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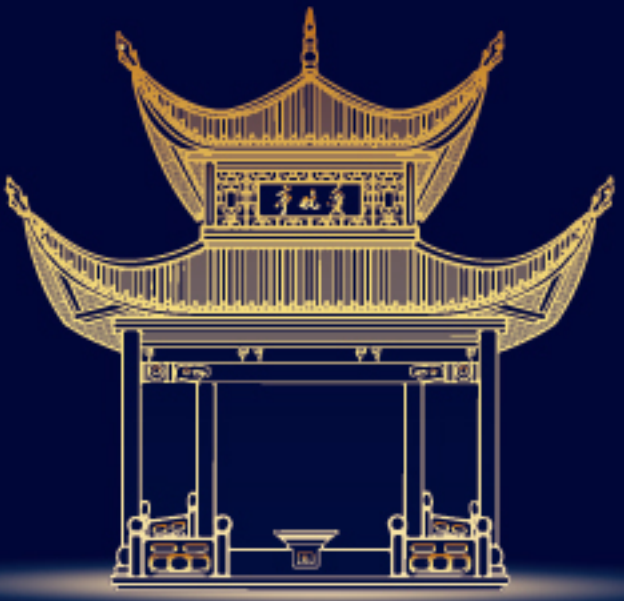
论文汇编



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口头发言

OR-001

加拿大医学检验教育经验与借鉴

刘征
桂林医学院

目的 作者于 2014 年至 2017 年在加拿大医学检验技术专业学习，回国后从事医学检验教学工作。本文从课程设置和教学方法两个方面分析加拿大医学检验教育的经验和对国内医学检验教育的借鉴。
方法 选取加拿大 10 所和国内 6 所开设医学检验技术专业的大学，通过对比专业课程设置，分析加拿大医学检验技术专业课程设置的不同和优缺点。通过作者在加拿大医学检验技术专业学习的体会，对比与国内医学检验技术教学方法的异同。
结果 加拿大医学检验技术专业的专业课设置以医院检验科工作为导向，分为临床生物化学检验技术、临床微生物检验技术、临床血液检验技术、输血技术、组织技术 5 门课，上课内容、教具、材料、化验单直接取自医院检验科。国内院校没有开设组织技术课，但是将一部分临床生化和血液检验技术融合成了一门临床检验基础课程，同时微生物、血液、输血技术 3 门课内容过于陈旧，注重大而全，以讲述基础理论和经典检测方法为主，对当前检验科开展的项目讲述含糊不全。加拿大医学检验技术专业严格遵循宽进严出的毕业政策，所以在教学方法上注重知识点的理解和拓展，死记硬背教材内容很难达到毕业要求。
结论 与国内相比，加拿大医学检验技术专业课程设置与当前检验科开展项目密切关联，值得国内学习。由于录取的学生基本都已经完成了 4 年的大学课程，所以在基础知识讲述方面较为省略，这也使得教学工作虽较为实用，但是过于技术化。

OR-002

检验医学科住院医师规范化培训临床教学模式的研究与探讨

李林璋、曹永彤
中日友好医院

住院医师规范化培训是医学生毕业后再教育的重要组成部分，在医学教育体系中起着承前（医学院校教育）启后（继续医学教育）的作用。检验医学科住院医师规范化培训推进了检验医学的发展，在住院医师规范化培训中，临床实践对于提高住院医师的临床能力有着重要作用，这种临床实践和临床思维的培养对检验医学住培学员也非常重要。因检验医学科由于未设立床位，不需要管理住院患者，检验科住培的临床教学就要与临床科室医师住培有所不同。临床科室的培训内容侧重于临床工作方法，规范体格检查、常见疾病的诊疗常规和临床路径，而检验医学培训则侧重于在具备临床知识和实验室检验技术能力的基础上，能够将实验室检验与临床相结合，为临床疾病的诊断、预防等提供建议和咨询。根据检验医学培训细则要求，检验医师在培训期间需要进行病例讨论、教学查房和临床巡诊等。检验医学的临床教学内容主要有：①以检验结果为切入点式病例讨论，通过检验报告寻找此患者所有的病例资料，分析其检验结果可能的影响因素，从标本检验报告单入手，提高检验医师实际工作运用能力和建设临床思维；②改革临床医学教学查房的基本模式，在临床带教老师的组织下进行教学查房，突出检验学科内容式教学查房，通过教学查房对检验医师言传身教，培养检验医师正确解读分析检验结果的能力，同时加强检验医师临床思维的训练和与临床信息关联的能力；③到相关临床科室进行临床巡诊，比如在血液组轮转的学员可以安排到血液科进行临床巡诊。检验医学科的住培工作是一项新的挑战，也是检验医学发展的必由之路。检验医学科现在已成为与临床内、外科等并列、平行的学科，目前国内已有少量检验科可出具检验诊断性报告，可指导临床医师合理申请检验项目，帮助临床医师深入挖掘检验报告的详细信息，拓展报告的作用，并参与临床的某些决策。这种进步与检验医学住培的临床教学息息相关，希望检验医学科专业住培能够得到更多的关注与重视，使检验医学得到更好的发展。

OR-003

网络平台建设在医学检验形态学人才培养中的应用研究

周玉利[1]、吴茅[2]、龚道元[3]、茹进伟[4]
1. 杭州市第一人民医院
2. 浙江省人民医院
3. 佛山科学技术学院检验学院
4. 广东省乐昌人民医院

目的 通过医学检验细胞形态学网络平台建设，促进形态学人才培养。
方法 通过企业微信、微信群、视频号、公众号、抖音、小程序等多种互联网形式开展细胞形态学教学，邀请更多的国内形态学专家录制视频课、微课、慕课，为学生免费开放，可重复试听。按照血液、骨髓形态学，体液形态学，寄生虫学，微生物学等分类，创建电子形态学图文资源库和试题库，系统、全面收集图片和案例，方便实时检索学习；设形态识别和病例分析等多种题型，学生可以自测训练，也可以运用于教学效果评定。举办形态学线上比赛，调动学生学习积极性，巩固教学质量，使学生更好掌握形态学的难点和重点。
结果 1.交流平台的建立，初步建立全国性的形态学医学检验交流群 3-5 个，每个微信群满员可容纳学员 500 名，定期有老师分享病例，或者转发分享其他微信群里较有学习价值的图片和病例；每周的周一、周三和周五，分别安排血液学病例、体液学病例和基础形态教学分享，动员群成员积极参与病例讨论和学习。2.资料库建设和公众号推送，成立病例资料整理组和公众号编辑组，病例整理组人员对图片和病例进行筛选和整理，选择高清典型的形态学图片收录资料库。公众号编辑组将精美图片和完善病例编辑成文，邀请专家审核后以公众号推文推送，供学生学习。3.专家库建设，吸引更多的临床检验专家和大专院校教授加盟，录制视频课、微课，丰富平台微课堂。4.形态学专家共识的推广，由国内知名形态学专家起草浆膜腔积液、肺泡灌洗液和脑脊液形态学检验专家共识，突出形态学教学的标准化、正规化的重要性。形态检验学生在校期间应该接受严格的规范化训练，为今后的临床工作打下坚实的理论和实践基础。
结论 多模态网络形态学教学大大推动形态学人才培养，值得大力推广和普及。

OR-004

Association of CDK6 and its upstream miRNAs with tuberculosis susceptibility in a Chinese population

Hao Bai、Binwu Ying
Department of Laboratory Medicine, West China Hospital, Sichuan University

Background Tuberculosis remains a serious global health threat. Recent studies revealed that cyclin-dependent kinase 6 (CDK6) participated in the regulation of inflammation. We aimed to investigate the association between CDK6 and upstream miRNAs with tuberculosis susceptibility in a Chinese population.
Methods We included 436 tuberculosis patients and 566 healthy individuals from West China Hospital. We first selected and genotyped 5 single nucleotide polymorphisms of CDK6 (rs4272, rs42032, rs42045, rs10254840, and rs6975474). And then the expression levels of CDK6 mRNA and its upstream regulatory microRNAs (miR-26a, miR26b, miR-29a, and miR-29b) were measured.
Results We found rs6975474 and rs10254840 were associated with tuberculosis susceptibility. And the expression of CDK6 mRNA was significantly down-regulated in tuberculosis patients. Further analysis revealed that CDK6 expression level was negatively correlated to the serum C-reactive protein level and the erythrocyte sedimentation rate. In addition, the expression levels of miR-26a and miR-26b were significantly increased, while miR-29a and miR-29b were decreased in tuberculosis patients.

Conclusion Our study roughly provided a comprehensive association of CDK6 and its upstream miRNAs with tuberculosis susceptibility in a Chinese population. More studies with functional verification will refine our understanding of the role of CDK6 in tuberculosis.

OR-005

基于 TCGA/GEO 数据库识别 GNG2 基因在乳腺癌中的作用与机制研究

赵安江[1]、李伶[2]、张玫[1]
1. 四川大学华西医院
2. 重庆医科大学

目的 G 蛋白 γ 亚基 2 (GNG2)参与多种细胞信号通路，对细胞增殖和血管生成至关重要。然而，GNG2 在乳腺癌(BC)发生发展中的作用尚不清楚。本研究旨在基于 TCGA/GEO 数据库探究 GNG2 在乳腺癌发生发展及临床诊治中的作用。
方法 利用 GEO 和 TCGA 数据库筛选出乳腺癌组织中的所有差异表达基因，利用 KEGG 富集分析探究所有差异基因可能参与的信号通路，利用 STRING 构建所有差异基因的相互作用网络，并筛选出对乳腺癌发生发展具有重要作用的候选差异基因。采用 Cox 回归分析 GNG2 与乳腺癌患者总体生存率的相关性。采用受试者工作曲线探究 GNG2 在乳腺癌中的诊断价值。通过体外和体内实验观察 GNG2 对细胞周期、增殖和凋亡的影响。通过共定位试验和免疫共沉淀技术揭示 GNG2 和 MRAS 之间的相互作用。
结果 我们从前 5 个差异基因中筛选出了 GNG2，其在乳腺癌组织中的表达明显减少。GNG2 与乳腺癌患者的总生存率独立相关，且在乳腺癌中具有较好的诊断价值（灵敏度 79.6%，特异度 85.8%）。过表达 GNG2 可显著抑制乳腺癌细胞增殖和肿瘤生长。此外，我们发现 GNG2 以 MRAS 依赖性的方式显著抑制 ERK 和 AKT 的活性。重要的是，GNG2 和 MRAS 在细胞膜上存在共定位并相互作用。
结论 GNG2 可能作为一种潜在的肿瘤标志物，为乳腺癌的诊断提供重要价值。机制上，GNG2 与 MRAS 的相互作用可能抑制 Akt 和 ERK 活性，从而促进乳腺癌细胞凋亡和抑制增殖。因此，在体内增加 GNG2 表达或破坏 GNG2-MRAS 的相互作用可能是治疗乳腺癌的一种潜在策略。

OR-006

Long-read sequencing enables the detecting of complex HBV integrated genome structures in hepatocellular carcinoma patients

Zhongling Zhuo、Fei Xiao
Beijing Hospital

Objective The integration of HBV into the human genome is a crucial mechanism of Hepatocellular carcinoma (HCC), but the intricate HBV integration pattern is still unclear. In this study, we evaluated the feasibility of identifying complex HBV integrated genome structures by Nanopore and PacBio platforms.
Methods The DNA library was sequenced using the long-read sequencing on GridION and PacBio Sequel II, respectively. Simultaneously the DNA and mRNA were sequenced using next-generation sequencing on Illumina NextSeq. We established a workflow, analyzed HBV integration patterns using BLAST and local scripts, and verified the accuracy of this workflow.
Results In this study, we evaluated the feasibility of identifying complex HBV integrated genome structures through Nanopore and PacBio platforms and established an analytical strategy. Based

on the long-read sequences of the Nanopore and PacBio platforms, we can not only identify the breakpoints of HBV integration but also obtain complex HBV integrated genome structures. We obtained the entire HBV integration patterns in sequences, not based on algorithm predicting for the first time. The HBV integration pattern was extremely complicated, HBV was not integrated with a complete genome, but the genome was fragmented and integrated into the human genome in different orientations.

Conclusion Our results proved that long-read sequencing enables detecting complex HBV integrated genome structures in HCC patients. It provides evidence to support the potential application of long-read sequencing in virus integration identification and helps people fully elucidated the role of HBV integration in carcinogenesis.

OR-007

Exploration of Microvascular Invasion Biomarkers for Hepatocellular Carcinoma Based on Cancer Genome Mutations

Zhaodan Xin、Juan Zhou、Liting You、Yi Zhou、Xingbo Song、Xiaojun Lu、Binwu Ying
West China Hospital, Sichuan University

Objective Microvascular invasion (MVI), has increasingly been recognized to be one of the most significant risk factors for hepatocellular carcinoma (HCC) recurrence and metastasis after hepatectomy, which is probably caused by tumor gene mutations. While it is tough to detect tumor tissue mutation before hepatectomy, non-invasive circulating tumor DNA (ctDNA) detection for HCC mutation is feasible. In this study, we focus on cancer genome mutations to explore new MVI markers and provide clues to the mechanisms of invasion and metastasis.

Methods 36 patients with initially suspected HCC who were undergoing hepatectomy at West China Hospital of Sichuan University in 2019 were prospectively recruited. Peripheral blood samples were collected preoperatively, and fresh tumor tissues were resected during the operation. High-throughput sequencing using hybrid capture library was performed on the Gene+2000 platform, for tumor tissues and ctDNA. The hybrid probes targeted 1021 genes related with tumorigenesis. Fisher's exact test was performed in MVI/non-MVI groups to find the differentially mutated genes and Wilcoxon test was utilized to compare VAF between groups. In all analyses, $P < 0.05$ indicated statistical significance.

Results 36 individuals including 11 MVI and 25 non-MVI samples underwent gene mutation analysis of tumor tissues, and mutations were detected in all samples; 33 individuals underwent ctDNA gene mutation analysis, and 26 samples (78.8%) were detected mutations. The HCC gene mutation profile was widely distributed and genes with the highest frequency of ctDNA mutations were similar to tumor tissues such as TP53, LRP1B and CTNNB1. We found the incidence of several gene mutations such as ACIN1 and CSF1R was higher in MVI group than non-MVI group both in tumor tissues and ctDNA analysis, although there was no statistical difference ($P>0.05$). Moreover, ctDNA variant allele frequency (VAF) was further compared between MVI group and non-MVI group, and VAF maximum value of MVI group was higher than non-MVI group (0.037 vs 0.015, P=0.0092). A total of 32 HCC patients had both tumor tissue and ctDNA sequencing results, among these patients, 7 samples (7/8, 87.5%) in MVI group and 16 samples (16/24, 66.7%) in non-MVI group were detected tissue consistent mutation in ctDNA, indicating great potential of ctDNA in HCC, especially in HCC patients with MVI. Remarkably, 13 samples (40.6%) detected undetected mutations of tissues in ctDNA, indicating great heterogeneity in HCC, and ctDNA might be a good choice by overcoming tumor heterogeneity.

Conclusion Genes with higher mutation rate in MVI patients deserve our further attention for HCC invasion. VAF of ctDNA, especially the maximum value of VAF, can be used as a new biomarker to distinguish MVI patients from non-MVI ones. Designing a panel of specific gene mutations and using the VAF maximum value of ctDNA to predict MVI might be a potential choice.

OR-008

数字 PCR 检测血流感染常见病原菌的临床应用研究

刘芳瑞、吕琳婷
上海交通大学医学院附属仁济医院(东院)

背景 血流感染是指细菌、真菌等病原微生物入侵血循环，在血液中繁殖,释放毒素和代谢产物,并诱导细胞因子释放,引起全身感染性疾病。目前血流感染的主流病原菌有大肠埃希菌、肺炎克雷伯菌、鲍曼不动杆菌、铜绿假单胞菌以及各类葡萄球菌。大多入侵为呼吸道感染、泌尿系统感染以及腹腔感染。近些年由于抗生素和介入治疗的使用，血流感染的发病率呈持续增高趋势。目前检测血流感染最重要的检查手段是血培养。但血培养周期时间长、用血量大、且无法定量，早期诊断及准确的抗菌治疗对降低疾病死亡率至关重要。
目的 运用领航数字 PCR 系统检测临床血浆样本中的病原菌，以测评该技术的临床应用价值。
方法 采用领航基因五色荧光数字 PCR 系统检测 169 份临床血浆样本，并与传统血培养方法进行比较，计算数字 PCR 技术检测血流感染的敏感度、特异性和符合率。
结果 本次实验检测的 169 份样本中，血培养阳性 27 例，阴性 142 例，阳性率 16%；数字 PCR 阳性 15 例，阴性 154 例，阳性率 8.9%。与传统血培养鉴定技术相比，领航五色荧光数字 PCR 系统检测血流感染样本的敏感度为 24%，特异性为 97.2%，阳性预测值为 60%，阴性预测值为 88%，总体符合率为 88.8%。数字 PCR 系统鉴定阳性的病原菌包括绿假单胞菌（1 例）、大肠埃希菌（5 例）、肺炎克雷伯菌（4 例）、鲍曼不动杆菌（2 例）、屎肠球菌（3 例）、粪肠球菌、嗜麦芽窄食单胞菌（5 例）、表皮葡萄球菌（3 例）。但由于血培养阴性而数字 PCR 检测阳性的病原菌主要集中在嗜麦芽假单胞菌和表面葡萄球菌，所以不能排除污染的可能性。
结论 数字 PCR 技术是一种新型血流感染的检测技术，检测时间短，具有较好的特异性，但敏感性还有待提高，未来或许可以成为临床早期诊断与优化感染治疗的新方法。

OR-009

Development and Validation of a Novel Glycolysis-Related Risk Signature for Predicting Survival in Pancreatic Adenocarcinoma

Ang Li[1]、Sinan Hou[2]、Jian Chen[3]、Yanfang Jiang[1]
1. The First Hospital of Jilin University
2. 连云港市中医院
3. 东南大学附属中大医院

Background Pancreatic adenocarcinoma (PAAD) is one of the leading causes of cancer-related deaths worldwide. Through data mining, anincreasing number of biomarkers have been identified to predict the survival of patients with PAAD. However, the ability of single gene biomarkers to predict patient survival is still insufficient. This study aimed to develop a novel risk signature for predicting the survival of patients with PAAD.
Methods mRNA expression profiling was performed for a large PAAD cohort (n =177) identified using The Cancer Genome Atlas database (TCGA). Geneset enrichment analysis (GSEA) was performed to detect whether the gene sets showed significant differences between PAAD and adjacent normal tissues. Univariate Cox regression was used to analyze and identify genes related to overall survival (OS). Multivariate Cox regression was subsequently used to confirm the prognostic genes and obtain the coefficients. By analyzing the expression level of selected genes weighted by their coefficients through linearly combining, we constructed a risk score formula for prognostic prediction. The three-mRNA signature for survival prediction was validated using the Kaplan–Meier method.

Results We demonstrated that a set of three genes (KIF20A, CHST2, and MET) were significantly associated with OS. Based on this three-gene signature, 177 PAADpatients were classified into high-risk and low-risk groups using the median risk score as the cut-off value. We also validated the reliability of this three-gene signature in the GSE28735 dataset from the Gene Expression Omnibus (GEO) database. Additionally, multivariate Cox regression analysis revealed that the three-gene signature had an independent prognostic value.
Conclusion To the best of our knowledge, this is the first study to develop a glycolysis-related risk signature for predicting the survival of patients with pancreatic adenocarcinoma. Our findings provide insight into the identification of PAAD patients with poor prognosis. We also identified novel therapeutic targets for this disease.

OR-010

Rapid electrochemical biosensor for sensitive profiling of exosomal microRNA based on multifunctional DNA tetrahedron assisted catalytic hairpin assembly

Xiaohe Zhang、Ye Zhang、Bo Situ、Yuan Wu、Shihua Luo、Lei Zheng、Yurong Qiu
Southern medical university Nanfang hospital

Profiling of exosomal microRNA (exo-miRNA) is very important for cancer diagnosis and treatment. However, rapid and sensitive determination the trace of exo-miRNA in clinical samples has not been developed. Herein, a robust electrochemical biosensor was proposed using multifunctional DNA tetrahedrons assisted catalytic hairpin assembly (MDTs-CHA) for exo-miRNA analysis. The MDTs-CHA, contained two multifunctional tetrahedrons (T1 and T2), leverage localized reaction and cascade amplification to enable rapid and ultrasensitive exo-miRNA analysis. Employing the MDTs-CHA, the electrochemical platform allowed quantitative measurement of exo-miRNA down to 7.2 aM in 30 min with good specificity. Furthermore, by profiling four tumor-associated exo-miRNAs (miR-1246, miR-221, miR-375, and miR-21) in a breast cancer cohort, this platform showed high efficiency (AUC: 0.989) and high sensitivity of 90.5% for breast tumors diagnoses, with 80% sensitivity for early diagnoses (stage I-IIa). Therefore, this platform has great potential in bioanalysis and clinical diagnostics.

OR-011

The establishment of neuron-specific enolase reference interval for the healthy population in southwest China

Qiang Miao、Bei Cai、Xuedan Gao、Zhenzhen Su、Junlong Zhang
West China Hospital, Sichuan University

Aim To investigate and establish a reference interval (RI) of neuron-specific enolase (NSE) in southwest China's healthy population by using the laboratory information system database.
Method A total of 86957 periodic health examination individuals of the medical examination center in West China Hospital from 2016 to 2018 were included in the study. We used the Box-Cox conversion combined with the Tukey method to normalize the data and eliminate the outliers, and the normal distribution method and the nonparametric method to estimate the 95% distribution RI.
Results The NSE 95% distribution RI we established in healthy populations in southwest China through normal distribution and nonparametric method were 0-19.64 ng/ml and 0-20.46 ng/ml, respectively. The obtained RIs verification conformed to the standard and was significantly different from the reagent instruction($P < 0.05$). The RI established by the nonparametric method was superior to the RI of the normal distribution method and reagent instruction($P < 0.05$).

Conclusion We initially established an NSE RI that was suitable for the healthy southwest China population. The Box-Cox conversion combined with the Tukey method and nonparametric method is a reliable and straightforward indirect method for reference interval acquisition, which is suitable for the promotion and application of clinical laboratory.

OR-012

上海市临床生物化学实验室诊断项目成本核算

邵文琦[1]、王海银[2]、赵瀛[1]、王蓓丽[1]、郭玮[1]、潘柏申[1]
1. 复旦大学附属中山医院
2. 上海市医学科学技术情报研究所

目的 实验室诊断是医疗服务项目规范的重要板块之一，价格构成不同于其他技术劳务为主的诊疗项目。政策要求创建“以成本和收入结构变化为基础”的价格动态调整机制，医疗服务价格调整箭在弦上，却由于缺乏科学的成本测算标准悬而未发。
方法 医院检验科临床生化室作为技术较为成熟的组室之一，日均标本量高，开展项目多。本文以检验科临床生化室的诊断项目成本作为切入点，通过客观、公正、科学、合理的数据分析兼顾各方利益，建立标准化实验室模型，构建价值分析框架，分版块，分类测算临床生化室诊断项目成本。
结果 大部分临床生化检验项目检测成本略高于收费价格，仅有少数方法较新的项目成本低于收费价格。
结论 临床生化检验项目价格制定按照 2012 年出台的成本价格进行计算，而没有考虑十余年间的通货膨胀，物价上涨和技术进步等因素，收费标准中也没有将人力成本和物耗成本等核算在内。需要在政府物价和医疗保险支付部门、病人、医院检验科间建立桥梁，提出完善实验室临床生化检验项目诊断价格制定和支付的政策建议。

OR-013

时间就是生命：探索心血管病医院急诊检验能力建设之道

于金星、崔凯、冯子秋、高小晶、周洲
中国医学科学院阜外医院

目的 中国心血管病患病率、死亡率持续上升，已成为重大公共卫生问题。尤其急性胸痛相关的致死性心血管疾病，如急性心肌梗死、主动脉夹层、肺栓塞等的救治，更需准确与快速，时间就是生命。而急诊检验的检测结果影响着 70%-85%的临床决策。阜外医院是心血管病专科医院，作为抢救的“最前线”的急诊检验承担着包括急诊室、ICU、CCU、HFCU、小儿 PICU、成人术后恢复室等急重症患者的检测服务，工作中涉及临床基础检验、临床血液学检验、临床生物化学检验、临床免疫学检验、临床微生物学检验、临床分子生物学检验等各检验专业学科，探索急诊检验能力建设对于提高心血管病急危重症患者救治能力具有重要意义。
方法 中国医学科学院阜外医院作为心血管专科医院，急诊检验通过信息化与自动化系统的运用升级流水线设备、丰富急诊检测项目、精益管理的实施：5S 精益改善、利用人工智能等一些列措施。
结果 通过精益的改善项目，急诊检验的流程得到了进一步的优化，对能力建设前与建设后进行数据分析，结果发现急诊检验内周转时间（标本签收与报告审核发送之间的时间）平均缩短了 34.2%。
结论 急诊检验通过升级流水线设备、丰富急诊检测项目、5S 精益改善、利用人工智能等一些列措施，提升了运营效率和服务水平，大大缩短了检测时间，为临床端及患者端提供准确及时的检测报告，提高了患者救治率。急诊检验的工作任务就是开展必要的检验项目以满足临床的急需，提供准确、及时的检验结果是临床对急诊检验的基本要求。心血管疾病的救治需要多学科医务人员协作，规范、及时的急诊检验尤为重要。急诊检验是检验科中综合性强、报告要求及时性高、工作量多、挑战性大的实验室。本项研究的探索，希望通过心血管病医院急诊检验的能力建设，对于提高心血

管病医院急危重症患者的救治能力、合理利用医疗资源、以及促进未来交叉学科的发展等方面提供一些参考数据和实践依据。

OR-014

检验过程的生物安全风险管理和实践体会

公衍文
山东大学第二医院

目的 总结实验室检验过程生物安全风险管理的实践体会，以期能够提供可以落地有效的风险管理办法。
方法 风险管理是质量管理的根本落脚点，但在实施过程中，多数实验室未能将静态评估和动态监测结果结合起来，一味地依靠所谓的头脑风暴，导致风险管理流于形式，没能识别出真正可能存在的风险，相应的风险控制措施也就没有效果，无法实现持续改进。我们将静态风险评估（基于工作流程和操作，明确每个岗位和操作在实验室环境、生物安全柜、个人防护措施等方面选择，并在此基础上评估存在的风险，以及风险的严重程度和可识别能力）和动态监测（安全管理组定期检查监测安全措施执行情况、风险管控措施执行情况，以及生物安全实验室良好工作行为遵守情况，统计风险可能发生的频次）相结合，计算 RPN 指数，进行客观的风险评估。
结果 共识别出高风险 5 项，中风险 11 项，低风险 25 项。对高风险立即实施针对性的纠正措施，并作为后续监测的重点，评估措施的有效性；对中风险项目，评估其可能的发展趋势，必要时采取预防措施，并监测措施的有效性；对低风险项目，继续列入日常监测项目，持续关注。
结论 检验过程风险管理必须将静态评估和动态监测结合起来，才能真正有效。

OR-015

检验科员工满意度与需求的多维度分析

牛书敏、姜宏兵、刘春燕、刘艳雯、张新、邓朝晖
新疆生产建设兵团医院

目的 采用多维度问卷了解检验科员工工作满意度与需求，并分析其主要影响因素，为科室管理提供决策依据。
方法 通过问卷调查法分析新疆生产建设兵团医院检验科 34 名员工的工作满意度，以明尼苏达满意度量表为雏形，马斯洛“需求层次理论”为基础，结合中国检验科实践工作设计相关评价指标。满意度调查分为 5 个维度，共 20 个项目，采用净推荐值(NPS)打分系统(1-6 分)及排序量化记分，评价科室不同专业组、不同年资员工对工作环境、收入和机遇、尊重与归属感、员工管理、组织承诺与结构 5 个维度的满意度。
结果 34 名员工平均满意度为 5.0 分，感到满意的员工达到 98%；其中，工作不满 5 年的员工满意度最高，微生物组、样本前处理组员工满意度最高，临检组满意度较低。满意度调查的 5 个维度中，收入和机遇维度满意度最低，平均满意度为 4.6 分；组织承诺与结构维度满意度最高，平均满意度高达 5.4 分；其他三个维度满意度居中。在收入和机遇维度满意度调查中，工作大于 10 年和临检组的员工满意度较低，平均满意度为 4.4 分、4.2 分，其中分别有 54%和 60%的员工持中性甚至负面态度。
结论 检验科员工对工作总体较为满意，收入和机遇是影响科室员工满意度的主要因素，科室有的放矢地采取改进措施，提高员工满意度。

OR-016

特殊蛋白检测项目基于患者风险的室内质量控制程序的设计

刘佳丽[1]、郭拥军[2]、刘向祎[2]、王薇[1]、王治国[1]
1. 北京医院 国家老年医学中心 国家卫生健康委临床检验中心/北京市临床检验工程技术研究中心
2. 首都医科大学附属北京同仁医院检验科

目的 用具有批长度的 Westgard 西格玛规则为九项特殊蛋白项目设计基于风险的统计质量控制（SQC）程序。
方法 收集北京同仁医院检验科 IgG、IgM、IgA、C3、C4、类风湿因子（RF）、抗链球菌溶素 O（ASO）、转铁蛋白（TRF）和前清蛋白（PA）半年（2018 年 12 月-2019 年 5 月）的累积在控变异系数（CV）作为不精密度的估计值，将该实验室参加室间质量评价（EQA）计划中的百分差值绝对值的均值作为偏倚（Bias）的估计值，采用国家卫生健康委临床检验中心 EQA 的评价标准作为允许总误差(TEa)，计算各项目的西格玛度量值（σ），采用具有批长度的 Westgard 西格玛规则为各项目设计合适的 SQC 程序。
结果 IgG、IgA、IgM、C4 和 TRF（σ>6）采用 13s 规则（N=2，R=1），批长度为 1000 个患者样品的 SQC 程序；C3（σ=5.86）采用 13s/22s/R4s 规则（N=2，R=1），批长度为 450 的 SQC 程序；RF、ASO、PA（3<σ<4）采用 13s/22s/R4s/41s/6X 规则（N=6，R=1），批长度为 45 的 SQC 程序。
结论 具有批长度的 Westgard 西格玛规则可帮助实验室设计基于风险的 SQC 程序，保证检验结果的质量和患者安全。

OR-017

基于生化免疫流水线的全流程智能化探索

尹利民、孟国艳、徐宏忍、白敏凤
昆明市第一人民医院

目的 为提高临床检验的工作效率，减轻工作人员劳动强度，依托生化免疫流水线系统，通过不断流程优化，进行全流程智能化探索。
方法 收集昆明市第一人民医院检验科 2015 年 6 月至 2021 年 5 月生化免疫检测项目的运行数据，开展回顾性研究。
结果 标本转运、标本接收、标本分拣、编号、离心、录入 LIS 系统、仪器上输入检测项目、去盖、分杯、转移到样品架，仪器检测、查看结果，稀释、复检审核、打印报告、报告发放、标本入库等多环节均实现自动化。
结论 自动化极大地提高了实验室的工作效率，优化了流程。

OR-018

一项回顾性观察研究：血清白蛋白水平升高与重症监护病房急性肾损伤 2 年死亡率降低相关

唐琪、王佳佳、夏鹏程、王榕榕、李明、白晓卉、王勇、卢志明
山东第一医科大学附属省立医院临床医学检验部

背景 血清白蛋白浓度与多种危重疾病的预后有关。急性肾损伤是一种严重的临床疾病，可能增加重症监护病房患者的死亡率。然而，在重症监护病房中血清白蛋白浓度与急性肾损伤 2 年死亡率之

间的关系尚未被探讨。本研究旨在调查重症监护病房的患者血清白蛋白与急性肾损伤 2 年全因死亡率之间的关系。
方法 我们对 2016 年 1 月至 2018 年 11 月在山东第一医科大学附属省立医院内科和外科重症监护室招募的患者进行回顾性观察分析。我们采用多元回归模型研究血清白蛋白与急性肾损伤 2 年全因死亡率之间的关系。我们还使用了分层分析来验证我们的研究在不同的患者亚组中的稳定性。
结果 本研究共纳入 392 例患者(男性 254 例，女性 138 例)。血清白蛋白与急性肾损伤两年全因死亡率呈负相关和非线性相关。校正模型 I 调整了两个变量(性别和年龄)，校正模型 II 调整了 8 个变量，包括性别、年龄、血尿素氮、C 反应蛋白、氯离子、钠、基础肌酐和葡萄糖。此外，在许多亚组中，包括男性患者、无糖尿病患者、手术 4 级、急性肾损伤 I 期、血尿素氮< 5.7 mmol/L、甘油三酯< 1.05 mmol/L、血容≥ 40.1 vol%、血红蛋白≥ 136 g/L、红细胞 ≥ 4.5×10^{12}/L、白细胞 < 6.15×10^{9}/L 等亚组中，血清白蛋白与急性肾损伤两年全因死亡风险显著相关。
结论 血清白蛋白与重症监护病房中急性肾损伤患者的 2 年全因死亡率呈非线性负相关。我们的发现需要进一步的研究来验证。

OR-019

运用 PDCA 循环法在三级医院检验科三年质量管理上的研究

周慧聪
南京大学医学院附属泰康仙林鼓楼医院

目的 运用 PDCA 循环法管理检验科检验前、检验后质量指标，探索检验科质量管理方法，提高检验科的工作质量，更好的服务患者。
方法 1、由科主任确定检验科“年度重点质量管理项目”，制定“质量目标”，包括“体液标本采集时间缺失率<10%”、“血液标本采集时间缺失率<10%”、“不合格标本比例<1%”、“门诊患者实验室内周转时间超时率<5%”。2、将上述数据“快捷统计功能”维护到检验科 LIS 系统里，可以按照“时间”、“标本来源”等检索条件获取每月数据。3、每月 5 号前由专人统计并分析上述质量指标涉及的数据，形成图表，清晰可见，内容包含以上四项质量管理项目在上月的数据。4、召开“检验科月度质量小组会议”，分析导致质量目标不佳的原因，由专人根据会议内容撰写“质量小组活动记录”，内容包括“针对本月的质量分析及改进项目”、“针对下月的改进目标和措施”、“对上月质控活动改进措施的落实和成效评价”。5、从人、机、料、法、环五方面进行根因分析，针对不同问题积极整改并与临床沟通，增强培训及考核力度。6、每月按照上述方法进行质量管理，循环往复，计算三年来质量管理成效。
结果 2020 年全年较 2018 年全年体液标本采集时间缺失率下降 31.24%；血液标本采集时间缺失率下降 82.59%；不合格标本率下降 40%；门诊患者实验室内周转时间超时率下降 54.14%。2019 年及 2020 年全年质量目标均在目的范围内。
结论 PDCA 循环法运用到检验科质量管理中可以起到很好的作用，可以大大提高检验科的质量目标，此方法可以运用到更多的检验科质量管理项目中，使检验质量不断进步。

OR-020

应用室间质评变异系数评价和推进检验结果互认的可行性研究

张娟、李红燕、蒋黎
电子科技大学附属医院·四川省人民医院

目的 回顾性分析四川省 2016-2020 年全省各级医院参加四川省临床检验中心举办的血细胞分析和临床化学检验项目室间质评结果变异系数 (Coeficient of Variation，CV)，分析近 5 年各项目 CV

值变化趋势，探讨依据 CV 值变化趋势判断和指导全省各级医院之间逐步推进临床检验项目结果互认的可行性。
方法 回顾性分析四川省临床检验中心 2016-2020 年连续 5 年临床血细胞分析共 8 个项目以及临床化学检验项目共 33 个项目，总共 41 个检验项目，每年 2 次，每次 5 个质评物的室间质评 CV 值，分析各项目各等级医院各浓度近 5 年 CV 值的变化趋势。由于项目较多，生化项目仅选取 11 个互认项目进行详尽分析。以 1 年为单位，将参与单位分为三个组，分别是三级医院组、二级医院组和其它检测机构组，对数据进行分组、分年进行分析，正态分布数据采用方差分析，非正态分布数据采用 Kruskal-Wallis 检验，$P<0.05$ 为差异有统计学意义。
结果 1. 参加血细胞分析和生化项目室间质评的实验室分别由 2016 年第一次 696 家增加到 2020 年 1014 家，生化为 682 家增加到 2020 年 989 家，总体合格率在逐年上升。2. 以医院等级进行分组，汇总近 5 年 CV 值结果分析，不同等级医院全血检测项目在低浓度和中浓度之间，CV 值均有差异，P 分别为 0.0039 和 0.0015，在高浓度间未见明显差异。生化项目根据各自参考范围分为低浓度和高浓度两个水平，除 TG 和 Mg 以外，其余项目 CV 均有显著性差异，且在三级医院的 CV 值均最低。3. 近 5 年各项目变化趋势为总体趋势均是各项目 CV 值中位数逐年递减，提示在推动全省检验项目结果互认基础上，总体检验结果一致性在逐年提高。
结论 室间质评项目 CV 值可以较好地客观反映全省各级医疗机构检验结果的差异和变化趋势，为全面推进检验项目的结果互认提供可靠的实验室参考依据。

OR-021

Sample pooling of COVID-19 RT-qPCR without sacrificing sensitivity

Dong Zhang、Juan Du、Guanhua Wang、Yu Chen、Xuesong Shang、yingying Ding、Ziyi Wang、Jie Wu、Jie Yi、Qiwen Yang、Yingchun Xu
PUMCH

A more efficient and costly method for COVID-19 testing has attracted much interest in recent times. Given the limited testing capacity available in the world, several studies have proposed sample pooling to increase testing capacity. However, the high rate of false negatives for sample pooling may undermine efficient tracking and good policymaking. We provide a detailed analysis and validation of the original sample pooling strategy and extracted RNA sample pooling strategy. The original samples and the extracted RNA samples were mixed in parallel to get a range of 2-specimen pool to 16-specimen pool size. For the pooled samples, we scaled up the PCR reaction volume to 50 ul, 75 ul, and 100 ul. No false-negative results were observed in Case 3 (Ct < 30), while a total of 43 (17.9%) false-negative results were acquired in 240 pooling samples containing Case 1 or Case 2 (Ct > 35). By scaling up the reaction volume, all the weak positive samples with low viral load could only be detected in RNA pools at dilutions of 1:1, 1:2, and 1:3, while the repeatability was unsatisfactory in other pooling strategies. Overall, the sensitivity of pooling RNA samples with scaling up reaction volume had about the same sensitivity as individual testing.

OR-022

泛癌分析显示同源重组缺乏评分可作为免疫治疗反应者的预测指标

杨璨[2,3]、唐雪梅[1]、张心菊[2]、吴之源[1,2,3]、关明[1,2,3,4]
1. 复旦大学附属华山北院中心实验室
2. 复旦大学附属华山医院中心实验室
3. 复旦大学附属华山医院检验科
4. 复旦大学附属华山北院检验科

背景和目标 肿瘤微环境(TME)的免疫背景是免疫学干预成功的决定性因素，但对免疫敏感性 TME 和免疫治疗反应者识别的 DNA 水平的生物标志物的探索较少。同源重组缺陷(HRD)疤痕是肿瘤基因组不稳定的一个新兴特征，可以触发免疫反应。本研究旨在全面研究主要癌症类型的 HRD 疤痕（评分），并揭示它们与肿瘤微环境和免疫治疗反应的联系。
材料和方法 使用来自癌症基因组图谱(TCGA)的 9088 个肿瘤的基因组学、转录基因组学和免疫表型数据对 HRD 评分进行了功能分析。与 HRD 相关的癌症类型由 HRD 评分累积频率分类来定义。对 HRD 高或低基因型的肿瘤突变负荷(TMB)和新抗原进行比较。肿瘤微环境(TME)用 CIBERSORT、xCell、MCP-counter、EPIC 和 quanTIseq 这五种算法进行了数字分析。微卫星不稳定性(MSI)、TMB 和 HRD 的敏感性和特异性。
结果 来自 TCGA 的 32 种癌症的 9088 名肿瘤患者的 HRD 评分分析显示，7 种主要癌之间的广泛关联，包括膀胱癌、乳腺癌、头颈鳞癌、肺腺癌、肺鳞细胞癌、卵巢癌和肉瘤。HRD 评分高的肿瘤有白细胞浸润和淋巴细胞分数增加，并表现出免疫敏感的 TME。最后，通过 TIDE 模型，我们证实了 HRD 评分的高基因型是 TCGA 乳腺癌队列中免疫反应的潜在预测因子。
结论 HRD 评分高的肿瘤具有免疫敏感的 TME。HRD-高基因型是乳腺癌患者免疫治疗反应的重要指标。

OR-023

Tfr-Tfh index: a new predicator for recurrence of hepatocellular carcinoma patients with HBV infection after curative resection

Beili Wang、JIE ZHU、BAI-SHEN PAN、JIAN ZHOU、JIA FAN、XIN-RONG YANG、WEI GUO
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University

Background T follicular helper (Tfh) cells and T follicular regulatory (Tfr) cells were newly identified as the subsets of cluster of CD4+ T cells. As major components of human immune system, they were found in tumor microenvironment and reported to play vital roles in the progression of cancer. But their clinical significance in Hepatocellular carcinoma (HCC) was not elucidated. Thus, this research aimed to investigate their prognostic value in HCC.
Materials and Methods A total of 210 subjects (including 110 HCC patients, 50 chronic hepatitis patients and 50 healthy individuals) were enrolled in the research. Tfh, Tfr cells and Treg cells from peripheral blood were measured by flow cytometry. Receiver operating characteristic (ROC) curves were used to evaluate the diagnostic performance of Tfr-Tfh Index (TTI) in early HCC and relapse status. Its further prognostic valve was assessed by Kaplan-Meier survival estimate and log rank tests.
Results Tfh cells, Tfr cells, Treg cells and TTI were all higher in HCC patients than in chronic hepatitis patients and healthy control. TTI was found to have positive correlation with the load of HBV. The AUC of TTI for early HCC and relapse status was better than other clinical indices in HBV positive patients. An optimal cutoff point for the TTI stratified the HCC patients into high

(>21.96) and low index (≤21.96) groups. High TTI was significantly correlated with recurrence. Univariate and multivariate analyses revealed TTI could be a predictor for recurrence. Moreover, it retained prognostic performance for patients with lower recurrence risk.
Conclusion Our research showed that TTI could be a promising indicator for early recurrence in HCC patients with HBV infection.

OR-024

Establishment of Coamplification at Lower Denaturation Temperature PCR/Fluorescence Melting Curve Analysis for Quantitative Detection of Hepatitis B Virus DNA, Genotype, and Reverse Transcriptase Mutation and Its Application in Diagnosis of Chronic Hepatitis B.

Can Liu、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

Dynamic and real-time hepatitis B virus (HBV) DNA, genotype, and reverse transcriptase mutation analysis plays an important role in diagnosing and monitoring chronic hepatitis B (CHB) and in assessing the therapeutic response. We established a highly sensitive coamplification at lower denaturation temperature PCR (COLD-PCR) coupled with probe-based fluorescence melting curve analysis (FMCA) for precision diagnosis of CHB patients. The imprecision with %CV and detection limit of HBV DNA detected by COLD-PCR/FMCA were 2.58% to 4.42% and 500 IU/mL, respectively. For mutation, the imprecision and detection limit were 3.35% to 6.49% and 1%, respectively. Compared with Sanger sequencing, the coincidence rates of genotype and mutation were 96.0% and 82.5%, respectively, whereas the inconsistent data resulted from a low proportion (<20%) of mixed genotypes or mixed mutations. The mutation ratio in HBV infection patients was as follows: hepatitis B e antigen (HBeAg)-positive infection (0/0.0%) < HBeAg-negative infection (16/4.5%) < HBeAg-positive hepatitis (30/5.5%) < HBeAg-negative hepatitis (36/6.5%). In patients with entecavir therapy, the proportion of mutation at baseline or week 4 in virologic response (VR) group was <4%, whereas in the partial VR group, it was mostly ≥4%. COLD-PCR/FMCA provides a novel tool with high sensitivity, convenience, and practicability for the simultaneous quantification of HBV DNA, genotype, and mutation. It might be used for distinguishing the different phases of HBV infection and predicting VR of CHB patients.

OR-025

Peripheral blood mononuclear cell DNA methylation markers enables early non-invasive detection for breast cancer

tiantian wang[2]、chuanxin wang[1]
1. The Second Hospital of Shandong University
2. The Second Hospital of Shandong University

Background The immune system can monitor the development of tumors, while DNA methylation is involved in the body's immune response to tumors. Peripheral blood mononuclear cell (PBMC) DNA carrying cancer-specific epigenetic aberrations may become a non-invasive approach for early detection of breast cancer (BC).
Methods we examined the genome-wide methylation profile of PBMCs from 50 BC patients and 30 normal controls using Infinium 850K BeadChips and identified BC-specific methylation

markers. The BC prediction diagnostic model was built in a training cohort (n = 100) using pyrosequencing and validated in a validation cohort (n = 200) using MethylTarget sequencing. Compared with mammogram and ultrasound, the performance of this diagnostic model was analyzed.
Results We discovered a total of 282 differentially methylated CpG positions (DMPs) between BC patients and match normal controls, of which 10 significant DMP markers were selected further pyrophosphate validation. We built and validated a BC diagnostic model based on four markers, which had high accuracy (90.0%,92.0%) sensitivity (85.7%,84.6%) and specificity (94.3%,86.6%) in both the training and validation cohort. More importantly, compared with mammogram and ultrasound, this diagnostic model achieved a great improvement in sensitivity in the detection of early-stage tumors(stage I-II 81.0% vs. 78.1%, 69.3%).
Conclusions DNA methylation markers in PBMC can provide a noninvasive, accurate, rapid and high-throughput method for early diagnosis of BC, and are more sensitive than traditional imaging examination for early-stage and minimal tumors.

OR-026

CD83+CCR7+ NK cells induced by interleukin 18 promote experimental autoimmune uveitis

Xin Wang[1]、Wei Lin[2]、Yi Zhang[1]
1. Qilu Hospital of Shandong University
2. 山东第一医科大学基础医学院基础研究所

Objective Uveitis, an inflammatory disease involving the uvea, retina, retinal vessels and/or vitreous body, can result in visual impairment and blindness. A disorder of the immune system represents an essential pathogenesis for autoimmunity uveitis. In specific, the large number of lymphocytes, including mature dendritic cells (DCs), T cells and natural killer (NK) cells infiltrating the eye may be a critical factor which drives this disorder of the immune system to result in tissue damage. Natural killer (NK) cells have been reported to play a pathological role in autoimmune uveitis. However, the underlying mechanisms of NK cells in uveitis remain unclear.
Methods Experimental autoimmune uveitis (EAU) mice were established by immunizing human interphotoreceptor retinoid-binding protein peptide (IRBP)1–20 and pertussis toxin (PTX) intraperitoneally. To analyze the role of CD83+CCR7+NK cells in EAU, CD83+CCR7+NK or CD83-CCR7-NK cells were isolated from the inflamed spleen on days 12-16 post-immunization by flow sorting instrument. These cells were then adoptively transferred into EAU mice that had been immunized 4 days prior. The cells from eyes, lymph nodes and spleens were analyzed by flow cytometry The severity of retinal tissue damage was assessed by H&E staining. DCs were isolated from spleens or ocular cells from EAU mice using a CD11c+isolation kit. For anti-IL-18R treatment, NK cells were isolated from the eyes of EAU mice and were pretreated with anti-IL-18R for 24h, and then were added to the DCs, T cells or combination of DCs and T cells.
Results We found CD83+CCR7+ NK cells were increased within the eyes in the EAU mice. Both clinical and histopathological scores of eyes from mice receiving CD83+CCR7+ NK cell-transfers were greater higher than those of mice without cells transfer or those receiving CD83-CCR7- NK cell-transfers. The number of lymphocyte subsets generated, including CD4+IFN-γ+ T cells, CD4+IL-17+ T cells, CD4+GM-SCF+ T cells, CD11c+ MHC-II+ DCs and CD3-NK1.1+ cells within the eyes of mice receiving CD83+CCR7+ NK cell-transfers were greater than that in mice without a CD83+CCR7+ NK cell transfer or those with a CD83-CCR7- NK cell-transfer. Furthermore, we found CD83+CCR7+ NK cells promote maturation of DCs when CD83+CCR7+ NK cells co-cultured with immature DCs in vitro. Since it has been found that CD83+CCR7+NK cells could secrete IFN-γ to influence the statues of DCs, we used anti-IFN-γR antibody to block IFN-γR on DCs, then we found the expression levels of CD80, CD86 and CD54 in above DC were lower than non-blockage when co-cultured with CD83+CCR7+ NK cells. As IL-18 has been reported to be an important factor involved in inducing subsets of CD83+CCR7+ NK cells, we examined IL-

18 in this EAU model. IL-18, as well as IFN-γ, were significantly increased both in the aqueous humor of inflamed eyes and serum of EAU mice. When IL-18 Binding Protein (IL-18 BP) was injected into EAU mice to neutralize IL-18, the symptoms of EAU and percent of CD83+CCR7+NK cells within the eyes were decreased. Furthermore, we found Anti-IL-18R antibody treatment relieved EAU symptoms and decreasd NK cell infiltration within inflamed eyes.
Discussion Our current data provide further evidence that the increasing CD3-NK.1.1+CD83+CCR7+cells in EAU play a pathological role in the development of EAU by promoting the activation of DCs and T cells. IL-18 is a cytokine that belongs to the IL-1 super-family and is an inflammatory factor in many diseases. However, the mechanisms of IL-18 as related to uveitis remain unknown. In our study, we now provide evidence indicating that IL-18 is a pathogenic factor in EAU and provide a description for some possible mechanisms of IL-18 in uveitis. IL-18 can induce NK cell activation to secrete IFN-γ and increase expression levels of CCR7, CD83, NKG2D and CD69 on NK cells. Thus, IL-18 has the capacity to promote NK cell activity and migration to inflammatory sites, where it may then function as a critical factor in EAU through induction of CD83+CCR7+ NK cells. IL-18 is mainly produced by macrophages, neutrophils and DCs. In our experiments, we found that macrophages, neutrophils and DCs were all increased in EAU and secreted IL-18. But macrophages and neutrophils were not primary increasing cells in inflamed eyes of EAU. DCs as an important pathogenic factor for EAU, might participate in producing IL-18 to promote pathogenic CD83+CCR7+NK cell activation in the eyes of EAU. And then, these NK cells migrate into lymph nodes to promote DC maturation and T-cell activation. Thus, IL-18 might play a key role in inducing the cycle of DC maturation and NK activation. An axis may exist between DC-NK interactions to regulate Th1 responses in this EAU model. Furthermore, anti-IL-18R antibody might serve as a possible therapeutic candidate for the treatment of autoimmune uveitis.

OR-027

血清自噬相关蛋白 7 在 HBV 相关肝癌中的诊断价值

卓传尚、冯惠娟、叶治、林英、陈力、彭菲、柳丽娟
福建医科大学孟超肝胆医院

目的 探讨自噬相关蛋白 7（ATG7）对乙型肝炎病毒相关肝癌（HBV-HCC）的诊断价值。
方法 采用 ELISA 技术检测 67 例 HBV-HCC、22 例非 HBV 相关肝癌（nonHBV-HCC）、50 例慢性乙型肝炎（CHB）和 20 例健康对照者（HC）血清中 ATG7 表达水平，分析各组 ATG7 及 AFP 的表达，比较 ATG7、AFP 及二者联合检测的诊断效率。
结果 HBV-HCC 组血清 ATG7 表达水平为 22.88(19.79,23.04)ng/m，显著高于 nonHBV-HCC 组（17.06 (14.45, 19.40) ng/mL）、CHB 组（19.21 (16.65, 20.82) ng/mL ）和健康对照组（13.82 (8.70, 17.82) ng/mL）；ATG7 诊断 HBV-HCC 的 AUC 为 0.818（95%CI：0.743～0.879），略高于 AFP（AUC=0.777, 95%CI：0.698~0.843）差异无统计学意义(P=0.3941)；ATG7 和 AFP 联合检测诊断 HBV 相关肝癌的 AUC 为 0.859（95%CI：0.790～0.913），显著高于 ATG7(P=0.0284）和 AFP（P=0.0379）。
结论 ATG7 是诊断 HBV 相关肝癌的良好标志物，ATG7 和 AFP 联合检测可显著提高 HBV 相关肝癌的诊断率。

OR-028

Four potential broad-spectrum neutralizing epitopes in the spike protein of SARS-CoV-2 were predicted by bioinformatics

Yunyi He[1]、Ning Zhang[1]、Ying Qu[1]、Hanyu Zhu[2]、Qiliang Liu[2]、Hongbo Liu[1]
1. The Second Affiliated Hospital of Guilin Medical University
2. College of Bio-technology, Guilin Medical University

Objectives To date, seven human coronaviruses (HCoVs) have been discovered. SARS-CoV-2 is a newly emerged HCoV, which can induce fatal pneumonia infection, and thus seriously threatens human health and life safety. Coronavirus is a single-stranded RNA virus that is susceptible to mutation, making it difficult to develop vaccines. Broad-spectrum vaccines based on conserved neutralizing epitopes can not only prevent epidemic strains, but also have broad-spectrum antiviral property. In this study, bioinformatics was used to predict broad-spectrum neutralizing epitopes of HCoVs.

Methods The spike (S) protein amino acid sequence of SARS-CoV-2 Wuhan-Hu-1 strain (GenBank ID: YP_009724390.1) was used as the template for epitope prediction. Four linear B-cell epitope prediction online servers with different algorithms, namely, ABCpred2006 (threshold: 0.51), BepiPred2.0 (threshold: 0.5), COBEpro (threshold: 0.5) and SVMTriP (default threshold), were employed to preliminarily predict the linear B-cell epitopes, and the peptide fragments were selected according to their common prediction results. To increase prediction accuracy, VaxiJen2.0 (threshold: 1.0), the online server with another different algorithm and a higher prediction accuracy rate (70%~89%), was used for further screening, shortening the peptide fragments scope by deleting the amino acid one by one, and the top three highest-scoring peptides in each scope were chosen as the candidate epitopes. The spatial position of candidate epitopes in S protein was analyzed by the PyMOL software, and the conservation of candidate epitopes was analyzed by Clustal X2 software.

Results Four potential broad-spectrum linear B cell neutralizing epitopes were predicted, which include P6(aa496-501), P12 (aa811-816), P14 (aa1163-1168) and P15 (aa1196-1201). These epitopes were all in the loop structures of SARS-CoV-2 S protein, which is the dominant structure recognized by functional antibodies. P6 was a potential cross-neutralizing epitope against SARS-CoV-2 and SARS-CoV in the RBD domain, containing four amino acids related to RBD/ACE2 binding, and its amino acid and spatial structure were highly conserved in SARS-CoV. P12 was a potential broad-spectrum neutralizing epitope against SARS-CoV-2, SARS-CoV and HCoV-OC43, located in the second cleavage site S2' of the S protein, and its amino acid was highly conserved in SARS-CoV and HCoV-OC43. P14 and P15 were located in the HR2 domain, and both contain the important amino acids related to HR2 and HR1 binding. P14 was the potential cross-neutralizing epitope against SARS-CoV-2 and SARS-CoV, and its amino acid was completely conserved in SARS-CoV. P15 might be a potential broad-spectrum neutralizing epitope against SARS-CoV-2, SARS-CoV and MERS-CoV, and its amino acid was completely conserved in SARS-CoV and highly conserved in MERS-CoV.

Conclusions In this study, bioinformatics methods were employed to predict the epitopes, and four potential broad-spectrum linear B cell neutralizing epitopes in the S protein of SARS-CoV-2 were predicted, laying a foundation for the development of HCoVs broad-spectrum vaccines.

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OR-029

The potential value of serum chemerin in patients with breast cancer

Xianjin Zhu、yingping cao
Fujian Medical University Union Hospital

Breast cancer (BC) is one of the most dangerous malignant diseases in females. However, the reliable serum biomarkers of BC still need to be explored. Chemerin levels have been found to be associated with different types of cancer. This study aimed to evaluate the role of serum chemerin as a biomarker of BC diagnosis, as well as the correlation between serum chemerin levels and clinicopathological features. The serum from 248 BC patients, 30 breast benign tumor patients, and 103 healthy controls were collected and serum chemerin levels were determined with enzyme-linked immunosorbent assay. We found that serum levels of chemerin in BC patients were higher than those in healthy control individuals ($P<0.05$). The area under the ROC curve (AUC) for chemerin, CA15-3 and CEA was 0.704, 0.662 and 0.581, respectively, in distinguishing between breast cancer patients from healthy individuals, and the chemerin cutoff value was 100.327 ng/ml with a sensitivity of 56.60% and a specificity of 98.10%. The AUC for chemerin + CA15-3 was 0.822, which was higher than that for chemerin + CEA and CEA + CA15-3. Moreover, serum levels of chemerin were significantly associated with histologic grade, Ki67 expression, and menopausal status. However, no significant association was found between serum levels of chemerin and age, tumor size, metastase, ER status, PR status, and HER-2 status. Overall, our study suggested that the combination of chemerin with CA15-3 achieves relatively better diagnostic performance in the breast cancer. Elevated serum chemerin is associated with Ki67 expression levels and histologic grade.

OR-030

2,5-dimethylcelecoxib improves immune microenvironment of hepatocellular carcinoma by promoting ubiquitination of HBx-induced PD-L1

Zhanfei Chen[2]、Haijian Tu[1]、Liumin Yu[1]、Nanhong Tang[3]
1. The Affiliated Hospital of Putian University
2. The Affiliated Hospital of Putian University, Putian Univeristy
3. Department of Hepatobiliary Surgery and Fujian Institute of Hepatobiliary Surgery, Fujian Medical University Union Hospital

Background 2,5-dimethylcelecoxib (DMC) is a targeted inhibitor of microsomal prostaglandin E synthase-1 (mPGES-1), a key enzyme in the PGE2 synthesis pathway of inflammatory mediators. Previous studies have confrmed that DMC can inhibit the growth of hepatitis B virus (HBV)-related hepatocellular carcinoma (HCC). However, it is not known whether DMC is involved in the changes of tumor immune microenvironment.
Methods In this study, we explored the effects of DMC on HBV-related HCC immune microenvironment, and deeply analyzed its unique effect and mechanism on programmed death receptor 1 (PD-1)/and its ligand 1 (PD-L1) pathway.
Results Clinical hepatoma tissues detection showed that compared with non-virus-related HCC, the level of CD8 of HBV-related HCC was signifcantly lower, while the levels of PD-L1 and CD163 were higher. In vivo experiments indicated that DMC could increase the level of tumor infltrating CD8+ T cells in hepatitis B virus X (HBx) (+) hepatoma cells implanted mouse models, and inhibit the expression of PD-L1 and CD163 in tumor tissues. DMC combined with atezolizumab had more signifcant antitumor effect and stronger blocking effect on PD-1/PD-L1 pathway. Mechanism studies have shown that DMC can promote ubiquitin degradation of HBx-

induced PD-L1 protein in HCC cells by activating adenosine 5′-monophosphate-activated protein kinase pathway. Further experiments confrmed that this process was mainly mediated by E3 ligase RBX1.
Conclusions Our results uncover a role for DMC in promoting HBV-related HCC immune microenvironment, which not only enrich the relationship between inflammatory factors (mPGES-1/PGE2 pathway) and immunosuppression (PD-L1), but also provide an important strategic reference for multitarget or combined immunotherapy of HBV-related HCC.

OR-031

Exosomal circPACRGL promotes progression of colorectal cancer via the miR-142-3p/miR-506-3p- TGF-β1 axis

Anquan Shang 、Dong Li
Tongji Hospital of Tongji University

Background Colorectal cancer (CRC) is the leading cause of cancer-related death worldwide. Exosome shave emerged as crucial regulators of intercellular communication and that abundant Circular RNAs (circRNAs) are enriched within exosomes. CircRNAs are novel members of noncoding RNAs regulating cancer proliferation and progression. However, the function and regulatory mechanism of cancer-derived exosomal circRNAs in CRC remains unclear.
Methods CRC cells-derived exosomes were characterized using transmission electron microscopy, nanoparticle tracking analysis (NTA) and western blot. CCK-8, wound healing and transwell assays, and flow cytometry assays were conducted to assess whether exosomes would affect the proliferation, metastasis, and apoptosis of CRC cells, respectively. Moreover, we performed the RNA sequencing and RT-qPCR to identify circRNAs in exosome-stimulated CRC cells. Fluorescence in situ hybridization (FISH) assay was used to detect the cellular distribution of circPACRGL. Bioinformatic analyses (StarBase 2.0) were used to pool the miRNA targets of circPACRGL. Luciferase assays were performed to verify the direct interaction. Finally, flow cytometry was used to detect the differentiation of N1-N2 neutrophils.
Results Our study identified a novel CRC-derived exosomal circRNA, circPACRGL. We found circPACRGL was significantly upregulated in CRC cells after tumor-derived exosomes addition. Moreover, circPACRGL serves as a sponge for miR-142-3p/miR-506-3p to facilitate the transforming growth factor-β1 (TGF-β1) expression. As a result, circPACRGL promoted CRC cell proliferation, migration and invasion, as well as differentiation of N1 to N2 neutrophils via miR-142-3p/miR-506-3p-TGF-β1 axis.
Conclusion Our study, the first to reveal that cancer-derived exosomal circPACRGL plays an oncogenic role in CRC proliferation and metastasis, providing mechanistic insights into the roles of circRNAs in CRC progression and a valuable marker for CRC treatment.

OR-032

Genetic testing and clinical relevance of patients with thoracic aortic aneurysm and dissection in northwestern China

Liu Yang、jinjie li、yanjun diao、lei zhou、yijuan xin、rui li、juan wang、jiayun liu
Air force medical uiversity xijing hospital

Thoracic aortic aneurysm and dissection (TAAD) is a life-threatening pathology that remains a challenge worldwide. Up to 40% of TAAD cases are hereditary with complex heterogeneous genetic backgrounds. The purposes of this study were to determine the diagnostic rate of patients with TAAD, investigate the molecular pathological spectrum of TAAD by next-generation

sequencing (NGS), and explore the future preclinical prospects of genetic diagnosis in patients at high-risk of study.
METHODS NGS was used to screen 15 genes associated withgenetic TAAD in 212 patients from northwestern China. Clinical data of patients were gathered by Electrocardiography, transthoracic echocardiography and computed tomography.
RESULTS Of the 212 patients, 67 (31.60%) tested positive for a (likely) pathogenic variant, 42 (19.81%) had a variant of uncertain significance (VUS), and 103 (48.58%) had no variant (likely benign/benign/negative). A total of 135reportable variants were detected in our test, among which 77(57.04%) are first reported in this paper.

OR-033

ddPCR 检测循环肿瘤 DNA 甲基化水平在肝细胞性肝癌诊断中的应用

王娟[1]、杨柳[1]、刘家云[1]、刁艳君[1]、郑良宏[2]、张康[3]、马越云[4]、郝晓柯[1]
1. 空军军医大学西京医院
2. 广州优泽生物技术有限公司
3. 澳门科技大学医学院
4. 解放军空军总医院检验科

近年来，一些新型蛋白质生物标志物、基因突变位点和表观遗传修饰常用于分子诊断癌症。作为一种非侵入性液体活检分析新策略，循环肿瘤 DNA(circulating tumor DNA，ctDNA)甲基化异常的分析在多种癌症的早期诊断中已有大量研究，其中也包括原发性肝细胞性肝癌(hepatocellular carcinoma,HCC)。本研究旨在通过基于数字微滴聚合酶链反应(digital droplet PCR, ddPCR)的检测方法，评价甲基化探针 cg23612220 在肝癌早期诊断中的应用。方 法 采集原发性肝癌患者 97 例，健康人 80 例，慢性肝炎 46 例。提取 ctDNA 并进行亚硫酸氢盐转化，利用 ddPCR 方法定量 DNA 甲基化水平。结 果 我们分析了不同健康状况下 cfDNA 含量的变化。肝细胞癌组 cfDNA 含量明显高于健康对照组。随后，我们研究了与肝癌病情进展相对应的外周游离 DNA 甲基化比率的动态变化。在晚期(BCLC C)和晚期(BCLC D)也检测到较高的游离 DNA 甲基化状态和 DNA 含量。另外，我们还探讨了甲基化标签 cg23612220 对肝癌诊断的价值。在肝癌的诊断中，结合 AFP 水平和 cfDNA 含量，采用 15.70%的 DNA 甲基化为 cutoff 值检测 HCC、慢性肝炎和健康个体之间的甲基化状态差异，敏感性为 78.57%，特异性为 89.38%，诊断正确率为 89.27% 。

OR-034

Serum GFAP, NfL, and UCHL1 as potential biomarkers of disease activity in AQP4-IgG+NMOSD

Jinyang Wang[1,2]、Jianan Wang[3]、Ruibing Li*[1]、Chengbin Wang*[1,2,3]
1. 中国人民解放军总医院第一医学中心检验科
2. 潍坊医学院医学检验学院
3. 解放军医学院

Objective Neuromyelitis optica spectrum disorder(NMOSD) is a frequently disabling neuroinflammatory syndrome with a relapsing course. Blood tests to monitor disease activity in NMOSD have not been developed. Here, we investigated the potential of serum glial fibrillary acidic protein(GFAP), neurofilament light chain(NfL), Tau protein and Ubiquitin C-terminal hydrolase L1(UCHL1) levels in NMOSD with aquaporin-4 antibody-positve(AQP4-IgG+NMOSD), myelin oligodendrocyte glycoprotein-antibody-associated disease(MOGAD) and multiple sclerosis(MS).

Methods Using ultra sensitive single molecule array(simoa), levels of sGFAP, sNfL, sTau and sUCHL1 were measured in a prospective cohort of 29 AQP4-IgG+ NMOSD, 13 MOGAD, 20 MS and 9 healthy controls(HCs). Serum biomarker levels were compared between patients in relapse and remission stages, and the correlation with clinical parameters in the AQP4-IgG+NMOSD group was further determined using multiple linear-regression.
Results The median levels of sGFAP[155.11pg/ml, p<0.0001], sNfL[10.71pg/ml, p=0.0001] and sUCHL1[14.34pg/ml, p=0.001] were significantly higher in the AQP4-IgG+NMOSD group than those in HCs group[sGFAP, 61.89pg/ml; sNfL, 5.28pg/ml; sUCHL1, 4.90pg/ml]. sUCHL1 levels in the AQP4-IgG+NMOSD group[14.34pg/ml] were higher compared to those in MOGAD groups[6.48pg/ml, p=0.02] and MS groups[8.51pg/ml, p=0.038]. For AQP4-IgG+NMOSD subgroups, sGFAP [233.29pg/ml, p=0.001], sNfL[18.35pg/ml, p=0.002] and sUCHL1[16.76pg/ml, p=0.004] levels remarkably increased during relapse. Meanwhile, patients in MOGAD relapse stage displayed higher sGFAP[144.27pg/ml] and sNfL[10.46pg/ml] levels than those in the remission stage[59.28pg/ml, 4.75pg/ml, all p<0.05], but only sNfL[21.29pg/ml, p=0.017] levels distinguished patients with MS in relapse from those in remission. During relapse in these disease groups, both sGFAP[233.29pg/ml, p=0.044] and sUCHL1[16.76pg/ml, p=0.007] levels were significantly higher in the AQP4-IgG+NMOSD group than those in MS group[136.72pg/ml, 9.00pg/ml, respectively], while only elevated sUCHL1 levels can discriminate the relapse stage of AQP4-IgG+NMOSD group from that of MOGAD group[6.48pg/ml, p=0.004]. Univariate and multiple analysis indicated that sGFAP and sNfL levels were higher in patients with brain lesions and sUCHL1 levels was higher in those with spinal cord lesions during a recent relapse. Additionally, combination with sGFAP, sNfL and sUCHL1 can significantly improved the diagnosis of AQP4-IgG+NMOSD[AUC=0.771, sensitivity:58.62%, specificity:90.24%, p<0.001].
Conclusions These findings suggest that sGFAP, sNfL and sUCHL1 can monitor AQP4-IgG+NMOSD disease activity, and were associated with phenotype of the recent relapse. Besides, sUCHL1 levels can exhibit good discrimination between these disease, and the combiation with sGFAP, sNfL and sUCHL1 can significantly improve AQP4-IgG+NMOSD diagnostic efficacy.

OR-035

Prognostic and immunological role of inhibin B receptor in lung adenocarcinoma: A study based on bioinformatics analysis

Guoying Zou、Ying Wu
The Second People's Hospital of Hunan Province

Objective Inhibin B (INHBB) is one of the transforming growth factor β (TGF-β) superfamily, consisting of α (INHA) and βB (INHBB) subunits. INHB is mainly secreted by germ cells, and acts as a negative feedback regulator of Follicle-stimulating hormone (FSH).The β subunit combines specifically with the activin receptor type-2 (ACVR2)， performs biological functions by competitively inhibiting the pathway of Activin (ACT). The study found that transforming growth factor β recetor 3 (TGFBR3) binds to a convex α subunit on the surface of INHB, and enhances the binding affinity of ACVR2A/B to INHβ subunit. So INH-ACVR2A/B-TGFBR3 can form a high affinity ternary complex that antagonizes ACT signal transduction. The research of INHB in oncology is largely limited to reproductive system tumors. Our previous research has found INH βB inhibited invasion and metastasis of nasopharyngeal carcinoma cells thought TGF-β/Smads signaling pathway. This study aimed to visualize the prognostic landscape of INHB subunit and its receptors in lung adenocarcinoma (LUAD) and investigate the relationship between INHB subunit and its receptors expression and immune infifiltration.
Methods INHB subunit and its receptors(INHA, ACVR2A, ACVR2B, INHBB, TGFBR3) expression were primarily screened in LUAD tissues and normal tissues from

Oncomine, UALCAN and GEPIA databases, and further analyzed the correlation between the expression of INHB and its receptors and the prognosis of LUAD patients using Kaplan–Meier plots database. Then, we investigated the functional relevance of INHB and its receptors in LUAD across CancerSEA database, and further validated the differential expression and co-expression of INHB in metastasis samples of LUAD from HCMDB database. And the proteins network with TGFBR3 and co-expression proteins were also built using the online STRING website, functional annotation and enrichment analysis of genes were performed. Meanwhile, we investigated the relationships between TGFBR3 expression and infiltrated immune cells and their corresponding gene marker sets with TIMER databases.
Results INHB subunit and its receptors(INHA, ACVR2A, ACVR2B, INHBB, TGFBR3) expression were differential in LUAD tissues and normal tissues ($P < 0.01$). The expression of INHA, ACVR2A, ACVR2B, INHBB were up-regulated while the expression of TGFBR3 was down-regulated in LUAD tissues. Only INHA, ACVR2A, and TGFBR3 expression levels were closely associated with high-grade malignancy and advanced TNM stage ($P < 0.05$). High INHA expression levels were significantly associated with poor overall survival (OS) and the expression of ACVR2A and TGFBR3 were the opposite in LUAD patients. The expression of TGFBR3 was negatively correlated with the metastasis of LUAD probably mainly through the regulation of lipolysis in adipocytes and PI3K-Akt signaling pathway.Univariate and multivariate analysis indicated the overall survival of LUAD cases with low TGFBR3 level is shorter than those of patients with high TGFBR3 expression ($P < 0.05$). LUAD with TGFBR3 deficiency presented the paucity of infiltrated immune cells and their matching marker sets.
Conclusion The expression of TGFBR3 was down-regulated and negatively correlated with the metastasis in LUAD. Deficient TGFBR3 expression was related to disease progression and poor prognosis, as well as impaired infiltration of immune cells in LUAD.

OR-036

Thrombin-activated platelets induce vascular endothelial leakage by a PECAM-1-dependent mechanism

Liqin Ling、Jing Zhou
West China Hospital, Sichuan University

Objective Acute lung injury (ALI) has a high mortality as it causes pulmonary vascular endothelial leakage leading to acute lung edema. It has been known that platelets can contribute to vascular endothelial leakage during ALI, therefore in this study, we aimed to figure out the mechanism involved in this process.
Methods Mice were injected intraperitoneally with lipopolysaccharide (0.1 mg/kg), followed 24 h later by intravenous injection of anti-H2d antibody (1 mg/kg), to creat ALI models. A custom-designed intravital confocal microscopy system was developed to study the pulmonary vasculature in vivo. Platelet, or its agonist (thrombin) or antagonist (anti-Pselectin, anti-PECAM1 or anti-GPIIbIIIa) was injected intravenously.
Results Thrombin injection could aggravate ALI endothelial leakage, blocking its activation on platelets (protease-activated receptor-4 antagonist) could interrupt this reaction. In vitro assay showed that thrombin-activated platelets could adhered to the lumen surface of pulmonary vascular endothelial cells, leading to intercellular junction breakage and cellular contraction, forming endothelial leakage, while thrombin or platelets alone didn't have this effect. Furthermore, by utilizing a self-developed device, which supported direct visual observation and/or video recording of cell-cell interactions in the pulmonary microvasculature under confocal intravital microscopy, we found that the number of adhesion platelets on pulmonary vascular endothelium was associated with the severity of endothelial leakage. While PECAM-1 antagonist could block this adhesion and reduce endothelial leakage, P-selectin antagonist or GPIIbIIIa antagonist did not have this effect. Moreover, by immunofluorescence techniques, only PECAM-1 was found to be localized at the edge of activated platelets, mainly at where the platelet-endothelium

adherence existed. P-selectin was found to be evenly distributed on activated platelets, mainly protruded towards the vascular lumen of the vessel, supporting its role in mediating the interaction between activated platelets and neutrophils in the vessels. GPIIbIIIa was found at where platelet aggegation existed, demonstrating its well-known role in hemostasis.
Conclusions With all the results above, we concluded that thrombin-activated platelets might induce vascular endothelial leakage by a PECAM-1-dependent mechanism in ALI mice, although we have yet to figure out the mechanism of how PECAM-1 signal mediates endothelial leakage.

OR-037

Risk predictive value of antiphosphatidyserine-prothrombin complex antibodies in lupus anticoagulant-positive patients

Yaxin Chu、Rui Qiao
Peking University Third Hospital

Objective To investigate the risk prediction value of antiphosphatidylserine/prothrombin complex antibodies(aPS/PT) in the clinical events of the patients with positive lupus anticoagulant(LA).
Methods A total of 167 patients with LA positive tested for two or more times at intervals of 12 weeks or more were enrolled in the study from Peking University Third Hospital from January 2018 to September 2019. The patients were divided into the group with clinical events(n=115) and group without clinical events(LA carrier group, n=52), and the former were divided into the thromboembolism(TE)group (n=18), adverse pregnancy outcome(APO) group(n=91) and TE+APO group(n=6). The anticardiolipin antibody(aCL), anti-β2glycoprotein I antibody(anti-β2 GPI) and aPS/PT of the patients were detected by the chemiluminescence immunoassay, and the results among different groups were compared.
Results The aPS/PT IgG positive rate(37.4% vs 9.6%, P<0.001) and the concurrence of aPS/PT IgG and IgM positive rate(31.3% vs 5.8%, P<0.001) in the clinical event group were significantly higher than in the LA carrier group. Besides, the titres of aPS/PT IgG in clinical event group was significantly higher than LA carrier group[16.050（5.100～73.083）units] vs[16.914（14.736～24.646）units], P=0.881). The clinical event group can be further divided into thromboembolism group(TE, n=18), adverse pregnancy outcomes group(APO, n=91) and the concurrence of two events group(TE+APO, n=6). Compared with LA carrier group(9.6%), the positive rate of aPS/PT IgG in TE+APO (100.0%), TE (55.6%) and APO (29.7%) were significantly higher, P<0.05. And the titres of aPS/PT IgG in TE+APO[150.000（89.305～150.000）units], TE [54.654（12.093～135.943）units] were significantly higher than LA carrier group [(16.359（14.737～24.473）units], P<0.05. The positive rate of aPS/PT IgM was only significantly higher in TE+APO (100.0%) than in the LA carrier group(38.5%), P<0.05, the titres of it was significantly higher in TE+APO than in LA carrier group[116.395（82.663～150.000）units] vs [40.871（15.925～127.643） units, P<0.05]. The positive rate of the concurrence of aPS/PT IgG and IgM were significantly higher in TE+APO(100.0%), TE(44.4%) and APO(24.2%) than in LA carrier group(5.8%), P<0.05. Positivity of aPS/PT showed good consistency with triple positive group of antiphospholipid antibodies profiles(aCL, aβ2GPI and LA), Kappa=0.114，P=0.012. And the titres of aPS/PT IgG and IgM in triple positive group [30.617（5.100～150.000）units], [76.212（33.420～150.000） units] were significantly higher than in only LA positive group[15.143（14.690～17.004）units], [13.458（9.598～20.611） units], P<0.05.
Conclusions The risk of clinical events of APS patients is increased in the cases of aPS/PT and LA positive, aPS/PT has the value of risk stratification for LA positive patients.

OR-038

血浆中 D-二聚体和 IL-6 与抗 PD-1 治疗晚期 NSCLC 的疗效和 PFS 相关性研究

陈冲
天津医科大学肿瘤医院

目的 寻找预测抗 PD-1 治疗晚期 NSCLC 患者的疗效和 PFS（无进展生存期）的外周血生物标志物，用来指导抗 PD-1 治疗方案调整，为 NSCLC 患者带来更大的临床获益；
方法 系统回顾 2018 年 1 月至 2021 年 4 月期间在天津医科大学肿瘤医院住院接受抗 PD-1 治疗（纳武利尤单抗（O 药）、帕博丽珠单抗（K 药）信迪利单抗和卡瑞丽珠单抗）的 103 名晚期或复发性 NSCLC 患者。记录患者的临床病理特征：包括开始治疗时的年龄、性别、ECOG PS、治疗线、吸烟史、放疗史、临床分期（根据国际肺癌研究协会指南第七版）、驱动肿瘤基因突变状态、组织学、BM、血清 Alb、血清 LDH、肺部肿瘤标志物（CEA、CYFR21-1 和 SCC 等）、血清炎症标志物-NLR、dNLR、 PLR、IL-6 和血浆中纤溶指标：D-dimer，利用 SPSS16.0 分析患者的临床病理特征与抗 PD-1 治疗晚期 NSCLC 患者的疗效和 PFS 相关性。
结果 仅有 85 名患者（82.5%）进行驱动肿瘤基因突变（EGFR 或 ALK）检测。仅有 86 名患者（83.5%）进行 PD-L1 肿瘤表达检测。IL-6 和 D-dimer 可以预测抗 PD-1 治疗 6-8 周的治疗效果临床价值，AUC 面积对应 0.765 和 0.804。利用新的 cut-off 值建立抗 PD-1 治疗 NSCLC 的 PFS 预测模型：利用 IL-6 ≥ 8.03 pg/mL 为“1”分，IL-6 ＜ 8.03 pg/mL 为“0”分；DD ≥ 917.2 ng/dL 为“1”分，DD ＜917.2 ng/dL 为“0”分；将 103 例研究对象分为：0 分、1 分和 2 分三组，比较三组抗 PD-1 治疗的 PFS。结果表明联合 IL-6 和 D-dimer 评分，评分越高，PFS 时间越短。
结论 联合应用炎症指标（IL-6）和纤溶指标（D-dimer）评分可以预测抗 PD-1 治疗 NSCLC 患者的疗效。

OR-039

急性中毒患者血栓弹力图和常规凝血指标检测的相关性及应用分析

闫彬、翟素平、胡天喜
南阳市中心医院

目的 探讨急性中毒患者血栓弹力图（TEG）和常规凝血指标检测之间的一致性。**方法** 回顾性分析 102 例急性中毒患者的 TEG 和常规凝血指标参数。
结果 （1）中毒后继发肝功能损害组的 R 值显著高于非肝功能损害组，而继发心肌损伤组的 MA 值和 G 值均显著高于非心肌损伤组；（2）PLT 值与 MA 值、CI 值和 G 值之间均呈正相关（r 分别为 0.397、0.234、0.401，P 均<0.05）；APTT 值与 R 值呈正相关（r=0.323，P=0.001），与 CI 值呈负相关（r=-0.201，P=0.043）；TT 值与 Angle 值、MA 值、CI 值和 G 值之间均呈负相关（r 分别为-0.197、-0.246、-0.232、-0.242，P 均<0.05）；FIB 值与 MA 值和 G 值之间均呈正相关（r 分别为 0.335、0.332，P=0.001）；（3）在评估患者低凝状态时，PLT 值和 MA 值、PLT 值与 CI 值之间具有一致性（κ 分别为 0.243、0.203，P 均<0.05）；TT 值和 CI 值之间具有一致性（κ=0.224，P=0.020）；FIB 值与 K 值、FIB 值与 MA 值之间具有一致性（κ 分别为 0.193、0.213，P 均<0.05）。FIB 值与 Angle 值、FIB 值和 MA 值之间在评估患者高凝状态时具有一致性（κ 分别为 0.214、0.274，P 均<0.05）；（4）PLT 值判断 MA 值<50mm 的敏感度和特异度分别为 99.0%、81.5%，AUC 为 0.933；FIB 值判断 MA 值<50mm 的敏感度和特异度分别为 70.0%、70.7%，AUC 为 0.678。

结论 TEG 和常规凝血指标检测在急性中毒患者中的相关性较弱，两者在评估患者低凝状态时的一致性较好。常规凝血指标对预测 TEG 检测的低凝结果价值较大，但不能取代 TEG 检测，两者联合应用将有助于更好地评估急诊中毒患者的凝血状态，预防出血事件。

OR-040

一例复合杂合突变导致的遗传性凝血因子 XII 缺陷症家系分析

陈静
成都市新都区人民医院

目的 分析 1 例遗传性凝血因子Ⅻ（FⅫ）缺陷症家系的临床表型及基因突变情况，探讨其分子致病机制。
方法 检测先证者及其家系成员（共 3 代 5 人）血浆凝血酶原时间（PT）、活化部分凝血活酶时间（APTT）、纤维蛋白原含量（FIB）、D-D 二聚体（D-D）、凝血因子 XII 促凝活性（FXII:C）和凝血因子 FXII 抗原（FXII:Ag）等凝血指标。采用高通量测序方法分析先证者 F12 基因所有的外显子编码区及外显子-内含子交界处的基因突变情况，对检出的可疑致病突变进行 Sanger 测序验证，并对家系成员的相应突变位点进行检测。采用 Mutation Taster 在线生物信息学软件预测突变位点对蛋白功能的影响。
结果 先证者 APTT 结果为 180.9s，明显延长；FXII:C 和 FXII:Ag 分别降低至 0.8%和 4.17%。高通量测序分析发现先证者 F12 基因存在复合杂合突变，即第 11 号外显子 c.1261G＞T 杂合无义突变（p.Glu421*）和第 4 号外显子 c.251dupG 杂合移码突变(p.Trp85fs)。这两个突变均为功能缺失型突变，将导致蛋白质合成提前终止，产生丧失重要功能区域的截短蛋白，具有极强的致病性；Mutation Taster 软件预测这两个突变均为致病突变。Sanger 测序家系验证结果显示，先证者 c.1261G＞T 杂合突变遗传自其母亲，其哥哥和女儿均为 c.1261G＞T 杂合突变携带者。在此家系中基因检测结果与血液学检查结果相符，即基因型和表型共分离。
结论 F12 基因第 11 号外显子 c.1261G＞T 杂合无义突变和第 4 号外显子 c.251dupG 杂合移码突变是该家系遗传性凝血因子Ⅻ缺陷症的分子发病机制，这两个突变均为国际上首次报道的新突变。

OR-041

尿液分析智能审核系统的建立、验证及临床应用评价

王刚强、程翔、何娟、杨若凡、闫宏斌、汪沛、卢佩、李程华、肖凤静、刁艳君、郑善銮、郝晓柯、刘家云
空军军医大学西京医院

目的 建立尿液分析智能审核系统，并评价其临床应用效果。
方法 应用 Sysmex 公司 UN9000 尿液流水线（2 台 UC-3500 尿液干化学分析仪、3 台 UF-5000 尿液有形成分分析仪）操作平台检测尿液样本，依据 CLSI 发布的 AUTO 10-A《临床实验室定量检验结果的自动审核》指南、国家卫生健康委员会发布的 WS/T 616-2018《临床实验室定量检验结果的自动审核》卫生行业标准，通过仪器检测结果与双盲法镜检结果间比对，结合自建的 UF-5000 尿液参考区间、干化学 Hb 与 RBC 及干化学 LEU 与 WBC 的等级对应确认关系、患者临床信息等，设计并验证智能审核规则，分别计算真阴性率、假阴性率（漏检率）、真阳性率、假阳性率、镜检率、智能审核通过率以及人工审核和智能审核结果之间的一致率，同时比较近两年同期尿液审核效率。

OR-042

全自动血细胞分析仪高敏体液模式快速识别胸腹水恶性肿瘤细胞的价值探讨

龚继涛、曲林琳
吉林大学第一医院

目的 探讨全自动血细胞分析仪高敏体液（hsA）模式对胸腹水游离肿瘤细胞的快速识别价值。
方法 收集 2021 年 1 月~3 月在吉林大学第一医院检验科行脱落细胞学检查的胸腹水标本 100 份，应用全自动血细胞分析仪 hsA 模式检测胸腹水标本中高荧光细胞百分比（HF%）和高荧光细胞绝对值（HF#）。依脱落细胞学检查结果分为肿瘤细胞阳性组和肿瘤细胞阴性组，比较两组间 HF%和 HF#的差异；通过受试者工作特征（receiver operating characteristic，ROC）曲线分析 HF%和 HF#筛查胸腹水游离肿瘤细胞的 cutoff 值、灵敏度、特异度、阳性预测值和阴性预测值，评价 HF%和 HF#与脱落细胞检查的一致性。
结果 ①100 份胸腹水标本中，脱落细胞学检查肿瘤细胞阳性 69 份，肿瘤细胞阴性 31 份，阳性组 HF#和 HF%水平显著高于阴性组，差异具有统计学意义（P<0.05）；②HF#检出肿瘤细胞 cutoff 值为 27.65×106/L 时，最大曲线下面积（AUC）为 0.824，灵敏度为 69.57%，特异度为 93.55%，阳性预测值为 96.00%，阴性预测值为 58.00%；HF%检出肿瘤细胞 cutoff 值为 2.05%时，AUC 为 0.856，灵敏度为 81.16%，特异度为 77.42%，阳性预测值为 88.89%，阴性预测值为 64.86%；③HF#、HF%与脱落细胞学检查结果的 Cohen’s kappa 系数分别为 0.54、0.56，95%置信区间分别为 0.385-0.727（P<0.001）、0.385-0.727（P<0.001）。
结论 希森美康 XN9000 全自动血细胞分析仪 hsA 模式下检测高荧光细胞对胸腹水游离肿瘤细胞具一定的筛查作用，与脱落细胞学检测结果具有一定程度的相关性，在临床工作中应依据筛查目的、人群与疾病的分布特点对 HF#和 HF%的 cutoff 值做出一定调整，以提高筛查效果。

OR-043

血小板-中性粒细胞聚集体与中性粒细胞胞外诱捕网及深静脉血栓形成的关系研究

周景艺、张艺镜、沈薇
上海交通大学医学院附属仁济医院

目的 分析深静脉血栓 (deep venous thrombosis, DVT) 患者体内血小板-中性粒细胞聚集体（Platelet-Neutrophil Aggregates，PNAs）和中性粒细胞胞外诱捕网 (neutrophil extracellular traps, NETs)的量化关系，明确 PNAs 在 NETs 形成中的作用以及 NETs 在 DVT 产生中的价值，同时摸索 PNAs 形成的生理条件。
方法 采集 20 例深静脉血栓患者（DVT 组）和 20 例正常对照（正常对照组）新鲜枸橼酸钠抗凝全血。检测血浆游离 DNA、血小板-中性粒细胞聚集体（PNAs）以及血小板活化水平。比较两组上述三个指标之间的差异，明确 PNAs 与 NETs 的量化关系以及两者在 DVT 中发挥的作用。分离正常人外周血中性粒细胞和血小板，在血小板中加入不同种类和不同剂量的血小板诱导剂活化后，加入分离所得的中性粒细胞共孵育，通过涂片染色计数 PNAs 的数量，同时检测上清液中游离 DNA 水平，进而明确不同种类和不同浓度的血小板诱导剂对 PNAs 形成的影响，摸索 PNAs 体外形成的最佳条件。
结果 对 DVT 组和正常对照组两组人群的 PNAs、血小板活化以及血浆游离 dsDNA 水平进行统计学分析和比较，发现 DVT 患者的 PNAs 表达明显上升。DVT 组的总血小板活化水平也显著高于正常对照组。 PNAs 的表达与血小板的活化呈正相关。同时，DVT 患者的游离 dsDNA 水平显著高于

正常对照组，且 dsDNA 水平与 PNAs 水平呈现明显的正相关性。体外研究表明，血小板诱导剂 ADP 可诱导体外 PNAs 的形成以及 NETs 的产生，且呈现时间和浓度依赖性，同时 ADP 诱导的血小板活化所产生的 NETs 水平显著高于花生四烯酸诱导的血小板活化所产生的 NETs。
结论 DVT 患者体内 PNAs 的存在与 NETs 的产生密切相关。血小板活化是 PNAs 形成以及 NETs 产生的前提基础。

OR-044

核心抗体定量在乙肝相关慢加急性肝衰竭中的表达水平及与预后的关系

李静[1]、龚启明[2]、谢培琳[1]、林君玉[1]、陈嘉[1]、韦栋[1]、于德敏[1]、韩悦[1]、张欣欣[1]
1. 上海交通大学医学院附属瑞金医院临床病毒室
2. 上海交通大学医学院附属瑞金医院感染科

目的 研究乙肝相关慢加急性肝衰竭（HBV-ACLF）患者血清核心抗体定量（qAnti-HBc）的表达水平及与预后的关系。
方法 选取上海交通大学附属瑞金医院 2014 年 1 月-2019 年 12 月 HBV-ACLF 患者 168 例（88 例为训练集，80 例为验证集），和同期慢性乙型肝炎（CHB）患者 216 例（对照组），比较两组 qAnti-HBc 水平。进一步比较 HBV-ACLF 患者生存组与死亡组 qAnti-HBc 水平，建立预后模型，并在验证集验证。动态观察 16 例 HBV-ACLF 组患者入院后 1 月内，3 月，6 月，9 月，12 月时 qAnti-HBc 的变化。
结果 HBV-ACLF 组血清 qAnti-HBc 水平明显高于 CHB 组。HBV-ACLF 患者中，qAnti-HBc 水平在生存组明显高于死亡组，血清 qAnti-HBc 水平与 MELD 评分呈轻度负相关。HBV-ACLF 组患者中合并其他感染患者相比未合并者血清 qAnti-HBc 水平明显降低；合并肝性脑病患者相比未合并者 qAnti-HBc 水平明显降低；合并肝肾综合征患者相比未合并者 qAnti-HBc 水平明显降低；在有无肝硬化患者中无明显统计学差异。ROC 曲线提示血清 qAnti-HBc 水平对 HBV-ACLF 的预后预测价值与 MELD 评分相当。 进一步建立包含 qAnti-HBc 在内的预测模型，预测价值明显优于 MELD 评分，且在验证组中加以验证。16 例 HBV-ACLF 患者在入院 1 月内 qAnti-HBc 水平无明显变化，3 月时显著下降，6 月时再次下降，后趋于稳定。
结论 HBV-ACLF 患者 qAnti-HBc 水平显著高于 CHB 患者，在 HBV-ACLF 患者中，生存组明显高于死亡组，qAnti-HBc 水平对 HBV-ACLF 患者预后的预测价值与 MELD 相当。随着 HBV-ACLF 患者病情好转，于第 3 月和第 6 个月时明显下降，后趋于稳定。

OR-045

一个基于临床检验的银屑病分型诊断模型

高骞
中南大学湘雅医院

目的 通过调查银屑病患者的临床资料及临床检验，分析相关性，探究临床检验项目在银屑病分型中的作用；选取相关性显著的临床检验项目进行机器学习，建立银屑病分型的预测模型并对模型进行评价。
方法 采用回顾性研究的方法，分析自 2016 年 11 月至 2021 年 3 月于中南大学湘雅医院皮肤科门诊就诊，诊断为“银屑病”患者的临床资料及各项临床检验。以银屑病的不同类型为变量进行与临床检验项目之间的描述性、显著性及相关性分析；最后利用检验项目与疾病类型的高度相关性进行机器学习，建立预测模型。

结果 分析 291 例银屑病患者，PASI（Psoriasis lesions area and severity of the disease index，银屑病皮损面积和病情严重程度指标）评分最低 0.3，最高 48.3，BSA（The surface area of the affected body，受累体表面积）评分最低 0，最高 93，通过 K-W H 检验发现年龄、PTGA（A doctor's general assessment of a condition，医生对病情的总体评估）、BSA 评分、风湿全套检验和皮肤病生活质量评分具有统计学意义，将这些指标并加入一些填充率较高（45%）的项目进行建模，发现分型诊断预测模型效果较好。
结论 在这项研究中可以发现银屑病患者通过一些临床检验指标可以建立预测模型，模型的效能良好，在测试集中可以区分出银屑病的分型情况，由此可见建立的模型可以对免疫性疾病银屑病的分型具有重要作用且效果好，该模型可以用于银屑病分型。

OR-046

Pancreatic stellate cells regulate branched-chain amino acid metabolism in pancreatic cancer

LU QIAO
Tianjin Medical University Cancer Institute and Hospital

Background Pancreatic ductal adenocarcinoma (PDAC) is the most lethal malignancy: it has a 5-year survival rate of less than 9%. Although surgical resection is an effective treatment for PDAC, only a small number of patients can have their tumors surgically removed. Thus, an urgent need to find new therapeutic targets for PDAC exists. Understanding the molecular mechanism of PDAC development is essential for the treatment of this malignancy. This research aimed to study the mechanisms of pancreatic stellate cells (PSCs), which regulate branched-chain amino acid (BCAA) metabolism in PDAC.
Methods Differentially expressed proteins were detected via nanoliquid chromatography coupled to mass spectrometry (nano-LC-MS/MS). Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment methods were used to find the valine-leucine-isoleucine (BCAA) degradation pathway. The levels of BCAAs in the sera and tissues of patients with PDAC were measured by using nuclear magnetic resonance (NMR). The functions of BCAA concentrations and the effects of activated pancreatic stellate cells (aPSCs) were also evaluated by performing Cell Counting Kit-8, colony formation, and wound healing assays.
Results A total of 1,519 proteins with significantly differential expression were discovered in PDAC and adjacent tissues by using nano-LC-MS/MS. KEGG pathway enrichment analysis identified the BCAA degradation pathway. The content of BCAA in PDAC clinical samples was up-regulated. However, the addition of different concentrations of BCAA to PDAC cell culture medium failed to promote the proliferation and migration of PDAC cells. Given that analysis based on The Cancer Genome Atlas database showed that the number of aPSCs gradually increased with the progression of PDAC, the effects of aPSCs on PDAC cells were explored. After coculture with aPSCs, PDAC cell proliferation showed a significant increase, and the proteins involved in the BCAA degradation pathway in PDAC cells had also changed.
Conclusions aPSCs could regulate BCAA metabolism to enhance the progression of PDAC, indicating that the regulation of BCAA metabolism may serve as a new therapeutic direction for PDAC.

OR-047

lncRNA profiles enable prognosis prediction and subtyping for esophageal squamous cell carcinoma

Shujun Zhang、Chuanxin Wang
The Second Hospital of Shandong University

Objective Esophageal Cancer (EC) ranks seventh and sixth in terms of incidence and mortality in the world, respectively. Although various therapies are used to treat EC, the long-term outcome is still dismal. The prognostic power of traditional prognostic factors such as sex, smoking and alcohol history are very limited. Therefore, Novel prognostic markers might be helpful for better clinical outcome prediction. Growing evidence has suggested that lncRNA profiles can provide important prognostic information for patients with cancer. We aim to explore the role of lncRNA in EC prediction and subtyping.

Method We used publicly available TCGA RNA-seq expression data and focused on evaluating the potential usefulness of lncRNA markers for EC surveillance and the efficacy. We first identified EC-specific lncRNA signatures by DESeq2 package. Then, we applied Kaplan-Meier (KM) method combined univariate cox proportional hazards regression (UniCox) method to single out prognostic lncRNAs. Combined the differential and prognostic lncRNAs, we develop a prognostic model using cox stepwise regression analysis. Time-dependent ROC for 3-year and 5-year survival were predicted by lncRNA model, TNM stage, lymph node metastasis, distant metastasis, and all combined. We further generated a lncRNA-based molecular classification of EC using an unsupervised clustering method (k-means). Last, we found that a novel lncRNA AC007128.1 was upregulated in both EC cells and tissues, associated with poor prognosis. And we validated the biological role of a novel lncRNAs AC007128.1 by cellular assays in EC progression.

Results 257 upregulated and 165 downregulated lncRNAs were identified by DESeq2 package based on TCGA RNA-seq data. 413 prognostic lncRNAs was single out based on Kaplan-Meier method combined UniCox method. Combined the differential and prognostic lncRNAs, a total of 13 overlapping lncRNAs were selected as candidate biomarkers for EC. 13 lncRNAs were subjected to cox stepwise regression analysis and find an optimal model with 11 lncRNAs. Kaplan-Meier curves showed that the high risk-score group was significantly related to EC patients' poor prognosis. Patients with high risk score prognostic s had more deaths than low-risk-score patients.The obtained prognostic prediction model could effectively predict the 3-year and 5-year prognosis and survival of patients with EC by time-dependent ROC (area under curve = 0.87 and 0.89, respectively). The model had better ability to predict prognosis compared with clinical prognostic factors. The combination of lncRNA model and clinical characteristics improved the ability to predict 5-year prognosis (AUC=1.00). Multivariate Cox regression analysis indicated that the prognostic model was an independent factor of survival for EC. In the analysis of subtype, we used 111 EC patients in TCGA as training dataset, and obtained two clusters of EC samples with 50 lncRNAs that were different between the clusters and with significantly association with race and barretts esophagus (BE) (both $P<0.001$). We also verified the robustness of 50 lncRNAs in another independent dataset from GEO (GSE53625). Last, we found that a novel lncRNA AC007128.1 was upregulated in both EC cells and tissues, associated with poor prognosis, and could promote EC cell epithelial-mesenchymal transition (EMT) by increasing activation of MAPK/ERK and MAPK/p38 signaling pathways.

Conclusion by using lncRNA expression profiles, we construct an 11 lncRNA prognostic model with high ability to predict prognosis, and generate lncRNA-based subtypes of EC with high robustness. We also have demonstrated a significant upregulation of AC007128.1 in EC tumor and cell lines and association with poor survival in EC patients. Mechanistic analysis demonstrated that AC007128.1 may function to promote cancer cell EMT by aberrantly activating MAPK signal pathway.

OR-048

Four Familial Hypercholesterolemia causing LDLR mutations were identified using the Next Generation Sequencing based laboratory developed sceening test

Shitong Cheng、Xiaoxu Han
The First Affiliated Hospital of China Medical University

Objective To establish an appropriate genetic screening protocol for Familial hypercholesterolemia (FH) that can be used in clinical laboratories and to explore the FH mutation spectrum in Shenyang.
Methods Firstly, a Next Generation Sequencing (NGS) based laboratory developed test (LDT) was established. The customized sequencing panel was designed to cover the exonic regions of 24 lipid metabolism related genes. Then, the clinical records of 41803 patients whose blood lipid profile had been tested during the period from Nov.11, 2019 to Jan. 13, 2020 in the First Affiliated Hospital of China Medical University were investigated and 18 patients were clinically diagnosed as Definite FH according to the Dutch Lipid Clinical Network Criteria (Chinese Revised Version) (DLCN-CRV) established by Shi et al. The whole blood samples of 16 (out of 18) definite FH patients were collected following by the DNA extraction and NGS for screening, In-silico analyses (including SAMtools and ANNOVAR) for identifying the pathogenic mutations according to the ACMG criteria and finally the Sanger Sequecing for confirmation.
Results The prevalence of FH was found to be 0.043% for the 41803 individuals mentioned above according to the DLCN-CRV Criteria (grade>8) and 5/16 (31.25%) definite FH patients were confirmed carrying FH pathogenic mutations (ACMG Class 4 or above), including LDLR(NM_000527): exon12: c.C1783T: p.R595W, exon4: c.T493G: p.W165G, exon13: c.G1879A: p.A627T, and exon4: c.G682T:p.E228X. In addition, one Familial Combined Hypercholesterolemia pathogenic mutation (LPL(NM_000237): exon9: c.C1421G: p.S474X, ACMG Class 4) and one Statin response related genetic variant (SLCO1B1(NM_006446): exon6: c.T521C: p.V174A) were also identified using the LDT protocol, as well as five possible FH pathogenic mutations (ACMG Class 3, including APOB(NM_000384): exon12: c.C1594T: p.R532W, exon26: c.C10579T: p.R3527W, exon29: c.G12809C: p.R4270T and LDLR(NM_000527): exon10: c.G1432A: p.G478R, exon7: c.1060+7T>C) and three variants (APOA5(NM_001166598): c.*158C>T, EPHX2(NM_001256483): exon7: c.G662A: p.R221Q, USF1(NM_001276373): c.*187C>T) considered as risk factors for dyslipidemia. All genetic variants screened by the LDT protocol were then confirmed using Sanger Sequencing with a positive rate of 100%.
Conclusion The NGS based FH genetic screening protocol was reliable and could be used in the clinical laboratories to improve the rate of FH identification and to expand the local FH pathogenic mutation spectrum. More effort will be needed to discover the appropriate target population in order to make the screening test more cost-effective.

OR-049

miR-133b targets NCAPH to promote β-catenin degradation and reduce cancer stem cell maintenance in non-small cell lung cancer

Qiuxia Xiong、Yong Duan
The First Affiliated Hospital of Kunming Medical University;Yunnan Key Laboratory of Laboratory Medicine;
Yunnan Institute of Experimental Diagnosis

Non-small cell lung cancer (NSCLC), one of the most common lung cancers, is well known to have diverse pathological features. Although many signaling pathways and therapeutic targets have been defined to play important roles in NSCLC, limiting efficacies have been achieved. Here, we identified that non-SMC condensin I complex subunit H (NCAPH), which is highly expressed in NSCLC, correlates with worse clinical outcome. We found that NCAPH is increased in cancerous cell lines (H1299, A549, H1975, SPC-A1, H838 and GLC-82) than that in normal human bronchial epithelium cell line (BEAS-2B), and NCAPH knockdown inhibits cell proliferation and migration. Furthermore, we validated that miR-133b directly targets NCAPH, and that miR-133b is downregulated in both cancerous cell lines and peripheral blood serum isolated from NSCLC patients. Forced expression of miR-133b inhibits the proliferation, migration and xenograft tumor formation abilities of tumor cells. In addition, mechanistic study showed that NCAPH promotes cancer stem cells (CSCs) maintenance in NSCLC through inhibiting Akt1-mediated phosphorylation and degradation of □-catenin proteins, which in turn leads to suppressed Wnt signaling activity and tumorigenesis. In summary, our findings reveal the critical role of miR-133b/NCAPH axis during NSCLC progression, indicating that miR-133b or NCAPH can be used as novel therapeutic targets in the future.

OR-050

基于轮状催化发夹组装和框架杂交链反应的无酶扩增策略灵敏检测循环肿瘤 DNA

罗世华、张晔、黄国妮
南方医科大学南方医院

循环肿瘤 DNA (circulating tumor DNA, ctDNA)作为一种理想的液体活检生物标志物候选，在肿瘤的非侵入性诊断中发挥着重要作用。ctDNA 的准确分析对促进临床应用具有重要意义。为此，我们开发了一种轮状催化发夹组装(WCHA)和框架杂交链反应(FHCR)的新型 ctDNA 电化学生物传感器。ctDNA 通过立足点链位移与 DNA 传感器结合，释放引发剂促进 WCHA 的循环扩增，与固定在金电极表面的捕获探针杂交形成大量的轮状 DNA 产物。此外，还设计了亚稳态哑铃探针(DSH1 和 DSH2)用于杂交链反应。与传统的 HCR 相比，这种新型的 HCR (FHCR)可以折叠更致密的 DNA 纳米结构，大大降低了空间电位电阻，提高了电子传输能力。双信号扩增策略(WCHA/FHCR)的结合显著提高了 ctDNA 检测的灵敏度，使检测限(LOD)低至 8.3 fM。更重要的是，该方法成功地应用于临床样本的分析，具有有效的分类器，AUC 为 0.909，对乳腺肿瘤的诊断灵敏度为 86.7%，特异性为 80.0%。因此，该平台在生物分析和临床诊断方面具有巨大的潜力。

OR-051

脑脊液的宏基因组测序技术用于诊断神经外科与脑室外引流和腰椎引流相关性脑室炎和脑膜炎

钱玲烨[1]、史一君[1]、李方强[1]、王玉飞[1]、马淼[1]、张艳芳[1]、邵阳[2,3]、郑光辉[1]、张国军[1]
1. 首都医科大学附属北京天坛医院
2. 南京迪飞医学科技有限公司
3. 南京医科大学公共卫生学院

宏基因组二代测序技术 (mNGS) 目前已成为一种广泛应用的可以快速准确检测感染病原体的技术。本研究是一项于 2019 年 2 月至 2019 年 9 月在中国最大的临床神经外科中心之一开展的大队列前瞻性研究。本研究旨在评估神经外科患者脑脊液的 mNGS 检测对脑室外引流和腰椎引流相关性脑室炎和脑膜炎(external ventricular and lumbar drainage-associated ventriculitis and meningitis, EVD/LD-VM) 的诊断价值。我们收集了神经外科滞留 EVD/LD 超过 24 小时的患者脑脊液标本进行常规微生物培养和 mNGS 检测。并探讨了脑脊液 mNGS 对 EVD/LD-VM 的诊断价值。共有 102 名患者被纳入本研究，并分为三组，包括确定感染组 (confirmed VM, cVM) (39) 、疑似感染组 (suspected VM, sVM) (49) 和无感染组 (non-VM, nVM) (14)。在所有患者中，mNGS 共检测到 21 株革兰阳性菌，20 株革兰阴性菌和 5 株真菌。检出的三种主要细菌分别为表皮葡萄球菌 (9) 、鲍曼不动杆菌 (5) 和金黄色葡萄球菌 (3) 。证实 EVD/LD-VM 的 mNGS 阳性符合率为 61.54% (24/39)，在 nVM 组中 mNGS 阴性符合率为 100% (14/14) 。cVM 组中有 15 例 VM 的感染病原菌未被 mNGS 鉴定出，包括 8 例 mNGS 结果阴性，7 例 mNGS 结果与常规微生物鉴定结果不一致。此外，对 22 例常规方法检测为阴性的患者进行了 mNGS 检测并成功鉴定出病原体，其中有 10 例患者获得了及时有效的临床治疗，这也显示了 mNGS 在指导 EVD/LD-VM 治疗的优势。

OR-052

The Emergence of Multidrug-Resistant Candida haemulonii : Using Whole-Genome Sequencing to Describe the Population Structure

Xinfei Chen、Xin Hou、Meng Xiao、Xinmiao Jia、Yingchun Xu
Peking Union Medical College Hospital

Background The emergence of a multidrug-resistant yeast, *Candida auris*, has drawn attention to the closely related species from the *Candida haemulonii* complex includeing *C. haemulonii*, *C. duobushaemulonii*, *C. pseudohaemulonii*, and *C. haemulonii var. vulnera.* The goal of this study was to investigate the genetic relationships and drug-resistance profiles among isolates of the *C. haemulonii* from different cities and to examine possible evidence of transmission if it existed.
Materials/methods The 61 *C. haemulonii* isolates causing invasive fungal diseases were collected from twenty three tertiary hospitals through CHIF-NET. We used antifungal susceptibility testing and whole-genome sequencing (WGS) to investigate drug resistance and genetic diversity among isolates of *C. haemulonii* from different geographic areas of China.
Results Between 2010 and 2017, 61 isolates of *C. haemulonii* from China; In the China, 69% of *C. haemulonii* was isolated from blood, and other invasive sites (Table 1). Phylogenetic analysis using SNPs called against the *C. haemulonii* reference strain BMU05228. Genetic relationships among *C. haemulonii* isolates are shown in (Figure 1). The average pairwise difference between the isolates was 347 SNPs (range 6–581), and there was distinct phylogeographic population structure. Most isolates were different from each other by fewer than 57 SNPs and formed some small, well-supported cluster in the phylogenetic tree based on bootstrap analysis. Three isolates, F4450, F4454, and F4456, were different from each other by fewer than 10 SNPs. These three

isolates were recovered from different patients treated at the same hospital in Shanghai. In addition, five isolates from Nanjing，F4474, F4486, F4500, F4516, F4518, differed by fewer than 45 SNPs recovered from same hospital. We observed variable levels of susceptibility to amphotericin B among 61 tested C. haemulonii isolates: 48 (79%) had elevated MICs from 2μg/mL to >8μg/ ml, and the rest had MICs below 2μg/ml. All isolates had elevated MICs of fluconazole ranging from32 to 256μg/ml (Table 2).
Conclusions Our results indicate that, although we are not observing the widespread of the *C. haemulonii*, at least these isolates can be transmitted within a healthcare facility and may cause healthcare associated outbreaks.

OR-053

外周血宏基因组二代测序对血液病患者肺孢子菌感染的诊断价值

徐春晖[1,2]、许颖出[2]、朱国庆[1]
1. 中国医学科学院血液病医院（中国医学科学院血液学研究所）
2. 中国医学科学院血液病医院 协和博精实验室

目的 探讨血液病患者外周血宏基因组二代测序技术在耶氏肺孢子菌肺炎诊断和治疗中的应用价值，为该类患者肺孢子菌感染的诊治提供依据。
方法 回顾性分析中国医学科学院血液病医院 2020 年 6 月 10 日至 2021 年 6 月 10 日采用外周血进行二代测序检出的耶氏肺孢子菌肺感染患者的实验室和临床特征，分析外周血病原二代测序对血液病患者合并该类真菌感染的应用价值。
结果 1 年内共 242 位患者送检外周血病原二代测序检测， 11 位患者检出肺孢子菌，检出率为 4.5%。11 例患者中男性 4 例（36.4%），中位年龄 38（2-57）岁。4 例为急性髓系白血病，4 例急性淋巴系白血病，1 例再生障碍性贫血，1 例骨髓增生异常综合征，1 例自免溶贫，其中 10 例患者发病前有糖皮质激素用药史。临床表现主要为发热（100%,11/11）、血氧饱和度减低（81.8%，9/11）、咳嗽(3/11,27.3%)等。除 1 例患者未进行影像检查外，其余患者均表现为肺间质纹理增多，磨玻璃样改变。实验室数据显示，11 例患者的白细胞中位数为 2.9（0.3-12.0）×109 /L，粒缺期患者占 9.1%（1/11）。使用糖皮质激素患者中共 6 例患者进行了 CD4 细胞计数检测，均低于正常值，中位数为 153（5-227）cells/μL。 1,3-β-D-葡聚糖增高见于 36.4%（4/11）的患者，11 例患者乳酸脱氢酶均有增高，中位数为 406（256.4-946.8）U/L。二代测序检出耶氏肺孢子菌序列的中位数为 2（1-184）条。10 例患者应用磺胺甲噁唑/甲氧苄啶治疗，9 例好转，接受治疗患者的平均发热时间为 8（4-17）天，无死亡病例。
结论 血液病患者外周血二代测序检出肺孢子菌具有较高的临床符合度，其创伤性小、报告周期短的特征可作为无法进行支气管镜检查和肺泡灌洗患者肺孢子菌感染的诊断方法之一。

OR-054

在肺活检组织中使用 mNGS 鉴定肺部感染病原体的性能研究

郭一凡、李荷楠、王辉
北京大学人民医院

背景 宏基因组下一代基因组学 (mNGS) 具有改善肺部感染病原体鉴定的潜力。关于 Illumina 和 Nanopore 平台对肺活检组织的诊断性能的报告很少见。
方法 2018 年 7 月至 2020 年 5 月，收集 140 份肺活检组织，应用临床微生物学检测和 mNGS（Illumina 和 Nanopore 平台）进行病原体鉴定。基于 Illumina 结果计算肺部菌群多样性。
结果 我们基于 Illumina 结果检测了 α 多样性，与不确定感染患者相比，检出病原体患者的 shannon 多样性显着降低。下呼吸道感染 (LRTIs) 患者的 α 多样性显着低于癌症患者。与临床综合

判定结果相比，Illumina 的灵敏度为 77.55%，特异性为 97.62%，阳性预测值（PPV）为 95.00%，阴性预测值（NPV）为 88.17%。然而，Nanopore 的灵敏度为 34.69%，特异性为 98.65%，PPV 为 94.44%，NPV 为 69.52%。Illumina 中，细菌和真菌 cutoff 为 3516.21 和 1987.85，对于 Nanopore，cutoff 为 57 和 30。Illumina/Nanopore 平台可以比临床微生物检测更多的真菌，但对结核分枝杆菌的诊断性能较弱。

结论 α 多样性可以作为诊断不同类型疾病的指标。Illumina 平台的阴性符合率更高，比传统微生物检测鉴定出更多的真菌病原体。对于高人类背景标本时，应在湿实验过程中优化 Nanopore 流程。我们首先确定了肺活检组织的 cutoff，这可能是临床诊断的一种有前途的标本类型。

OR-055

基于全基因组测序技术的碳青霉烯耐药肺炎克雷伯菌毒力溯源

王若冰、王辉
北京大学人民医院

目的 近年，越来越多的报道发现碳青霉烯耐药肺炎克雷伯菌携带了毒力基因。这意味着治疗肺炎克雷伯菌感染不仅面临大多数抗生素不起作用，还会对人体造成毒力较大的严重损伤。为此，我们借助第三代测序技术，通过获得碳青霉烯耐药肺炎克雷伯菌的完整毒力质粒数据，探索耐药菌株的毒力质粒来源。

方法 对我国流行的 ST11 型肺炎克雷伯菌进行三代测序，获得包括质粒在内的全基因组数据。下载公开数据库中的菌株序列及其相关菌株信息，整合为信息较为完整的数据集。对这些序列进行 MLST、毒力基因、血清型、耐药基因的鉴定等注释，选择血清型为 K1、K2、K47 和 K64 的菌株，用毒力基因定位毒力序列，随后构建毒力序列基于时间的系统发育树。

结果 从 9738 条非重复肺炎克雷伯菌的全基因组数据中筛选出 256 株 ST11 型肺炎克雷伯菌、毒力质粒 205 个和 217 条毒力序列。发现大多数 K1、K2 和 K64 型菌株的毒力序列相似程度较高，ST11-K64 型的毒力质粒类型以 IncHI1B(pNDM−MAR)/repB 为主。从中随机选择一株与经典 ST23-K1 型高毒力肺炎克雷伯菌相似的 ST11-K64 型的碳青霉烯耐药肺炎克雷伯菌的毒力序列作为参考序列，在数据集中寻找与之相似的毒力序列并做有时间尺度的系统发育分析。系统发育树显示 ST11-K64 型肺炎克雷伯菌的毒力质粒与 ST23-K1 型的同源，推断 ST11-K64 型菌株的毒力质粒可能是由 ST23-K1 型菌株的毒力质粒演变而来。

结论 我国流行的 ST11 型碳青霉烯耐药肺炎克雷伯菌可能从 ST23 型经典高毒力肺炎克雷伯菌中获得了毒力质粒，演变为毒力更强的耐药株。

OR-056

A liquid chromatography-tandem mass spectrometry (LC-MS/MS)-based assay for simultaneous quantification of aldosterone, renin activity, and angiotensin II in human plasma

Fangjun Chen、ZI-YUN CHEN、YING-FEI PENG、ZHEN-XIN WANG、BEI-LI WANG、BAI-SHEN PAN、WEI GUO
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University

Accurate quantification of plasma aldosterone (ALD) and renin activity (PRA) is critical for the diagnosis of primary aldosteronism (PA). Liquid chromatography-tandem mass spectrometry (LC-MS/MS) is considered the “gold standard” method for the determination of ALD and PRA. The aim of this study is to develop a new LC-MRM/MS assay for quantifying plasma ALD, PRA, and

angiotensin II (Ang II) simultaneously and validate its effectiveness. To be more specific, plasma samples were prepared by solid-phase extraction and separated in an ultra-performance reversed-phase column. MS detection was performed via a triple quadrupole mass spectrometer containing both positive and negative ion monitoring modes. The developed assay was then validated according to the standard guidelines and the influence of sample incubation on ALD and Ang II concentration was evaluated. In addition, the variation of endogenous Ang I was explored. The proposed LC-MRM/MS method was compared another LC-MS/MS method, which detects ALD, Ang I, and Ang II separately. Analytes were separated and quantified within 5 min. The assay was validated to be linear up to 5000 pg/ml for ALD and Ang II and 33.3 ng/ml/h for PRA. The lower limit of quantification (LLOQ) was 15 pg/ml, 15 pg/ml, and 0.1 ng/ml/h for ALD, Ang II, and PRA respectively. Specificity, precision, accuracy, and stability were tested to meet the requirements of the guidelines. Significant changes were not found in ALD and Ang II concentrations over the 3h-incubation. In addition, it was demonstrated that the result of PRA was not strongly influenced by the endogenous Ang I. Comparison with another LC-MS/MS method was performed using the same apparatus and the proposed method was proved to be in good coincidence with the correlation coefficients ranging from 0.955 to 0.996. A sensitive and reliable method for simultaneous quantification of ALD, PRA, and Ang II has been developed and this study will significantly promote laboratory workflow efficiency and throughput.

OR-057

基于发光 QDs 的选择性识别和 Ce3+的配位聚合的可视化和双荧光均相传感器用于临床甲亢样品中焦磷酸酶的检测

陈飘飘、应斌武
四川大学华西医院

目的 现有医学分子诊断技术主要是依靠单个信号分子实现目标物的定量，且难以可视化读取。该体系致力于①使用双荧光信号分子，定量一种分析物，提高方法的准确性；②将发光纳米材料引入医学诊断中，实现可视化 POCT 分析；③以焦磷酸酶（PPase）为例，在考察其作为甲亢疾病标志物的潜在性的同时，验证该体系的分析性能。

方法 该方法主要是基于两个选择性识别反应：①CdTe QDs 选择性识别 Cu2+和 PPi-Cu2+-PPi 复合物（PPi，焦磷酸盐），以及②Ce3+选择性识别 PPi 和其它磷酸盐。如图 1 所示为 PPase 的分析原理图，利用 PPase 水解 PPi 生成 Pi（磷酸），而 Pi 对 Cu2+无络合力，以及 Pi 对 Ce3+荧光信号产生可忽略的影响的现象，可轻松构建 PPase 的双荧光信号均相可视化分析策略。

结果 该方法可实现 0.15 U/L 浓度级别 PPase 的准确定量，肉眼可显著区分 5 U/L 焦磷酸酶和空白溶液。已在 53 例临床甲亢病人血清样品上进行了验证，与临床甲亢诊断结果一致。使用 PPase 为甲亢标志物，其诊断准确率达 100%，具有较好的可靠性和临床应用价值。此外，我们推荐以 500 U/L PPase 含量为甲亢病人诊断的临界值。

结论 该方法无论在分析速度和通量（1 小时内），分析成本（单次检测成本低于 1 元）、分析操作（均相分析，仅仅需要将反应物质混合，不需要专业研究人员）上均显著优于现有方法。

OR-058

Serum glycated albumin can serve as a good indicator of early diabetic nephropathy

Yunlai Liang[1]、ying liu[2]、kangkang huang[1]、kun wang[1]、jingzhong liao[1]、bin yi[1]
1. Xiangya Hospital of Central South University
2. 中南大学湘雅医学院

Object To explore the clinical application of GA in EDN diagnosis.
Methods 119 patients with T2DM and 36 healthy subjects were enrolled from Xiangya Hospital of Central South University and classified into 4 groups: healthy group, T2DM group (UACR < 30mg/g), early diabetic nephropathy group (30mg/g < UACR < 300mg/g) and advanced diabetic nephropathy group (UACR < 300mg/g). SPSS25.0 was used for statistical analysis.
Results The EDN group showed significantly higher GA values compared with the other 3 groups. The correlation analysis showed GA was negatively correlated with ALB and positively correlated with HbA1C in EDN group. Multivariate linear regression found GA was influenced by HbA1C, BMI and ALB. GA, TG and HLR were identified by univariate logistic regression analysis as independent variables that predicted the presence of EDN. ROC analysis found GA had the largest area under the curve (AUC = 0.800, CI 0.727 - 0.960, P < 0.01) among all indexes. Combined diagnosis of EDN by GA, GFR and age was the optimum scheme (AUC = 0.833, CI 0.758 - 0.907, P < 0.01). Interestingly, it exhibited better diagnostic efficacy in female patients. Finally, GA, GFR and age were eventually introduced by discriminant analysis and optimal discriminant formula was Y = 0.195X1 + 0.323X2 + 1.048X3 (X1 = GA, X2 = Age, X3 = GFR), which classifued 75% of patients with T2DM, 42.9% of patients with EDN and 76.6% of patients with ADN correctly.
Conclution GA might be a potential molecular marker for the diagnosis of EDN.

OR-059

Determination of tryptophan and its 9 metabolites in fluid from the anterior chamber of the eye in patients with glaucoma by ultra-high performance liquid chromatography-mass spectrometry

Lin Li[2]、Kecheng Li[1]、Honglang Huang[1]、Wenna Liu[1]、Ting Zhang[1]、Yuheng Cheng[1]、Haibo Wang[1]、Liangmin Chuan[1]、Li Jiang[1]
1. Sichuan Academy of Medical Sciences & Sichuan Provincial People's Hospital
2. 电子科技大学附属医院·四川省人民医院

Objective Tryptophan (Trp) is to an essential amino acid and its metabolites are significant to human health. The dysregulation of Trp is implicated in diseases such as cancer, neurodegenerative (i.e. glaucoma) and auto immune disorders. The objective of this study was to measure the levels of Trp metabolites in the anterior chamber of the eye of both primary open-angle glaucoma (POAG) and primary angle-closure glaucoma (PACG), and to help elucidating the involvement of these metabolites in the disease pathology.
Methods Ultra-high performance liquid chromatography-mass spectrometry (UPLC-MS/MS) was used to measure the levels of Trp and its 9 major metabolites, namely kynurenine (Kyn), kynurenic acid (KYNA), 3-hydroxy kynurenine (3-OH Kyn), xanthurenic acid (XANA), 3-hydroxy anthranilic acid (3-OH AA), picolinic acid (PICA), quinolinic acid (QUIA), serotonin (5-HT) and melatonin (Mel) in fluid from the anterior chamber of the eye of 50 POAG, 50 PACG and 50 cataract patients. The analysis was carried out on a Waters ACQUITY UPLC HSS T3 (100×2.1mm, 1.8μm) column using gradient elution mode. For quantitative determination, Trp-d5,

Kyn-C13, KYNA-d5, 3-OH Kyn-C13N15, XANA-d4, 3-OH AA-d3, PICA-d3, QUIA-d3, 5-HT-d4 and Mel-d4 were used as an internal standard.
Results The method was linear in the concentration range 10.29-2058.00 ng/mL for Trp, 5.40-1080.00 ng/mL for Kyn, 0.38-76.88 ng/mL for KYNA, 5.24-1048.00 ng/mL for 3-OH Kyn and XANA, 5.63-1125.00 ng/mL for 3-OH AA, 9.42-1884.00 ng/mL for PICA, 5.22-1044.00 ng/mL for QUIA, 5.30-1060.00 ng/mL for 5-HT and 0.22-44.04 ng/mL for Mel. The mean recoveries measured at 3 concentration levels for Trp, Kyn, KYNA, 3-OH Kyn, XANA, 3-OH AA, PICA, QUIA, 5-HT and Mel were all within the range of 91.3-107.4%. The intra-day precision parameters were smaller than 6.4%. The developed method was applied to study the level of Trp, Kyn, KYNA, 3-OH Kyn, XANA, 3-OH AA, PICA, QUIA, 5-HT and Mel in the anterior chamber of the eye in POAG, PACG and cataract patients (n = 50). The results showed that the levels of Kyn, KYNA, 3-OH-Kyn were significant higher in glaucoma patient group (especially PACG) than those of cataract patient group ($P<0.05$), while the other analytes showed no significant difference among POAG, PACG and cataract patient groups.
Conclusion A UPLC-MS/MS method was successfully developed for the quantification of Trp and its 9 metabolites in the anterior chamber of the eye of POAG, PACG and cataract patients.

OR-060

Exploration of Potential Biomarkers of Anthracycline-induced Cardiotoxicity Based on Targeted Amino Acid Metabolomics

Wendi Li、Ming Su、Zhenju Cao、Mei Jia
Peking University People's Hospital,

Objective Anthracyclines have become the cornerstones of cancer chemotherapy due to their significant anti-cancer effects. Although anthracyclines improve the long-term survival rate of cancer patients, severe and irreversible myocardial damage limit the clinical applications. Amino acids (AAs) play a critical role in protein synthesis, regulation, and energy metabolism in the function of cardiomyocytes. AA metabolism disorder will be caused when cardiomyocytes are seriously damaged. We can further explore the mechanism of anthracycline-induced cardiotoxicity by studying AA metabolism. In the present study, we established adriamycin (ADR)-induced cardiac injury models. By using targeted AA metabolomics, we screened the changes of AA metabolism in order to find potential biomarkers of anthracycline-induced cardiotoxicity.
Methods Fifteen C57BL/6 male mice were randomly divided into control group (n=7) and ADR group (n=8). Mice in ADR group were intraperitoneally injected with ADR 15 mg/kg to establish anthracycline-induced cardiotoxicity model. Echocardiography was performed to determine the cardiac function. H9c2 cells were treated with 1μM ADR for 18 hours and the culture medium supernatant samples were collected. A targeted AA metabolomics approach based on UPLC-MS/MS was established to detect the serum and culture medium supernatant samples. Multivariate statistical analysis was performed using Simca-P 14.1, and the integral differences of metabolic profiling were described by orthogonal partial least squares discriminant analysis (OPLS-DA). The AA profiles of ADR groups and control groups were analyzed using multivariate statistical analysis with significant alterations identified through Student-t test and variable importance in projection (VIP). Metabolites that satisfied both VIP > 1.0 and $p < 0.05$ were identified as candidate biomarkers.
Results Compared with the control group, ADR-treated mice showed significant decrease of ejection fraction (EF%), indicating that the ADR induced a significant cardiac injury. We found that there were 14 AA metabolites changed in the serum samples of ADR-treated mice, including 10 increased and 4 decreased. There were 15 AA metabolites changed in the medium supernatant of ADR treated H9c2. OPLS-DA analysis showed that the ADR groups could be clearly separated from the control groups, indicating that significant AA metabolism changes occurred after ADR

treatment. Nine AAs including L-glutamic acid, L-lysine, L-serine, L-tryptophan, L-methionine, L-histidine, L-asparagine, L-tyrosine, O-phosphorylethanolamine and five AAs including L-tyrosine, L-alanine, L-glutamine, L-serine, L-glutamic acid with VIP > 1 and $p < 0.05$ were selected as potential biomarkers of serum and medium supernatant samples, respectively. By using overlap analysis, we found that L-glutamate, L-serine and L-tyrosine were increased in the two models, suggesting that a possible mechanism of AA utilization impairment during anthracycline-induced cardiotoxicity.

Conclusion A targeted amino acid metabolomics approach based on UPLC-MS/MS detection can be used to explore the biomarkers and mechanism of anthracycline-induced cardiotoxicity and provide new clues for the prevention and treatment of anthracycline cardiotoxicity in the early clinical stage.

OR-061

PD-1+ CXCR5+CD8+ T 细胞在肾移植物失功中作为诊断标志物的应用

樊吉文、严琳、万正利、李亚梅、李壹
四川大学华西医院

目的 肾移植是肾病终末期最理想的治疗方式，而移植物失功是肾移植常见的并发症之一，其中导致其发生的最主要原因是抗体介导的排斥反应。有研究表明，PD-1+CXCR5+CD8+ T 细胞表现出滤泡辅助性 T 细胞的作用，具有免疫调节功能，并受到 STAT5 负调控。我们以肾移植患者为研究对象，通过分析 CD8+CXCR5+T 细胞频率及信号传导子及转录激活子 4（STAT4）、信号传导子及转录激活子 5（STAT5）和程序性死亡受体 1（PD-1）的表达，探讨其在肾移植患者移植物失功中的作用。

方法 纳入曾在四川大学华西医院行肾移植术的 82 例患者，收集研究对象的基本资料，包括年龄、性别、BMI、移植时间、生化检查、病理活检结果等，并收集全血标本做横断面分析，使用流式细胞术分析测定 CD8+CXCR5+T 细胞频率及 STAT4、STAT5 和 PD-1 等的表达，以 eGFR =60ml/min 为界限分为慢性移植肾功能减退（CAD）组（eGFR< 60ml/min）和肾功能正常组(eGFR> 60ml/min)，根据病理活检结果分为抗体介导的排斥反应（AMR）和 T 细胞介导的排斥反应（CMR）两组，使用 SPSS 分析 CD8+CXCR5+T 细胞的频率及 STAT4、STAT5 和 PD-1 的表达与移植物失功的相关性及 PD-1+CXCR5+CD8+ T 细胞诊断肾移植失功和抗体介导的排斥反应的 ROC 曲线。

结果 根据肾功分组且排除药物影响后，CXCR5/CD3CD8 在肾功正常组显著高于慢性移植肾功能减退组（P<0.05），STAT4/CD8CXCR5、STAT5CXCR5/CD3CD8 在肾功正常组显著高于慢性移植肾功能减退（P<0.05）， PD -1/CD8CXCR5 在慢性移植肾功能减退组表达显著高于肾功正常组（P<0.05）。根据病理类型分组后，CXCR5PD-1/CD3CD8 在 AMR 组显著高于 CMR 组（P<0.05）、PD-1/CD8CXCR5 在 AMR 组显著高于 CMR 组（P<0.05）。PD-1+CXCR5+CD8+ T 细胞诊断 CAD 的 AUC 为 0.647，PD-1+CXCR5+CD8+ T 细胞诊断 AMR 的 AUC 为 0.742。

结论 PD-1 高表达于移植物失功组和抗体介导的排斥反应组，且 CD8CXCR5 上 STAT5 和 STAT4 的表达在移植物失功组中明显下调，PD-1+CXCR5+ CD8+T 细胞可能促进抗体产生，参与体液反应，且 PD-1+CXCR5+CD8+ T 细胞诊断 AMR 的诊断效能较好。因此，PD-1+CXCR5+CD8+ T 细胞在移植物失功中可作为诊断标志物帮助诊断 AMR。

OR-062

GPR56 及颗粒酶 B 在肺癌患者 T 淋巴细胞中的共表达及其临床价值研究

刘忱[1]、刘天赐[1]、曾星月[1]、王平章[2]、王辉[1]
1. 北京大学人民医院
2. 北京大学医学部基础医学院

目的 本项目旨在研究 GPR56 在肺癌患者外周血 T 淋巴细胞中的表达情况，分析 T 细胞中 GPR56 的表达与肺癌分类分期等的关系，从临床角度探讨 GPR56 在肺癌中的表达变化及其潜在诊断价值。
方法 使用生物信息学方法分析 GPR56 在淋巴细胞中的差异性表达情况，通过虚拟分选的方法分析同 GPR56 表达相关的分子。收集 68 位肺癌患者和 29 位健康对照组(HC)的外周血，采用流式细胞术分析 CD4 和 CD8 细胞的 naïve（CCR7+CD45RA+）、记忆(CCR7+CD45RA-Tcm 以及 CCR7-CD45RA-Tem)和效应(CCR7-CD45RA+)细胞亚群中 GPR56 表达比例，比较不同分类分期肺癌患者 CD4 和 CD8 细胞中 GPR56 相关亚群的比例变化，并利用 ROC 曲线来探索 GPR56 对肺癌的潜在临床诊断价值。
结果 GPR56 在 T 淋巴细胞中具有显著的差异性表达趋势，虚拟分选预测其与颗粒酶 B 表达相关。细胞学研究表明 GPR56 与颗粒酶 B 在 CD4 和 CD8 细胞中均具有显著共表达。与健康对照相比，肺癌患者 GPR56 表达水平升高。肺癌患者外周血中的 Tem 细胞比例显著升高，而 T naïve 细胞显著降低；GPR56 在肺癌患者的 CD4+T em 细胞和 CD8+Teff 细胞表面显著升高。肺鳞癌患者 T 细胞中 GPR56+占比显著高于健康对照；GPR56 的表达随着肺癌 TNM 分期而呈现上调趋势。颗粒酶 B 在肺癌患者和健康对照的外周血的表达均与 GPR56+以及 GPR56+Granzyme B+细胞的变化趋势一致。ROC 曲线分析表明了 GPR56+、Granzyme B+以及 GPR56+Granzyme B+细胞水平对于肺癌具有潜在的辅助诊断价值。
结论 肺癌患者中的 GPR56 和颗粒酶 B 显著共表达，提示其发挥作用可能与颗粒酶 B 有关，并且对肺癌具有潜在诊断价值，可用于肺癌发病以及疾病进展恶性程度的辅助诊断。

OR-063

A Rapid, Simple and Low-Cost Paper-based Time-resolved Fluorescence Lateral Flow Immunoassay for CD8 Cell Count

Wei Xiao[1]、Yong Tang[2]
1. Guangdong Second Provincial General Hospital
2. 暨南大学生物工程学系

CD8+ T lymphocytes play an important role in the body's anti-infective immunity, autoimmunity and anti-tumor immunity. The number of CD8+ T lymphocytes (CD8 cells) in peripheral blood can directly reflect the immune status of the body and is widely used for auxiliary diagnosis and prognostic evaluation of diseases. There is an urgent need to develop a simple CD8 cell-counting platform to meet clinical needs.
Methods Our group designed a paper-based cell-counting method based on a blocking competition strategy. In addition, we developed a time-resolved fluorescence-blocking competitive lateral flow immunoassay (TRF-BCLFIA) for point-of-care CD8 cell counting that functions by measuring europium nanoparticle (EuNP)-labeled CD8 antibody probes that are not captured by CD8 cells, and we indirectly calculated the concentration of CD8 cells in samples. Within 30 min, four operation steps can provide an accurate CD8 cell count for a 75-μL whole-blood sample, and this approach can be implemented on a handheld device.

Results The TRF-BCLFIA reliably quantified CD8 cells in whole-blood samples, in which the assay exhibited a linear correlation (R2=0. 989) readout for CD8 cell concentrations ranging from 137 to 821 cells/μL. To validate the clinical suitability of the detection system, 33 clinical blood samples were tested, and the results showed a high correlation with flow cytometry analysis (R2=0.97).
Conclusions RF-BCLFIA can be used to count CD8 cells in blood samples, and has a high coincidence rate with FCM analysis.This analysis approach is a promising alternative for the costly standard flow cytometry-based tools for CD8 cell counting in tumor patients in community clinics, small hospitals, and low medical resource regions. This technology would deliver simple diagnostics to patients anywhere in the world, regardless of geography or socioeconomic status. This technology would deliver simple diagnostics to patients anywhere in the world, regardless of geography or socioeconomic status.

OR-064

结肠癌微环境中免疫细胞浸润模式及其预后评估

梁艳玲[1,2]、吴智聪[1,2]、马尊雅[3,4]、陈华[3]、吴妮莎[2]、邓凡[3]、曾方银[2]
1. 南方医科大学南方医院检验科
2. 南方医科大学第五附属医院检验医学科
3. 南方医科大学基础医学院细胞生物学教研室
4. 南方医科大学基础医学院基础医学

目的 结直肠癌（colorectal cancer，CRC）是主要的致死性恶性肿瘤之一。其中，结肠癌是结直肠癌中的最常见类型。目前，免疫疗法已被临床验证为许多肿瘤有效治疗的选择。肿瘤浸润免疫细胞作为肿瘤免疫微环境中的主要成分，其与结肠癌患者预后之间的关联尚未明确。本研究旨在探索结肠癌微环境中免疫细胞的浸润模式及其预后价值，为临床个体化治疗提供新方向。
方法 利用 CIBERSORT 软件包从癌症基因组图谱 TCGA（The Cancer Genome Atlas）数据库、GEO（Gene Expression Omnibus）数据库共筛选 38 例正常结肠组织样本及 316 例结肠癌组织样本，基于标准化后的基因表达谱对 22 种浸润免疫细胞进行提取和量化，分析免疫细胞在正常组织和癌组织中的浸润差异。利用多因素 COX 回归构建 Nomogram 风险预测模型。
结果 本研究发现活化的 CD4+记忆性 T 细胞、M0 巨噬细胞、M1 巨噬细胞在结肠癌组织中浸润显著增多，幼稚 B 细胞、浆细胞、单核细胞及未活化的肥大细胞显著减少。高水平活化的肥大细胞及调节性 T 细胞浸润与肿瘤转移和分期进展密切相关（$p<0.05$），低水平活化的 CD4+记忆性 T 细胞和滤泡辅助性 T 细胞与肿瘤淋巴结播散及分期进展相关（$p<0.05$）。利用患者年龄、性别、临床病理分期、TNM 分期、组间分析具有差异的免疫细胞构建 Nomogram 风险预测模型，模型预测 1 年、3 年和 5 年生存率的 ROC 曲线 AUC 分别为 0.828、0.794 和 0.754。将 COAD 患者按照风险评分分为高低风险组并进行 Kaplan-Meier 分析，结果显示高风险组 COAD 患者预后较差（$p<0.001$），提示模型具有良好预测效能。
结论 结肠癌患者中免疫细胞的浸润差异可能在疾病进展中具有重要作用，其预后模型可能为结肠癌患者的生存评估提供理论和数据支持。

OR-065

肺腺癌外泌体 miR-1290 靶向抑制 SOCS3 调控巨噬细胞极化

吴逸宁、王雪滢、顾嘉慧、徐建
江苏省人民医院（南京医科大学第一附属医院）

目的 肺腺癌严重威胁人类健康。阐明肺腺癌的发病机制，寻找免疫治疗的新方法，对改善预后十分重要。本研究旨在明确肺腺癌外泌体 miR-1290 对巨噬细胞极化的调控作用及其分子机制，为靶向 miR-1290 的治疗提供理论依据。
方法 利用重组慢病毒构建 miR-1290 稳定敲低的肺腺癌细胞株并分离及鉴定其外泌体。流式细胞术和 Transwell 细胞侵袭实验检测与敲低 miR-1290 的外泌体共培养后巨噬细胞表型和功能的改变。通过裸鼠皮下瘤模型在体内验证肺腺癌外泌体 miR-1290 对巨噬细胞极化的作用。采用双荧光素酶报告基因实验、qRT-PCR 和 Western blot 鉴定 miR-1290 的靶基因 SOCS3。改变 miR-1290、SOCS3 的表达水平或与肺腺癌外泌体共培养后，qRT-PCR 和 Western blot 检测巨噬细胞极化标志物及相关信号通路分子的表达变化。
结果 与敲低 miR-1290 的肺腺癌外泌体共培养抑制巨噬细胞向 M2 型极化并减弱其促肺腺癌细胞侵袭的能力。敲低肺腺癌外泌体 miR-1290 可减少裸鼠皮下移植瘤中浸润的 M2 型巨噬细胞数量并减小肿瘤体积。过表达 miR-1290 可活化巨噬细胞 STAT3 通路，同时促进其向 M2 型极化；阻断 STAT3 通路削弱 miR-1290 促巨噬细胞 M2 型极化的效应。miR-1290 能特异性结合 SOCS3 的 3'UTR，靶向抑制 SOCS3 的表达。敲低 SOCS3 可活化 STAT3 并促进巨噬细胞向 M2 型极化；回补 SOCS3 可抵消 miR-1290 上调对 STAT3 活化及 M2 型极化的促进作用。敲低 miR-1290 的肺腺癌细胞外泌体可上调巨噬细胞中 SOCS3 表达, 进而抑制 STAT3 通路及 M2 型极化。
结论 肺腺癌外泌体 miR-1290 通过调控 SOCS3-STAT3 轴, 促进巨噬细胞向 M2 型极化。

OR-066

Reference intervals for glomerular filtration function markers among pregnant women of Shandong Province, east China

Fang Luan
Department of Clinical Laboratory, Shandong Provincial Hospital Affiliated to Shandong First Medical University, Shandong, China

Background The aim of the study was to establish reference intervals (RIs) for glomerular filtration function markers among pregnant women of Shandong Province, east China.
Methods From Janunary 2017 to December 2018, we retrospectively analyzed serum samples from 360 pregnant women and a control cohort of 60-non-pregnant women. The glomerular filtration function markers included Cystatin C (CysC), Creatinine (Cr), and Estimated Glomerular Filtration Rate (eGFR). BeckmanAU5800 detection system was used to determine the serological level of CysC by immunonephelometry method and Cr by enzyme method, eGFR was calculated according to age, gender and Cr results. We calculated the RIs according to the guidelines in C28-A3 published by the Clinical and Laboratory Standards Institute (CLSI).
Results The calculated RIs for serum CysC were (0.40-0.67) mg/L, (0.5-0.85) mg/L, (0.77-1.49) mg/L in 1st, 2nd, and 3rd trimester respectively. Cr were (37.26-57.47) μmol/L, (33.70-54.82) μmol/L, (33.66-62.69) μmol/L in each cohort . eGFR based on Cr were (115.24-140.05) ml/min per 1.73m2, (117.42-141.88) ml/min per 1.73m2 , (109.00-146.00) ml/min per 1.73m2.

Conclusions The results show the necessity to establish special RIs for glomerular filtration function markers during pregnancy, even in each trimester. CysC levels increase obviously, so we also should cautiously treat it in the three trimesters.

OR-067

Effects of Different Doses of rAAV5-mCherry on the Transcriptome of Hippocampal Pyramidal Neurons in Male Mice

刘忆思
南方医科大学珠江医院

Recombinant adeno-associated virus (rAAV) vectors have been widely used in neuroscience for gene transduction, and high-dose rAAV induces unexpected side effects. However, little is known about the mechanisms underlying rAAV-induced toxicity in brain cells. Here, we evaluated the effects of three different doses of rAAV5 vectors, which are widely used for functional studies in the brain, on hippocampal pyramidal neurons in male mice. There was a strong correlation between rAAV dose and toxicity. As the dose increased, rAAV5-mCherry upregulated genes related to immune and inflammatory responses and neuronal apoptosis and downregulated genes associated with synaptic and axonal compartments and mitochondria, suggesting that higher doses of rAAV-5-mCherry may induce pyramidal neuronal fragility and impair synaptic transmission. Thus, the dose should be taken into consideration when rAAV vectors are used for gene transduction studies.

OR-068

AKR1B10 confers resistance to radiotherapy via FFA/TLR4/NF-κB axis in nasopharyngeal carcinoma

DIXIAN LUO
HUAZHONG UNIVERSITY OF SCIENCE AND TECHNOLOGY UNION SHENZHEN HOSPITAL

Nasopharyngeal carcinoma (NPC) is one kind of human head and neck cancers with high incidence in Southern China, Southeast Asia and North Africa. In spite of great innovations in radiation and chemotherapy treatments, the 5-year survival rate is not satisfactory. One of the main reasons is resistance to radiotherapy which leads to therapy failure and recurrence of NPC. The mechanism underlying remains to be fully elucidated. Aldo-keto reductase B10 (AKR1B10) plays a role in the formation and development of carcinomas. However, its role in resistance to radiotherapy of NPC is not clear. In this research, the relationships between AKR1B10 expression and the treatment effect of NPC patients, NPC cell survival, cell apoptosis, and DNA damage repair, as well as the effect and mechanism of AKR1B10 expression on NPC radioresistance were explored. A total of 58 paraffin tissues of NPC patients received radiotherapy were collected including 30 patients with radiosensitivity and 28 patients with radioresistance. The relationships between AKR1B10 expression and the treatment effect as well as clinical characteristics were analyzed by immuno-histochemical experiments, and the roles of AKR1B10 in cell survival, apoptosis and DNA damage repair were detected using the AKR1B10 overexpressed cell models. Furthermore the mechanism of AKR1B10 in NPC radioresistance was explored. Finally, the radioresistance effect of AKR1B10 expression was evaluated by the tumor xenograft model of nude mice and the method of radiotherapy. The results showed AKR1B10 expression level was correlated with radiotherapy resistance, and AKR1B10 overexpression promoted proliferation of NPC cells, reduced apoptosis and decreased cellular

DNA damage after radiotherapy. The probable molecular mechanism is that AKR1B10 expression activated FFA/TLR4/NF-κB axis in NPC cells. This was validated by using the TLR4 inhibitor TAK242 to treat NPC cells with AKR1B10 expression, which reduced the phosphorylation of NF-κB. This study suggests that AKR1B10 can induce radiotherapy resistance and promote cell survival via FFA/TLR4/NF-κB axis in NPC, which may provide a novel target to fight against radiotherapy resistance of NPC.

OR-069

检验科开展腹膜透析评估试验的临床意义

梁珊珊[1]、钟慧[2]、贾成瑶[1]
1. 四川大学华西医院实验医学科
2. 四川大学华西医院肾内科

目的 腹膜透析评估试验包括了腹膜平衡试验和溶质清除，这是腹膜透析患者进行腹透过程中两个重要评估数据，目前需要人工录入所有检测结果到第三方软件中，才能获得相应数据。因此检验科联合肾内科腹透中心对此进行改革。
方法 检验科通过 LIS 后台的设置，直接通过抓取数据的方式，代替之前的手工录入，直接完成腹膜平衡试验和溶质清除的完整报告。
结果 2019 年 3 月，检验科、肾内科腹透中心启动腹膜透析评价报告改革项目。在整个过程中，经历了不同批次腹膜透析液的更换、肌酐检测的变化方法和计算公式的更新等问题。截至目前，已成功完成 1000 余份腹膜透析评价报告。完全替代了以往的第三方软件，将人工输入造成的错误概率降低到 0，节省了大约 1 小时/天的人力；可根据不同批次腹膜透析液及时改变校正系数，更符合临床诊治需要；临床医生获得腹膜透析评估试验的报告时间至少缩短 15 小时，加快临床诊治进程；达到数据完整、客观、永久保存的目的，便于临床医生和护士及时查阅和分析动态数据。
结论 检验科联合腹膜透析中心完成腹膜透析评估报告新模式改革，是国内首次在 LIS 平台上开展的创新方法，结合腹膜透析患者持续健康管理项目的实施，医疗、护理、技术团队的配合，显示了医疗工作的有效改善。员工满意度和患者满意度提高，促进学科交叉和多学科发展。

OR-070

Development and validation of a prediction model for malignant pulmonary nodules

Zhen Ren 、Hongmei Ding、Zhenzhen Cai
The First Affiliated Hospital of Nanjing Medical University

Background To develop and validate a preoperative prediction model for malignancy of pulmonary nodules (PNs).
Methods Data from 409 patients who underwent PN resection at the First Affiliated Hospital of Nanjing Medical University between June 2018 and December 2020 were retrospectively collected. Then, the patients were nonrandomly split into[Y. Mu1] a training cohort and a validation cohort. Logistic regression analysis was used to identify variables significantly associated with malignant pulmonary nodules (MPNs) that were then included in the nomogram. We evaluated the discrimination and calibration ability of the nomogram by using R software.
Results MPNs were confirmed in 215 (52.6%) patients by a pathological examination. Multivariate logistic regression analysis identified six risk factors independently associated with MPN: Gender [Female, odds ratio (OR) =2.487; 95% confidence interval (CI): 1.313–4.711; P = 0.005], location of nodule (upper lobe of lung, OR = 2.576; 95%CI: 1.380–4.806; P = 0.003), density of nodule (pure ground glass, OR = 16.899; 95%CI: 7.572-37.716; P < 0.001; part-solid

nodules, OR = 24.096; 95%CI: 10.153–57.186; P < 0.001), nodule size (OR = 1.100; 95% CI: 1.058–1.145; P < 0.001), GAGE7 (OR = 1.085; 95%CI: 1.011–1.165; P = 0.023) and GBU4-5 (OR = 1.126; 95%CI: 1.054–1.204; P < 0.001). The concordance index was 0.88 (95%CI: 0.83–0.91) and 0.92 (95%CI: 0.85–0.97) in the training and validation cohorts, respectively. The calibration curves showed good agreement between the predicted risk by the nomogram and real outcomes.

Conclusions We have developed and validated a preoperative prediction model for MPNs. The model could aid physicians in clinical treatment decision making.

OR-071

Exosome-mediated secretion of CST1 promotes colorectal cancer metastasis

Weili Duan、chuanxin wang
The Second Hospital of Shandong University

Cystatin SN (CST1) , encoded by CST1, is a secretory peptide and belongs to the type 2 cystatin superfamily. Emerging evidence has demonstrated that CST1 has diverse critical biological functions, especially its roles in tumor development and metastasis. In the present study, CST1 was commonly upregulated in CRC tissues and predicted a poor prognosis. Upregulation of CST1 promoted, whereas downregulation of CST1 inhibited cell migration, invasion and EMT of CRC in vitro. Most interestingly, we found that CRC-derived exosomes transferred CST1 between HCC cells promoted cell migration by activating the MAPK pathway. In addition, CRC-derived exosomes transferred CST1 to human umbilical vein endothelial cells (HUVECs) to promote angiogenesis. Taken together, our results demonstrate a novel function of CST1 in tumor metastasis mediated by exosomes through regulation of the MAPK pathway and angiogenesis in CRC.

OR-072

一组血清外泌体 miRNA 作为肾透明细胞癌新型液体活检指标的临床价值研究

王成[1]、田亚萍[1]、张辰宇[2]、张春妮[1]、汪俊军[1]
1. 中国人民解放军东部战区总医院
2. 南京大学生命科学院，医药生物技术国家重点实验室

目的 探讨肾透明细胞癌（ccRCC）患者血清特定变化外泌体 miRNA 作为 ccRCC 新型分子标志物潜能。

方法 收集治疗前 ccRCC 患者血清 126 例，同时收集 124 例年龄、性别匹配的正常对照血清。分别提取患者和对照组血清外泌体后，运用低密度芯片技术检测 miRNA 表达谱。运用 qRT-PCR 分别在复筛组（27 例 ccRCC 和 26 例正常）、验证组（72 例和 72 例正常）和测试组（27 例 ccRCC 和 26 例对照）逐步进行验证。对部分 ccRCC 患者术前、术后样本比较分析。最后评价特定变化外泌体 miRNA 及其组合的临床价值。

结果 低密度芯片显示 ccRCC 患者血清外泌体中 miRNA 的表达谱与正常对照有明显差异，44 种 miRNA 在 ccRCC 中明显上调（变化倍数 > 5）。qRT-PCR 技术验证发现 6 种 miRNA 包括 miR-28-3p、miR-200a、miR-1826、miR-103、miR-1249 和 miR-640 在 ccRCC 患者中的水平均显著且稳定高于正常对照，在早期 ccRCC 中即显著升高，且在患者术后明显下降。ROC 曲线下面积（AUC）分析显示，6 种 miRNA 及其组合对复筛组、验证组、测试组诊断的 AUC 范围分别是 0.751 ～ 0.893、0.620 ～ 0.808、0.744 ～ 0.920，具有较高的诊断准确性。此外，6-miRNA 组合

对早期 ccRCC 诊断的 AUC 为 0.832（95%CI = 0.774 ～ 0.889），敏感度 84%，特异性 83%。逻辑回归分析显示，6 种 miRNA 及 6-miRNA 组合的 OR 值均具有统计学意义。

结论 6 种血清外泌体 miRNA miR-28-3p、miR-200a、miR-1826、miR-103、miR-1249 和 miR-640 组合在一起对 ccRCC 早期诊断、手术效果评估方面具有较高的准确性，有望成为 ccRCC 潜在的液体活检指标。

OR-073

肽核酸功能化的纳米通道生物传感器高灵敏检测肿瘤外泌体 MicroRNA

孙忠月、张玉林、涂济源、路淑敏
湖北中医药大学

目的 本研究构建了一种肽核酸（PNA，peptide nucleic acid）功能化纳米通道生物传感器，实现对肿瘤外泌体 miRNAs 超灵敏检测。

方法 采用不对称化学蚀刻的方法制备聚对苯二甲酸乙二醇酯（Polyethylene terephthalate，PET）锥形纳米通道，将探针 PNA 共价修饰在通道表面，并通过皮安计电流、X 射线光电子能谱及激光共聚焦显微镜等表征实验证明 PNA 功能化纳米通道生物传感器的成功构建，利用传感器检测提取的外泌体总 RNA 中的 miRNA-10b，PNA 识别靶标 miRNA-10b 并杂交，通道内产生电荷变化，从而导致离子电流的改变，通过记录检测前后电学信号的差异来区分胰腺癌细胞与正常细胞组。并从当地医院收集了 20 例临床血浆标本(10 例健康志愿者和 10 例胰腺癌患者)，利用 exoRNeasy Serum/Plasma Midi Kit 试剂盒分别提取外泌体总 RNA，随后使用我们的传感器进行分析。

结果 成功制备得到锥形纳米通道生物传感器，通过激光共聚焦和 XPS 表征进一步验证在纳米通道内表面 PNA 确实与 miRNA 杂交，该传感器可高度区分靶标 miRNA-10b 与单碱基错配及非互补序列，且检测限可低至 75aM，同时与健康样本信号值相比，发现胰腺癌患者样本的平均电流信号明显强于每个健康样本。

结论 本研究成功构建肽核酸功能化纳米通道生物传感器，可实现对 miRNA 高特异、灵敏检测及临床样本检测，为将来该传感器应用于临床癌症的早期筛查提供实验基础，并且该策略具有普适性，可通过转换不同序列的 PNA 探针，以检测不同癌症相关的核酸标志物。

OR-074

基于外泌体 DNA 的肿瘤相关基因突变临床检测的方法学研究

王哲颖[1,2]、王瑞娴[2]、潘晓蓉[2]、童建华[2]
1. 山东大学齐鲁医院
2. 上海交通大学医学院附属瑞金医院

背景 研究发现外泌体 DNA 中肿瘤相关基因的突变与肿瘤患者的疾病进展和预后密切相关。但是，目前有关外泌体的分离方法以及针对外泌体 DNA 的分析研究均无法确保相关的操作是在最佳条件下进行的，不同的研究之间也缺乏可比性。本研究旨在建立一种适于临床应用的基于外泌体 DNA 的检测肿瘤相关基因突变的实验方案。

方法 以胰腺癌的 KRAS 突变检测为例，针对血液样本的不同类型以及外泌体分离、外泌体 DNA 制备和微滴式数字 PCR（ddPCR）检测基因突变过程中的一些潜在因素进行了研究，并分析其对外泌体 DNA 检测可能产生的影响。

结果 本研究发现血清样本中外泌体 DNA 的含量高于血浆样本，但血清来源的外泌体 DNA 中 KRAS 突变的等位基因突变频率（MAF）则明显低于血浆样本。在外泌体分离的过程中，基于膜亲和原理的柱膜法与传统的超速离心法相比，在外泌体 DNA 的得率和 KRAS MAF 方面均无明显差异。

对分离得到的外泌体用 DNase I 进行预处理可以有效去除外泌体外部黏附的野生型 DNA，从而提高阳性样本中 KRAS MAF 的检测值。PBS 缓冲液会干扰 DNase I 的作用，如果后续实验需对外泌体 DNA 进行检测，则应避免将 PBS 作为外泌体的重悬缓冲液。此外，使用 ddPCR 进行相关基因突变检测时，若在微滴形成之前对外泌体 DNA 进行变性解链可以有效提高 KRAS 的总拷贝数和突变的阳性微滴数。

结论 本研究为外泌体 DNA 分析最佳实验条件的选择和不同实验室研究结果的比较提供了方法学的依据，并提出了一种能适于临床应用的有关外泌体 DNA 基因突变检测的实验方案。

OR-075

可编程的工程化外泌体模拟物通过协同光免疫疗法和化学免疫疗法促进有效的癌症治疗

王毅超[1]、樊志金[2,3]
1. 台州市中心医院（台州学院附属医院）
2. 台州市中心医院（台州学院附属医院）
3. 广东省人民医院

人们迫切希望开发有效的治疗策略，选择性地破坏原发实体肿瘤，同时对正常组织的副作用最小，以消除转移性病变，并防止肿瘤复发。在此，我们通过将光热(PTT)剂金纳米棒(GNR)和化疗(ChemoT)剂吉西他滨(gemcitabine)加载到 m1 型巨噬细胞来源的纳米囊泡中来设计外泌体模拟物(EEMs)，将快速和局部光疗与进展性和广泛化疗结合起来。为增强 PTT 和 ChemoT 同时诱导的免疫原性细胞死亡(ICD)的免疫效应，将免疫激动剂 CpG ODN 和免疫检查点阻断剂 PD-L1 适配体包裹于 EEMs 中。随着肿瘤组织穿透能力的增强，GNR 可以通过光诱导的热膨胀实现对肿瘤细胞的局部机械损伤和药物释放，从而实现对原发肿瘤的精确清除。更重要的是，GNR 介导的 PTT 可通过释放肿瘤相关抗原和免疫激动剂 CpG ODN 促进强抗肿瘤免疫应答。随后 CD8 阳性 T 细胞比例增加，肿瘤细胞免疫被激活。为了防止 PD-L1 对细胞免疫的干扰，PD-L1 适配体竞争性地与 PD-L1 结合，从而发挥免疫检查点的阻断作用。EEMs 还通过吉西他滨诱导远端肿瘤的免疫原性细胞死亡，导致免疫系统激活和转移性肿瘤的崩溃。EEMs 将局部光热治疗与广泛化疗相结合，并将 ICD 放大以实现长期的肿瘤特异性免疫过程，以实现原位肿瘤和转移肿瘤清除。

OR-076

核受体 NR2F6 介导乳腺癌铂类药物耐药的分子机制研究

黄玲
广州医科大学附属第六医院

目的 NR2F6 与多种癌症预后不良有关，再此探讨核受体亚族 2，F 组第 6 号成员（NR2F6）对乳腺癌细胞顺铂耐药的影响及其可能的作用机制。

方法 Western blot 和 real-time PCR 检测乳腺癌正常上皮细胞 MCF-10A，5 种乳腺癌细胞 MCF7,MDA-MB-231,UACC812,SK-BR3,BT474 和乳腺癌顺铂耐药细胞株 MCF-7/DDDP 中 NR2F6 的表达水平。CCK8 法检测上述细胞的半抑制浓度 IC50，探究 NR2F6 的表达水平是否与 IC50 有关，根据 NR2F6 表达水平选择 MDA-MB-231 细胞构建 NR2F6 稳转细胞，MCF7 构建敲低细胞，Western blot 法验证细胞是否构建成功。CCK8 细胞增殖，流式凋亡实验，划痕，transwell 法验证 NR2F6 对乳腺癌细胞增殖、侵袭、迁移的影响，CCK8 法验证顺铂的最适浓度，在顺铂作用下，重复上述实验验证顺铂作用下 NR2F6 对乳腺癌细胞增殖、侵袭、迁移的影响。CCK8 法检测过表达细胞及其亲本细胞，敲低细胞及其亲本细胞的半抑制浓度 IC50。运用 RNA-seq，蛋白质

质谱，CHIP 筛选下游分子行进一步机制研究，并进一步行 rescue 实验，双荧光素酶报告基因实验验证其下游基因。
结果 NR2F6 过表达可增加顺铂对 MDA-MB-231 细胞的杀伤活性，而 NR2F6 敲低可降低顺铂对其杀伤活性，根据 RNA-seq 及蛋白质质谱筛选并验证下游基因 BCL2A1。
结论 NR2F6 可通过下调 BCL2A1 增加乳腺癌细胞对顺铂的敏感性。

OR-077

泛素连接酶 TRIM7 通过调控 HIF-1α 信号抑制肾透明细胞癌的转移与侵袭

袁超、赵敬杰
山东大学第二医院

目的 肾透明细胞癌是一种具有独特发病机制的恶性肿瘤，发生机制尚未完全阐明。我们前期研究结果表明，泛素连接酶 TRIM7 在肾透明细胞癌中低表达。本课题将探讨泛素连接酶 TRIM7 抑制肾透明细胞癌发生发展的机制研究。
方法 本课题结合细胞模型、动物模型和临床病理标本，明确 TRIM7 在肾透明细胞癌中的作用；利用干扰 shRNA、RNA-seq 等分子生物学手段和基因组学方法研究 TRIM7 对 HIF-1α 信号通路的影响，进而阐明 TRIM7 影响肾透明细胞癌发生的分子机制。
结果 我们收集了 40 例 ccRCC 患者的石蜡切片和 25 例 ccRCC 患者的新鲜癌组织，免疫组化、qRT-PCR 和 Western Blot 的结果显示 TRIM7 在 ccRCC 组织中显著低表达。过表达 TRIM7 基因可以抑制乏氧条件下细胞转移和侵袭，并显著降低 HIF-1α 的蛋白水平。我们将不同量的 TRIM7 野生型过表达质粒和 CA 突变体与恒量的 Src 过表达质粒共转染 HEK293 细胞，野生型 TRIM7 可以显著降低 Src 的蛋白水平，而泛素连接酶活性缺失的 CA 突变体对 Src 蛋白水平没有影响；与 CA 突变体相比，野生型 TRIM7 可以明显缩短 Src 的半衰期；蛋白酶体抑制剂 MG132 可以废除 TRIM7 对 Src 蛋白水平的影响。
结论 本研究明确了 TRIM7 在肾透明细胞癌中的作用，揭示了 TRIM7 调控 HIF-1 信号通路的分子机制，将为肾透明细胞癌的防治提供新的策略。

OR-078

Dysregulated Glutamate Transporter SLC1A1 Propels Cystine Uptake via Xc_x0001_ for Glutathione Synthesis in Lung Cancer

Wenzheng Guo[1,2]、Kaimi Li[3]、Beibei Sun[4]、Shuhai Lin[5]、Jiong Deng[2]
1. 上海市东方医院 检验科 Department of Laboratory Medicine，Shanghai East Hospital, Tongji University School of Medicine
2. 上海交通大学医学院 Shanghai Jiao Tong University School of Medicine
3. 北京协和医学院 Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College
4. 上海交通大学转化医学中心 Translational Medical Research Center, Shanghai Jiao Tong University
5. 厦门大学生命科学学院 School of Life Sciences, Xiamen University

Cancer cells need to generate large amounts of glutathione (GSH) to buffer oxidative stress during tumor development. A ratelimiting step for GSH biosynthesis is cystine uptake via a cystine/ glutamate antiporter Xc_x0001_. Xc_x0001_ is a sodium-independent antiporter passively driven by concentration gradients from extracellular cystine and intracellular glutamate across the cell membrane. Increased uptake of cystine via Xc_x0001_ in cancer cells increases

the level of extracellular glutamate, which would subsequently restrain cystine uptake via Xc_x0001_. Cancer cells must therefore evolve a mechanism to overcome this negative feedback regulation. In this study, we report that glutamate transporters, in particular SLC1A1, are tightly intertwined with cystine uptake and GSH biosynthesis in lung cancer cells. Dysregulated SLC1A1, a sodium-dependent glutamate carrier, actively recycled extracellular glutamate into cells, which enhanced the efficiency of cystine uptake via Xc_x0001_ and GSH biosynthesis as measured by stable isotope-assisted metabolomics. Conversely, depletion of glutamate transporter SLC1A1 increased extracellular glutamate, which inhibited cystine uptake, blocked GSH synthesis, and induced oxidative stress-mediated cell death or growth inhibition. Moreover, glutamate transporters were frequently upregulated in tissue samples of patients with non–small cell lung cancer. Taken together, active uptake of glutamate via SLC1A1 propels cystine uptake via Xc_x0001_ for GSH biosynthesis in lung tumorigenesis.

OR-079

FUT7 Promotes the Epithelial-Mesenchymal Transition and Immune Infiltration in Bladder Urothelial Carcinoma

Mulin Liu[1]、Siyi Chen[2]、Shijun Li[1]
1. The First Affiliated Hospital of Dalian Medical University
2. 大连医科大学

Background Bladder urothelial carcinoma (BLCA) is one of the most frequently appearing, lethal and aggressive malignancies of the genitourinary system with growing morbidity and mortality, which affects human health seriously. Protein glycosylation, catalyzed by specific glycosyltransferase, has been found to be abnormal in several diseases, especially cancer. Fucosyltransferase VII (FUT7), one of the fucosyltransferases, was observed abnormally expressed in various cancers, however, the role of FUT7 in BLCA, and the association between its expression and clinical outcomes or immune infiltration remains unclear.
Methodology FUT7 expression in BLCA was analyzed in Oncomine database, which was further confirmed with immunohistochemistry and ELISA. The prognostic value of FUT7 for BLCA was evaluated with PrognoScan database, and its genetic alteration was examined in cBioPortal database. The proliferation, migration, invasion and epithelial–mesenchymal transition (EMT) changes of bladder cancer cells after FUT7 siRNA or cDNA transfection were determined by CCK8, colony formation, transwell and Western blot, respectively. The correlation between FUT7 expression and immune infiltration levels was analyzed in TIMER and TISIDB databases, and the methylation level of FUT7 was detected in UALCAN database.
Results The results showed that the expression of FUT7 was increased in BLCA, and patients with high FUT7 level were predicted to have lower overall survival and diseasespecific survival rates, which were not influenced by FUT7 genetic alterations. Downregulation FUT7 inhibited the proliferation, migration, invasion and EMT of bladder cancer cells, whereas upregulation of FUT7 showed the opposite effects. We found that FUT7 was positively correlated with immune cell infiltration levels (CD8+ T cells, CD4+T cells, macrophage, neutrophil and dendritic cells), and also the expression of gene markers of immune cells. The negative correlation between FUT7 expression and FUT7 methylation level was observed, among which FUT7 expression was positively correlated with the abundance of 28 kinds of tumor-infiltrating lymphocytes (TILs), while FUT7 methylation level was negatively correlated with TILs.
Conclusion Altogether, these findings suggested that FUT7 possessed the potential to serve as a detection biomarker or immunotherapeutic target for BLCA.

OR-080

Free fatty acid is a promising biomarker in triage screening for patients with colorectal cancer: a case-control study

Bin Zhu、Yingping Cao
Fujian Medical University Union Hospital

Purpose The aim of our study was to identify the diagnostic ability of Free fatty acid (FFA) in younger CRC by comparing carcinoembryonic antigen (CEA) and carbohydrate antigen 19-9 (CA19-9).
Methods Patients screened for CRC at Fujian Medical University Union Hospital from January 2011 to December 2014 were recruited. Patients pathologically diagnosed with CRC or colorectal adenoma (CA) and healthy control participants were included. The enzyme endpoint method was applied to measure FFA levels. Receiver operating characteristic (ROC) curve analysis was performed to further evaluate the diagnostic ability of FFAs.
Results FFA levels for patients in the late-stage (TNMstage III-IV, tumour-node-metastasis-stage) were higher than that in the early-stage (TNMstage I-II) (P=0.02). The FFA levels in CRC patients were higher than controls in all ages, younger than 50, males and females (P<0.001), and there was a dramatic increase in patients younger than 50 which is bigger than all ages, also, the increase in female is bigger. There was no significant difference in the FFA level between CA patients and healthy participants (P=0.53). The area under the curve (AUC) values of FFA, CEA, CA19-9, FFA+CEA, FFA+CA19-9 and FFA+CEA+CA19-9 distinguished CRC patients from controls at all ages, with values of 0.604, 0.731, 0.640, 0.754, 0.678 and 0.758, respectively; however, in the younger CRC patients (age≤50), the AUC values were 0.701, 0.735, 0.669, 0.798, 0.749, and 0.801. The AUC in female patients younger than 50 was larger than that in males (0.769 vs 0.660) and it was also larger than males (0.739) and females (0.729) of CEA.
Conclusion FFA has not only a complementary ability of CEA and CA19-9, but also a superior ability in female and younger patients with CRC; it may have a potential role in triage screening early CRC.

OR-081

长链非编码 RNA SCARNA10 促进肝癌细胞增殖及其机制研究

韩亚伟
天津医科大学肿瘤医院

目的 探究长链非编码 RNA SCARNA10 对肝癌细胞增殖的影响及其机制。
方法 在人肝癌细胞系 HepG2、MH97H 及正常肝细胞系 L-7702 中，采用实时荧光定量 PCR（qPCR）法检测 SCARNA10 的表达水平。将 HepG2 和 MH97H 细胞各分为两部分，分别转染小干扰 RNA（siRNA）和阴性对照 RNA（NC）36 h；收集细胞，采用 qPCR 法检测细胞中的增殖细胞核抗原（PCNA） mRNA，CCK-8 法检测波长 450 nm 处的吸光度（OD）值表示细胞增殖活性，克隆形成实验计数克隆形成数。核质分离提取实验观察 SCARNA10 在肝癌细胞胞核、胞质中的分布情况，RNA 结合蛋白免疫沉淀（RIP）实验验证 SCARNA10 与 SUZ12、EZH2 的相互作用。
结果 HepG2、MH97H 细胞中 SCARNA10 相对表达量均高于 L-7702 细胞（P 均＜0.05）。与转染 NC 比较，转染 siRNA 的 HepG2、MH97H 细胞中 PCNA mRNA 表达量、细胞增殖 OD 值均降低，细胞克隆数均减少（P 均＜0.05）。核质分离提取实验显示，SCARNA10 在 HepG2、MH97H 细胞胞核内的表达比例高于胞质内表达比例（P＜0.05）。HepG2 细胞中 SCARNA10 与 SUZ12、EZH2 的相对富集量分别为 5.05±1.39、3.95±0.67，MH97H 细胞中分别为 6.71 ±2.60、4.47±1.75。
结论 在细胞核中 SCARNA10 可能通过与 SUZ12、EZH2 结合而促进肝癌细胞增殖。

OR-082

Recommendations for proficiency testing criteria for hemoglobin A1c based on the Shanghai Center for Clinical Laboratory's study

Yi Ju[1]、Zhimin Cao[2]、qing li[1]、liping tang[1]、yuanzhu ou[1]、xiaoxuan yu[1]、wenbin liu[1]
1. Shanghai Center for Clinical Laboratory,Shanghai,China
2. Upstate Medical University, Syracuse, New York, USA

ObjectiveThe US Centers for Medicare & Medicaid Services proposed in 2019 that glycated hemoglobin A1c (HbA1c) be a CLIA'88 regulated analyte . People who commented expressed concerns that the proposed acceptance limit (AL, HbA1c in NGSP unit) ±10% for proficiency testing (PT) would be unable to maintain already improved analytical performance and guarantee the clinical utility of HbA1c testing. Assessing impact of various ALs on PT performance is needed to provide scientific evidence for adopting an appropriate AL.
Methods Ten patient's EDTA-whole blood specimens were distributed to 318 and 336 laboratories in the 2018 and2019 PT events organized by Shanghai Center for Clinical Laboratory (SCCL). HbA1c concentrations were measured by participants using various methodologies commonly used in the USA and China. Targets were determined using secondary reference measurement procedures (SRM) at SCCL. Failed Results were results outside the SRM-defined target ±AL (5% through 10%). Laboratories with Failed Results ≥ 2 out of 5 samples per PT event obtained Event Unsatisfactory Status.
Results HbA1c target values ranged 33.3 mmol/mol (5.2 NGSP%) 102.2 mmol/mol (11.5 NGSP%) for 2018 event, and 33.3 mmol/mol (5.2 NGSP%) 84.7 mmol/mol (9.9 NGSP%) for 2019 event. Overall Laboratory Event Unsatisfactory Rates ranged 11.3-12.2%, 4.8-5.3%, 0.9-3.1%, 0.6-2.2%, 0.6-1.4% and 0.6-1.4%, at AL of ±5%, ±6%, ±7%, ±8%, ±9% and ±10%, respectively.
Conclusions The AL (in NGSP unit) of ±6% or ±7% for PT evaluation of HbA1c results would be appropriate, with satisfactory event score for about 95% of participant laboratories in a PT event.

OR-083

Epidemiological, clinical and laboratory features of patients with bloodstream infection of Brucella in Anhui Province, China

Cuixiao Shi[1]、Lianzi Wang[1]、Dongmei Lv[1]、Gang Wang[1]、Hylemariam Mihiretie Mengist[2]、Tengchuan Jin[2]、Bo Wang[1]、Ying Huang[1]、Yajuan Li[1]、Yuanhong Xu[1]
1. Department of Clinical Laboratory, the First Affiliated Hospital of Anhui Medical University
2. 中国科学技术大学

Background Brucellosis is currently one of the most widespread zoonotic diseases caused by Brucella genus, and the Brucella melitensis is the major pathogen. The number of people infected with Brucella has gradually increased in Anhui Province.
Purpose To retrospectively evaluate the epidemiological, clinical, and laboratory data of brucellosis patients in Anhui Province.
Patients and Methods A total of 109 brucellosis patients were admitted to the First Affiliated Hospital of Anhui Medical University from January 2012 to March 2021. Data from all patients were retrieved from the hospital's electronic medical system. The final results were grouped and compared according to the presence or absence of bacteremic brucellosis and three phases of brucellosis.

Results The most common symptoms among all 109 brucellosis patients were fever (89.0%), followed by chills (52.3%), arthralgia (48.6%), and weight loss (30.3%), and laboratory results presented with anemia (65.1%), elevate of C-reactive protein (CRP) (91.7%), erythrocyte sedimentation rate (ESR) (86.2%), aspartate aminotransferase (AST) (40.4%), and lactate dehydrogenase (LDH) (43.1%). The percentage of fever (96.1%), arthralgia (58.8%), anorexia (35.3%), leukopenia (31.4%), and the AST (51.0%) were higher in bacteremic than nonbacteremic group. Additionally, the median level of LDH (332.0 mg/ L, IQR, 209.0–553.0) was higher in bacteremic than nonbacteremic group. Nevertheless, the albumin (36.0 mg/L, IQR, 33.9–38.2) was lower in the bacteremic group. The percentage of fever (94.9%) and the median LDH level (316.0 U/L (IQR,218.0–517.5)) in the acute phase of brucellosis were higher than the percentage of fever (72.0%) and the median LDH level (209.0 U/L (IQR,162.0–276.0)) in the subacute phase of brucellosis.
Conclusions Brucellosis has become an important public health issue in Anhui Province. Brucellosis is a disease with diverse clinical manifestations. Our data showed that unex-plained fever, arthralgia, and elevated AST and LDH should be considered as a diagnosis of bacteremia brucellosis for early treatment intervention.

OR-084

HNRNPA2B1 Affects the Prognosis of Esophageal Cancer by Regulating the miR-17-92 Cluster

Kexin Li[1]、Xiaoying Lou[1]、Benheng Qian[2]、Yiling Li[1]、Shaohui Ma[1]、Wei Cui[1]
1. 中国医学科学院肿瘤医院
2. 温州医科大学附属第二医院

N6-methyladenosine (m6A) is the most abundant RNA modification in eukaryotes. Accumulating evidence suggests that dysregulation of m6A modification significantly correlates with tumorigenesis and progression. However, the function of HNRNPA2B1 in miRNA regulation in esophageal cancer (ESCA) has not been fully elucidated to date. In this study, we observed an increased expression and positive correlations of all 25 m6A regulators in ESCA data obtained from the TCGA database. Next, we used 25 m6A regulators to classify the ESCA patients into two subgroups (EC1 and EC2). We found EC2 subgroup was remarkably correlated with advanced clinical stage, distant metastasis, lymph node metastases and overall survival of ESCA. Through expression profiling of these regulators, a prognostic score model containing HNRNPA2B1, ALKBH5 and HNRNPG was established, and the high-risk subgroup exhibited strong positive correlations with ESCA progression and outcome. The risk score obtained from this model may represent an independent predictor of ESCA prognosis. Notably, the gene most frequently associated with increased risk was HNRNPA2B1. Recent study reported that HNRNPA2B1 might be involved in the progression of ESCA by regulating miRNA expression. In addition, bioinformatics analysis showed that HNRNPA2B1 was significantly positively correlated with the expression of miR-17-92 clusters, and there were binding sites for m6A and HNRNPA2B1 at miR-18a. In ESCA, the increased expression of HNRNPA2B1 alone might predict poor prognosis by affecting tumor-promoting signaling pathways through miR-17-92 clusters. An experimental study demonstrated that elevated HNRNPA2B1 expression was positively associated with distant metastasis and lymph node stage, and predicted the poor outcomes of ESCA patients. We also collected the 14 paired esophagus cancer tissues and tumor-adjacent tissues to validate the bioinformatic analysis in TCGA datasets. We found that the significantly positive correlation between HNRNPA2B1 and miR-17/miR-18a/miR-106b in 14 paired esophagus cancer tissues and tumor-adjacent tissues. Moreover, HNRNPA2B1, miR-17, miR-20a, miR-93, and miR-106b showed the higher expression in tumor tissues than tumor-adjacent tissues. We also found the positive correlation between HNRNPA2B1 and miR-17, miR-18a, miR-20a, miR-93 and miR-106b in 7 ESCA cell lines. Furthermore, m6A and HNRNPA2B1 could co-immunoprecipitate on the miR-17-92 cluster in TE1, which is consistent with our

predicated result. Knockdown of HNRNPA2B1 significantly decreased the expression of miR-17, miR-18a, miR-20a, miR-93, and miR-106b and inhibited the proliferation of ESCA cells. Therefore, our study indicated that the dynamic changes in 25 m6A regulators were associated with the clinical features and prognosis of patients with ESCA. Importantly, HNRNPA2B1 alone may affect the prognosis of patients with ESCA by regulating the miR-17-92 cluster.

OR-085

长链非编码 RNA LUCAT-1 通过 miR-4316/VEGF-A 轴促进肺腺癌转移的机制研究

谢艳
山东大学第二医院

背景与目的 肺腺癌（Lung adenocarcinoma，LA）是全球癌症死亡的主要原因之一，大量研究发现，长链非编码 RNA (Long non-coding RNA, lncRNA)作为 miRNA 分子海绵参与 LA 细胞的增殖、迁移、侵袭和凋亡等病理生理学过程。本文拟探讨 LA 细胞来源 lucat-1 介导的细胞间通讯调控对 LA 进展的影响及其作用机制。

方法 选取 5 例 LA 患者血清样本为观察组，以及 5 例健康体检者血清样本作为对照组；利用测序筛选出 LA 患者及健康体检者血清差异表达的 lncRNA LUCAT-1，通过实时荧光定量 PCR(RT-qPCR)技术在大量样本集（100 例 LA 患者及 100 例健康对照者）中进行验证，受试者工作特征曲线（ROC）分析示 lucat 对结直肠癌的诊断效能。通过 tcga 数据库分析 LA 在 LA 组织中的表达情况，设计 lucat-1 过表达及敲减质粒，通过 Transwell 侵袭迁移实验检测 LUCAT-1 对 LA 细胞侵袭迁移能力的影响。双荧光素酶实验明确 lucat-1 及下游 miRNA 的靶基因，并设计挽救实验。

结果 与非癌症人群血清外泌体相比，在 LA 血清外泌体及组织中中 LUCAT-1 的表达水平均上调。LUCAT-1 能够促进 LA 细胞的迁移能力。采用生物信息软件预测 LUCAT-1 与 miR-4316 的作用靶点及 VEGF-A mRNA 的 3’非翻译区（3’-untranslated region，3’-UTR）miR-4316 结合位点，通过荧光素酶报告基因实验证实靶点；通过转染上调 miR-4316 后 VEGF-A 蛋白表达明显下降，而下调 miR-4316 后 VEGF-A 蛋白表达明显升高；上调 LUCAT-1 后 VEGF-A 蛋白表达明显升高，而下调 LUCAT-1 后 VEGF-A 蛋白表达明显下降。细 胞功能回复实验结果显示，同时上调或下调 LUCAT-1 和 miR-4316 时 VEGF-A 蛋白表达水平变化不显著。体内实验显示， LUCAT-1-KD 组瘤体中 LUCAT-1 含量及 VEGF-A 蛋白的表达水平降低，而 LUCAT-1-OE 组瘤体中 LUCAT-1 含量及 VEGF-A 蛋白的表达水平显著升高。

结论 LA 外泌体中 LUCAT-1 通过吸附 miR-4316 促进 VEGF-A 表达进而进肿瘤转移。敲低 LA 细胞中的 LUCAT-1 有望通过调控 miR-4316/VEGF-A 轴来抑制 LA 的侵袭和转移。

OR-086

Consistency of aminotransferase analysis in China: Comparison of six mainstream aminotransferase routine methods and recalibration using human serum pool preparations supplemented with human recombinant aminotransferases

Zhenni Liu[1]、Qichen Long[1]、Tianqi Qi[1]、Jing Wang[2]、Haijian Zhao[2]、Jie Zeng[2]、Tianjiao Zhang[1]、Ying Yan[2]、Weiyan Zhou[2]、Jiangtao Zhang[2]、Wenxiang Chen[2]、Chuanbao Zhang[1]

1. 北京医院 国家老年医学中心 中国医学科学院老年医学研究院 国家卫生健康委临床检验中心 北京市临床检验工程技术研究中心 中国医学科学院北京协和医学院

2. 北京医院 国家老年医学中心 中国医学科学院老年医学研究院 国家卫生健康委临床检验中心 北京市临床检验工程技术研究中心

Background The purpose of this study is to evaluate the consistency of six mainstream homogeneous systems for aminotransferase measurements and improve the consistency of routine aminotransferase activity measurements through uniform calibrators.

Methods A total of 200 individual samples were grouped into four sets for the assay groups with and without pyridoxal-5-phosphate (P-5'-P) for ALT and AST. The routine assays of the P-5'-P group were compared with reference measurement procedures (RMP). In the no P-5'-P group, four routine assays were pairwise analyzed in six method pairs. Recalibration was performed using human serum pools (HSPs) supplemented with human original recombinant aminotransferases (HOR). Data were analyzed with the Passing–Bablok regression and the Bland–Altman plots.

Results In the P-5'-P group, the mean biases of Ortho and Dimension for ALT were 17.0% and -25.4%, while for AST, their mean biases were -9.5% and -9.6%, respectively. In the no P-5'-P group, the mean deviation of six method pairs ranged from -5.9% to 5.9% for ALT. For AST, the slopes and relative deviation ranged from 0.86 to 1.03 and -19.1% to 6.5%, respectively. After recalibration, in the P-5'-P group, the relative biases reduced to -12.2% ~ 7.7% for ALT and -6.9% ~ 0.8% for AST. In the no P-5'-P group, the mean deviations between the method pairs remarkably reduced for AST (-3.0% ~ 3.3%).

Conclusion Assays with P-5'-P supplemented both showed undesirable performance against RMP for ALT and AST. For assays without P-5'-P, the results for AST showed unsatisfying comparability for almost all method pairs. Using HSP preparations as the uniform calibrators could be hopeful to propel harmonization among mainstream homogeneous systems for aminotransferase activity measurement, especially for variable AST routine measurements.

OR-087

An Extraction free Isothermal System for Rapid Detection of Eight Common Pathogens Causing Lower Respiratory Tract Infections

Yuying Si 、Lieying Fan
Shanghai East Hospital

Lower respiratory tract infections (LRTIs) are a leading cause of morbidity and mortality worldwide and lack of a rapid diagnostic method. To improve the diagnosis of LRTIs, we established an available loop-mediated isothermal amplification (LAMP) assay for the detection of eight common lower respiratory pathogens, including Klebsiella pneumoniae, Pseudomonas aeruginosa, Acinetobacter baumannii, Staphylococcus aureus, Escherichia coli, Haemophilus

influenza, Streptococcus pneumoniae, and Moraxella catarrhalis. Furtherly, we established a rapid, high throughput and extraction free detection planform for LRITs using direct nucleic acid releasing strategy without extra nucleic acid extraction steps and encapsulated assay agents saved multiple labor. The whole progress can be shortened to 45min from sample in to results out. 528 sputum samples collected from patients with suspected LRTIs were detected by LAMP assays (8 tests in each sample, a total of 4224 tests), which compared with standard culture method (SCM), and then samples with inconsistent results were verified by Sanger sequencing and High-throughput sequencing (NGS). The results showed that all the Kappa coefficients between LAMP assay and SCM for detecting eight kinds of bacteria exceeded 0.4 as well as $P < 0.001$, indicated fair to good agreement. Besides, LAMP method (44.51%) detected more multiple infections than SCM (12.69%), and 367 inconsistent tests between the two methods were verified by Sanger sequencing. Results showed that 231 tests (62.94%) were concordant with LAMP, presenting higher sensitivity and detection rate than SCM, especially for multiple infection samples. 50 inconsistent samples were randomly selected for NGS and the diagnostic efficiency of LAMP assay was as follows: specific 94.49%, sensitive 75.00%, positive predictive value 90.44%, negative predictive value 84.47%, positive likelihood ratio 13.62, and negative likelihood ratio 0.26. In summary, an extraction free and high throughput LAMP platform was established to detect eight common pathogens causing LRTIs, which was significant for point of care testing and can be implemented in primary hospitals.

OR-088

我国部分地区区域检验中心建设及运营情况调查

吴炯[1]、殷杏[1]、樊绮师[2]
1. 上海嘉会国际医院
2. 上海交通大学医学院附属瑞金医院

目的 随着我国医改政策的持续推进，各地先后建立了不同模式和规模的区域医学检验中心。据不完全统计，目前全国已建立的区域医学检验中心已达数十家之多。区域检验中心在我国建设、运营情况如何，目前尚无调查及研究。我们对我国不同区域及地区的区域检验中心进行调研，了解其类型及规模、相关政策及制度、建设情况及人员利用率情

方法 对我国华东、华北、西北、西南地区正在运营的 9 家区域检验中心进行调研。通过问卷调查、电话访谈及现场调研的方式收集相关信息资料。问卷内容包含：区域检验中心类型及规模、区域检验中心相关政策及制度、区域检验中心建设情况、区域检验中心人员利用率情况等。

结果 调查中的区域检验中心主体是以公立医疗机构为主（77.8%）。此类型区域检验中心依附于其附属的公立医疗机构，大多无独立法人资质。区域检验中心建设及运营过程中，无 1 家由国家投资，部分经济发达地区区域检验中心（22.2%）有运营补贴。区域检验中心建设资金来源中，集中采购补贴是一种较为特殊的方式。区域检验中心建设存在规模（面积、设备投入、收入）差异，较小规模的区域检验中心并未设立分子诊断亚专科（22.2%），实验室整体质量建设尚有待提高（实验室认可通过率 44.4%）。区域检验中心建设中设备投入 3.01±1.60 万元/平方米，其中临床免疫亚专科单位面积设备投入最高（3.75±2.21 万元/平方米）。区域检验中心由于集中化检测，其人员利用率较普通实验室更高，区域检验中心临床化学亚专科最低（0.065 小时/项），而分子诊断及微生物亚专科相对较高。

结论 目前我国区域检验中心建设及发展正处于起步阶段。不同类型、不同地区的区域检验中心在发展模式、规模等各方面均存在较大差异。希望本文的研究内容和成果，可为今后全国各类型、各模式的区域医学检验中心的建设运营提供有价值的参考标准。使已建和新建的区域医学检验中心达到更好的“社会效益”和“经济效益”。

OR-089

中高危甲状腺癌患者术后血清甲状腺球蛋白水平与临床结局的相关性研究

刘茜辉、李贵星、贺勇、银梦婷
四川大学华西医院

目的 探究中高风险分化型甲状腺癌（DTC）患者术后血清 Tg 水平对远期临床结局的预测价值。
方法 以 2011 年 1 月至 2015 年 12 月就诊于四川大学华西医院的 194 名 DTC 患者为研究对象，依据最后一次随访结果分为三组：A 组：存在结构性的复发；B 组：生化反应不全；C 组：无病生存。三组患者均接受甲状腺全切手术和碘 131（131I）放射治疗，并规律随访，中位随访时间为 62 个月（2~120 个月）。比较三组患者术后刺激性甲状腺球蛋白水平（ps-Tg）和抑制性甲状腺球蛋白水平（bTg）的差异；通过 ROC 曲线确定 ps-Tg 和 bTg 预测患者无病生存的最佳临界值；采用多因素 logistic 回归分析疾病复发的危险因素。
结果 A 组和 B 组的 ps-Tg、bTg 水平高于 C 组（P＜0.01），A 组和 B 组间 ps-Tg、bTg 水平没有显著差异（P＞0.05）。ps-Tg 和 bTg 预测患者无病生存的最佳临界值分别为 5.18ng/mL（AUC：0.949，95%CI：0.913-0.986）和 0.85ng/mL（AUC：0.911，95%CI：0.867-0.956）。颈部淋巴结转移分期（OR：3.42，95%CI：1.33-8.76，P＜0.01），ps-Tg 水平（OR：1.43，95%CI：1.23-1.67，P＜0.001）是患者出现生化反应不全或疾病结构性复发的危险因素。此外，血清 Tg 倍增时间小于一年的患者，更容易出现疾病结构性的复发。
结论 淋巴结转移分期较高、术后 ps-Tg 高于 5.18ng/mL、bTg 高于 0.85ng/mL、Tg 倍增时间小于 1 年的中高风险 DTC 患者疾病复发的可能性较大。

OR-090

Identification of potential core gene GMPS in Hepatocellular Carcinoma using bioinformatics analysis

Xiaoli Zhou[1]、Shu Feng[1]、Renwei Jing[2]、Li Jiang[1]
1. Department of Laboratory Medicine, Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China.
2. Department of Cell Biology and Key Laboratory of Immune Microenvironment and Disease (Ministry of Education), Tianjin Medical University, Qixiangtai Road, Heping District, Tianjin, 300070, China

Background Hepatocellualr carcinoma (HCC) is one of the most malignant cancers in the world. It has the characteristics of high incident rate, high mortality rate and limited treatment options.Therefore, it's urgent to find out more new targets related to hepatocellular carcinoma.
Materials and Methods To explore potential therapeutic targets for HCC, we analyzed two microarray datasets (GSE117361 and GSE46408) derived from the Gene Expression Omnibus (GEO) database. The GEO2R tool was used to screen out differentially expressed genes (DEGs) between HCC and normal liver tissue. Gene Ontology(GO) function and Kyoto Encyclopedia of Genes and Genomes(KEGG) pathway enrichment analysis were performed using the Database for Annotation, Visualization and Integrated Discovery to identify the pathways and functional annotation of DEGs. Protein–protein interaction of these DEGs was analyzed based on the Search Tool for the Retrieval of Interacting Genes database and visualized by Cytoscape software. In addition, we used the online Kaplan–Meier plotter survival analysis tool to evaluate the prognostic value of hub genes expression in HCC patients.
Results A total of 363 up-regulated DEGs and 122 down-regulated DEGs were identified. Among them, ten hub genes with a high degree of connectivity were picked out. Over-expression of genes VCL, LOX and GMPS was associated with unfavorable prognosis of HCC, down-

expression of gene CXCL12 was associated with unfavorable prognosis of HCC. Especially, GMPS over-expression was observed and indicated poor outcome of HCC.
Conclusion Our study suggested that GMPS was over-expressed in HCC compared with normal liver tissue, and over-expression of GMPS was an unfavorable prognostic factor of HCC patients. Further study is needed to explore the value of GMPS in the treatment of HCC.

OR-091

EGFR 介导 FRK 抑制 β-catenin 入核影响脑胶质瘤

石琼、马萍
徐州医科大学附属医院

目的 研究 FRK 是否通过 EGFR 抑制 β-catenin 入核，从而影响胶质瘤细胞的凋亡。
方法 1.将 FRK 质粒转染入脑胶质瘤 U251 细胞中，Western blot 检测过表达 FRK 对细胞浆，细胞核和整个细胞中 β-catenin 水平的影响，验证 FRK 是否影响 β-catenin 入核。2. Western blot 检测过表达 FRK 对 EGFR 和磷酸化的 EGFR-Y1173 水平的影响。3.转染 EGFR(WT)和 EGFR(Y1173F)质粒，流式细胞仪检测细胞凋亡情况，研究 EGFR(WT)、EGFR(Y1173F)对脑胶质瘤 U251 细胞凋亡的作用。4. 共转 FRK 和 EGFR(WT)、EGFR(Y1173F)质粒，分别检测细胞浆，细胞核和整个细胞中 β-catenin 水平，验证 FRK 是否通过影响 EGFR-Y1173 磷酸化从而抑制 β-catenin 入核。5. 共转 FRK 和 EGFR(WT)、EGFR(Y1173F)质粒，流式细胞术检测细胞的凋亡情况，检测 FRK 是否通过影响 EGFR-Y1173 磷酸化从而促进胶质瘤的凋亡。
结果 1. 与对照组相比，过表达 FRK 降低细胞核内 β-catenin 蛋白水平，但不改变细胞内总的 β-catenin 蛋白水平。2. 与对照组相比，过表达 FRK 增加 EGFR-Y1173 磷酸化水平（$P<0.05$），而对 EGFR 总蛋白水平无影响。3. 流式细胞术结果显示：过表达 EGFR(WT)、EGFR(Y1173F)质粒，细胞凋亡均减少（$P<0.05$）。4. 与对照组相比，过表达 FRK 抑制了 β-catenin 的核转位，EGFR 促进了 β-catenin 的核转位，且转染 EGFR（Y1173F）质粒组的作用比转染 EGFR（WT）的效果更明显，此外，转染 EGFR（Y1173F）质粒逆转了过表达 FRK 对 β-catenin 核转位的抑制作用（$P<0.05$）。5. 流式细胞术结果显示：与对照组相比，过表达 FRK 促进了细胞凋亡，EGFR 抑制了细胞凋亡，且转染 EGFR（Y1173F）质粒组的作用比转染 EGFR（WT）的效果更明显，此外，转染 EGFR（Y1173F）质粒可逆转过表达 FRK 对胶质瘤细胞的促凋亡作用（$P<0.05$）。
结论 FRK 可以通过促进 EGFR-Y1173 磷酸化抑制 β-catenin 入核，从而促进胶质瘤细胞凋亡。

OR-092

Withaferin A reduces doxorubicin-induced cardiac injury by inducing MAPK phosphatase-1

Jun Qiu、Dong Zheng
The First Affiliated Hospital of Soochow University

Aims Doxorubicin is widely used as a first-line chemotherapeutic drug for various malignancies. However, doxorubicin causes severe cardiotoxicity which limits its clinical use and therapeutic approaches are limited. Recent studies demonstrated that impaired autophagic flux contributes to doxorubicin cardiotoxicity. This study investigated whether withaferin A (WFA) protects against doxorubicin cardiotoxicity by improving autophagic flux via inducing MAPK phosphatase-1.
Methods Cardiac injury was induced in mice by intraperitoneal injection of doxorubicin (20 mg/kg). WFA (1, 2 or 5 mg/kg) was intraperitoneally given 30 min before doxorubicin injection. Five days later, myocardial function and myocardial injury were analyzed. Cultured cardiomyocytes were incubated with WFA followed by doxorubicin for 24 hours. Cell death and

oxidant stress were determined. Autophagy and autophagic flux were analyzed in cardiomyocytes and mouse hearts.
Results Administration of WFA reduced oxidant stress, inhibited cardiac cell death and attenuated myocardial dysfunction in doxorubicin-injected mice in a dose-dependent manner. These protective effects of WFA were recapitulated in cultured cardiomyocytes stimulated with doxorubicin. Mechanistically, WFA prevented autophagic flux block and accumulation of autolysosomes in doxorubicin-induced cardiomyocytes and a mouse model of doxorubicin cardiotoxicity, the effects of which were associated with inducing MKP-1 expression. Furthermore, blocking autophagic flux with chloroquine or knock-down of MKP-1 with siRNA abrogated these protective effects of WFA in doxorubicin cardiotoxicity.
Conclusions WFA prevents doxorubicin cardiotoxicity by improving autophagic flux and autolysosome clearance via MKP-1 signaling. Thus, WFA may be a potentially useful drug to prevent doxorubicin cardiotoxicity.

OR-093

CD73 severed as a potential prognostic marker and promote lung cancer cells migration via enhancing EMT progression

Zhao-wei Gao、Ke Dong
Tangdu hospital， Air Force Medial University

Objective To investigate the expression levels and prognostic value of CD73 in lung cancer. And moreover, to identify the effect and potential mechanism of CD73 on lung cancer cells proliferation and migration.
Method CD73 expression levels in lung cancer were analyzed base on GEPIA2 and GEO database. GEPIA2 and Kaplan-Meier Plotter (KM Plotter) was used to analyzed the correlation between CD73 expression and prognosis. GEO dataset were analyzed via GEO2R. CD73 overexpression cell model was construction via recombinant lentivirus transfection into A549 cells. CCK8 and colony formation assay were used to investigate cells proliferation. Migration and invasion ability were evaluated by scratch and transwell method.
Results Base on GEPIA2, GSE32683, GSE116959 and GSE37745 dataset, we found that CD73 expression were significant higher in tumor tissues of lung adenocarcinoma (LUAD) compared with that in non-tumor normal tissues and in lung squamous cell carcinoma (LUSC), while there were no significant difference of CD73 expression between LUSC and normal control tissues. Moreover, a high CD73 level predict poor overall survival (OS) of LUSC. However, GEPIA2 and KM plotter showed the opposite conclusion of prognostic value of CD73 in LUAD. By using cell experiment, we found that CD73 overexpression promoted proliferation, migration and invasion of lung cancer A549 cells. Furthermore, CD73 overexpression facilitates epithelial to mesenchymal transition (EMT) progression.
Conclusion Our results indicated that higher CD73 expression in LUAD and might be an poor prognostic marker for LUSC patients. CD73 play an important role in lung cancer cells proliferation and migration. These data allowed to support CD73 as a therapeutic target for lung cancer.

OR-094

基于液相色谱-串联质谱技术骨关节结核血清生物标志物的初步研究

陈汐濛、温新宇、王成彬
中国人民解放军总医院第一医学中心

目的 骨关节结核是结核分枝杆菌直接感染或迁延至骨关节组织所引起的一种肺外结核病。该病早期临床表现特异性差，现有临床影像学和实验室检查对该病早期检出率低，极大地影响患者的治疗和预后。针对骨关节结核早期诊断较为困难的情况，本课题利用液相色谱-串联质谱 (LC-MS/MS) 筛选骨关节结核患者血清中特异性表达的血清差异蛋白并进行临床验证和诊断评价，从实验室诊断的角度为骨关节结核早期诊断提供思路。
方法 收集临床上已确诊的骨关节结核、风湿免疫性骨关节炎患者血清样本，同时收集健康成人血清样本作为对照，并据此设置相应的疾病分组。应用 LC-MS/MS 对所收集血清样本的蛋白质成分进行分析，以 $p<0.05$ 且差异倍数>1.5 为标准，筛选在骨关节结核患者血清中特异性表达的血清差异蛋白。根据蛋白差异表达情况挑选特异性较好的数种蛋白，使用另一批次相同纳入排除标准的血清样本进行酶联免疫吸附试验 (ELISA) 验证以评估差异蛋白的诊断效能。
结果 经过 LC-MS/MS 分析，共筛选出 56 种在骨关节结核患者血清中特异性表达的血清差异蛋白，包含 29 种表达上调蛋白和 27 种表达下调蛋白。根据差异蛋白表达情况及 ELISA 验证的结果，初步得出人类血清补体 H 因子相关蛋白 1 (CFHR1)、人类血清补体 H 因子相关蛋白 2 (CFHR2) 为诊断效能较好的潜在血清差异蛋白标志物，其 ROC 曲线下面积值分别为 0.8733 和 0.8176。
结论 应用 LC-MS/MS 初步筛选出两种诊断效能较好的在骨关节结核患者血清中特异表达的潜在血清差异蛋白标志物，为骨关节结核早期实验室诊断的生物标志物研究和骨关节结核机体相关免疫机制研究提供了参考。

OR-095

The changes of vanA gene cluster mediate the collateral sensitivity between daptomycin and glycopeptide antibiotics in Enterococcus faecium

Weiliang Zeng[2]、lingbo wang[2]、相阔 zheng[2]、huaiyu jia[1]、wenya xu[2]、liqiong chen[1]、tieli zhou[2]、yao sun[2]、jianming cao[1]
1. Department of Medical Lab Science, School of Laboratory Medicine and Life Science, Wenzhou Medical University, Wenzhou, Zhejiang Province, China.
2. 温州医科大学附属第一医院

Objective Collateral sensitivity (CS), where resistance to one antimicrobial increases susceptibility to other drugs, is a good example against bacterial resistance. The aim of this study was to explore the molecular mechanisms of CS between daptomycin (DAP) and glycopeptides in Enterococcus faecium.
Methods 2 vancomycin-resistant and DAP-susceptible E. faecium strains (SC1174 and SC1762) were surveyed. Adaptation laboratory evolution was carried out to investigate CS by DAP induction experience in vitro. The susceptibility of strains to DAP and antibiotics was detected by antimicrobial susceptibility testing. Polymerase chain reactions (PCR), quantitative Real-time PCR (qRT-PCR), overlapping PCR and efflux pump inhibition testing were performed to explain the molecular mechanisms of CS.
Results Both strains exhibited high level resistance to DAP after exposure DAP for 36 days. CS between DAP and glycopeptides was observed in SC1762 and SC1762-D (highly DAP-induced SC1762 mutant) strains. The vanH gene mutations (Gly899Ala and Val914Asp) were only found

in SC1762-D. Compared with corresponding parental strains, the transcriptional expression level of vanA gene cluster in SC1174-D (highly DAP-induced SC1174 mutant) was significantly up-regulated, inversely, those in SC1762-D was obviously down-regulated except for the vanX gene. Overlapping PCR showed that the reversed insertion of IS1216 element between vanXY in SC1762 and SC1762-D. Besides, the results of efflux pump inhibition testing indicated that all strains had positive efflux pump phenotype.
Conlusions The decrease of vanA gene cluster expression was the main mechanism of CS between DAP and glycopeptides, and vanH mutation might also be related to resensitization.

OR-096

Nosocomial transmission and rearrangement of large resistance-virulence hybrid plasmids between two bacteremic ST11 carbapenem-resistant hypervirulent Klebsiella pneumoniae strains with low fitness cost

Yang Liu 、si chen、qisen huang
First Affiliated Hospital of Nanchang University

Objectives To characterize nosocomial transmission and rearrangement of the resistance-virulence plasmid between two ST11-K64 carbapenem-resistant hypervirulent Klebsiella pneumoniae (CR-hvKP) strains (JX-CR-hvKP-10 and JX-CR-hvKP-9) with low fitness.
Methods The serum killing assay, the quantitative biofilm formation assay, the Galleria mellonella infection model, and the mouse lethality assay were used to assess the virulence of JX-CR-hvKP-10 and JX-CR-hvKP-9. Whole-genome sequencing was used to analyze JX-CR-hvKP-10 and JX-CR-hvKP-9 chromosomes and plasmids. Fitness and conjugation experiments were also conducted using these two CR-hvKP isolates.
Results Clinical characteristics and phenotypic tests indicated that both JX-CR-hvKP-10 and JX-CR-hvKP-9 were multidrug-resistant and hypervirulent K. pneumoniae. Whole-genome sequencing and clinical information demonstrated that the super large resistance-virulence fusion plasmid pJX10-1 formed precisely by the fusion of pJX9-1 and pJX9-2 via the nosocomial transmission. Interestingly pJX9-1 itself was also a classic resistance-virulence fusion plasmid by way of the blaKPC-carrying resistance plasmid and pLVPK-like virulence plasmid. While pJX9-2 included numerous genes encoding for nucleotide transport and metabolism such as exonuclease, DNA polymerase, DNA ligase, integrase, recombinase. Compared with classic K. pneumoniae ATCC700603, fitness analysis revealed no significant difference in growth was observed between JX-CR-hvKP-10 and JX-CR-hvKP-9.
Conclusion Nosocomial transmission and rearrangement of a blaKPC-harboring plasmid and a pLVPK-like virulence plasmid with a low fitness cost in ST11 K. pneumoniae enhances drug resistance and virulence simultaneously. This can enhance the environmental adaptability of CR-hvKP, and promote its spread and prevalence. Thus, active surveillance of this hybrid plasmid is needed to prevent these efficient resistance-virulence plasmids from disseminating in hospital settings.

OR-097

肺炎链球菌疫苗蛋白 ΔA146Ply 的矿化纳米颗粒在鼻咽部感染中的研究

吴静雯
成都市第三人民医院

目的 本文旨在研究肺炎链球菌蛋白疫苗 ΔA146Ply 的矿化纳米颗粒在鼻咽部感染中的免疫保护作用。
方法 利用大肠杆菌原核表达系统，通过分子克隆技术表达肺炎链球菌疫苗蛋白 ΔA146Ply 及含有生物矿化肽的疫苗蛋白 ΔA146Ply-PA44，分别经 Ni2+柱纯化、去除内毒素。将 ΔA146Ply-PA44 置于富含 Ca2+和 PO43-的弱碱性溶液中处理后制备成纳米级的生物矿化颗粒（ΔA146Ply-PA44@CaP）。以 ΔA146Ply、ΔA146Ply-PA44@CaP 及 PBS 分别免疫小鼠后取其末梢血检测特异性抗体效价；于末次免疫后取小鼠脾细胞，再刺激并检测上清液中细胞因子分泌量。末次免疫后经鼻腔攻毒肺炎链球菌 CMCC31693，于 3 天后取肺泡灌洗液计数鼻腔及肺部细菌载量，同时取其肺部行 HE 染色评估炎症情况。
结果 以 ΔA146Ply、ΔA146Ply-PA44@CaP 及 PBS 分别免疫小鼠后，测得 ΔA146Ply-PA44@CaP 免疫组小鼠产生的特异性抗体效价较 ΔA146Ply 及 PBS 组均有显著升高；ΔA146Ply-PA44@CaP 免疫组小鼠脾细胞再刺激后产生的细胞因子 IL-4，IFN-γ 较 ΔA146Ply 及 PBS 免疫组均有显著增高。末次免疫后经鼻腔攻毒肺炎链球菌 CMCC31693，于 3 天后取肺泡灌洗液计数鼻腔及肺部细菌载量，结果显示 ΔA146Ply-PA44@CaP 免疫组小鼠肺泡灌洗液中细菌载量较 ΔA146Ply 及 PBS 免疫组明显减少，同时小鼠肺部 HE 染色提示，ΔA146Ply-PA44@CaP 免疫组的小鼠肺部炎症反应较 ΔA146Ply 及 PBS 免疫组明显较弱。
结论 以上结果提示肺炎链球菌蛋白疫苗 ΔA146Ply 的矿化纳米颗粒能诱导小鼠产生较强免疫保护效应并可有效抵抗肺炎链球菌的鼻咽部定植及感染。

OR-098

肺炎克雷伯菌肝脓肿不同临床特征分组的比较分析

鲁敏仪、郑佳佳
北京大学第三医院

目的 通过比较分析肺炎克雷伯菌肝脓肿（KPLA）与其他细菌肝脓肿（NKPLA）的临床特征以及对肺炎克雷伯菌肝脓肿亚分组的临床特征和实验室指标差异分析，为 KPLA 的诊断治疗提供参考和依据。
方法 分析北京大学第三医院 2016 年 1 月至 2020 年 12 月收治的 215 例肝脓肿患者的临床资料，比较 KPLA 患者和 NKPLA 患者、KPLA 是否合并糖尿病、是否患有胆道疾病、是否患有消化道疾病亚分组的临床特征，实验室检测指标，病原学结果、治疗方法及预后情况，$P<0.05$ 认为具有显著性差异。
结果 215 例肝脓肿病例中细菌培养结果阳性 98 例，其中 72 例为肺炎克雷伯菌，KPLA 分离的肺炎克雷伯菌对除氨苄西林外的大部分抗菌药物敏感。与 NKPLA 相比，KPLA 患者多同时患有糖尿病（$P=0.013$），且临床表现以畏寒或寒战（$P=0.010$）为主，KPLA 组 AST 水平较高（$P<0.01$）；而 NKPLA 患者多同时患有胆道疾病（$P<0.01$），且 NKPLA 组血红蛋白水平较低（$P=0.029$）。KPLA 合并糖尿病患者相比于不合并糖尿病患者白细胞计数（$P=0.049$）、中性粒细胞绝对计数（$P=0.041$）高于非糖尿病组，而 KPLA 非糖尿病组的 AST 水平高于糖尿病组（$P=0.043$）；两组在并发症、治疗方法、治疗结果上无明显差异，但糖尿病组的治疗时间明显长于非糖尿病组（$P=0.017$）。KPLA 合并胆道疾病患者血小板计数（$P=0.035$）及 GGT（$P=0.016$）水平高于无

胆道疾病的患者，且治疗效果差（*P*=0.033）。而 KPLA 是否合并消化道疾病两组间除年龄外无显著差异。
结论 肺炎克雷伯菌是引发细菌性肝脓肿的主要致病菌，KPLA 患者多同时患有糖尿病，易发生其他部位脓肿，眼内炎等侵袭性并发症，且炎症指标升高，治疗时间长；此外 KPLA 合并胆道疾病治疗效果差，应早期合理应用抗菌药物治疗，脓肿液化应及时穿刺引流。

OR-099

Profile analysis of circRNAs in osteoclasts infected by intracellular Staphylococcus aureus

Haifang Zhang、Hong Du
Department of Clinical Laboratory, The Second Affiliated Hospital of Soochow University, Suzhou, Jiangsu, 215004, China.

Circular RNAs (circRNAs) play important roles in multiple physiopathological processes. However, little is known about the roles of circRNAs in the pathogenesis of osteomyelitis, which is primarily caused by Staphylococcus aureus infection. It has been reported that S. aureus can survive in osteoclasts, but the function of osteoclast circRNAs in response to intracellular S. aureus infection remains unclear. In this study, the circRNA expression profile of mouse osteoclasts intracellularly infected with S. aureus was investigated by RNA sequencing. In total, 24 upregulated and 62 downregulated differentially expressed circRNAs (DEcircRNAs) were identified. Subsequently, Gene Ontology annotation and Kyoto Encyclopedia of Genes and Genomes pathway enrichment analysis were used to further study biological functions of the DEcircRNAs. Interestingly, the phospholipase D signaling pathway, bacterial invasion of epithelial cells, and Fc gamma R-mediated phagocytosis were the most significant pathways enriched for the host genes of upregulated DEcircRNAs, while T cell and B cell receptor signaling pathways and axon guidance were the most significantly enriched pathways of downregulated DEcircRNAs. Moreover, we constructed circRNA-microRNA and protein-protein interaction networks that may be associated with intracellular S. aureus infection in osteoclasts. Finally, we confirmed that circPum1 regulated Pmp22 expression via miR-767 by quantitative reverse transcription PCR and Western blot analyses. This study provided the first profile analysis of circRNAs in osteoclasts infected by intracellular S. aureus and a novel idea for understanding the pathogenesis of osteomyelitis.

OR-100

Hypoxia stimulats adipogenesis at the expense of the osteogenesis via leptin in fibroblast-like synoviocytes from patients with rheumatoid arthritis

Menglei Ding、Lieying Fan
Shanghai Dongfang Hospital Affiliated Tongji University

Objective This study aimed to investigate the role of hypoxia on rheumatoid arthritis fibroblast-like synoviocytes (RA-FLSs) osteogenesis and adipogenesis.
Methods RA-FLSs and osteoarthritis (OA)-like synoviocytes (OA-FLSs) were isolated and cultured, The expression of CD73, CD90, CD105, and CD45 as well as apoptotic cells in both groups was examined by flow cytometry. The self-renewal capacity was measured by the clone-forming assay. The osteogenic or adipogenic differentiation potential was confirmed by specific staining after continuous cultivation in osteogenic or adipogenic induction medium, respectively. All these experiments were performed in parallel under hypoxia (3% O2). The gene expression

profiles GSE21959, GSE32006, and GSE5587 were downloaded from the Gene Expression Omnibus (GEO) database. The differentially expressed genes (DEGs) between normoxic and hypoxic cells were identified and overlapped. Subsequently, the role of leptin in osteogenesis and adipogenesis of RA-FLSs was assessed by RNA interference. the mRNA and protein expression levels of leptin as well as osteogenic and adipogenic markers were measured using qRT-PCR and western blotting.
Results RA-FLSs presented a mesenchymal stem cell (MSC)-like phenotype and showed limited self-renewal capacity and multi-differentiation potential. Hypoxia inhibited RA-FLSs osteogenic differentiation by downregulating the expression of runt-related transcription factor 2 (Runx2), osteocalcin (Ocn), alkaline phosphatase (Alp) and osteostrix (Osx). In contrast, hypoxia significantly promoted RA-FLSs adipogenic differentiation by upregulating CCAAT enhancer-binding protein α (C/EBPα), peroxisome proliferator activated receptor γ (PPARγ) and fatty acid binding protein 4 (FABP4). Bioinformatics analysis indicated that leptin was the only overlapping gene among the three gene expression profiles. The expression of leptin increased when RA-FLSs responded to hypoxic stimuli. Konckdown of leptin rescued the imbalance of adipogenesis and osteogenesis induced by hypoxia in RA-FLSs.
Conclusion RA-FLSs possess MSC-like characteristics. Hypoxia readily stimulated RA-FLSs to differentiate into adipocytes instead of osteoblasts via leptin. Our results indicate that leptin could be a new molecular target for therapy in RA.

OR-101

Association of serum total cholesterol with pegylated interferon-α treatment in HBeAg-positive chronic hepatitis B patients

Zhen Xun 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Background Recent studies suggest that serum lipids are associated with pegylated interferon-alpha (PegIFNα) treatment response in chronic hepatitis C patients. However, the role of serum lipids in influencing the outcome of HBV treatment is not well understood. This study aims to investigate the association of serum lipids with the response to interferon-alpha treatment for chronic hepatitis B (CHB) patients.
Methods We dynamically measured 11 clinical serum lipid parameters of 119 HBeAg-positive CHB patients, including 53 patients who achieved sustained response (SR) and 66 patients who achieved nonresponse (NR) induced by PegIFNα treatment for 48 weeks.
Results The dynamic analysis showed that the baseline serum total cholesterol (TCHO) level was higher in the NR group than that in the SR group (P = 0.004). Moreover, the correlation analysis demonstrated a significant positive correlation between TCHO and HBsAg at baseline (P = 0.009). In addition, CHB patients with the high baseline TCHO levels exhibited higher HBV DNA, HBsAg, HBeAg and HBeAb levels during early treatment periods (weeks 0, 4, 12 and 24) than those with the low TCHO levels. Furthermore, the logistic regression analysis identified that baseline serum TCHO was a risk factor of NR achievement (OR = 4.94, P = 0.047).
Conclusions Our results indicated that serum TCHO was associated with PegIFNα therapeutic response in HBeAg-positive CHB patients which suggested that serum TCHO could be useful as an auxiliary clinical factor to predict poor efficacy of PegIFNα therapy.

OR-102

Anti-Citrullinated Protein Antibodies Induce Trained Immunity in RA Synovial Tissues and Its Gene Signature Correlates with the Response to Clinical Therapy

Qiao Zhong[1]、Xiaoli Dai[2]、Xiaoqiu Dai[3]、Fangyuan Gong[3]、Xiaoming Gao[3]
1. the Affiliated Suzhou Hospital of Nanjing Medical University, Suzhou Municipal Hospital, Suzhou, China
2. 苏州大学附属第二医院
3. 苏州大学生物医学研究院

Much evidence suggests that trained immunity is inappropriately activated in the synovial tissue in rheumatoid arthritis (RA), but the underlying mechanism remains unclear. Here, we describe how RA-specific autoantibody deposits can train human monocytes to exert the hyperactive inflammatory response, particularly via the exacerbated release of tumor necrosis factor α (TNFα). Comparative transcriptomic analysis by plate-bound human IgG (cIgG) or β-glucan indicated that metabolic shift towards glycolysis is a crucial mechanism for trained immunity. Moreover, the cIgG-trained gene signatures were enriched in synovial tissues from patients with ACPA- (anticitrullinated protein antibody-) positive arthralgia and undifferentiated arthritis, and early RA and established RA bore a great resemblance to the myeloid pathotype, suggesting a historical priming event in vivo. Additionally, the expression of the cIgG-trained signatures is higher in the female, older, and ACPA-positive populations, with a predictive role in the clinical response to infliximab. We conclude that RA-specific autoantibodies can train monocytes in the inflamed lesion as early as the asymptomatic stage, which may not merely improve understanding of disease progression but may also suggest therapeutic and/or preventive strategies for autoimmune diseases.

OR-103

A novel class of tsRNA signature as a biomarker for diagnosis and prediction of nephritis in SLE

Ping Yang、han shen
Department of Laboratory Medicine，Drum Tower Hospital，Nanjing University Medical School

Object To explore the value of a novel class of tsRNA signature as a biomarker for diagnosis and prediction of nephritis in SLE.
Methods First, 110 normal controls and 191 SLE patients of which 75 SLE without LN patients and 116 SLE with LN patients were recruited from The Affiliated Drum Tower Hospital of Nanjing University Medical School. A total of 10 mL serum was respectively mixed in each group (24 normal controls , 23 SLE without LN patients and 33 SLE with LN patients) were performed initial screening by small RNA sequencing. Real-time fluorescence quantitative Polymerase Chain Reaction (RT-qPCR) was used to verify the screened out 10 differentially expressed tsRNAs. Differentially expressed tsRNAs were further validated by RT-qPCR in residual 52 SLE without LN patients, 83 SLE with LN patients and 86 healthy controls. The severity degree in SLE patients was assessed by the systemic lupus erythematosus disease activity index 2000 (SLEDAI-2K). The diagnostic efficacy was assessed by Receiver Operating Characteristic Curve (ROC). Further more, correlations of tsRNAs with clinical manifestations of SLE patients were analyzed. Finally, a bioinformatic analysis was performed to investigate the potential functions of differentially expressed genes.
Results 393 tsRNAs were differentially expressed between the SLE without LN patients and NC patients. Among which, significantly upregulated expression levels of tRF-1:23-chrM.Ala-TGC, tRF-27:42-Gly-GCC-1-M3, tRF-1:28-His-GTG-1, tRF-68:85-Ser-GCT-3-M4, tRF-1:22-Val-AAC-1-

M7, tRF-68:85-Ser-TGA-4, tRF-65:86-Leu-CAA-1-M5, tRF-53:71-chrM.Pro-TGG, tRF-57:76-Tyr-GTA-2-M2,
tRF-57:75-Gln-CTG-2-M3 were further validated in serum from SLE with LN patients by RT-qPCR. Meanwhile, we identified the area of the tsRNA under the AUC curve of distinguishing SLE group and normal group was 0.67, LN group and normal group was 0.73, SLE without nephritis group and nephritis group was 0.81. The area under the AUC curve of tsRNA combined with dsDNA in distinguishing SLE group and normal group was 0.95, the area under the AUC curve of tsRNA combined with 24-hour urine protein in distinguishing SLE without nephritis group and nephritis group was 0.89. We also identify tsRNA biomarkers for the classification of both dsDNA-positive and negative SLE patients, as well as anti-smith antibodies-positive and negative RA patients. Bioinformatic analysis suggested several gene ontology (GO) and KEGG terms and signal pathways may play important roles in the development of SLE.
Conclusion In summary, Our data provided comprehensive evidence regarding the differential expression of tsRNAs in serums from SLE patients indicating that these tsRNAs may be a potential biomarker for diagnosis and prediction of nephritis in SLE.

OR-104

In-depth plasma proteomics analysis identifies the vascular involvement biomarkers of Behcet's disease progression

Linlin Cheng [1]、Dongxue Wang[3]、Guibin Wang[2]、Ziyan Wu[1]、Meng Xu[2]、Xiaomei Zhang[2]、Te Liang[2]、Liubing Li[1]、Chenxi Liu[1]、Chundi Wei[2]、Songxin Yan[1]、Fengchun Zhang[1]、Xiaobo Yu[2]、Yongzhe Li[1]
1. Peking Union Medical College Hospital, Peking Union Medical College and Chinese Academy of Medical Sciences, Beijing, China
2. 国家蛋白质科学中心(北京)，北京蛋白质组研究中心
3. 国家蛋白质科学中心(北京)，北京蛋白质组研究中心

Objectives Behcet's disease (BD) is a heterogeneous chronic vasculitis, with the highest prevalence along the ancient Silk Road. However, the pathogenesis is still unclear and satisfactory biomarkers for diagnostics and prognostics are lacking. The clinical heterogeneity further increases the difficulty of marker discovery. To address this challenge, we executed the largest proteomics analysis of plasma proteins in BD to reveal the potential pathogenesis and identify markers that are expected to be used in diagnosis and treatment.
Methods The plasma proteins from 98 BD patients with various manifestations and 31 healthy controls (HC) were measured using our in-depth proteomics platform comprised of data-independent acquisition mass spectrometer (DIA-MS) and Antibody Microarray (AA) to screen candidate protein markers for BD. Functional annotation and pathway analysis of significant proteins were applied to uncover their pathogenic roles in BD. Potential markers for diagnostics, phenotypes and severity evaluation were identified and further validated in an independent cohort by ELISA comprised of 39 BD patients and 10 HC.
Results 228 significantly expressed proteins were identified between BD patients and HC ($P<0.05$). The most extensively enriched biological process by 130 proteins ($P<0.01$) are 1) complement and coagulation cascades, 2) immune and inflammatory response, 3) serine-type endopeptidase activity, 4) platelet activation and coagulation dysfunction, 5) plasma lipoprotein metabolism, highlighting the vital role of complement, serine-type endopeptidase, lipoprotein in BD, and the involvement of complement, leukocyte, platelet and immunoglobulin during the inflammation, immune response and coagulation dysfunction in BD. KEGG analysis further highlighted the role of pathogenic infection in BD. Specifically, different proteins panels and pathologic pathways underline various phenotypes of BD. In the subsets with vascular involvement, the role of platelet, component of complement systems and IGF/IGFBPs (Insulin-like Growth Factor/Insulin-like Growth Factor Binding Proteins) were further highlighted and present potential therapeutic values in BD. The protein markers of HABP2, TNC and SERPINA3 were discovered and validated to indicate vascular involvement and disease risk in BD.

Conclusion We performed the largest proteomics study in BD. The results obtained from this proteomics study provide the in-depth insight in the BD pathogenesis and different phenotypes. Three biomarkers (HABP2, TNC and SERPINA3) were associated with the vascular lesion and severity of BD progression.

OR-105

The value of AMA-M2, gp210 and sp100 antibody levels in disease progression of primary biliary cholangitis

Zhan Wang、Mingjun Liu、Tiantian Xu、Wenshuai Li
The Affiliated Hospital of Qingdao University

Objective In this study, multiplex bead-based flow fluorescent immunoassay (MBFFI) was used to quantitatively detect serum AMA-M2, gp210 and sp100 antibodies in patients with PBC, and to explore the clinical value of antibody level in evaluating the disease progression of PBC.
Methods The case group included 340 patients with PBC. Other disease groups included 81 patients with autoimmune hepatitis (AIH) and 62 patients with systemic lupus erythematosus (SLE). And there are 171 healthy subjects served as healthy control group. We used MBFFI to detect the AMA-M2, gp210 and sp100 antibodies quantitatively in all serum samples. The difference in serum autoantibody contents between PBC, other disease and healthy control groups were compared. Another purpose of this study is to explore the relationship between the level of antibodies to AMA-M2, gp210 and sp100 antibody and the disease progression, especially with the natural course of disease. In PBC group, the difference in antibody levels between PBC cirrhosis patients and non-cirrhosis patients was compared. And the correlation between antibody level and other laboratory indexes was also evaluated. In addition, we analyzed AMA-M2, gp210 and sp100 antibody levels in 25 patients with PBC at two visits before and after a 1-year interval to evaluate the changes in antibody levels and their relationship with disease progression.
Results The serum levels of AMA-M2, gp210 and sp100 antibodies in PBC group were significantly higher than those in other disease groups and healthy controls (P=0.000). The serum gp210 antibody levels of patients in natural course stage I [3.09 (2.16-18.08) AU], natural disease stage II [3.46(2.16-6.61) AU] and natural disease stage III [6.28(2.13-16.33) AU] were lower than that of patients with natural disease stage IV [27.90 (4.28-169.56) AU] (P=0.000). The level of serum gp210 antibody in cirrhosis group [27.90 (4.28-169.56) AU] was higher than that in non-cirrhosis group [3.57 (2.16-12.46) AU] (P=0.000). However, there was no significant difference in the antibody levels of AMA-M2 and gp210 between cirrhosis group and non-cirrhosis group (P>0.05). Serum AMA-M2 level was positively correlated with ALP (r=0.186, P=0.001) and GGT (r=0.143, P=0.013), but not with other laboratory indexes. Serum gp210 antibody level was positively correlated with ALT (r=0.150, P=0.007), AST (r=0.257, P=0.000), TBIL (r=0.241, P=0.000), DBIL (r=0.263, P=0.000), ALP (r=0.266, P=0.000) and GGT (r=0.188, P=0.001), and it was negatively correlated with ALB (r=-0.240, P=0.000). However, there was no correlation between gp210 antibody and PLT. Serum sp100 antibody level was negatively correlated with ALP (r=-0.123, P=0.034) and GGT (r=-0.142, P=0.013), but there was no significant correlation between other laboratory indexes. In this study, twenty-five PBC patients had a second visit in our hospital during sample collection, the interval between two visits was 12.2 ± 3.38 months. The patients with serum AMA-M2, gp210 and sp100 antibody levels ≥ 20AU at the first visit had different degrees of changes in antibody levels during the follow-up. However, in the patients with serum antibody levels＜20AU at first visit, their antibody levels were stable and did not fluctuate significantly during the treatment of the disease.
Conclusion The level of serum gp210 antibody in PBC patients is correlated with the disease natural course. And High level of gp210 antibody may indicate rapid progression of the disease. PBC patients with higher levels of gp210 were more likely to develop cirrhosis. In addition, the level of AMA-M2 and sp100 may be an indicator of cholestasis.

OR-106

无精症患者精液代谢组学分析

轩冉
解放军总医院

目的 无精子症（Azoospermia），是指在所射出的精液中连续 3 次找不到一个精子，约占男性不育症患者的 15%-20%，病因繁多，根据输精管道有无阻塞分为梗阻性无精症（obstruction azoospermia，OA）和非梗阻性无精症（non-obstruction azoospermia, NOA）。研究精液成分可以提高临床诊断的准确性，更好的了解无精症患者的病理生理学。代谢组学为评价生物标志物和更好的理解病理机制提供了新的平台。本研究目的是利用代谢组学的方法分析无精症患者的精浆，找到能鉴别诊断无精症类型的生物标志物，从而为无精症患者的临床诊断治疗提供更多的信息。
方法 收取门诊健康查体患者（n=30）和无精症患者（n=40）精液，并将无精症患者根据诊断分为 OA 组（n=23）和 NOA（n=17）。在 LC-MS 分析之前，将标本进行混合模式固相萃取和两步衍生化；预处理好的标本上机进行 LC-MS 质谱分析（系统包括 LC-30AD 超高性能 LC 系统、离子陷阱-飞行时间质谱仪、LCM solution3.72 程序）；质谱系统得出的数据导入到 MZmine2.0 软件中进行峰检测、同位素峰分组、峰积分和特征对比，然后在三个水平对代谢物数据进行鉴（第一级是通过比较保留时间和 MS/MS 信息与商业标准的特征阳性鉴定代谢物；第二级将特征的 MS/MS 信息与 HMDB、脂质组学谱、MSFINDER 软件中的预测/报道片段进行比较；第三级对没有 MS/MS 谱的特征通过在 HMDB 数据库中搜索准确的特征量进行推定识别，并且选择具有最低 Δppm 的候选物质）；最后得到预期结果。
结果 研究发现健康对照组和无精症组存在差异性代谢物，且差异具有统计学意义；OA 组和 NOA 组存在具有鉴别诊断的生物标志物。
结论 无精症是目前男性不育中常见的疾病，部分患者的发病机制目前尚不明确。代谢组学是新兴的组学技术，与基因组学、蛋白组学不同的是，该技术分析的是整个代谢组，即生物系统内代谢的最终产物；代谢组的组成决定了细胞当前的表型状态，以及对细胞和细胞外刺激的相应变化，从而使代谢组学研究比其他组学方法提供更多的信息，特别是在研究细胞对外源性刺激的反应或在病理情况下。基于此，对精液的代谢组学分析具有重要意义。

OR-107

POU4F3 基因两个新突变致常染色体显性遗传非综合征型耳聋家系的鉴定分析及其分子标志物价值研究

白晓卉[1]、张凤国[2]、肖云[2]、卢志明[1]、徐磊[2]
1. 山东第一医科大学附属省立医院
2. 山东大学附属省耳鼻喉医院

目的 分析两个遗传性非综合征型耳聋家系的临床听力学特征，并利用遗传性耳聋基因目标区域捕获测序技术鉴定致聋基因,并评价致病突变作为分子标志物的诊断价值及意义。
方法 通过家系调查，收集到两个感音神经性聋家系的临床资料，整理并分析该家系成员的临床听力学和遗传学特征，对家系成员进行调查并绘制系谱图。我们利用进行耳聋基因目标区域捕获技术和大规模平行测序技术，对先证者的 DNA 标本进行了已知耳聋基因突变筛查。继而对获得的测序结果进行分析，确定候选基因。利用 Sanger 测序技术对所有家系成员进行候选基因突变验证，并对氨基酸保守性进行分析。结合临床患者资料，评价 POU4F3 基因 2 个新突变作为分子标志物的价值。
结果 根据绘制的系谱图，该耳聋家系遗传方式为常染色体显性遗传。该家系耳聋特征为双侧对称性的全频感音神经性耳聋，发病特点为语后发病、进展性听力损失。耳聋基因目标区域捕获测序技

术分析结果提示，耳聋基因 POU4F3 存在 2 个新突变 c.704_705del (p.T235fs) 和 c.593G>A(p.R198H)，分别为这两个耳聋家系的致病病因。这 2 个位点在多物种之间保守，Sanger 测序确认 2 个新突变与家系耳聋表型共分离，在 200 个正常人群中未发现。

结论 耳聋基因 POU4F3 存在 2 个新突变 c.704_705del (p.T235fs) 和 c.593G>A(p.R198H)，分别是两个耳聋家系的致病病因，在诊断常染色体显性遗传性耳聋致病病因中具有重要意义和临床价值。

OR-108

A Homologous Recombination Deficiency Signature-Derived Gene Expression Panel Predicts Chemotherapeutic Response of Breast Cancer

Zhiyuan Wu[1,2,3]、Can Yang[1]、Xinju Zhang[4]、Xuemei Tang[2]、Qingyun Zhng[2]、Ming Guan[1,2,3,4]

1. 复旦大学附属华山医院检验科
2. 复旦大学附属华山医院北院中心实验室
3. 复旦大学附属华山医院北院检验科
4. 复旦大学附属华山医院中心实验室

Objective Homologous Recombination Deficiency (HRD) is the emerging genomic marker for malfunction of homologous recombination and determines the surgical intervention, chemotherapy, and targeted medication of breast cancer. However, detection of HRD requires the quantification of genomic scars by high-throughput DNA sequencing, which is both labor- and technical-intensive. The aim of this study is to establish a gene expression panel (GEP) representing the HRD status and evaluate its clinical significance in breast cancer management.

Methods A 23 differentially expressed gene (DEG) list was generated with the transcriptomic data of HRD-high and HRD-low subgroup from the cancer genomic atlas (TCGA) breast cancer cohort (n = 981). Lasso regression model was performed on the DEG list to establish a GEP with the best performance fitting. The pathway specificity of the GEP was determined by gene set enrichment analysis (GSEA) and DNA repair score ranking test in the TCGA group and further validated by HRD quantification with an independent cohort of 20 breast cancer tissues collected in the Department of General Surgery, Huashan Hospital. Survival analysis was performed to evaluate the clinical significance of the GEP in 5 breast cancer cohorts with over 5,000 cases (TCGA, n = 1,020; METABRIC, n = 1,903; GSE42568, n = 104; GSE20685, n = 327; GSE96058, n = 3,273). The sensitivity and specificity of GEP, OncotypeDX Breast Cancer Assay and PAM50 in overall survival prediction were compared by receiver operating characteristic (ROC) curve analysis. Drug response of breast cancer chemotherapy agents was compared with the pharmacogenomic data from two cell line databases [Genomics of Drug Sensitivity in Cancer (GDSC) and Cancer Therapeutics Response Portal (CTRP)] and cancer tissue database (TCGA ncRNA model).

Results A three-gene (*PHGR1*, *CAPN8*, and *PRAME*) expression based GEP was generated to represent the HRD status in TCGA. GSEA analysis revealed cell cycle, DNA replication, homologous recombination repair, oxidative phosphorylation and proteasome as the top 5 enriched pathways of GEP. Decreased RPPA DDR score, recombination proficiency score, and increased TP53 inactive score and PARPi7 was enriched in TCGA samples with high GEP (Kolmogorov–Smirnov test, $P < 10^{-5}$). In the 20 fresh breast cancer tissues, GEP score was significantly increased in the HRD high group (Fisher's exact test, $P = 2.03\times10^{-3}$). Breast cancer with higher GEP demonstrated unfavored overall survival in TCGA [HR = 1.87 (95% CI = 1.33-2.63), $P = 2.90\times10^{-4}$], METABRIC [HR = 1.20 (95% CI = 1.07-1.35), $P = 2.41\times10^{-3}$], GSE42568 [HR = 2.84 (95% CI = 1.39-5.82), $P = 4.30\times10^{-3}$], GSE20685 [HR = 1.90 (95% CI = 1.21-2.96), $P = 5.04\times10^{-3}$], and [HR = 2.04 (95% CI = 1.63-2.56), $P = 2.45\times10^{-6}$]. Moreover, the GEP score outperformed the 21 gene OncotypeDX and PAM50 in the overall survival prognosis in TCGA [AUC = 0.634 (GEP) vs 0.619 (OncotypeDX) vs 0.585 (PAM50)]. Subgroup analysis further revealed the association between high GEP and chemotherapy sensitivity in TCGA [n = 434, HR

= 2.4 (95% CI = 1.15-5.02), *P* = 0.02], which was further supported by the drug response analysis in the GDSC and CTRP cell lines and TCGA tissue samples (Olaparib, Rucaparib, 5-Fluorouracil, Cisplatin, Doxorubicin, Methotrexate, IC50 comparison by two sample t-test, all *P* < 0.05).
Conclusion The three-gene (*PHGR1*, *CAPN8*, and *PRAME*) GEP represents the HRD status of breast cancer. This gene expression marker sets a promising index for the prognosis and drug response prediction of breast cancer patients.

OR-109

长链非编码 RNA AC012073.1 对乳腺癌细胞迁移侵袭的影响及临床价值研究

孔雪、王传新
山东大学第二医院

目的 探讨长链非编码 RNA（lncRNA）AC012073.1 在乳腺癌（BC）中的表达及对细胞迁移侵袭的影响，并对其临床价值进行研究。
方法 运用高通量芯片和 TCGA 数据挖掘分析在 BC 组织中高表达并与患者预后不良相关的 lncRNAs。利用实时荧光定量 PCR（qRT-PCR）检测 AC012073.1 在乳腺癌细胞和血清中的表达水平。通过小干扰或质粒转染技术敲减或过表达 AC012073.1 并利用 Transwell 和划痕实验检测其对细胞迁移和侵袭能力的影响。利用 TargetScan 等数据库对下游作用靶点和功能富集分析进行预测，并运用 Cytoscape 软件绘制 ceRNA 调控网络。采用受试者工作曲线（ROC）分析血清 AC012073.1 对乳腺癌的诊断效能。
结果 筛选发现一种新型 lncRNA AC012073.1，在乳腺癌组织中高表达且与患者预后不良显著相关（P=0.031），乳腺癌细胞系中 AC012073.1 表达水平明显高于正常乳腺上皮细胞。选择 MDA-MB-231 和 MCF-7 两株细胞进行功能实验，结果显示，敲减 AC012073.1 显著抑制细胞迁移和侵袭能力，反之过表达 AC012073.1 后，细胞的迁移和侵袭能力明显增强。下游靶点和基因通路分析显示 AC012073.1 可能通过调控肿瘤经典信号通路促进乳腺癌的进展。此外，qRT-PCR 结果显示，与健康对照相比，乳腺癌患者血清中 AC012073.1 显著升高，ROC 曲线结果显示曲线下面积（AUC）为 0.833，表明其对乳腺癌具有良好的诊断价值。
结论 研究表明 AC012073.1 在乳腺癌中显著高表达,促进乳腺癌细胞的迁移和侵袭，并可能成为乳腺癌诊断和预后的潜在生物标志物。

OR-110

Epithelial circulating tumor cells with a heterogeneous phenotype are associated with metastasis in NSCLC

Yujuan Zhang
National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Objectives To analyze the clinical relevance of heterogeneous phenotypes of peripheral circulating tumor cells (CTCs) in non-small cell lung cancer (NSCLC).
Materials and Methods CTCs in 5 mL venous blood were enriched by using the CanpatrolTM CTC technique in 82 NSCLC patients. 60 patients did not receive any treatment and 22 patients had received chemoradiotherapy or targeted therapy. And then CTCs were subjected to RNA in situ hybridization with a combination of epithelial (EpCAM and CK8/18/19) and mesenchymal (vimentin and TWIST1) markers.
Results In 82 NSCLC cohort, only 2 patients didn't detect CTCs, the overall CTCs detection rate was 97.5% (80/82). The median number of total CTCs per 5mL blood was 21 (range 0-90).

Across all the patients, the median number of hybrid E/M phenotype CTCs was 17 cells/5mL (range 0-83), and the median number of E-CTCs and M-CTCs was 1 cells/5mL (range 0-17 and 0-47, respectively).
For 60 treatment naïve NSCLC, only one patient didn't detect CTCs and 27 patients showed all three phenotypes. A total of 13 patients showed both M-CTCs and hybrid E/M-CTCs, 7 patients showed both E-CTCs and hybrid E/M-CTCs, 11 patients showed pure E/M-CTCs and 1 patient showed pure M-CTCs.
The total number of CTCs detected in the 59 treatment naïve NSCLC ranged from 1-90 cells/5mL with the median value being 22 cells/5mL. The number of hybrid E/M phenotype CTCs, the most common phenotype observed in each patient, ranged from 0-83 cells/5mL with a median value of 13 cells/5mL. The number of E-CTCs and M-CTCs ranged from 0-17 cells/5mL and 0-47 cells/5mL, respectively, with the median value being 1 cells/5mL.
According to the fluorescence intensity of epithelial and mesenchymal markers, hybrid E/M phenotype CTCs were further divided into three subtypes, including the number of E>m CTCs, e=m CTCs and e<M CTCs that contained ranges of 0-17 cells/5mL, 0-65 cells/5mL and 0-21 cells/5mL, with median values being 1 cells/5mL, 15 cells/5mL and 1 cells/5mL, respectively.
The distribution of total CTCs/5ml blood between advanced versus early stages showed no significant differences. However, the non-E/M CTCs, especially the M-CTCs, were significantly greater more in advanced stage NSCLC patients compared to patients in early stages. The ROC curve with a cutoff value of M-CTCs being 2 cells/5 mL blood demonstrated that the sensitivity of M-CTCs in the diagnosis of advanced NSCLC was 58.62% and the specificity was 77.42% (AUC=0.6974, 95% CI, 0.5609 to 0.8340).
The distribution of total CTCs/5ml blood between patients with versus without distant metastasis showed no significant difference, while hybrid E/M CTCs, especially the e=m-CTCs, significantly differed between them. Interestingly, compared to distant metastasis cohort, patients without distant metastasis had more number of hybrid E/M CTCs and e=m-CTCs.
Findings showed that 1/15patients (7%) with distant metastasis showed pure hybrid E/M-CTCs and pure M-CTC, a total of 3/15 (20%) showed both E-CTCs and E/M-CTCs (E+E/M CTCs), a total of 5/15 (33%) showed both E/M CTCs and M-CTCs (E/M+M CTCs) and a total of 6/15 (40%) showed three phenotypes (E+E/M+M CTCs). In patients without distant metastasis, a total of 10/45 (22%) showed pure hybrid E/M CTCs, a total of 4/45 (9%) showed E+E/M CTCs, a total of 9/45 (20%) showed E/M+M CTCs, a total of 21/45 (47%) showed E+E/M+M CTCs and only one did not show detectable levels of CTCs. Though statistical analysis showed that the distribution of CTCs subpopulations in patients with and without distant metastasis was not statistically significant, from the figures, we found that patients with pure hybrid E/M-CTCs showed a lower proportion in distant metastasis positive cohort compared to negative ones(7% vs 22%); while patients with E+E/M CTCs (20% vs 9%) and E/M+M CTCs (33% vs 20%) showed a higher proportion.
Conclusion We concluded that E-CTCs with a hybrid E/M phenotype are associated to metastasis in therapy-naïve NSCLC patients.

OR-111

Membrane feature-inspired identification biosensor assists extracellular vesicle differentiation and pancreatic cancer diagnosis

Ping Li、Mengqiu Gao、Zijian Hu、Yueqing Gu
China Pharmaceuticle University

Purpose To demonstrate the benefits and promote the practicality of liquid biopsy based on extracellular vesicles for pancreatic cancer diagnosis, realizing precise and sensitive EV

identification and eliminating macromolecule disturbances, biomarker heterogeneities and EV abundance limitations in current EV assay.
Methods The sensor synergistically integrates EV capture and detection by virtue of EV membrane features (membrane protein and lipid bilayer). Firstly, specific antibody-conjugated magnetic beads (AbMBs) and bivalent cholesterol (biChol, cholesterol modified on the adjacent end of each signal strand)-modified RNA-DNA duplexes served as the EV capturer and signal transporter, respectively. Then duplex-specific nuclease (DSN), a unique nuclease that is preferable to cleave DNA in RNA-DNA duplexes and practically inactive toward RNA, was introduced for signal amplification. The fluorescent signal emerged and amplified after selective digestion of DNA probe, followed by recurrent RNA detection cycles (Scheme 1). Bivalent cholesterol (biChol)-modified RNA-DNA duplexes were designed to insert into the EV membrane, transforming EV signals into RNA signals and initiating the signal amplification. The membrane-based signal production pattern eliminated protein interference. Finally, after modified with antibodies specific to four PCa-related protein biomarkers (EGFR, EpCAM, GPC-1 and EphA2), the AbMB-biChol platform was applied in plasma collected from PCa patients (n=21) and healthy donors (n=29).
Results The bivalent cholesterol strategy improved the anchoring efficiency of the duplex, allowing it to irreversibly bind to the EV membrane. The antibody modified magnetic beads along with bivalent cholesterol based amplification detection system enabled profound EV capture and detection efficiency, achieving an LOD of 10 particles/μL, which is competitive with current EV analysis methods. A linear relationship was observed between the change in FL intensity and the EV concentrations (R2 = 0.978). Moreover, the AbMB-biChol system allowed differentiation of EVs originated from various cancer cells, realizing cell-traceable EV identification. After inosculated with antibodies against PCa-related biomarkers, the proposed biosensor exhibited great promise for PCa-related EV identification and PCa diagnosis, demonstrating superior characteristics to CA19-9 (AUC: 0.714) and four PCa-related protein combination analysis (AUC: 0.737), achieving impressive diagnostic efficacy in discriminating between PCa patients and healthy donors (AUC: 0.909). In addition, KRAS mutation rates in the captured EVs were 79% (G12D), 62% (G12V), and 17.2% (G12R) for PCa patients and 6.8% (G12D) and 0% (G12V, G12R) for healthy donors, further confirming the strong correlation between captured EVs and PCa.
Conclusion The proposed platform paves the way for the implementation of precise and sensitive EV differentiation and noninvasive PCa detection, embracing great potential in clinical applications.

OR-112

流式细胞术检测多发性骨髓瘤患者 NK 细胞及其表面 PD-1 表达的初步研究

王亚奇[1]、张琳[1]、岳保红[2]
1. 郑州大学第五附属医院
2. 郑州大学第一附属医院

目的 本研究旨在探讨多参数流式细胞术（multiparameter flow cytometry，MFCM）检测多发性骨髓瘤患者 NK（CD3-CD56+）细胞及其细胞表面 PD-1 表达，从而为病人的诊断、治疗和预后提供依据。
方法 回顾性分析 2018 年 07 月至 2020 年 11 月收治的多发性骨髓瘤患者的临床资料，随访至少半年时间，并将研究对象分为对照组、初诊组、复发难治组。
结果 97 例患者均经组织病理活检及免疫组化确诊为多发性骨髓瘤，其中男性 55 例，女性 42 例，发病年龄为 60 岁（40~84 岁）。流式细胞术检测显示，相比于对照组，初诊组、复发难治组 NK 细胞的比例增高，但是初诊组 NK 细胞增高没有统计学意义（P > 0.05），复发难治组 NK 细胞比

例显著增高，差异具有统计学意义（P < 0.05）。复发难治组患者骨髓中 NK 细胞与初诊组相比比例增高，差异具有统计学意义（P < 0.05）。进一步对 PD-1 在 NK 细胞表面的表达情况进行分析，流式细胞术检测结果显示相比于对照组，在复发难治组多发性骨髓瘤患者骨髓中 NK 细胞上的 PD-1 表达增高，差异有统计学意义（P < 0.05）。并且复发难治组多发性骨髓瘤患者骨髓中 NK 细胞上 PD-1 的表达比初诊组增高，差异有统计学意义（P < 0.05）。

结论 流式细胞术检测到 PD-1 在多发性骨髓瘤患者的 NK 细胞上表达，并且 PD-1 在多发性骨髓瘤患者骨髓中的表达与疾病的进展相关，PD-1/PD-L1 通路可能与多发性骨髓瘤的预后有关。

OR-113

基于 SERS 技术鉴别急性髓系白血病亚型相关血液特征

叶旻璐[1]、段正伟[1]、肖丽荆[1]、王玉婷[1]、林秋[2]、陈阳[1]、冯尚源[3]、曹颖平[2]
1. 福建医科大学， 医学检验系
2. 福建医科大学附属协和医院，检验科
3. 福建师范大学，医学光电科学与技术教育部重点实验室

目的 本文应用表面增强拉曼光谱（surface-enhanced Raman spectroscopy, SERS）技术对急性髓系白血病（AML）患者的血浆进行分析，以期找寻 M3、M5 亚型相关特征性血浆标志物及其变化趋势，为 SERS 技术用于 AML 的快速分型、诊断及预后分析提供实验依据。

方法 按 WHO MICM 分型标准将采集的急性髓系白血病患者血浆样本分为 4 组，M3、M5、其他 AML（包括 M0、M2 和 M4 亚型）及正常对照组。应用基于银纳米粒子的 SERS 技术用于探索不同 AML 患者血浆之间存在的生化差异。后续应用相关多元统计分析方法及通路分析手段，探寻不同组间谱带强度的差别是否具有显著统计学意义，找寻可能的特征标志物，进一步评价 SERS 技术识别不同亚型 AML 的性能。

结果 谱带 495（L-精氨酸）、725（腺嘌呤和辅酶 A）、1002（苯丙氨酸）、1070（胶原蛋白）、1616（苯丙氨酸和酪氨酸）以及 1653（酰胺 I）cm-1 的强度在多个 AML 组与对照组之间存在显着差异且有着良好的检验效能（受试者工作曲线（ROC）曲线下面积 AUC≥0.9），且与 AML 患者的亚型分化有关。分析显示 725/1653、533/1002 、 1070/1653 和 1616/1653 的谱带强度比值能够在对照组与几种 AML 亚型之间进行有效鉴别。这些强度比值经多指标联合 ROC 分析，在不同亚型 AML 患者与健康人以及 M3 和 M5 亚型的鉴别方面具有显著性意义。

结论 本文发现的特征性谱带相应变化可能是通过血浆标本区分不同亚型 AML 的关键。研究证明了 SERS 技术作为一种新型分析方法，在临床检验实践中作为一种无创、微量检测方法的巨大潜力。

OR-114

伴有-5/del(5q)和/或-7/del(7q)的骨髓增生异常综合征的（相关）基因表观遗传学研究

虞亚菲
中国人民解放军总医院第一医学中心

目的 骨髓增生异常综合征(MDS)是一种克隆性血液学疾病，以造血细胞发育不良、外周血细胞减少和易发生急性髓系白血病(AML)为特征。5 和 7 号染色体的全部或部分缺失[-5/del(5q)和-7/del(7q)]被认为是最常复发的遗传异常，包括骨髓增生异常综合征(MDS)和急性髓系白血病(AML)在内的10-20%的髓系恶性肿瘤。有研究认为，5、7 号染色体常见缺失区域(common deleted regions, CDRs)的肿瘤抑制基因的单倍性是 MDS 和 AML 的发病机制之一。而表观遗传变化，包括启动子区高甲基化和翻译后组蛋白修饰，可能使肿瘤抑制基因失活，从而导致肿瘤的发生。本研究拟应用高通量测序（NGS）技术，对[-5/del(5q)和-7/del(7q)]阳性患者的常见缺失区域（CDRs）相关基因

启动子区的甲基化水平检测，分析表观遗传变化，进一步评估其在携带 del(5q)和/或-7/del(7q)的 MDS/AML 患者中的临床意义。
方法 通过常规细胞遗传学、荧光原位杂交（FISH）筛选出-5/del(5q)和/或-7/del(7q)阳性骨髓标本，对 5、7 号染色体 CDRs（5q32-q33，7q31、7q34、7q35-q36）的候选基因启动子区进行生物信息学预测及验证，并应用二代测序（NGS）方法进行基因启动子区甲基化验证，并结合血液常规及血细胞形态、骨髓细胞形态与骨髓活检病理、染色体核型分析等相关临床检查，进行单因素和多因素分析，Kaplan－Meier 法和 COX 回归模型分析其生存情况。
预期结果和结论 通过高通量测序技术提取靶向基因特异的甲基化状态，并结合相关临床检查，不同分组之间的预后进行单因素和多因素分析，分析其生存情况。建立和完善 MDS 发生和发展分子评估模型，为 MDS 患者的潜在遗传机制提供了新的见解。

OR-115

Aberrant lactate dehydrogenase A signaling contributes metabolic signatures in pancreatic cancer

LU QIAO
Tianjin Medical University Cancer Institute and Hospital

Background Pancreatic cancer (PC) has the lowest 5-year survival rate; therefore, new early screening methods and therapeutic targets are still urgently required. Emerging technologies such as metabolomic_x0002_based liquid biopsy may contribute to the field. We found aberrant lactate dehydrogenase A (LDHA) signaling to be an unfavorable biomarker for PC.
Methods A total of 9 genes of the glycolysis pathway were detected by enrichment analysis in the PC Gene Expression Omnibus (GEO) dataset. The relationship between LDHA/pyruvate kinase (PKM)/ fructose biphosphate aldolase A (ALDOA)/glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and patient survival was analyzed by Kaplan-Meier plotting analysis of The Cancer Genome Atlas (TCGA). The detection of changing metabolites in the serum of PC patients was performed using a nuclear magnetic resonance (NMR) spectrometer.
Results We found LDHA was an independent predictor of overall survival (OS) in PC patients ($P<0.001$). Consistent with genetic aberrance of LDHA, we identified significant alterations in patients' glycolysis_x0002_related metabolites, including upregulation of lactic acid and downregulation of pyruvic acid. A 0.956 area under the curve (AUC) was achieved using the combinative metabolites score of lactic acid, pyruvic acid, citric acid, and glucose to distinguish PC from healthy controls.
Conclusions Aberrant LDHA signaling is an unfavorable biomarker for PC and consequential metabolic changes constitute potential diagnostic signatures of PCs.

OR-116

Plasma D-Dimer can be used as an independent predictor for stroke-associated pneumonia: A cohort study from northeastern China

Yinting Xing、Feifan Ding、Wei Yang、Yingyu Jin、Caijun Zha、Yanhong Liu
The First Affiliated Hospital Of Harbin Medical University

Purpose Stroke-associated pneumonia (SAP), a complication with many negative effects on acute ischemic stroke (AIS) patients, is in urgent need to find laboratory test items as its predictive factors. The study was aim to investigate whether D-Dimer can be used as a predictor for SAP and long-term prognosis of AIS.

Methods According to whether the AIS patients had SAP or not during hospitalization, 392 AIS patients were divided into two groups: SAP group and non-SAP (NSAP) group. The basic clinical information was collected, and blood samples were collected twice within 24 h and 48 h after admission to test clinical laboratory items, especially D-Dimer. Patients were followed for up to 18 months to check the long-term prognosis. The receiver operating characteristic (ROC) curves of SAP were drawn, and the sensitivity and specificity of D-Dimer were calculated. To verify the correlations, multivariate regression models were established. Cox regression was used for univariate and multivariate survival analysis. A nomogram was used for predicting 1-year unfavorable outcomes in Chinese AIS patients.
Results The D-Dimer levels in the SAP group were significantly higher than that in the NSAP group (P<0.001). D-Dimer showed the highest AUC compared with the other clinical laboratory items (0.763, 95% CI: 0.694-0.832, P<0.0001). When the maximum level of YI in D-Dimer was 0.441, the D-Dimer level was 0.515 DDU: μg/mL. The sensitivity and specificity of D-Dimer for SAP diagnosis were 0.972 and 0.469, respectively. After adjusting for confounding and risk factors, the multivariate logistic regression relationship between D-Dimer and SAP was significant (P=0.031, adjusted OR: 1.174). The multivariate Cox regression analysis showed that D-Dimer was significantly correlated with long-term prognosis in the NSAP group (P<0.001, RR: 2.480, 95% CI: 1.811-3.396) but not in the SAP group.
Conclusions Plasma D-Dimer was a strong predictor for SAP at an early stage in Chinese AIS patients. D-Dimer might be a useful tool to evaluate the long-term poor prognosis of patients without SAP.

OR-117

ID1 表达水平指示肝癌患者 sorafenib 药物敏感性

牛蕾蕾
山东大学第二医院

研究背景 Sorafenib 是 FDA 批准用于治疗晚期 HCC 的靶向药。然而，HCC 患者耐药性的出现大大削弱了 sorafenib 的药效。因此，揭示并探明有关 sorafenib 的耐药机制变得尤为重要。越来越多的数据表明衰老细胞内部的新陈代谢依然活跃，它们可以分泌多种生物活性分子，如促炎细胞因子和生长因子等。人们将这种现象定义为衰老相关分泌表型（SASP）。许多促使肿瘤发生发展的恶性因子如 IL6 等都属于 SASP 的关键成分。本研究旨在观察衰老对 sorafenib 药效的影响，并进一步揭示衰老是如何介导的 sorafenib 耐药。
方法与结果 首先，我们利用 MTT 检测了 sorafenib 在五种不同的 HCC 细胞系中的毒性。Sorafenib 在 HepG2, SK-Hep-1 和 huh7 中的细胞毒性明显强于 Hep3B 和 PLC5。结合 western blot 和 qRT-PCR 实验，我们观测到衰老诱导基因 p16 和 SASP 标志物 IL6 在 Hep3B（非敏感）中的表达水平显著高于 HepG2（敏感）。此结果说明，sorafenib 在 SASP 水平高的 HCC 细胞中药效弱。利用干扰 RNA 将 p16 敲除可提高 sorafenib 在 Hep3B 中的细胞毒作用。深入研究发现衰老介导的 sorafenib 耐药源于 ID1 对 p16 的负调控。在五种细胞株中 ID1 的表达水平与药物敏感性高低成正相关，与 p16 成负相关。过表达或敲除 ID1 可抑制或刺激 p16 的表达，引起 sorafenib 药效增强或减弱。此结论在人肝癌细胞的裸鼠移植瘤模型中得到了验证。采用体外低浓度梯度递增法成功将 HepG2 诱导为了耐药细胞株。和亲代敏感细胞株相比，ID1 在耐药细胞株中的表达水平降低，而 p16/IL6 表达水平升高。
结论 ID1 介导的 SASP 可被认为是 sorafenib 的潜在耐药机制。确定 ID1 的表达水平有助于判定何类患者更适于接受 sorafenib 治疗。

OR-118

分化抑制因子 1 通过与新型 cccDNA 结合蛋白 E2F4 相互作用介导 HBV 的转录抑制

魏杰、江咏梅
四川大学华西第二医院

目的 乙型肝炎病毒(HBV)是肝细胞肝癌(HCC)发展的主要危险因素，尽管对 HBV 生命周期的了解逐渐加深，乙肝疫苗和抗病毒药物的应用，全球仍超过 2 亿人患有慢性乙肝，长期的慢乙肝又会导致肝硬化和肝癌的发生，对人类的健康造成严重威胁。因此希望从 HBV 的多个生命周期环节联合用药实现治愈乙肝，于是我们探索了不同的靶点来开发靶向抑制 HBV 复制和转录的新疗法。
方法 我们在体外细胞学实验和体内动物实验研究了分化抑制因子 1 (Id1) 和转录因子 E2F4 在 HBV 转录和复制中的作用。这两种 DNA 复制的调控因子和 HBV cccDNA 之间的相互作用通过亚细胞定位、蛋白-蛋白相互作用、染色质免疫沉淀和荧光素酶等试验进行分析评估。
结果 过表达 Id1 在 HBV 表达细胞和 HBV 转基因小鼠中均显著降低了 HBV 的转录和复制，相反下游分子 E2F4 对 HBV 的转录和复制产生促进作用。Id1 通过和 E2F4 形成异源二聚体，阻止 E2F4 与 cccDNA 结合并失活 HBV 的核心启动子。此外，SPR 及 ITC 实验证实，1758'-TTAAAGGTC-1766'是 E2F4 同源二聚体的结合靶点，该位点在 HBV A-D 的基因型中高度保守，为 E2F4 成为治疗靶点提供了理论基础。同样在 HCC 组织中存在 HBV 的表达水平与 Id1 负相关，与 E2F4 正相关的现象。
结论 该发现强调了 E2F4，一种新的 cccDNA 结合蛋白，作为一个潜在的治疗 HBV 转录靶点能被 Id1 所抑制，提示对 E2F4 的抑制可能成为一种新的抗 HBV 策略。

OR-119

肉桂醛通过抑制粘附发挥对白念珠菌生物膜滞留菌的抑制作用研究

陈丽华、刘雅婷、郝治云、魏于涵、李思、曾莫琦裔、伍勇
中南大学湘雅三医院

目的 研究肉桂醛对白念珠菌生物膜滞留菌的影响及其相关机制。
方法 用微量肉汤稀释法检测肉桂醛对白念珠菌 2 株标准菌株 90028 和 14053、8 株氟康唑耐药性不同的白念珠菌临床菌株的最低抑菌浓度（MIC），用结晶紫染色法和 XTT 法检测肉桂醛对白念珠菌生物膜的影响，用平板培养法检测肉桂醛对白念珠生物膜滞留菌的影响，用棋盘实验检测肉桂醛与氟康唑联合对耐氟康唑白念珠菌的作用。检测 30 株白念珠菌临床菌株各菌株的黏附能力、生物膜形成能力及生物膜滞留菌生成能力，并分析它们的相关性；用 real-time PCR 方法检测白念珠菌生物膜滞留菌中粘附分子 MP65 的表达。检测肉桂醛对白念珠菌粘附的影响。
结果 肉桂醛对所测白念珠菌的 MIC 值均为 32μg/mL；结晶紫染色法结果显示 0.5×MIC 的肉桂醛即可抑制白念珠菌生物膜总量（$P<0.05$），且呈现剂量依赖性；XTT 法结果显示 2×MIC 的肉桂醛可以显著抑制白念珠菌生物膜的代谢（$P<0.01$）；1×MIC 肉桂醛即可抑制白念珠生物膜滞留菌的形成（$P<0.05$），并呈剂量依赖性；联合药敏检测结果显示，肉桂醛与氟康唑具有相加作用，可使对氟康唑的 MIC 从 128μg/mL 降到 32μg/mL；白念珠菌黏附能力与生物膜滞留菌生成能力之间（$r=0.4275$, $P<0.0001$）呈正相关关系；real-time PCR 结果显示生物膜滞留菌中 MP65 表达显著升高，0.5×MIC 肉桂醛即可显著抑制白念珠菌粘附，并具有剂量依赖性。
结论 肉桂醛可以抑制白念珠菌生物膜滞留菌形成，其机制可能与肉桂醛抑制白念珠菌黏附分子 MP65 表达有关。

OR-120

金黄色葡萄球菌磷霉素 MIC 动态变化及主要耐药基因

陈天驰、李敏
上海交通大学医学院附属仁济医院(东院)

目的 本研究旨在探究上海地区 ST5 及 ST239 金黄色葡萄球菌磷霉素最低抑菌浓度（MIC）动态变化及磷霉素相关耐药基因。
方法 对 2008-2019 年某三甲医院分离金葡菌进行 MLST 分型。通过标准纸片扩散法检测所有金葡菌的磷霉素耐药表型，琼脂稀释法检测耐药菌株磷霉素 MIC。随机挑选 ST5 金葡菌 169 株及 ST239 金葡菌 62 株进行全基因组测序（NGS）。通过文献搜集目前已知磷霉素耐药相关基因，CLC Genomics Workbench 12.0 分析上述耐药相关基因突变情况。根据菌株耐药表型，去除磷霉素敏感菌株中良性突变，筛选出磷霉素耐药菌株中突变频率最高的关键基因，使用 MAFFT 进行多序列比对，PhyloSuite 进行多基因联合建树。后续拟敲除关键耐药相关基因进行验证。
结果 12 年间 MLST 分型结果显示临床 ST5 金葡菌分离率及磷霉素耐药率常年处于较高水平，而 ST239 分离率和磷霉素耐药率则逐年下降，同时 MIC 检测发现 ST5 金葡菌大多属于磷霉素高水平耐药（>1024mg/l）而 ST239 则多为低水平耐药（64-128mg/l）。通过阅读文献共搜集 11 种磷霉素耐药相关基因（*uhpT*, *glpT*, *hptR*, *hptS*, *hptA*, *ptsI*, *cyaA*, *murA*, *fosB*, *tet38*, *mgrA*）。经过全基因组测序数据分析及各基因突变情况统计筛选得到金葡菌中突变频率最高的 5 个基因（*uhpT*, *glpT*, *hptR*, *hptS*, *hptA*），同时发现 ST5 耐药株中突变多发生于 *glpT* 及 *uhpT*，而 ST239 耐药株则以 *hptA* 居多。多基因联合建树结果表明金葡菌中可能存在关键基因突变导致磷霉素高水平耐药，同时也可能多个基因突变累加导致耐药水平升高，需后续敲除实验进一步验证。
结论 与 ST239 不同，ST5 金葡菌在 12 年间长期对磷霉素高水平耐药，提示磷霉素的使用可能为 ST5 金葡菌提供生长优势。磷霉素高水平耐药金葡菌多由 *glpT* 及 *uhpT* 突变所致，而低水平耐药则可能为 *hptA* 导致。

OR-121

铁载体毒力基因 entB 对碳青霉烯类耐药肺炎克雷伯菌毒力的影响

韩睿辉[1,2,3]、刘淑敏[1,2,3]、毕建蝶[1,2,3]、杜艳[1,2,3]
1. 昆明医科大学第一附属医院
2. 云南省检验医学重点实验室
3. 昆明医科大学第一附属医院临床检验诊断省创新团队

目的 以临床分离的碳青霉烯类耐药肺炎克雷伯菌(CRKP)为野生株(WT)，构建 entB 基因缺失株△entB 和回补株 C-△entB。探究与铁载体毒力因子肠杆菌素相关的 entB 基因，对 CRKP 菌落形态、黏液表型、生物膜形成能力、生长情况以及其毒力对小鼠生存率的影响。
方法 1.通过 Crispr Cas9 基因敲除技术构建 entB 基因缺失株△entB 和回补株 C-△entB，并用 PCR 验证敲除及回补是否成功。2.通过观察 WT、△entB、C-△entB 菌株的菌落形态和拉丝实验结果，了解 entB 基因对 CRKP 菌落形态及黏液表型的影响。3.通过结晶紫染色法了解 entB 基因对 CRKP 生物膜形成的影响。4.绘制生长曲线，探究 entB 基因对 CRKP 生长的影响。5.通过预实验选择合适菌液浓度后，腹腔注射相同浓度的等量菌液感染 4～5w 龄 ICR 小鼠，根据小鼠生存率直观地了解 entB 基因对 CRKP 毒力的影响。
结果 1.PCR 结果显示 entB 基因在缺失株△entB 中不表达，在回补株 C-△entB 中重新表达，表明通过 Crispr Cas9 基因敲除技术构建 entB 基因缺失株和回补株成功。2.通过观察菌落形态及拉丝实验，结果显示 entB 基因对 CRKP 的菌落形态及黏液表型并无明显影响。3.结晶紫染色结果显示三组之间差异无统计学意义(P> 0.05)，说明 entB 基因对 CRKP 生物膜形成能力无明显影响。4.生长

曲线显示△entB 组生长能力更强，且与 WT 组、C-△entB 组差异均有统计学意义(P< 0.05)。5.将 $0.8x10^7$cfu/mL 0.1mL 菌液分别通过腹腔注射感染 ICR 小鼠，结果显示△entB 组小鼠生存率明显高于 WT 组和 C-△entB 组，且差异有统计学意义(P< 0.05)，表明 entB 基因缺失显著降低了 CRKP 的毒力。

结论 铁载体毒力基因 entB 缺失导致 CRKP 生长能力增强而使毒力显著下降。

OR-122

SPR741 联用大环类酯类抗生素治疗泛耐药及全耐药肺炎克雷伯菌

刘亚倩、佘鹏飞、徐兰兰、伍勇
中南大学湘雅三医院

目的 广泛耐药(XDR)及全耐药（PDR）肺炎克雷伯菌的出现对全球医疗保健系统造成了巨大威胁，本研究旨在探究 SPR741 和大环类酯类抗生素联用对 XDR 及 PDR 肺炎克雷伯菌的体外及体内协同作用。

方法 采用微量肉汤稀释法检测 SPR741 和大环类酯类抗生素对肺炎克雷伯菌的最低抑菌浓度（MIC）及最低杀菌浓度（MBC)，应用棋盘稀释法、纸片扩散法检测 SPR741 与大环类酯类抗生素的两药及三药联合抗菌作用，采用时间-杀菌曲线评价其联合抗菌效果。利用微孔板构建生物膜，检测 SPR741 和大环类酯类抗生素联用对肺炎克雷伯菌生物膜的抑制和成熟生物膜分散作用以及对膜内菌的杀灭作用。通过 CCCP 法诱导形成持留菌，检测 SPR741 和大环类酯类抗生素联用对持留菌的杀灭效果。构建小鼠中性粒细胞缺少的大腿肌肉感染模型，评估 SPR741 和大环类酯类抗生素联用的体内抗菌效果。

结果 棋盘稀释法、纸片扩散法显示，SPR741 与克拉霉素（CLA）、红霉素（E）具有协同抗菌作用，并且三药联用时抗菌效果更显著。杀菌曲线进一步验证三药联用组与对照组相比，细菌细胞数显著降低。SPR741 与 CLA 或 E 联用可以抑制肺炎克雷伯菌生物膜形成，并杀死膜内细菌。对 CCCP 诱导的持留菌有明显清除作用。在中性粒细胞缺少的小鼠大腿肌肉感染模型中，SPR741 与 CLA 和 E 三药联用使右侧大腿肌肉细菌数从 8.72log10 减少至 0，展现出显著的体内疗效。

结论 SPR741 联用大环类酯类抗生素在体内和体外对 XDR 及 PDR 肺炎克雷伯菌均具有良好的协同抗菌效果，本研究成果有望为泛耐药及全耐药肺炎克雷伯菌的治疗提供新的途径。

OR-123

An outbreak of ST859-K19 Carbapenem-Resistant Hypervirulent Klebsiella pneumoniae in a Chinese teaching hospital

Junying Zhu [1]、Xuemei Jiang[2]、Min li[1]
1. Department of Laboratory Medicine, Renji Hospital, School of Medicine, Shanghai Jiao Tong University, Shanghai,
2. 新疆维吾尔自治区妇幼保健院

Objectives Carbapenem-resistant and hypervirulent K. pneumoniae（CR-hvKP）has recently attracted extensive attention worldwide. In this study, we report an outbreak caused by a new and rare sequence type (ST859) CR-hvKP strains.

Methods The outbreak occurred in intensive care unit (ICU) of Renji Hospital Affiliated to Shanghai Jiao Tong University (Shanghai, China). Eleven CR-hvKP strains were collected from 11 patients. We performed antimicrobial susceptibility, multilocus sequence types (MLST), and

whole genome sequencing for the 11 isolates. One representative isolate (RJ-K9299) was selected for further sequencing with the Nanopore platform. Hypervirulence phenotype potential was established using serum resistance assay and Galleria mellonella model for all the CR-hvKP strains.

Results The 11 patients aged 36-70 years had various underlying diseases, including hypertension, cerebral hemorrhage and tumour，and admitted to ICU between Oct. 2019 and Feb. 2020. All the 11 patients received antimicrobial treatment. In the end, 7 patients developed pneumonia and of which 3 patients died of CRKP infection, the other 4 patients discharged. MLST results showed all the 11 CR-hvKP isolates belonged to ST859 type, which is single locus variant of ST11, and KL19 serotype. Antimicrobial susceptibility assays results showed that all the isolates exhibited high-level resistance to carbapenems, cefotaxime, cephalosporin, aztreonam, cefoperazone/sulbactam and levofloxacin, while remaining susceptible to colistin, tigecycline and ceftazidime/avibactam. When comparing the other 10 CR-hvKP isolates against reference genome of RJ-K9299, our analysis revealed 15 single-nucleotide polymorphisms (SNPs) at most (minimum, 0). Furthermore, the phylogram also showed a homogenous picture with all the 11 CR-hvKP isolates clustered in one clade, which indicated probable interbacterial transmission. WGS data analysis showed the 11 isolates had same resistance genes profile (blaKPC-2, blaTEM-1B, blaSHV-187, rmtB, fosA6 positive) and virulence genes (rmpA, rmpA2, iutAiucABCD, iroE, irp1, irp2 positive) profile, which hint clone transmission again. Five plasmids were assembled in RJ-K9299, including one virulence plasmid, namely pVir-RJ9299 and one resistance plasmid harboring blaKPC-2 carbapenem resistance gene, namely pKPC-RJ9299. Similar to pLVPK plasmids (~230kb) which belonged to the 'IncHI1B-IncFIB' replicon incompatibility type, pVir-RJ9299 is an IncHI1B -type plasmid with a length of 215959 bp and an average GC content of 49.87%. Comparative genomics of pVir-RJ9299 showed that they possess over 99% similarity (with 92% query coverage) to pLVPK (GenBank AY378100). However, unlike previous version of ~170kb KPC-2-producing plasmids, pKPC-RJ9299 belonged to IncFII-IncR type plasmid of ~109kb with IS26 located upstream and downstream of blaKPC-2. Serum resistance assays showed that survival of 3 isolates (RJ-9299, RJ-9582, RJ-9717) significantly increased in the presence of human serum over 3h while survival of the other 8 isolates decreased. Using Galleria mellonella model, Mouse lethality assay showed that the LD50 of all the 11 CR-HMKP strains was 104 ~105.5CFU, suggesting that they were hypervirulent.

Conclusion This is the first report of outbreak caused by ST859 CR-hvKP isolates. The emergence of ST859 clone isolates which converged carbapenem resistance and hypervirulence maybe the next threat for public threat.

OR-124

Anticardiolipin IgA may be an independent risk factor for pregnancy morbidity in APS patients

Xiaodan Di、Shuo Yang、Liyan Cui
Peking University Third Hospital

Objective Antiphospholipid syndrome (APS) is an autoimmune disorder characterized by venous or arterial thrombosis and/or obstetric morbidity, along with persistently present antiphospholipid antibodies (aPLs). However, the relationship between the immunoglobulin A isotype of aPL positivity and its clinical utility in APS with pregnancy morbidity is controversial. Thus, we determine the clinical utility of IgA–aPL from female APS patients.

Methods 3265 female APS patients were evaluated. Six antiphospholipid antibodies (aPLs) were tested using commercial kits, including aβ2GPI of the IgA/IgG/IgM isotypes and aCL of the IgA/IgG/IgM isotypes.

Results The overall prevalence of aCL IgA was 43.7% and aβ2GPI IgA was 1.8%. Only 4.9%(31/628) of the aCL-positive subjects with isolated aCL IgA. Similarly, isolated aβ2GPI IgA only accounted for 6.4%(18/281) of the aβ2GPI-positive subjects. aCL IgA showed the largest

area under the curve(AUC=0.671,95%CI: 0.647-0.694,P ＜ 0.05), followed by SCT ratio(AUC=0.535,95%CI: 0.511-0.560,P ＜ 0.05). The combination of aβ2GPI IgG/IgM/IgA provides perfect performance for fetal loss in APS patients.
Conclusion the positive rates of aCL IgA and aβ2GPI IgA were very low when it comes to each isolated isotype of aPL. ACL IgA showed perfect diagnostic efficacy for fetal loss in APS patients., But the combination of IgA aPLs and IgG or IgM aPLs provide poor performance for fetal loss in APS patients. And aCL IgA can be used as an independent risk factor for the development of APS-related fetal loss. Besides, it is important to establish the standardized diagnosis of IgA aPLs.

OR-125

Analysis of BCR characteristics of antigen-specific single memory B cells in patients with long-term HIV-1 infection

Mingyu Li、Ya Li
The First Affiliated Hospital of Kunming Medical University

Objective Human immunodeficiency virus type 1, HIV-1 antigen-specific B cell receptor (BCR) of single memory B cell was analyzed objective to understand the BCR characteristics and functional correlation of memory B cells, so as to provide theoretical basis for exploring the humoral immune mechanism of broad-spectrum neutralizing antibodies and antibody affinity maturation in patients with long-term non progression of HIV-1 infection, and further provide new ideas for the prevention and treatment of HIV-1 infection.
Methods The antigen-specific single memory B cells were sorted by flow cytometry The variable region genes of BCR heavy chain and light were amplified by reverse transcription, nested polymerase chain reaction (nested PCR) and touch up nested PCR, Then the PCR products were recovered and purified by agarose gel electrophoresis, they were digested, linked to expression vector, transformed into E.coli competent cells, and clones were picked up and sequenced , Paired heavy chain and light chain plasmids were expressed in 293T cells and 293F cells,respectively Recombinant protein A was used to purify the antibody secreted by 293F cells ,and the purified antibodies were identified by SDS polyacrylamide gel electrophoresis (SDS-PAGE)and Coomassie brilliant blue staining, The binding and neutralizing activities of the antibodies were detected by enzyme linked immunosorbent assay (ELISA) and TZM-bl cell neutralization assay.
Results (1) 407 heavy chain variable regions and 258 light chain variable regions of PT15 antigen-specific single memory B cells were obtained by gene amplification; (2)Touch-up nested PCR can effectively improve the positive rate of light chain variable region gene amplification; (3) different antigen-specific single memory B cells have different sources of BCR heavy light chain genes, AE, YU2-gp140 specific single memory B cells have rare types of BCR light chain, and the types of germline genes are more abundant; (4) different sorting antigens can get single memory B cells BCR heavy chain variable region SHM; (5) somatic hypermutation (SHM) of heavy chainand light variable region gene from different embryo lines mostly occurred in the complementary determining region, The light chain variable region gene SHM mostly occurs in CDR1、CDR2 ,the heavy light chain variable region gene with high level of SHM had high mutation in CDR1 region; (6) with the increase of time, the BCR gene of memory B cells in pt sample appeared the phenomenon of old germline gene disappearance and new germline gene production, and the length of SHM and CDR3 increased; (7) eight antibodies were successfμlly expressed in T cells; (8) 293F cells expressed and expressed successfμlly Purified three monoclonal antibodies P1A2-2、P1B4-1、P1A9-1; (9) monoclonal antibodies P1A2-2、P1B4-1、P1A9-1 have high binding activity to different subtypes of HIV-1 pseudovirus, low binding activity to gp120, and weak neutralization activity to global panel HIV-1 pseudovirus.
Conclusions The neutralization antibody needs to mature for a long time and evolve under the stimulation of various antigens. The long-term progress of HIV-1 infection provides an appropriate

immune environment for the production and maturity of broad-spectrum neutralization antibody. The BCR characteristics of single memory B cells with different sorting antigens and different time points sμggest that the memory B cells of the long-term non progressors of HIV-1 infection gradually evolve towards the trend of increasing broad-spectrum reactivity and affinity under the condition of long-term exposure to different antigens.

OR-126

Treponema pallidum Tp0768 protein enhances endothelial cell migration and adhesion through ER stress and NF-κB/HIF-1α pathway

Yun Tang、xiangping zhou、shuangquan liu
The First Affiliatd Hospital Of University Of South China

Objective To explore the mechanism of recombinant Treponema pallidum lipoprotein Tp0768 on vascular endothelial cells attracting THP-1 cells to migrate and adhere to it, and to screen the key signal pathway of Tp0768 in promoting migration and adhesion, so as to provide a new idea for revealing the pathogenic mechanism and therapeutic target of Tp.
Methods After human umbilical vein endothelial cells were stimulated by Tp0768, the viability of endothelial cells was detected by CCK8, and the levels and contents of ICAM-1, MCP-1 and IL-8mRNA in endothelial cells were detected by qRT-PCR and ELISA to determine the effect of TP0768 on them. The migration rate of THP-1 cells to endothelial cell culture supernatant was detected by Transwell method, and the adhesion degree of THP-1 cells to endothelial cells by adhesion test, so as to observe the effect of Tp0768 on these adhesion factors and the ability of these factors to promote the migration and adhesion of THP-1 cells to endothelial cells. The subtle structural changes of endoplasmic reticulum were observed by transmission electron microscope, the protein level of endoplasmic reticulum stress marker by WesternBlot, the degree of nuclear translocation of NF- κB P65 and the expression of p65 protein by immunofluorescence and WesternBlot. After transfection, HIF-1α in endothelial cells was knocked out, and the expression levels of ICAM-1, MCP-1 and IL-8mRNA in endothelial cells in negative / positive control group and knockout group were detected by qRT-PCR. After pretreatment with endoplasmic reticulum stress inhibitor 4-PBA, PERK pathway inhibitor GSK, IRE1α pathway inhibitor STF and NF- κB pathway inhibitor PDTC, the expression levels of ICAM-1, MCP-1 and IL-8mRNA were detected by qRT-PCR. In order to detect the relationship between endoplasmic reticulum stress and NF- κB pathway, HIF-1α pathway and the relationship between these pathways and the above adhesion molecules.
Results (1) .Tp0768 can up-regulate the expression of ICAM-1, MCP-1 and IL-8 mRNA in vascular endothelial cells in a dose-and time-dependent manner, and promote the migration and adhesion of THP-1 cells to vascular endothelial cells.
(2) .Tp0768 could cause endoplasmic reticulum deformation, enlarge endoplasmic reticulum lumen and form vacuoles, and increase the protein expression of PERK, IRE1a and ATF6. ER stress inhibitor 4-PBA, PERK inhibitor GSK and IRE1α inhibitor STF significantly down-regulated the levels of ICAM-1, MCP-1 and IL-8mRNA induced by Tp0768.
(3) .After Tp0768 stimulation, the protein level of NF-κB p65 was up-regulated and nuclear translocation occurred in a time-and dose-dependent manner; after inhibition of ER stress, the nuclear translocation of NF- κB p65 decreased and the expression of p65 protein decreased; inhibition of NF-κB pathway decreased the levels of ICAM-1, MCP-1 and IL-8mRNA induced by Tp0768.
(4) After Tp0768 stimulation, the mRNA level of HIF-1α was up-regulated in a dependent manner, and the mRNA level of HIF-1α was significantly decreased after inhibition of ER stress pathway and NF-κB pathway, respectively. After knocking down HIF-1α, the levels of ICAM-1, MCP-1 and

IL-8 mRNA decreased, the protein expression of ICAM-1 decreased, and the adhesion rate of THP-1 cells to endothelial cells decreased.
(5)Tp0768 could regulate the secretion of ICAM-1, MCP-1 and IL-8, by endothelial cells and the migration and adhesion of THP-1 cells to vascular endothelial cells through ER stress and NF-κB / HIF-1α pathway, and significantly down-regulated the migration and adhesion rate of THP-1 cells to vascular endothelial cells after inhibiting ER stress pathway and NF-κB pathway, respectively. Pretreatment with anti-MCP-1 neutralization antibody could significantly reduce the migration rate of THP-1 cells to the supernatant of vascular endothelial cell culture medium, and anti-ICAM-1 neutralization antibody could significantly reduce the adhesion rate of THP-1 to vascular endothelial cells.
Conclusion The promotion of migration and adhesion of Tp0768 for endothelial cells is mediated by ER-stressed PERK and IRE-1α pathways through NF-κB, which also involves the activation of downstream pathway HIF-1α, thus promoting endothelial cell production of migration-promoting adhesion molecules ICAM-1, MCP-1 and IL-8.

OR-127

In vitro activity of antirheumatic drug auranofin in combination with aztreonam-avibactam against metallo-β-lactamase (MBL)-producing Enterobacterales

Siqiang Niu
Department of Laboratory Medicine, The First Affiliated Hospital of Chongqing Medical University

Objectives Auranofin (AUR), an antirheumatic metallo-drug, was recently demonstrated to be a potent metallo-β-lactamases (MBLs) inhibitor. To assess the efficacy of ceftazidime-avibactam-auranofin (CAZ-AVI-AUR) and aztreonam-avibactam-auranofin (ATM-AVI-AUR) against a collection of 88 carbapenemase-producing Enterobacterales (CPE) clinical isolates (37 single KPC-producers, 33 single MBL-carriers, and 18 dual/triple carbapenemase-producers) and 6 in vitro selected ATM-AVI-resistant CPE with CMY-16 Tyr150Ser and Asn346His mutants or transformants.
Methods Minimum inhibitory concentrations (MICs) of imipenem (IPM), auranofin (AUR), CAZ-AVI, ATM-AVI, CAZ-AVI-AUR and ATM-AVI-AUR were determined via the broth microdilution method. Genetic background and carbapenemase genes were determined by PCR and Sanger sequencing.
Results The addition of AUR (16 mg/L) reduced the CAZ-AVI MIC50 from >64 to 1 mg/L in the 88 clinical CPE isolates. The addition of AUR (16 mg/L) resulted in an 8-fold reduction of ATM-AVI MIC50 (from 0.5 to 0.0625 mg/L) and a 4-fold reduction of MIC90 (from 1 to 0.25 mg/L) against these 88 clinical CPE isolates, respectively. Notably, the reduced ATM-AVI MIC values were mainly found in MBL-producers, and the MIC50 and MIC90 reduced by 4 folds (from 0.25 mg/L to 0.0625 mg/L) and 8 folds (from 2 to 0.25 mg/L) respectively by 16 mg/L AUR among the 51 MBL-producers. By contrast, the addition of AUR (16 mg/L) did not showed significant effects of ATM-AVI MIC50 (0.0625 mg/L) and MIC90 (0.125 mg/L) among single KPC-producers (n = 37). Interestingly, the addition of AUR (16 mg/L) re-sensitized the ATM-AVI susceptibility against the 6 in vitro selected ATM-AVI-resistant CMY-16 Tyr150Ser and Asn346His mutants or transfromants, with the MICs reduced from ≥32 mg/L (32->256 mg/L) to ≤8 mg/L (0.0625-8 mg/L).
Conclusions Our results demonstrated that AUR potentiated the activities of CAZ-AVI and ATM-AVI against MBL-producing isolates in vitro. Importantly, AUR restored the ATM-AVI activity against ATM-AVI resistant mutant strains. As a clinical approved drug, AUR might be repurposed in combination with other β-lactams (e.g. ATM-AVI) to treat infections caused by highly resistant MBL-producing Enterobacterales.

OR-128

Identification of the conjugative and mobilizable plasmid fragments in the plasmidome using sequence signatures

Zhencheng Fang、Hongwei Zhou
Department of Laboratory Medicine, Zhujiang Hospital, Southern Medical University.

Aim Plasmids are the key element in horizontal gene transfer in the microbial community. Recently, a large number of experimental and computational methods have been developed to obtain the plasmidomes of microbial communities. Distinguishing transmissible plasmid sequences, which are derived from conjugative or at least mobilizable plasmids, from non-transmissible plasmid sequences in the plasmidome is essential for understanding the diversity of plasmids and how they regulate the microbial community. Unfortunately, due to the highly fragmented characteristics of DNA sequences in the plasmidome, effective identification methods are lacking. This work addresses a challenge associated with plasmid characterization, more precisely, the identification of transmissible plasmid sequences in plasmidome data.
Method In this work, we first used information entropy from information theory to assess the randomness of synonymous codon usage over 4424 plasmid genomes. We then further developed a novel algorithm named PlasTrans. PlasTrans takes the triplet code sequences and base sequences of plasmid DNA fragments as input and uses the convolutional neural network of the deep learning technique to further extract the more complex signatures of the plasmid sequences and identify the conjugative and mobilizable DNA fragments.
Result The results showed that for all amino acids, the choice of a synonymous codon in conjugative and mobilizable plasmids is more random than that in non-transmissible plasmids, indicating that transmissible plasmids have different sequence signatures from non-transmissible plasmids. Moreover, Tests showed that PlasTrans could achieve an AUC of as high as 84–91%, even though the fragments only contained hundreds of base pairs.
Conclusion To the best of our knowledge, this is the first quantitative analysis of the difference in sequence signatures between transmissible and non-transmissible plasmids, and we developed the first tool to perform transferability annotation for DNA fragments in the plasmidome. We expect that PlasTrans will be a useful tool for researchers who analyse the properties of novel plasmids in the microbial community and horizontal gene transfer, especially the spread of resistance genes and virulence factors associated with plasmids. PlasTrans is freely available via https://github.com/zhenchengfang/PlasTrans

OR-129

Outbreak of Invasive Infections Caused by Rhodotorula mucilaginosa in a Tertiary Hospital

Jingjing Huang 、Yingchun Xu
Peking Union Medical College Hospital

Rhodotorula mucilaginosa is a rare opportunistic yeast. It often infects immunocompromised persons and most infections have been associated with intravenous catheters. In China, relatively little is known of identification of *R. mucilaginosa* and of its antifungal susceptibility patterns and ability of biofilm formation before 2020. As a part of the National China Hospital Invasive Fungal Surveillance Net (CHIF-NET) Program, we found outbreak of invasive infections caused by *R. mucilaginosa* in a tertiary hospital in northern China.

Here we studied 78 non-duplicate *R. mucilaginosa* isolates from patients at 22 hospitals participating in CHIF-NET program (2010-2018). Molecular sequencing of ITS region and D1/D2 domain of rDNA and MALDI-TOF MS identification methods were compared for their performance in species identification. Antifungal susceptibility testing was performed using Sensititre

YeastOne™ YO10 methodology. The biofilm formation assay was carried out by crystal violet staining. Microsatellite typing (MT) method was also established to study the genetic relationships between the 78 strains isolated from different provinces in China. Phylogenetic analysis was performed with software Molecular Evolutionary Genetic Analysis (MEGA_X software) using the neighbor-joining (NJ) method based on single nucleotide polymorphisms (SNPs) in genome, compared with reference genome in NCBI database.

All isolates were identified correctly by the Vitek MALDI-TOF MS system (bioMérieux) and the Clin-TOF MS system (Bioyong Technology Company Inc). The Bruker MS system (Bruker Daltoniks) also correctly identified all *R. mucilaginosa* isolates but using a lowered (≥1.700) cut-off score for species assignment. MICs of ≥256μg/ mL for fluconazole were seen for all 78 isolates, whilst MICs of ≥4 μg/mL for voriconazole, ≥4 μg/mL for itraconazole and ≥2 μg/mL for posaconazole were seen for 78.2, 10.3 and 74.4% of isolates, respectively. All sequences can be divided into 4 ITS types compared to the reference sequence NR_073296.1 from *R. mucilaginosa* CBS316. Differences of biofilm quantification between 78 isolates were significant ($P<0.001$) with three classification.

There were 30 strains isolated from one hospital in northern China. Only 24 to165 SNPs were calculated between the 30 isolates. 96.7% of strains were collected from peripheral blood and 63.3% of patients were admitted in Intensive Care Unit. A total of 53 MT types for 78 isolates were identified. Among them, 38 genotypes were distributed sporadically and the 30 strains causing outbreak infections accounted for 15 MT types.

The study has provided a global picture of the identification, antifungal susceptibility profile, phylogenetic situation and ability of biofilm formation of *R. mucilaginosa* in China during the period of the study. We should look out these emerging, pathogens especially in immunodeficient and immunocompromised patients.

OR-130

Interleukin-11 Is Upregulated By Hypoxia-inducable factor-1α Under Hypoxia To Promote Breast Cancer Progression

Yahui Liu 、Li Ren
Tianjin Medical University Cancer Institute and Hospital

Background Interleukin-11(IL-11), a member of the IL-6 family of cytokines, is found expressed abnormal in human cancers. Nevertheless, the relationship between hypoxia and IL-11 in human breast cancer are little understood. In this study, we explored the expression of IL-11 in hypoxia microenvironment of breast cancer and the detailed mechanism behind it, and IL-11's role in breast cancer.

Methods The expression of IL-11 in breast cancer cell incubated either in normoxia condition or hypoxic condition was detected by Quantitative real-time PCR and ELISA; The level of IL-11 was also detected when hypoxia-inducable factor-1α(HIF-1α) was silenced under hypoxic condition; The ability of cell proliferation induced by IL-11 were measured by assays of colony formation and MTS; Cell motility in response to IL-11 was measured by assays of transwell. Serum samples were obtained from 166 patients with breast cancer for analyzing of relationship between the level of IL-11 and clinicopathological features. Immunohistochemical staining of surgically resected specimens of 30 patients with breast cancer was performed to detect the correlation between hypoxia markers and IL-11 in vivo.

Results We found the expression of IL-11 significantly increased in hypoxic condition compared with normoxia condition and in a time-dependent pattern. Furthermore, silencing of HIF-1α dramatically abrogated the increased expression of IL-11 mediated by hypoxia. Cell proliferation，migration and invasion were also enhanced by IL-11.In the clinical aspect, the level of serum IL-11 was related to CA15-3, CA-125, CEA, lymph node metastasis, tumor stage, clinical stage, tumor size. Immunohistochemical staining showed that the expression of IL-11 was significantly correlated with the expression of HIF-1α and CA-IX.

Conclusions IL-11 is a novel hypoxia-inducible and HIF-1α-regulated gene and elevated IL-11 promotes the malignant progress of breast cancer.

OR-131

ILF2 cooperating with E2F1 to maintain mitochondrial homeostasis is a potential biomarker for small cell lung cancer progression

Meng Zhao
Tianjin Medical University Cancer Institute and Hospital

Objective Mitochondria playing multifunctional roles in carcinogenesis. Deciphering uncertainties of molecular interactions within mitochondria will promote further understanding of cancer. Interleukin enhancer binding factor 2 (ILF2) is upregulated in several malignancies, however, much remains unknown regarding ILF2 in small cell lung cancer (SCLC). In the current study, we explored ILF2's role in SCLC and demonstrated its importance in mitochondria quality control.
Methods Colony formation, cell proliferation, cell viability and xenograft studies were performed to examine ILF2's role on SCLC progression. Glucose uptake, lactate production, cellular oxygen consumption rate and extracellular acidification rate were measured to examine the effect of ILF2 on glucose metabolism. RNA-sequencing was utilized to explore genes regulated by ILF2. E2F1 transcriptional activity was determined by dual luciferase reporter assay. Mitochondria quantification and mitochondrial membrane potential assays were performed to examine mitochondrial quality. Gene expression was determined by RT-qPCR, western blotting and IHC assay.
Results LF2 promotes SCLC tumor growth in vitro and in vivo. ILF2 elevates oxidative phosphorylation expression and declines glucose intake and lactate production. Genome-wide analysis of ILF2 targets identified a cohort of genes regulated by E2F1. In consistent with this, we found ILF2 interacts with E2F1 in SCLC cells. Further studies demonstrated that suppression of E2F1 expression could reverse ILF2-induced tumor growth and enhanced mitochondria function. Significantly, expression of ILF2 is progressively increase during SCLC progression and high ILF2 expression is correlated with higher histologic grades, which indicates ILF2's oncogenic role in SCLC.
Conclusions Our results demonstrate that ILF2 interacts with E2F1 to maintain mitochondria quality and confers SCLC cells growth advantage in tumorigenesis.

OR-132

Sensitive detection of Escherichia coli O157:H7 and Salmonella typhimurium in food samples using two-channel fluorescence lateral flow assay with liquid Si@quantum dot

Shuai Zheng、Xingsheng Yang、Chongwen Wang、Rui Xiao
Beijing Institute of Radiation Medicine

Background Foodborne diseases, which are mainly caused by bacterial contamination, are major threats to human health and result in one-third of global deaths each year. Common foodborne bacteria, such as S. typhi and E. coli are spread through contaminated water and food (e.g., meat and vegetables) and could result in serious illness (e.g., gastroenteritis, diarrhea, and shock).

Methods Here, we proposed a silica–quantum dot (QD)-based fluorescent lateral flow immunoassay (LFA) method with high sensitivity for the simultaneous qualification of Salmonella typhimurium (S. typhi) and Escherichia coli (E. coli) O157:H7 in food samples. To meet the demand of rapid, sensitive, and simultaneous detection of the highly pathogenic E. coli O157:H7 and S. typhi in the food samples, we proposed a two-channel fluorescent LFA strip by using novel silica-quantum dot nanocomposites with dual-QD shell (Si@DQD) as the signal tags. The high-performance Si@DQD tags were fabricated by coating two layers of CdSe/ZnS MPA QDs onto the surface of 190 nm SiO_2 spheres by using our previously proposed polyethyleneimine (PEI)-mediated electrostatic adsorption method. The new Si@DQD with a dual QD-shell has adsorbed hundreds of carboxylated QDs onto its surface, thus greatly enhancing the fluorescence performance and the antibody conjugation. Second, the excellent stability and monodispersity provided by the big SiO_2 core (~190 nm) allowed the tags used to detect two different bacteria via the LFA strip without interfering.
Results The fluorescence intensities of Si@DQD tags observed on the two test lines can be quickly measured for quantitative E. coli O157:H7 and S. typhi analysis. The IUPAC protocol (LOD = yblank + 3 SDblank) was used to define the limit of detection (LOD) of the assay, where yblank and SDblank are the mean fluorescence intensity and standard deviation of the blank control, respectively. Based on the analysis of the fluorescence signal, the LOD of the proposed method for target S. typhi/E. coli O157:H7 was determined to be 50 cells/mL. Thus, the sensitivity of Si@DQD-LFA strip for bacterial detection was at least 200 times higher than that of AuNP-LFA strip. Moreover, the fluorescence intensities of T1 line for S. typhi and T2 line for E. coli O157:H7 exhibited wide dynamic relationships with the concentrations of two target bacteria with $R2 = 0.9997$ for S. typhi and $R2 = 0.9998$ for E. coli O157:H7. These results show the excellent quantitative analysis capability of the Si@DQD-LFA by fluorescence mode. Subsequently, the repeatability and precision of our method were evaluated by recovery test of the spiked bacterial samples (including meat extraction, vegetable extraction, and milk). The average recovery values of spiked S. typhi and E. coli O157:H7 were calculated to be 75%–121%, with RSD values ranging from 2.2%–12.7%.
Conclusions To our knowledge, this work is the first to simultaneously detect two foodborne bacteria by using QD-based LFA strip. Therefore, the proposed method has great potential for food safety monitoring and the actual detection of pathogens.

OR-133

Serum GSDMD as a Novel Predicting Biomarker for the Natural Courses of HBeAg-positive and HBeAg-negative HBV-Chronic Hepatitis

Lijing Zhou、Pu Li
重庆医科大学附属第二医院检验科

BACKGROUND & AIMS Hepatitis B virus (HBV) infection which causes about 1 million deaths every year is a major global health care problem and always accompanied by hepatocyte inflammation, as well as the imbalance of the host's immune system. The natural course of chronic HBV infection is generally divided into four sequential phases according to HBeAg seroconversion: hepatitis B e antigen (HBeAg)-positive chronic infection (EPCI) and hepatitis (EPCH), followed by HBeAg-negative chronic infection (ENCI) and hepatitis (ENCH) with reference to the European Association for the Study of the Liver guidelines and the guidelines of prevention and treatment for chronic hepatitis B (2019 version) in China. To monitor the natural history and distinguish the sequential phases of chronic hepatitis B virus (HBV) infection is still extremely desired. The pore-forming protein Gasdermin D (GSDMD), controlling pyroptosis in cells, contributed to the inflammation-associated liver cell damage and chronic liver inflammation. We aimed to investigate the expression and to evaluate

the diagnostic efficacy of serum GSDMD levels during the four natural courses of chronic HBV infection: hepatitis B e antigen (HBeAg)-positive chronic infection (EPCI) and hepatitis (EPCH), followed by HBeAg-negative chronic infection (ENCI) and hepatitis (ENCH).
Methods We enrolled 273 healthy individuals, 614 liver patients containing 126 autoimmune hepatitis (AIH) patients, 110 hepatocellular carcinoma patients, 378 viral hepatitis patients and 480 chronic HBV infection consecutive patients including 127 with EPCI, 105 with EPCH, 139 with ENCI, and 109 with ENCH. HepG2-NTCP-HBV infected cell platform systems were created to evaluate the performance of GSDMD in vitro. Immunofluorescence and western blot analysis were applied to vitro expriments. Sandwich ELISA kits we invented previously was applied to detect the GSDMD levels both in the clinical specimen and cell systems. The viral markers of HBV were detected by chemiluminescent enzyme immunoassays. HBV DNA was detected by real-time PCR. The receiver operating characteristic (ROC) curve was conducted to explore the diagnostic and predictive performance of GSDMD. The spearman's Correlation coefficients were calculated the correlation among GSDMD, biochemical parameters and virological biomarkers.
Results The serum GSDMD was prominent higher in liver disease groups compared with that in healthy individuals groups. In liver disease groups, GSDMD secretion of HBV infection patients had significant strengths than the others. The same phenomenon was observed in vitro experiments. And the gradually significantly elevated tendency of serum GSDMD with the development of chronic HBV infection nature course, especially in EPCI, EPCH and ENCH. While the levels of serum GSDMD in ENCI was slightly lower than that in EPCH. The mean values of these two groups were relatively closer. Even though the other biochemical parameters and virological biomarkers had significant differences in four phases of chronic HBV infection, there existed no obvious tendency changes in the development. Moreover, areas under ROC curves (AUCs) of serum GSDMD in healthy individuals, EPCI, EPCH, ENCI and ENCH were 0.982, 0.713, 0.593, 0.595 and 0.756; optimal cutoffs were ≤ 4.8, ≥ 104.3, ≤ 143.8, ≤161.1 and ≥ 178.0 ng/mL with sensitivities and specificities 100% and 99.35%, 92.92% and 39.37%, 44.27% and 80.95%, 52.17% and 71.429%, 54.13% and 85.98% , respectively. The serum GSDMD levels remarkably correlated to serum ALT, AST, HBsAg and HBV DNA levels in different nature phases of chronic HBV infection, respectively.
Conclusions Serum GSDMD levels had relatively diagnostic and predictive performance in predicting HBeAg-positive and HBeAg-negative Chronic Hepatitis sequential phases and strongly correlated with ALT. The cell system detection also identified the results in clinical specimens. These mentioned above provided convincing evidence that serum GSDMD may be an early and efficacious serum biomarker for auxiliary definitions of the natural course of HBeAg-positive and HBeAg-negative Chronic Hepatitis.

OR-134

Development of Spike Protein-based Fluorescence Lateral Flow Assay for the Simultaneous Detection of SARS-CoV-2 Specific IgM and IgG

Chongwen Wang、Rui Xiao、Shengqi Wang
Beijing Institute of Radiation Medicine

Background The pandemic outbreak of the 2019 coronavirus disease (COVID-19), which caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is still spreading rapidly and poses a great threat to human health. As such, developing rapid and accurate immunodiagnostic methods for the identification of infected persons is needed.
Methods We developed a high-performance fluorescence LFA strip for the rapid, sensitive, and specific detection of SARS-CoV-2-specific IgM/IgG in clinical samples by using S protein-conjugated quantum dot nanotags. Advanced silica–core@dual QD–shell nanocomposites

(SiO2@DQD) with superior luminescence and stability were prepared to serve as a fluorescent nanotags in the LFA strip and guarantee the high sensitivity and reliability of the assay. The novel SiO2@DQD NP with 200 nm monodisperse SiO2 core and dual layer of carboxylated QD shell was fabricated for practical application in the clinical samples and possessed monodispersity, good stability, and high luminescence. The SARS-CoV-2 spike protein was immobilized onto the surfaces of SiO2@DQD NPs, whereas anti-human IgM and IgG antibodies on the two test lines enabled the simultaneous and highly specific detection of anti-SARS-CoV-2 IgM and IgG in one human sample.
Results By optimization of the assay conditions, the proposed SiO2@DQD-based LFA strip can sensitively and simultaneously detect the low concentration of IgM/IgG (1:107 dilution) from 1 μL serum within 15 min. The performance of SiO2@DQD-strip was fully optimized and confirmed by using 10 positive serum samples from COVID-19 patients and 10 negative samples from patients with other respiratory diseases. The practical clinical value of the assay was further evaluated by testing 316 serum samples (114 positive and 202 negative samples). The overall detection sensitivity and specificity reached 97.37% (111/114) and 95.54% (193/202), respectively, indicating the huge potential of our proposed method for the rapid and accurate detecting of SARS-CoV-2-infected persons and asymptomatic carriers.
Conclusions The proposed research demonstrated that the strategy of combined IgM/IgG detection via SiO2@DQD-based LFA allows the early and accurate identification of SARS-CoV-2-infected persons and can be used in monitoring the progress of the disease.

OR-135

Identification of Novel Autoantibodies for Idiopathic Inflammatory Myopathies Using Human Proteome Microarray

Liubing Li[1]、Li Yongzhe[2]
1. Peking Union Medical College Hospital, Chinese Academy of Medical Sciences
2. 北京市东城区北京协和医院东院检验科

Objectives Idiopathic inflammatory myopathies (IIMs) are a group of clinically heterogeneous, inflammatory muscle disorders characterized by proximal and symmetric muscle weakness and multisystem involvement. Autoantibodies are important biomarkers for IIMs, aiding in diagnosis, classifying patients into more homogeneous groups, and understanding additional clinical complications and responses to treatment. We aimed to employed human proteome microarrays, each composed of about 20,000 unique human proteins, to identify IIMs-specific autoantibodies.
Methods A Three-Phase strategy was used. To screen candidate autoantigens, in Phase I, 90 serum samples collected from 40 IIMs patients, 30 autoimmune disease controls and 20 healthy subjects were probed individually to human proteome microarrays. To verify these candidates, in Phase II, a focused array with candidate IIMs-associated autoantigens was constructed, and this was used to profile a much larger cohort, comprised of serum samples collected from 397 IIMs patients (100 polymyositis, 217 dermatomyositis, 45 cancer-associated myositis, and 35 juvenile dermatomyositis), 197 disease controls (40 systemic sclerosis, 39 systemic lupus erythematosus, 40 primary Sjogren's syndrome, 39 rheumatoid arthritis, and 39 other chronic diseases), and 98 healthy controls. In Phase III, sera with high signal values (value > 3 standard deviation of the mean of the healthy group) for verified proteins were validated using western blot analysis.
Results Ninety-one candidate autoantigens that were significantly associated with IIMs were identified in Phase I. After verification in Phase II, glycine n-methyltransferase (GNMT) was considered as a new IIMs-specific autoantigen. Twenty-five polymyositis, ten dermatomyositis, six cancer-associated myositis, two juvenile dermatomyositis, and two disease controls had high signal values for GNMT, while no healthy subject showed high signal values. In Phase III, 13 of the 25 polymyositis, four of the ten dermatomyositis, five of the six cancer-associated myositis,

two of the two juvenile dermatomyositis, and one of the two disease controls were positive for anti-GNMT autoantibodies using western blot.
Conclusion Anti-GNMT autoantibodies serve as a novel biomarker for IIMs and is expected to help clinical diagnosis. The prevalence of anti-GNMT autoantibodies in different ethnic populations and the association between anti-GNMT autoantibodies and clinical features should be further studied.

电子壁报

PO-0001

Serum Exosome MiRNA Sequencing Identifies Diagnostic Biomarkers for Alzheimer's Disease

Zhiwu Dong[1]、Hongjun Gu[2]、Qiang Guo[1]、Shuang Liang[1]、Jian Xue[3]、Feng Yao[3]、Xianglu Liu[1]、Feifei Li[1]、Huiling Liu[1]、Li Sun[1]

1. Jinshan Branch of Shanghai Sixth People's Hospital
2. 上海市金山区中西医结合医院
3. 上海市金山区众仁老年护理院

Aim Alzheimer's disease (AD) is a common neurodegenerative disease leading to dementia in the eldly. Till now, few diagnostic biomarkers, such as amyloid-β, and phosphorylated tau, were clinically used. It is in urgent need to identify novel peripheral blood-based biomarkers. Exosomes (30–150 nm in diameter) are endosome-derived small extracellular vesicles which function in cellular communication. They are found in many kinds of biofluids, such as blood, CSF, saliva, breast milk and urine. However, the circulating exosomal miRNA expression patterns in AD remain largely unknown.

Methods Eight AD patients (4 females, 4 males) and 8 matched healthy controls (HC, 4 females, 4 males) were included in the NGS experiment. Another 40 AD patients (20 females, 20 males) and 40 age- and gender-matched HC (20 females, 20 males) were enrolled in the validation test. The circulating exosomes were collected using the Exosome Isolation Q3 kit for serum (Wayen Biotechnologies, Shanghai, China) according to the manufacturer's instructions. The exosome morphology was observed with transmission electron microscope (TEM). Exosome markers CD63 and CD9 were detected by western blot assay. The exosomal miRNA profile was characterized by RNA sequencing to evaluate the potential for AD diagnosis. Quantitative reverse transcription PCR was applied to validate the sequencing data. Subsequently, Gene Ontology analysis and pathway analysis were performed for the genes targeted by the differentially expressed miRNAs. All statistical analyses were performed by SPSS 19.0, MedCalc 12.1.4.0, and GraphPad Prism 5.01 software. $P < 0.05$ was considered statistically significant.

Results The NGS data revealed that 207 miRNAs in exosomes were differentially expressed in the AD compared with the normal controls (p-value < 0.05, and ± 1.2-fold change;), including 113 miRNAs up-regulated, and 94 miRNAs down-regulated. Twenty-four miRNAs showed significant difference when ± 2.0-fold change at p-value <0.05 and at least 50 reads for each sample. Gene Ontology analysis showed that the differentially enriched basic functions include cell adhesion, regulation of transcription, and the ubiquitin system. Functional network analysis revealed the pathways including proteoglycans in cancer, viral carcinogenesis, signaling pathways regulating pluripotency of stem cells, and cellular senescence in AD pathology. Serum exosomal hsa-miR-30b-5p, hsa-miR-22-3p, hsa-miR-375-3p, hsa-miR-378a-3p, and hsa-miR-22-5p were validated by RT-PCR on a larger cohort. The data showed that miR-30b-5p, miR-22-3p and miR-378a-3p were significantly associated with AD, with the area under the curve (AUC) of 0.668, 0.637 and 0.718, respectively. Compared with healthy controls, AD patients had a lower level of hsa-miR-30b-5p (X1), with odds ratio (OR) 0.987, 95% confidence interval (CI) 0.980-0.994, a higher hsa-miR-22-3p (X2) with OR 1.017, 95% CI 1.004-1.031, and hsa-miR-378a-3p (X3) with higher OR value 4.454, 95% CI 2.060-9.629. Logistic regression analysis established a diagnostic model for AD by serum exosomal miR-30b-5p, miR-22-3p and miR-378a-3p:$Y = -0.909 - 0.013 \times X1 + 0.017 \times X2 + 1.494 \times X3$ The combination of the three miRNAs had an AUC of 0.880, 95% CI: 0.802-0.959.

Conclusions Exosome miRNA profile may distinguish AD patients from healthy controls. The circulating exosome hsa-miR-30b-5p, hsa-miR-22-3p and hsa-miR-378a-3p were differentially expressed and independently associated with AD. These data emphasized the potential clinical use of exosomal miRNA for AD diagnosis.

PO-0002

全自动样本前后处理系统提升临床分子检测效率

刘朝晖[1]、崔凯[2]、赵娟[2]、周洲[2]
1. 云南省阜外心血管病医院
2. 中国医学科学院阜外医院

目的 分子诊断广泛应用于传染性疾病、肿瘤个体化诊疗、血液筛查、产前筛查、遗传性疾病筛查、药物代谢基因组学等领域。COVID-19 的到来极大推动了分子诊断特别是 PCR 检测技术的发展，而目前在 PCR 检测的实际应用中，在效率上仍有非常大的提升空间。本文旨在研究临床分子检测效率的提升方案，探究自动化技术对核酸检测技术发展的意义。
方法 本文针对核酸检测流程中操作最为繁杂的核酸提取环节，在实验室已有核酸提取仪的基础上，引入了全自动样本前后处理系统，可自动完成核酸提取前处理的扫码传输、拧盖、吸取样本移液至核酸提取 96 孔板等步骤。同时可实现在提取结束后，独立后处理的产物分配、反应体系构建等操作。由于样本前后处理系统可与核酸提取仪同步处理运行，因此效率将远高于步骤自动顺序运行核酸提取工作站。此次实验对病毒采集管拧盖吸样成功率进行了 200 批 48 样本/测试。对于全流程的交叉污染率实验进行取 48 人份试剂、3 个样本架阳性、阴性样本交叉放置的方式，测试 30 次，根据扩增检测结果观察加样过程及提取产物分配过程的污染情况。在此过程中同时评估该方案与纯手工操作及工作站时的检验人效比，根据实验效果对临床分子检测效率提升方案进行研究。
结果 在超过 200 次开盖实验中，开盖及加样成功率均达到了 99%以上，无错加漏加情况发生。在进行 30 次交叉污染实验之后，均未出现交叉污染率的情况。在使用样本前后处理系统之后，保持原有测试数相同条件时，实验室操作人员可由 4 人调整为 1 人，较工作站方案时间缩短 70%，人效比提升 300%。
结论 本文所研究的临床分子检测效率的提升方案，仅需 1 人，即可完成大量样本核酸提取工作，免人工拧盖，样本进结果出，交叉污染及人员感染风险极低，样本信息自动扫码传输，进一步推动核酸检验报告自动化。因此，方案能较好地提升提升临床分子检测效率。

PO-0003

Development of a reverse transcription recombinase polymerase amplification coupled with nanoparticle-based lateral flow biosensor (RT-RPA-LFB) assay for rapid detection of SARS-CoV-2 RNA

Qiuyue Xu、yong duan
Department of Clinical Laboratory,the Frist Affiliated Hospital of Kunming Medical University

Background The ongoing global pandemic (COVID-19), caused by the SARS-CoV-2, has become a huge public health issue. Currently, the standard molecular techniques for SARS-CoV-2 detection include RT-PCR and RT-qPCR. These diagnostic methods are highly sensitive but time consuming, labor intensive and require sophisticated expensive instruments, thus not suitable for point-of-care use. The objective of this study was to develop and optimized a rapid, sensitive, robust, reliable, and highly specifc reverse transcription-RPA technique coupled with nanoparticle-based lateral flow biosensor (RT-RPA-LFB) assay.
Methods Using two RPA primer sets, the ORF1ab and N genes of SARS-CoV-2 were simultaneously amplified in a single-tube reaction, and detected with the diagnosis results easily interpreted by LFB. In presence of FITC (fluorescein)-/digoxin- and biotin-labeled primers, RT-RPA produced numerous FITC-/digoxin- and biotin-attached duplex amplicons, which were determined by LFB through immunoreactions (FITC/digoxin on the duplex and anti-FITC/digoxin on the test line of LFB) and biotin/treptavidin interaction (biotin on the duplex and strptavidina on

the polymerase nanoparticle). The accumulation of nanoparticles leaded a characteristic crimson band, enabling multiplex analysis of ORF1ab and N gene without instrumentation. We also evaluated this RT-RPA-LFB for clinical use using SARS-CoV-2 reference standard material (GBW(E)091099) ， 53 clinical samples， and spiked samples (including Streptococcus pneumoniae, Staphylococcus aureus, Streptococcus pyogenes, Mycobacterium tuberculosis, Haemophilus influenzae, Klebsiella pneumoniae, Mycoplasma pneumoniae, Legionella pneumophila, influenza A virus and influenza B virus).
Results We achieved rapid detection of SARS-CoV-2 within an hour. The assay could detect SARS-CoV-2 with high sensitivity (20 copies/μL for each detection target), and no cross-reactivity was generated from non-SARS-CoV-2 templates. The analytical sensitivity of SARS-CoV-2 was 100% (3/3 nasopharyngeal swab samples collected from COVID-19 patients), and the assay's specificity was also 100% (50/50 nasopharyngeal swab samples collected from non-COVID-19 patients).
Conclusions RT-RPA-LFB was established in this study to detect SARS-CoV-2, a method that was highly specific, sensitive, cost-effective and easy to operate, and provides a new method for the prevention and diagnosis of COVID-19,especially in locations without access to large platforms or sophisticated equipment.

PO-0004

基于 BI-HSV-TK/GCV 系统抑制胃癌细胞增殖的作用研究

皇海
空军军医大学西京医院

目的 探讨双歧杆菌-单纯疱疹病毒胸苷激酶基因-丙氧鸟苷（BI-HSV-TK/GCV）系统对裸鼠体内成瘤的抑制效应和分子机制。
方法 建立裸鼠胃癌实验模型，观察裸鼠的的体重、荷瘤的体积等参数；运用 Western blot 试验，TUNEL 法，Real-time PCR 试验，观察裸鼠胃癌组织和裸鼠胃癌组织中 casepase3、casepase8、Fas 及 FAP-1 的 mRNA 表达、增殖，凋亡相关基因和蛋白的改变。
结果 BI-HSV-TK/GCV 系统能够有效抑制裸鼠体内成瘤的体积和重量，并能够促进胃癌组织细胞的凋亡发生，诱导体内胃癌细胞凋亡相关蛋白 Caspase3，Caspase8，FAP-1，Fas 蛋白水平以及 mRNA 的表达增加，促进凋亡的发生。
结论 BI-HSV-TK/GCV 系统能够有效抑制胃癌细胞在裸鼠体内成瘤的体积和重量，并促进胃癌细胞凋亡的发生。

PO-0005

一组神经胶质瘤恶性分级及临床预后评估分子标志物

刘春芳、刘爱平
复旦大学附属华山医院

神经胶质瘤是对人类健康和生命威胁最大的恶性肿瘤之一，按病理形态学特征 WHO 将神经胶质瘤分为：WHO II、WHO III 、WHO IV。WHO 病理分级是诊断神经胶质瘤的金标准，然而病理形态学诊断具有耗时长、主观性强、病理改变常具有滞后性、难以自动化，而且对病人预后的判断并不太好。尤其是对较低级别胶质瘤，它们在病理组织学上非常接近，但预后却千差万别，从几个月到十年以上。1p19q 状态 1p19q-codel 还是 1p19q-non 是神经胶质瘤预后评估的重要指标。
目的 分子生物学技术具有快速、微量、高通量、客观等巨大优势。因而，用分子生物学方法对神经胶质瘤进行分型、恶性分级及预后评估是未来的发展方向。在本研究中，我们旨在寻找用于神经胶质瘤快速临床预后评估的分子生物学指标。

结果 通过生物信息学，对与神经胶质瘤相关的肿瘤标志物做大规模筛查后，我们找到一组用于神经胶质瘤恶性分级及预后评估的分子生物学指标，包括 WEE1、ISL2、HOXD10、IGF2BP2、EN1、ZNF217、EFNB1、TNFRSF11B、CABP4、UBE2C 等 10 个基因的 mRNA Sequencing 表达量与神经胶质瘤的预后密切相关，P<0.0001；该基因组（Molecular group， MG）的联合应用可提高诊断效率。该 MG 的 mRNA Sequencing 表达量对神经胶质瘤进行分类，表达量高值组和低值组的总体生存期（Overall Survival, OS）具有显著性差异 (高值组 OS 中位数=438，n=513；低值组 OS 中位数=3299，n=457；P<0.0001)。
该 MG 组与 WHO 的神经胶质瘤病理分型相结合，可以将神经胶质瘤分为六种不同亚型的肿瘤；可以根据不同亚型对病人进行预后评估及恶性分级（P<0.0001）。IV+MG （高值组=356，n=310；低值组=694，n=64)；III+MG（高值组=564，n=147；低值组=2633，n=175）。II+MG（高值组=2199，n=52；低值组>5000，n=218）。
该 MG 组与 1p19q 状态相结合，可以将神经胶质瘤分为四种不同亚型的肿瘤；可以根据不同亚型对病人进行预后评估及恶性分级（P<0.0001）。1p19q-codel+MG(高值组=1048， n=32；低值组>5000，n=167)；1p19q-non+MG（高值组=415，n=464；低值组=2367，n=233）。
结论 本研究为神经胶质瘤恶性分级、预后评估提供了一组高效、快速的分子标志物。

PO-0006

催化发夹自组装快速检测甲型流感病毒

吴绘娜
东南大学附属中大医院

目的 甲型流感病毒是一种常见的呼吸道病毒，传染性强，可以引起季节性流行和全球大流行，对公共卫生造成严重负担。目前流感检测的金标准为逆转录聚合酶链式反应（RT-PCR），然而 RT-PCR 操作复杂，对操作人员技术要求高。早期筛查流感病毒对于患者治疗及流感控制至关重要，而本研究基于催化发夹自组装（CHA）原理检测甲型流感病毒的方法操作简便、成本低、检测快速非常适用于流感病毒早期大规模筛查。
方法 催化发夹自组装涉及三个基本成分：目的 RNA 片段及基于目的 RNA 片段设计的两个发夹称为 H1 和 H2，在发夹 H2 的两端标记荧光基团和淬灭基团用于监测反应的可行性，最终通过检测标记生物素的 H1 和标记地高辛的 H2 双链反映目的 RNA 的含量。
结果 荧光结果及电泳分析证明方案可行，在优化反应条件后，本研究最低检出限达到 fM，反应的特异性结果好。
结论 本实验研发了一种操作简便、快速检测甲型流感病毒的方法，可以用于流感病毒大规模筛查。

PO-0007

14 种 VWF 基因剪切位点突变的致病性研究

梁茜、丁秋兰、王学锋
上海交通大学医学院附属瑞金医院检验科

目的 从 mRNA 水平证实 14 种 VWF 基因剪切位点突变的致病性。
方法 抽提先证者外周血白细胞及血小板来源的 mRNA，逆转后通过 PCR 特异性扩增 VWF 转录产物，分析突变对 VWF 基因剪切方式的影响。通过荧光定量 PCR 检测 VWF 基因总体转录水平，并联合 VWF 基因 SNP 位点通过单碱基延伸进行等位基因表达不平衡检测，验证异常转录产物是否存在无义突变介导的 mRNA 降解（NMD）。
结果 5 种突变（c.322A>T 、 c.875-5T>G 、 c.7884C>G 、 c.8116-2delA 和 c.1534-13_c.1551delinsCA）导致了外显子缺失；5 种突变（c.221-2A>C、c.323+1G>T、c.1730-2A>G、

c.2547-13T>A 和 c.7464C>T）激活了隐匿的剪切位点；1 种突变（c.2968-14A>G）产生了新的剪切位点。其余 3 例患者中（c.-1+3A>C、c.2684A>G 和 c.5171-9delT）未检测到异常转录产物。等位基因表达不平衡检测显示 c.5171-9delT 突变除外的其余突变均存在不同程度的 NMD 现象，且血小板中 NMD 程度远高于白细胞。

结论 13 种 VWF 基因剪切位点突变均有致病性，突变 c.5171-9delT 很可能是多态性。本研究提供了 VWF 剪切位点突变致病性研究的通用方案，所有剪切位点突变的分子致病机制均需在 mRNA 水平进行验证。

PO-0008

外周血循环甲状腺乳头状癌细胞 NTRK1 融合基因检测方法的初步建立

张玉娟
中国医学科学院肿瘤医院

目的 预期建立一种外周血 NTRK 融合基因检测方法，以利于复发或转移甲状腺癌患者临床检测治疗。

方法 收集 27 例甲状腺乳头状癌（papillary thyroid carcinoma，PTC）患者和 13 例健康对照的外周血并在 4 小时内进行 CD45 阴性富集外周血循环肿瘤细胞（circulating tumor cell, CTC），然后采用免疫荧光化学染色联合 FISH 法进行 NTRK1 基因融合检测，自动荧光显微镜扫描仪 IMSTAR-CYTTEL 扫描记录结果。

结果 NTRK1 断裂探针阳性表现为 3’端的绿色信号和 5’端的红色信号的分离（3’+5’）或者单个绿色信号（3’）；NTRK1 基因融合阳性细胞为 DAPI 阳性、CD45 表达阴性、NTRK1 断裂探针表现阳性（DAPI+ CD45-/NTRK1+）的细胞。16/27 例 PTC 患者检测到了 3’/5’,3’+5’断裂，检测范围为 1~3 个/3.75ml；2/27 例患者检测到了 3’/5’≥2,3’断裂，3/27 例患者检测到了 3’+5’≥2 断裂，均检测到 1 个/3.75ml； 3/13 例正常对照组中检测到 3’/5’,3’+5’断裂，检测个数均为 1 个/3.75ml。ROC 曲线分析显示，cutoff 值为 2 个/3.75ml 时，NTRK1 断裂诊断 PTC 的敏感性为 14.8%，特异性为 100%。数据初步显示 PTC 患者外周血 NTRK1 基因融合阳性率为 14. 8%。

结论 首次在 PTC 患者外周血中检测到了 NTRK1 基因融合，虽然检测到的阳性个数以及例数均比较低，但是该检测方法仍为无法获得病理组织的肿瘤患者提供了一种新的检测治疗思路。

PO-0009

Potential clinical value of plasma circ_0004592 as an auxiliary diagnostic biomarker for gastric cancer

Yanhua Xu、Shan Kong、Ming Zheng、Shaoqing Ju
Affiliated Hospital of Nantong University

Background Gastric cancer (GC) is one of the world’s most common cancers with high mortality which lacks of ideal diagnostic biomarkers. Circular RNAs (CircRNAs) are a new class of non-coding RNAs which is closely related to GC. However, the clinical application value of circRNAs in GC are largely unknown. Therefore, we studied the role of a novel circRNA named circ_0004592 in early screening and prognosis of GC.

Methods High-throughput sequencing of circRNAs was performed to screen out the target molecule. Real-time fluorescent quantitative PCR (qRT-PCR) was used to detect the expression level of circ_0004592 in GC tissues, cells and plasma. The correlation between the expression level of plasma circ_0004592 and clinicopathological data of GC patients was further analyzed.

Receiver operating characteristic curve (ROC) and the area under ROC curve (AUC) were used to evaluate the diagnostic performance.
Results Has_circ_0004592 was first found up-regulated in both tissues (P=0.0009) and plasma of GC patients (P=0.0001). Circ_0004592 was resistant to RNA exonuclease digestion and had a long half-time. The expression level of circ_0004592 was significantly correlated to tumor pathological differentiation (P=0.002), tumor depth (P=0.004), lymph node metastasis (P=0.022). The AUC of plasma circ_0004592 was 0.787 (95%CI: 0.719-0.854) with high sensitivity (66.00%) and specificity (84.00%) in discriminating GC patients from healthy donors. More importantly, the combined diagnosis of circ_0004592, CEA and CA199 achieved the superior AUC of 0.831 (95%CI: 0.773-0.889) with a highest sensitivity (85.00%).
Conclusion Plasma circ_0004592 may prove to be a potential non-invasive auxiliary diagnostic biomarker for GC patients.

PO-0010

Lower respiratory tract samples are reliable for severe acute respiratory syndrome coronavirus 2 nucleic acid diagnosis and animal model study

Cuixian Yang 、Mi Zhang 、xingqi Dong
Yunnan Infectious Diseases Hospital

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and coronavirus disease 2019(COVID-19) continue to impact countries worldwide. At present, inadequate diagnosis and unreliableevaluation systems hinder the implementation and development of effective prevention and treatmentstrategies. Here, we conducted a horizontal and longitudinal study comparing the detection rates ofSARS-CoV-2 nucleic acid in different types of samples collected from COVID-19 patients and SARS-CoV-2-infected monkeys. We also detected anti-SARS-CoV-2 antibodies in the above clinical and animal model samples to identify a reliable approach for the accurate diagnosis of SARS-CoV-2 infection. Results showed that, regardless of clinical symptoms, the highest detection levels of viral nucleic acid were found in sputum and tracheal brush samples, resulting in a high and stable diagnosis rate. Anti-SARS-CoV-2 immunoglobulin M (IgM) and G (IgG) antibodies were not detected in 6.90% of COVID-19 patients. Furthermore, integration of nucleic acid detection results from the various sample types did not improve the diagnosis rate. Moreover, dynamic changes in SARS-CoV-2 viral load were more obvious in sputum and tracheal brushes than in nasal and throat swabs. Thus, SARS-CoV-2 nucleic acid detection in sputum and tracheal brushes was the least affected by infection route, disease progression, and individualdifferences. Therefore, SARS-CoV-2 nucleic acid detection using lower respiratory tract samples aloneis reliable for COVID-19 diagnosis and study.

PO-0011

Association of Polymorphism rs1045411 in the HMGB1 Gene with Cancer Risk

Quansong Xia
The Third Affiliated Hospital of Kunming Medical University, Kunming 650118, China.

The high-mobility group box protein 1 (HMGB1) rs1045411 polymorphism has been demonstrated to be associated with cancer risk in some studies. However, the results regarding this topic are inconsistent. A meta-analysis was applied to elucidate the association between the HMGB1 rs1045411 polymorphism and cancer risk. Ten relevant studies were subjected to our analysis, and pooled odds ratios (ORs) and 95% confidence intervals (CIs) were calculated. In

total, of 3,918 cases and 5,296 controls were included in this study. The pooled ORs were calculated using a random-effects or fixed-effects model according to the heterogeneity. The pooled results revealed that TT genotype was significantly related to increased cancer risk in the comparisons of TT vs. CC+TC (OR=1.35; 95% CI: 1.09–1.67; p=0.005). Though no statistical significance was achieved between HMGB1 rs1045411 polymorphism and cancer risk in other four genetic models (T vs. C: OR=1.08, 95% CI 0.90-1.30; TC vs. CC: OR=1.01, 95% CI 0.82-1.24; CC vs. TC+TT: OR=0.95, 95% CI 0.77-1.18; TT vs. CC: OR=1.42; 95% CI 0.98-2.05), a trend of increased risk could be drawn. In the subgroup analysis by type of malignancy and ethnicity, no obvious difference was found in the tumour risk regarding the HMGB1 rs1045411 polymorphism amongst the cancer types except for breast cancer (OR=1.94; 95% CI: 1.05-3.59; p=0.03) and hepatocellular carcinoma (OR=1.82; 95% CI: 1.15-2.88; p=0.01), while rs1045411 polymorphism was positively associated with risks of cancer amongst Hans (OR=1.37; 95% CI: 1.11-1.69; p=0.004) rather than Caucasians (OR=0.89; 95% CI: 0.26-3.02; p=0.85). These results suggest that the HMGB1 rs1045411 polymorphism might be associated with increased cancer risk.

PO-0012

Dynamic changes of IgM and IgG antibodies in asymptomatic patients as an effective way to detect SARS-CoV-2 infection

Ping Li
First Affiliated Hospital, Hunan University of Chinese Medicine

Background COVID-19 has become a global pandemic, and close contacts and asymptomatic patients are worthy of attention.
Methods A total of 1844 people in close contact with 76 COVID-19 patients were investigated, and nasopharyngeal swabs and venous blood were collected for centralized medical quarantine observation. Real-time fluorescence was used to detect SARS-CoV-2 nucleic acid in nasopharyngeal swabs of all close contacts, and the colloidal gold method was used to detect serum specific antibodies. Levels of IgM and IgG specific antibodies were detected quantitatively through chemiluminescence from the first nucleic acid negative date (0 week) and on weekly intervals of:1, 1-2, 2-3, and 6-7 weeks.
Results The total positive rate of the colloidal gold method (88.5%,23/26) was significantly higher ($\chi2 = 59.182$, $P < 0.001$) than that of the healthy control group (2.0%, 1/50). There was significant difference in IgG concentration at different time points (0-7week) after negative nucleic acid conversion ($\chi2 = 14.034$, $P = 0.029$).
Conclusions The IgG concentration in asymptomatic cases remained at a high level after nucleic acid turned negative. Nucleic acid detection combined with IgM and IgG antibody detection is an effective way to screen asymptomatic infections.

PO-0013

Internally controlled recombinase-aided amplifcation (IC-RAA) assays for the detection of human papillomavirus genotypes 16 and 18 using extracted DNA and samples treated with nucleic acid releasing agent

Jinrong Wang[1,2,3]、Jianli Liu[4]、Guowei Song[1]、Zhi Cao[5]、Jing Pan[1]、Xinna Li[3]、Yuan Gao[2,3]、Juju Qi[1]、Ziwei Chen[3]、Guohao Fan[3]、Xueding Bai[3]、Ruiqing Zhang[2,3]、Ruihuan Wang[3]、Qingxia Duan[2,3]、Lixin Li[1]、Xinxin Shen[3]、Xuejun Ma[3]

1. Shijiazhuang People's Hospital
2. 河北医科大学
3. 中国疾病预防控制中心
4. 海关总署(北京)国际旅行卫生保健中心
5. 北京市朝阳区妇幼保健院

Objectives Cervical cancer is primarily caused by persistent infection with high-risk human papillomavirus (HPV), and 70% of cases are associated with HPV16 and 18 infections. The objective of this study was to establish rapid, simple, and sensitive internally controlled recombinase aided amplification (IC-RAA) assays for the detection of HPV16 and 18. And we explored a nucleic acid release agent suitable for the IC-RAA assay to combine the extraction free nucleic acid method with the IC-RAA assay.

Methods In the E6/E7 gene regions of HPV16 and HPV18, probes and primers were designed based on RAA design principles, and competitive internal control was added to establish a method for detecting HPV16 and HPV18 by IC-RAA assay. A nucleic acid release agent was used to process the sample, and the extraction-free nucleic acid method was combined with the IC-RAA assay. The assays were performed at 39℃ and were completed within 30 minutes. A total of 277 clinical samples of exfoliated cervical cells were tested by IC-RAA assays and commercial HPV real-time fluorescent PCR kits using extracted DNA and samples treated with a nucleic acid releasing agent.

Results The analytical sensitivity of the IC-RAA assay was found to be 10 copies/μL for the detection of HPV16 and 18 when using recombinant plasmids as targets. The optimal analytical concentration of the internal control (IC) plasmid was 1000 copies/μL for HPV16 and 100 copies/μL for HPV18. The clinical sensitivity of the IC-RAA assays for HPV16 using extracted DNA and samples treated with the nucleic acid releasing agent was 98.73% and 97.47%, respectively, with Kappa values of 0.977 ($P < 0.01$) and 0.955 ($P < 0.01$), respectively. The specificity of both were 100%. The sensitivity and specificity of each assay for IC-RAA detection of HPV18 were 100%, and the Kappa value was 1 ($P < 0.01$).

Conclusion We have successfully established highly sensitive, specific and rapid IC-RAA assays for the detection of HPV16 and 18 using extracted DNA and samples treated with the nucleic acid releasing agent. In addition, the method for detecting HPV16 and HPV18 without nucleic acid extraction combined with IC-RAA assay does not require nucleic acid extraction equipment, complex nucleic acid extraction, and purification steps, and simplifies the operating steps of the IC-RAA assay, making it possible for the development of RAA assay to POCT. The IC-RAA assay is a promising tool for detecting HPV16 and 18, and provides a new strategy for realizing HPV16 and HPV18 screening in the grassroots and resource-limited areas.

PO-0014

一例 F11 基因复合杂合变异导致的遗传性凝血因子XI缺陷症的家系分析

程晓丽、杨柳、郝晓柯、刘家云
空军军医大学西京医院

目的 对 1 个遗传性凝血因子XI（coagulation Factor FXI，FXI）缺陷症家系进行临床表型和基因变异分析，探讨其分子致病机制。
方法 提取基因组 DNA，sanger 测序法测定 F11 基因所有外显子及侧翼序列；用 ClustalX-2.1-win 及 MutationTaster 软件分析突变氨基酸的保守性及对蛋白质功能的影响；通过 Swiss-Pdb Viewer 软件分析突变氨基酸对蛋白结构的影响。
结果 基因测序结果显示先证者 F11 基因第 10 和 13 外显子分别存在 c.1067C>T 和 c.1556G>A 变异，导致 p.Pro338Leu 错义变异和 p.Trp501stop 无义变异；先证者父亲和姐姐存在 p.Pro338Leu 杂合错义变异；先证者母亲和儿子存在 p.Trp501stop 杂合无义变异，先证者丈夫为正常野生型。
结论 p.Pro338Leu 和 p.Trp501stop 复合杂合变异是该家系遗传性 FXI缺陷症的分子致病机制，并且 p.Pro338Leu 为国内外首次发现的新变异。

PO-0015

Genetic landscape of DNA repair defects in human monogenic disorders

Niu Li、Yufei Xu、Ru-en Yao、Tingting Yu、Xiumin Wang、Jian Wang
Shanghai Children's Medical Center, Shanghai Jiaotong University School of Medicine

Purpose To provide an unbiased and global view of the proportion of the disorders with DNA repair defects (DRD) in human monogenic diseases.
Methods we retrospectively analyzed the genetic and clinical data of 9,107 unrelated patients from a single center, and sort relevant genes from literature retrieval.
Results From the 127 candidate DNA repair genes, three groups based on the functional study evidence were identified: 26 well-known DNA repair genes, 69 with strong evidence, and 32 with limited evidence. Deleterious variants of these genes were collected from 539 patients, including 72 (13.4%), 249 (46.2%), and 218 (40.4%) for each gene group, respectively. Patients with multiple system involvement as the main manifestation accounted for the largest proportion (47.7%, 257/539), followed by those with prominent neurological symptoms (13.7%, 74/539). We obtained an overall diagnostic rate of 33.5% (3052/9107) and proposed that DRD disorders account for 21.7% (539/2,488) of human monogenic diseases after excluding 564 patients with copy number variations.
Conclusion This is the first report to survey the contribution of DRDs in monogenic diseases from a large cohort. This study expands the DNA repair gene and phenotype spectra and demonstrates that DRD disorders are much more complex than our traditional knowledge.

PO-0016

血浆 cfDNA 结直肠癌 14 基因检测性能及临床应用评估

朱赟洁、沈敏娜、王蓓丽、郭玮
复旦大学附属中山医院

目的 基于 IonS5XL 二代测序平台对 OncomineColoncfDNAAssay（以下简称结直肠癌 cfDNApanel）进行性能确认和临床应用评价。
方法 根据《我国医学检验部门自建检测方法发展与管理建议》和《实验室自建分子诊断项目基本要求专家共识》的试剂盒性能评价相关要求评估结直肠癌 cfDNApanel 的准确性、精确性、参考范围、可报告范围、抽提起始量和投入量、空白限和分析灵敏度、分析特异性等指标。比较本平台与 IlluminaMiseqDx 二代测序平台及突变扩增阻滞系统（amplificationrefractorymutationsystem，ARMS）PCR 的一致性。分别检测临床标本 17 例和 22 例例结直肠癌患者血浆中 cfDNA。
结果 结直肠癌 cfDNApanel 准确性为 99.97%，同时具有很好的精确性。最低可兼容的血浆抽提量为 1ml，血浆投入量为 10ng。分析灵敏度是 0.2%。结直肠癌 cfDNApanel 兼备较好的抽提抗干扰能力和检测特异性。与 IlluminaMiseqDx 二代测序平台一致率为 94.12%，KRAS/NRAS/BRAF/PIK3CA 的阳性符合率（PPA）和阴性符合率（NPA）分别为 100%和 99.60%。与分子病理（组织 ARMS）结果一致率为 90.91%。
结论 结直肠癌 cfDNApanel 性能确认数据符合临床应用需求，在治疗前晚期结直肠癌患者中，血浆 cfDNA 结果与匹配的肿瘤组织结果高度一致，是组织活检的有益补充。

PO-0017

Novel therapeutic evaluation biomarkers of lipid metabolism targets in uncomplicated pulmonary tuberculosis patients

Jiaxi Chen
Enze Hospital of Enze medical center group

Currently, the management of pulmonary tuberculosis (TB) lacks potent medications and accurate efficacy evaluation biomarkers. In view of the fact that the host lipids are the important energy source of Mycobacterium tuberculosis (Mtb), UPLC-MS/MS based on lipid metabolism was used to monitor the plasma lipid spectrum of TB patients from the initial diagnosis to cured. The analysis showed that TB patients presented aberrant metabolism of phospholipids, glycerides, and sphingolipids. Upon the treatment, the abnormal expression of Cer (d18:1/24:0), CerP (d18:1/20:3), LPE (0:0/22:0), LPA (0:0/16:0) and LPA (0:0/18:0) in TB patients were gradually normalized, indicating that the intervention of lipid metabolism could block energy metabolism and inhibit the cell wall synthesis of Mtb. Furthermore, the increase in ceramide (Cer) levels could promote the autophagosome-lysosome fusion. LPA (0:0/16:0) and LPA (0:0/18:0) had a great potential in the early diagnosis (both sensitivity and specificity were 100%) and efficacy evaluation (both sensitivity and specificity were 100%) of TB, indicating that the above lipid metabolites could be used as potential biomarkers for TB.

PO-0018

APN-mediated phosphorylation of BCKDK promotes hepatocellular carcinoma metastasis and proliferation via the ERK signaling pathway

Mengying Zhai
Tianjin Hospital
天津医科大学

Background Hepatocellular carcinoma (HCC) is one of the most prevalent human malignancies worldwide and has high morbidity and mortality. Elucidating the molecular mechanisms underlying HCC recurrence and metastasis is critical to identify new therapeutic targets. This study aimed to determine the roles of aminopeptidase N (APN, also known as CD13) in HCC proliferation and metastasis and its underlying mechanisms.
Method We detected APN expression in clinical samples and HCC cell lines using immunohistochemistry, flow cytometry, real-time PCR and enzyme activity assays. The effects of APN on HCC metastasis and proliferation were verified in both in vitro and in vivo models. RNA-seq, phosphoproteomic, Western blot, point mutation, coimmunoprecipitation and proximity ligation assays were performed to reveal the potential mechanisms.
Findings We found that APN was frequently upregulated in HCC tumor tissues and high metastatic cell lines. Knockout of APN inhibited HCC cell metastasis and proliferation in vitro and in vivo. Functional studies suggested that loss of APN impedes the ERK signaling pathway in HCC cells. Mechanistically, we found that APN might mediate the phosphorylation at serine 31 of BCKDK (BCKDK^{S31}), promote BCKDK interacting with ERK1/2 and phosphorylating it, thereby activating the ERK signaling pathway in HCC cells.
Interpretation Our findings indicate that APN mediates the phosphorylation of BCKDK^{S31} and activates its downstream pathway to promote HCC proliferation and metastasis. Therefore, the APN/BCKDK/ERK axis may serve as a new therapeutic target for HCC therapy, and these findings may be helpful to identify new biomarkers in HCC progression.

PO-0019

PRISMA-compliant meta-analysis of diagnostic value of microRNA-375 in prostate cancer

Xin Wang、Zhuo Li、Jian Zhou、Li Wang
The First Affiliated Hospital of Xi'an Medical University

Objectives MicroRNA-375 (miR-375) plays an important role in the diagnosis of prostate cancer (PCa). However, the diagnostic parameters in previous studies are inconsistent. In order to evaluate the diagnostic value of miR-375 in PCa, we conducted a meta-analysis.
Methods We searched for PubMed, Medline, Cochrane Library, Embase, Web of Science and Chinese database (CNKI and Wanfang database), comprehensively from the inception to November 31, 2020. Meta disc 1.4 and StataSE15 were used to analyze the data. The bivariate meta-analysis model was employed to summarize sensitivity (SEN), specificity (SPE), positive likelihood ratio (PLR), negative likelihood ratio (NLR) and diagnostic odds ratio (DOR) for miR-375 in the diagnosis of PCa. Summary receiver operating characteristic curve (SROC) analysis and the area under the curve (AUC) were used to check the overall test performance.
Result Sixteen studies, evaluating the diagnostic value of miR-375 in patients with prostate cancer, were included in this meta-analysis. The combined sensitivity and specificity of miR-375 in the diagnosis of PCa were 0.75 (95% CI: 0.73-0.77) and 0.77 (95% CI: 0.74-0.79), respectively. The PLR was 2.94 (95% CI: 2.30-3.76), and the NLR was 0.29 (95% CI: 0.23-0.38). In addition, we noted that the overall DOR of miR-375 for PCa was 12.90 (95% CI: 8.84-18.83). The AUC of

total area under receiver operating characteristic curve (ROC) was 0.86 (95% CI: 0.82-0.89). Multiple regression analysis showed that the heterogeneity mainly came from the total number of samples. Subgroup analysis showed that the diagnostic efficiency of serum was the highest and the heterogeneity was the lowest among the different sample types. Fagan nomogram results showed that miR-375 detection significantly increased the diagnosis of PCa.
Conclusion Serum miR-375 has a high diagnostic value for prostate cancer. Rigorous and high-quality prospective studies are required to verify our conclusion.

PO-0020

Urea as a By-product of Ammonia Metabolism can be a Potential Serum Biomarker of Hepatocellular Carcinoma

Changsen Bai、Li Ren
Tianjin Medical University Cancer Institute and Hospital

Objective Hepatocellular carcinoma (HCC) is highly malignant; nearly half of the new cases and deaths are in China. The poor prognosis of HCC is mainly due to late diagnosis; many new biomarkers have been developed for HCC diagnosis. However, few markers are quickly translated into clinical practice; early and differential diagnosis of HCC from cirrhosis and/or hepatitis is still a clinical challenge. We set out to find a biomarker that could be used to distinguish HCC from other liver diseases.
Methods The metabolites of the serum were analyzed by quantitative targeted metabolomics for differential analysis to find specific potential markers of HCC patients. The biochemical analysis method was used for in-depth analysis and verification. The serum of 115 cases of healthy controls, 69 cases of HBV, 108 cases of HBV positive cirrhosis, 95 cases of HCV, 294 cases of HBV positive HCC patients, and 77 cases of metastatic HCC patients (other cancers metastasize to the liver) were preliminary verified as the training set. Next, the serum of 118 normal healthy controls, 142 cases of lung cancer patients, 150 cases of breast cancer patients, 140 cases of colorectal cancer patients, and 165 cases of HBV positive HCC patients were analyzed as the validation set. Besides, we have demonstrated the underlying mechanism through multiple cell models and co-culture models.
Results Most of the elevated metabolites in HCC and HBV patients were overlapped compared with controls. Urea was the specifically elevated serum biomarker of HCC patients. Moreover, urea combined with AFP and CEA can improve the sensitivity of HCC diagnosis. The plasma ammonia of HCC patients was significantly higher than healthy controls. Co-culture cell model revealed normal liver cells cooperated with cancer cells to metabolize ammonia into urea. The urea metabolism in cancer cells marginally depended on the expression of CPS1. However, the expression of CPS1 did not change with ammonium chloride, which might regulate the urea cycle through enzyme activity. The urea cycle could detoxify high concentrations of ammonia to promote cancer cell proliferation.
Conclusion Urea was a by-product of ammonia metabolism and could be a potential serum biomarker for HCC. The combined application of metabolomics and biochemical methods can discover new biomarkers for the early diagnosis of HCC and be quickly applied to clinical diagnosis.

PO-0021

Novel evidence for an oncogenic role of SOX9 in lung cancer stem cells

Qingli Bie、Haixin Dong、Fenglian Shan、Bin Zhang
Department of Laboratory Medicine, Affiliated Hospital of Jining Medical University, Jining, Shandong, P. R. China

Lung cancer is the second most common malignant tumor and is the leading cause of cancer death worldwide. SOX9 is an important transcription factor that functions in development, and it has been demonstrated to be abnormally expressed in various cancers. In the present study, we found that SOX9 was overexpressed in lung cancer tissues and that SOX9 could promote proliferation, migration, invasion and self-renewal by gain- and loss-expression of SOX9 in vitro. Clinicopathological characteristics analysis showed a significant relationship between SOX9 expression and TNM stage, sex, VEGF and EGFR; moreover, overexpression of SOX9 predicted a poor outcome in lung cancer patients. Transcriptome profiles revealed 364 differentially expressed genes between A549 cells transfected with shControl and those transfected with shSOX9. Potential signaling pathways associated with malignant biological behavior were identified, including GnRH, MAPK, and PPAR. In conclusion, SOX9 is an important transcription factor promoting malignancy in lung cancer, and it may be a novel therapeutic target for lung cancer.

PO-0022

ISO15189 质量管理体系在医院检验科实习生带教工作中的实践和运用

周庆丰、曹辉、陈洪卫、刘军
上海市松江区中心医院

随着医学的不断进步，医院对于检验科实习生的带教要求也越来越高，借鉴 ISO15189 质量管理体系对实习教学过程进行全面质量控制，培养学生独立操作、发现问题、分析问题和解决问题的能力，综合运用医学检验与理论知识的能力，加强与临床医患沟通的能力。将 ISO15189 质量管理体系融入实习带教中，引导实习生关注影响检验结果的各个环节，训练其从检验和临床的角度全面分析问题，有助于拓宽实习生的知识面，帮助实习生形成系统全面的综合判断思路，从而有效地提高实习生的理论知识与专业技能，提高实习生的实习效果。

PO-0023

不同教学模式对培养创新型检验人才的临床效果评估

邓文平、谢小义、刘琪、黄琳淋
重庆市涪陵中心医院（重庆市微创外科研究所）

目的 为提高医学检验的教学质量，提升实习学生的学习能力和临床思维方式，本文探讨不同教学模式下对医学检验创新型人才的培养效果。
方法 选择 40 名实习学生随机分成两组，实验组和对照组，以传统讲授教学模式与分段联合 EBLM 与 PBL 的教学模式，进行比较，分别对实习学生的基础理论成绩、实际操作成绩、临床思维能力、提出问题解决问题能力、沟通与合作能力等内容进行评价。
结果 在初期传统教学模式下，学生对理论定义掌握与其它教学模式相比，基本一致，较全面，教学中花费的时间最少；分段联合 EBLM 与 PBL 教学模式学生对于检验项目在临床的应用比较有更

为直接的证据，对临床应用的接收程度和临床思维能力提高较为显著；学生在实际工作中发现的问题提出解决问题的能力提高也较为明显。
结论 对医学检验创新型人才的培养中，以分段联合 EBLM 与 PBL 的方式，在实习不同的时间段，分配不同的教学模式主体能更好地提高学生的学习水平和综合素质，促进创新型检验人才的培养，顺应时代赋予医学检验专业培养检验人才的要求。

PO-0024

多元化教学与过程性考核相结合在临床生化检验带教中的探索与实践

高佳
中国医学科学院肿瘤医院

临床生化检验是医学检验的重要亚专业之一，其知识点繁杂、与临床结合紧密，带教难度颇大，而与此同时，临床生化室又是自动化程度较高的实验室，容易出现只教仪器操作，而忽略了更深层次的仪器检测原理、项目临床意义的情况。中国医学科学院肿瘤医院检验科自 2006 年首批取得北京市检验住院医师培训基地资格以来，针对临床生化检验的教学特点和难点做了大量的探索。本文将结合中国医学科学院肿瘤医院检验科检验医师规范化培训基地在检验医学住院医师规范化培训的具体实施情况与经验，对临床生化检验的带教模式进行探讨。
1 解读培训及考核要求，根据培养对象的特点及背景确定培养目标
依据《临床住院医师规范化培训大纲》及《检验医师培训细则》对在培检验医（技）师进行培训，但不同培训人员的培训要求和培训重点不尽相同。即使对于同类的培训人员，培训侧重点也应根据其学历和工作背景个性化设置。
2 确认培训要点、制订培训计划
结合《临床住院医师规范化培训大纲》和《临床生物化学检验》课本，由带教老师集中讨论，确认并列举本专业组的所有培训要点。按照循序渐进的原则，将培训要点分类并确定每一大类的培训时长，制订规范的培训计划及培训方案。
3 采用导师负责制与日常带教相结合的带教模式，灵活运用操作演示、专题小讲座、结合案例教学等多种教学手段，辅以面试、笔试、PPT 汇报等过程性考核形式。
通过一系列的改进，极大地提高了临床生化检验的教学质量，形成了涵盖实验室常规操作、检验相关的质量控制、临床诊疗知识的教学培训体系。临床生化检验的带教工作是繁重的，但“教学相长”，带教本身也是一个查缺补漏、自我提高的过程，只有合理地安排培训周期、设计培训计划，不断在教学过程中进行监督和考核，才能使教学管理渐趋科学化、规范化，最终提高教学质量。

PO-0025

Development, application, and evaluation of a problem-based learning method in clinical laboratory education

Chunyan Peng[1,2]、xiandong Li[1]、Fei X[1]
1. Taihe hospital, Hubei University of Medicine
2. 湖北医药学院

Background There is a big gap between theory and real clinical practice with respect to the structure of clinical laboratory medicine (CLM) education in China. An integrated teaching method is urgently required, to improve student competency and prepare students to deal with complex challenges in the working environment.

Methods A total of 122 fourth-year CLM students studying at Hubei University between 2018 and 2019 were randomly assigned to a traditional teaching methods group or a problem-based learning (PBL) group. In the PBL group students were instructed to exchange their thoughts, identify information gaps, rehearse and perform simulated clinical scenarios, and incorporate the new information into cases in small groups. Theory tests, questionnaires, and clinical performance assessments were used to evaluate the effectiveness of PBL and compare it with that of traditional teaching methods.
Results PBL resulted in significantly better theory test scores, better student feedback scores, and clinical performance assessments, and a higher rate of satisfaction among students and teachers.
Conclusion PBL is an effective way to help CLM students develop comprehensive abilities to deal with real clinical laboratory work. It is a promising education method and should be generalized to all subtypes of clinical laboratory curriculums in the future.

PO-0026

带有样本相关信息二维码的载玻片示教片应用与形态学示教的优势

张玲
阿克苏地区第一人民医院

背景 在临床或医学教学时，载玻片是医学实验中重要的材料。通常将包含细菌、真菌、细胞或组织切片等的样本放在载玻片上，然后将其放置在显微镜下对样本的病理、形态学进行观察与分析。而用于临床检验、病理病例资料及教学的示教载玻片保存时需要对其进行标记。由于载玻片的尺寸小，那么可用于标记的内容也就极其有限。目前载玻片上标记的信息一般包括样本编号或类别及名称-具体的病理及形态学还需要根据标签上的编号或类别、名称通过电脑或其他的途径另作查询。这给实验人员尤其医学教学人员造成了极大的不便。基于上述原因，对现有载玻片标记方式进行改进。提供一种带有样本信息二维码贴在载玻片上，只需通过扫描二维码即可调取储存在载玻片上的与样本有关的各种形式（文档、图谱、PPT 甚至视频）的信息。方便了病历资料整理及保存，也为教学人员的教学提供了便利。
方法 根据载玻片上样本包含的内容制作需要展示的文档、图谱、PPT 甚至视频；信息化解码；生成二维码；扫码提取信息。选取 2020 年我院检验科学员及新进员工 16 人随机分组，A 组 8 人采用传统培训模式，集中授课、现场演示练习等；B 组 8 人，在传统培训模式的基础上，加用二维码示教片进行自主学习。两组干预周期均为两个月，干预后比较两组人员学习的效果，指标包括形态学理论知识与实践操作考核、培训的满意度。
结果 传统培训的基础上，加用二维码示教片进行自主学习后理论考试操作考试均高于 A 单纯的传统培训模式；并且培训的满意度也比单纯的传统培训模式高，且差异具有统计学意义。
结论 带有二维码信息的教学载玻片示教片是将现代信息技术与临床技能教学结合，有效激发了学员、新进员工及工作人员的学习兴趣，可提高对形态学教学的培训效果。让现代化信息技术为临床技能教学添彩加翼。

PO-0027

多模式教学在医学检验实习带教中的应用

武睿
重庆医科大学附属第一医院

目的 为提高医学检验科本科生实习教学质量，将 PBL、CBL 结合翻转课堂多模式教学应用于实习带教管理程序中，探讨多模式教学在医学检验科实习带教中的应用效果。
方法 2018 年进入本科室的 18 名医学检验技术专业的本科实习生以传统管理方式进行实习带教，为对照组，2019 年进入本科室的 20 名医学检验技术专业的本科实习生以多模式教学方式进行实习带教，即将 PBL、CBL 结合翻转课堂教学方式加入实习带教中，设为实验组，将两组毕业考试成绩及满意度评价进行对比。
结果 实验组出科考试的理论成绩与操作成绩均高于对照组，差异有统计学意义（$P < 0.05$），并且实习满意率明显高于对照组($P < 0.05$)。
结论 采用 PBL、CBL 结合翻转课堂多模式教学进行医学检验科实习带教，可有效提高教学质量，提高实习生的满意度。

PO-0028

瑞金医院检验医师规范化培训的模式和体会

孟俊
上海交通大学医学院附属瑞金医院

住院医师规范化培训是高层次医学生毕业后教育的重要组成部分，是，其中检验医师规范化培训是培养检验专科医师的有效手段和重要措施，；是专业检验科医生成长的必由之路，也是为其之后行医奠定关键基础的关键阶段，，也是一个专业检验科医生成长的必由之路。同时也在扩大检验医学影响力和提高检验科在医院地位等方面具有同等重要价值。本文结合上海交通大学医学院附属瑞金医院十多年来检验医师培养方面的一些措施和体会，为检验医师的工作及其规范化培训过程提供一些意见和建议。

PO-0029

临床血液学检验规范化培训教学模式探索与实践

沈迪、车轶群、王力、宋桂瑜、崔巍
中国医学科学院肿瘤医院

目的 通过建立系统的临床血液学检验规范化培训教学体系，为培养高素质应用型临床血液学检验医师和技师提供教学支撑作用。
方法 制定合理的规范化培训规程，建设完整的组织管理体系；指导教师的选拔和培训，内容涉及基地管理、教学方法改进、教学能力提升、科研能力提高等；规培学员的录取和培训，根据规范化培训大纲和标准细则要求，制定临床血液学检验的教学计划和培训细则；建立系统的考核模式，考核形式包括组内阶段性考核、出科考核和年度模拟考核；实行师生双向评价和反馈机制，设置规培学员与指导教师互评体系，定期举办师生座谈会，收集学员对教学工作的意见和建议；带教教师采用多元式教学形式与教学方法进行教学，包括传统的教学形式，日常线上练习及讲解，充分应用案例教学法（case-based learning,CBL），以学员为主导的微课教学模式；注重医学人文的培养，应用人文关怀加强医患沟通。

结果 通过制定合理的规范化培训规程，有序实施教学活动，规范教师带教，促进教师带教能力的提升，提高了教学水平。学员通过系统的规范化课程培训，通过日常练习和系统考核，明确了学习的重点和难点，促进了学习兴趣，并且重视日常的积累，为以后步入工作岗位打下坚实基础。
结论 临床血液学检验是一门多学科交叉的课程，并且实践性强、发展迅速，在今后的教学过程中，我们在未来的实践中不断探索和研究，尝试更多更新的教学手段、理念，创造更加合理的人才培养模式。

PO-0030

多元化教学模式在检验科实习生带教中的应用

岳宏波
西安市阎良铁路医院

目的 探讨多元化教学模式在检验科实习生带教中的应用效果。
方法 将我科 2018 年 8 月-2019 年 3 月 13 名实习生作为对照组，2019 年 8 月-2020 年 3 月 15 名实习生作为观察组，对照两组实习效果。对照组实行传统带教模式，即学员轮转到各专业组由各专业组老师带教本专业组内容。学习没有系统性，学员的学习质量也受带教老师的带教态度和和能力影响很大；观察组采用多元化教学模式。实行带教导师负责制对所带教的学员全过程负责。在培训方法上注重多元化、趣味化、及时性，实习生接受度更高效果好。通过完善的考核机制，“师生双向”效果评价和反馈，不仅提升了带教老师工作责任心和教学技巧，同时调动了实习生的主动性。多元化具体教学模式为：1.确定教学组织架构，由科主任-教学组长-带教导师组成。科主任负责对整个培训计划和方案的制定与落实，对整个培训过程管理督导和检查；教学组长负责总带教，负责具体培训内容和考核内容的实施，对带教导师和教学计划进行工作督导和考评；带教导师进行“一对一”导师负责制。 2.培训方法采用多模式教学：每日晨课、理论督导、各专业组轮转学习；技能比赛、学员 PPT 授课比赛；情景模拟；突发事件应急演练；视频反馈教学和评价。3.采用 SPSS17.0 软件进行数据分析，计量资料使用（`X±S）表示，采用 t 检验；计数资料使用 X2 检验，以 P<0.05 则差异有统计学意义。
结果 观察组实习生理论知识考核评分为（94.25±4.31），操作技能考核评分为（95.05±3.82），教学质量评分为（96.36±2.23）；对照组实习生理论知识 考核评分别为（88.76±5.35），操作技能考核评分为（90.57±4.06），教学质量评分为（88.53±8.20）。观察组理论知识考核、操作技能考核、教学质量评分均高于对照组，差异均具有统计学意义（P<0.05）。观察组实习生对教学方法满意度调查中，满意为 100%；对照组实习生对教学方法满意度调查中，满意为 76.9%，一般为 23.1%。观察组实习生对教学方法满意度评价高于对照组，差异均具有统计学意义（P<0.05）。
结论 多元化教学模式在检验科实习生带教中应用效果显著，不仅提升实习生的实习质量，并且提高其对教学方法评价的满意度，同时也提升带教老师教的带教能力。

PO-0031

Explore the growth path of clinical laboratory graduate students with a background in clinical medicine from the perspective of "cultivation of laboratory physicians"

Yingmei Wu[1]、Yingchun Zhou[2]
1. Department of Clinical Laboratory, The First Affiliated Hospital of Guangzhou University of Chinese Medicine
2. 广州中医药大学第一附属医院白云医院

In September 2012, the Ministry of Education adjusted the medical laboratory specialty from five to four years. The specialty was thus classified as a science degree and no longer belonged

to a bachelor of medicine. This decision in turn made it impossible for students who enrolled in the future to participate in the physician qualification examination. The COVID-19 epidemic has brought the normally unknown clinical lab staff to the front line of the response teams and also made the entire society aware of the importance of building a team of clinical lab doctors. At present, the clinical labs and clinical departments usually lack in-depth communication, and medical staff has limited understanding of many reports issued by the lab. The cultivation of lab physicians is conducive to mutual understanding and growth of departments and labs, and improves the efficiency of hospital diagnosis and treatment services.

In this context, clinical lab graduate students with a bachelor's degree in clinical medicine are particularly suitable to take the path of clinical lab physicians. It is reasonable to say that graduate students who have just entered the lab have little knowledge of the diagnostic techniques available. Therefore, the process of learning for each professional group in the laboratory is particularly important. First of all, in the rotating learning process of the laboratory, the staff should master every process of the lab work, and become involved in more hands-on operations, from daily reagent preparation, quality control, calibration to report review, and so on. Students should understand the various inspection projects, the settings and work content of each professional group, etc. Additionally, it is necessary for students to master the principles, methods, and clinical significance of each test item, and become familiar with the factors that affect the test results. For example, when the test results do not match the clinical symptoms, they should be able to further analyze and find out the reasons. Through practical training in the clinical lab, graduate students with a clinical background can have a deep understanding of the work and its limitations.

Later, in the training of clinical departments, graduate students should learn to treat and manage patients independently, and be proficient in various basic clinical skills, including medical history collection, physical examination, and preliminary diagnosis and treatment of diseases. In addition, lab physicians should focus their training on the interpretation of various test reports, learn to look at test results from the perspective of clinicians, maintain a flexible clinical thinking mode and guide and help clinicians to choose test items correctly and reasonably. When doctors or patients have questions or doubts about the test results, they can provide professional answers. Training experience will inevitably broaden the scientific research thinking of laboratory physicians and will bring great benefits to their future scientific research in the hospital. The cooperation and promotion of laboratory and clinical departments is inseparable from the cultivation of laboratory physicians.

PO-0032

以“强化科研素养”为成果导向的《分子生物学检验技术》课程模式构建

林艳凤、林东红、林旎
福建医科大学

培养具备科研能力与创新能力的医学人才是 21 世纪高等医学教育教学承载的责任与使命。反思分子生物学检验技术教学现状，引入成果导向教育理念，提出“强化科研素养教育，培养卓越型医学人才”学习成果目标，从教学理念、教学模式、教学手段和考核评价等方面进行改革，解决学生科研素养与未来需求不相适应的问题，满足当代医学对临床实验室医学检验专业高素质应用型人才的需求。

PO-0033

线上与线下混合式教学在临床检验诊断学研究生深度学习中的应用探讨

张利霞、张启声、王娜
内蒙古科技大学包头医学院第一附属医院

目的 在线上线下混合教学情境下，明确哪些因素可以促进临床检验诊断学研究生的深度学习(反思性与整合性学习），从而为临床检验诊断学研究生制定线上与线下深度融合的优质教学模式，并进一步探索检验高级人才培养新策略。

方法 1.通过文献查阅、哲学思辨对深度学习的核心进行理论界定，提出影响深度学习的主要因素。通过 NSSE 中国改良版（NSSE-China）心理学问卷调查，确定临床检验诊断学研究生在教学过程中影响深度学习的实际主要因素，由此制定深度学习的在教育学中的评价标准。2.将深度学习的评价标准与临床检验诊断学的研究生教学相结合，通过教师访谈，学生调查问卷，分析教学内容的特点，制定基于线上线下混合的教学新模式。

结果 1.促进临床检验诊断学研究生深度学习的方式有：师生互动分析讨论，学生积极有效表达想法；以小组为单位的文献阅读共同体的建立；线上资源包括知识点视频、开放性试验、专题讨论资料、创新性前沿信息分享讨论等。

2.结合深度学习的评价标准制定了学科中每节课的深度学习的评价标准和实际评价方法。基于此通过整合和制作线上教学资源和线下教学调整，构建了新的教学模式。

结论 线上与线下混合式教学深度融合，能根据学生的个性化需求，重置学习的时间与空间，有效提升了学生学习的有效性，增强了学生的实践和创新能力。但混合式教学设计在国内临床检验诊断学硕士研究生培养中仍处于探索阶段，在实践中需要不断创新和总结经验。

PO-0034

BOPPPS 教学法在《临床免疫学检验技术》实验教学中的应用探索

张丽翠、马雅静
石河子大学医学院第一附属医院

目的 探讨基于 BOPPPS 教学法在《临床免疫学检验技术》实验教学中的应用效果及其评价。

方法 选取 2020 年 09 月-2020 年 11 月在石河子大学医学院进行《临床免疫学检验技术》实验课的医学检验专业的本科 2018 级 1 班 40 名学生作为实验对象，并随机分为实验组与对照组(每组 20 名)。对照组采用传统教学方法，实验组采用 BOPPPS 教学方法。在教学实验结束后比较两组学生理论考核成绩、技能操作考核成绩、案例分析能力得分，并建立学生对教学满意度评价、自我提升能力等多方面建立评价机制。

结果 实验组学生理论知识、技能操作以及案例分析成绩均明显高于对照组($P<0.05$)。实验组学生对教学的满意度(100%)明显高于对照组(85%)，$P<0.05$，实验组学生综合能力提升显著高于对照组 $P<0.01$。

结论 在《临床免疫学检验技术》实验教学中应用 BOPPPS 教学法可取得较好的教学效果，学生能同时具有实验操作技能及与临床案例相结合的思维和认知能力相融合，建立系统的临床思维能力。为培养以“检验技术”为核心的医学检验人才，对现如今的临床免疫学技术的实验课教学方法进行革新能够有效提高学生的临床与检验综合分析能力，同时有助于学生更好地培养其临床检验思维能力与兴趣，并显著提高了学生对教学质量的满意度，值得进一步研究及推广。

PO-0035

检验医学规培模式探讨培养实用型人才

宋立兴[1]、余晓林[1]、宋自阆[1]、刘孝桢[2]
1. 自贡市第四人民医院
2. 四川省卫生康复职业技术学院

目的 对检验医学规培人员探索在新形势下，如何培养适应时代发展要求的新型复合型检验医学人才。
方法 通过改革教学内容、创新教学方法和改进教学形式，致力于学员的操作能力、临床思维能力、适应社会能力的培养。
结果 在检验医学规培带教中采用多种教学模式，培养学员临床思维能力，检验结果与临床相结合的意识，可以激发学员主动学习的兴趣，教会学员如何发现问题、分析问题、解决问题，可以大大增强学员对自我能力的认识和对检验专业的认同感。
结论 通过创新规培模式，改革规培方法和内容，有利于培养学员良好的临床沟通能力、临床思维能力和解决临床实际问题的能力，有利于培养适应现代医学发展的新型实用型人才

PO-0036

医学检验专业本科生专业思想稳定性的调查与分析

黄奔、王洁、张祥、赵鸿
南京医科大学第一附属医院（江苏省人民医院）

目的 为了解新形势下医学检验专业本科生专业认知的情况，了解医学检验本科生的专业基本情况、专业思想稳定性、专业评价与专业学习的现状。
方法 采用分层整群的抽样方法，调查江苏省某医学院校医学检验学专业三个年级的在校本科生，发放问卷 336 份，回收有效问卷 269 份，有效率为 80.59%。采用 Epidata3.1 软件建立数据库，双人双录入的方式来确保数据输入的准确性。采用 IBM SPSS Statistics 25.0 统计软件进行一般性统计学分析。
结果 此次调查分析中，共有男生 78 名，女生 191 名；大一学生 93 名，大二学生 95 名，大三学生 81 名。调查显示，所学专业为报考第一志愿的学生仅有 99 人（36.80%），其中，因自身兴趣爱好而报考的仅占 20.20%。在专业思想稳定性方面，有 5 名（1.85%）学生想过要转专业，只有 79 人（22.07%）认为自身适合医学检验专业学习，并且有 207（76.95%）人选择毕业后会从事所学专业工作。在专业社会地位评价方面，只有 11 人（4.08%）认为医学检验专业的社会地位较高。在专业学习方面，只有 19 人（7.06%）认为专业课程学习设置合理。
结论 此次调研显示，超过半数的医学检验专业本科生认为所学专业社会地位不高，并且对专业学习课程评价度低，医学检验专业本科生的专业思想稳定性存在问题，亟待重视。

PO-0037

临床医学本科《实验诊断学》课程教学改革实践

张翔、郝晓柯、杨柳、周柯、周磊、刁艳君、李蕊、贺文芳、刘家云
空军军医大学西京医院

目的 实验诊断学是临床医学专业的一门必修专业课程，是诊断学中重要部分，也是重要的医学“桥梁”课程。以往课程局限于检验项目原理逐条单一讲授，学员反映知识繁杂难记、运用困难；而实验诊断学发展迅速，教学与临床相脱节的矛盾日趋明显。

方法 为引领学员顺利进入后续临床专业课程学习，尽早建立临床思维，空军军医大学西京医院实验诊断学教研室近年来对课程设置和内容进行了大幅度改革，调整如下：（1）优化内容，调整教学方法以系统、器官、疾病为主线进行排课，形成“五位一体“的板块式教学模式，即在理论按照临床血液学检验、体液检验、生化检验、免疫学检验、微生物学检验五个部分知识体系重点学习的基础上，分别结合各相关疾病的实验室诊断来进行系统讲授；（2）强调实用性：舍弃老旧、传统的检验项目，把与临床联系密切、实用性强的内容作为课程的主要内容，增加新技术、新方法讲授和病例分析，使学生在日后临床工作中学有所用；（3）重点培养学以致用的能力：重实践，改变传统实验课只重技术操作的方式，增加用学生自己的实验结果分析病例，穿插以报告单解读和实诊病例讨论为主要内容进行的讨论式教学，加之观摩实验室了解临床工作流程，激发学习的兴趣，提高动脑与动手能力；(4)通过结合学习通、雨课堂等学习 APP 和虚拟仿真（VR）软件“沉浸式“实践教学，辅以翻转课堂、知识竞赛等多维形式为补充，搭建信息化、混合式立体教学平台，更好地培养学员综合素质和整体临床医学观。

结果 经过几学期的教改和实施，教学取得良好成效。回收调查问卷提示，临床学员普遍反映学习兴趣增加，临床思维得到训练。

结论 “学生为主体，教师为主导”的教学原则下，多种手段相结合的混合式教学方法给实验诊断学教学改革提供了新的方向。

PO-0038

从“人机法料环”浅谈临床检验诊断学学术型研究生的科研能力培养

吴洪坤
海军军医大学第二附属医院（上海长征医院）

科研能力的培养对临床检验诊断学研究生、尤其是学术型研究生至关重要，但目前临床检验诊断学学术型研究生的科研培养存在科研水平不足及科研环境欠佳等诸多问题。结合多年培养经验，提出从“人机法料环”五个因素方面入手，通过发挥自身内驱力、增强导师引导力、提高培养工具性、提高思维科学性、提升环境友好性等对策来提高临床检验诊断学学术型研究生的科研能力和水平，为其以后的职业发展奠定坚实的科研基础，为临床检验诊断学的发展贡献新生力量和高水平人才。

PO-0039

医学检验技术专业 PBL 课程建设与应用探讨

程龙、李小宁、徐五琴、张鹏、邢子禾
皖南医学院弋矶山医院

为满足新时代综合性专业人才培养，我校在医学检验技术专业尝试建设 PBL 课程。本文主要论述 PBL 课程在医学检验技术专业中建设与应用，在课程的建设中重点加强课程导师队伍建设已经课程案例库建设；课程实施过程要坚持 PBL 小组讨论的主要形式并且重点关注课程的考核与评价。在课程建设与实施阶中发现 PBL 课程在学生临床思维能力培养方面较传统教学方法有显著优势。在医学检验技术专业教学教改中起到了积极作用。

PO-0040

互联网+医学检验高等教育的数字化资源库建设研究

林旎[1]、欧启水[2]
1. 福建医科大学
2. 福建医科大学附属第一医院

在"互联网+教育"跨界融合大背景下,阐述了当前环境下创建数字化资源库对推进教学模式和学习形态变革的必要性。创建数字化资源库符合信息时代教育网络化、数字化、智能化的要求,有助于改进教学效果和提升学习体验,有助于推动网络共享课程建设,有助于实现兄弟院校资源共享和学习型社会建设,具有一定的社会效益。

PO-0041

改良 Mini-CEX 在医学检验专业硕士研究生教学中的应用探索*

任美英、王翠峰
内蒙古科技大学包头医学院第一附属医院

目的 探讨改良迷你临床演练评估（Mini-CEX）在医学检验专业硕士研究生教学中的应用价值。
方法 将医学检验专业 2018~2020 级硕士研究生共 18 名作为研究对象，分别在检验科 5 个亚专业组（临检组、细胞组、微生物组、生免组，急诊检验组）轮转实习，分三轮进行，每轮 6 名学生，随机分为实验组和对照组，每组各 9 名。对照组遵循传统的带教模式；实验组在传统教学的基础上，实施 Mini-CEX 教学。 具体的研究**方法** 1.师资培训 2.操作流程，包括：时间预约、地点选择、学生准备、学生操作、当场评分、及时反馈 3.测评指标，采用医学检验科自制的评分表。4.评分标准，Mini-CEX 评估量表采用 9 分制评分。所有学生完成实习后，参加统一的理论和操作技能考评。
结果 在轮转结束时，两组学员的 Mini-CEX 考核成绩中实验组成绩（ 包括标本接收与处理、标本检测、检验结果审核与报告、标本保存与废弃物处理、临床思维、医患沟通、整体表现 7 个方面） 均优于对照组，差异具有统计学意义（ $P<0.05$）；两组学生轮转结束后的出科考核包括理论知识和操作技能考核。两组的理论知识考核成绩，差异无统计学意义（ $P> 0.05$）；而实验组的出科操作技能考核成绩高于对照组，差异具有统计学意义（ $P< 0.05$）。
结论 将改良 Mini-CEX 应用于医学检验专业硕士研究生的轮转考核中，能够更加全面客观地评价学生在临床实习中的表现，逐步建立一套具有临床检验专业特点的研究生综合实践能力评价体系，其信度和效度均优于传统的评估方法，有效提高我科临床教学质量，值得在医学检验带教硕士研究生教学活动中推广应用。

PO-0042

临床检验诊断学专业硕士研究生住院医师规范化培训的带教体会

张静[1,2]、李芳[1,2]、马雯[1,2]、樊瑞军[1,2]、朴文花[1,2]
1. 宁夏回族自治区人民医院
2. 西北民族大学第一临床医院

作为西北民族大学第一临床学院，本院开展临床检验诊断学硕士研究生住院医师规范化培训九年，在培训的过程中发现学员对培训目标定位不明确、师资带教水平参差不齐，缺乏临床思维的培养、与住院医师规范化培训共用的培训大纲落实不到位、教学模式单一、与导师和带教老师沟通的主动性欠佳等问题。通过归纳总结带教中的一些体会，医院建立了住院医师规范化培训导师、带教老师遴选制度，季度、年度考核制度、出科汇报、导师谈话制度。结合执业医师资格通过情况优化培训轮转的模式。各专业组制定分层递进的培训计划，保证每个阶段的学习内容和深度逐层有所提

高。尝试将案例教学法引入临床检验诊断学专业硕士研究生教育，让学员自己动手动脑寻找病例的蛛丝马迹，加强师生之间的互动，提升团队精神和合作意识，不断提高检验诊断学专业的培训能力，提高学员分析、解决问题的能力，为检验医学高层次临床应用型人才队伍培养出优秀的检验医师。

PO-0043

牢固课堂教学主阵地，打造来华留学生实验诊断学“金课”

张洁心、王芳
江苏省人民医院（南京医科大学第一附属医院）

目的 根据 2019 年教育部发布《关于深化本科教育教学改革全面提高人才培养质量的意见》的内容和要求，以坚持立德树人，围绕学生忙起来、教师强起来、管理严起来、效果实起来的目标为导向，我校医学检验学系在来华留学生实验诊断学课程三年改革的基础上继续探索，旨在突出来华留学生教学特色，深化课堂教学质量标准建设与评估，同时加强师资培训以提高教师综合素质。
方法 我们将改革前后共十年间留学生课堂表现、课后作业、实验操作及笔试成绩分别计算制表，以调查问卷方式获得学生反馈信息，运用统计学方法进行量化分析。
结果 近三年来留学生绩点与改革前、改革开始前两年相比有显著差异，综合成绩显著提高，尤其是实验操作部分。多数学生反馈在小班教学中实验操作能够从零快速提高到熟练，结合带课教师的逐步讲解、一对一实练和小组讨论，能够更好掌握理论知识，完善作业。
结论 在来华留学生实验诊断学的教改过程中，应增强先进教学理念、技术与实验课堂教学的密切联系，逐步达成“金”益求精、与时俱进的“金课”建设目标，实现知行合一，学以致用。

PO-0044

临床寄生虫学检验实现“浇花浇根、育人育心” 的探索与实践

丁淑琴、张玮、张爱君
宁夏医科大学

目的 牢固树立“立德树人”理念,坚决贯彻“浇花浇根、育人育心”。在临床寄生虫学检验专业知识传授中，秉承专业知识与价值引领相结合的基本原则，以“德”为中心，引导学生树立正确的人生观、世界观和价值观，继承和发扬传统中国文化，关注公众健康，提高职业认同感，培养良好的社会责任意识。
方法 秉承“课程承载思政”和“思政寓于课程”的理念，充分发挥课堂教学的主渠道作用，将医学检验技术专业在我国发展的历程、学校学科的成长积淀、以及伴随国家的发展壮大本专业同步建设过程等各类丰富详实、激动澎湃的教学资源等融入课程教学中，把国家成长发展中所积累的传统文化精髓、名人壮士的传奇跌宕爱国情怀融入课程教学中，把为国为民为科技进步所奉献终身的仁人志士的一生学习及教育理念等融入课程教学中，润物细无声地浇灌育人。开展专题演讲、作业评比、寄生虫形态绘图比赛、寄生虫知识科普宣传手册制作等丰富多彩的第二课堂活动提升学生的职业认同感及职业素养。
结果 学生的学习态度明显改观、学习目的更加明确，学习兴趣更加浓厚，学习成绩大大提高。大部分学生对融入专业的思政育人要素表现了极大热情和关注。教师在良好的课程氛围中教学更富有激情。通过课程中出现的思政案例潜移默化地教育学生爱党爱国、敬业守信、勇于创新，同时专业课程的理解和认知得到了升华。
结论 通过将思政课程与临床寄生虫学检验专业教学进行有机结合，把学生价值观培育和塑造的重任以“基因嵌入式”教学模式融入临床寄生虫学检验专业课程，使学生在丰富多彩、有血有肉的感性实例中步入理性认识的殿堂，在“润物细无声”的知识学习中实现理想信念层面的精神指引。

PO-0045

新型冠状病毒肺炎疫情背景下检验科实习生带教思考

王馨、李卓、何天娇
西安医学院第一附属医院

在新型冠状病毒肺炎（COVID-19）疫情“全球大流行”的背景下，随着现阶段复工复产复学逐步推进、疫情境外输入压力不断增大以及无症状感染者频频出现，对我国当前 COVID-19 疫情的防控和检测工作提出了新的挑战。在 COVID-19 的诊疗中，因对病原体的传染途径和致病力尚未完全明确，作为近距离接触病原体样本的实验室一线工作人员，存在较大的感染风险，因而检验科实习学生的心理状况、生物安全以及工作质量也是此次疫情防控工作中各教学医院的重要关注点。本文旨在从疫情中暴露出不足的方面（医德教育、安全防护、质量管理等）进行探讨，促进实习生的综合分析能力和临床批判性思维的形成，为培养合格的医学检验专业人才提供参考。

PO-0046

临床检验渗透人文教育实践的探索

王睿霞
哈尔滨医科大学附属第一医院

目的 当前医学检验的迅猛发展，检验设备的仪器化、自动化，人文意识逐渐淡化，医护人员与检验者之间相互信任度不够，故加强检验技术人员的人文教育非常重要。
方法 尝试在医学检验专业课程临床基础检验技术教学中进行专业教育与人文精神相结合的教学改革尝试，对提升检验医学专业人员职业认同感的价值的作用。**结论** 探索既能促进培养提高独立思考问题的能力，又能开拓视野、拓展知识的方法，了解本学科领域的新进展、新动态，将知识进行整合。网络平台可方便群聊讨论或私聊沟通，帮助学生逐渐树立自信心，并且鼓励学生提出批判性的创新性观点。课内与课外结合、理论与实践结合、素质与技能结合的“三结合” 模式，可进一步加强专业与人文教育的融合与并行，体现了科学与人文的紧密结合，使人文教育不受时间、场所和空间的限制，从而达到事半功倍的效果。
结果 作为检验技术工作者，虽然更多是面对自动化仪器操作，接触人体各种标本，很少与人直接交涉，但却关系到患者的重要疾病信息，所以加强人文素养，对每一份标本负责，对每一个生命负责尤为重要。在医学检验专业课程教学中全程贯穿 人文素质教育，通过转变思想认识、学会换位思考、拓宽交流渠道、提升实战能力等方式，使专业与人文精神相互融合、相互渗透，学生的职业素养及工作能力明显有所提高。通过问卷调查和座谈讨论，学生自我评价较好。教学改革是一个需要长期坚持和不断改进的过程，故需要进一步探索，以期更好地为临床、为社会服务，培养出具有服务意识、法律意识、竞争意识、创新意识的新型医学检验人才。

PO-0047

医学检验技术线上实习的实践及思考

聂鑫、贾成瑶、付阳、罗俐梅、唐思诗、周燕虹、陈春霞、谢轶
四川大学华西医院

目的 通过问卷调查对新冠疫情期间医学检验技术线上实习进行分析并结合线下实习教学的经验，探索出医学检验“线下”+“线上”交互式实习教学模式，让线下、线上实习相互取长补短，进一步发展和完善医学检验实习教学。

方法 采用问卷星对医学检验技术师生进行网络调查分析，对实习同学进行线下、线上实习满意度调查，对带教老师进行线下、线上实习教学评估，同时请所有研究研究对象分别对线下和线上实习进行优缺点评价并对改进实习教学提出建议。
结果 学生线上、线下实习总体满意度评分分别为 95.84±1.81 分和 97.24±1.74 分，差异无统计学意义。相较线下实习教学，大多数带教老师认为线上实习教学的带教前准备更复杂耗时、带教中的讲授更困难且更不能达到预期效果。带教老师认为，在线教学软件的学习与在线教学视频的录制是带教前准备中最复杂和最花费时间的环节，实景演示和引导互动是线上实习讲授中面临的最大困难，线下实习不能被线上实习完全取代。被调查师生认为线上、线下实习各有优缺点，应将两者结合，取长补短。
结论 以线下实习为主体，在线下实习前、中、后分别增加不同内容与形式线上教学的交互式实习教学模式能给广大医学检验教育工作者提供一种新的实习教学思路与方法，可提高医学检验实习教学效率与质量，为探索实习教学新模式、培养新时代医学检验人才贡献力量。

PO-0048

加强医学检验专业学生临床思维培养提高临床诊断能力教学模式的探讨

赵欣、龙军
南方医科大学珠江医院

目的在于结合目前医学检验专业学生培养现状来探讨医学检验专业学生如何加强临床思维的培养。临床思维培养对检验人员至关重要，但是目前医学检验专业学生培养存在着不重视临床思维培养，检验与临床脱节的现象，希望通过本院检验临床教学模式的改革与探讨，提出几点建议希望能有所改善此现象。

近年来，随着现代医学的飞速发展，检验医学在临床诊疗工作中的作用越 来越重要。作为未来检验工作的直接参与者，医学检验专业学生仅仅掌握检验 相关知识，认为为临床提供准确数据为最终目标是远远不够的，还应该具备良 好的临床思维能力，能够快速准确地将实验数据转化成临床信息，并能有效且 合理地应用这些数据，充分发挥医学检验的导向作用。为了更好地服务于临床， 更大程度上辅助临床诊疗工作，加强医学检验专业学生临床思维的培养势在必 行。然而就目前医学检验专业学生培养现状来说，普遍存在着不重视临床思维 培养的现象。因此，本文旨在探讨如何加强医学检验专业学生临床思维能力的 培养。

PO-0049

The utility of competency-oriented clinical laboratory teaching combined with case-based learning (CBL)

Jingfang Sun、hongchun li、shuang ding、yi guo、ping ma
Affiliated Hospital of Xuzhou Medical University

Background This study aimed to evaluate the benefit and efficiency of competency-oriented clinical laboratory teaching combined with case-based learning (CBL), to improve the examination of students' competence of laboratory medicine.
Methods On their voluntary basis of students, a total of 107 medical laboratory medicine interns at the Affiliated Hospital of Xuzhou Medical University from June 2017 to July 2019 were assigned into a control group with training of the traditional teacher-centered method, and an experimental group under a CBL teaching program. Student theory tests and skill assessment were designed to evaluate what the students gained from their internship when they completed their studies at the Affiliated Hospital of Xuzhou Medical University.

Results Compared to students in control group with traditional method, those in CBL teaching program had significantly higher theory test scores and skill assessment scores in average, especially in identification and processing of instrument alarm information, analysis of test results, identification and solution of the problem, as well as identification and reporting of the critical value and clinical communication.
Conclusion The competency-oriented teaching method combined with CBL is effective in improving students' professional knowledge, interpersonal relationship, language expression and teamwork, which is worthy of being carried out in laboratory medicine teaching.

PO-0050

关于医学专业"大创计划"参与度调查及近六年大创项目分析

王霞、张玫
四川大学华西医院

目的 为提高医学类大学生创新创业型人才的建设质量，以"大创计划"为出发点，从大学生参与情况及近年来获奖项目详情两个角度进行深入分析，为创新创业型人才的建设提供可靠的数据支持。
方法 结合文献及学生访谈对问卷进行设计，采用"问卷星"进行线上匿名问卷调查大学生"大创计划"的参与情况并对 2015 年至 2020 年我校国家级和省级"大创项目"的项目学院、项目类型、项目类别、项目级别进行统计描述，卡方检验进行不同专业组间的比较，SPSSAU. (Version 20.0)对数据进行统计分析及可视化。
结果 医学类大学生参与度明显高于非医学类大学生，"大创计划"中兴趣度最高的项目类型是"创新训练类项目"，未参与"大创计划"的主要原因是"不知道参加途径"。2015 年至 2020 年我校 6 个医学类学院申请的国家级和省级"大创项目"占比最高的项目类型是"创新项目类"，项目类别占比最高的是"科学探索类"。
结论 目前我校医学类大学生"大创计划"参与度尚可，对于未参与"大创计划"的大学生需要提供更多的参与机会和多样化结题标准；医学类大学生对创业型项目的兴趣度有待提高，项目类别上"科学探索类"热度最高。

PO-0051

新冠疫情影响下多元化模式教学方案在线上教学中应用的探索 ——以《临床血液学》为例

金咏梅、蒋能刚、廖红艳、粟军、郑沁
四川大学华西医院

目的 始于 2020 年初的一场惊世新型冠状病毒肺炎席卷全球，人类正面临着一个包括生存、生产以及生活的全方位的大挑战。在新冠肺炎疫情防控的特殊时期，教育部发文要求全国高校"停课不停教"、"停课不停学"，充分利用现有资源积极开展线上教学。
方法 以《临床血液学》为例，组织师生建立 qq 聊天群及微信群，线上教学期间 qq 群主打，利用各种群功能，如打卡、作业星等，课前发放相关课程的彩色图谱（来源于 2012 版 WHO 白血病与淋巴组织相关疾病分册）及生动形象的幻灯片讲解视频，高效利用慕课资源，建立语音聊天室，实时语音答疑交流，翻转课堂教学。微信群以备不时之需（网络拥堵时）。分小组进行多人协作病案讨论，基于维普在线专业考核进行期末实验及理论双考试。
结果 学生及教师对本学期该课程满意度较高，教学效果评估优秀。
结论 若是能实施显微镜实时投影，并增加骨髓片全片扫描上传到网络，由学生在 PC 端自主学习并进行分类计数，完成骨髓形态学报告，将会更大程度提高学生的学习积极性，进一步提升《临床血液学》的教学质量。

PO-0052

新型冠状病毒疫情下如何加快培养和提升中医检验人员科研能力的思考

刘佳[1]、孙鲁英[1]、陶庆春[2]
1. 北京中医药大学房山医院
2. 北京中医药大学第三附属医院

目的 全球新型冠状病毒引起的肺炎确诊病例超过 1 亿 1662 万例、死亡病例超过 259 万例，已有 21 个国家确诊病例超过 100 万例。新型冠状病毒(下文简称"新冠")疫情流行传播速度快，世界性范围广，造成危害极大。疫情下，中西医特色治疗鲜明、新冠疫苗副作用小、检测试剂盒创新等均取得阶段性胜利，并获得国内外肯定和赞誉。医学检验技术涵盖生化检验、微生物检验、免疫学检验等，为临床诊断和治疗提供较多的便利，更具有科研前瞻性优势。PCR 快速核酸检测、观察中西医药物联合治疗新冠患者疗效的检验指标变化、新冠患者检验指标在中医证型鉴别等研究方向与检验科研工作有密切联系。本文作者 2020 年 2 月支援区级收治新冠病人定点医院检验科 28 天，对中医检验人员参与新冠科研工作有一定亲身经历，阐述加快培养和提升科研能力的几点思考。
方法 采用问卷星 APP 制作和开展中医检验人员新冠疫情下从事研究现状调查，共收集六所三甲中医院检验人员有效问卷 175 份，总结科研能力停滞不足的四个因素，并提出应对措施。
结果 中医与检验相关的继续教育学习机会较少、科研投入时间与岗位工作有冲突、科研难于得到专业指导或领导支持及个人主观意识缺乏科研创新精神等造成新冠疫情下检验人员科研能力不足。
结论 提出鼓励检验人员积极参加科研能力提升班或西学中课程学习、成立多专业协作的科研团队定期交流和搜集研究热点、有条件实验室设立科研岗位加大补贴和技术支持、加强中医检验的科研思维培养，可以起到提升科研能力作用。

PO-0053

房水、玻璃体液白介素-6 和白介素-10 水平在眼内淋巴瘤中的诊断价值

陈锟[1,2]、李向宇[1,2]、王庆平[1]、陈波斌[1]、关明[1]
1. 复旦大学附属华山医院
2. 复旦大学附属华山医院北院

目的 眼内淋巴瘤（VRL）是一种罕见的眼部恶性肿瘤。分析玻璃体液、房水中白介素 10（IL-10）、IL-10/白介素 6（IL-6）比值和眼内淋巴瘤诊断的白细胞介素评分（ISOLD）水平对玻璃体视网膜淋巴瘤的诊断价值。
方法 回顾性分析 2018 年-2020 年 38 例可疑 VRL 行玻璃体切除术的临床资料。采用流式细胞微球阵列术（CBA）检测玻璃体及房水中 IL-6、IL-10 细胞因子水平，比较分析最终诊断为 VRL 和非 VRL 的患者玻璃体、房水中 IL-10、IL-10/IL-6 比值和 ISOLD 水平差异及诊断效能。
结果 38 例可疑 VRL 玻璃体、22 例房水 IL-6、IL-10 及 IL-10/IL-6 比值与 40 例玻璃体、15 例房水标本的非 VRL 有显著统计学差异（$p<0.001$）；两组患者房水与玻璃体之间 IL-10、IL-6 水平无显著统计学差异($p>0.05$)； IL-10 水平与玻璃体细胞数呈正相关（$r=0.581$，$p<0.01$）；玻璃体液 IL-10、IL-10/IL-6 比值及 ISOLD 在诊断 VRL 的 ROC 曲线下面积（AUC）分别是 93.5%、93.6%和 93.8%；房水中 IL-10、IL-10/IL-6 比值及 ISOLD 在诊断 VRL 的 ROC 曲线下面积分别是 82.9%、72.1%和 84.8%。IL-6 水平异常升高的 VRL 患者有严重的视网膜下色素上皮剥离表现。
结论 检测玻璃体液 IL-10、IL-10/IL-6 比值及 ISOLD 评分对诊断 VRL 具有较高的敏感性和特异性，房水较之玻璃体标本易获取、稳定性好、操作风险小，使用房水进行诊断效能评价与玻璃体液相当，两组房水细胞因子水平与玻璃体液无明显统计学差异。虽然 IL-10 水平升高与 VRL 相关，但 IL-10、

IL-10/IL-6 比值及 ISOLD 评分低于 Cutoff 值并不能完全排除 VRL。因此无临床表现房水 IL-10 升高可能预示 VRL 的复发，一旦明确诊断 VRL，房水 IL-10 可以作为随访监测和治疗评估。特别是使用 ISOLD 评分具有较高的敏感性和特异性。

PO-0054

TLR4 通路的活化诱导 CD11b+髓系细胞增殖促进 HBV 清除

王琴、张浩、张云云、周强
安徽医科大学第二附属医院

目的 有效的免疫应答在清除乙肝病毒（HBV）感染中发挥关键作用。然而天然免疫应答在病毒清除过程中发挥的具体作用仍不十分清楚。本研究旨在探讨 LPS 刺激 TLR4 通路活化后对天然免疫细胞 CD11b+髓系细胞增殖分化的影响，及其对病毒清除的作用。
方法 采用高压水尾静脉注射 HBV 质粒的方法，在 C57BL/6 小鼠体内建立 HBV 复制模型，给予小鼠腹腔注射 TLR4 配体 LPS，观察小鼠病毒血症变化的情况，分离小鼠肝脾内免疫细胞，流式分析肝脾内 CD11b+髓系细胞增殖及其分化情况。分析 LPS 活化 TLR4 通路后天然免疫细胞 CD11b+髓系细胞的变化及其在 HBV 感染过程中对病毒清除的作用。
结果 给予小鼠 LPS 刺激 TLR4 通路活化诱导小鼠肝脏和脾脏内 CD11b+髓系细胞增殖分化为中性粒细胞和炎症性单核巨噬细胞，其中肝脏内单核巨噬细胞表面 F4/80 蛋白的表达水平低于对照小鼠，表明 LPS 刺激后小鼠肝脏内促进免疫耐受的 Kupffer 细胞减少，促进 HBV 感染病毒的清除。
结论 TLR4 通路活化后诱导 CD11b+髓系细胞增殖分化为炎症性天然免疫细胞中性粒细胞和单核巨噬细胞，并且肝内免疫耐受细胞 Kupffer 细胞减少，促进 HBV 感染过程中病毒的清除

PO-0055

抗 PAD2 和抗 PAD4 自身抗体对类风湿关节炎的临床应用价值研究

詹明华、刘昱东
北京大学人民医院

目的 评估中国 RA 人群中抗 PAD2 抗体和抗 PAD4 抗体与 RA 的相关性及对 RA 并发 ILD 风险的临床预测应用价值。
方法 本研究共入选 227 名受试者，其中包括 148 名 RA 患者，35 名非 RA 关节炎患者（疾病对照，DCs）和 44 名健康对照（HCs）。通过 ELISA 确定血清抗 PAD2 抗体和抗 PAD4 抗体水平。
结果 抗 PAD2 抗体分别存在于 26.4％的 RA、5.7％的 DC 和 4.5％的 HC 患者中。RA、DC 和 HC 患者中抗 PAD4 抗体的阳性率分别为 20.9％，5.7％和 2.3％。与抗 PAD4 抗体阴性的 RA 患者相比，抗 PAD4 抗体阳性的 RA 患者病程更长、肺间质性疾病（ILD）发生率更高（p=0.002）。在 RA 患者中，抗 PAD4 抗体与 ILD 之间存在显著正相关（OR=3.521，p=0.002），而加入抗 PAD2 抗体的检测后（即抗 PAD2 抗体阴性且抗 PAD4 抗体阳性的患者）可以进一步将 OR 提升到 5.429。在血清阳性的 RA 中，抗 PAD4 抗体与 ILD 表现出较弱的相关性（OR=2.324，p=0.046），而联合应用抗 PAD2 抗体和抗 PAD4 抗体，可以显著提高抗 PAD4 抗体对于 ILD 的临床预测价值（OR=4.059，p=0.007）。
结论 本研究探讨了抗 PAD2 抗体和抗 PAD4 抗体与 RA 的相关性，发现抗 PAD2 抗体和抗 PAD4 抗体的联合检测有助于识别具有 RA-ILD 风险的患者。抗 PAD2 抗体和抗 PAD4 抗体的检测可以作为现有 RA 血清学标志物的重要补充。

PO-0056

Tp0136 targets fibronectin (RGD)/Integrin β1 interactions promoting human microvascular endothelial cell migration

tianci yang
Center of Clinical Laboratory, Zhongshan Hospital, School of Medical, Xiamen University, Xiamen, China,

In this research, we purposed to analyze the role of Tp0136 in the migration of human microvascular endothelial (HMEC-1) cells and to explore the related mechanism.

First, Tp0136 significantly promoted HMEC-1 cell migration. Furthermore, the levels of C–C motif ligand 2 (CCL2) mRNA and protein expression rose with the concentration and time increasing of Tp0136. The migration of HMEC-1 cells was significantly suppressed by an anti-CCL2 antibody and a CCR2 (the CCL2 receptor) inhibitor. Additionally, after pretreatment with an anti-fibronectin antibody, an anti-integrin β1 antibody or RGD, the migration of HMEC-1 cells treated with Tp0136 was obviously suppressed. These results show that Tp0136 promots the migration of HMEC-1 cells by inducing CCL2 expression via the interaction of the fibronectin RGD domain with integrin β1 and the CCL2/CCR2 signaling pathway, and these interactions may contribute to the mechanisms that increase the capacity for self-healing syphilis infection.

PO-0057

基于 SLE 家系高通量芯片检测自身抗体对 SLE 诊断价值初探

张苹
四川大学华西医院

目的 通过自身抗体检测芯片对系统性红斑狼疮（Systemic lupus erythematosus，SLE）三个不同家系的样本进行检测，探讨不同 SLE 家系自身抗体反应的差异，寻找针对不同遗传背景家系患者的自身抗体检测模型。

方法 纳入四川大学华西医院确诊的 7 例 SLE 患者（来自 3 个 SLE 家系）、健康对照 4 例作为研究对象，采用包被有 120 种自身抗原的 OmicsArrayTM 自身抗体检测芯片进行检测，并将结果绘制热图。使用 SPSS25.0 软件进行统计学处理，定量资料数据符合正态分布，采用`x±s 表示，数据不符合正态分布时采用中位数与四分位数表示，定性资料用例数表示。两组间比较，若数据符合正态分布且方差齐，使用两独立样本 t 检验，否则采用 Wilcoxon 秩和检验，多组间比较采用 Kruskal-Wallis H 秩和检验，两两比较采用 Dunnett-t 检验。当 P＜0.05 时，认为差异具有统计学意义。

结果 热图显示，SLE 病例组 120 种自身抗体表达水平总体较对照组上调。SLE 家系 1、2、3 分别与对照组分析，筛选出包括抗 dsDNA 抗体、抗 ssDNA 抗体、抗染色体 DNA 抗体、抗胶原 VI 抗体 4 种自身抗体在 SLE 患者显著升高（P＜0.05），将 3 个 SLE 家系病例汇总为一组（SLE 家系 1+2+3）与对照组进行分析，得到抗 dsDNA 抗体、抗 ssDNA 抗体、抗染色体 DNA 抗体、抗胶原 VI 抗体、抗硫酸软骨素 C 抗体、抗 GP210 抗体、抗 U1-snRNP 68/70 抗体、抗 U1-snRNP C 抗体 8 种自身抗体在 SLE 患者显著升高（P＜0.05）。

结论 SLE 家系内表现出自身抗体表达聚集性，而不同家系间表现出不同自身抗体的异质性，且差异性项目随样本量的扩大而增多，可作为辅助 SLE 疾病预防与诊断的方法之一。

PO-0058

SERS-based immunoassay enhanced with silver probe for selective separation and detection of Alzheimer' s disease biomarkers

Shibao Li
The Affiliated Hospital of Xuzhou Medical University

The demand for simple and sensitive detection method is urgent, owing to the key role of Aβ-amyloid and P-Tau-181 in the early diagnosis of Alzheimer's disease (AD). In this study, a novel SERS-based sandwich immunoassay, which consists of tannin-capped silver nanoparticles and magnetic graphene oxide (Fe3O4@GOs), was firstly developed to detect quantitatively serum biomarkers (Aβ-amyloid and P-Tau-181) of AD in standards and to differentiate AD from non-AD dementia patients. The detection linear range of Aβ1-42 and P-Tau-181 standards was observed to range from 100 pg mL-1 to 10 fg mL-1 and 100 pg mL-1 to 1 fg mL-1 respectively. And the concentration of proteins in human serum samples was calculated firstly by regression equation obtained from standards. The results confirmed that even a very small amount of biomarkers in human serum can be caught by the proposed SERS-based immune method. We finally explored the clinical application of this method in 63 serum samples. As a result, the P-tau-181 levels differentiated AD from non-AD dementia patients (AUC = 0.770), with a more favored ROC than Aβ1-42 (AUC = 0.383). These findings indicated that this developed SERS-based immunoassay was successfully applied to the determination of Aβ-amyloid and P-Tau-181 in human serum specimens, which provided a promising tool for the early diagnosis of AD.

PO-0059

细胞因子及 PCT 检测在经皮肾镜手术治疗上尿路结石术后脓毒症诊疗中的应用价值

于宝丹、赵晓颖、刘冠炤、林勇平
广州医科大学附属第一医院

目的 尿源性脓毒症是经皮肾镜手术（percutaneous nephrostolitho tomy，PCNL）治疗上尿路结石术后风险最大的并发症之一，其早期诊断、病情评估对降低病死率和改善预后具有重要意义。细胞因子和降钙素原(procalcitonin, PCT)是脓毒症患者常见感染性炎症指标，本文研究了 IL-6、IL-8、IL-10、IL-1β、TNF-α、IFN-γ 及 PCT 在经 PCNL 治疗上尿路结石术后尿源性脓毒症早期诊断、病情评估及预后中的作用。

方法 收集本院 2020 年 4 月至 2021 年 4 月期间收治的经 PCNL 治疗上尿路结石患者 49 例，分为脓毒症组（17 例）、全身性炎症反应综合征（Systemic Inflammatory Response Syndrome, SIRS）组（12 例）和对照组（20 例），检测 3 组患者术前、术后 2 － 4 小时、术后第 2 天、第 4 天、第 7 天血清中 6 种细胞因子 IL-6、IL-8、IL-10、IL-1β、TNF-α、IFN-γ 及 PCT 含量。

结果 术前 3 组患者细胞因子及 PCT 无差异；术后脓毒症组及 SIRS 组 6 种细胞因子升高迅速，术后 2-4 小时各细胞因子最高，其后逐日下降；PCT 上升速度不及细胞因子，脓毒症组及 SIRS 组 PCT 在术后第 2 天达到高峰，其后逐日下降；诊断尿源性脓毒症的 ROC 曲线显示：单因子中 IL-8 的 AUC 最高（0.958），敏感性、特异性分别为 94.1%、87.5%；IL-6 的 AUC 次之（0.954），敏感性、特异性分别为 82.4%、96.6%；单个细胞因子联合 PCT 结果显示，PCT+IL-8 的 AUC 最高（0.971），敏感性、特异性分别为 94.1%，87.5%；PCT+IL-6 的 AUC 次之（0.961），敏感性、特异性分别为（88.2%，96.9%）；相关分析结果显示，脓毒症组术后 2-4h 的 IFN-γ、术后第 2 天 PCT 浓度与 SOFA 评分中度相关；脓毒症组术后第 4 天 IL-6 浓度与 ICU 住院天数高度相关；术后 2-4h 的 IFN-γ、第 2 天、第 7 天的 PCT 浓度与 ICU 住院天数中度相关。

结论 术后 2-4h 的 PCT 联合 IL-8 检测可作为上尿路结石 PCNL 术后尿源性脓毒症较好的早期诊断指标；术后 2-4h IFN-γ、第 2 天的 PCT 和 SOFA 评分相关，可作为病情严重程度评估指标；术后第 4 天 IL-6 浓度对预后的指导意义最大，此外，术后 2-4h IFN-γ、第 2 天及第 7 天 PCT 浓度与对尿源性脓毒症预后评估有一定价值。总之，本研究表明 IL-6、IL-8、IFN-γ 及 PCT 检测对尿源性脓毒症早期诊断、病情评估及预后具有重要价值。

PO-0060

血清特异性抗体对儿童麸质敏感性肠病诊断价值的研究

鄂建飞、赵 铭、杨 浩、詹 璐、郑 茂
德阳市人民医院

目的 通过分析麸质敏感性肠病（GSE）患儿血清特异性抗体 TGA、EMA、DGP 的检出情况，为临床筛查和诊断 GSE 提供依据。
方法 选取 2018 年 1 月至 2020 年 10 月 GSE 患儿 50 例作为 GSE 组，选取同期同年龄段健康儿童 50 例作为对照组，分别进行 TGA、EMA、DGP 检测，并对结果进行分析。
结果 50 例 GSE 患儿主要临床表现为慢性腹痛腹泻（34.0%，17/50）、贫血（28.0%，14/50）、生长发育迟缓（20.0%，10/50）、营养不良（16.0%，8/50）和焦虑抑郁（2.0%，1/50）。GSE 组 TGA-IgA、TGA-IgG、EMA-IgA、EMA-IgG、DGP-IgA、DGP-IgG 阳性率分别为 90.0%、66.0%、92.0%、94.0%、92.0%、96.0%，均显著高于对照组（P<0.01）。在对 GSE 的诊断效能上，DGP-IgG 的 AUC 最高（98.0%），而 TGA-IgG 的 AUC 最低（83.3%），TGA、EMA、DGP 的 IgA 和 IgG 特异性均大于 95.0%，EMA、DGP 的 IgA 和 IgG 敏感性均大于 90.0%，但 TGA-IgG 敏感性较低（66.0%）；DGP-IgG 的 PLR 最高，且 NLR 最低。≤7 岁年龄组 DGP-IgG 诊断效能最好，敏感性、特异性、阳性预期值、阴性预期值均为 100%；>7 岁年龄组 TGA-IgA 诊断效能最好，敏感性、特异性、阳性预期值、阴性预期值均为 96.2%。≤7 岁年龄组 TGA-IgG 敏感性为 45.8%，>7 岁年龄组 TGA-IgG 敏感性为 84.6%，两组相比差异具有统计学意义（P<0.05）；≤7 岁年龄组 TGA-IgA 敏感性为 75.0%，>7 岁年龄组 TGA-IgA 敏感性为 96.2%，两组相比差异具有统计学意义（P<0.05）。
结论 TGA、EMA、DGP 检测是儿童 GSE 筛查和诊断的重要手段，其中以 DGP-IgG 敏感性和特异性最佳，可作为首选筛查抗体；TGA-IgA 和 TGA-IgG 在诊断 GSE 时受年龄影响较大，不建议作为≤7 岁儿童的 GSE 筛查实验。

PO-0061

甲胎蛋白异质体比率联合异常凝血酶原诊断原发性肝癌的相关性研究

谈艳芳、刘利洪、袁成良
德阳市人民医院

目的 检测原发性肝癌患者血清中的甲胎蛋白（AFP）、甲胎蛋白异质体(AFP-L3)与甲胎蛋白的比率，以及异常凝血酶原(PIVKA-Ⅱ)，通过分析并探讨各项指标及联合运用三项指标在原发性肝癌中的诊断价值。
方法 收集 2019 年 4 月—2020 年 4 月原发性肝癌患者 50 例，良性肝病组患者 50 例（包括急慢性肝病，肝硬化、继发性肝癌等）。采用 Centaur XP 全自动化学发光免疫分析仪、亲和吸附离心和 LUMIPULSEG1200 全自动免疫分析仪分别检测 AFP、AFP-L3、PIVKA-II 水平。

结果 原发性肝癌组血清 AFP、AFP-L3/AFP、PIVKA-II 的表达水平明显高于良性肝病组（P<0.05）。血清 AFP 诊断原发行肝癌的敏感性为 64%，特异性为 58%，；AFP-L3/AFP 敏感性为 84%，特异性为 90%，PIVKA-II 敏感性为 76%，特异性为 84%，采用 AFP+AFP-L3/AFP+PIVKA-II 三者联合诊断的敏感性为 94%，特异性为 78%。原发性肝癌的工作特征（ROC）曲线显示 AFP、AFP-L3/AFP、PIVKA-II、AFP+AFP-L3/AFP+PIVKA-II 分别为 0.581，0.843，0.770，0.905。

结论 三种指标联合检测原发性肝癌的敏感度和特异性都优于各项指标单独检测，可为原发性肝癌的早期诊断奠定坚实的基础。

PO-0062

LncRNA GAS5 promotes autophagy process and antimicrobial responses via miR-221-3p/ATG12 axis during mycobacterial infection

Zikun Huang 、Yongqin Guo、Peng Fu、Qing Luo、Junming Li
The First Affiliated Hospital of Nanchang University

Objectives Autophagy plays a key role in activating the antimicrobial host defense against Mycobacterium tuberculosis (Mtb). The emerging roles of long non-coding RNAs (lncRNAs) in regulating host antimicrobial responses against Mtb have gained widespread attention. However, the process by which lncRNAs specifically influence antibacterial autophagy during mycobacterial infection is largely uncharacterized.
Methods The present study assessed lncRNA GAS5 for antimicrobial immune functions and defined mechanisms wherein lncRNA GAS5 regulates Mtb growth, autophagy and microRNA in macrophages.
Results The Mtb infection leads to downregulation of lncRNA GAS5 in a time- and dose-dependent manner and concomitant downregulation of ATG12 in THP-1 macrophages. Overexpression of lncRNA GAS5 dramatically promoted Mtb-induced activation of autophagy in human THP-1 macrophages, whereas inhibitors of lncRNA GAS5 remarkably inhibited Mtb-induced autophagy. Mechanistically, lncRNA GAS5 targets an inhibiting element miR-221-3p, as shown by bioinformatics, dual-luciferase reporter gene analysis and pull-down assay, respectively. Notably, miR-221-3p inhibited autophagy via suppressing autophagy protein ATG12 by binding to its 3'-UTR in Mtb-infected macrophages and thus promoting intracellular Mtb growth. Concurrently, lncRNA GAS5 enhanced autophagy in Mtb-infected macrophages by blocking the ability of miR-221-3p to inhibit ATG12.
Conclusion These data indicate that lncRNA GAS5 regulates the innate host defense by promoting the activation of autophagy and antimicrobial effects against Mtb via the miR-221-3p/ATG12 axis.

PO-0063

外周血 CD3+CD4-CD8-双阴性 T 淋巴细胞在复发性流产患者中的表达及意义

张吟眉、吴宇鑫、郑佳佳
北京大学第三医院

目的 分析复发性流产（RSA）患者外周血淋巴细胞亚群以及双阴性 T 淋巴细胞（DNT）水平, 并探讨 DNT 在 RSA 发病中的意义。

方法 选取 2018~2019 年北京大学第三医院有 RSA 病史的非妊娠患者 106 例以及健康非妊娠对照者 50 例。采用流式细胞术分析 RSA 患者及对照组外周血淋巴细胞亚群以及 DNT 细胞的表达，比较 RSA 与对照组淋巴细胞亚群及 DNT 细胞比例差异, 以及 RSA 患者中抗核抗体（ANA）和阴性组 DNT 比例差异。
结果 RSA 患者与健康对照组相比，CD3+ CD8+T 细胞以及 DNT 细胞显著高于对照组（P=0.006，P<0.001）。在 RSA 患者中，ANA 阳性患者 DNT 水平高于 ANA 阴性患者(P<0.05)；此外，RSA 患者中抗磷脂抗体阳性患者 NK 比例高于与阴性患者(P<0.05)，但 DNT 比例无明显差异，DNT 水平与抗磷脂抗体水平无相关。
结论 RSA 患者的 DNT 水平较正常对照组显著升高，可对 RSA 发生提供一定预测价值

PO-0064

Combining Calcitonin and Procalcitonin and Rheumatoid Arthritis-related Biomarkers Improve Diagnostic Outcomes in Early Rheumatoid Arthritis

Yingwen Liu[1]、Jing Shi[2]、Bo Wang[3]、Lijing Zhou[3]、Xiaolan Zhou[3]、Yane Du[3]、Dandan Li[3]、Liang Duan[3]、Qin Hu[3]、Weixian Chen[3]、Pu Li[3]
1. Department of Laboratory Medicine, Peoples Hospital of Deyang City
2. Department of Laboratory Medicine, the First Hospital of Chongqing Medical University
3. The Second Hospital of Chongqing Medical University

Objective To demonstrate whether procalcitonin (PCT) combined with calcitonin (CT) could provide additional diagnostic value to other clinically available rheumatoid arthritis (RA)-related biomarkers in the early diagnosis of RA.
Method The blood samples aseptically collected by venipuncture were centrifuged within 1 hour and frozen at -80°C. PCT and CT levels were measured using electrochemiluminescence immunoassay (ECLIA) in 260 subjects (48 patients with early RA, 34 patients with established RA, 37 patients with systemic lupus erythematosus, 30 with osteoarthritis, 31 with gouty arthritis, and 80 healthy participants). Anti-cyclic citrullinated peptide (Anti-CCP) and anti-RA33 antibodies (Anti-RA33) were analyzed by ELISA. RF was detected by transmission immunoturbidimetry. Mann-Whitney U tests and Kruskal-Wallis tests compared differences among groups. Spearman's rank correlation analysis determined the relationship between biomarkers. Receiver-operator characteristic (ROC) curves were generated and diagnostic performance was assessed by area under the curve (AUC), as well as specificity, sensitivity, likelihood ratios (LR).
Results Median serum PCT concentrations were significantly higher ($p < 0.0001$) in patients with early RA (0.065 ng/ml) when compared with healthy controls (0.024 ng/ml), and patients with osteoarthritis (0.025 ng/ml). When compared with gouty arthritis (GA) controls (0.072 ng/ml) and systemic lupus erythematosus (SLE) controls (0.093 ng/ml), median serum PCT concentrations were not significant in patients with early RA (0.065 ng/ml). Median serum CT concentrations were significantly lower ($P < 0.0001$) in patients with early RA (0.880 pg/ml) compared with healthy controls (3.159 pg/ml), patients with SLE (2.480 pg/ml), patients with GA (2.550 pg/ml). When compared with osteoarthritis controls (0.586 pg/ml), median serum CT concentrations were not significant in patients with early RA (0.880 pg/ml). ROC curve analysis comparing early RA with healthy controls demonstrated that the AUC of RF, anti-CCP and anti-RA33 were 0.66, 0.73 and 0.64, respectively, the additions of PCT and CT further improved the diagnostic ability of early RA with the AUC of 0.97, 0.98 and 0.97, respectively ($p < 0.01$). The sensitivities of RF, anti-CCP and anti-RA33 for early RA were 33.33%, 44.74% and 58.33%, respectively, and the additions of PCT and CT showed very high sensitivities of 83.33%, 92.11%, 87.50%. The high-value groups of PCT moderately correlated with the anti-RA33 levels ($r = 0.417$, $P < 0.05$). CT had no significant correlation with disease duration, radiographic progression

or clinical/serological variables, such as ESR levels, CRP levels, RF, anti-CCP, anti-RA33 levels in early RA.
Conclusions Serum PCT and CT combined with clinically available RA-related biomarkers could further improve the diagnostic efficiency of early RA.

PO-0065

SARS-CoV-2 灭活疫苗接种后机体免疫系统动态变化的研究

殳洁、盛慧明
上海交通大学医学院附属同仁医院

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic has dramatically expedited global vaccine development efforts. The first vaccine to be used in China is an inactivated SARS-CoV-2 vaccine. Here, we investigated the dynamic changes of the immune system in volunteers upon SARS-CoV-2 inactivated vaccine. We found that total SARS-CoV-2 antibodies and specific neutralizing antibodies both increase upon the inactivated vaccine inoculation (post second dose). Subsequently plasma protein peptide microarray detection of subjects showed high expression of RBD and S protein sequences of IgM and IgG in plasma post second dose vaccination. Furthermore, the expansion of ICOS+CXCR5+ Follicular helper T cell (Tfh) and CD27+CD19+ B cells in PBMC upon the inactivated vaccine inoculation, providing a potential biomarker for testing vaccine efficacy. Overall, although subjects upon the inoculation of inactivated SARS-CoV-2 vaccine have shown a variety of features, including production of neutralizing antibodies and associated immune cells suggests that more research is needed.

PO-0066

血清学标志物检测对酒精性肝病肝脏纤维化程度的诊断价值探讨

车媛媛、黄晶、金宇亭
吉林大学第一医院

目的 探讨血清学肝纤维化检测标志物透明质酸酶、III 型前胶原、IV 型胶原和层粘连蛋白在酒精肝纤维化进程中的诊断价值。
方法 本研究纳入北京解放军 302 医院 88 例临床明确诊断为酒精性肝病的患者，诊断标准全部符合《2018 年美国胃肠病学院酒精性肝病诊治临床指南》。根据其无创肝硬度值（LSM）以及肝穿病理活检分期（S）结果将患者分成酒精性肝纤维化（AHF）、酒精性肝硬化（AC）以及酒精相关性肝癌组（ARHC），对照组选自同期体检中心年龄、性别匹配的健康人群 15 例（HC）。根据 MELD 评分和 CTP 评分/分级标准对全部患者进行疾病严重程度评估。血清透明质酸酶（HA）、III 型前胶原（PIIINP）、IV 型胶原（IV-Col）和层粘连蛋白（LN）浓度检测采用安图生物工程有限公司的化学发光试剂盒。数据分析应用 GraphPad Prism 和 medcalc 软件。
结果 HA、PIIINP 和 IV-Col 在各组患者血清中水平均高于对照组，AHF 与 AC 两组比较 HA 和 LN 差异有统计学意义，AC 与 ARHC 两组比较只有 LN 差异无统计学意义，AHF 与 ARHC 组比较四项差异均具有统计学意义；相关性分析显示：HA、PIIINP、IV-Col 和 LN 与 MELD 评分、CTP 评分和无创肝硬度值正向相关；根据无创肝硬度值及病理分期将患者分成轻度纤维化（LSM<7.7/S<2）和中重度纤维化及硬化（LSM≥7.7/S≥2）组，ROC 分析结果显示：血清 HA、PIIINP、IV-Col 和 LN 的诊断敏感性分别为 0.82、0.62、0.72 和 0.51，特异性分别为 0.56、0.70、0.55 和 0.85，AUC 值分别为 0.709、0.669、0.734 和 0.722；根据无创肝硬度值及病理分期将患者分成轻中度纤维化（LSM≤12.5/S≤3）和重度纤维化及硬化（LSM＞12.5/S＞3）组，ROC 分析结果显示：血清 HA、PIIINP、IV-Col 和 LN 的诊断敏感性分别为 0.67、0.64、0.97 和 0.78，特异性分别为 0.87、0.63、0.37 和 0.63，AUC 值分别为 0.818、0.664、0.680 和 0.754；

结论 传统肝纤维化四项联检在酒精性肝病患者肝脏纤维化严重程度的分级诊断中意义明确，其中血清 HA 在纤维化早期的诊断敏感性优于 PIIINP、IV-Col 和 LN，可能更适用于过度饮酒者肝纤维化早期筛查。

PO-0067

长链非编码 RNA MALAT1、SNHG14 和 HIF1A-AS2 在膀胱尿路上皮癌的表达及意义

高娟、李卓
西安医学院第一附属医院

目的 通过研究 MALAT1、SNHG14 和 HIF1A-AS2 在膀胱尿路上皮癌的表达，探讨其在膀胱尿路上皮癌发生、发展中的作用。
方法 运用免疫组织化学 Envision 法检测 MALAT1、SNHG14 和 HIF1A-AS2 在 143 例膀胱尿路上皮癌和 35 例癌旁正常组织中的表达。
结果 MALAT1、SNHG14 和 HIF1A-AS2 在膀胱尿路上皮癌及癌旁正常组织中的表达分别为 79.7%(114/143)和 22.9%(8/35)、40.6%(58/143)和 17.1%(6/35)、75.5%(108/143)和 20%(7/35)，且差异均具有统计学意义(P＜0.05)。同时，MALAT1、SNHG14 和 HIF1A-AS2 的表达随着肿瘤浸润程度的增加，表达呈上升趋势，浸润性膀胱尿路上皮癌阳性表达显著高于非浸润性尿路上皮癌，差异具有统计学意义（P＜0.05）。且膀胱尿路上皮癌中 MALAT1、SNHG14 及 HIF1A-AS2 的表达均呈正相关。
结论 MALAT1、SNHG14 及 HIF1A-AS2 蛋白在膀胱尿路上皮癌中均有异常表达，并与膀胱尿路上皮癌的分化和浸润程度密切相关，提示 MALAT1、SNHG14 及 HIF1A-AS2 可能参与膀胱尿路上皮癌的发生、发展。

PO-0068

CpG-modified plasmid DNA encoding flagellin inhibits dissemination of Treponema pallidum in C57BL/6 mice

Kang Zheng、liqun peng、qiguo xiao、xi deng
Hengyang Central Hospital

Treponema pallidum (T. pallidum), an obligate extracellular bacterium, is the causative agent of sexually transmitted bacterial diseases. In this study, the CpG motifs cloned into the plasmid DNA backbone encoding the flaB3 gene of T. pallidum were injected intramuscularly into C57BL/6 mice, resulting in higher levels of specific anti-FlaB3 antibodies and FlaB3-specific splenocyte proliferation than those in the mice immunized with pcDNA3/FlaB3. Cytokine (IL-4, IL-6, IL-10, IFN-γ, and TNF-α) analysis of splenocytes showed that the CpG-modified plasmid DNA could slightly trigger the Th1-biased immune response. Furthermore, immunization of mice with pcDNA3/CpG-FlaB3 elicited a significant production of IFN-γ by CD4+ T-cells in the spleen. Subsequently, mice were inoculated intradermally (between the scapulae), intraperitoneally, intrarectally and via the corpora cavernosa with 2.5×106 organisms per site (1×107 total organisms). The bacterial organ burden detected in the blood, spleen, liver, testes or brain of immunized mice suggested that CpG-modified plasmid DNA enhances protective immunity to inhibit T. pallidum colonization in distal tissues. Therefore, CpG-modified plasmid DNA vaccination enhances FlaB3-specific immunogenicity and provides protection against T. pallidum dissemination.

PO-0069

The potential application of serum free light chain in the early diagnosis and and staging of chronic kidney disease

Fan Zhang 、Mianyang Li、Chengbin Wang
Chinese People's Liberation Army General Hospital

Objective Three kinds of serological biomarkers were analyzed in the diagnosis and staging of chronic kidney disease (CKD), including serum free light chain (sFLC), serum creatinine (Scr) and cystatin C (Cys C).
Methods 155 patients with CKD of 5 stages were divided into CKD1 group (2 cases), CKD2 group (10 cases), CKD3 group (22 cases), CKD4 group (43 cases), CKD5 group (78 cases). 64 healthy subjects were selected as normal control group. The sFLC was detected by immunoturbidimetry. Scr and serum Cys C were detected by enzymic method.
Results In CKD1 group, κ-type serum free light chain (κFLC) was significantly different compared with that of normal control group, but the other indicators including λ-type serum free light chain (λFLC), Scr and Cys C were not significantly different compared with that of normal control group. In CKD2 group, κFLC, Scr and Cys C were significantly different compared with that of normal control group, but λFLC was not significantly different compared with that of normal control group. From CKD3 to CKD5 group, κFLC, λFLC, Scr and Cys C were all significantly different compared with that of normal control group.
Conclusion The detection of sFLC, Scr and Cys C play important roles in the early diagnosis and clinical staging of CKD.

PO-0070

Apoptosis inhibitor of macrophage/CD5L：A novel marker for assessing disease activity in rheumatoid arthritis

Xianan Wu
Tangdu Hospital, Airforce Military Medical University

Objective Cytokines are implicated in many of the immune processes that are associated with the pathogenesis of rheumatoid arthritis. Here we investigate the association between Apoptosis inhibitor of macrophage (AIM) and disease activity in patients with rheumatoid arthritis (RA).
Methods In this study, concentrations of serum AIM in 110 RA patients, 38 patients with osteoarthritis (OA) and 50 sex&age- matched control subjects were determined by enzyme-linked immunosorbent assay (ELISA). Meanwhile, we also detected the expression of AIM in the articular fluid of patients with OA and RA.
Results Serum AIM concentrations in RA patients were dramatically higher than those from patients with OA or healthy controls. The levels of synovial fluid AIM displayed a significant increase as compared with OA patients. we also found that circulation of serum AIM was significantly elevated in the RA-associated comorbidities including RA-associated metabolic syndrome (RA-MS) and RA-associated interstitial lung disease (RA-ILD). More importantly, AIM levels was significantly correlated with RA disease activity features such as ESR, CRP and DAS28. The predictive value of AIM on high disease activity was superior to those of CRP and ESR. A noteworthy correlation in our study was observed between the serum AIM levels and laboratory parameters, particularly serum lipids. Furthermore, serum AIM levels could be significantly down-regulated after effective integrative treatment.
Conclusion AIM may be served as a novel sensitive biomarker to assist disease activity assessment and monitor therapeutic effects in active RA patients.

PO-0071

风湿病合并 COVID-19 患者的临床和实验室特征及预后

赵军、夏欣一
中国人民解放军东部战区总医院

目的 COVID-19 患者合并风湿免疫性疾病的特点鲜有报道。风湿病患者由于长期服用免疫抑制的药物导致其自身免疫功能受到抑制，可能会增加其对 COVID-19 的易感性。然而，患者免疫低下的状态可能在 SARS-CoV-2 引起的细胞因子风暴中对机体产生保护性的作用。
方法 在这项回顾性研究中，我们对武汉火神山医院确诊的 3059 例 COVID-19 患者的电子病历进行数据提取，并使用 SPSS(version 25.0)分析临床和实验室特征。
结果 3059 例患者中有 29 例合并风湿免疫性疾病，类风湿关节炎（Rheumatoid arthritis,RA)15 例，系统性红斑狼疮（Systemic lupus erythematosus,SLE)5 例，重叠综合症（Rhupus）1 例，重症肌无力（Myasthenia gravis,MG)2 例，干燥综合征（Sjogren's syndrome,SS)1 例，强直性脊柱炎（Ankylosing spondylitis,AS)1 例，皮肌炎(Dermatomyositis ,DM)1 例，自身免疫性肝病(Autoimmune hepatitis ,AIH)1 例，未分化结缔组织病(Undifferentiated connective tissue disease ,UCTD)2 例。研究人群包括 4 名男性和 25 名女性，平均年龄 61 岁，危重症患者占 3.4%（1/29），重症患者占 58.6%（17/29），轻症患者占 38%(11/29)。临床症状表现为，咳嗽 21 例；乏力 21 例；腹泻 3 例；不同程度呼吸困难 14 例；均有发热。实验室检查结果主要表现为，D-二聚体和 C 反应蛋白的增高以及血红蛋白的降低，与普通人群的检查结果无显著性差异。29 例患者中 28 例治愈出院，1 例患者死亡，死亡病例感染新冠前合并多种基础疾病且多脏器衰竭。
结论 初步研究表明，风湿病患者感染 SARS-CoV-2 的风险较高，但可能不会有发展为危重病程的风险，需要进一步研究以了解这些疾病的免疫学特征。免疫疗法作为一种替代疗法，可能在维持免疫功能、延缓或防止疾病恶化以及进一步减少机械通气的治疗方面发挥作用。（本文部分内容已发表于 Ann Rheum Dis, IF=16.102，Correspondence）

PO-0072

Identification and Verification of Ubiquitin D as a gene associated with HCV-induced HCC

Kai Yang
Department of Clinical Laboratory, First Affiliated Hospital of Kunming Medical University

Introduction Accumulated studies have suggested that hepatitis C virus (HCV) infection is one of the leading causes for hepatocellular carcinoma (HCC). However, the mechanisms underlying the effect of HCV on the occurrence of HCC is still poorly understood.
Methods HCV infection datasets (GSE82177 and GSE17856) and HCC datasets (TCGA-LIHC (The Cancer Genome Atlas Liver Hepatocellular Carcinoma) and GSE89377) were downloaded from Gene Expression Omnibus (GEO) or TCGA for analysis.The common differentially expressed genes (DEGs) in the above four datasets were identified by R software. The expression of Ubiquitin D (UBD) in HCV infected HepG2 cells was detected by RT-qPCR and western blot, respectively.The interaction between NS3 and p53 was detected by Co-Immunoprecipitation. The influence of UBD on the proliferation and migration ability of HepG2 cells was evaluated by CCK-8 and wound healing assay, respectively.
Results UBD was upregulated in both HCV infected samples and HCC samples. HCV NS3 interacted with p53 and inhibited its expression. HCV NS3 induced UBD could promote the proliferation and migration of HepG2 cells.
Conclusion Our results suggest that HCV NS3 induced UBD is positively correlated with the development of HCV-related HCC during HCV infection. Targeting UBD could be a potential strategy for preventing and treating HCV-induced HCC.

PO-0073

SARS-CoV-2 感染期和恢复期患者抗体变化的动力学特征

夏欣一
中国人民解放军东部战区总医院

目的 检测 1,850 例 COVID-19 患者抗 SARS-CoV-2 总抗体 IgM、IgG 水平，与 spike 蛋白(S)-、受体结合结构域(RBD)-和核蛋白(N)特异性抗体 IgM、IgG 水平在入院、住院和出院时的变化，以及病毒脱落与抗体反应的关系，全面阐述不同抗体在 SARS-CoV-2 感染期和恢复期过程中的动态变化。
方法 纳入 2 月 4 日至 3 月 30 日在武汉火神山医院的所有 COVID-19 确诊病例，患者的临床特征和实验室诊断数据均取自医院电子病历。使用化学发光磁酶免疫分析法(MCLIA)在不同时间点连续测定总抗体 IgM 与 IgG 水平，S-、RBD-和 N-特异性抗体 IgM 与 IgG 水平。
结果 （1）抗体动态变化与临床分型有关：与轻/中度患者相比，重症/危重型患者 S-、RBD-和 N-特异性 IgG 晚于 1 周产生，且重症/危重型患者住院期间 S-和 RBD-特异性 IgG 水平高出轻/中度患者 1.5 倍(P=0.005 和 P=0.006)。（2）抗体动态变化与年龄有关：住院期间，老年患者的 RBD 特异性 IgG 水平比年轻患者高 4 倍(P＜0.0001)。（3）抗体动态变化与核酸载量有关：核酸阴性康复患者的 S-和 RBD-特异性 IgG 水平是核酸阳性患者的 2 倍。（4）抗体动态变化与临床指标有关：较低的 S-、RBD-和 N-特异性 IgG 水平与较低的淋巴细胞百分比、较高的中性粒细胞百分比和较长的病毒脱落持续时间显著相关。（5）出院时抗体水平低下的患者在恢复后可能有较高的核酸检测再次阳性的风险，表明抗体水平对 COVID-19 出院患者的预后具有重要价值。
结论 抗体动态变化与临床分型、年龄、病毒载量等密切相关，尤其是 S-，RBD-特异性抗体 IgG 在 COVID-19 患者的病毒清除和康复中发挥了重要作用。部分患者出院后核酸复阳，可能有两个原因：第一，采集鼻咽拭子样本可能会导致假阴性；第二，部分出院患者缺乏足够的抗体，可能发生再次感染。因此，出院前抗体检测十分重要，对于 S-、RBD-特异性 IgG 水平较低的鼻咽拭子阴性患者，应提高出院标准，或在出院后加强保护和监测。本研究的局限性包括：核酸假阴性标本的存在；最初收治的部分患者来自非定点医院，难以追溯更早的抗体水平数据；并不是所有患者都有连续的观察数据；疫情初期未检测中和抗体水平。总之，研究各种抗 SARS-CoV-2 抗体的动态变化，可为 COVID-19 的诊断、监测和预后以及疫苗研发提供重要参考。（本文部分内容已发表于 Nat CommunIF=12.121）

PO-0074

A combined test strips with fluorescent microspheres as tracer to detect rotavirus and adenovirus

Qingjun PAN、Na Jiang、Han Wu、Ping Wu
Affiliated Hospital of Guangdong Medical University

Background Rotavirus (RV) and enteric adenovirus (AdV) mainly cause infantile infectious gastroenteritis. Several separate test methods for the detection of RV or AdV are currently available, but few tests are able to simultaneously detect both RV and AdV viruses, especially in primary medical institutions.
Methods The present study was mainly designed to compare the performance of two combined test strips for the detection of RV and AdV: a rotavirus-adenovirus strip with fluorescent microspheres for tracers (FMT); and the CerTest rotavirus-adenovirus blister strip with colored microspheres for tracers (CMT). To test the strips cultures of RV, AdV and from other enteric pathogens were used, in addition to 350 stool specimens from 45 symptomatic patients with gastrointestinal infections.

Results Detection thresholds for RV and AdV cultures using serial dilutions showed that the sensitivity of FMT was significantly higher than that of CMT (both $P < 0.05$). Specificity evaluation demonstrated that with culture mixtures of Coxsackie (A16), ECHO (type30), and entero- (EV71) viruses there was no detection of cross reaction using the two test strips, i.e., all the results were negative. With regard to the detection of RV in 350 clinical specimens, the total coincidence rate was 92.9%, the positive coincidence rate was 98.2%, and the negative coincidence rate was 90.8%. With regard to AdV detection, the total coincidence rate was 95.4%, the positive coincidence rate was 95.2%, and the negative coincidence rate was 95.5%.
Conclusions FMT performed better than CMT with regard to the combined detection of RV and AdV.

PO-0075

光激化学发光法检测 CA242，CA19-9、CA50 在胰腺良恶性疾病中的诊断价值研究

周剑锁、甘奕箫、王攀、崔丽艳
北京大学第三医院

目的 评估酶联免疫检测系统与光激化学发光检测系统之间检测结果的相关性和一致性，评价光激化学发光检测系统检测 CA242、CA19-9、CA50 在胰腺良恶性疾病诊断中的临床价值。
方法 连续留取 530 例临床酶联免疫法检测 CA242 剩余血清样本，使用光激化学发光系统(LiCA)检测，对两种检测系统的检测结果进行相关性分析。另留取 149 例患有胰腺疾病患者的血清样本，其中 65 例胰腺癌患者为恶性疾病组，31 例胰腺癌术后患者为术后对照组、53 例胰腺良性疾病患者为良性对照组，检测三组患者血清中 CA19-9、CA50、CA242 的表达水平，描述其差异并绘制 ROC 曲线，分析不同的血清标志物的联合诊断效能。
结果 两种方法检测 CA242 线性回归分析，$R^2 = 0.9093$。单独检测患者 CA19-9、CA242、CA50 的血清浓度对鉴别胰腺疾病良恶性质的 AUC 分别为 0.777、0.771、0.798；CA19-9 与 CA242、CA19-9 与 CA50、CA242 与 CA50 以及三项指标联合诊断的 AUC 分别为 0.772、0.798、0.800、0.799。CA242 与 CA50 联合诊断的效能最优。胰腺癌患者、胰腺癌术后患者、良性疾病患者之间的非参数检验结果显示，胰腺癌患者的三种标志物血清浓度与其他两组的差异具备统计学意义（$P<0.05$），术后对照组 CA19-9、CA50 的血清浓度均高于良性对照组，差异具备统计学意义（$P<0.05$），术后对照组与良性对照的 CA242 血清浓度无显著性差异（$P=0.262$）。
结论 对照系统 ELISA 与考核系统 LiCA 之间相关性较好，具有可比性。在 CA19-9 水平升高时，CA242 与 CA50 的表达水平可作为判断胰腺良恶性疾病的辅助鉴别指标，CA242 表达水平可作为胰腺癌术后预后判断的指标。

PO-0076

成都地区 1887 例患儿呼吸道感染病原体检测结果分析

黄潇苇
成都市第三人民医院

目的 了解本地区呼吸道感染患儿病原体分布及流行特点。
方法 收集于 2018 年 11 月至 2020 年 11 月在本院就诊的 1887 例呼吸道感染患儿血清标本，采用间接免疫荧光法检测九种呼吸道感染病原体的 IgM 抗体，分别为嗜肺军团菌(Legionella pneumophila,LP) 、肺炎支原体(Mycoplasma pneumoniae,MP) 、肺炎衣原体(Chlamydia pneumoniae, CP)、Q 热立克次体(Q fever rickettsia,COX)、腺病毒(adenovirus,ADV)、呼吸道合

胞病毒(respiratory syncytial virus,RSV)、甲型流感病毒(influenza A vi-rus,FluA)、乙型流感病毒(influenza B virus, FluB)和副流感病毒(parainfluenza virus，PIV)。

结果 1887 例标本中 1042 例检测到至少 1 种病原体抗体阳性，阳性率 55.22%。单一病原体感染 645 例，占 61.9%。最常见感染病原体 MP,共 807 例，感染率达 42.77%；其次为 FluB,感染率 20.45%。混合感染 397 例，占阳性标本的 38.10%，其中以 MP 合并 FluB 感染最为常见，共 185 例，占混合感染的 52.86%。女性患儿感染率低于男性患儿，差异有统计学意义（P<0.05）。呼吸道感染患儿中，1 岁以下婴儿感染率最低，为 22.01%；学龄前组感染率最高，达 66.67%，差异有统计学意义（P<0.05）。春季感染率最高，与另外三个季节相比具有显著差异（P<0.05），夏秋冬三季阳性率无显著差异（P>0.05）,夏秋冬三季感染率最高的均为 MP,其次为 FluB 和 PIV,春季 MP 和 FluB 均有较高的感染率。

结论 MP、FluB 和 PIV 是引起成都地区儿童呼吸道感染的主要病原体，各种病原体的检出率在不同年龄段患儿和不同季节具有差异性，混合感染较为常见。因此，对于易发生呼吸道感染的儿童有针对性地进行预防和治疗具有重要意义。

PO-0077

膜性肾病患者 PLA2R 抗体定量水平与肾损伤标志物的相关性

黄宇、洪国斧
厦门大学附属第一医院

目的 探讨膜性肾病患者 PLA2R 抗体定量水平与肾损伤标志物的相关性。

方法 回顾性分析 60 例膜性肾病患者（男性 39 例、女性 21 例）临床资料、血清和尿液检测结果，采用酶联免疫吸附法定量检测血清抗磷脂酶 A2 受体（PLA2R）抗体水平、仪器法测定尿液 24h 尿蛋白（24-UTP）、ACR，以及血清尿素氮（UREA）、肌酐（CREA）、半胱氨酸蛋白酶抑制剂 C（CYSC）、总蛋白（TP）、白蛋白（ALB）、降钙素（PCT）。采用统计学分析不同年龄组 PLA2R 抗体定量水平变化、比较不同性别 PLA2R 抗体定量水平差异，按血清 PLA2R 抗体不同定量水平（150 RU/mL，KDIGO 指南）分为高、低浓度两组，分析比较两组各肾损伤标志物的差异以及相关性。

结果 ①PLA2R 抗体定量水平随年龄增加而升高，不同年龄分组年龄≤40 岁组、41～60 岁组、＞60 组中位数水平分别为 48.83 RU/mL、119.72 RU/mL、200.56 RU/mL；

②不同性别 PLA2R 抗体定量水平无统计学差异（P=0.186），男性、女性 PLA2R 抗体定量中位数水平分别为 96.30 RU/mL、143.87 RU/mL；

③不同 PLA2R 抗体浓度水平分组比较提示尿液标志物中 PLA2R 抗体高浓度组 24-UTP 水平（6675mg/24h）显著高于低浓度组（5446mg/24h），ACR 值在两组无统计学差异；血清标志物中 PLA2R 抗体高浓度组 UREA 水平（7.76 mmol/L）显著高于低浓度组（5.54 mmol/L），CYSC、CREA、TP、ALB、PCT 等标志物两组无显著差异。24-UTP、UREA 表达水平与 PLA2R 抗体定量水平存在一定的相关性（P=0.002、0.034）。ACR、CYSC、CREA、TP、ALB、PCT 表达水平与 PLA2R 抗体定量水平无显著相关（P=0.800、1.000、0.728、0.270、0.146、0.726）。进一步进行相关性分析提示 24-UTP、UREA 与 PLA2R 抗体定量水平呈正相关关系。

结论 PLA2R 抗体定量水平随年龄增加而升高，PLA2R 抗体定量水平与 24-UTP、UREA 存在正相关，本研究结论为膜性肾病的临床诊断治疗提供参考。

PO-0078

应用肿瘤标志物评估 COVID-19 患者预后的初步探索

何帮顺、吴秋月、夏欣一
东部战区总医院

目的 探讨与肺癌相关的肿瘤标志物对新型冠状病毒肺炎（COVID-19）患者预后的指导意义，为临床病例诊治应用提供参考。
方法 纳入武汉火神山医院 129 例 COVID-19 确诊病例和 80 例健康对照，采集临床资料，包括年龄、性别、基础疾病和预后等数据进行统计分析；采用化学发光法对 COVID-19 患者和对照组肿瘤指标 CEA, CYFRA21-1, NSE, SCCA 和 ProGRP 进行检测，比较两组之间指标差异，同时对不同临床特征 COVID-19 患者进行肿瘤指标的比较分析。
结果 该研究共纳入 129 例 COVID-19 确诊患者，其中 20 例轻症（15.50％），73 例重症（56.59％）和 36 例危重症（27.91％），危重症患者的平均年龄显著高于重症和轻症患者。糖尿病、慢性肾脏病和其他合并症患者的分布在疾病不同严重程度之间具有显着差异。129 例 COVID-19 患者中，114 例（88.37％）经治疗康复出院，15 例（11.63％）治疗无效死亡。与对照组相比，COVID-19 患者中 5 种肿瘤生物标志物的血浆浓度均明显升高（Pall<0.01）。此外，根据疾病严重程度和临床结局分组，各组间 CEA，CYFRA21-1 和 SCCA 的血浆水平存在显著差异，并且 CEA，CYFRA21-1，SCCA 的血浆水平随疾病严重程度增加而显著提高。采用逻辑回归分析来衡量肿瘤生物标志物水平与死亡风险之间的关系，结果显示 CEA、CYFRA21-1、NSE 和 SCCA 水平的升高分别与死亡风险增加相关。同时，还评估了 22 例出院和 11 例死者的生物标志物动力学与预后的相关性，结果表明，CYFRA21-1，SCCA 和 NSE 浓度升高是死亡的风险。ROC 曲线显示 SCCA（AUC：0.937，P= 0.000，临界值：2.57 ng / ml），CYFRA21-1（AUC：0.882，P= 0.000，临界值：7.29 ng / ml）和 CEA（AUC ：0.737，P= 0.003，截断值：8.55 ng / ml）可以预测 COVID-19 患者的临床结局。
结论 COVID-19 患者 CEA，CYFRA21-1，NSE，SCCA，ProGRP 肿瘤标志物浓度升高，且 CEA，CYFRA21-1，SCCA 可预测 COVID-19 患者的临床结局，本文为相关成熟生物标志物在突发疫情中的探索应用提供了新思路。（本文部分内容已发表于 J Infect， IF=4.842）

PO-0079

Four myositis-specific autoantibodies—anti-Mi-2, anti-MDA5, anti-TIF1γ and anti-ARS—in adult dermatomyositis in a Chinese cohort

Liubing Li
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences

Objective Dermatomyositis (DM) is an idiopathic inflammatory myopathy, characterized by muscle weakness and cutaneous lesions. Our study aimed to determine the prevalence of anti-Mi-2, anti-melanoma differentiation-associated gene 5 (MDA5), anti-transcription intermediary factor 1γ (TIF1γ) and anti-aminoacyl-transfer RNA synthetase (ARS) autoantibodies, and their associations with clinical features in DM patients of Han Chinese.
Methods There were 428 subjects including 189 DM, 36 polymyositis, 89 connective tissue diseases (CTD) and 114 healthy individuals who underwent testing for four myositis-specific autoantibodies (MSA) including anti-Mi-2, anti-MDA5, anti-TIF1γ and anti-ARS autoantibodies. Clinical characteristics of DM patients were compared between those with and without these autoantibodies.
Results The prevalence of anti-Mi-2, anti-MDA5, anti-TIF1γ and anti-ARS autoantibodies in our DM cohort were 9.0%, 43.9%, 26.5% and 9.5%, respectively. Patients with anti-Mi-2 autoantibody

had higher risk of developing muscle tenderness and lower risk of developing ILD than patients without anti-Mi-2 autoantibody. Patients with anti-MDA5 autoantibody had higher risk of developing skin ulceration, ILD, and fever and lower risk of developing gastroesophageal reflux than patients without anti-MDA5 autoantibody. Patients with anti-TIF1γ autoantibody had higher risk of developing periungual erythema and malignance, and had lower risk of developing arthralgia, ILD and fever than patients without anti-TIF1γ autoantibody. Patients with anti-ARS autoantibody had higher risk of developing mechanic hands and gastroesophageal reflux than patients without anti-ARS autoantibody.
Conclusion The clinical features determined by these myositis-specific autoantibodies differ from each other. Detection of MSA is helpful for the diagnosis and prediction of complications of patients with DM.

PO-0080

Impact of heat-inactivation on the detection of SARS-CoV-2 IgM and IgG antibody by ELISA

Xiumei Hu
Nanfang Hospital, Southern Medical University

Background To establish a safe and accurate method for detecting SARS-CoV-2 IgM and IgG, we assessed the impact of sera after heat-inactivation on the SARS-CoV-2 IgM and IgG levels measured by ELISA-immunoassay.
Methods The serum samples of 62 patients with COVID-19 and 18 healthy controls were collected in Hankou's Hospital of Wuhan from February 27 to March 6, 2020. Before and after the samples were inactivated, the levels of IgM and IgG antibodies were measured.
Results The indexes of antibodies after inactivated were signifificantly higher than those in fresh sera, while the positive rates in all participants or in patients with COVID-19 did not change. The positive coincidence rate, negative coincidence rate and total coincidence rate of IgM antibodies before and after inactivation were 100.00% (55/55), 96.00% (24/25) and 98.75% (79/80), respectively ($\kappa = 0.971$, $P < 0.001$), while those for IgG antibodies were 98.21% (55/56), 91.67% (22/24) and 98.75% (79/80) respectively ($\kappa = 0.910$, $P < 0.001$). These results showed a good consistency.
Conclusions Heating-activation does not decrease the diagnostic effifffifficacy of SARS-CoV-2 IgM or IgG antibodies. Sera inactivated by heating at 56 °C for 30 min should be recommended to minimize the risk of virus con_x0002_tamination of laboratory staff.

PO-0081

基于微流控技术的肺癌循环肿瘤细胞检测及其在诊疗中的应用研究

魏雪菊[1,2]、洪国斐[1,2]
1. 厦门大学附属第一医院检验科
2. 厦门市基因检测重点实验室

原发性肺癌是常见的恶性肿瘤之一，其发病率和死亡率始终居于恶性肿瘤的首位，严重威胁人类的健康和生活质量。肺癌的主要亚型为非小细胞型肺癌（non-small cell lung cancer ,NSCLC），约占 80%-85%，并且大多数患者确诊时已经处于中晚期。随着人们对肺癌驱动基因的发现和相应靶向药物的研究与应用，肺癌的治疗模式已经进入分子靶向治疗时代。以表皮生长因子受体（epidermal growth factor receptor，EGFR）和间变淋巴瘤激酶（anaplastie lymphoma kinase，ALK）为靶点的药物临床应用使得 NSCLC 患者个体化治疗具有重大意义。液体活检（liquid

biopsy）是指从体液中获得来源于组织的生物标志物，并通过对所得标志物的分析来反应来源组织的相关信息。相比于传统的活检技术，液体活检的优势在于快速、方便、侵袭性小、可重复操作、能够密切监测肿瘤对治疗的反应和预测癌症的复发。循环肿瘤 DNA（ctDNA）是死亡肿瘤细胞释放出的核酸物质，在肿瘤的早期释放量少，所包含信息有限；外泌体是肿瘤细胞释放的小囊泡，包含肿瘤细胞的 DNA、RNA 和蛋白组，现有基础研究少，临床意义有限；而循环肿瘤细胞（CTCs）可以提供肿瘤病灶的基因组变异、mRNA 表达异常、细胞形态与功能等信息，更能全面、系统地反应整个肿瘤发展进程的液体活检内容，是一个极具潜力的检测靶标。该课题拟采用的方法是发展基于微流控技术的肺癌循环肿瘤细胞液体活检技术。对循环肿瘤细胞进行捕获、计数及分析，可用于肺癌患者靶向治疗的用药指导，预测靶向治疗的疗效、以及复发监测等伴随诊断领域。

PO-0082

新型冠状病毒肺炎患者不同血清模式下淋巴细胞亚群细胞数量比较

叶巍
湖北省新华医院

目的 探讨因新型冠状病毒肺炎（COVID-19）患者新型冠状病毒（2019-CoV-2，2019-nCoV）抗体免疫球蛋白 M（IgM）和免疫球蛋白 G（IgG）抗体检测结果，比较不同结果间的淋巴细胞数量区别。
方法 收集 2020 年 3 月 4 日至 3 月 18 日在湖北省中西医结合医院因新型冠状肺炎入院 245 例患者检测结果，回顾性研究入院患者核酸检测结果、血清学 IgM 和 IgG 抗体以及流式细胞学检测结果，并对根据血清学结果将患者分为 IgM（+）/IgG（+）、IgM（-）/IgG（+）以及 IgM（-）/IgG（-）3 组，对 3 组人群分别抽取 20 名患者，比较其淋巴细胞检测结果。
结果 245 例患者中，血清学 IgM（+）/IgG（+）95 例，IgM（-）/IgG（+）126 例,IgM（-）/ IgG（-）24 例。2019-nCoV IgM 抗体检测的灵敏度为 38.77%， 2019-nCoV IgG 抗体检测的灵敏度为 90.20%。IgM（-）/IgG（-）组和 IgM（+）/IgG（+）以及 IgM（-）/IgG（+）组在外周血淋巴细胞总数、CD4+T 细胞、CD8+T 细胞、B 细胞均有显著性差异。
结论 应将核酸检测和抗体检测结果结合进行诊断，采用免疫疗法提高淋巴细胞数量可能作为治疗 COVID-19 的一种潜在重要疗法。

PO-0083

Combined Detection of Norovirus GI and GII: An Innovative Fluorescent Particles Test Strip

潘庆军、张莉芳、蒋娜、吴晗、吴平、刘华锋
广东医科大学附属医院

We used selected chromatographic materials and antibodies specific to Norovirus GI and GII, the Norovirus GI and GII fluorescent particles combined detection test strip (tested method) was prepared as a conventional double antibody sandwich. The samples assayed included cultured rotavirus and 465 specimens from patients with symptoms of gastrointestinal infection. Norovirus was detected using the tested method and a reference method (CerTest Norovirus GI-GII test card). The results indicated that the sensitivity of the tested method was 4 (for GI detection) or 8 times (for GII detection) greater than the reference method. Neither of the two methods cross-reacted with rotavirus and so on. For specimens, 29 were found to be negative by the reference method and positive by the tested method, and 8 were found to be negative by the tested method and positive by the reference method. Furthermore, a retesting of these samples by qPCR

showed that 28 of the 29 were positive, and 3 of the 8 were positive. so, our test strip was successfully prepared and had good detection performance.

PO-0084

One-step-combined test strips with fluorescent microspheres as the tracer to detect influenza A and B

Qingjun PAN、Na Jiang、Lifang Zhang、Han Wu、Ping Wu
Affiliated Hospital of Guangdong Medical University

Background Influenza A and B viruses mainly cause respiratory infectious disease. Till now, few tests are able to simultaneously detect both, especially in primary medical establishments.
Methods This study was designed to compare the performance of two different one-step-combined test strips for the detection of influenza A and B: one strip with fluorescent microspheres for tracers (FMT); and the other strip with colored microspheres for tracers (CMT). To test the strips, cultures of influenza A, B, and other pathogenic viruses were used, in addition to 1085 clinical specimens from symptomatic patients with respiratory infections. Real-time RT-PCR was also considered as a reference method used to detect the different results of FMT and CTM.
Results Detection thresholds for influenza A and B cultures using serial dilutions revealed that the sensitivity of FMT was higher than that of CMT (both $P < 0.05$). With the culture mixtures of Coxsackie virus (A16), enteric cytopathic human orphan virus (ECHO type30), enterovirus (EV71), rotavirus (LLR strain), and enteric adenovirus (AdV 41), specificity assessment demonstrated that there was no cross reaction during the usage of the two test strips as shown by the results which were negative. In the detection of influenza A in 1085 clinical specimens, the total coincidence rate was 96.7%, the positive coincidence rate was 97.1%, and the negative coincidence rate was 96.7%. In the case of influenza B detection, the total coincidence rate was 99.1%, the positive coincidence rate was 92.6%, and the negative coincidence rate was 98.5%. In addition, with influenza A or B real-time RT-PCR detection method, the results showed that, for influenza A, 26 of the 33 specimens that negative with CMT but positive with FMT, showed positive results, and none of the 3 specimens that positive with CMT but negative with FMT showed a positive result; For influenza B, 12 of the 15 specimens that negative with CMT but positive with FMT, showed positive results, and none of the 5 specimens that positive with CMT but negative with FMT showed a positive result.
Conclusions FMT performed better than CMT in the combined detection of influenza A and B viruses.

PO-0085

Emerging Molecular Markers for Developing Disease Biomarker Panels in Lupus

Gongjun Tan
zhuhai center for maternal and children healthcare

Systemic lupus erythematosus (SLE) is a multifactorial autoimmune disease which affects various organs and tissues, posing significant challenges in clinical diagnosis and treatment. It is known that elevated autoantibody production and hyper-proliferation and activation of autoreactive T cells and B cells are major hallmarks of this devastating disease, however, the etiology of SLE is highly complex, contributed by environmental factors, stochastic factors and genetic susceptibility. The current criteria for diagnosis of SLE are mainly based on the combination of clinical manifestations and traditional laboratory tests. However, these tests are

suboptimal in sensitivity and specificity and are not able to inform disease cause or guide physicians in decision-making for medication. Therefore, there is an urgent need to develop a more accurate and robust biomarker of SLE for effective clinical management and drug development for lupus patients. It is fortunate that the emerging Omics has empowered the discovery and identification of potential novel biomarkers of SLE, especially markers from blood, urine, cerebral spinal fluids (CSF) and other body fluids. In this review, we summarize the sensitivity, specificity and performance of detection of these novel disease markers and discuss the potentials of these markers for the development of biomarker panel based diagnostics or disease monitoring system in SLE.

PO-0086

Establishment and evaluation a high selective, sensitive method to separated and identified antigens in immune complexes

Gongjun Tan
zhuhai center for maternal and children healthcare

Comprehensive identification and profiling of antigens in immune complexes (ICs) in biological fluids, such as serum and other body fluid, is useful for developing early diagnostic biomarkers and specific therapy for many diseases. “immune complexes analysis” method include separation of ICs from serum with protein A/G, papain-digestion and elution, then tryptic digestion, and nano-LC–MS/MS for the identification and profiling of antigens in CICs, that method is selective and sensitive. However, Protein G or Protein A bind the fragment of crystallization (Fc) domain of antibodies is nonselective, the separation efficiency of the immune complex by this method is not high selective because the binding antibodies and the unbinding antibodies cannot be distinguished by Protein G or Protein A, and the amount of the unbinding antibodies in the serum is greater than the binding antibodies. To selectively purified CICs with enhanced sensitivity, in this study, complement 1q (C1q) was applied for the specific recognition of antibody–antigen complex to separated CICs from specimens, combined papain-digestion and elution, tryptic digestion, and nano-LC–MS/MS. Result showed that C1q capture Method provided the high selective and sensitive detection of CIC-antigens, without interference by antibodies and proteins non-specifically bound to the beads. These data suggest that t C1q capture CIC separation technique is a good general pretreatment technique for the identification of antigens incorporated in CICs.

PO-0087

LATS2 is a prognostic biomarker and correlated with immune infiltrates in colorectal cancer

chengwen zhao[1]、jianping chen[1]、yonghui liu[2]、xiaoyu gu[1]、shunhao zhang[1]、shaoqing ju[1]
1. Department of Laboratory Medicine
2. 南通大学附属医院分院

Background Colorectal cancer (CRC) is one of the most common malignancies with high prevalence and low five-year survival. Although immunotherapy has made impressive progress in the treatment of CRC, it still faces huge challenges. LATS2, as a critical molecule of Hippo signaling pathway, has been well accepted that its expression level is associated with cancer progression. How-ever, the prognostic and immune response roles of LATS2 expression in CRC remain unclear.

Methods To investigate the value of LATS2 in prognosis and immune infiltration, a retrospective study of 213 CRC patients was carried out. Immunohistochemi-stry analysis on tissue microarray and qRT-PCR were used to determine the expression of LATS2. Besides, bioinformatics was used to analyze the level of immune infiltration and related pathways of LATS2.
Results indicated that LATS2 levels were decreased in CRC tissues compared with those in non-tumor tissues, which was notably associated with tumor differentiation (P=0.002) and tumor stage (P=0.002). Multivariable analysis showed that low LATS2 protein expression was a significantly independent predictor in CRC. In the Kaplan-Meier analysis, patients with high LATS2 expression had significantly better overall survival than those with low LATS2 expression. Furthermore, we identified that LATS2 was involved in the regulation of immune-related pathways and its expression had positive correlation with tumor immune infiltrating cells like T cells, macrophages and dendritic cells by GSEA, TIMER and ssGSEA analysis.
Conclusion In summary, our data suggested that LATS2 may act as a cancer suppressor gene in CRC and be associated with prognosis and immune infiltration. Thus, LATS2 can be used as a novel biomarker for predicting prognosis and immune infiltration in CRC.

PO-0088

新型分泌蛋白冠层成纤维细胞生长因子信号调节因子 2 在甲状腺乳头状癌中的临床应用价值

段文冰
山东第一医科大学附属省立医院临床医学检验部

目的 通过分析冠层成纤维细胞生长因子信号调节因子 2(CNPY2)在甲状腺乳头状癌(PTC)患者癌组织及血清上的表达，探讨其临床应用价值。
方法 甲状腺乳头状癌(PTC)组为 2010-2012 年山东省立医院两腺外科收治并行手术的患者 92 例，良性病变组 45 例，组织切片做免疫组化(IHC)；PTC 组术前患者血清样本 102 例、良性病变组 64 例及正常对照 54 例，进行血清酶联免疫(ELISA)实验。采用 t 检验、秩和检验、卡方检验及 ROC 曲线进行分析。
结果 ① PTC 患者癌组织 CNPY2 的 IHC 得分[9.74(8,12)]均显著高于癌旁组织[5.78(4,8)](Z=8.25,P=0.000)和良性病变组织[5.87(4,8)](Z=6.82,P=0.000)。②CNPY2 蛋白在年龄≥55 岁与<55 岁 PTC 患者[11.47(12,12)比 9.40(8,12);Z=3.08,P=0.002]、女性与男性患者[10.05(8,12)比 8(8,8);Z=3.42,P=0.001]、淋巴结转移与未转移患者[10.44(8,12)比 9.28(8,12);Z=2.03,P=0.042]、恶性肿瘤分期(TNM 分期)II 期与 I 期患者[12(12,12)比 9.58(8,12);Z=2.45,P=0.014]均有显著差异。③ PTC 患者血清 CNPY2 的浓度(ng/ml)[0.19(0.13,0.23)]显著高于正常组[0.13(0.13,0.15)](Z=4.27,P=0.000)及良性组[0.15(0.10,0.17)](Z=2.79,P=0.005);PTC 患者中女性血清 CNPY2 浓度(ng/ml)[0.22(0.14,0.29)]显著高于男性[0.16(0.13,0.17)](Z=3.70,P=0.000)。④根据受试者工作特征曲线确定的最佳截断值 0.159ng/ml，分 CNPY2 高值组和低值组，并将 PTC 患者分为 PTC 组(42 例)、合并淋巴细胞性甲状腺炎的 PTC 组(21 例)及合并结节性甲状腺肿或腺瘤样增生的 PTC 组(39 例)，发现 PTC 组中抗甲状腺球蛋白抗体在 CNPY2 高值与低值组中有明显差异[31.17(10.10,61.01)比 10.39(10.21,10.43);Z=2.04,P=0.044]。
结论 通过检测 PTC 患者组织及血清 CNPY2 的表达水平，分析其与病理因素及甲功血液指标的相关性，推测 CNPY2 对于 PTC 的预测有着一定的临床应用价值。

PO-0089

全血细胞及肺泡灌洗液组织研磨匀浆后培养测 IFN-γ 实验室技术对诊断肺结核效能比较研究

方晓露、刘德扬
襄阳市第一人民医院

目的 不同来源组织全血细胞及肺泡灌洗液研磨的匀浆组织培养后测 IFN-γ 释放试验技术对诊断肺结核效能比较研究，以提高临床早期诊断肺结核的水平。
方法 选择襄阳市第一人民医院检验科 2019 年 5 月-2021 年 4 月期间接收的 137 例成年疑似肺结核患者送检标本，包括 91 例 TB 组患者（确诊组 46 例, 很有可能组 33 例, 可能组 12 例)及 46 例非肺结核组患者，然后将送检肺泡灌洗液研磨后的匀浆及全血组织分别设置阴性对照组，本底实验组，阳性对照组三组 进行培养，24 小时候后用 ELISA 方法对 IFN-γ 释放进行检测（北京万泰结核感染 T 细胞检测试剂盒 体外释放酶免疫法）；评价上述 2 种不同来源组织 IFN-γ 释放试验对诊断肺结核的效能。
结果 结果以临床诊断为标准，检测技术诊断肺结核的阳性率分别为全血组织培养后 IFN-γ 释放试验阳性率为 19.2%(15/78), 肺泡灌洗液组织研磨匀浆培养测 IFN-γ 实验室技术阳性率 85.8%(67/78)。肺泡灌洗液组织研磨匀浆测 IFN-γ 实验室技术的敏感度高于全血细胞培养测血清 IFN-γ，差异均有统计学意义（p<0.05）。
结论 在肺结核的早期诊断中，选取肺泡灌洗液组织研磨后，取匀浆培养测得 IFN-γ 的释放试验对肺结核诊断的敏感性高于全血组织培养后 IFN-γ 的释放试验，肺泡灌洗液检测实验可有效提高临床肺结核检出率，肺泡灌洗液组织研磨匀浆测 IFN-γ 实验室技术方法值得在临床推广。

PO-0090

广西玉林市 2015-2020 年 HIV 抗体不确定结果的随访分析

庞晓泸[1]、叶瑞国[1]、庞贤武[2]、宁珺茹[1]、林瑞玲[1]、黄佐妮[1]、蒋宁[1]
1. 玉林市疾病预防控制中心
2. 广西壮族自治区疾病预防控制中心

探讨 HIV 抗体不确定结果转归特点及 HIV-1 病毒载量检测在 HIV 抗体不确定诊断中的应用。
方法 收集 2015-2020 年全市 HIV 抗体筛查为 HIV 抗体有反应的标本，使用两种快速法检测试剂复核，出现单反应或双反应的标本使用免疫印迹法（WB）进行补充试验，结果为不确定的使用 HIV-1 病毒载量检测作为补充试验。
结果 2015-2020 年共 HIV 抗体确证检测样本 4906 人份，不确定结果 153 人份（3.12%），最终完成随访并有检测结果 91 例。在 91 例中有 59 例阳转，32 例阴转；复核双反应和单反应的阳转率分别为 94.74%和 14.71%；第一次 WB 结果为两条带以上的阳转率为 87.76%，WB 结果仅有 1 条带的阳转率为 35.71%。91 例随访中病毒载量＞5000CPs/m 的有 59 例，病毒载量≤5000CPs/ml 的有 32 例。
结论 HIV 抗体复核均有反应且 WB 至少 2 条带型的样本阳转率比较高，HIV 抗体复核仅单反应且 WB 仅有 1 条带型的也有感染的高风险，同时采用 HIV 抗体确证结果结合 HIV 病毒载量检测方法作为补充试验尽早确定是否感染。

PO-0091

An analysis of predictive value of HIV serology COI for confirmation of HIV infection using Elecsys® HIV combi PT assay

Mengying Zhang
The First Affiliated Hospital of Nanjing Medical University

Background 4-th generation assays performed high sensitivity and specificity, greatly improved early diagnosis of HIV. While false positive rate (FPR) was high in low prevalence region, which caused inconvenience for clinical practice and anxiety for patients.
Objectives To analyze the relation between COI values and HIV confirmatory results, and explore new COI threshold in our own laboratory to predict HIV infection.
Methods We retrospectively analyzed primarily reactive results by Elecsys® HIV combi PT assays and their confirmatory results by WB at Nanjing CDC. The mean COI values of true positives (TP), false positives (FP) and indeterminate group were compared to understand the COI values distribution. And ROC analysis was performed to determine the optimal COI value for predicting HIV infection status.
Results Totally 150980 HIV serological results by Elecsys® HIV combi PT assays were reviewed, 305(0.2%) were primarily reactive. There are 82(26.89%) true positives, 210(71.92%) false positives and 11 indeterminate by WB tests, another 2 patients rejected WB tests. Mean COI values of TP (3.174) were greatly higher than that of FP (643.5) ($P < 0.0001$), but there is no significant difference between FP and indeterminate group. Combining the requirement of HIV diagnosis and ROC analysis, 9.87 was established as the optimal threshold to predict the infection, with 100% sensitivity and 99.99% specificity.
Conclusions By adjusting the COI cutoff, the false positive rate (FPR) can be reduced and the efficiency of screening assays can be increased, which can save much additional reagent and staff costs and much time for delivery of HIV test results.

PO-0092

结肠癌 TP53 相关外泌体定量蛋白质组学研究

朱琳
中国人民解放军总医院第一医学中心检验科

目的 比较分析 TP53 突变、敲除及野生的肿瘤细胞分泌外泌体的蛋白质组差异，探讨突变的 TP53 对肿瘤微环境中的分泌蛋白质的影响。
方法 从 TP53 野生型（HCT116-p53(WT)）、敲除型（HCT116-p53(-/-)）和构建的 273 位点突变型的结肠癌 HCT116 细胞（HCT116-p53(R273H)）培养上清中分别提取外泌体，通过透射电镜观察其形态和免疫印迹法检测外泌体标志性蛋白，并经 iTRAQ-LC-MS/MS 策略分析三种细胞外泌体蛋白组成的差异并通过酶联免疫吸附测定（ELISA）进行差异蛋白验证。
结果 HCT116-p53(WT)分泌的外泌体和 HCT116-p53(R273H)分泌的外泌体相比有 144 个差异蛋白，HCT116-p53(WT)分泌的外泌体和 HCT116-p53(-/-)分泌的外泌体相比有 480 个差异蛋白，大部分差异蛋白主要参与代谢和细胞的生物学过程以及凋亡、应激、增殖、细胞粘附等功能。通路分析（IPA）显示 HCT116-p53(WT)分泌的外泌体相比于 HCT116-p53(R273H)分泌的外泌体的差异蛋白主要富集在泛素化、mTOR、DNA 损伤修复通路中；HCT116-p53(WT)分泌的外泌体相比于 HCT116-p53(-/-)分泌的外泌体的差异蛋白主要集中在泛素化、EIF2、糖酵解通路中。而且，结肠癌患者的血清视网膜母细跑瘤蛋白（RB1）水平明显高于健康对照（P=0.0012）
结论 TP53 突变和缺失会改变外泌体的蛋白组成，富集许多泛素化蛋白，结肠癌患者的血清 RB1 水平明显高于健康对照，这为深入探讨 TP53 状态对外泌体蛋白组成和肿瘤微环境的影响奠定基础。

PO-0093

A nonlinear time-series analysis to identify thresholds in associations between antimicrobial consumption and rates of resistance at a Chinese tertiary care hospital, 2009-2020

Xiaohan Hu
Nanjing drum Tower Hospital

Background Antibiotic abuse is the major cause of increasing antimicrobial resistance. Infections caused by drug-resistant bacteria carry significant mortality. However, many studies supported the hypothesis that resistance of antibiotic is associated with 'fitness cost' which reduces virulence of these pathogen. Therefore, the numbers of cases caused by drug-resistance bacteria only increase when the selection pressures from antibiotics exceed critical thresholds. Our purpose is to investigate the association between the usage of antibiotics and the number of infections caused by drug-resistance bacteria and find the critical thresholds.
Methods Data regarding monthly consumption of six kinds of antibiotics (daily defined doses (DDDs)/1,000 inpatient-days) and the number of cases caused by five kinds of drug-resistance bacteria (occupied bed days (OBDs)/10,000 inpatient-days) from inpatients during 2009 to 2020 were retrieved from the electronic prescription system at a tertiary hospital in Jiangsu Province, China. Generalized additive models (GAM) was used to analyze correlations and trends between antibiotics consumption and antimicrobial resistance on a monthly basis.
Results Six kinds of antibiotics and five kinds of drug-resistance bacteria established 30 models. And 8 models (carbapenems-CRAB, lag=0; carbapenems-CRKP, lag=0; carbapenems-P.aeruginosa, lag=1; carbapenems-E.coli, lag=2; glycopeptides-CRAB, lag=0; glycopeptides-CRKP, lag=0; glycopeptides-P.aeruginosa, lag=1; fluoroquinolones-E.coli, lag=0) were considered statistically significant. 5 of 8 above-mentioned models had definite thresholds showing selection pressures overweigh the fitness costs while other models hardly to find typical thresholds.
Conclusions We identified significant correlations between antibiotics consumptions and the incidence density of drug-resistance bacteria. Our study suggested threshold can be interpreted as a limit and it may guide rational compromises between the selection pressure and the survival advantage for providing targets for access to effective treatments.

PO-0094

PLR、D-二聚体和 CA125 对上皮性卵巢癌诊断的研究价值

蔡针针
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨血小板（Platelet，PLT）/ 淋巴细胞（Lymphocyte）、D-二聚体（D-dimer）和糖类抗原 125（CA125）在上皮性卵巢癌诊断中的应用价值。
方法 回顾性分析南京医科大学第一附属医院 2015 年 1 月−2020 年 12 月收治的上皮性卵巢癌患者 136 例[年龄：57.00(49.00,64.00)]、卵巢良性疾病患者 126 例[年龄：40.00(29.00,51.00)]。首先采用单因素分析和多因素 Logistic 回归分析与上皮性卵巢癌诊断相关实验室指标。其次用 ROC 曲线分析 PLR（PLT/Lymphocyte)、D-dimer、CA125 单独检测和联合检测对上皮性卵巢癌的诊断效能，最后分析上皮性卵巢癌患者 PLR、D-dimer、CA125 水平与其临床病理特征的关系。
结果 经 Logistic 回归分析，患者年龄、PLR、D-dimer 和 CA125 水平为上皮性卵巢癌独立危险因素。PLR、D-dimer 和 CA125 联合检测时诊断效能最好（AUC=0.955, 95%CI 0.922～0.977)。在上皮性卵巢癌组中，PLR 和 D-dimer 水平与肿瘤大小显著相关（P<0.05)；晚期患者与早期患者相比，PLR、D-dimer 和 CA125 水平均显著升高（P<0.05)；腹水<1000ml 的上皮性卵巢癌患者，

PLR 水平明显低于腹水≧1000ml 的患者（P<0.05)；PLR、D-dimer 和 CA125 水平与上皮性卵巢癌淋巴结转移有关，有淋巴结转移的患者 PLR、D-dimer 和 CA125 水平均升高（P<0.05)。
结论 联合 PLR、D-dimer 和 CA125 有利于上皮性卵巢癌的诊断。

PO-0095

Establishing Reference Intervals for Islet Autoantibody Assay and its Potential Utility in Type 1 Diabetes

yu fu
the First Affiliated Hospital of Nanjing Medical University, Nanjing, People's Republic of China.

Background Currently, islet autoantibodies (IAbs) constitute the most reliable marker for detecting the autoimmune process of type 1 diabetes (T1D). However, there are no appropriate reference intervals (RIs) to interpret the results of IAbs in China.
Objective In this study, we aimed to establish the RIs of four common IAbs based on the Chinese Han population and evaluate their clinical diagnostic values in patients with T1D.
Methods We collected 177 blood samples from healthy volunteers to detect the levels of IAbs directed against insulin (IAA), glutamic acid decarboxylase-65 (GADA), insulinoma antigen 2 (IA-2A), and zinc transporter-8 (ZnT8A) using a chemiluminescence immunoassay. RIs were calculated using nonparametric 95th percentile intervals in accordance with the Clinical and Laboratory Standards Institute guidelines, and their clinical diagnostic values were evaluated by detecting the levels of IAbs of 140 blood samples from patients with T1D in a clinical setting.
Results We defined 138 individuals as the apparently healthy population. No association between the levels of the four IAbs and gender ($p > 0.05$) and age ($p > 0.05$) were found in the apparently healthy population. The combined RIs for GADA, IA-2A, ZnT8A, and IAA were 0–1.78 IU/mL, 0–3.91 IU/mL, 0–2.36 AU/mL, and 0–0.58 COI, respectively. Collectively, the diagnostic efficiency for the four IAbs, especially for GADA and IAA, were improved by using the RIs established in this study.
Conclusions The RIs for IAbs established in this study, for the first time, will be a valuable tool for disease diagnosis and the therapeutic management of T1D in a clinical setting.

PO-0096

新冠疫苗接种者体内抗体水平变化和外周血淋巴细胞亚群相关性分析

刘阳、侯彬、袁丹、王芳、杨平、蔡志龙、王丹、方堃
四川省科学城医院

目的 研究新冠疫苗接者体内抗体水平变化及临床意义，分析其水平与外周血淋巴细胞亚群相关性。
方法 收集某单位 2021 年 3 月至 2021 年 5 月期间完成第二剂新冠灭活疫苗接种者 56 例作为研究对象，同时收集未接种疫苗志愿者 20 例作为对照组。分析疫苗接种人群抗体水平变化，比较各组间外周血体液免疫指标差异，分析中和抗体水平与外周血免疫细胞相关性。
结果 同对照组相比，中和抗体水平、IgM、IgG 显著升高（P<0.001）；疫苗接种组：（6-8 天）、（13-15 天）两组中和抗体水平阳性率 100%，在 3 天组和（27-35 天）组分别是 20%和 88.6%; 疫苗接种组间比较，3d 组和（6-8d）组 IgM 有差异（P<0.05）；而 IgG 水平在 3d 组同（6-8d）、（13-15d）、（27-35d）间均具有显著差异（P<0.05，P<0.01，P<0.01）。中和性抗体的表达在 3d 组同（27-35d）组间差异非常显著（P<0.01）,同（6-8d）、（13-15d）组，P<0.05。总抗体水平的结果显示：3d 组与（6-8d）、（13-15d）（27-35d）相比，分泌显著增加，差异明显，P

值分别为 P<0.01，P<0.01，P<0.05。接种疫苗组 CD3+CD4+辅助性 T、CD3+CD8+杀伤性 T、CD3-CD19+B 淋巴细胞比例增加，其中 CD3+CD4+辅助 T 升高最明显，而 CD3+T 淋巴细胞百分比轻度下降，差异具有统计学意义（P<0.05）。
结论 新冠疫苗第二剂接种 13-15 天以后，产生了较高水平的 IgG、中和性抗体和总抗体水平，能激发人体体液免疫和细胞免疫应答，产生免疫力，这对我们估计疫苗疗效提供了一定的临床依据。

PO-0097

GPC3 联合 PIVKA-Ⅱ在 AFP 阴性肝癌的诊断预后价值

林莺莺、陈燕
福建省肿瘤医院

目的 探讨磷脂酰肌醇蛋白聚糖-3（GPC-3）和异常凝血酶原（PIVKA-Ⅱ）联合检测对 AFP 阴性肝癌的诊断和预后价值，为患者的临床治疗提供参考。
方法 从福建省肿瘤医院 408 例肝癌首诊患者中筛选出 101 例 AFP 阴性肝癌患者作为实验组，并对其中 13 例接受肝癌手术治疗的患者进行疗效监测，同时选择同期入院的 114 例良性肝病患者以及 60 例体检的正常人群作为对照组进行前瞻性队列研究。收集肝癌实验组临床诊疗数据进行生存随访。检测研究对象血清中 GPC3 及 PIVKA-Ⅱ的表达水平，建立 ROC 曲线并计算两者诊断指标以及在不同肿瘤分期的诊断敏感性；单因素分析 GPC3 和 PIVKA-Ⅱ与 AFP 阴性肝癌患者临床特征的相关性；分析手术患者治疗前后 GPC3 及 PIVKA-Ⅱ的表达水平变化；比较治疗前 GPC3 和 PIVKA-Ⅱ与肝癌患者预后相关性。
结果 AFP 阴性肝癌患者血清中 GPC3 及 PIVKA-Ⅱ的表达水平显著高于良性肝病患者和正常对照者，差异有统计学意义。在 AFP 阴性肝癌患者中，GPC3 和 PIVKA-Ⅱ单项及组合的 ROC 曲线下面积分别为 0.792，0.928 和 0.862；GPC3 和 PIVKA-Ⅱ单项及联合检测的敏感性分别为 77.2%、86.1%和 83.2%，特异性分别为 82.2%、93.1%和 83.3%。GPC3 及 PIVKA-Ⅱ随着肿瘤分期的增高而增高，在Ⅰ期肝癌中的敏感性高达 86.5%和 83.8%。GPC3 水平与 AFP 阴性肝癌患者年龄相关，PIVKA-Ⅱ水平与 AFP 阴性肝癌患者门脉癌栓情况相关；肝癌患者术后 GPC3 及 PIVKA-Ⅱ血清水平较术前明显减少。肝癌患者的生存时间与治疗前 GPC3 及 PIVKA-Ⅱ的表达水平无关，与临床分期显著相关。
结论 GPC3 及 PIVKA-Ⅱ检测对于 AFP 阴性肝癌尤其是Ⅰ期肝癌有较高的诊断价值，可用于 AFP 阴性肝癌术后疗效监测。

PO-0098

Logistic 回归结合 ROC 曲线分析标志物模型在肝硬化合并肝癌患者中的诊断价值

林莺莺、陈燕
福建省肿瘤医院

目的 评价血清异常凝血酶原（PIVKA-Ⅱ）、高尔基体蛋白 73（GP73）、甲胎蛋白（AFP）和甲胎蛋白异质体（AFP-L3）四种肝癌标志物不同检测模型在肝硬化合并肝癌患者中的诊断价值，建立最佳诊断模型。

方法 以治疗前 170 例肝硬化合并肝癌、60 例肝硬化、60 例慢性乙型肝炎患者和 60 例健康体检者为研究对象，检测 PIVKA-Ⅱ（化学发光酶免疫检测法）、GP73（酶联免疫法）、AFP（电化学发光法）和 AFP-L3（微量离心柱法）的血清水平，建立单项检测的 ROC 曲线，确立各指标的最佳诊断临界值（cutoff 值）。使用 SPSS 做多变量观察值的 ROC 曲线，建立 Logistic 回归方程，评价多变量检测模型的诊断指标，确定最佳诊断模型。

结果 单项检测时，PIVKA-Ⅱ的曲线下面积（AUCROC）最大（0.920），敏感性和特异性分别为 91.2%和 85.6%。多项联合检测时，PIVKA-Ⅱ和 AFP 联合检测的多变量检测模型曲线下面积（AUCROC）最大（0.951），敏感性和特异性分别为 87.6%和 91.1%，为乙肝肝硬化合并肝癌的最佳诊断模型。最佳诊断模型的肝癌风险概率值在早期肝癌患者中的敏感性为 66.7%，在小肝癌的敏感性为 67.7%。

结论 PIVKA-Ⅱ和 AFP 联合检测为乙肝肝硬化合并肝癌的最佳诊断模型，利用肝癌风险概率值可从乙肝肝硬化患者中及时诊断出早期肝癌和小肝癌，提高患者生存率。

PO-0099

Chi3L1 在肝纤维化诊断分期中的作用

刘爱平、胡尧、张弢、刘春芳
复旦大学附属华山医院

目的 研究 Chi3L1 水平在慢性肝脏纤维化诊断分期中的作用

方法 收集肝脏穿刺病人的血清进行 Chi3L1 的检测，并与传统肝纤维化指标 FIB4 和 APRI 进行比较，观察其在肝脏不同纤维化分期中的水平，计算其诊断价值。

结果 在区分慢性肝炎有无肝纤维化、S1 期与 S2-4 期，chi3L1 ROC 曲线下面积分别为 0.718 和 0.792，略高于 APRI 和 FIB4。但是在区分 S1、2 期和 S3、4 期时，Chi3L1 ROC 曲线下面积为 0.727，并不优于 APRI 和 FIB4.

结论 Chi3L1 在区分有无早期肝纤维化阶段有重要作用，在区分肝纤维化晚期分期中作用不显著。

PO-0100

新冠疫苗接种后新冠病毒 IgM 和 IgG 抗体检测结果分析

王宁、吕金娥、张丽晶
云南省曲靖市第二人民医院

目的 分析新冠疫苗接种后新冠病毒抗体检测结果。

方法 我院医务人员 152 人接种新冠疫苗（2 针）1 月后检测新冠病毒 IgM 和 IgG 抗体。

结果 IgM 抗体阳性 33 例，弱阳性 1 例，阳性率 22.36%，IgG 抗体阳性 133 例，弱阳性 5 例，阳性率 90.79%。

结论 新冠病毒抗体检测对于新冠肺炎诊断、病情监控具有辅助作用，疫苗接种后进行新冠病毒 IgM 和 IgG 抗体检测阳性率与中和抗体检测阳性率相符，若能用新冠病毒 IgM、IgG 抗体检测作为新冠疫苗接种成功的实验室检测依据，将大大提高广大人民群众对疫苗接种的积极性，为我国快速、有效推进疫苗接种工作起到积极的作用，同时尽快形成群体免疫，在国内甚至世界范围内筑起新冠肺炎免疫屏障，最终达到消除新冠病毒的终极目标。

PO-0101

GALAD 和 BALAD-2 模型在原发性肝细胞癌诊断及短期疗效评价中的临床意义研究

陈岩松、崔兆磊、陈燕
福建肿瘤医院

目的 探讨 GALAD 模型在原发性肝细胞癌患者诊断价值以及 BALAD-2 模型在肝细胞癌短期疗效评估中的价值。
方法 收集某院 2017 年 8 月—2018 年 2 月 87 例首诊肝癌（HCC）患者、53 例肝脏良性疾病（BLD）患者、49 例表观健康体检者(HC)血清，采用微流控免疫荧光电泳技术检测血清中 AFP、AFP-L3 和 DCP 水平，建立基于性别、年龄和血清中 AFP、AFP-L3 和 DCP 水平的 GALAD 模型，分析 GALAD 模型对于肝癌患者的诊断价值；采用溴甲酚紫法检测血清中白蛋白及重氮法检测血清中胆红素水平，建立基于 ALB、BIL、AFP、AFP-L3 和 DCP 的 BALAD-2 模型，对随访资料完整的 41 例原发性肝癌患者动态观察治疗前后 BALAD-2 模型变化，分析 BALAD-2 模型与肝癌患者短期疗效的关系。
结果 GALAD 模型评分与患者的性别和年龄显著相关，差异有统计学意义,多数肝癌患者伴有乙肝病毒感染，肝硬化是肝癌的高危因素；肝癌患者血清 AFP、AFP-L3、DCP 水平以及 GALAD 模型评分均显著高于肝脏良性疾病组(P<0.05)和表观健康对照组(P<0.05)，差异均有统计学意义；GALAD 的特异性（94.3%）和准确性（60.8%）均高于 AFP（分别为 85.1%和 55.7%）、AFP-L3(分别为 71.3%和 55.0%）、DCP（分别为 85.1%和 59.1%）,特异性(95.1%)低于 AFP-L3(97.1%)和 DCP(97.1%)，高于 AFP(90.2%),研究表明，GALAD 模型诊断肝癌优于单一指标；肿瘤控制组治疗后 AFP、AFP-L3、DCP 水平以及 BALAD-2 较治疗前均显著下降（P<0.05）差异有统计学意义；肿瘤进展组 AFP、AFP-L3、DCP 和 BALAD-2 均未显著下降（P>0.05）。
结论 GALAD 模型可提高原发性肝癌的早期诊断率，BALAD-2 模型有助于肝细胞癌患者短期疗效评估。

PO-0102

聚乙二醇沉淀法预处理甲状腺激素异常增高 1 例

胡家伦
复旦大学附属华山医院

聚乙二醇（Polyethylene glycol，PEG）是一种水溶性的非离子多聚物，最早用于提纯免疫球蛋白、沉淀一些细菌和病毒，近年来广发用于核酸和酶的分离提纯。PEG 试剂溶解度大，在水中占据大部分空间，由于空间和水的排斥作用，PEG 具有改变蛋白质溶解度的非特异性能力，因此能作为蛋白质沉淀剂。当血清中存在一系列蛋白质均可能干扰甲状腺激素的检测，而使测定结果出现假性增高，从而导致误诊和误治。本文以 PEG 沉淀法预处理甲状腺激素异常增高病例进行分析讨论。

PO-0103

分析 2808 例 7 种肿瘤相关抗原自身抗体联合检测在肺癌早期筛查中的诊断意义

孙璐璐
吉林大学第一医院

由于疾病的隐匿性和复杂性，北方地区的肺癌发病特点通常表现为：确诊肺癌的多数患者发现即处于晚期，远期存活率较低。除影像学检查和传统的肺癌血清学标志物检测外，即使是处于肺癌发病的高风险人群，可以提供肺癌的早期筛查诊断的检测手段仍很少。

目的 探讨联合检测 7 种肿瘤相关抗原自身抗体（p53、GAGE7、PGP9.5、CAGE、MAGEA1、SOX2、GBU4-5 抗体）在肺癌早期筛查患者中的检出水平，评估自身抗体检测在早期肺癌筛查策略中的诊断潜力。

方法 收集我院 2019 年 1 月至 2021 年 4 月期间，共 2808 例初次行 7 种肺癌相关抗原自身抗体检测的患者（包括肺癌患者、体检健康者、肺部良性疾病和患有其他疾病或癌症的患者）。用酶联免疫吸附法联合检测其血清中 7 种自身抗体的水平，对不同分组的患者进行敏感性、特异性、年龄和性别、不同病理特征的阳性率进行比较分析，绘制 ROC 曲线分析其对肺癌的诊断效能。

结果 7 种自身抗体联合检测可以区分肺部疾病的良、恶性病变，其结果与健康体检人群差异明显。对已确诊肺癌的患者，7 种自身抗体水平均高于健康体检人群、肺部良性疾病患者和其他疾病或癌症患者，差异均有统计学意义(P 均<0．05)。7 种自身抗体联合检测在确诊肺癌的患者中的敏感性为 69.00 %，特异性为 87.30 %，在肺癌患者血清中检测的 7 种抗体中，至少有 1 项抗体浓度显著升高，多表现为 2 至多项抗体浓度同时升高。对患者不同年龄或性别、不同病理特征、或同一疾病的不同进展阶段进行统计分析 7 种抗体浓度水平，其表现没有明显统计学差异。同时对全部受试群体中的 352 例进行影像学检查患者的结果比较，为影像学上发现的直径小于 8mm 的肺部结节的判断及后续治疗方案提供了一项新的辅助诊断方法。

结论 联合检测 7 种肿瘤相关抗原自身抗体可以提供较为灵敏和特异的血清学检查，弥补传统血清学标志物在肺癌早期诊断方面的限制，降低肺癌的早期筛查成本。临床患者对此类仅需采血即可实现的便捷检查方法的接受程度较高。同时，此类血清学检测方法可与放射影像学和其他诊断策略配合使用，促进早期临床干预，实现早发现早治疗，提高患者的远期存活率，并为评估肺癌患病风险和鉴别诊断提供有效参考信息。

PO-0104

2016 年 11 月~2018 年 4 月哈尔滨医科大学附属第一医院胃泌素释放肽前体在肺癌中的临床意义

史永胜、金英玉
哈尔滨医科大学附属第一医院

研究目的和背景肺癌是世界上各国家和地区发病率和死亡率最高的恶性肿瘤之一，在我国城市肺癌的发病率和死亡率占所有恶性肿瘤的第一位，而且在我国农村上升速度也很快，肺癌对我国人民健康危害最严重。肺癌又分小细胞肺癌和非小细胞肺癌，小细胞肺癌和少数非小细胞肺癌肿瘤细胞产生和分泌胃泌素释放肽前体(Pro-GRP)小细胞肺癌患者(SCLC)血清中胃泌素释放肽前体(Pro-GRP)浓度升高显著，胃泌素释放肽前体(Pro-GRP)对小细胞肺癌(SCLC)诊断灵敏性和特异性明显高于其他十一项肺癌相关肿瘤标志物，对可疑肺癌而不能获得病理的患者:胃泌素释放肽前体有助于鉴别诊断小细胞肺癌和非小细胞肺癌患者。对小细胞肺癌患者疗效监测和再次病发诊断都优于神经元特异性烯醇化酶(NSE)等

PO-0105

天花粉蛋白通过影响 Foxp3 的泛素化水平增强 CD4+Treg 的体外诱导的初步研究

宣彬彬[1]、丁旭苹[2]、侯亚菲[2]、王雪[2]、武娇祥[1]、孙寒晓[1]、谭美玉[1]、盛慧明[1]、路丽明[2]
1. 上海交通大学医学院附属同仁医院
2. 上海市免疫学研究所

目的 我们前期研究发现中药天花粉蛋白（Trichosanthin，Tk）具有负向免疫调节的特性，体外低浓度即可提高 CD4+CD25+Foxp3+Treg 细胞诱导比例，但分子机制不明。Foxp3 作为 Treg 细胞的特异性转录因子，驱动 Treg 细胞的分化和功能行使。最新研究显示 Foxp3 蛋白的表达和稳定性受控于泛素化水平的修饰，如去泛素化酶成员 USP7（Ubiquitin specific peptidase 7）在维持 Foxp3 蛋白稳定性方面发挥着重要作用。我们研究关注 Tk 提高 Foxp3+Treg 细胞诱导比例，发挥免疫调节作用是否与其对 Foxp3 蛋白的泛素化水平的作用相关，Tk 是否通过激动去泛素化酶 USP7 的活性促进 Foxp3 蛋白的稳定性，换言之，本部分论文旨在探讨 Tk 是否可通过激动 USP7 来抑制 Foxp3 蛋白的泛素化降解，进而诱导增强 Treg 细胞发挥免疫调节功能。
方法 1．将 C57BL/6 雌性小鼠脾脏取出并制备淋巴细胞悬液，并通过与 Anti-CD3 mAb、Anti-CD28 mAb、TGF-β、IL-2 以及 Tk 进行共培养，使用流式细胞术检测 Tk 在体外对 Treg 细胞诱导增殖的影响；2. 构建稳定表达 Foxp3 基因的 HEK293T 细胞系，使用 Western Blot 检测 Tk 对 Foxp3 蛋白表达以及泛素化水平的作用；3.使用蛋白芯片、BLI 和 SPR 分析检测 Tk 与 USP7 之间的分子互作，并进一步探究 Tk 对 USP7 酶活性的影响。
结果 1.体外 Treg 细胞诱导体系中，Tk 的加入使 Treg 细胞的诱导增殖比例显著提升，Foxp3 蛋白的表达量明显升高；2.蛋白芯片、BLI 和 SPR 亲和力检测结果表明 USP7 与 Tk 可在体外发生紧密结合，BLI 检出二者 KD 值为 2.59×10-11（2.59E-11），提示二者亲和力很强；3.酶和底物实验表明 Tk 可显著增强 USP7 的酶活性，从而降低 Foxp3 蛋白的泛素化降解水平。

PO-0106

基于纳米抗体和介孔碳的电化学免疫传感及其在 CP4-EPSPS 检测中的应用研究

孙倩[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学附属中大医院临床检验医学中心
3. 东南大学江苏省重症医学重点实验室

转基因作物的商业化种植在提高农业生产力的同时也引发了一系列涉及环境安全、人类健康等方面的问题。农杆菌 CP4 株的 5-烯醇式丙酮酰莽草酸-3-磷酸合酶（CP4-EPSPS）对光谱高效除草剂草甘膦具有较高的天然抗性，被认为一种潜在的转基因作物筛选的生物标志物。因此，实现 CP4-EPSPS 的灵敏特异性检测对转基因作物种植工程具有重要意义。而传统的液相色谱质谱联用法、聚合酶链式反应、酶联免疫吸附法等 CP4-EPSPS 检测策略往往因灵敏度较低、耗时较长或需要昂贵的设备，不适合日常使用。电化学免疫传感具有检测限较低、灵敏度较高、特异性较好和操作简便等优点，是一种在高效灵敏检测分析领域颇具潜力的检测方式。本工作通过耦合纳米抗体、有序介孔碳（OMC）和硫堇（Th）成功构建了对 CP4-EPSPS 具有高灵敏度和高选择性的电化学免疫传感器。其中，以免疫的双峰驼中筛选出的纳米抗体作为捕获剂比传统抗体表现出更高的稳定性和更强的耐热性；OMC 为组装氧化还原探针 Th 提供了具有高表面积、导电性和生物相容性的平台，并进一步耦联了大量捕获纳米抗体。通过差分脉冲伏安法在 0.001 至 100 $ng \cdot mL^{-1}$ 的宽线性范围内对 CP4-EPSPS 进行测定，检测限低至 0.72 $pg \cdot mL^{-1}$，比先前报道的工作低了 3 个数量级。该

电化学免疫传感器在 CP4-EPSPS 的筛选和检测中表现出巨大的应用潜力并为食品安全检测领域开辟了新的前景。

PO-0107

一种基于微流控免疫磁珠法的新型快速 ELISA 检测平台建立

蔡栋昊[1,2]、段朝晖[2]、罗晓红[2]、周小棉[3,4]
1. 广东省第二中医院
2. 中山大学孙逸仙纪念医院
3. 广州市宝创微流控产业化研究院
4. 广州市宝创生物技术有限公司

目的 本研究以华支睾吸虫检测为对象，利用微流控与免疫磁珠的技术优势，建立一种新型快速 ELISA 分析平台，以期解决传统 ELISA 法步骤繁琐、检测时间长、自动化成本高等不足。
方法 利用 Solidwork 软件进行微流控芯片设计，采用“六连孔”设计，机械加工及化学封接方法进行生产组装。同时，通过化学偶联方式制备华支睾吸虫抗原包被免疫磁珠，以 HRP-TMB-H_2O_2 作为显色体系，利用抗原抗体特异结合原理检测华支睾吸虫 IgG 抗体。经过临床样本检测，初步建立基于微流控免疫磁珠检测平台，并从灵敏度、特异性、符合率等方面进行对比评价。
结果 经过条件优化和验证，初步建立了一种基于微流控免疫磁珠原理的华支睾吸虫 IgG 抗体检测平台，整个实验过程仅需少量试剂用量，耗时约 30min 即可完成检测。方法学评价显示，与粪检结果比较，自建微流控免疫磁珠检测平台符合率为 97.2%，满足定性检测方法要求。灵敏度、特异性分别达到 96.6%、97.9%。
结论 本研究初步建立了一种基于微流控磁珠免疫原理的新型 ELISA 检测平台。该方法具有操作简便、耗时短、试剂及样本用量少等特点，满足临床定性检测项目要求，解决了传统 ELISA 检测方法的不足，具有良好的市场应用前景。

PO-0108

PD-L1 exosomes as predictive markers of immunotherapy for head and neck squamous cell carcinoma

Juan Wang[1]、Qing Wang[1]、Guoqiang Du[2]
1. The Affiliated Hospital of Qingdao University
2. 青岛市市立医院东部院区

Objective Head and neck squamous cell carcinoma (HNSCC) seriously affects the life quality of patients. PD-1/PD-L1 immune checkpoint inhibitor therapy has become the first-line treatment for HNSCC, however, it is not effective for all patients. Study has reported that the upregulation of PD-L1 is associated with tumorigenesis and poor prognosis of gastric cancer. Thus, PD-L1 exosomes can be used as predictive markers for the choice of PD-1/PD-L1 immune checkpoint inhibitor treatment.
Method In the present study, the expression of PD-L1 in HNSCC was detected by immunohistochemistry staining and Western blot in clinical samples. The exosomes were extracted from the cultural supernatant of HNSCC cells. In addition, the expression of PD-L1 on the exosomes was detected by FCM flow cytometry.
Result The results showed that PD-L1 was overexpressed in HNSCC tissues. Moreover, PD-L1 was overexpressed on the exosomes extracted from the cultural supernatant of HNSCC cells.
Conclusion The detection of the expression of PD-L1 on the exosomes will provide predictive value for the treatment of HNSCC via immune checkpoint inhibitors, which will help us to identify the patient population more likely to benefit from the immune checkpoint inhibitors.

PO-0109

妊娠期糖尿病患者肠道菌群代谢产物 TMAO 的检测意义初探

乐江漫[1,2]、盛慧明[2]
1. 上海市嘉定区妇幼保健院
2. 上海交通大学医学院附属同仁医院

目的 探讨血浆氧化三甲胺（TMAO）水平与妊娠期糖尿病（GDM）的相关性。
方法 回顾性分析 2019 年 3 月至 12 月于上海市嘉定区妇幼保健院定期进行产前检查的单胎妊娠孕妇 272 例，其中妊娠期糖尿病组（GDM 组）178 例，正常孕妇组（non-GDM 组）94 例。分别记录两组的年龄、孕前 BMI 等一般特征、孕早期血糖、血脂等血清学检测指标和口服糖耐量试验（OGTT）0h、1h、2h 血糖水平。采用液相色谱质谱联用分析法检测血浆 TMAO 浓度，多因素 Logistic 回归分析血浆 TMAO 与妊娠期糖尿病的相关性。
结果 GDM 组与 non-GDM 组孕妇孕早期甘油三酯（TG）、空腹血糖（FBG）、孕中 TMAO 水平及 OGTT 0h、1h、2h 血糖水平分别为 1.56mmol/L（1.22,2.10）与 1.43mmol/L（1.08,1.68）（ t=2.995,p=0.003 ） 、 4.55mmol/L （ 4.25,4.91 ） 与 4.34mmol/L （ 4.14,4.59 ）（t=3.774,p=0.000）、1.35umol/L (1.01,1.86)与 1.14umol/L (0.82,1.67)（t=2.390,p=0.017）、4.74mmol/L (4.41,5.24)与 4.34mmol/L (4.17,4.60)（t=7.050,p=0.000）、9.88mmol/L (8.80,10.50)与 6.68mmol/L (5.68,7.82)mmol/L（t=11.100,p=0.000）、8.78mmol/L (8.13,9.56)与 6.12mmol/L (5.40,6.80)（t=11.219,p=0.000），差异均有统计学意义（p<0.05）。多因素 Logistic 回归分析结果显示，在校正了多个单因素变量后，TMAO（OR1.514,95%CI:1.079-2.125）水平高仍是 GDM 发病的独立危险因素。
结论 孕中期血浆 TMAO 水平与发生妊娠期糖尿病的风险呈正相关，肠道菌群有望成为 GDM 防治新靶点。

PO-0110

CX3CR1 肠道巨噬细胞通过平衡肠道菌群和调节免疫功能治疗溃疡性结肠炎的机制研究

田文杰、王学锋
上海交通大学医学院附属瑞金医院

目的 肠道巨噬细胞与肠道菌群之间的相互影响对平衡肠道稳态，预防溃疡性结肠炎（ulcerative colitis，UC）的发生至关重要。$CX3CR1^{high}$ 肠道巨噬细胞在抗炎、保护肠粘膜和吞噬菌群中都发挥着重要的作用，然而减少 $CX3CR1^{high}$ 肠道巨噬细胞是否能引起肠道菌群组成的改变进而影响 UC 的发生是未知的，因此本研究主要探讨了 $CX3CR1^{high}$ 肠道巨噬细胞是否能够改变肠道菌群组成以及这个改变对溃疡性结肠炎的作用。
方法 把 10 只正常 C57 小鼠平均分成 2 组，分别是实验组和对照组，实验组予以腹腔注射巨噬细胞耗竭剂氯氟松，对照组注射同等剂量的 PBS，24h 后予以处死，首先，留取结肠组织提取肠固有层淋巴细胞进行流式细胞术分析巨噬细胞耗竭情况；其次，留取粪便 DNA 进行 16SrRNA 测序分析肠道微生物多样性；最后，借助菌群敲除和粪便移植实验评估受 $CX3CR1^{high}$ 肠道巨噬细胞影响的菌群对葡聚糖硫酸钠（dextran sulphate sodium，DSS）诱导的肠炎的作用。
结果 在稳态下，$CX3CR1^{high}$ 肠道巨噬细胞对巨噬细胞耗竭剂较为敏感，耗竭效率约为 60%；$CX3CR1^{high}$ 巨噬细胞减少后，肠道菌群的多样性显著下降，菌群组成也发生了明显变化，主要表现为变形杆菌属、肠球菌属和葡萄球菌属等有害菌明显减少，拟杆菌属等有益菌明显增多；借助广谱抗生素敲除小鼠的肠道菌群，然后移植氟氯松处理 24h 后的小鼠的粪便，发现 DSS 诱导肠炎的症状明显减轻，肠道固有层淋巴细胞中 Th17 和 $IL\text{-}17A^{+}$ $INF\text{-}\gamma^{+}T$ 细胞的比例也明显下降。

结论 CX3CR1^{high}巨噬细胞耗竭有可能通过平衡肠道菌群，调节 Th17 和 IL-17A^{+} INF-γ^{+}T 细胞比例从而改善 DSS 肠炎。本研究为有效治疗肠炎提供了新的实验依据。

PO-0111

2016-2020 年南京地区住院患儿呼吸道合胞病毒感染的流行特点分析

温忠亭、徐静茹
南京医科大学第二附属医院

目的 回顾 2016-2020 年本院住院 14 岁以下儿童因合胞病毒（RSV）引发的呼吸道疾病的感染情况，分析南京地区儿童 RSV 的流行特点。为临床防治儿童 RSV 感染提供理论指导和科学依据。
方法 收集 2016 年 4 月-2020 年 4 月南京城区及周边江宁、浦口、六合郊区等地 14 岁以下因呼吸道感染住院患儿病例共 10625 例，用直接荧光法检测呼吸道分泌物中 RSV 抗体。应用 SPSS18.0 软件对 RSV 感染资料进行统计学分析。
结果 1. RSV 感染儿 533 例，感染率为 5.01%。男女感染率分别是 5.41%和 4.50%.有显著差异。
2. RSV 感染年龄分布于 0-14 岁之间，其中 0-28 天(新生儿组）、29 天-1 岁（婴儿组）、1-3 岁（幼儿组）、3-14 岁（儿童组）感染率分别为 4.12%、8.14%、4.45%、2.22%，婴儿组感染率最高，各年龄段有显著差异。
3. RSV 感染引发的疾病主要为肺炎、毛细支气管炎和哮喘。其中肺炎感染最多，占所有疾病的 71%，婴儿组感染率最高为 5.64%。
4. RSV 感染主要分布于秋冬两季,占全年感染人数的 75%，其中冬季感染率最高为 7.44%，其次是秋季，感染率为 6.03%。
5. 针对近四年南京流行季节气温研究，气温平稳 RSV 无明显变化,阳性率在较冷气温偏高。
6. 南京地区 RSV 感染符合华东、华中、华北地域流行特点，与东北、华南、西南、西北、台湾等地区的 RSV 感染有地域性差异。
结论 近年来南京地区 RSV 感染趋于平稳，儿童 RSV 感染的防治工作需要全年全区域进行，其重点是针对秋冬季节对 0-3 岁儿童（尤为男性）肺炎的防治。

PO-0112

流式荧光免疫法检测肝病相关自身抗体的评价及其对原发性胆汁性胆管炎的诊断价值

王战、王麟、姚远、刘静、孙桂荣、刘明军
青岛大学附属医院

目的 应用多重微球流式荧光免疫法（MBFFI）检测肝病相关自身抗体，将 MBFFI 定量检测肝病相关自身抗体的结果与免疫印迹法（IBT）进行比较与分析评价，进一步评估其对原发性胆汁性胆管炎（PBC）的诊断价值。
方法 选取 2018 年 8 月至 2020 年 12 月于青岛大学附属医院就诊并临床确诊的 PBC 患者 340 例。其他疾病组包括自身免疫性肝病（AIH）患者 81 例与系统性红斑狼疮（SLE）患者 62 例。健康对照组包括健康体检者 117 例。分别应用 MBFFI 与 IBT 两种检测方法检测 600 例受试者血清中五种肝病相关自身抗体，应用一致性检验比较检测结果的一致性；应用灵敏度、特异度、阳性预测值、阴性预测值、约登指数及 AUC 值等指标评估 MBFFI 检测 AMA-M2、gp210 与 sp100 抗体对 PBC 的诊断价值。

结果 总体样本中两种方法检测一致性最好的抗体为 AMA-M2（Kappa=0.895）。MBFFI 与 IBT 检测 PBC 患者血清 AMA-M2、gp210、sp100、SLA 与 LC-1 抗体的一致率分别为 95.00%，88.24%，92.05%，97.94%，96.76%；Kappa 值分别为 0.874，0.713，0749，0.393，0.361；AIH 组五种抗体的一致率分别为 85.19%，91.36%，91.36%，97.53%，96.30%；Kappa 值分别为 0.289，0.318，0.327，0.738，0.556。PBC 组患者检测 AMA-M2、gp210、sp100 抗体的一致性高于 AIH 组。AIH 组患者检测 SLA、LC-1 抗体的一致性高于 PBC 组。MBFFI 检测 PBC 组 AMA-M2、gp210 与 sp100 抗体的灵敏度分别为（72.06%、28.24%、22.35%）；gp210 与 sp100 两种抗体联合检测的灵敏度（44.71%）高于该两种抗体的单项检测，AMA-M2、gp210 与 sp100 三种抗体联合检测的灵敏度（82.65%）高于该 3 种抗体的单项检测。三种抗体联合检测诊断 PBC 的 AUC 值最大（0.9070）。
结论 MBFFI 检测 AMA-M2、gp210 与 sp100 抗体与 IBT 检测结果相比一致性较好。MBFFI 联合检测 AMA-M2、gp210 和 sp100 抗体对 PBC 的诊断价值更大。
MBFFI 可能成为 PBC 相关自身抗体的常用检测方法。

PO-0113

ZNF148 在儿童类风湿关节炎中的作用机制及信号通路研究

黄伟
江西省儿童医院

目的 本课题前期研究显示，ZNF148 对儿童类风湿关节炎的发生发展具有显著相关性并且 ZNFΔN 与 ZNF148FL 存在着功能的拮抗性。另有实验证实 TNF-α 可通过上调类风湿关节炎人滑膜肉瘤细胞系（SW982）细胞中的 miR-147 表达，miR-147 通过再调控转录因子 ZNF148 的表达，从而影响 SW982 细胞的凋亡。然而，类风湿关节炎有关 ZNF148 的下游信号通路并未十分明确，这使得我们研究探索 ZNF148 下游特异的靶基因变得更加有意义。
方法 通过分析 TCGA data，检测 ZEB-AS1 表达水平与儿童类风湿关节炎是否存在相关性。Q-PCR 分析儿童类风湿关节炎 SW982 细胞中 ZEB-AS1 和 SDHA、SDHB 的表达水平。
结果 Q-PCR 分析结果表明 ZEB-AS1 水平和 SDHA/SDHB 的表达水平均呈负相关，且 ZEB-AS1 水平与 SDHB 的相关性更高。在 ZEB1-AS1 高表达 SW982 细胞株中，转染 ZEB1-AS1 SiRNA, 然后利用 QPCR 分析 ZEB-AS1 表达水平降低后，细胞 SDHA 和 ZEB 的表达水平变化。结果表明 ZEB-AS1 表达水平降低后，SDHA mRNA 表达水平升高约 1.7 倍；ZEB-AS1 表达水平降低后，转录因子 ZEB1 mRNA 表达水平降低 90%（均 P<0.05）。
结论 RNA ZEB-AS1 通过调控转录因子 ZEB1 的表达，影响了线粒体三羧酸循环相关蛋白 SDH 的表达，引起细胞内琥珀酸含量升高；琥珀酸含量升高抑制了 TET 家族蛋白活性，细胞内 CIMP 水平升高，最终影响 SW982 细胞的凋亡可能是导致类风湿关节炎发生的重要原因。

PO-0114

The imbalance of TIGIT and CD226 on Treg in recurrent spontaneous abortion patients

段忠亮、应春妹
复旦大学附属妇产科医院

Objective To evaluate the role of TIGIT and CD226 on peripheral Treg cells in the patients of recurrent spontaneous abortion (RSA).
Methods Detecting the proportion of CD226 and TIGIT on Tregs in pregnant women and RSA patients, as well as cytokines TGF-β, IL-10 and IFN-γ in different Treg subsets, from 31 normal pregnant women and 26 RSA patients.

Results Compared with normal pregnant women, the expression of TIGIT on Tregs was lower in RSA patients (34.35±8.59% vs 47.52±9.52). The ratio of CD226 to TIGIT in RSA group (2.44±1.02) was higher than that in control group (1.56±0.95). TGF-β and IL-10 in TIGIT+ Treg were higher than that in TIGIT- Treg, and IL-10 in CD226+ Treg was higher, while IFN-γ in these subsets showed no significant difference. The TIGIT+CD226+ Treg cells subset was significantly higher in RSA patients.
Conclusions TIGIT and CD226 molecules may play a role in maintaining maternal-fetal immune tolerance through Treg, and there is an imbalance of TIGIT and CD226 on Treg in recurrent spontaneous abortion patients.

PO-0115

Non-neutralizing epitopes induce robust hepatitis C virus (HCV)-specific antibody-dependent CD56+ natural killer cell responses in chronic HCV-infected patients

Lu Long[1]、Tao Shen[2]
1. Shanghai Ninth People's Hospital, Shanghai JiaoTong University School of Medicine
2. 北京大学医学部基础医学院病原生物学系

Natural killer (NK) cell-mediated antibody-dependent cellular cytotoxicity (NK-ADCC) is of considerable interest in viral infection. However, little is known about NK-ADCC responses in chronic hepatitis C virus (HCV) infection. In this study, impaired non-specific antibody-dependent CD56+ NK cell responses were observed in chronic HCV infection, as shown by decreased degranulation (extracellular CD107a expression) and interferon (IFN)-γ production in response to antibody-bound P815 cells. A peptide pool composed of epitopes recognized by anti-HCV-E1/E2 antibodies could induce pronounced HCV-specific antibody-dependent NK cell responses in sera from approximately half the chronic HCV carriers. Additionally, HCV-specific epitopes with the capacity to induce robust NK-ADCC activity were identified. Five linear NK-ADCC epitopes (aa211-aa217, aa384-aa391, aa464-aa475, aa544-aa551 and aa648-aa659 of the HCV envelope) were identified and do not overlap with putative linear neutralizing epitopes. This study revealed the dysfunctional characteristics of antibody-dependent CD56+ NK cell responses in chronic HCV carriers. The key non-neutralizing NK-ADCC epitopes identified in this study may act as new targets for immunological intervention.

PO-0116

Comparison of analytic and clinical performance of two immunoassays for detecting thyroid-stimulating receptor antibody in the diagnosis of Graves' disease

Yao Hu、Ming Guan、Buyue Zhang、Yi Cen、Wenqing Wu、Mingying Huang
Department of Laboratory Medicine, Huashan Hospital, Shanghai Medical College, Fudan University

Objective Differentiate between Thyroid stimulating hormone (TSH) receptor (TSHR) autoantibodies (TRAbs) types and its heterogeneous molecular is essential for Graves' disease (GD) diagnosis. The aim of the present study was to evaluate the analytical and clinical performance of two immunoassay for diagnosis of GD, the Immulite thyroid-stimulating immunoglobulin (TSI) and Elecsys Anti-TSH receptor (TSHR) assay.
Methods Precision and analytical measurement range were assessed using pooled samples of patients. The comparison between the two methods was evaluated using 579 clinical samples (81 patients with untreated GD, 85 patients with treated GD, 79 patients with Hashimoto's thyroiditis,

103 patients with thyroid nodules, 96 patients with hypothyroidism, 59 patients with nontoxic goiter, and 56 patients with thyroid cyst and 20 euthyroid healthy subjects), and receiver operating characteristic (ROC) curves were drawn using the final diagnosis as reference. Clinical sensitivity and specificity, accuracy, positive predictive value (PPV) and negative predictive value (NPV) were calculated for the two tests. The inconsistent results of the two methods were investigated and confirmed by the clinical diagnosis.
Results The repeatability and intermediate imprecision coefficient of variation (CV%) of the TSI assay were 3.8% and 4.1% at 0.95 IU/L, and 3.5% and3.6% at 19.5IU/L, respectively. The assays were linear over a range of 0.27 to 38.5 IU/L. The Anti-TSHR assay had repeatability and intermediate imprecision 7.0% and 7.8% at 1.5IU/L, and 1.7% and 2.0% at 21.0 IU/L, respectively. The analytical measurement range was from 1.0 to 38.5 IU/L. There was a high correlation between the quantitative results of the two methods (correlation coefficient r= 0.930). The cut-off value obtained by ROC analysis for TSI assay was 0.7 IU/L with sensitivity of 93.7% and specificity of 85.1%, while it was 2.5 IU/L for Anti-TSHR assay with sensitivity of 92.5% and specificity of 86.7%. An overall qualitative agreement of 91.5% between two methods was observed. Among 44 patients with discordant qualitative results, the TSI assay provided more satisfactory results consistent with clinical diagnoses.
Conclusion The TSI assay showed excellent analytical performance and provided a high PPV for GD.

PO-0117

Establishment of reference intervals of monomeric prolactin to identify macroprolactinemia in Chinese patients with increased total prolactin

Yao Hu、Ming Guan、Jiajin Ni、Buyue Zhang、Wei Cheng、Huating Zhang
Department of Laboratory Medicine, Huashan Hospital, Shanghai Medical College, Fudan University

Background Macroprolactin is responsible for pseudohyperprolactinemia and is a common pitfall of the prolactin immunoassay. We aimed to determine the frequency of macroprolactinemia in Chinese hyperprolactinemic patients using monomeric prolactin discriminated by precipitation with polyethylene glycol (PEG).
Methods Post-PEG monomeric prolactin gender-specific reference intervals were established for the Elecsys immunoassay method (Roche Diagnostics) using sera from healthy female (n = 120) and male (n = 120) donors. The reference intervals were validated using 20 macroprolactinemic (as assessed by gel filtration chromatography (GFC)) sera samples, and presence of monomeric prolactin was discriminated by GFC. Patients with high total prolactin were then screened by PEG precipitation to analyze macroprolactin. The demographic and biochemical details of patients with true hyperprolactinemia and macroprolactinemia were compared.
Results Reference intervals for monomeric prolactin in females and males were 3.4–18.5 and 2.7-13.1 ng/mL, respectively. Among 1140 hyperprolactinemic patients, macroprolactinemia was identified in 261 (22.9%) patients while the other 879 (77.1%) patients were diagnosed with true hyperprolactinemia. Menstrual disturbances were the most common clinical feature in both groups. Galactorrhea, amenorrhea, and visual disturbances occurred more frequently in true hyperprolactinemic patients ($P < 0.05$).
Conclusions The prevalence of macroprolactin in Chinese patients with hyperprolactinemia was described for the first time. Monomeric prolactin concentration, along with a reference interval screening with PEG precipitation, provides a diagnostic approach for hyperprolactinemia with improved accuracy.

PO-0118

抗中性粒细胞胞浆抗体间接免疫荧光法和免疫印迹法不一致结果原因分析

刘婷、陈国敏、龙贵萍、彭潮燕、付正乾、苏蒙
贵州金域医学检验中心有限公司

目的 对中性粒细胞胞浆抗体的间接免疫荧光法和免疫印迹法不一致结果进行分析。
方法 采用间接免疫荧光法和免疫印迹法同时检测 10178 例临床样本的抗中性粒细胞胞浆抗体，并对不一致的结果进行回顾性分析。
结果 分析 10178 例样本结果，109 例 C-ANCA 和 PR3 结果不符合；628 例 P-ANCA 与 MPO 结果不符合。排除病人资料不全的病例，共 301 例不一致结果入选进行分析。301 例样本中男女比例为 1:2.46；疾病分类中血管炎疾病为 26 例，其中包含 ANCA 相关性血管炎 5 例，自身免疫性疾病 127 例，最常见为系统性红斑狼疮和类风湿性关节炎，其他非自身免疫疾病 148 例，其中慢性肾功能衰竭最常见。ANCA 结果不一致的分型四种中以第一型 C-ANCA(+)/PR3(-)（53/301,17.6%）和第三型 P-ANCA(+)/MPO(-)（209/301,69.4%）为常见。
结论 间接免疫荧光法和免疫印迹法两种方法学联合检测 ANCA 因方法学不同和检测原理需要根据临床病例情况和实际结果具体分析，对血管炎和相关疾病的诊断、分类和预后有重要意义。

PO-0119

AFP 和 PIVKAⅡ检测对肝癌的诊断价值及其与肝癌大小的相关性研究

张凤、司元全
山东第一医科大学附属省立医院

目的 探讨甲胎蛋白（AFP） 和异常凝血酶原Ⅱ（PIVKAⅡ）检测对原发性肝癌(PHC)的诊断价值以及二者浓度与肝癌肿瘤大小、病理分级的相关性。
方法 收集 77 例 PHC 患者和 80 例良性肝病患者的血清，分别进行 AFP 和 PIVKAⅡ的检测，采用受试者工作特性曲线(ROC)评估二者在 PHC 诊断的应用价值，同时分析二者含量与肝癌患者病理分级、癌灶大小的关系。
结果 经 Mann-Whitney U 检验，PHC 组与对照组比较，AFP 和 PIVKAⅡ二项指标检测结果差异均具有统计学意义（Z 值分别为 4.94、8.03，P 均<0.01）；AFP 和 PIVKAⅡ单独运用诊断 PHC 的 ROC 曲线下面积（AUC）分别为 0.728(95% CI，0.650～0.807)、0.871(95% CI，0.814～0.929)，血清 PIVKAⅡ用于诊断 PHC 的诊断价值优于 AFP（Z=1.75，P<0.05）；PHC 患者血清 AFP、PIVKAⅡ浓度与肿瘤切面积呈正相关(r 值分别为 0.310，0.686，P 均<0.01)；不同病理分级的 PHC 患者血清 AFP、PIVKAⅡ浓度差别具有统计学意义（P 均<0.05）。
结论 检测 PHC 患者血清 AFP 和 PIVKAⅡ对肝癌诊断具有重要意义，同时发现 PIVKAⅡ的诊断价值优于 AFP，且 AFP 和 PIVKAⅡ浓度对于判断癌灶的大小及病理分级具有重要临床价值。

PO-0120

血清 PIVKA-II 联合 FIB 对 AFP 阴性肝癌患者的预后监测价值

张永瑞[1]、孙娅红[2]
1. 云南省肿瘤医院
2. 昆明医科大学

目的 探讨 PIVKA-II、FIB 及其联合应用在 AFP 阴性肝癌中的预后价值，为肝癌患者的预后评估提供实验室依据。
方法 选取 2017 年 10 月至 2019 年 12 月期间云南省肿瘤医院收治的确诊为 AFP 阴性的原发性肝癌患者，回顾性收集其初诊时的肝功能及凝血指标检测值，并进行跟踪随访。运用 R 语言、SPSS22.0 统计分析，探讨 PIVKA-II 联合 FIB 在 AFP 阴性肝癌患者预后评估中的临床价值，评估单个指标、联合指标对 AFP 阴性肝癌患者预后之间的关系并对其进行验证。
结果 本研究共纳入研究对象 135 人。截止随访时间，失访 23 人（17%）根据随访结局分为存活组（48 例，占 42.9%）和死亡组（64 例，占 57.1%）。本研究结果表明年龄、FIB 与 AFP 阴性 PHC 预后独立相关，可作为 AFP 阴性 PHC 的预后因素。联合 PIVKA-II 和 FIB（AUC=0.728，95%置信区间 0.634-0.822, P=<0.001，最佳临界值 0.55，灵敏度 58.3%，特异度 87.5%）对 AFP 阴性肝癌患者的预后监测效果优于 PIVKA-II（AUC=0.625，95%置信区间 0.521-0.729,P=0.024<0.05，最佳临界值 156.825mAU/ml，灵敏度 91.7%，特异度 41%）、FIB（AUC=0.274，95%置信区间 0.180-0.368，P=<0.001，最佳临界值 3.245g/l，灵敏度 41.7%，特异度 12.5%）单个指标对 AFP 阴性肝癌患者的预后监测效果。基于患者年龄、性别、乙肝病史、FIB 与 PIVKA-II 联合建立 Cox 回归预测模型，对模型进行验证评估后，显示模型预测能力、准确性和临床实用性较好。
结论 本研究结果表明了年龄、FIB 与 AFP 阴性 PHC 预后的独立相关。可作为 AFP 阴性 PHC 的预后因素。联合 PIVKA-II 和 FIB 对 AFP 阴性肝癌患者的预后监测效果优于 PIVKA-II、FIB 单个指标对 AFP 阴性肝癌患者的预后监测效果。联合患者年龄、性别、乙肝病史、FIB 与 PIVKA-II 建立预测模型，并对模型进行验证评估后，显示模型预测能力、准确性和临床实用性较好。表明建立的 Cox 预测模型可作为监测 AFP 阴性 PHC 预后的工具。具有一定的临床使用价值。

PO-0121

第四代 HIV 诊断试剂在重组新型冠状病毒疫苗受试者中 HIV 抗体假阳性原因分析

许成新
上海交通大学附属第一人民医院嘉定分院

目的 与免疫印迹试验(WB)结果比较，分析第四代人类免疫缺陷病毒(HIV)抗体化学发光免疫分析(CLIA)诊断试剂筛查结果在重组新型冠状病毒疫苗受试者中 HIV 抗体阳性与免疫印迹试验(WB)结果不同，分析引起假阳性的原因，评估 CLIA 法 HIV 筛查在艾滋病诊断中的临床价值。
方法 CLIA 法对 2020 年 8 月－2021 年 5 月本院 5969 例患者进行 HIV 抗体初筛检测，其中选取接受 19 例重组新型冠状病毒疫苗受试者患者，HIV 第四代诊断试剂检测初筛阳性的标本，送 HIV 确诊实验室用 WB 法确证 HIV 抗体结果，记录结果并进行对比分析，探讨出现假阳性的原因。
结果 CLIA 法初筛阳性 19 例，WB 确证阳性 2 例，4 例 HIV 抗体不确定，13 例 HIV 抗体阴性。CLIA 初筛方法确证阳性率为 10.52%。WB 确证阳性患者 CLIA 法 S/CO 值为 303.20(146.50，645.68)，与确证阴性患者 S/CO 值［1.8(1.24，2.98)］和确证不确定患者 S/CO 值［1.48(1.20，3.36)］差异有统计学意义(P＜0.05)。比较 1＜S/CO≤10、10＜S/CO≤50 及 S/CO＞50 三组，WB

法获得的阳性率的差异有统计学意义(P＜0.05)。随着 S/CO 值的增高，初筛结果与确证结果阳性符合率也随之升高。

结论 重组新型冠状病毒疫苗受试者患者，CLIA 法筛查 HIV 抗体灵敏度较高，HIV 四代检测试剂存在较高的假阳性率，尤其是低 S/CO 值的标本，这与试剂同时检测 HIV 抗体和 P24 抗原有关。较高的 S/CO 值的患者 HIV 感染的风险较大，但是高 S/CO 值并不代表 HIV 感染，应进一步推进诊断试剂的研发和改进进程，助力临床精准医疗，当 1<S/CO≦10 时，实验室检测人员应依据实验检测结果，结合受检者相应病史和个体状况进行综合分析。

PO-0122

慢性乙型病毒性肝炎相关肝细胞癌患者免疫功能与性激素分泌关系的研究

袁梦娇、龚倩
复旦大学附属中山医院青浦分院

目的 探讨不同慢性乙型肝炎病毒（chronic hepatitis B virus，CHB）感染期男性患者及 CHB 相关肝细胞癌（Hepatocellular Carcinoma，HCC）患者免疫功能表达差异，及各组免疫功能与性激素分泌之间的关系，为疾病治疗监测、进展及后续治疗方面研究提供一定的临床数据。

方法 收集 CHB 患者 57 例，按照 2017 版欧洲肝病学会指南分为 4 个期：HBeAg+慢性感染期、HBeAg+慢性肝炎期、HBeAg-慢性感染期、HBeAg-慢性肝炎期，根据术中病理结果筛选出确诊为 HCC 的患者。利用检验科 FACS Canto II 流式细胞仪进行 T 淋巴、B 淋巴、Th 淋巴、NK 细胞亚群检测，HITACHI 7600 全自动生化分析仪检测补体 C3、C4，CobasE 801 全自动电化学发光分析仪采用竞争法、电化学发光法定量检测 E2、睾酮。非正态分布数据采用 t 检验非配对分析。

结果 1）病例中 HBeAg 阳性的慢性 HBV 感染和慢性 HBV 肝炎，HBeAg 阴性的慢性 HBV 感染和 HBV 肝炎各期患者年龄主要以 40 岁以上分布，其中大于 60 岁患者占 36.84%，50-59 岁患者占 29.82%，40-49 岁患者占 22.81%。2）淋巴细胞表达差异：HBeAg 阳性的慢性 HBV 感染和慢性 HBV 肝炎，HBeAg 阴性的慢性 HBV 感染和 HBV 肝炎各期各组间淋巴细胞表达，除 B 淋巴细胞外（p＜0.05），其余各组间无明显差异。3）CHB 与 CHB-HCC 患者补体、细胞因子表达差异：各组间 C3 表达差异明显（p＜0.01），各组 IL-2 表达有明显差异（p＜0.01）。4）CHB、CHB-HCC 患者性激素表达差异：CHB 与健康对照组间睾酮（TESTO）的表达有明显差异，CHB 患者 TESTO 表达高于健康对照组（p＜0.05）。

结论 随着疾病的进展，慢性 HBV 感染患者免疫状态发生变化，免疫指标可作为慢性 HBV 感染临床病情演变、治疗效果及疾病预后的参考依据。不同感染期 CHB 患者性激素睾酮表达有差异。

PO-0123

HBx 基因对 HepG2．2．15 细胞 MICA－A5．1 表达及侵袭、迁移的影响

李沛
南华大学附属第一医院

目的 探究 HBx 基因对 HepG2．2．15 细胞侵袭、迁移及主要组织相容性复合体(MHC) Ⅰ类链相关基因 A (MICA)－A5. 1 表达的影响。

方法 体外培养 HepG2．2．15 细胞系(插入 HBV 全基因组并持续表达的 HepG2 细胞) ，随机分为对照组、HBx 过表达质粒组、HBx 空载质粒组、HBx siＲNA 组、HBx siＲNA 阴性对照组，分

别转染质粒及 siRNA 后，以 CKK － 8 法分别检测 24 h、48 h 后细胞增殖情况，筛选合适药物作用时间; 以 Transwell 侵袭实验和细胞划痕实验检测各组细胞侵袭迁移能力; 以免疫印记法检测 HBx、MI- CA － A5． 1 蛋白和上皮间质转化标志蛋白 E － cadherin、Vimentin 的表达; 以酶联免疫吸附法检测各组细胞培养基中 sMICA 水平。计量资料多组间比较采用单因素方差分析，进一步两两比较采用 SNK q 检验。

结果 与对照组比较，24 h 后，HBx 过表达质粒组细胞活力升高，HBx siRNA 组细胞活力降低，差异均有统计学意义(q 值分别为 8． 268、4． 365，P 值分别为 ＜ 0． 001、0． 036) ; 48 h 后，HBx 过表达质粒组细胞活力升高，HBx siRNA 组细胞活力降低，差异均有统计学意义(q 值分别为 12. 680、7． 523，P 值均 ＜ 0． 001) 。与对照组比较，HBx 过表达质粒组细胞 HBx、MICA 及 Vimentin 蛋白表达、细胞培养基中 sMICA 水平、迁移细胞数目、侵出 Transwell 小室的细胞数目均升高，E － cadherin 表达降低(q 值分别为 9． 427、6． 697、10． 500、5． 042、22． 740、15． 720、5． 258，P 值均 ＜ 0． 05) ; HBx si R - NA 组细胞 HBx、MICA 及 Vimentin 蛋白表达、细胞培养基中 sMICA 水平、迁移细胞数目、侵出 Transwell 小室的细胞数目均降低，E － cadherin 表达升高(q 值分别为 8． 133、8． 828、7． 616、7． 673、5． 391、7． 694、6． 226，P 值均 ＜ 0． 05) 。

结论 HBx 基因调控 HepG2． 2． 15 细胞 MICA － A5． 1 表达及侵袭、迁移，上调该基因可促进 MICA － A5． 1 表达，增强 HepG2． 2． 15 细胞侵袭转移能力。

PO-0124

细胞焦亡在肿瘤发生发展及抗肿瘤免疫中的研究进展

李可馨、崔巍
中国医学科学院肿瘤医院

目的 细胞焦亡是一种不同于细胞凋亡和坏死性凋亡的促炎性细胞程序性死亡方式，研究发现细胞焦亡在肿瘤发生发展和抗肿瘤免疫反应方面均发挥一定作用。将细胞焦亡的分子机制其对肿瘤治疗中的作用，尤其是在抗肿瘤免疫中研究进展进行总结及展望，旨在为肿瘤联合免疫治疗提供新的思路。

方法 本文总结了近年来细胞焦亡在肿瘤发生发展尤其是抗肿瘤免疫中的作用，分析了基于细胞焦亡的抗肿瘤机制在肿瘤免疫治疗和联合治疗中的潜在价值。

结果 细胞焦亡主要特征为炎症小体和含半胱氨酸的天冬氨酸蛋白水解酶家族的活化及切割 Gasdermin 家族成员，从而使细胞膜出现孔洞并伴随炎性细胞因子的释放及一系列炎症反应。其中 Gasdermin 家族作为细胞焦亡发生的主要执行者。细胞焦亡在肿瘤的发生发展中常表现出促进和抑制肿瘤细胞生长的双重作用。一方面细胞焦亡可以抑制肿瘤生长，另一方面过度激活的焦亡途径也可引起大量炎症反应的发生，使正常组织或细胞长期处于炎症环境中，而增加肿瘤发生的风险，为肿瘤细胞提供适宜生存的微环境。细胞焦亡可通过促进抗肿瘤免疫反应而影响肿瘤免疫治疗的疗效。由于细胞焦亡能够激活抗肿瘤免疫反应，使肿瘤微环境由“冷”向“热”转变，因此可在免疫活性低或对免疫检查点抑制剂及其他免疫疗法无反应的肿瘤患者中诱导焦亡，或在表观遗传上沉默的肿瘤患者中诱导 GSDMD/GSDME 的表达从而促进焦亡途径的激活。T 细胞可能通过影响肿瘤细胞焦亡从而影响肿瘤免疫对肿瘤细胞的抑制作用。

结论 细胞焦亡参与肿瘤的发生发展中，并影响抗肿瘤免疫反应。通过合理的焦亡诱导剂联合免疫检查点抑制剂治疗可能增强抗肿瘤免疫活性，提高患者获益程度。

PO-0125

CCL15 在脓毒症免疫病理过程中的作用及机制研究

黄丽莉
重庆医科大学附属第一医院

目的 检测脓毒症中 CCL15 的含量，探究 CCL15 在脓毒症免疫病理中的作用和机制。
方法 ELISA 检测脓毒症患者和建立脓毒症模型后小鼠血清中 CCL15 含量；给脓毒症小鼠补充重组 CCL15 蛋白或者 PBS，探究 CCL15 对生存率的影响；通过 HE 染色和生化指标检测评估器官损伤；用流式细胞术检测吞噬细胞比例变化，用细菌感染巨噬细胞，探究 CCL15 对细胞吞噬杀伤的影响。
结果 脓毒症患者血清中 CCL15 含量较健康对照者显著增加，且脓毒症小鼠血清中 CCL15 水平也较对照小鼠显著升高；给脓毒症小鼠补充 CCL15 蛋白后，与对照组相比，小鼠生存率明显增加，生化及 HE 染色切片显示器官损伤显著改善，细菌载量降低，促进腹腔灌洗液中细胞募集。
结论 CCL15 在脓毒症中表达增加，通过促进细菌清除、改善器官损伤发挥免疫保护作用，从而改善生存率。

PO-0126

恶性肿瘤患者血清抗 Stathmin 自身抗体检测方法的建立及初步评价

陈曦、董轲
空军军医大学唐都医院

恶性肿瘤是引起患者死亡的主要诱因之一，且其发病率及死亡率呈逐年上升趋势。如能早期发现和治疗，恶性肿瘤的死亡率及预后将会大幅改善，因此探索适用于早期诊断和预防性筛查的新型肿瘤标志物至关重要。
目的 探讨不同类型肿瘤患者血清中是否存在癌蛋白 Stathmin 的自身抗体并对其检测方法进行初步评价。
方法 表达、纯化人源 Stathmin 蛋白并建立酶联免疫吸附实验（Elisa）检测血清 Stathmin 自身抗体的操作流程。应用新建立的 Elisa 方法检测 483 例恶性肿瘤患者血清和 230 例正常人血清中 Stathmin 自身抗体，统计学分析检测结果差异性。
结果 Elisa 分析显示 483 例肿瘤患者血清 1:50 稀释条件下，Stathmin 自身抗体阳性患者为 217 例，阳性率为 45%；230 例正常血清 1:50 稀释条件下，仅有 2 例为阳性，阳性率为 0.9%。不同肿瘤患者的结果如下：88 例胃癌患者血清有 48 例阳性，阳性率为 54%；96 例肝癌患者血清有 40 例阳性，阳性率为 42%；88 例直肠癌患者血清有 36 例阳性，阳性率为 41%；98 例乳腺癌患者有 35 例阳性，阳性率为 36%；113 例肺癌患者有 58 例阳性，阳性率为 51%。恶性肿瘤患者阳性率与正常人对照比较，均有统计学差异（$P<0.05$）。
结论 我们成功建立了血清 Stathmin 自身抗体检测方法，且 Stathmin 自身抗体在多种恶性肿瘤中高表达，为恶性肿瘤患者的诊断、治疗及预后判断提供了一种新型标志物。

PO-0127

First Case of Mixed Phenotype Acute Leukemia (B/T-lymphoid type) with t (9; 22) (q34; q11.2) BCR-ABL1 in a pediatric patient and review of the literature

Zie Wang
Shandong provincal hospital

Mixed phenotypic acute leukemia (MPAL) is a rare disorder with an incidence of less than 2% in all acute leukemia using the recent 2016 WHO criteria. Common subtypes are the B/myeloid and T/myeloid, B/T and trilineage MPAL being extremely rare. Here we discuss a case of a 9-year-old male child who presented with fever and skin ecchymosis. Peripheral blood smears showed 3% blast cells and bone marrow with 75% blasts. Immunophenotyping by multicolor flow cytometry showed two distinct populations: the major one with T-lineage (45.94％) and the minor one with B-lineage (25.02％). Conventional karyotyping done on bone marrow sample showed t(9;22)(q34;q11)(Ph+). BCR/ABL1 (P190) positive was confirmed by multiplex nested reverse transcription-PCR (RT-PCR). The case was diagnosed as MPAL with double Philadelphia chromosome Ph+. Mixed phenotype B/T acute leukemia is an extremely rare disease, particularly those with fusion gene BCR/ABL1 and clinically presents challenges in diagnosis and treatment.

PO-0128

流式细胞术检测巨球蛋白血症患者淋巴细胞亚群分析

王子娥
山东省立医院

目的 总结巨球蛋白血症患者采用流式细胞术检测淋巴细胞亚群的工作体会。

方法 取 500ul 全血+2ml PBS 震荡混匀，置于 37℃水浴箱中 10 分钟，然后 300g，5 分钟，离心，去上清后取细胞沉淀物再加 2mlPBS，5 分钟，300g，离心。去上清后取 50ul 处理后的细胞沉淀物用相应的荧光抗体去标记。
结果 温浴洗涤处理后的全血标本可以正常进行流式细胞术检测。
结论 巨球蛋白血症患者血清中存在大量单克隆免疫球蛋白 IgM，导致高粘滞血症，应予全血温浴洗涤处理后再做血液细胞成分荧光抗体标记。

PO-0129

SLE 患者慢性肾病的发生与血清抗核抗体特异荧光模型的相关性分析

胡冬
四川省绵阳市中心医院

目的 分析系统性红斑狼疮（systemic lupus erythematosus，SLE）患者发生慢性肾病（Chronic kidney disease，CKD）的风险程度与血清抗核抗体（antinuclear antibody，ANA）荧光模型特征的相关性，探讨特异性 ANA 荧光模型对 SLE 发生 CKD 的预测价值。
方法 回顾性分析 2019 年 1 月～2021 年 5 月绵阳市中心医院 SLE 患者 796 例，收集其性别、年龄、肾小球滤过率（glomerular filtration rate，GFR）、随机尿蛋白/肌酐比值（random urinary

albumin/creatinine ratio，UACR）和 ANA 检测结果；以血清 eGFR 值联合 UACR 值对受试者进展为 CKD 的风险程度进行评估，受试者按照风险高低分组，分析不同风险程度 SLE 患者荧光模型特征，筛选与 CKD 发生进展相关的特异荧光模型。
结果 1.受试者总共检出 ANA 荧光模型 13 种，累计 1564 次，按照进展为 CKD 的风险程度分 4 组：低风险组 319 例，中风险组 161 例，高风险组 186 例和极高风险组 130 例。2.SLE 患者进展为 CKD 的风险程度高低与性别、年龄不相关，与荧光模型叠加数量和滴度高低相关，叠加数量越多、滴度越大，进展为 CKD 的风险越高；核斑点型、核仁型和核均质型在不同 CKD 风险分组中的构成比差异有统计学意义。3.核均质型受试者进展为 CDK 的风险可能更高，单一荧光模型的受试者中，核均质型受试者的 eGFR 中位数最低，UACR 中位数最高，差异有统计学意义；混合荧光模型的受试者中，核均质型参与的混合模型受试者 eGFR 中位数最低，UACR 中位数最高，差异有统计学意义。
结论 SLE 患者 CKD 的发生和进展与抗核抗体荧光模型类别、叠加数量和滴度高低相关，核均质型 SLE 患者发生 CKD 风险更高，SLE 患者 CKD 的防治宜重视患者抗核抗体荧光模型特征的分析。

PO-0130

雅培 i4000SR 化学发光免疫分析仪检测乙肝五项的性能评价

史静
重庆医科大学附属第一医院

目的 评价雅培 i4000SR 化学发光免疫分析仪对乙型肝炎病毒血清标志物检测的分析性能。
方法 参考行业标准和规范文件，对 i4000 化学分析仪检测乙肝表面抗原（HBsAg）、乙肝表面抗体（HBsAb）、乙肝 e 抗原（HBeAg）、乙肝 e 抗体（HBeAb）、乙肝核心抗体（HBcAb）从精密度、临界值分析物浓度重复性、正确度、比对实验、分析测量范围、参考区间、分析灵敏度、携带污染和最大稀释度九个方面评价仪器分析性能。
结果 i4000 分析仪两个模块检测乙肝五项批内及批间不精密度均符合厂商要求；检测 HBeAg、HBeAb、HBcAb 临界值附近浓度标本阳性、阴性结果出现频率均大于 0.95。乙肝五项 2 个水平室间质评检测结果均与反馈结果相符。与 I2000SR 进行比对实验，结果一致性满足要求。HBsAg、HBsAb 项目两个模块间比较偏差均小于 1/2 Tea（15.0%）， HBsAg 携带污染量均小于允许误差范围。HBsAg、HBsAb 两个模块参考个体测定值均落在厂商提供的参考区间内。HBsAg 分析灵敏度为 0.03 IU/mL ，小于厂家给定的灵敏度 0.05 IU/mL；HBsAg 最大稀释度为 1：200，参考区间验证结果一致率 100% 。
结论 雅培 i4000 化学发光免疫分析仪检测乙型肝炎血清标志物的精密度、临界值分析物浓度重复性、正确度、比对实验、分析测量范围、 参考区间、分析灵敏度、携带污染和最大稀释度性能均达到质量文件和临床检验要求，可用于临床标本的常规检测。

PO-0131

35618 例 ANCA 检测患者就诊情况的分析

王丽
四川大学华医院

目的 分析抗中性粒细胞胞浆抗体（ANCA）检测在临床科室中的送检情况、阳性患者的基本情况、就诊症状、抗体谱分布及阳性结果疾病分布等，为进一步探讨 ANCA 在各种疾病中的临床意义奠定基础。
方法 通过四川大学华西医院信息系统，收集 2019 年 6 月-2020 年 10 月检测 ANCA（酶联免疫吸附法）的患者，记录其检测结果及其他临床信息。

结果 共收集 ANCA（ELASA）检测患者 35618 例，男女比例为 1：1.27，阳性者 2529 例，男女比例为 1：1.22，男女性都是随着年龄增长 ANCA 检出阳性率逐渐增高。阳性率最高的科室前三位依次是风湿免疫科（20.51％）、肾内科（17.03％）、呼吸内科（12.08％）；ANCA 阳性结果中除外常见的靶抗原 MPO 和 Pr3，其他靶抗原如 BPI、EL、LF、CAT 等阳性也很常见，各抗原相关的疾病除外大家熟知的 AAV 还有其他疾病也很常见如感染、炎症性肠病及类风关、干燥综合征、自身免疫性肝病等其他自免疾病。

结论 ANCA 阳性者多见于中老年人，且女多于男，ANCA 阳性者多就诊于肾内科，应与 ANCA 多累及肾脏有关，临床诊疗中遇肾损伤症状应考虑 ANCA 损害可能；此外，除 AAV 外，ANCA 阳性还可见于多个临床科室的多种疾病，其临床意义有待进一步明确。

临床诊断最多的前三类疾病依次为感染相关（20.92%）、ANCA 相关性血管炎相关（9.63%）、肺间质疾病相关（8.23%）；AAV 阳性 255 例，男女比例为 1：1.32，前三科室是肾脏内科（55.29%）、风湿免疫科（18.04%）、呼吸内科（9.80%）。

PO-0132

免疫球蛋白和临床实验室指标的综合分析鉴定免疫调节治疗的白塞病患者相关功能性关联和诊断标志物

程琳琳[1]、李阳[2]、吴子燕[1]、李柳冰[1]、刘晨曦[1]、刘建华[3]、代佳宇[2]、郑文洁[1]、张奉春[1]、唐刘军[2]、于晓波[2]、李永哲[1]

1. 中国医学科学院北京协和医院
2. 国家蛋白质科学中心(北京)，北京蛋白质组研究中心
3. 中国医科大学附属盛京医院检验科

背景 白塞病（BD）是一种全身复发性血管炎性/自身免疫性疾病。已经有大量关于 BD 的研究，然而尚未发现 BD 的实验室诊断标志物，且发病机制在很大程度上尚不清楚。此研究的目的是通过相关性分析来探索不同临床实验室变量之间的相互作用，以鉴定变量之间的功能性关联以及潜在的 BD 诊断标志物。

方法 我们测量了 66 名健康对照者和 63 名 BD 患者的免疫球蛋白蛋白质组（IgG，IgG1-4，IgA，IgA1-2）和 29 个临床实验室指标。我们进行了全面的临床变量关联分析并定义了指标间的生理，病理和药理学关联。为了能在临床中起到更好地指示作用，我们进一步计算了关联变量之间的相对变化。最终在包括 76 例 BD 患者、30 例健康对照、18 例大动脉炎和 18 例抗中性粒细胞胞浆抗体相关性血管炎的独立验证集中验证了潜在诊断标志物。

结果 在生理，病理和药理条件下，BD 患者中的临床变量协同而非单独执行功能。皮质类固醇和免疫抑制剂可以抑制免疫和炎症。对粒细胞，血小板和相关变量的综合分析可能会提供对疾病活动性、血栓形成风险以及组织损伤的更全面的了解。与对照组相比，BD 患者中总蛋白/平均红细胞血红蛋白，总蛋白/平均红细胞血红蛋白浓度，总蛋白/平均红细胞体积，血小板压积/单核细胞计数显著升高（在发现集和验证集中 $P<0.05$），这有助于 BD 的诊断和鉴别诊断。BD 中的慢性贫血与总蛋白增加可能导致这些生物标志物的水平升高，并且血小板与单核细胞之间的相互作用可能与血管受累有关。

结论 所有这些结果证明了我们的方法在阐明发病机理和鉴定自身免疫性疾病的新型生物标志物方面的实用性。

PO-0133

Association between 17-β-estradiol and IL-8 and visual field progression in postmenopausal women with primary angle closure glaucoma

Shengjie Li、wenjun cao
Eye & ENT Hospital, Shanghai Medical College, Fudan University

Purpose To investigate an association between sex hormones and inflammatory cytokines, and to determine whether baseline 17-β-estradiol (E2) and interleukin (IL)-8 are associated with visual field (VF) progression in postmenopausal women with primary angle closure glaucoma (PACG).
Methods A prospective cross-sectional and cohort study. The cross-sectional study enrolled 200 postmenopausal women with PACG and 151 healthy postmenopausal women as normal controls. A total of 105 postmenopausal women with PACG were included and followed up for at least 2 years in the cohort study. All participants were evaluated for levels of baseline sex hormones (follicle-stimulating hormone, prolactin, progesterone, testosterone, luteinizing hormone, and E2) and inflammatory cytokines (IL-1, IL-2, IL-6, IL-8, IL-10, and CRP) and underwent VF examinations. The cross-sectional study was conducted to establish risk factors for postmenopausal women with PACG using logistic regression analysis. The cohort study was designed to identify the factors, which could be used to predict VF progression in postmenopausal women with PACG using multivariate Cox regression analyses.
Results Decreased E2 (OR=0.88, 95% CI=0.78–0.99, p=0.007) and increased IL-8 (OR=1.12, 95% CI=1.01–1.23, p<0.001) levels were risk factors in postmenopausal women with PACG. A significant negative correlation was observed between IL-8 levels and E2 (r=-0.21, p=0.02). Multivariable regression analyses revealed a significant correlation between E2 levels and visual field mean deviation (MD) (B=-0.16, p=0.04, 95% CI=-0.09–-0.003), and between IL-8 levels and MD (B=0.36, p<0.001, 95% CI=0.01–0.02). During follow-up, 48 (45.71%) patients showed VF progression. Lower baseline E2 (hazard ratio [HR]=0.85, 95% CI=0.82–0.88, p=0.04) and higher baseline IL-8 levels (HR=1.01, 95% CI=1.00–1.02, p=0.004) were associated with progression of glaucoma. Patients with lower E2 levels had a significantly higher rate of PACG progression (log-rank test p<0.001), similar to those with higher IL-8 levels (log-rank test p=0.04).
Conclusions Decreased E2 and increased IL-8 levels at baseline are significant predictors of VF progression in postmenopausal women with PACG.

PO-0134

白塞病中红细胞参数的变化：与疾病严重程度和血管受累相关

程琳琳、李柳冰、刘晨曦、晏颂欣、陈海震、李昊隆、张奉春、陈华、李永哲
中国医学科学院北京协和医院

目的 白塞病（BD）是一种病因不明的全身性和慢性炎症性血管炎。通过临床症状进行诊断，然而由于缺乏特异性的实验室诊断标志物使 BD 的诊断更加困难。本研究的目的是确定 BD 患者血液学检查指标的变化，探究与 BD 临床特征的关系。
方法 本研究共纳入 48 位 BD 患者和 96 位健康对照。对每个 BD 患者的严重程度进行评分。评估了几项实验室检查指标在 BD 患者与健康对照之间的差异；研究了实验室指标与 BD 患者临床特征的关联；通过相关分析以揭示指标间的相互关联。
结果 与健康对照相比，BD 患者的 C 反应蛋白（CRP），平均红细胞血红蛋白（MCH），平均红细胞血红蛋白浓度（MCHC），中性粒细胞计数，血小板计数和血小板比容显着增加（P <0.05）。皮肤病变患者的 CRP 较高，血管受累患者的 MCH 和 MCHC 较低，皮肤病变和生殖器溃疡的患者

中性粒细胞计数较高。较高的 CRP，较低的 MCH 和 MCHC 与严重状况有关。此外，MCH 和 MCHC 与血小板计数，血小板计数和中性粒细胞计数呈负相关。
结论 这项研究表明，MCH 和 MCHC 是 BD 的有价值的实验室指标，有助于评估疾病的严重程度并指示 BD 存在的血管受累。

PO-0135

风湿性骨骼肌疾病中前白蛋白与 C 反应蛋白相关

程琳琳、李柳冰、刘晨曦、晏颂欣、陈海震、陈华、张奉春、李永哲
中国医学科学院北京协和医院

目的 前白蛋白检查可用于监测病人的营养状况，然而研究报道该评估受到炎症的影响。在这项研究中，我们旨在探究在五种炎性风湿性骨骼肌肉疾病（RMDs）中前白蛋白和 C 反应蛋白（CRP）以及其他免疫或炎性相关参数的关系：大动脉炎，抗中性粒细胞胞浆抗体相关性血管炎，系统性狼疮红斑，白塞氏病和多发性肌炎/皮肌炎。
方法 研究总共纳入 52 名健康对照者和 508 名 RMDs 患者的 3714 条记录。我们收集了患者从 2011 年 6 月至 2019 年 8 月临床和实验室信息，其中最长的随访期为 11 年。我们全面分析了 RMDs 患者和健康对照人群中前白蛋白与 CRP，球蛋白间隙，白蛋白与球蛋白之比以及 IgG 之间的关系。
结果 前白蛋白与 CRP 的相关系数高（r=-0.497，P<0.001），前白蛋白诊断 CRP 的曲线下面积高（AUC=0.777（95％CI 0.76-0.795）），并且前白蛋白水平与 CRP 随时间变化一致。前白蛋白和 CRP 之间的统计学关联不受性别，种族和年龄的影响，但是男性、中国非汉族和年轻患者人群中前白蛋白和 CRP 的相关性相对较高。在五种 RMDs 中，前白蛋白在与 CRP 的相关性大动脉炎患者人群中最强（r = 0.607，P <0.001）。另外，还观察到前白蛋白和 IgG，球蛋白间隙和白蛋白与球蛋白之比之间也存在中度的相关性。
结论 在患有五种慢性炎症性 RMD 的中国患者中，前白蛋白与 CRP 密切相关，这可能是由于疾病过程中慢性炎症的影响所致。

PO-0136

抗酿酒酵母抗体作为白塞病胃肠道受累诊断标志物的荟萃分析

程琳琳、李柳冰、刘晨曦、晏颂欣、李永哲
中国医学科学院北京协和医院

目的 由于在酒精和烘焙行业中普遍接触酵母，据报道，有胃肠道症状的白塞氏病(GIBD)患者的抗酿酒酵母抗体(ASCA)阳性率很高。我们进行了一项荟萃分析，以评估 ASCA 在区分 BD 患者与其他慢性炎症性肠病患者中的诊断价值。
方法 荟萃分析与流行病学检查表中系统评价和荟萃分析的首选报告项目和观察性研究的荟萃分析一起呈现。2019 年 7 月 12 日从 PubMed、EMBASE、Web of Science、SCOPUS 和 Cochrane 数据库检索了调查 BD 患者 ASCA 水平的相关研究；搜索于 2020 年 2 月 12 日重新运行。按 ASCA 的同种型分类，运用 Stata/SE V.12.0 和 Meta-DiSc V.1.4 用于执行荟萃分析和敏感性分析.
结果 九项研究被纳入荟萃分析。结果显示 ASCA 和 GIBD 之间有很强的关联，尤其是 ASCA-IgG(OR=5.50(95%CI 2.58~11.55),p=0.000) 和 ASCA-IgG+IgA(OR=5.36(95% CI 1.40~20.45)，p=0.014）。GIBD 中 ASCA 的阳性率明显高于溃疡性结肠炎（UC）：IgA（OR=2.13（95% CI 1.30 ～ 3.50 ）， p=0.003 ）； IgG+IgA （ OR=2.19 （ 95% CI 1.03~4.66 ）， p=0.042 ）； IgG/IgA((OR=2.03 (95% CI 1.30~3.17), p=0.002)。然而，克罗恩病患者的 ASCA-IgG 频率显着高

于 GIBD (OR=0.48 (95% CI 0.28~0.83)), p=0.009)。无胃肠道受累的 BD 与健康对照之间以及 GIBD 与肠结核(iTB)之间的 ASCA 阳性率无显着差异(p>0.05)。
结论 ASCA 可能在胃肠道受累的发病机制中起作用。当与克罗恩病相鉴别时，IgG 阴性结果有利于 GIBD/BD 的诊断。ASCA-IgA 在区分 GIBD 和 UC 方面表现出中等的诊断性能，与 IgG 联合使用的诊断性能更好。然而，ASCA 可能不是区分 GIBD 和 iTB 的有用血清学标志物。

PO-0137

端粒酶催化亚基在卵巢肿瘤中的表达研究

李牧
复旦大学附属中山医院青浦分院

目的 研究端粒酶催化亚基（human telomerase reverse transcriptase hTERT）在卵巢肿瘤中的表达及意义。
方法 应用免疫组织化学 SP 法检测 99 例恶性卵巢上皮肿瘤、12 例交界性卵巢上皮肿瘤、10 例良性卵巢上皮肿瘤和 7 例卵巢囊肿中 hTERT 的阳性表达率。
结果 hTERT 在癌、交界性肿瘤、良性肿瘤、囊肿不同类型肿瘤组织中阳性率分别为 79.8%(79/99)、91.7%（11/12）、70.0%（7/10）、57.1%（4/7），hTERT 在四种不同类型肿瘤组织中核表达强度有显著性差异(P<0.05)；hTERT 核表达水平与卵巢癌患者淋巴结转移情况、FIGO 分期、患者初诊年龄及绝经状况无关(P>0.05)，与肿瘤大小有关(P＜0.05)。
结论 hTERT 的表达与卵巢癌的发生发展有关。

PO-0138

Association between L-FABP and acute kidney injury in critically ill patients: an observational cohort study

Tao Sun、Shufang Qu、Ying Ping、Zhihua Tao
The Second Affiliated Hospital of Zhejiang University School of Medicine

Background Acute kidney injury was a common clinical complication in intensive care unit with high morbidity and mortality. We explored the clinical application of L-FABP, a renal tubular biomarker, early prediction for acute kidney injury.
Methods The concentration and concentration change rate of L-FABP were analyzed to explore the relationship with AKI. Logistic regression analysis and ROC curve analysis were used to predict the risk of AKI on 1 day before diagnosis, 2 days before diagnosis and 3 days before diagnosis Evaluating the role of L-FABP by comparing concentration change in different stages of AKI.
Results There were significant differences between AKI group and non-AKI group on the day of diagnosis, 1 day before diagnosis and 2 days before diagnosis, however, there were not significant differences on 3 days before diagnosis. The concentration and concentration change rate of L-FABP both were an excellent predictor for risk analysis of acute kidney injury. The predictive power of L-FABP was similar to CAF, NGAL, β2MG and CysC on 1 day before diagnosis and 2 days before diagnosis which was superior to other biomarkers on 3 days before diagnosis. Higher concentration of L-FABP was associated with increased risk of AKI. The closer time before AKI occurred, the better predictive value was. the concentration of L-FABP was increased with the higher stage which meant the higher risk. L-FABP had a good effect on the staging of AKI and could facilitate clinically early diagnosis.
Conclusion L-FABP was a potentially predictive biomarker of AKI and might provide benefit for clinical decision-marking for early intervention.

PO-0139

B 亚型 HIV-1 V3 区氨基酸变化与病毒感染能力及亲嗜性的研究

林春艳、蒋丽鑫
哈尔滨医科大学附属第一医院

目的 通过分析不同嗜性 B 亚型 HIV-1 感染者 V3 区氨基酸序列差异及感染实验，探讨 V3 区 11、22、25 位点与病毒感染能力及亲嗜性的关系。
方法 从 HIV 数据库中以 FASTA 格式下载 B 亚型 V3 区氨基酸序列，并将其分为 R5 亲嗜性组和 X4 亲嗜性组，利用 CLUSTAL W 软件分别对两组序列进行多重序列比对，计算每个位点氨基酸出现的频率，并进行降幂排列。对 HIV-1 HXB2 和 SF162 株包膜糖蛋白 V3 区进行修饰，并构建伪病毒及进行感染实验。
结果 研究结果显示 R5 亲嗜性和 X4 亲嗜性病毒中 V3 区 Consensus 序列在 11、22 和 25 位上具有差别。在 R5 亲嗜性毒株中这三个位点最常出现的氨基酸频率分别为 71.9% S，66.7% A 和 56.0% D；在 X4 亲嗜性毒株中这三个位点最常出现的氨基酸频率分别为 50.0% R，57.1% T 和 26.2% Q。V3 区 22 氨基酸残基与病人 CD4+T 细胞数具有明显的相关性。R5 亲嗜性或 X4 亲嗜性毒株 V3 区 11、22、25 位氨基酸残基的改变都使其感染能力降低，并且 SF162 的 11 位氨基酸残基 S 转变为 R 时，病毒由 R5 嗜性变为 R5X4 双嗜性。
结论 我们的研究结果发现在 B 亚型的 HIV-1 中 V3 区 22 位氨基酸残基与病毒的感染能力及病人的疾病进展具有明显的相关性。可以和 11、25 位氨基酸一起作为生物学表型预测的位点。

PO-0140

利用聚多巴胺-碳纳米管纳米复合物进行信号放大的酶联电化学免疫分析

尹斐[1]、张越[1]、潘登[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学中大医院临床检验医学中心
3. 东南大学危重症医学江苏省重点实验室

开发灵敏、快速的生物分析方法对疾病早期诊断具有重要意义。[1,2] 酶联免疫分析是临床诊断、药物发现、食品安全检测和环境分析中最常用的方法之一。[3-4] 通过偶联酪氨酸酶（Tyr）和β-将半乳糖苷酶（Gal）转化为一种氧化还原循环方案，采用聚多巴胺功能化多壁碳纳米管（MWCNTs-PDA）纳米杂化修饰电极，构建了一种选择性和灵敏度均提高的酶级联型电化学免疫传感器。MWCNTs-PDA 纳米杂化物的抗体结合能力提高了 5 倍，这是信号放大的主要原因。在提出的酶级联方案中，Gal 被夹在免疫传感器的表面，通过催化苯基的免疫反应被捕获 β-D-半乳吡喃糖苷（P-GP）在苯酚的基础上发生水解反应。所得苯酚被用作酪氨酸的底物，酪氨酸被催化生成邻苯二酚，然后生成邻醌。然后将邻醌电化学还原为邻苯二酚，在邻苯二酚和邻醌之间形成氧化还原循环。基于酶级联的免疫分析不仅显著放大了电化学信号，而且具有很高的选择性。以 CEA 的检测为例，酶级联型电化学免疫传感器的检测范围为 10 pg ml-1 至 10 ng mL-1 最低检出限为 8.39 pg mL-1（S/N=3），这比以前报告中使用其他方法优越。酶级联免疫传感器的选择性比单一酶免疫传感器高 44-80%。这项工作显示了偶联酶级联在免疫诊断中的巨大潜力，提高了选择性和敏感性。

PO-0141

血清抗 PLA2R 抗体与特发性膜性肾病患者肾脏足细胞数及 Nephrin 的临床相关性分析

陈施晓、秦晓松
中国医科大学附属盛京医院

目的 了解肾组织中足细胞数及 Nephrin 在特发性膜性肾病（IMN）的变化与表达情况，探索血清中抗 M 型磷脂酶 A2 受体（PLA2R）抗体与足细胞损伤的关联。
方法 选取了我院肾脏内科经肾活检病理诊断为 IMN，且肾组织 PLA2R 免疫荧光染色阳性的 45 例住院患者作为 IMN 组，且收集其肾组织；同时收集 7 例癌旁组织作为正常组织对照组。使用免疫组化方法检测 WT1、Nephrin 在肾组织中的表达情况，以 WT1 阳性标记细胞计算足细胞数及密度。收集研究对象的临床资料、血清抗 PLA2R 抗体表达水平，比较足细胞数、Nephrin 在 IMN 及正常组织对照组的表达特点。并在抗 PLA2R 抗体阳性及阴性以及不同的尿蛋白水平分组下 IMN 患者足细胞密度、Nephrin 平均光密度值的差异，并探讨其相互关系。
结果 1、WT1 在肾小球足细胞胞核及胞浆内表达，且 IMN 组的 WT1 阳性细胞数较正常对照组明显减少，染色更浅，足细胞绝对数及足细胞密度均低于对照组（P＜0.05）。Nephrin 沿毛细血管襻分布，IMN 组 Nephrin 染色不均、呈弥漫、细颗粒状或团块状，多数染色线性消失；Nephrin 平均光密度值较对照组明显降低（P＜0.05）。2、抗 PLA2R 抗体阳性组的 TC、HDL-C、LDL-C、24h-UP、Urea 均显著高于阴性组（P＜0.05），Nephrin 平均光密度值、Alb 均显著低于阴性组（P＜0.05）；两组间足细胞密度不具有统计学差异（P＞0.05）。3、大量蛋白尿组的抗 PLA2R 抗体、Urea、Scr 水平显著高于少量蛋白尿组（P＜0.05），而肾组织 Nephrin 平均光密度值、足细胞密度、Alb、完全缓解比例显著低于少量蛋白尿组（P＜0.05）。4、Nephrin 平均光密度值与 24h-UP、不完全缓解呈负相关（P＜0.05），足细胞密度与不完全缓解呈负相关（P＜0.05），Nephrin 平均光密度值、足细胞密度与血清抗 PLA2R 抗体水平之间无显著相关性（P＞0.05）。
结论 IMN 患者肾组织存在足细胞损伤。血清抗 PLA2R 抗体与 IMN 肾脏足细胞数、Nephrin 表达之间无相关性，血清抗 PLA2R 抗体与 IMN 肾足细胞损伤程度并不完全一致。肾组织 Nephrin 及足细胞密度损失越少，足细胞损伤程度越轻，IMN 的预后越好。

PO-0142

IgG 亚型与甲状腺功能相关抗体检测对自身免疫性甲状腺疾病的诊断价值

刘珏
山东第一医科大学附属省立医院

目的 探讨 IgG 亚型与甲状腺功能相关抗体检测在自身免疫性甲状腺疾病的诊断价值。
方法 选取 2015 年 1 月至 2020 年 12 月于山东第一医科大学附属省立医院就诊的自身免疫性甲状腺疾病患者 294 例，其中 Graves 病患者 168 例作为 GD 组，年龄为 11~73 岁；桥本甲状腺炎患者 126 例作为 HT 组，年龄为 13~50 岁；选取健康志愿者 100 例作为对照 NC 组，年龄为 20~80 岁。分别检测各组的 TSH、FT4、FT3、TgAb、TPOAb 和 TRAb 以及 IgG 亚型水平。
结果 通过比较自身免疫性疾病患者分组与健康对照者血清中各项指标，发现 HT 组 TSH、TgAb 和 TPOAb 明显高于对照组（P＜0.05），FT4 和 FT3 明显低于对照组（P＜0.05）；GD 组 FT4、FT3、TgAb、TPOAb 和 TRAb 明显高于对照组（P＜0.05），TSH 明显低于对照组（P＜0.05）；GD 组 TSH、TgAb 和 TPOAb 明显低于 HT 组（P＜0.05），FT4、FT3 和 TRAb 明显高于 HT 组（P＜0.05）；GD 组 IgG1 水平为（8.11 ± 0.53）g/L，明显高于对照组和 HT 组（P＜0.05）；HT 组 IgG2 水平为（7.24 ± 0.60）g/L，明显高于对照组和 GD 组（P＜0.05）；HT 组和 GD 组 IgG3、

IgG4 水平分别为（0.26 ± 0.11）g/L 和（0.24 ± 0.12）g/L、（0.49 ± 0.21）g/L 和（0.47 ± 0.22）g/L，明显低于对照组（P＜0.05）；GD 组、HT 组患者 IgG1、IgG2、IgG3 和 IgG4 水平与 TSH、FT4、FT3、TgAb、TPOAb 和 TRAb 无显著性差异（P＞0.05）。
结论 不同自身免疫性疾病中甲状腺功能血清学检测指标水平存在明显不同，且不同 IgG 亚型有所差异，联合检测对鉴别诊断具有临床意义。

PO-0143

铁蛋白在 COVID-19 中的价值：系统评价和荟萃分析

程琳琳、李昊隆、李柳冰、刘晨曦、晏颂欣、陈海震、李永哲
中国医学科学院北京协和医院

目的 COVID-19 已迅速发展为大流行病。在严重的 COVID-19 患者中发现由于细胞因子风暴和继发性噬血细胞淋巴组织细胞增生症引起的铁蛋白水平升高。因此，本研究的目的是确定铁蛋白在 COVID-19 中的作用。
方法 从 PubMed、EMBASE、CNKI、SinoMed 和万方收集调查 COVID-19 中铁蛋白的研究。该荟萃分析比较不同患者组之间的铁蛋白水平：存活着与死亡者；严重患者与非严重患者；有合并症与无合并症；ICU 与非 ICU；机械通气与不机械通气。
结果 该荟萃分析共纳入 52 项研究，涉及 2019 年 12 月 25 日至 2020 年 6 月 1 日期间 10614 名 COVID-19 确诊患者，18 项研究纳入定性综合分析。与非重症患者相比，重症患者的铁蛋白水平显着升高 [WMD 397.77 (95% CI 306.51-489.02), P < .001]。与幸存者相比，非幸存者的铁蛋白水平显着更高 [WMD 677.17 (95% CI 391.01-963.33)，P < .001]。有一种或多种合并症（包括糖尿病、血栓并发症和癌症）的患者的铁蛋白水平显着高于没有合并症的患者（P < .01）。严重的急性肝损伤与高水平的铁蛋白显着相关，其水平与重症支持治疗相关，包括 ICU 转移和机械通气。
结论 铁蛋白与不良预后相关，可以预测 COVID-19 患者的恶化。

PO-0144

超敏肌钙蛋白 hs-cTnT 联合 NLR 诊断急性心肌梗死的研究

王琳
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 随着检测技术灵敏度不断提高，一些非急性心肌梗死的病人包括老年人、不稳定型心绞痛、心肌损伤等，在实际临床检测中血浆 cTnT 水平也会增加，从而增加临床诊断急性心梗的难度，甚至导致过度治疗，因此寻求更加高效的诊断方案，是目前急性心梗的一项重要研究方向。本课题研究 hs-cTnT 联合 NLR 诊断 AMI 的效果，以及在众多 hs-cTnT 低水平升高患者中，鉴别出 AMI（actue myocardial infarction，急性心肌梗死）患者的能力。
方法 筛选苏大附一院 2019 年 10 月至 2020 年 5 月期间，收治的 236 例疑似心梗（胸痛、胸闷等）症状同时伴有 hs-cTnT 轻度增高的病人为观察组，同时并选 100 例同期非 AMI 患者为对照组。观察于入院 0 小时，hs-cTnT、中性粒细胞计数（Neutrophil，N）、淋巴细胞（Lymphocyte，L）以及中性粒细胞/淋巴细胞比 (Neutrophil lymphocyte ratio，NLR)水平。3 小时后以及治疗后，再次检测 hs-cTnT 和 NLR 的水平，观察其变化。
结果 在 hs-cTnT 低水平升高患者中，AMI 患者 hs-cTnT 水平明显高于非 AMI 患者，且该差异与年龄及性别无关。AMI 患者 NLR 水平明显高于非 AMI 患者，NLR 对 AMI 鉴别诊断有一定的临床应用价值。同时，AMI 患者 3 小时后 hs-cTnT 与 NLR 水平呈正相关，动态分析 hs-cTnT 与 NLR 水平变化，结果显示 NLR 随 hs-cTnT 升高而升高，降低而降低，表明 hs-cTnT 与 NLR 动态相关。

结论 NLR 以及 NLR 0/3h 比值可以有效预测急性心肌梗死，动态监测 NLR 0/3h 可以预测 AMI 的进展进程；NLR 联合 hs-cTnT 可用于鉴别诊断 AMI 和 UA 等心血管疾病。

PO-0145

HLA-B27 抗体剂量减半应用对临界值结果的影响

王子娥
山东省立医院

目的 研究 HLA-B27 抗体剂量减半在临床应用中的可行性
方法 用 EDTA 抗凝的真空采血管采集 2ml 外周血。取 50μl 抗凝全血，加入 15μlAnti-HLA-B27 FITC/ CD3 混匀，室温避光静置 15min。加入 2 m l用蒸馏水 1 : 9 稀释的溶血素，低速混匀，室温避光静置 10 min 后 300 g 离心 5 min，弃上清。加入 2 ml PBS，混匀，300 g 离心 5 min 后弃上清。加入 0. 5 m l PBS，低速混匀，上机检测。根据定标微球确定临界值，样本 FL1 平均荧光强度大于或等于临界值判断为阳性，小于临界值为阴性，见图 1，图 2。若样本 FL1 平均荧光强度处于 130 至 marker 之间，加 30ul Anti-HLA-B27 FITC/ CD3 重复检测此样本。
结果 实验组一 63 例中有 73.02%病例在加入 30ul 抗体后结果转为阳性，差异有统计学意义，P<0.01。实验组二加入 30ul 抗体，所测结果仍为阴性；实验组三加入 30ul 抗体，所测结果仍为阳性，结果无差异。实验组一中，加入 30ul 抗体后，HLA-B27 抗体荧光强度明显增强，差异有统计学意义（P<0.01）（见表 2）。实验组二和实验组三荧光强度虽增强，差异有统计学意义,但检测结果阴阳性判定无变化，阴性为阴性，阳性为阳性。
结论 HLA-B27 荧光抗体试剂量减半使用在临床应用中切实可行，但在遇到荧光强度在 140 至 marker 之间的临界值病例时，则应全量抗体重新检测，并以全量检测结果报告。遵循这个原则，即不影响临床检测结果，又可以有效降低损耗，节约支出。从而使 HLA-B27 的检测在相关疾病的诊断和预后判断等方面发挥更大的作用。

PO-0146

Elevated systemic immune inflammation index level is associated with disease activity in ulcerative colitis patients

Yiyi Xie、Tingting Zhuang、Yin Ping、Xiuzhi Duan
The Second Affiliated Hospital of Zhejiang University School of Medicine

Background It has been confirmed that high Systemic immune-inflammation index (SII) levels usually indicate poor outcomes in various diseases, especially on malignancies. However, the clinical significance of the SII in ulcerative colitis (UC) patients is remain unclear. Therefore, the purpose of our paper is to analyze the levels of SII in UC patients and assess the relationship between the SII and disease activity.
Materials and Methods We studied 187 consecutive patients with UC and 185 age- and sex-matched healthy controls retrospectively. The Mayo scoring system was adopted to evaluate disease activity in UC patients. We collected clinical characteristics and laboratory parameters from hospital electronic medical records.
Results The SII levels were significantly higher in UC patients than those in healthy subjects (P<0.001). Higher SII levels were observed in moderate and severe UC subgroups compared to mild or remission subgroups. Correlation analysis displayed that the SII levels were positively relatived with Mayo score (r = 0.469, P <0.001), C reactive protein (CRP) (r = 0.480, P <0.001), and erythrocyte sedimentation rate (ESR) (r = 0.336, P <0.001), but negatively with haemoglobin

(Hb) (r = -0.271, P <0.001). A multiple linear regression analysis suggested that there was an independent correlation between Mayo score and SII (beta = 0.324, t = 4.241, P <0.001). The receiver operating characteristic (ROC) curve revealed that the maximum area under the curve (AUC) was 0.711 (95% CI, 0.630–0.791, P < 0.001), and the cut-off value for diagnosing active UC was 485.95, the sensitivity was 0.641, and the specificity was 0.75.
Conclusions We demonstrated that the SII was elevated significantly in UC patients and was closely related to the UC disease activity. In addition, the SII had a high discriminative capacity for active UC.

PO-0147

甲状腺刺激素受体兴奋抗体在 Graves 病中的应用评价及检测策略优化

童明宏、盛慧明
上海交通大学医学院附属同仁医院

目的 评价甲状腺刺激素受体兴奋抗体(TSI)检测对 Graves 病检测策略的优化作用。
方法 采集 2019 年 8 月至 2020 年 4 月上海市同仁医院检验科 544 份明确诊断的血清样本。血清样本分别是 52 例未治疗 GD 患者、155 例已治疗 GD 患者、83 例桥本甲状腺炎患者、70 例甲状腺结节患者、83 例甲状腺癌患者和 101 例健康受试者。所有样本均检测 TSI 和 TSH 受体自身抗体(TRAb)。此外，对 23 例首次就诊时未明确诊断甲状腺疾病的患者进行 6 个月的监测以作出最终诊断。
结果 TSI 和 TRAb 检测的临床敏感性分别为 98.10%和 94.20%，临床特异性分别为 92.30%和 96.70%。以 UT-GD(新诊断 GD 患者)血清为基础进行 ROC 曲线分析，TSI 检测的曲线下面积(AUC)为 0.974。最佳临界值为 0.58 IU/L(敏感度 98.0%，特异性 92.8%)。TRAb 检测的 AUC 为 0.961。结合 TSI 和 TRAb 结果，曲线下面积为 0.981。在对 23 例初始诊断不确定的患者进行的试点研究中，随访结果显示，23 例患者中有 22 例临床诊断与 TSI 检测结果一致，1 例与 TRAb 检测结果一致。
结论 TSI 检测具有良好的临床应用前景，可提高 GD 的诊断水平。TSI 检测在 GD 与其他甲状腺疾病的初步鉴别诊断中可能优于 TRAb 检测。

PO-0148

Research on the CD3 × CD155 Bispecific Antibody Targeted T Cells for Gastric Cancer

Wanru Ma
Affiliated Hospital of Xuzhou Medical University

China is a country with a high incidence of gastric cancer, accounting for about 50% of the world's morbidity and deaths. The disease burden is very serious, which seriously endangers the health of our residents. Due to its characteristics of recurrence and drug resistance, the therapeutic effects of surgery, radiotherapy and chemotherapy are limited. Therefore, the development of a new treatment method, immunotherapy, is very important for patients with bladder cancer. Anti-CD155 antibody is an effective target for mediating the immunotherapy of tumors expressing CD155. Using anti-CD155 antibody to target tumor cells overexpressing CD155 can inhibit tumor growth. This subject takes gastric cancer as the research object, and analyzes the expression of CD155 in gastric cancer cells by flow cytometry; constructs a CD3 × CD155 bispecific antibody (CD155Bi-Ab) by chemical coupling method; and performs flow cytometry, LDH, ELISA, and fluorescence detection The killing effect of T cells bound to bispecific

antibodies on gastric cancer cells was analyzed. In addition, an animal model was established to analyze the inhibitory effect of CD155Bi-Ab-modified ATC on gastric cancer cells.

PO-0149

结核感染 T 细胞 IFN-γ 释放实验临床应用分析

张培莉
山东第一医科大学附属省立医院

目的 探讨结核感染 T 淋巴细胞 γ 干扰素释放实验（IGRAs）在临床检测结核病中的应用价值。
方法 利用 IGRAs 方法检测 2013-2016 年 11968 例门诊及住院结核筛查患者。按科室分布分析，同时对检测阳性病例按性别、年龄进行分析比较，并对不确定结果进行分析，不同方法进行比较。
结果 11968 例筛查者中，2048 例阳性，阳性率为 17.11%，不确定结果 107 例，占总检测数的 0.89%。2013-2016 年检测阳性率分别为 19.65%，21.35%，15.82%，13.56%。 肺内及肺外结核检测筛查中，呼吸科、消化科、肿瘤科、神经科、妇科阳性率分别为 22.07%、20.27%、23.38%、12.84%、11.86%。阳性筛查者中，男性占 62.11%，女性占 37.89%，男性明显高于女性。按年龄分组，≤15 岁、16～25 岁、26～45、46～65、≥66 岁，各年龄段阳性率分别为 1.96%、18.51%、16.54%、21.25%、25.73%。分析不确定结果数据，风湿免疫科、血液科比例最高，分别占 1.99%、2.35%。与其它实验室检测方法对比，IGRAs 方法具有明显优势。
结论 结核好发于全身各个器官，结核菌感染存在性别、年龄差异。IGRAs 是灵敏和特异的快速检测结核分枝杆菌感染的方法，虽不能作为确诊指标，但为进一步确诊疾病，在结核疑似患者筛查中具有较大临床应用价值。

PO-0150

桥本氏甲状腺炎 Fas 系统表达水平的研究

徐兆珍、郭欣
哈尔滨医科大学附属第一医院

目的 为了研究 Fas/FasL 介导的细胞凋亡在桥本氏甲状腺炎发病机制中的作用，评价其在治疗中的意义。
方法 采用流式细胞仪、双抗体夹心 ELISA 法及免疫组化方法分别测定桥本氏甲状腺炎(HT)及正常对照组外周血 T 淋巴细胞 Fas 抗原表达情况，血浆中 sFas 水平及甲状腺腺泡细胞 Fas 抗原及 Fas 配体的表达情况。
结果 发现 HT 组甲状腺细胞 Fas 和 FasL 表达强度显著高于正常对照组(P<0.01)，血浆 sFas 水平(2.05±0.54ng/ml)明显低于正常组(3.59±0.68ng/ml，P<0.001)，HT 外周血 T 淋巴细胞 Fas 抗原阳性细胞数(79.99%±16.08%)显著高于正常对照组(57.22%±11.57%，P<0.001)。
结论 Fas 系统与桥本氏甲状腺炎发病密切相关。

PO-0151

靶向人类自然杀伤细胞活性化合物的筛选——瑞香素增强 IFN-γ 分泌

阳青兰、邓亚飞、彭红艳、吴舒婷、王莉莉、张树菊、李梨平
湖南省儿童医院儿科医学研究所

目的 寻找具有增强 NK 细胞效应功能的活性化合物作为新的候选抗癌药物。
方法 单个核细胞(PBMCs)，在 IL-12 或 IL-15 (10 ng/ml)存在的条件下，化合物（287 个）处理 18 小时后，通过流式细胞仪评估 NK 细胞中 IFN-γ 蛋白的胞内染色情况，发现 5 个候选化合物；进一步通过 ELISA 确定候选化合物处理后 PBMCs 上清分泌的干扰素含量；通过流式细胞分选从 PBMCs 得到纯化的原代人类 NK 细胞，用以区分候选化合物是否直接或间接促进了 NK 细胞 IFN-γ 的产生；利用流式细胞术检测候选化合物处理后 NK 细胞 CD107a 变化以及 NK 细胞中激活和抑制受体 NKp46、NKp30、NKp44、NKG2D、2B4、CD16、TRAIL、DNAM-1、NKG2A 和 FasL 的表达用以确定其杀伤作用；最后通过 RNA-测序找到候选化合物增强 NK 细胞分泌 IFN-γ 的信号通路，进一步使用信号分子抑制剂处理后，通过免疫印迹法确定信号通路。
结果 筛选 287 个化合物后，我们发现 5 个化合物，包括瑞香素、MK-8617、LW6、JIB-04 和 IOX1，增加了 NK 细胞中 IFN-γ+的比例。进一步研究发现瑞香素直接促进 NK 细胞中 IFN-γ 的产生，而其他 4 种化合物则间接作用于 NK 细胞。瑞香素还能提高 NK 细胞对肿瘤细胞的直接细胞毒性。通过 RNA 测序，我们发现 PI3K-Akt 信号通路是介导 NK 细胞活化的中心通路。进一步发现，PI3K-Akt 抑制剂及其主要下游信号通路 mTOR、LY294002 和雷帕霉素能分别逆转瑞香素增加的 IFN-γ 生成。
结论 我们鉴定了一种天然产物——瑞香素，具有通过 PI3K-Akt-mTOR 信号促进人类 NK 细胞活化的能力。

PO-0152

基于流式细胞平台的淋巴细胞交叉配型实验方法研究

王琳[1]、尹利民[2]
1. 眉山市人民医院
2. 昆明市第一人民医院

目的 提高抗供体 HLA 抗体检测灵敏度，建立基于流式细胞平台的淋巴细胞交叉配型（Flow Cytometry Crossmatch, FCXM）实验方法。
方法 采集 2 例 AB 型男性血清作为阴性对照，采集 30 例供体全血并使用免疫磁珠特异性分离供体淋巴细胞，加入荧光抗体对 B 淋巴、T 淋巴及抗供体 HLA 抗体进行识别，通过流式细胞仪采集荧光信号，使用 FLOWJO 软件对数据进行分析建立 FCXM 实验方法。采集 14 例供体全血及 48 例受体血清，进行 57 次 FCXM 实验及补体依赖的细胞毒（Complement Dependent Cytotoxicity, CDC）实验，通过 Wilcoxon W、McNemar 检验及 Kappa 检验进行统计学分析。
结果 FCXM 实验 T 淋巴细胞 anti-IgG-FITC Cutoff 值为 226.6，B 淋巴细胞 anti-IgG-FITC Cutoff 值为 214.4。FCXM 与 CDC 两种方法的一致性极低（McNemar 检验 P 值<0.01；Kappa 值<0.01）。
结论 FCXM 是一种灵敏度更高的检测方法，可用于临床低浓度抗供者 HLA 抗体检测。

PO-0153

抗原特异性 T 细胞数量检测微孔反应板的研制

张雷、金岳心子、徐娟、孙子微、林明鑫、魏嘉、陈文秀
江苏省人民医院（南京医科大学第一附属医院）

目的 创建一种简单易行、可对抗原特异性 T 细胞进行数量检测的新方法。
方法 利用商品化的 H-2Kb-Ig/OVA257-264 二聚体作为靶向抗原,包被在直径 4.5 微米的磁珠表面制成磁珠式人工抗原提呈细胞（aAPC-beads）,以 OT-1 转基因鼠脾淋巴细胞群中的 OVA 抗原特异性 T 细胞作为待检的靶细胞,建立了磁性人工抗原提呈细胞微孔反应板技术（aAPC-microplate）,并进行方法学论证。
结果 准确性分析显示，磁珠分选所得细胞数与接种的淋巴细胞数之间呈现了良好的数量依赖关系和线性关系,R2 值达到 0.99 以上。特异性分析显示：用无关抗原肽的 Kb/TRP2-beads 同步分选 OT-1 鼠脾淋巴细胞群时,阳性细胞比例降为 0.45%左右；经 Kb/OVA-beads 磁珠分选后所得细胞群中的 OVA 抗原特异性 T 细胞比例经 H-2Kb-Ig/OVA257-264 二聚体荧光染色及流式分析为 89.80%，而分选前的比例为 10.13%。重复性分析显示：在 5 个检测数量组之间,阳性细胞比例的平均批内 CV 值为 4.4%；对同一份 OT-1 鼠脾淋巴细胞群进行三次重复实验时,批间 CV 值为 13.5%,阳性细胞比例分别为 9.40%、9.77%和 9.47%；R2 值分别为 0.9959、0.9970 和 0.9960。
结论 aAPC-microplate 检测方案具有较高的特异性、准确性和重复性以及与传统检测方法的相关性,提示了该技术检测抗原特异性 T 细胞数量的可行性。

PO-0154

前列腺小体外泌蛋白在慢性前列腺炎诊断中的临床价值研究

徐燕萍
上海交通大学医学院附属仁济医院

目的 通过检测尿液中前列腺小体外泌蛋白(prostatic exosomal protein,PSEP)评估 PSEP 再慢性前列腺炎（CP）诊断中的临床价值。
方法 纳入对象为仁济医院泌尿外科门诊的 CP 患者 156 例，体检中心的正常健康男性 82 例，采用前列腺小体外泄蛋白检测试剂盒（酶联免疫法）定量检测尿液标本中的 PSEP 含量。评价 PSEP 诊断慢性前列腺炎的灵敏度、特异度和临床总符合率等指标，绘制受试者工作曲线（ROC），比较 PSEP 与临床诊断结果的一致性。
结果 慢性前列腺炎患者 PSEP 检测结果为 2.316(1.306～3.247)ng/mL,明显高于健康体检者的 0.765(0.342～1.158)ng/mL, 两组存在显著差异(P＜0.001)。根据 ROC 计算 PSEP 的最佳临界值为 1.185 ng/mL, ROC 曲线下面积(the area under the ROC curve, AUC)为 0.873,对慢性前列腺炎的诊断敏感度为 80.15％,特异度为 81.03％。
结论 PSEP 用于慢性前列腺炎的临床诊断具有客观、无痛，简便、无创的特点，可作为诊断慢性前列腺炎的潜在分子标志物。

PO-0155

Hepatitis B virus protein preS2 promotes angiogenesis in hepatocellular carcinoma via its transcriptional activation of VEGFA promoter

Fang Luan
Department of Clinical Laboratory, Shandong Provincial Hospital affiliated to Shandong First Medical University, PR China

Background Angiogenesis is closely related to the development and progression of hepatocellular carcinoma (HCC) development. The overexpression of the angiogenic factors has been demonstrated in HCC. Hepatitis B virus protein preS2 is a transactivator that plays an important role in hepatitis B virus (HBV) related HCC. In this study, we investigated the potential of preS2 in inducing angiogenesis in HCC.
Methods Totally Sixty-three cases of HCC, aged 34-79, who were surgically treated and pathologically confirmed were enrolled. Levels of preS2, CD34 and vascular endothelial growth factor A (VEGFA) in HCC samples were evaluated by immunohistochemistry. The proliferation of vascular endothelial cells was detected by CCK-8. VEGFA was analyzed by Western blot in HCC cells. Luciferase reporter assays were used to measure the effect of preS2 on VEGFA promoter.
Results Microvascular density (MVD) and VEGFA were significantly higher in preS2-positive HCC samples than preS2-negative HCC samples. PreS2 over-expression upregulated VEGFA expression in HepG2 and activated vascular endothelial cell proliferation. While blocking preS2 expression reduced VEGFA expression in HepG2.2.15 and inhibited vascular endothelial cell proliferation. Furtherly, dual-luciferase assay showed that preS2 activated VEGFA promoter activity.
Conclusion The expression of preS2 protein promotes angiogenesis by transactivating VEGFA promoter in HCC.

PO-0156

正常成人粒细胞集落刺激因子动员外周血内皮祖细胞的生物学特性

白丽萍
天津市肿瘤医院（天津医科大学肿瘤医院）

目的 观察粒细胞集落刺激因子动员的外周血中内皮祖细胞的生物学特性。
方法 获取粒细胞集落刺激因子动员正常人的外周血单个核细胞，同时获取 8 例正常成人外周血单个核细胞作为对照。将获取的细胞接种在预铺纤维连接蛋白的培养皿中进行体外培养。FACS 和免疫组化法检测获取细胞的免疫表型；采用 MTT 比色法和黏附能力测定实验检测内皮祖细胞的增殖和黏附能力；实时定量 PCR 检测血管形成相关细胞因子的表达；荧光标记的乙酰化低密度脂蛋白(Dil-acLDL)吞噬实验鉴定内皮功能；将获取的细胞接种在含有血管内皮细胞生长因子和碱性成纤维细胞生长因子的基底膜胶中诱导血管生成。
结果 动员后外周血和未动员外周血内皮祖细胞具有相似的细胞形态和免疫表型，FACS 和免疫组化检测结果显示上述两种内皮祖细胞都表达内皮细胞特异性抗原 CD34、CD31、FLK-1、ve-Cadherin、vWF 和 CD133。内皮细胞生长因子和基质细胞衍生因子 1 在动员后外周血内皮祖细胞中的表达水平增加；两种来源的内皮祖细胞都具有吞噬 Dil-acLDL 和在体外诱导血管生成的能力。但是，动员的外周血中内皮祖细胞的数量和增殖能力明显强于未动员外周血中的内皮祖细胞。结果可见动员后的外周血中可以分离出具有内皮祖细胞特性的细胞群体，该群体具有体外诱导血管生成

的能力；与未动员的外周血内皮祖细胞相比，动员后外周血内皮祖细胞数量明显增加并具有更好的增殖能力。
结论 粒细胞集落刺激因子动员的外周血中内皮祖细胞具有更好的增殖能力

PO-0157

缺陷型金属有机骨架应用脂质探针高效无损分离细胞外囊泡

潘炜伦、李博、冯俊杰
南方医科大学南方医院

细胞外囊泡（EVs）在疾病治疗中具有巨大的临床应用前景，但目前仍缺乏快速有效的 EVs 分离平台。本文报道了一种以缺陷型金属有机框架（MOF）为载体，脂质探针 PSDC 为捕获元件的 EVs 高效分离平台 MOF@PSDC。该平台中的脂质探针能嵌入 EVs 的脂质双分子层中完成快速捕获及分离。我们首先合成了 MOF UiO-66-NH2 并在此基础上构建 MOF@PSDC，动态光散射结果显示其粒径增大，电位降低，证明了 MOF@PSDC 的成功合成。接下来，我们利用共聚焦成像技术与超分辨显微镜分别在细胞水平与 EVs 水平验证了所设计的脂质探针具有高效脂质双分子层识别能力，能够用于 EVs 的快速识别和分离。其次，通过投射电镜与原子力显微镜可知，MOF@PSDC 能够高效捕获 EVs，且所分离的 EVs 结构典型，背景杂质干扰少。进一步通过条件优化，MOF@PSDC 可在 10 分钟内实现 EVs 的富集，效率达到 77%，且通过常规表征证明所分离的 EVs 粒径、结构、蛋白表达皆符合国际细胞外囊泡学会发布的《细胞外囊泡最低研究标准 2018》中的定义。进一步，超分辨显微镜成像技术证明，平台所分离的 EVs 仍然保持活性，可应用于下游检测分析。综上所述，我们成功构建了一个基于脂质探针和缺陷型 MOF 的通用 EVs 分离平台 MOF@PSDC。其中，脂质探针可高效嵌入 EVs 的脂质双分子层中，而 MOF 载体可通过低速离心即可将 EVs 从繁杂溶液体系中分离出来，且保持 EVs 的结构完整性与生物学性质。本方法与传统金标准超速离心法相比，具有快速、高效、无损和杂质少的优点，而不需要昂贵的设备。本研究为发展临床适用的 EVs 快速分离平台提供了理论基础。

PO-0158

血清 2019-nCoV IgM、IgG 抗体阳性与其相关性分析

唐丽红、韩晓丽
乌鲁木齐市友谊医院

目的 分析血清 2019-nCoV IgM、IgG 抗体阳性与其相关性。
方法 本次研究收集 2020 年 3 月 9 日至 4 月 22 日收治我院采用新型冠状病毒 2019-nCoV 抗体检测试剂盒（胶体金法）进行检测 IgM 和 IgG 抗体的患者共 699 人。
结果 本次研究共检测了 699 人，IgM 检测阳性率为 1.89%；IgG 检测阳性率为 0.199%。研究结果显示，同一民族的不同性别间、同一性别的不同民族间患者的血清 2019-nCoV IgM 表达，不同性别间的阳性率及不同民族间阳性率差异均无统计学意义（P>0.05）。血清 2019-nCoV IgM 抗体检测阳性组白细胞、中性粒细胞百分比、中性粒细胞计数、单核细胞计数、血小板、血小板压积、血小板分布宽度、C-反应蛋白等值高于阴性组，而血清 2019-nCoV IgM 抗体检测阳性组淋巴细胞百分比、嗜碱性粒细胞百分比、红细胞、血红蛋白、红细胞压积等值低于阴性组，差异均具有统计学意义（P<0.05）。
结论 血清学检测有简便、快捷、经济的优点。特异性抗体阳性可以提示临床需对这些患者核酸检测样本的采样更加关注，此时需考虑进一步复查核酸检测。

PO-0159

ICOS 和 PD-1 协同刺激信号在四氯化碳致小鼠肝纤维化中的动态变化

丁海涛、王波、肖伟利、贺娟、李媛
内蒙古自治区人民医院

目的 探讨可诱导共刺激分子（inducible costimulatory molecular， ICOS）和程序性死亡受体 1（programmed cell death protein 1，PD-1）蛋白在四氯化碳致小鼠肝纤维化中的动态变化。
方法 将 80 只雄性 BALB/c 小鼠按随机数字表法分为正常对照组和肝纤维化模型组，每组 40 只。酶联免疫吸附测定法 （enzyme-linked immunosorbent assay，ELISA）检测小鼠不同周期脾淋巴细胞培养上清中的相关细胞因子白细胞介素（interleukin，IL）-21 /IL-33/转化生长因子-β1（transforming growth factor-β，TGF-β1）的分泌水平及小鼠血清中 PCⅢ的含量；流式细胞仪分析测定不同阶段滤泡辅助性 T 细胞（follicular helper cells，Tfh）群 ICOS 及 PD-1 的动态表达趋势及特征；并分析 PD-1+ CD4+ CXCR5+ T 细胞、ICOS+ CD4+ CXCR5+ T 细胞与肝纤维化标志物Ⅲ型前胶原肽（Procollagen type Ⅲ， PCⅢ）的相关性。
结果 与正常对照组相比，纤维化模型组中 CXCR5+ CD4+ T 细胞表面 PD-1 的表达比例均明显升高，并在 13 W 达到峰值，组间差异有统计学意义{（2.77±0.92）% 比[8 W：（6.53±2.12）%，13 W：（27.47±5.15）%，20 W：（19.20±6.64）%]， t 值分别为 4.60、13.35、6.93 ，P 值均<0.05}；CXCR5+ CD4+ T 细胞表面 ICOS 的表达比例亦逐渐升高，13 W 达到峰值，组间差异有统计学意义{（1.13±0.44）% 比[（8 W：（13.28±3.85）%，13 W：（33.62±6.28）%，20 W：（21.50±5.83）%]，t 值分别为 8.87、14.60、9.85 ，P 值均<0.05 }。随着病程进展，肝纤维化小鼠组 CD4+ CXCR5+ T 细胞群 IL-33，IL-21，TGF-β1 的表达从 8 W 开始上调，13 W 达到峰值，20 W 仍维持较高水平，且均显著高于对照组（P 值均<0.05）。PD-1+ CD4+ CXCR5+ T、ICOS+ CD4+ CXCR5+ T 细胞表达水平与 PCⅢ的水平成正相关（r 值分别为 0.6278 和 0.6036，P 值均<0.05）。
结论 肝纤维化慢性期 ICOS+ 和 PD-1+ 的循环 Tfh 细胞可能促进肝纤维化发病，IL-21 和 IL-33 作为主要的细胞因子参与炎症进展。

PO-0160

单细胞代谢调节组分析来表征代谢调节的单细胞以及他们的表型特征

马智颖
山东大学第二医院

目的 细胞代谢调节免疫细胞的激活、分化和效应功能，但目前的代谢方法缺乏单细胞分辨和同时表征细胞表型。在这里，我们开发了一种方法来表征代谢调节的单细胞以及他们的表型特征。生物组织具有很大的异质性，因此需要利用单细胞平台进行深入研究。技术进步正在从多个层面推动单细胞分析的前沿，包括基因组、转录组、表观基因组和蛋白质组。在这里，我们提出了 scMEP，一种利用基于抗体的检测结合单细胞水平上的细胞身份来分析代谢调节的方法。对代谢调节的关注使我们能够直接从有限的、离体的人体物质中定义代谢状态。
方法和结果 代谢调节体的靶向定量区分人类免疫群体。代谢调节体的靶向定量区分人类免疫群体。T 细胞激活的整合模型识别了代谢转换的检查点。组织特异性代谢调节组定义了人类 T 细胞亚群。人体组织隔间的细胞代谢与空间组织有关。肿瘤免疫边界代表一种独特的代谢生态位。

该方法，单细胞代谢调节组分析(scMEP)，使用高维抗体为基础的方法定量蛋白质调节代谢途径的活性。通过重建体外激活的原始和记忆性 CD8+ T 细胞的代谢重构，我们使用细胞计数仪(CyTOF)将 scMEP 作为整体代谢检测的基准。我们将该方法应用于临床样本，并在人类结直肠癌中鉴定出组织受限、代谢抑制的细胞毒性 T 细胞。将我们的方法与成像质谱(MIBI-TOF)相结合，我们发现了代谢程序的空间组织，这表明从肿瘤免疫边界排除了代谢抑制的免疫细胞。总的来说，我们的方法使单个细胞的代谢和功能状态的稳健近似。

结论 我们在这里提出了一个稳健的方法来研究使用基于抗体的多重技术的单细胞代谢。scMEP 的应用将有助于更好地理解人类免疫细胞生物学，有助于识别与疾病相关的代谢改变，这可能作为各种人类疾病的潜在生物标记物和治疗靶点。

PO-0161

ICOS 阻断后肝纤维化小鼠体内 IL-33/ST2 表达的动态变化及意义

王波、丁海涛、李媛、肖伟利、贺娟
内蒙古自治区人民医院

目的 探讨可诱导共刺激分子 （Inducible costimulator, ICOS）阻断后，四氯化碳诱导肝纤维化小鼠白细胞介素 33(interleukin-33，IL-33)/白细胞介素 1 受体样 1 (interleukin 1 receptor like 1，ST2) 表达的动态变化。

方法 将 80 只雄性 BALB/c 小鼠按随机数字表法分为正常对照组和肝纤维化模型组，每组 40 只。流式细胞术分别检测 ICOS 阻断组和未阻断组肝纤维化小鼠脾淋巴细胞中 T 细胞表面 ICOS 表达的动态变化；酶联免疫吸附测定法 （enzyme-linked immunosorbent assay，ELISA）检测小鼠不同周期脾淋巴细胞培养上清中 IL-33/ST2 水平；并分析小鼠血清中 AST 和 ALT 的水平以及 IL-33 的表达水平与 ICOS 的相关性分析。

结果 与未阻断组相比，阻断 ICOS 组纤维化模型组中 CD4+ T 细胞表面 ICOS 表达水平明显下调，差异有统计学意义{[6 W：（25.29±4.87）% 比（2.81±0.82）%，13 W：（41.62±7.10）%比（5.33±2.05）%，16W：（30.42±4.51）%比（4.95±1.98）%]， t 值分别为 12.88、13.89、14.63，P 值均<0.05}；ICOS 阻断组与未阻断组相比，6 周后 IL-33、ST2 的表达水平均明显下降，差异有统计学意义（t 值分别为：IL-33：5.52、5.70、4.57；ST2：3.68、6.11、4.50，P 值均<0.05）。阻断 ICOS 后，AST 和 ALT 的水平在肝纤维化的 6 周后均明显下调，差异有统计学意义（t 值分别为：AST：4.53、5.53、2.31；ALT：4.16、3.28、3.86，P 值均<0.05）。另外，肝纤维化模型组脾淋巴细胞培养上清中 IL-33 的水平与 ICOS 的表达成正相关（r=0.2170，P=0.0385）。

结论 肝纤维化慢性期 ICOS 可能促进肝纤维化发病，IL-33/ST2 作为主要的细胞因子参与炎症进展。

PO-0162

霉酚酸酯预处理对小鼠肝脏缺血/再灌注损伤的保护作用

杜振东[1]、熊丞[2]
1. 上海交通大学医学院附属仁济医院南院
2. 上海交通大学医学院附属瑞金医院

目的 霉酚酸酯(mycophenolate mofetil，MMF)是一种免疫抑制药，在缺血/再灌注损伤过程中对器官发挥抗炎作用。然而，MMF 在肝脏缺血/再灌注损伤中的确切作用仍然是个未知数。本研究旨在探讨 MMF 在肝脏缺血/再灌注损伤中的保护作用及其可能机制。

方法 用 MMF 或生理盐水腹腔注射雄性野生型(WT)和 TLR4 基因敲除(KO)小鼠。动物肝脏行局部缺血 90min，再灌注 1h、6h 或 24h。肝组织学、血清转氨酶、炎性细胞因子、肝细胞凋亡和肝细胞自噬检测评估肝脏损伤。
结果 MMF 治疗显著减少肝脏缺血/再灌注损伤，血清氨基转移酶水平降低，Suzuki 评分降低，总体坏死程度降低。MMF 处理显著抑制 TLR4 活化。MMF 还能显著抑制 NF-κB 通路的激活和促炎细胞因子的表达。在 TLR4 KO 的 鼠中，MMF 仍然对肝脏缺血/再灌注损伤有保护作用。MMF 处理可抑制肝细胞凋亡，表现为 TUNEL 染色减少，及裂解 Caspase-3 的表达增加。MMF 通过增加 LC3-II，P62，和 Beclin-1 的表达，在肝再灌注前后诱导自噬，增加自噬通量。MMF 诱导的自噬可能与 TLR4 激活有关。
结论 结果表明，MMF 治疗可以改善肝脏缺血/再灌注损伤。其作用机制可能与 MMF 在诱导细胞自噬的同时降低细胞凋亡和炎症反应有关。

PO-0163

新型冠状病毒感染者咽拭子病毒载量与抗体水平的动态分析

胡金曹、沈瀚、陶月
南京大学医学院附属鼓楼医院

目的 分析新型冠状病毒肺炎（COVID-19）患者的咽拭子病毒载量与其血清特异性抗体水平的相关性。
方法 选取 2020 年 1 月到 3 月期间在南京市第二医院汤山分院收治的 COVID-19 患者 19 例，包括 7 例重症感染者和 12 例非重症感染者。通过实时荧光逆转录聚合酶链反应动态监测其咽拭子 SARS-CoV-2 核酸病毒载量。利用新冠病毒的四种蛋白（NP、S1、RBD 和 ECD）作为包被抗原，ELISA 方法检测患者体内针对 RBD、S1、ECD 和 NP 蛋白的特异性 IgM 和 IgG 抗体水平，并分析病毒载量与抗体之间的动态变化模式。
结果 利用 ELISA 发现，72.2%～93.1%的 COVID-19 血清标本为阳性，且在 COVID-19 发病进程中，所有患者体内均能产生了针对新冠病毒抗原的特异抗体。COVID-10 重症患者和非重症患者的病毒载量和抗体的动态变化模式呈多样化。
结论 研究 COVID-19 患者的病毒载量和抗体水平的动态变化水平，将为新冠病毒的抗体检测、基于抗体的治疗策略以及 COVID-19 疫苗的研发提供参考。

PO-0164

ANCA 相关性血管炎的中医证型与实验室指标的相关性分析

马明坤[1]、刘晟铭[2]、朱黎娜[1]、武广晔[1]、温学红[1]
1. 天津中医药大学第二附属医院
2. 天津医科大学

目的 探讨 ANCA 相关性血管炎的中医证型与其实验室指标间的相关性
方法 选择我院 2016 年 1 月～ 2021 年 1 月间疾病诊断为 ANCA 相关性血管炎(ANCA associated vasculitis，AAV)患者的检验数据共 186 份作为研究对象。中医辨证分型大致分为脾肾亏虚证、痰浊瘀阻证、痰热癍肺证、湿热内蕴证四种证型。同时收集病人中性粒细胞胞浆抗体检测项目、C 反应蛋白（C-reactive protein，CRP）、D-二聚体（D-Dimer）、血小板（platelet，PLT）等实验室检测指标结果，结合中医辨证分型进行分组，比较其是否具有统计学意义。
结果 脾肾亏虚、痰浊瘀阻、痰热癍肺、湿热内蕴这四种 AAV 中医证型中，D-Dimer 和 PLT 均没有统计学意义（$p>0.05$），而在 CRP 这一指标中，脾肾亏虚证与痰热癍肺证（$p<0.05$），痰浊瘀阻证与痰热壅肺证（$p<0.05$）具有统计学意义。在 pANCA 和 cANCA 两项指标下，脾肾亏虚证、痰

浊瘀阻证、痰热瘫肺证、湿热内蕴证四种不同证型 AAV 患者的组间阴阳性没有统计学意义；在抗 MPO 抗体和抗 PR3 抗体两项指标下四组中医证型阴阳性具有统计学意义（$p<0.05$）。

结论 痰热瘫肺证 AAV 患者的 CRP 平均水平高于痰浊瘀阻证证 AAV 患者的 CRP 平均水平；痰热瘫肺证 AAV 患者的 CRP 平均水平高于脾肾亏虚证 AAV 患者的 CRP 平均水平。抗 MPO 抗体与抗 PR3 抗体在四组间的对比具有统计学意义，其中痰浊瘀阻证两项指标阳性占比最高。其他选取指标间比较结果无统计学意义。

PO-0165

布鲁氏菌感染中巨噬细胞极化通过 PD-1/PD-L2 途径对 T 细胞亚群的调控作用研究

李智伟[1]、王昌敏[1]、丁剑冰[2]
1. 新疆维吾尔自治区人民医院
2. 新疆医科大学

目的 布鲁氏菌病慢性程度高，免疫机制不清。研究为明确布病时巨噬细胞极化特点并阐明 M2 型巨噬细胞通过 PD-1/PD-L2 途径变化调控 Th 细胞的机制。

方法 收集 2017.9 -2019.6 就诊于新疆自治区人民医院的布病患者 126 例和健康对照 120 例。通过流式细胞术检测外周血 M1 和 M2 型巨噬细胞以及 PD-L2 的表达；Th1，Th2，Th17，Treg 细胞及其上 PD-1 的表达。qRT-PCR 和 Western Blot 检测 T-bet、GATA-3、IFN-γ、IL-4、iNOS、Arg-1、TNF-α、IL-1RA 的 mRNA 和蛋白表达。检测血清中 TNF-α、IL-1RA、IFN-γ 和 IL-4 水平。通过分选布病患者的 M2 细胞和对照组的 CD4+T 细胞，进行体外试验。分别对 PD-L2 进行增强或阻断，以及对 PD-1 阻断，观察 T-bet、GATA-3、IFN-γ、IL-4 的 RNA 和蛋白表达以及 IFN-γ 和 IL-4 的变化情况。

结果 布病组的 M2 细胞增加，且 M2 细胞上的 PD-L2 表达下调。iNOS、TNF-α、Arg-1 和 IL-1RA 增加，血清中 TNF-α 增高，IL-1RA 显著增高。布病组 Th1 降低，Th2 增多，Treg 增高，PD-1 在 Th1、Th2、Treg 细胞上的表达增高。血清中 IL-4 增加。T-bet 的 mRNA 和蛋白水平无明显变化，GATA-3 和 IL-4 的 mRNA 和蛋白水平则升高，IFN-γ 的 mRNA 和蛋白水平升高。体外试验结果发现，在加入了 PD-L2 后，M2 型巨噬细胞会上调 T-bet 和 IFN-γ 的表达水平，并下调 GATA-3 和 IL-4 的表达水平。在加入了 Anti-PD-L2 后，M2 型巨噬细胞会进一步下调 T-bet 的表达水平，并上调 GATA-3 和 IL-4 的表达水平，阻断 PD-L2 后则会得到相反的结果。加入 PD-L2 使 T-bet 和 IFN-γ 的表达水平升高后，进一步加入 Anti-PD-L2 阻断 PD-L2 可以下调 T-bet 和 IFN-γ 的表达水平。在加入 PD-L2 并阻断 PD-L2 后，T-bet、GATA-3、IFN-γ 和 IL-4 的表达水平恢复到与 M2 组相同的水平。在阻断 PD-L2 或者阻断 PD-1 后 T-bet、GATA-3、IFN-γ 和 IL-4 的表达水平无明显差异。

结论 布鲁氏菌病患者体内巨噬细胞以 M2 型极化占优势，且 M2 上的 PD-L2 表达下调。同时 Th1 降低，Th2 增多，Treg 增多。Th1、Th2 和 Treg 上的 PD-1 增高，PD-1 参与了 CD4+T 亚群的调控。体外试验表明 M2 型巨噬细胞通过 PD-1/PD-L2 途径影响 Th1/Th2 平衡参与布鲁氏菌病的发生发展。

PO-0166

Human Amniotic Mesenchymal Stem Cells Inhibit aGVHD in Humanized NPG Mice by Suppressing Effector T Cells

Ya Gao 、weiru Li、xiaoyin Bu、shengchun Cai、xiumei Hu、Lei Zheng、baohong Ping
Nanfang Hospital, Southern Medical University

Background Acute graft versus host disease (aGVHD) occurs when immunocompetent T cells in the donated tissue recognize the recipient as foreign after allo-HSCT, which can severely affect the quality of life.The aim of this study was to explore the therapeutic efficacy and underlying mechanisms of human amniotic mesenchymal stem cells (hAMSCs) transplantation for the humanized aGVHD mouse model.
Methods We established a humanized aGVHD mouse model by transplanting human peripheral blood mononuclear cells (PBMCs) into NOD-PrkdcscidIL2rγnull (NPG) mice. Mice were divided into control group (untreated), aGVHD group, and hAMSCs treatment group, the hAMSCs labeled with GFP were administered to aGVHD mice to explore the homing ability of hAMSCs. T effector and Treg cell levels and cytokines of each group in target organs were detected by flow cytometry and cytometric bead array (CBA) respectively.
Results We successfully established a humanized aGVHD mouse model using NPG mice. The hAMSCs have the ability to inhibit aGVHD in this mouse model. hAMSCs suppressed xenogenesis CD3+CD4+ T and CD3+CD8+ T cell proportion and increased the number of Treg cells, and besides, hAMSCs can reduce the levels of IL-17A, INF-γ, TNF, and IL-2 in aGVHD target organs.
Conclusions The NPG murine environment was capable of activating human T cells to produce aGVHD pathology to mimic aGVHD as in humans. The hAMSCs controlled aGVHD by decreasing inflammatory cytokine secretion within target organs by modulating the balance of Treg and T effector cells in humanized mice.

PO-0167

Serological characteristics of patients with rheumatoid arthritis carrying anti-SSA/Ro

Wei Wang 、Siyu Wu
Department of Clinical Laboratory, Xiangya Hospital, Central South University,

Objectives To analysis the serological characteristics of anti-SSA/Ro positive RA patients and to evaluate the associations between the serological characteristics observed in RA and synovitis.
Methods 971 RA patients were screened from the Xiangya Hospital’s original database for the availability of anti-ENA antibody data. The prevalence of each anti-ENA antibody in 971 RA patients was analyzed and the serological characteristics of anti-SSA/Ro positive RA patients were concluded. Among the 971 RA patients, 380 RA patients performed the ultrasound imaging to judge about synovitis. Binary logistic regression analysis was performed to evaluate the associations between the serological characteristics observed in RA and synovitis.
Results The prevalence of anti-SSA/Ro60 and anti-SSA/Ro52 in 971 RA patients were 12.26 % and 12.15 %. Anti-SSA/Ro60 positivity was associated with high titers of other autoantibodies (RF, ACPA, anti-SSA/Ro52 and anti-SSB), and anti-SSA/Ro52 positivity was associated with anti-SSA/Ro60 and anti-SSB. Levels of CRP, C4, ANC and PLT were showed lower, and levels of IgG and IgA showed higher in anti-SSA/Ro60-positive group. And levels of CRP and ANC were showed lower, and levels of IgG showed higher in anti-SSA/Ro52-positive group. Further logistic regression analysis revealed that anti-SSA/Ro60 antibody may be a protective factor for synovitis in RA.

Conclusions Anti-SSA/Ro-positive RA patients might be a distinct subset with high titers of other autoantibodies and low acute phase reactive proteins. And anti-SSA/Ro60 antibody might be a protective factor for synovitis in RA, which provide new insights into the association between anti-SSA/Ro and the pathogenesis of RA.

PO-0168

Anti-citrullinated protein antibodies are associated with neutrophil extracellular trap formation in rheumatoid arthritis

Wei Wang 、Siyu Wu
Department of Clinical Laboratory, Xiangya Hospital, Central South University,

Objectives We evaluated the associations of anti-citrullinated protein antibodies (ACPAs) and serological and cytological levels of neutrophil extracellular trap (NET) formation in rheumatoid arthritis (RA) patients.
Methods Serum levels of myeloperoxidase-DNA and elastase-DNA complexes (NET remnants) were examined in 51 patients with RA and 40 healthy controls using a modified enzyme-linked immunosorbent assay. Neutrophils were isolated by density gradient centrifugation. IgG antibodies were purified by affinity chromatography.NET formation in RA and control neutrophils was assessed by microscopy in vitro.NETs were purified and co-incubated with fibroblast-like synoviocyte (FLS) cells.Interleukin (IL)-6 and IL-8 mRNA expression and protein levels in FLS cells were determined by real-time polymerase chain reaction and enzyme-linked immunosorbent assay, respectively.
Results In RA patients, NET remnants in the peripheral circulation were higher in extremely high ACPA titers when compared to in moderate ACPA titers. And IgG antibodies containing ACPA can stimulate neutrophils to form NETs in a concentration-dependent manner. Furthermore, significantly higher expression of the pro-inflammatory cytokines IL-6 and IL-8 is detected after FLS cells interacted with NETs which derived from neutrophils stimulated with ACPA-containing IgG antibodies.
Conclusions Anti-citrullinated protein antibodies may enhance NET formation and contribute to inflammation development in RA by stimulating NET formation, such as by subsequent activation of FLS cells by NETs.

PO-0169

Human Amniotic Mesenchymal Stem Cells Inhibit Acute Graft versus Host Disease in Humanized Mice by Regulating the Balance of T cells and Treg Cells

Ya Gao、Baohong Ping、Xiaoyin Bu、Shengchun Cai、Xiumei Hu、Lei Zheng
Department of Hematology, Nanfang Hospital, Southern Medical University

Background Acute graft versus host disease (aGVHD) occurs when immunocompetent T cells in the donated tissue recognize the recipient as foreign after allo-HSCT, which can severely affect the quality of life.The aim of this study was to explore the therapeutic efficacy and underlying mechanisms of human amniotic mesenchymal stem cells (hAMSCs) transplantation for the humanized aGVHD mouse model.
Methods We established a humanized aGVHD mouse model by transplanting human peripheral blood mononuclear cells (PBMCs) into NOD-PrkdcscidIL2rγnull (NPG) mice. Mice were divided into control group (untreated), aGVHD group, and hAMSCs treatment group, the hAMSCs labeled

with GFP were administered to aGVHD mice to explore the homing ability of hAMSCs. T effector and Treg cell levels and cytokines of each group in target organs were detected by flow cytometry and cytometric bead array (CBA) respectively.
Results We successfully established a humanized aGVHD mouse model using NPG mice. The hAMSCs have the ability to inhibit aGVHD in this mouse model. hAMSCs suppressed xenogenesis CD3+CD4+ T and CD3+CD8+ T cell proportion and increased the number of Treg cells, and besides, hAMSCs can reduce the levels of IL-17A, INF-γ, TNF, and IL-2 in aGVHD target organs.
Conclusions The NPG murine environment was capable of activating human T cells to produce aGVHD pathology to mimic aGVHD as in humans. The hAMSCs controlled aGVHD by decreasing inflammatory cytokine secretion within target organs by modulating the balance of Treg and T effector cells in humanized mice.

PO-0170

肺癌七项自身抗体与相关肿瘤标志物联合检测对肺癌诊断的价值

高慎霞
天津市胸科医院

目的 分析七种自身抗体（seven autoantibodies，7-AABs，包括 PGP9.5、GBU4-5、p53、GAGE7、MAGE A1、SOX2、CAGE）和相关肿瘤标志物（CEA+NSE+CYFRA21-1）单独及联合检测对肺癌诊断的价值，并探究 7-AABs 的阳性率及表达水平在不同肺癌病理分型及临床 TNM 分期间的差异，为临床诊断提供新思路。
方法 选取天津市胸科医院 2020 年 9 月至 2021 年 1 月的肺癌患者 186 例，并选取同期就诊的肺良性病变患者 74 例作为对照组，采用酶联免疫吸附法检测两组患者血清中 7-AABs 含量，收集患者 CEA、NSE、CYFRA21-1 三种肿瘤标志物数据，比较两组患者 7-AABs 阳性率和表达水平的差异，同时比较肺癌组中不同病理分型及不同 TNM 分期患者中 7-AABs 的差异，通过 ROC 曲线判断 7-AABs 和肿瘤标志物（CEA+NSE+CYRFRA21-1）单独及联合检测对肺癌的诊断效能。统计学分析采用统计学软件 SPSS 进行。若 P<0.05，则认为差异有统计学意义。
结果 肺癌组 7-AABs 阳性率高于肺良性疾病组。p53 与 PGP9.5 在 III 期+IV 期组中的表达水平高于 I 期+II 期组；7-AABs 在小细胞肺癌组及鳞癌组中的阳性率高于腺癌组。在 ROC 曲线中，7-AABs+肿瘤标志物联合检测 AUC 值为 0.777，灵敏度为 0.919，特异度为 0.635，联合检测的灵敏度较 7-AABs 单独检测提升了 0.419，较肿瘤标志物单独检测提升了 0.209（P<0.05）。
结论 7-AABs 与相关肿瘤标志物联合检测可提高肺癌诊断的灵敏，可为临床上肺癌的辅助诊断提供新思路。

PO-0171

Soluble POSTN as a potential biomarker for early chemotherapy efficacy monitoring in breast cancer

Dong Dong
Tianjin Medical University Cancer Institute and Hospital

Background The limitations of the current use of imaging for and chemotherapy efficacy monitoring in BCa are high costs, time-consuming, side effects from exposure to radiation and contrast agents, and potential delays in therapy reorientation. Noninvasive biomarkers for the early assessment of tumor response in breast cancer (BCa) are essential for optimized therapeutic decision-making. The most commonly used blood markers in BCa management, CA153 and CEA, provide incompetent performances due to limited sensitivity and specificity.

Therefore, there is an urgent need to explore other novel and reliable non-invasive biomarkers. POSTN is a secreted extracellular matrix (ECM) glycoprotein, which was originally identified in osteoblasts. Overexpression of POSTN have been implicated in several types of human cancer. And recent studies have indicated that POSTN was involved in cancer cell survival, ECM degradation, invasion, metastasis and chemoresistance. In BCa, immunohistochemistry results indicated that POSTN was overexpressed mainly in cancer-associated stroma and/or slightly in cancer cells, usually associated with poor clinical outcomes. Moreover, there was a trend of increasing POSTN expression in metastatic lymph nodes, as well as other tissues and organs. However, the clinical significance of circulating POSTN in BCa remains to be fully assessed. The aim of this study is to evaluate the potential of soluble POSTN in circulating as a biomarker for early chemotherapy efficacy monitoring in BCa.

Experimental Design：

In prevalence assessment, the correlation between the level of soluble POSTN and tumor volume, as well as TNM stages of BCa was verified. And in longitudinal assessment, BCa patients receiving conventional or Her2-targeted chemotherapy were enrolled. Soluble POSTN, together with CA153 or CEA, were determined in serum collected at different time points (C0, C1 and C2) by enzyme linked immunosorbent assay (ELISA) or electrochemiluminescence immunoassays. Then we compared the performances of markers in recapitulating the early chemotherapy efficacy assessed by imaging.

Results Serum levels of soluble POSTN were significantly increased in BCa patients compared with benign disease and healthy controls. Its levels were significantly associated with tumor volume and TNM stages of BCa, and its dynamics could recapitulate the early chemotherapy efficacy much better than that of CA153 and CEA. A strong consistency of POSTN response was observed in all four cases with progressive disease at both C1 and C2. Moreover, further analysis indicated that, for partial response, the monitoring efficiency of soluble POSTN with high baseline (above 17.05 ng/mL) at C2 was significantly higher than that of with low baseline (below 17.05 ng/mL, $P < 0.05$), and the baseline levels were significantly correlated with the change ratios of POSTN in the fourteen consistent cases ($r = 0.684$, $P = 0.007$). Moreover, response of soluble POSTN after the first cycle of chemotherapy (at C1) could predict the early efficacy of chemotherapy assessed by CT (at C2). Finally, overall survival analysis showed that patients experienced a significant early decrease of POSTN at C1 and C2 tended to obtain more benefits from the treatments.

Conclusions The current study suggests that soluble POSTN is an informative serum biomarker to complement the current clinical approaches for early chemotherapy efficacy monitoring in BCa, and performing soluble POSTN analysis to complement the current clinical approaches for early chemotherapy efficacy monitoring may be beneficial to patients with breast cancer.

PO-0172

基于三维石墨烯水凝胶复合材料的电化学免疫传感器的研发及其对分泌型自噬小体的检测

张越[1]、王立新[2]、沈艳飞[2]、周成林[1]
1. 泰州市人民医院
2. 东南大学

目的 肿瘤细胞释放分泌型自噬小体(TRAP)通过多种途径影响肿瘤生长，且 TRAP 可释放入外周血，提示外周血 TRAP 有望反映肿瘤进程。目前尚未有方法直接定量检测 TRAP，且外周血 TRAP 含量较少，因此，建立 TRAP 富集与定量检测的新方法有重要意义。基于此，我们研发 TRAP 特异性纳米磁珠用于外周血 TRAP 的纯化富集，同时利用免疫传感器的高灵敏度和高特异性以及纳米材料三维石墨烯水凝胶的优良特性，设计研发新型免疫传感器，用于 TRAP 富集后定量检测，为探究外周血 TRAP 含量与肿瘤疾病的关系提供新思路。

方法 1、扫描电镜、紫外-可见吸收光谱分析 Fe_3O_4-Au；Fe_3O_4-Au 偶联 LC3B 特异性抗体制备 TRAP 特异性纳米磁珠，激光共聚焦显微镜鉴定其合成并分析性能。
2、扫描电镜、紫外-可见吸收光谱验证三维石墨烯水凝胶-亚甲基蓝(GH-MB)合成，循环伏安法分析 GH-MB 性能；循环伏安法监测免疫传感器的构建；通过差分脉冲伏安法检测免疫传感器修饰富集所得 TRAP 前后的电流相对变化值定量检测 TRAP，并分析免疫传感器性能。
3、免疫传感器检测癌症患者与健康人外周血 TRAP 含量，分析其与肿瘤疾病的相关性。
结果 1、Fe_3O_4-Au 合成成功；TRAP 特异性纳米磁珠制备成功且性能优异。
2、GH-MB 合成成功，可放大电信号；免疫传感器构建成功，检测 TRAP 的线性范围为 60 pg/mL-600 ng/mL 且性能较好。
3、癌症患者与健康人外周血均含有 TRAP，且癌症患者外周血 TRAP 含量明显高于健康人。
结论 1、TRAP 特异性纳米磁珠与基于氧化石墨烯水凝胶复合材料的电化学免疫传感器研发成功，可用于 TRAP 的富集与定量检测。
2、免疫传感器 TRAP 检测法可应用于癌症患者外周血 TRAP 含量的检测，且初步发现癌症患者外周血 TRAP 含量明显高于健康人。

PO-0173

Dynamic observation of antibody responses in COVID-19 convalescents and vaccinated individuals by five surrogate neutralization assays

Ruiwei Jiang、Min Li、Enyun Wang、Jiwen Hu、Dan Xiong、Xiaowen Dou、Xiuming Zhang
Medical Laboratory Center of Luohu Hospital Group

Background The ongoing severe acute respiratory syndrome coronavirus (SARS-CoV-2) infection has persisted for approximate to one half and a year. Resistance to SARS-CoV-2 persists in infected people and whether antibodies produced against natural infection provide protective immunity, it is crucial for prevent reinfection risk and vaccine development to assess how long immunity. To investigate the changes of serum antibody levels in participants vaccinated with COVID-19 vaccine and those recovered with COVID-19, and to compare the performance of five neutralizing antibody (Nab) kits against SARS-CoV-2.
Patients and Methods In this study, a total of 164 healthy participants were enrolled for a two-dose procedure of inactive vaccination, and 10 COVID-19 convalescent patients. Venous blood was drawn at different time point, for assessing SARS-CoV-2 IgM, IgG and Nab. The seroconversion rate of different antibodies was calculated at different time points. Dynamic changes of antibody levels were observed at different time points. Besides, the correlation of antibody level were evaluated with three SARS-CoV-2 chemiluminescent assays (Axceed, iFlash and Ecl) and one enzyme-linked immunosorbent (ELISA) assay (Yaneng) compared directly the cPass ELISA neutralization test.
Results The antibody levels changed significantly with time extension after vaccination. The seroconversion of Nabs on day 28 after the first vaccination schedule was 13%, while the result increased to 85% in one week after the second dose. Whereas at day 28 after completely immune seroconversion was seen in 97%. The levels of Nabs increased steadily after vaccination, and enhanced sharply after the second dose of vaccine and the peak value was 6.67 AU/mL on day14, that's 14 times the base value (median 0.44AU/mL). The correlation between cPass and yaneng was the strongest ($r = 0.917$), followed by Ecl, Axceed ($r = 0.726$ and $r = 0.723$, respectively), the medium correlation was iFlash ($r = 0.565$).After, a total of 25 different levels of samples were separated for the "gold standard" - VNT. The results of VNT test showed that the positive rate of Nabs was 32% (n=8/25), whereas the test results of Axceed was 76% (n=19/25).The correlation between the SARS-CoV-2 chemiluminescent assays kit (Axceed) and VNT was r=0.57. Besides, The level of Nabs induced by vaccine was 7.41 AU/mL (95%CI：

5.02~9.8AU/mL, n=120,60days), which was 0.14 times higher than that of 52.47 AU/mL (95%CI：45.18~59.76AU/mL, n=33, 30-60days) in COVID-19 convalescent patients.
Conclusion Inactivated vaccines induce a strong humoral immunity response. Rapid detection method can be used to effectively evaluate the change of Nabs in humoral immune response products of vaccinators and recovered patients.

PO-0174

可溶性共刺激分子 B7-H3 在结直肠癌中的表达及临床意义

王蕾
上海市第八人民医院

目的 检测结直肠癌（CRC）患者血清可溶性 B7-H3（sB7-H3）的水平，探讨其在 CRC 中的临床应用价值。
方法 选取 CRC 患者 232 例，结直肠良性疾病患者 87 例，以及健康体检者 59 例（正常对照组）。分别测定 sB7-H3、癌胚抗原（CEA）、糖类抗原 19-9（CA19-9）、糖类抗原 72-4（CA72-4）及糖类抗原 50（CA-50）水平。采用受试者工作特征（ROC）曲线评价 B7-H3 对 CRC 的诊断效能；探讨 CRC 患者血清 B7-H3 水平与肿瘤部位、浸润深度、淋巴结转移状态、远处转移状态及肿瘤分期的相关性。
结果 （1） CRC 组、结直肠良性疾病组和正常对照组三组间两两比较，sB7-H3 水平差异均有统计学意义（P<0.001）。（2）在 CRC 组中，B7-H3 与 CA-50、CEA、CA72-4 均呈正相关（r 值分别为 0.220、0.217、0.142，P<0.05），而与 CA19-9 无相关性。（3）ROC 曲线显示，B7-H3 的曲线下面积最大，为 0.862，cut-off 值为 20.50，此时的敏感度为 0.850，特异度为 0.759。（4）免疫组化显示，CRC 组阳性率为 58.6%，炎症息肉组阳性率为 6.7%，二组的阳性率比较差异有统计学意义（P<0.01）。（5）CRC 患者血清 B7-H3 水平与肿瘤远处转移状态及病理学分期相关（P<0.05），而与肿瘤患者的性别、年龄、肿瘤部位及淋巴结转移状态无关（P 均>0.05）。
结论 B7-H3 对于 CRC 具有较好的辅助诊断价值，且与肿瘤远处转移状态及病理学分期相关，有助于临床早期诊断。

PO-0175

Diagnostic value of anti-citrullinated α-enolase peptide 1 in patients with rheumatoid arthritis: A meta-analysis

Haolong Li
Department of Clinical Laboratory, Peking Union Medical College Hospital, Peking Union Medical College and Chinese Academy of Medical Sciences, Beijing, China

Objective Rheumatoid arthritis (RA) is a common systematic autoimmune disorder which is mainly characterized by inflammatory arthritis. In this study, we evaluated the diagnostic value of anti-citrullinated α-enolase peptide 1 (anti-CEP 1) in patients with RA by performing systematic review and meta-analysis.
Medthods Five electronic databases were searched for relevant studies published by February 29,2020, including PubMed, Web of Science, Embase, Scopus and Cochrane Library. The bivariate mixed-effects model was used to calculated the diagnostic indexes from primary data of eligible studies by using STATA 15.0 software. The included articles were assessed with Quality Assessment of Diagnostic Accuracy Studies 2 tool. Subgroup analysis and meta-regression were also performed.

Results Twenty articles that met inclusion criteria were performed meta-analysis, there were a total of 13,864 RA patients and 6459 control participants. The pooled sensitivity, specificity, and positive and negative likelihood ratios for anti-CEP 1 were 44% (95% CI, 39%-55%), 97% (95% CI, 95% -98%), 14.44 (95% CI, 10.50-20.75), and 0.57 (95% CI, 0.52-0.61), respectively. The area under summary receiver operator characteristic curve was 0.81. The meta-regression indicated that the detection method for anti-CEP 1 may be the source of heterogeneity. The subgroup analysis showed that the group detected anti-CEP 1 using a commercial ELISA kit shows the sensitivity was 59% (95% CI: 50%-68%), the specificity was 93% (95% CI: 85%-97%).
Conclusion In conclusion, anti-CEP 1 has a moderate diagnostic value of diagnosing RA with relatively low sensitivity and high specificity, but using the commercial ELISA kit may increase the sensitivity of diagnosing RA.

PO-0176

严重急性呼吸综合征冠状病毒 2 抗体检测及临床应用概述

李昊隆
中国医学科学院北京协和医院

目的 从严重急性呼吸综合征冠状病毒 2（SARS-CoV-2）特异性抗体的产生、抗体检测方法的建立及其临床应用价值等方面做一综述。
方法 检索 PubMed、Web of Science、Scopus、Embase、中国知网以及万方数据库中已发表的 SARS-CoV-2 抗体产生、检测方法的建立、临床应用价值的相关文献，对已发表的文献进行总结。
结果 SARS-CoV-2 IgM 抗体主要出现在发病早期，而 IgG 抗体主要出现在发病的中后期。各厂商多选择 S 蛋白或 N 蛋白作为抗体检测试剂盒的靶抗原。SARS-CoV-2 抗体检测方法有酶联免疫吸附试验、化学发光免疫分析技术、胶体金免疫层析技术、荧光免疫分析技术。SARS-CoV-2 IgM 抗体诊断的灵敏度约为 68.2%-93.1%，IgG 抗体的灵敏度约为 64.7%-96.1%。抗体检测是核酸检测的重要补充手段，可在疑似病例的诊断中与核酸检测联合应用或作为核酸检测阴性的疑似病例的补充检测指标。COVID-19 患者 SARS-CoV-2 抗体水平的变化可以反映患者的病情进展。SARS-CoV-2 抗体检测还可用于疫苗效果的评估及病毒感染的血清流行病学调查。
结论 SARS-CoV-2 抗体检测是核酸检测手段重要的方法学补充，对于 COVID-19 患者的辅助诊断具有重要意义，与核酸检测联合应用可减少 COVID-19 患者漏检的情况。

PO-0177

The Value of Hematological Indexes in Evaluating the Risk of Hip Involvement in Patients with Ankylosing Spondylitis

Sihui Li、xi li、wei zhou、yanting jiang、min jin、jian wang
First Affiliated Hospital of Guangxi Medical University

Objective To analyze the laboratory data of ankylosing spondylitis (AS) patients with hip involvement, and explore the value of neutrophil to lymphocyte ratio (NLR) and monocyte to lymphocyte ratio (MLR) in evaluating the risk of hip involvement in patients with AS.
Methods Retrospective analysis was performed on a total of 188 patients with AS. According to BASRI score, 84 AS patients with hip radiology score ≥2 were selected as hip involvement group, and 104 AS patients with hip radiology score<2 as non-hip involvement group. During the same period, 173 patients with osteoarthritis (OA) and 181 healthy people by age and sex were selected. The characteristics of hematological indexes of the three groups were compared, and the levels of NLR and MLR in hip involvement group and non-hip involvement group were observed.

Results The values of NLR and MLR in AS group were significantly higher than those in OA group and healthy controls (each P<0.05). The values of NLR and MLR in hip joint involvement group were significantly higher than those in non-hip involvement group (P<0.05). The diagnostic efficiency of combined detection of NLR and MLR in AS-hip involvement group was significantly higher than that in AS-non-hip involvement group and OA group (AUC-AS-hip involvement group=0.863, P<0.001; AUC-AS-non-hip involvement group=0.746, P<0.001; AUC-OA group=0.669, P<0.001).
Conclusion NLR and MLR have certain value in the evaluation of AS patients with hip involvement, and the combined diagnosis of them has higher value.

PO-0178

A Novel Prognostic Model for patients with Hemophagocytic Lymphohistiocytosis

Jun Zhou、Hua-Guo Xu
First affiliated Hospital of Nanjing Medical University / Jiangsu Provincial people's Hospital

PURPOSE Hemophagocytic Lymphohistiocytosis (HLH) is a type of rare disease with low survival rate. We aimed to develop a clinical prediction model to evaluate the six-month prognosis in HLH patients.
METHODS The post-treatment data for newly diagnosed HLH patients was collected and a stepwise regression analysis was performed to select independent prognostic variables for inclusion in the model.
RESULTS Three laboratory markers were confirmed to be the independent risk factors (ferritin: hazard ratio (HR) 0.101, 95% confidence interval (CI) 0.036-0.282, P＜0.001; platelets: HR 4.799, 95% CI 1.884-12.223, P=0.001; alanine aminotransferase (ALT): HR 0.423, 95% CI 0.180-0.997, P=0.049). These were included in the final clinical prediction model. Receiver operating characteristic (ROC) curves disclosed that this model had a better discrimination (area under the curve (AUC)=0.842, 95% CI 0.773 -0.910, P<0.001) than each of them alone and the calibration curves aligned completely with the model predictions and actual observations. Kaplan-Meier curves revealed a significant difference in the overall survival (OS) in patients stratified by the model with higher values associated with a better OS.
CONCLUSION These results point out that serum ferritin, platelets and ALT levels are independent elements of OS in patients with HLH, and that the proposed model have a better prognostic value than any of these markers alone.

PO-0179

自身免疫性肝病患者血清 Linc00324 和 Th17 细胞因子的表达及意义

王芳
山东大学第二医院

目的 检测自身免疫性肝病患者血清辅助性 T 细胞 17(Th17)因子和长链非编码 RNA 00324(Linc00324)的表达情况,探讨其在自身免疫性肝病发病中的作用及关系.
方法 选取自身免疫性肝病患者 86 例，选取同期 52 例体检健康者作为健康对照组。采用实时荧光定量 PCR 法(qRT-PCR)检测各组血清 Linc00324 表达水平;采用流式细胞仪对 Th17 细胞因子白细胞介素-4(IL-4)、白细胞介素-10(IL-10)水平进行检测;采用 Pearson 法分析自身免疫性肝病患者血清 Linc00324 及 Th17 细胞因子 IL-4、IL-10 表达水平的相关性.

结果 自身免疫性肝病患者血清 Linc00324 水平、Th17 细胞因子 IL-4、IL-10 水平均显著高于对照组(P<0.05)，自身免疫性肝病患者血清 Linc00324 表达水平与 Th17 细胞因子 IL-4、IL-10 水平呈明显正相关(r=0.528、r=0.508,P<0.05).
结论 Linc00324 在自身免疫性肝病患者血清中明显高表达,Th17 细胞因子 IL-4、IL-10 水平在自身免疫性肝病患者中明显高表达，提示 Linc00324 在自身免疫性肝病早期诊断及病情评估具有重要的临床意义。

PO-0180

Comprehensive characteristics of lymphocyte subsets alterations in COVID-19 patients

Wei Dai、Xinyi Xia
Jinling Hospital

Objectives Coronavirus disease 2019 (COVID-19) is a respiratory disorder caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which had rapidly spread all over the world and induced public health emergency. Although the diagnosis and treatment for COVID-19 have been well defined, the immune cell characteristics and the key lymphocytes subsets alteration in COVID-19 patients have not been thoroughly investigated.
Methods In this study, the level of immune cells including T cell, B cell, and natural killer (NK) cell in 548 hospitalized COVID-19 patients, and 30 types of lymphocytes subsets in 125 COVID-19 patients admitted in Wuhan Huoshenshan Hospital of China were measured by flow cytometry. The relationship with cytokines Interleukin- 6 (IL-6), and the characteristics of lymphocytes subsets in single-cell RNA sequencing (scRNA-seq) data obtained from peripheral blood mononuclear cell (PBMC) were also analyzed in COVID-19 patients.
Results Our results indicated that patients with critical COVID-19 exhibited an overall decline of lymphocytes including CD4+ T cell, CD8+ T cell, total T cell, B cell, and NK cell compared to mild and severe patients. Whereas the number of lymphocytes subsets including CD21 low CD38 low B cell, effector T4 cell, and PD1+ depletes T8 cell were moderately increased in critical COVID-19 patients in comparison to mild cases. Notably, except for effect memory T4 cell, plasmablast and Treg, the number of all lymphocytes subsets were remarkably declined in COVID-19 patients with IL-6 levels over 30 fold than normal. Moreover, scRNA-seq data showed obvious differences in distribution and numbers of lymphocytes subsets between COVID-19 patients and healthy person, subsets-specific marker genes of lymphocyte subsets including CD4, CD19, CCR7, and IL7R in COVID-19 patients were remarkable decreased than those in health.
Conclusion Our investigation indicated that the comprehensive decrease of immunity cells and lymphocytes subsets in critical patients with COVID-19 infection, peripheral lymphocyte subsets alteration showed a clear association with the clinical characteristics. Targeting inflammation such as IL-6 is a promising tool for the treatment of COVID-19 and provides an evidence of the biological mechanism to the clearance of COVID-19 infection.

PO-0181

IL35 通过诱导淋巴细胞转化维持妊娠期免疫耐受

刘佳、李亚丽
山东大学第二医院

目的 妊娠早期的母体中存在大量免疫耐受淋巴细胞与抑制性细胞因子，并抑制母胎界面 Th17 细胞的免疫效应。我们先前的研究表明，妊娠早期滋养细胞可表达并分泌免疫抑制细胞因子 IL-35，并且早孕妇女外周血中 IL-35 水平显著升高。考虑到 IL-35 的免疫抑制作用及其在滋养层细胞中的表

达，我们推测母胎界面中 IL-35 可能通过诱导 iTR35 细胞分化参与维持母胎耐受,此外，作为抑制性免疫细胞的重要组成部分，Breg 细胞可通过调节外周免疫应答在自身免疫性疾病和感染中发挥调节作用。由于 B 淋巴细胞很少存在于母胎界面，因此我们主要研究了 Breg 细胞在妊娠期间外周免疫耐受中的调节作用。

方法 1．构建自然流产小鼠模型 CBA/J XDBA/2J 和正常妊娠小鼠模型 CBA/J XBALB/c。

2．通过 WB 的方法检测孕鼠母胎界面 IL-35 含量。

3．将小鼠重组 IL-35 细胞因子及 IL-35 中和性抗体分别对不同组孕鼠进行腹腔注射治疗，观察其对流产的影响以及母胎界面 iTR35 含量变化。

4. 通过 WB 的方法检测妊娠相关激素及 IL-35 诱导产生 B10 和 IL-35Breg 的相关信号通路和转录因子。

结果 1.自然流产孕鼠胚胎丢失率明显高于正常妊娠孕鼠。

2．自然流产孕鼠母胎界面 IL-35 水平和 iTR35 细胞的比例显著低于正常妊娠孕鼠。

3．IL-35 治疗显著提高了母胎界面 iTR35 含量并抑制流产的发生；

4.IL-35 和 hCG 均能抑制小鼠脾脏 B 细胞的增殖，hCG 可促使小鼠 B 细胞内的 STST3 磷酸化，诱导其转化生成 B10。

结论 IL-35 可分别在母胎界面和母体外周诱导抑制性 iTR35 细胞和 IL-35Breg 细胞产生，从而促进了母胎局部及妊娠期外周的免疫耐受形成。妊娠相关激素 hCG 也在外周 B10 细胞的诱导中发挥着重要作用。我们的研究为 IL-35 在治疗复发性流产中的应用提供了新的依据，具有重要的临床应用价值。

PO-0182

TK1 及 CA153 联合检测在乳腺癌诊断中的应用

郭信蓉
滨州医学院烟台附属医院

目的 探讨血清胸苷激酶 1（TK1）和血清糖类抗原 153（CA153）联合检测在乳腺癌诊断中的应用价值。

方法 选取 40 名乳腺癌患者作为乳癌组，40 名乳房良性疾病患者为良性疾病组，40 名女性健康体检者为健康对照组，采用电化学发光的方法测定血清 CA153 的含量，应用免疫印迹增强化学发光法测定 TK1 含量。

结果 乳癌组血清 TK1、CA153 的水平以及阳性率明显高于良性疾病组和健康对照组，差异均有统计学意义（P＜0.05）。联合检测 TK1 和 CA153 灵敏度提高到 87.50%，准确性上升到 88.33%，特异性变化不明显。

结论 与单项检测相比，联合检测 TK1 和 CA153 能有效提高乳腺癌诊断的灵敏度，使乳腺癌的检出率大幅增加，在乳腺癌早期诊断中有一定的临床价值。

PO-0183

血清鳞状上皮细胞癌抗原在银屑病患者皮损及疗效评估中的临床价值

魏彬
四川大学华西医院

目的 本研究旨在探讨 SCCA 在银屑病患者辅助诊断及疗效评估的临床应用价值。

方法 纳入 2020 年 6 月至 2021 年 1 月我院临床确诊 401 例皮肤疾病患者，包括银屑病 187 例，天疱疮 147 例，湿疹 28 例，特发性皮炎 27 例，红皮病 12 例，另外选取同期 660 例健康体检正常人群作为对照组，检测血清 SCCA 水平，采用 SPSS 统计软件分析数据。
结果 SCCA 测定结果显示，SCCA 在银屑病、天疱疮、湿疹、特应性皮炎、红皮病、对照组中的阳性率分别为 66.84%、17.00%、28.57%、62.96%、91.67%、2.42%，中位数分别为 4.49 (2.05-11.30) ng/ml、0.89 (0.62-1.53) ng/ml、1.96 (0.90-2.80) ng/ml、5.31 (1.54-13.90)ng/ml、22.05 (9.26-37.70)ng/ml、1.16 (0.91-1.47) ng/ml。各组间 SCCA 定量比较有统计学差异，红皮病患者最高，其次为特应性皮炎和银屑病患者。进一步针对银屑病亚类分析，未分类银屑病阳性率 73.68%，寻常型银屑病（含点滴型和斑块状银屑病）阳性率 63.16%，各银屑病亚类间血清 SCCA 水平无显著性差异（P>0.05）。银屑病患者治疗前皮损面积和严重程度指数(Psoriasis area and severity index, PASI)及体表受累面积(body surface area, BSA)与 SCCA 水平呈指数相关（PASI R=0.675，BSA R=0.609），治疗后皮损好转者 SCCA 显著降低（P<0.001）。
结论 血清 SCCA 水平可因皮损等原因在银屑病、红皮病及特异性皮炎中明显增加；血清 SCCA 检测可有效评估银屑病患者皮损受累程度和治疗效果。

PO-0184

血清 25-羟基维生素 D3 检测在儿童社区获得性肺炎中的应用价值分析

陆媛
西安市第一医院

目的 探讨血清 25-羟基维生素 D3[25-（OH）D3]在儿童社区获得性肺炎中的变化及临床意义。
方法 选择 2018 年 1 月-2018 年 6 月间我院儿科收治的 128 例社区获得性肺炎患儿为研究对象，根据病情程度分为轻症组（n=80）及重症组（n=48），选择同期在我院体检的健康儿童 50 例纳入对照组。比较不同组别研究对象血清 25-（OH）D3、超敏 C 反应蛋白（hs-CRP）水平，以及维生素 D 充足组（n=51）及维生素 D 缺乏组（n=77）患儿临床疗效。
结果 社区获得性肺炎（轻症组及重症组）患儿血清 25-（OH）D3 水平分别为（73.45±12.63）nmol/L、（68.36±11.74）nmol/L，均明显低于对照组的（81.64±11.52）nmol/L，血清 hs-CRP 水平分别为（11.28±3.36）mg/L、（16.61±4.54）mg/L，均高于对照组的（3.67±1.17）mg/L，差异有统计学意义（P＜0.05）；重症组患儿血清 25-（OH）D3 水平低于轻症组，血清 hs-CRP 水平则高于轻症组，差异有统计学意义（P＜0.05）；维生素 D 充足组患儿临床症状体征消退时间、住院时间分别为（7.16±2.14）d、（9.24±3.25）d，明显短于维生素 D 缺乏组的（9.93±3.29）d、（12.26±4.42）d，差异均有统计学意义（P＜0.05）。
结论 血清 25-（OH）D3 的缺乏与儿童社区获得性肺炎的发生关系密切，并且 25-（OH）D3 水平可以反映疾病的轻、重程度，且可以影响临床疗效。

PO-0185

乙肝病毒感染采用 HBV DNA 定量与乙肝血清学标志物定量联合检测的效果分析

赵棉
西安市第一医院

目的 探讨乙肝病毒（HBV）感染采用 HBV DNA 定量与乙肝血清学标志物定量联合检测的效果。
方法 回顾性分析 2017 年 1 月~2017 年 12 月我院 988 例乙型肝炎患者的临床资料，根据 HBV 血

清学标志物定量检测水平将其分为三组，即大三阳组 285 例、小三阳组 358 例与其他模型组 245 例。所有患者均行乙肝血清学标志物定量与 HBV DNA 定量检测。观察并分析 HBV DNA 对 HBV 感染的检测结果，血清标志物与 HBV DNA 检测的阳性率，以及不同血清学标志物定量模式与不同 HBV DNA 定量水平的检测结果。

结果 三组对 HBV DNA 检测的阳性率对比差异具有统计学意义（P<0.05），即大三阳组 HBV DNA 检测的阳性率>小三组>其他模型组。三组 HBV DNA 定量检测水平对比差异具有统计学意义（P<0.05），即大三阳组>小三阳组>其他模型组。490 例 HBV DNA 阳性样本中，HBeAg 检出率为 48.98%（240/490），HBsAg 检出率为 96.94%（475/490）。HBV DNA 水平>7 lg copies/ml 时，以大三阳组居多，占 77.24%；5~7 lg copies/ml 时，以大三阳组居多，占 66.04%；2.7~5lg copies/ml 时，以小三阳组居多，占 44.66%；<2.7lg copies/ml 时，以其他模型组居多，占 55.83%。

结论 HBV DNA 定量与乙肝血清学标志物定量联合检测能够有效增强 HBV 的诊断准确率，为评价 HBV 传染性与感染程度提供了有效的参考，适于临床应用。

PO-0186

MDSC 外泌体诱导小鼠结直肠癌细胞 EMT 的实验研究

蔡婧姗、王胜军
江苏大学附属人民医院

研究 MDSCs 来源 exosomes（MDSC-exo）对小鼠结直肠癌细胞上皮间质转化（EMT）和肿瘤转移的影响，并对其中的分子机制进行探讨。结果发现，与对照组相比，MDSC-exo 处理组的 CT26 细胞中 E-cadherin 蛋白表达降低，N-cadherin 的蛋白表达增高；转录因子 Snail1、Snail2、Zeb1 和 Twist1 的 mRNA 水平增加（P<0.05）。为了探讨 MDSC-exo 通过 ROS 诱导 EMT 的可能性，我们首先通过 FCM 证实 MDSCs 胞内 ROS 水平高于 CT26 细胞，并且 MDSC-exo 处理 CT26 细胞后，CT26 细胞 ROS 水平明显增加（P<0.01）。利用 ROS 清除剂 NAC 预处理 MDSCs 后，MDSCs 胞内 ROS 水平降低（P<0.05），外泌体中 ROS 水平也明显降低（P<0.05）。将 MDSC-exo 和 MDSCNAC-exo 分别处理 CT26 细胞，MDSCNAC-exo 组 CT26 细胞胞内 ROS 水平低于 MDSC-exo 组（P<0.05），并与对照组无明显差异（P>0.05）。经 MDSC-exo 处理 CT26 细胞 E-cadherin 和 Claudin-1 的蛋白表达低于对照组（P<0.001），Vimentin、Snail1 和 Zeb1 的蛋白表达高于对照组（P<0.001）；而当抑制 MDSC-exo 中 ROS 水平后，MDSCNAC-exo 处理组中 CT26 细胞的 Claudin-1、Vimentin 和 Zeb1 的蛋白表达低于 MDSC-exo 组（P<0.05），Snail1 的蛋白表达高于 MDSC-exo 组（P<0.01），E-cadheirn 表达无明显差异（P>0.05）。MDSC-exo 具有诱导 CT26 细胞 EMT 的作用，同时 MDSC-exo 能够增强肿瘤细胞迁移和侵袭，其作用机制可能部分依赖于 MDSC-exo 中携带的 ROS。

PO-0187

Netrin-1 对肿瘤髓源性抑制细胞功能的影响及机制研究

夏雪莉、王胜军
江苏大学附属人民医院

目的 肿瘤细胞常分泌多种分子调节 MDSCs 的分化发育与功能，我们探究结直肠癌细胞分泌的 Netrin-1 对 MDSCs 功能的作用及机制。

方法 ①检测小鼠结肠癌细胞系的 Netrin-1 表达情况，体外用 Netrin-1 重组蛋白处理 MDSC，检测 MDSC 对 T 细胞增殖的抑制能力以及多种免疫抑制效应分子的 mRNA 和蛋白水平。②qRT-PCR 验证 Netrin-1 及其受体 在 MDSC 上的表达，筛选可能的 Netrin-1 受体。在体外用 Netrin-1 重组蛋

白，受体拮抗剂和受体激动剂处理 MDSC，检测 MDSC 免疫抑制功能变化。 ③利用慢病毒载体敲减 Netrin-1 的稳转结肠癌细胞株，监测小鼠移植瘤的生长情况。

结果 利用 Netrin-1 重组蛋白处理 MC38 荷瘤小鼠脾脏 MDSCs，关键的免疫抑制分子活性氧（ROS）产生显著增多，Arg1 活性增强，但没有改变 NO 产生水平。MDSC 培养上清中分泌的 IL-10 和 TGF-β1 升高。对 MDSCs 上不同的 Netrin-1 受体的分析表明，A2BR 高表达，而 UNC5H 家族受体，DCC，neogenin 或 DSCAM 低表达或不表达。Netrin-1 诱导的 MDSC 免疫抑制活性被 A2BR 选择性拮抗剂 PSB1115 显著减弱，证实了 A2BR 在 Netrin-1 信号转导中的作用。为了进一步研究 Netrin-1 调节 MDSC 免疫抑制功能的机制，我们发现 Netrin-1 通过受体 A2BR 激活 cAMP-PKA-pCREB 信号通路。磷酸化的 CREB 直接与 C /EBP-β 启动子的 CREB 响应元件结合，并随后增强 Arg1，IL-10 和 TGF-β1 的表达。

结论 肿瘤细胞衍生的 Netrin-1 通过 MDSC 表面的 A2BR 受体，进一步激活了 MDSCs 中的 cAMP / PKA / CREB 信号通路，促进 Arg1，IL-10 和 TGF-β1 的产生，从而增强 MDSCs 的免疫抑制功能。

PO-0188

Silencing of PRDX2 Inhibits the Proliferation and Invasion of Non-Small Cell Lung Cancer Cells

xu jing
The Second Hospital of Shandong University

Peroxiredoxin 2 (PRDX2), a member of the peroxiredoxin family of antioxidant enzymes, has been revealed to be an important player in cancer progression. However, the biological role of PRDX2 in the progression of non-small cell lung cancer (NSCLC) is poor reported. In the present study, the loss-of-function experiments were performed to investigate the specific role of PRDX2 in the growth and invasion of NSCLC. The results revealed that knockdown of PRDX2 by siRNA interference significantly suppressed the proliferation, migration, and invasion of A549 and H1299 cells, as well as diminished the activity of MMP9. Additionally, the decrease in PRDX2 expression significantly promoted apoptosis in NSCLC cells by downregulating expression of Bcl-2 and upregulating the expression of Bax, cleaved caspase 3 and cleaved caspase 9, but had no significant effect on the apoptosis of normal lung epithelial cells BEAS-2B. Moreover, PRDX2 inhibitor also inhibited the proliferation, migration, and invasion of A549 cells and promoted apoptosis. Further, our data demonstrated that silencing of PRDX2 markedly reduced the phosphorylation of Akt and mTOR and expression of downstream proteins Cyclin D1 and p70S6k. In conclusion, our findings

indicate that PRDX2 exerts a prooncogenic role in the progression of NSCLC and might be a potential therapeutic target for NSCLC treatment.

PO-0189

Signaling lymphocytic activation molecule regulates Tfh-like cells in allergic rhinitis patients

Jun Yang、Shengjun Wang
The Affiliated People's Hospital, Jiangsu University

Background Allergic rhinitis (AR) is characterized by type I hypersensitivity that is mediated by IgE-induced humoral responses. Follicular helper T cells (Tfh) comprise the key helper T cell (Th) subset that promotes antibody production. Signaling lymphocytic activation molecules (SLAMs) participate in regulation of the differentiation and function of Tfh cells, but whether this regulation is involved in the pathogenesis of AR is unknown.

Methods CD4+CXCR5+ Tfh-like cells from peripheral blood were detected by flow cytometry. The IL-21 and IgE levels in serum were measured by an ELISA. Blood CD4+CXCR5+ Tfh-like cells were sorted and cultured with anti-SLAM mAb in vitro.
Results The frequencies of circulating CD4+CXCR5+ Tfh-like cells appeared virtually unchanged in AR patients, but the expression of SLAMs and SLAM-associated protein (SAP) on circulating Tfh-like cells was significantly decreased. Meanwhile, the level of serum IL-21 was increased in AR patients, and a negative correlation was found between the IL-21 level and SLAM or SAP expression on CD4+CXCR5+ T cells. Treatment with anti-SLAM mAb resulted in reduced IL-21 production by Tfh-like cells in vitro. Additionally, SLAM expression on B cells was significantly decreased, although the percentages of B cells were increased in AR patients.
Conclusions SLAMs negatively regulate IL-21 production in CD4+CXCR5+ Tfh-like cells, which contributes to the pathogenesis of AR

PO-0190

The Landscape of Immune Cells Infiltrating in Prostate Cancer

Zhicong Wu[1]、Hua Chen[2]、Wenyang Luo[2]、Hanyun Zhang[1]、Guihuan Li[2]、Fangyin Zeng[3]、Fan Deng[2]
1. Department of Clinical Laboratory, Nanfang Hospital, Southern Medical University
2. 南方医科大学基础医学院
3. 南方医科大学第五附属医院

Background This study was to explore the infifiltration pattern of immune cells in the prostate cancer (PCa) microenvironment and evaluate the possibility of specifific infifiltrating immune cells as potential prognostic biomarkers in PCa.
Methods Infifiltrating percentage of 22 immune cells were extracted from 27 normalized datasets by CIBERSORT algorithm. Samples with CIBERSORT p-value < 0.05 were subsequently merged and divided into normal or tumor groups. The differences of 22 immune cells between normal and tumor tissues were analyzed along with potential infifiltrating correlations among 22 immune cells and Gleason grades. SNV data from TCGA was used to calculate the TMB score. A univariate and multivariate regression were used to evaluate the prognostic effects of immune cells in PCa.
Results Ten immune cells with signifificant differences were identifified, including seven increased and three decreased infifiltrating immune cells from 190 normal prostate tissues and 537 PCa tissues. Among them, the percentage of infifiltration of resting NK cells increased the most, whereas the percentage of infifiltration of resting mast cells decreased the most. In normal tissues, CD8+ T cells had the strongest infifiltrating correlation with monocytes, while activated NK cells and naive B cells were the highest in PCa tissues. Moreover, the infifiltration of fifive immune cells was signifificantly associated with TMB score and mutations of immune gene change the infifiltration of immune cells. The Area Under Curve (AUC) of the multivariate regression model for the fifive- and 10-year survival prediction of PCa reached 0.796 and 0.862. The validation cohort proved that the model was reproducible.
Conclusions This study demonstrated that different infifiltrating immune cells in prostate cancer, especially higher infifiltrating M1 macrophages and neutrophils in PCa tissue, are associated with patients' prognosis, suggesting that these two immune cells might be potential targets for PCa diagnosis and prognosis of treatment.

PO-0191

脑脊液肿瘤标志物联合检测对肺癌脑转移诊断的临床价值

张爱敏
天津医科大学肿瘤医院

目的 探讨脑脊液中肿瘤标志物癌胚抗原(CEA)、神经元特异性烯醇化酶（NSE）、细胞角蛋白 19 片断（CYFRA21-1）和鳞状上皮细胞癌抗原（SCC）联合检测对肺癌脑膜转移辅助诊断的临床价值。
方法 用电化学发光免疫分析法(ECLIA)和微粒子酶联免疫测定法（MEIA）检测 45 例肺癌脑膜转移患者、30 例脑部良性肿瘤患者血清和脑脊液中 CEA、NSE、CYFRA21-1 和 SCC 含量。
结果 肺癌脑膜转移患者血清和脑脊液中 4 项肿瘤标志物含量均明显高于脑良性肿瘤组，有显著性差异(P <0.01)，肺癌脑膜转移患者脑脊液中肿瘤标志物水平与血清中比较，无显著性差异(P 0.01)，CEA、NSE、CYFRA21-1 和 SCC 的敏感性为 92.3%，90.8%，52.9%和 49.8%，特异性分别为 95.7%、85.3%、95.2 和 94.3%。脑脊液肿瘤标志物的联合检测组合中，4 项指标任意 1 项阳性的诊断敏感性 100%，三项指标同时阳性的诊断特异性 100%。
结论 脑脊液中 4 项肿瘤标志物联合检测对于肺癌脑膜转移的诊断，具有重要的临床意义。

PO-0192

CD38 表达对 T 细胞功能及 HIV 感染治疗后疾病转归影响机制的研究

宋成博、张子宁、尚红
中国医科大学附属第一医院

AIDS 是由 HIV 感染引起的一种传染性疾病，感染可导致免疫缺陷和多种相关并发症。随着 ART 疗法的出现，HIV 感染的发病率及死亡率已大大降低，但 ART 治疗仍不能完全恢复免疫状态，部分感染者免疫功能恢复和临床转归较差。CD38 是机体主要的 NAD 水解酶，NAD 是细胞代谢过程中的重要辅酶，负责传递电子辅助 ATP 的合成，其的稳态对调节细胞代谢和线粒体功能起到重要作用。NAD 也是胞内重要的组蛋白去乙酰化酶 SIRT 的底物并影响细胞的蛋白修饰、转录调控、代谢等。CD38 对 HIV 疾病较强的预测能力提示它可能在感染者疾病进程中发挥重要作用，然而，HIV 感染者 T 细胞 CD38 的生物学功能尚不明确。

本研究通过流式检测发现 HIV 感染者 T 细胞上 CD38 表达均显著升高，且 ART 治疗后 CD38 表达水平无法完全恢复。我们还发现 HIV 感染者外周血 CD8+T 细胞的衰老水平与 CD38 的表达比例呈正相关，且 CD38 在 PD1+的耗竭 T 细胞上呈较高水平表达，CD38+T 细胞的 IFN-γ 分泌能力也明显降低，说明 CD38 会促进 T 细胞的衰老与耗竭并抑制 T 细胞功能；通过转录组分析发现 CD38 抑制 T 细胞功能、发育及细胞毒性相关的基因，并影响细胞线粒体平衡，且流式检测发现 CD38 能够促进线粒体损伤和 ROS 累积；本研究还使用 CD38 抑制剂处理细胞，发现 CD38 抑制剂能够提高 HIV 感染者 T 细胞的 NAD 浓度和 SIRT 酶活性，减少线粒体损伤、延缓 T 细胞衰老，提高 T 细胞的细胞因子分泌功能及增殖能力。这些结果为明确 CD38 在 HIV 感染中的生物学功能及 CD38 抑制类药物对 T 细胞的影响提供了新线索，也为改善 HIV 的免疫恢复和疾病转归提供新策略。

PO-0193

IL-18 诱导的单核细胞对肺癌细胞的影响

聂兆超
山东大学第二医院

目的 探讨外源性白介素 18 对单核细胞的活化作用以及 IL-18 激活诱导的单核细胞对肺癌细胞增殖、迁移和侵袭的影响。
方法 通过白介素 18 体外诱导单核细胞模拟激活体内肿瘤微环境中的肿瘤相关巨噬细胞的作用。应用 Transwell 法检测白介素 18 对单核细胞的趋化作用；外源性白介素 18 刺激后，流式细胞术检测 M1、M2 型肿瘤相关巨噬细胞的比例；白介素 18 激活诱导的单核细胞和肺癌细胞共培养，分别以克隆形成实验、细胞划痕实验、细胞侵袭实验检测共培养后肺癌细胞的增殖、迁移和侵袭的变化。
结果 IL-18 对单核细胞具有显著的趋化作用；外源性白介素 18 刺激后的细胞表型向 M2 型肿瘤相关巨噬细胞方向分化；克隆形成实验显示其克隆形成能力具有显著的统计学差异；两因素方差分析结果表明愈合率上有显著差别，随着时间增加，各组愈合率均增加，结果有统计学差异 ；刺激后，各组的侵袭能力具有显著的统计学差异，IL-18 诱导单核细胞促进了肺癌细胞增殖、迁移和侵袭能力。
结论 IL-18 可以诱导单核细胞并促进其活化，活化后的单核细胞促进肺癌细胞的增殖、迁移和侵袭。

PO-0194

Exosomal Cripto-1 serves as a potential biomarker for perihilar cholangiocarcinoma

Xin Zhang
Qilu Hospital of Shandong University

Background Perihilar cholangiocarcinoma (PHCCA) has a poor prognosis, mainly due to diagnosis at an advanced stage. Cripto-1 functions as an oncogene and is highly expressed in several human cancers, however, its clinical application in PHCCA is poorly understood.
Method Whether Cripto-1 can be secreted with exosomes from PHCCA cells was examined in vitro and in vivo. An ELISA method was developed to detect exosomal Cripto-1 in the serum of 115 PHCCA patients, 47 cholangitis patients and 65 healthy controls. Cripto-1 expression was detected in PHCCA tissues using immunohistochemistry.
Results We identified that Cripto-1 was released by PHCCA cells via exosomes in vitro and in vivo. Exosomal Cripto-1 was increased in sera of PHCCA patients and associated with metastasis. Compared with traditional serum tumor markers, CA19-9 and CEA, exosomal Cripto-1 demonstrated a larger area under ROC curve for PHCCA diagnosis. The cutoff value of exosomal Cripto-1 was 0.82, achieving a sensitivity of 79.1% and a specificity of 87.5%. As expected, exosomal Cripto-1 levels in immunohistochemically Cripto-1-high cases were significantly elevated compared to in Cripto-1-low cases. When measured 1-week postoperatively, Cripto-1 levels decreased on average from 1.25(0.96-3.26) to 0.85(0.62-1.82). Immunohistochemistry analysis showed Cripto-1 expression was negatively correlated with E-cadherin and was an independent prognostic biomarker for poor survival in PHCCA patients.
Conclusion Exosomal Cripto-1 in sera can reflect its expression in the tissue of PHCAA patients and has the potential be a non-invasive biomarker for diagnosis and prognosis of PHCCA.

PO-0195

肝细胞癌患者 TIM-3+ TIGIT+CD4+ T 细胞和 TIM-3+ TIGIT+CD8+ T 细胞免疫耗竭及其与疾病进展的关系

袁润林、陈正徐
合肥市第二人民医院

目的 探讨肝细胞癌（HCC）患者外周血中 $CD4^+$、$CD8^+$T 细胞免疫耗竭及其与疾病进展的关系。
方法 收集 30 例 HCC 患者，同时收集健康体检者(HC)20 例，利用流式细胞术检测外周血 $CD4^+$、$CD8^+$T 细胞表面抑制性受体 PD-1、TIGIT、TIM-3 以及胞内 IL-10 表达比例。
结果 HCC 患者组外周血 $TIM\text{-}3^+CD4^+$、$TIGIT^+CD4^+$、$PD\text{-}1^+CD4^+$、$TIM\text{-}3^+CD8^+$、$TIGIT^+CD8^+$、$PD\text{-}1^+CD8^+$T 细胞比例高于 HC 组(P<0.01)。$TIM\text{-}3^+TIGIT^+CD8^+$T 细胞比例高于 HC 组($P$<0.001)，$IL\text{-}10^+CD4^+$、$TIM\text{-}3^+TIGIT^+CD4^+$T 细胞比例高于 HC 组($P$<0.0001)。HCC 患者组 $PD\text{-}1^+TIM\text{-}3^+TIGIT^+CD4^+$、$PD\text{-}1^+TIM\text{-}3^+TIGIT^+CD8^+$T 细胞比例高于 $PD\text{-}1^+TIM\text{-}3^-TIGIT^-$ $CD4^+$、$PD\text{-}1^+TIM\text{-}3^-TIGIT^-CD8^+$T 细胞比例($P$<0.0001)。ROC 曲线分析 $TIM\text{-}3^+TIGIT^+CD8^+$、$TIM\text{-}3^+TIGIT^+CD4^+$T 细胞在 HCC 的诊断效能大于单分子阳性细胞。高 $TIM\text{-}3^+TIGIT^+CD8^+$、高 $TIM\text{-}3^+TIGIT^+CD4^+$T 细胞比例组 NLR 结果高于低 $TIM\text{-}3^+TIGIT^+CD8^+$、低 $TIM\text{-}3^+TIGIT^+CD4^+$T 细胞比例组($P$< 0.05)。
结论 HCC 患者外周血 $TIM\text{-}3^+TIGIT^+CD4^+$及 $TIM\text{-}3^+TIGIT^+CD8^+$T 细胞比例高于对照者，上述细胞高表达 PD-1；高 $TIM\text{-}3^+TIGIT^+CD4^+$及 $TIM\text{-}3^+TIGIT^+CD8^+$T 细胞比例与 HCC 疾病进展加快和不良预后有关，提示 HCC 患者 $CD4^+$、$CD8^+$T 细胞存在免疫耗竭，且有意义的双分子靶向治疗可能会为 HCC 提供了更新颖、更有效的治疗靶点，促进了 HCC 患者免疫检查点靶向治疗的发展。

PO-0196

Longitudinal transcriptome analyses show robust T cell immunity during recovery from COVID-19

Cuixian Yang 、mi zhang 、xingqi dong
Yunnan Infectious Diseases Hospital

Understanding the processes of immune regulation in patients infected with the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is crucial for improving treatment. Here, we performed longitudinal whole-transcriptome RNA sequencing on peripheral blood mononuclear cell (PBMC) samples from 18 patients with coronavirus disease 2019 (COVID-19) during their treatment, convalescence, and rehabilitation. After analyzing the regulatory networks of differentially expressed messenger RNAs(mRNAs), microRNAs (miRNAs) and long non-coding RNAs (lncRNAs) between the different clinical stages, we found that humoral immunity and type I interferon response were significantly downregulated, while robust T-cell activation and differentiation at the whole transcriptome level constituted the main events that occurred during recovery from COVID-19. The formation of this T cell immune response might be driven by the activation of activating protein-1 (AP-1) related signaling pathway and was weakly affected by other clinical features. These findings uncovered the dynamic pattern of immune responses and indicated the key role of T cell immunity in the creation of immune protection against this disease.

PO-0197

High-throughput sequencing-based serum exosomal differential miRNAs in high-grade gliomas and intracranial lymphomas

Shun Wang
Department of Clinical Laboratory, The Second Hospital, Cheeloo College of Medicine, Shandong University

Objective At present, there is no effective non-invasive method for the differential diagnosis of high-grade glioma and intracranial lymphoma. This study aims to use high-throughput sequencing technology to screen microRNA markers in serum exosomes for differential diagnosis of high-grade gliomas and intracranial lymphoma.
Methods Patients with intracranial lymphoma or high-grade glioma, and healthy controls were included in this study (training cohort n =10; validation cohort: intracranial lymphoma n =10, high-grade glioma n =32, healthy controls n =20). After extracting the RNAs of serum exosomes, the high-throughput sequencing technology was used to determine the serum exosome free microRNA expression profiles and screened for differential microRNAs. RT-qPCR was used to verify the expression of the selected microRNAs. The differences of microRNA expression levels between groups were measured by Kruskal-Wallis test. Analyzed the diagnostic value using the receiver operating characteristic (ROC) curve.
Results High-throughput sequencing demonstrated that 170 miRNAs, 109 of which were up-regulated and 61 down-regulated, were differentially expressed in serum exosomes between patients with intracranial lymphoma and high-grade glioma. While comparing with healthy controls, the differential serum exosomal miRNAs number of high-grade glioma and intracranial lymphoma patients were 130 and 173 respectively. RT-qPCR proved both miR-766-5p and miR-376b-5p of serum exosomes were significantly down-regulated in high-grade gliomas and intracranial lymphomas patients compared with healthy controls (all $p<0.001$), and serum exosomal miR-766-5p expression of intracranial lymphomas was lower than high-grade gliomas ($p<0.05$). The areas under ROC curve (AUCs) of serum exosomal miR-766-5p and miR-376b-5p for the diagnosis of gliomas were 0.8883 ($p<0.001$) and 0.7688 ($p=0.001$) respectively, and for the diagnosis of intracranial lymphoma were 0.9271 ($p<0.001$) and 0.8542 ($p<0.001$) respectively. The AUC value of serum exosomal miR-766-5p for the differential diagnosis for glioma and intracranial lymphoma was 0.7201 ($p=0.026$).
Conclusion MiR-766-5p and miR-376b-5p in serum exosomes might be used as auxiliary diagnostic indicators for high-grade gliomas and intracranial lymphomas, and miR-766-5p might be used as a differential diagnostic marker for both.

PO-0198

调节性 B 细胞及其相关分子在脓毒症小鼠中的作用

张英辉
中国人民解放军北部战区总医院

目的 探讨调节性 B 细胞（Regulatory B cells, Breg）及其相关分子在脓毒症小鼠中的作用机制，为脓毒症的免疫靶向药物研发及治疗奠定基础。
方法 建立小鼠脓毒症模型，收集小鼠脾脏和外周血，流式细胞术检测小鼠脾脏中调节性 B 细胞的表达，流式液相多重蛋白定量技术（Cytometric Beads Array, CBA）检测小鼠外周血中 IL-10、TGF-β1、IL-1β、TNF-α、IL-4、IFN-γ 的表达。Western blot 检测小鼠脾脏中（Toll Like Receptor 4, TLR4）的表达。
结果 小鼠建立脓毒症模型后 2 天，脾脏中 Breg 的表达明显升高（$P<0.05$ vs 对照组），外周血中 IL-1β、TNF-α、IFN-γ 的分泌明显升高（$P<0.05$ vs 对照组），IL-4、IL-10 和 TGF-β1 的水平明显

降低（P<0.05 vs 对照组），7 天后 Breg 的表达所有下降，但与对照组相比，差异具有统计学意义；外周血中 IL-1β、TNF-α、IFN-γ 的分泌有所下降，IL-4、IL-10 和 TGF-β1 的水平明显升高。15 天后，Breg 的表达明显下降，外周血中 IL-1β、TNF-α、IFN-γ 的分泌明显下降，IL-4、IL-10 和 TGF-β1 的水平明显升高。小鼠脾脏中 TLR4 的表达在建立模型后 2 天明显升高（P<0.05 vs 对照组），7 天仍然高表达，15 天时表达明显下降。

结论 脓毒症时，调节性 B 细胞明显抑制小鼠免疫反应，维持 Th1/Th2 细胞平衡；而 Breg 的调控作用可能是通过调控 TLR4 基因实现的。

PO-0199

HMGB1 与乳腺癌患者临床特征和免疫指标的相关性研究

张小艳[1]、李清祥[1]、刘勇[1]、李航[1]、仇丽娟[1]、封欣然[1]、谭立明[2]
1. 南昌市第三医院
2. 南昌大学第二附属医院

背景与目的 高迁移率族蛋白 B1(high mobility group box1,HMGB1) 参与 DNA 复制、转录及翻译过程，与恶性肿瘤的发生、发展、浸润及转移密切相关，并参与炎症、免疫、增殖、转移和自噬多种信号通路的调节。本研究旨在探究高迁移率族蛋白 B1（HMGB1）与乳腺癌患者临床病理特征、免疫功能以及新辅助化疗疗效的相关性。

方法 选取 2020 年 6 月至 2021 年 10 月南昌市第三医院收治并接受新辅助化疗的乳腺癌患者 120 例，酶联免疫吸附（ELISA）法测定患者空芯针穿刺活检物中 HMGB1 水平，以及调节性 T(Regulatory cells,Tregs)细胞相关指标 IL-10、TGF-β 含量；流式细胞术检测 CD3+、CD4+、CD8+ 和 NK T 淋巴细胞亚群百分比；速率散射比浊法检测免疫球蛋白(IgG、IgA、IgM)和补体(C3、C4)含量；按照 95%置信区间（95%CI）下限水平将研究对象分为高水平组（HMGB1>22.98ng/ml）和低水平组（HMGB1≤22.98ng/ml）；新辅助化疗方案疗程结束后，根据 Miller-Payne 病理反应性分级标准评价术后病理疗效，分析 HMGB1 水平和病理疗效的关系。

结果 HMGB1 和乳腺癌肿瘤临床分期、淋巴结是否发生转移相关（P<0.05）；HMGB1 和 Treg 细胞相关指标 IL-10、TGF-β 显著相关（r=0.734，P=0.000；r=0.686，P=0.000）；HMGB1 高水平组 CD4/CD3 低于低水平组，CD8/CD3 高于低水平组（P<0.05）；高水平 HMGB1 患者术后病理疗效差。

结论 HMGB1 水平和乳腺癌分期、淋巴结转移以及细胞免疫功能有关，并有助于预测新辅助化疗病理疗效。

PO-0200

基于新型免疫金纳米团簇的电化学发光免疫分析新方法

苏灿平[1,2]、邹志艳[1,2]、洪国裟[1,2]
1. 厦门大学附属第一医院
2. 福建医科大学

目的 基于新型免疫金纳米团簇，提出一种新的电化学发光免疫传感器构建策略，研制一种简单方便、灵敏特异的电化学发光免疫传感器，并探讨其在临床检验中的应用价值。

方法 在本研究中，我们提出了一种基于“二合一”免疫球蛋白修饰的金纳米团簇（IgG-AuNCs）的电化学发光免疫传感平台。得益于 IgG 生物分子独特的组成和功能，IgG-AuNCs 兼具识别和发光功能，不仅被用作生物识别元件，而且可以作为电化学化学发光（ECL）发光体，表现出较高的 ECL 信号、良好的水溶性、稳定性及低毒性。作为概念性验证，我们首次将该探针应用到一种竞争型免疫传感平台用于检测 IgG。

结果 在最佳条件下，检测 IgG 抗原的线性范围为 0.5 ~ 50000 ng/mL，检测限为 0.06 ng/mL，比先前构建的荧光方法低 4 个数量级。此外，已建立的 ECL 方法还具有样品体积小、制备简单、稳定性好等显著优点，适用于实际临床样品中 IgG 分子的高通量检测。
结论 相比传统的 ECL 免疫传感器，该平台具有更加省时、直接、节省生物样本等优势。该策略避免了添加蛋白质等非导电材料作为发光探针和抗体之间的连接器，这不仅简化了抗体标记探针的制备，而且无疑减少了传感界面的空间障碍，提高了电子转移和免疫识别的有效性，对其他 ECL 免疫探针的设计和应用具有重要的参考意义。我们认为，该策略可为设计制备其他特异性抗体功能化的纳米材料提供有力研究基础，并有望拓展到其他肿瘤标记物的高效检测、细胞检测和 ECL 成像等其他应用，在临床检验中有广阔的应用前景。

PO-0201

三阴性乳腺癌 4T1 细胞中过表达鼠白介素-10 对宿主抗肿瘤免疫应答的影响

王晓琴[1]、王晓倩[1]、贺龙梅[2]、马运峰[3]
1. 西安交通大学第一附属医院检验科
2. 陕西省中医医院检验科
3. 西安交通大学基础医学院病原生物学与免疫学系

目的 研究鼠白介素-10（mIL-10）在三阴性乳腺癌发生发展中的作用，为临床三阴性乳腺癌患者的诊疗提供新的思路。
方法 将重组质粒 pLenti-CMV-mIL-10-GFP-puro 以及 pLenti-CMV-GFP-puro 分别与慢病毒包装质粒（ΔR9、pVSVG）共转染 293T 细胞，收集细胞培养上清离心并感染小鼠三阴性乳腺癌 4T1 细胞，经药物 Puromycin 筛选后，构建过表达 mIL-10 的稳转细胞系即 4T1/ mIL-10（实验组）以及 4T1/GFP（对照组）；利用酶联免疫吸附实验、流式细胞术检测两组细胞 GFP 的表达情况以及 mIL-10 的表达水平。将 4T1/ mIL-10 以及 4T1/GFP 细胞皮下注射 BALB/c 小鼠，建立皮下移植瘤模型，利用流式细胞术检测肿瘤微环境中免疫细胞功能的变化。
结果 成功构建 4T1/ mIL-10、 4T1/GFP 稳转细胞系。结果表明，药物筛选后 4T1/GFP 的阳性率为 94.59%，4T1/mIL-10 的阳性率为 93.71%。与对照组相比，实验组 mIL-10 的表达水平显著增加（$P<0.05$）。小鼠荷瘤模型表明，与对照组相比，mIL-10 能够促进肿瘤组织中 CD8+T 分泌 IFN-γ，减少骨髓来源的抑制性细胞 MDSCs 的浸润（$P<0.05$），对肿瘤组织中 CD4+T 细胞 IFN-γ 的分泌、CD4+T 细胞以及 CD8+T 细胞颗粒酶 B 的分泌无显著影响（$P>0.05$）。与对照组相比，4T1/mIL-10 组荷瘤小鼠肿瘤于第 13 天开始逐渐减小，并于第 19 天时两组肿瘤大小具有统计学意义（$P<0.05$）。
结论 mIL-10 能够增强肿瘤组织中 CD8+T 细胞的活性，减少 MDSCs 细胞的浸润，增强宿主杀伤肿瘤的能力，抑制肿瘤的生长，从而为乳腺癌的诊疗提供理论与实验基础。

PO-0202

TNF-α 与 IFN-γ 协同诱导肝癌细胞表达 B7-H1 分子

李娜
山东大学第二医院

目的 B7-H1 是一种重要的免疫负调控分子，可以抑制 T 细胞功能，促进肿瘤细胞的免疫逃逸。所以，研究肝癌细胞中 B7-H1 升高的机制对于肝癌的治疗具有重要意义。本实验旨在研究肝癌微环境中细胞因子 IFN-γ、TNF-α 对于肝癌细胞表面 B7-H1 分子表达的影响及其机制的探究。
方法 本实验按照研究目标分成四大部分：

（1）选择四种不同的肝癌细胞系，采用实时荧光定量 PCR、流式细胞术和 Western-blot 方法检测 IFN-γ 对于肝癌细胞 B7-H1 分子表达的影响。
（2）采用实时荧光定量 PCR 以及流式细胞术方法检测 TNF-α 与 IFN-γ 是否可以协同诱导肝癌细胞在 RNA 以及蛋白质水平表达 B7-H 分子。
（3）进一步运用信号通路抑制剂和小干扰实验检测 TNF-α 与 IFN-γ 协同诱导肝癌细胞表达 B7-H1 分子的机制。
（4）采用动物实验以及肿瘤细胞与 T 细胞的共培养实验证明二者协同诱导的 B7-H1 分子是否具有免疫抵抗作用。
结果 在四种肝癌细胞中 IFN-γ 都可以诱导 B7-H1 分子的表达，并且 TNF-α 与 IFN-γ 可协同诱导肝癌细胞 B7-H1 分子的表达，二者协同诱导的机制是 TNF-α 通过 NF-κB 信号通路增强 IFNGR1 和 IFNGR2 的表达，进一步促进 IFN-γ 信号通路的活化。动物实验以及肿瘤细胞与 T 细胞共培养实验证明 TNF-α 与 IFN-γ 协同诱导肝癌细胞表达的 B7-H1 分子具有免疫抵抗作用，可以促进肿瘤细胞的免疫逃逸。
结论 肝癌微环境中 TNF-α 与 IFN-γ 可以协同诱导肝癌细胞表达 B7-H1 分子，诱导表达的 B7-H1 分子具有免疫抵抗作用。所有实验研究可能提供一些靶分子，针对这些靶分子的治疗可以减少肿瘤微环境中 TNF-α 和 IFN-γ 诱导的肝癌细胞中 B7-H1 分子的表达，进而有助于临床肝癌的治疗。
胞。

PO-0203

Nrf2 介导自噬缺陷对氧化低密度脂蛋白诱导巨噬细胞焦亡的影响

刘家汝、关秀茹
哈尔滨医科大学附属第一医院

目的 本实验旨在探 究 Nrf2 如何参与自噬缺陷对氧化低密度脂蛋白导致的巨噬细胞焦亡的调节，以期为 AS 的防治提供新靶点。
方法 本研究中，人类 THP-1 单核细胞在体外用药物诱导后形成巨噬细胞。 过量 ox-LDL 处理巨噬细胞构建实验模型。Western Blot 用以测定自噬和焦亡过 程的标志蛋白，同时测定 Nrf2 及其下游分子的蛋白量；通过细胞存活率检测、 LDH 释放试验和流式细胞术分别确定不同处理组的细胞活性以及细胞膜的完整 性；各组上清液中白细胞介素-1β（IL-1β）和白细胞介素-18（IL-18）用酶联免 疫吸附试验测定。综合以上多种 方法所得的结果对 Nrf2 在自噬缺陷调控 ox-LDL 诱导的巨噬细胞焦亡中的作用 进行全方位、多角度剖析。
结果 （1）ox-LDL 以浓度依赖性方式诱导 THP-1 源巨噬细胞焦亡。 （2）当细胞自噬过程受阻、自噬缺陷时，ox-LDL 处理的巨噬细胞焦亡程度 增加。（3）ox-LDL 和自噬抑制剂同时暴露于细胞时，胞核中 Nrf2 水平上调，其 下游效应蛋白 HO-1 含量也剧增。 （4）自噬受损时，在 Nrf2 促进剂或抑制剂的作用下，ox-LDL 处理的巨噬 细胞细胞焦亡程度分别增加或减轻。 （5）自噬缺陷时，在 Nrf2 促进剂或抑制剂作用下，ox-LDL 处理的巨噬细 胞自噬活性分别进一步降低或升高，这表明 Nrf2 可反馈性调节自噬活性。
结论 本研究证明， 在吞噬了 ox-LDL 的巨噬细胞中，Nrf2 分子因自噬缺陷而被激活，促进细胞焦亡， 进而影响 AS 斑块的不稳定性。

PO-0204

Elevated Serum IgG4 Was Found in Eosinophilic Granulomatosis With Polyangiitis

Ziyan Wu
Peking Union Medical College Hospital

Objective The aim was to determine the levels and clinical impact of immunoglobulin G4 (IgG4) and other IgG subclasses in a Chinese population with eosinophilic granulomatosis with polyangiitis (EGPA).
Methods We enrolled 49 patients who had EGPA, 27 who had granulomatosis with polyangiitis (GPA), 31 who had microscopic polyangiitis (MPA), and 30 healthy controls (HCs). Serum IgG subclasses were measured using commercial immunonephelometric assays and compared among different groups.
Results Fifteen EGPA patients (30.61%) had elevated IgG4 levels, based on a cutoff value of 135 mg/dL. In addition, 2 GPA patients (7.40%) and 1 MPA patient (3.33%) had elevated IgG4 levels. The EPGA group had a higher IgG4 level (65.60 mg/dL) than the GPA group (32.70 mg/dL, $p = 0.0021$), the MPA group (30 mg/dL, $p = 0.0021$), and the HC group (28.55 mg/dL, $p = 0.0002$). The EPGA group also had a higher IgG4/IgG ratio (0.0644) than the GPA group (0.0322, $p = 0.13$), the MPA group (0.0289, $p = 0.0055$), and the HC group (0.0212, $p < 0.0001$).
Conclusions Our results indicate that Chinese patients with EGPA have increased levels of serum IgG4. Further study is needed to determine the pathogenic role of IgG4 and IgG4 antineutrophil cytoplasmic antibodies in EGPA.

PO-0205

Antibodies to phosphatidylserine/prothrombin (aPS/PT) enhanced the diagnostic performance in Chinese patients with antiphospholipid syndrome

Shulan Zhang
Peking Union Medical College Hospital

Background Increasing evidence has highlighted the role of non-criteria antiphospholipid antibodies (aPLs) as important supplements to the current criteria aPLs for the diagnosis of antiphospholipid syndrome (APS). In this retrospective study, we evaluated the clinical relevance of antibodies to phosphatidylserine/prothrombin (aPS/PT) in Chinese patients with APS.
Methods A total of 441 subjects were tested, including 101 patients with primary APS (PAPS), 140 patients with secondary APS (SAPS), 161 disease controls (DCs) and 39 healthy controls (HCs). Serum IgG/IgM aPS/PT was determined by ELISA.
Results The levels of IgG/IgM aPS/PT were significantly increased in patients with APS compared with DCs and HCs. IgG and IgM aPS/PT were present in 29.7% and 54.5% of PAPS, and 42.1% and 53.6% of SAPS, respectively. For diagnosis of APS, IgG aCL exhibited the highest positive likelihood ratio (LR+) of 21.60, followed by LA (13.84), IgG aβ2GP1 (9.19) and IgG aPS/PT (8.49). aPS/PT was detected in 13.3% of seronegative PAPS patients and 31.3% of seronegative SAPS patients. LA exhibited the highest OR of 3.64 in identifying patients with thrombosis, followed by IgG aCL (OR, 2.63), IgG aPS/PT (OR, 2.55) and IgG aβ2GP1 (OR, 2.33). LA and IgG aCL were correlated with both arterial and venous thrombosis, whereas IgG aPS/PT and IgG aβ2GP1 correlated with venous or arterial thrombosis, respectively.
Conclusions Our findings suggest that the inclusion of IgG/IgM aPS/PT may enhance the diagnostic performance for APS, especially in those in whom APS is highly suspected, but conventional aPLs are repeatedly negative. In addition, IgG aPS/PT may contribute to identify patients at risk of thrombosis.

PO-0206

Antibodies against glycoprotein 2 display diagnostic advantages over ASCA in distinguishing CD from intestinal tuberculosis and intestinal Behçet's disease

Shulan Zhang
Peking Union Medical College Hospital

Objectives There is an increasing need to identify reliable biomarkers for distinguishing Crohn's disease (CD) from other gastrointestinal disorders sharing similar clinical and pathological features. This study aimed at evaluating the diagnostic potential of antibodies to zymogen granule glycoprotein GP2 (aGP2) in a large, well-defined Chinese cohort with a special focus on their role in discriminating CD from intestinal Behçet's disease (BD) and intestinal tubercolosis (ITB).
Methods A total of 577 subjects were prospectively enrolled, including 171 patients with CD, 208 patients with ulcerative colitis (UC), 71 with BD, 57 with ITB and 70 healthy controls (HC). aGP2 and anti-Saccharomyces cerevisiae antibodies (ASCA) were determined by ELISA. Perinuclear antineutrophil cytoplasmic antibodies were tested by indirect immunofluorescent assay.
Results aGP2 IgG and IgA levels were significantly elevated in patients with CD compared with those in patients with UC, intestinal BD, and ITB and HC. Conversely, ASCA IgG levels were not different between CD and intestinal BD patients, whereas ASCA IgA levels did not discriminate CD from intestinal BD and ITB patients. aGP2 IgA and IgG displayed a better assay performance (larger areas under the curve) over ASCA IgA and IgG in differentiating CD from disease controls ($P<0.05$). ASCA IgA did not discriminate CD from disease controls. aGP2 IgA and/or IgG was significantly associated with penetrating disease (B3) and ileal CD (L1) ($P<0.05$), whereas ASCA IgA and/or IgG was not.
Conclusions In comparison with ASCA, aGP2 distinguishes CD from intestinal BD or ITB as disease controls more efficiently, aiding in the differential diagnosis of IBD.

PO-0207

Correlation between cytokines and coagulation-related parameters in patients with coronavirus disease 2019 admitted to ICU

Dong Zhang
PUMCH

Background The novel SARS-CoV-2 caused a large number of infections and deaths worldwide. Thus, new ideas for an appropriated assessment of patients' condition and clinical treatment are of utmost importance. Therefore, in this study, the laboratory parameters of patients with coronavirus disease 2019 (COVID-19) were evaluated to identify the correlation between cytokine expression and other laboratory parameters.
Methods A retrospective and single-center study was performed in Wuhan, involving 83 severe or critical COVID-19 patients admitted to the intensive care unit (ICU). Laboratory parameters in ICU patients with laboratory-confirmed infection of SARS-CoV2 were collected. The association between parameters was assessed by Spearman's rank correlation.
Results Patients' median age was 66 years (IQR, 57-73), and 55 (66%) were men. Among the 83 patients, 61 (73%) had 1 or more coexisting medical condition. The median concentration of IL-2R, IL-6, IL8, IL10, and TNFα were above the normal range, without IL-1β. A significant negative correlation between IL-6 and platelet count was discovered ($r2 = -0.448$, $P < 0.001$) as well as a significant correlation between IL-6 and other platelet parameters. Finally, a correlation between multiple cytokines and coagulation indicators was found, pro-inflammatory factors were

found to be more associated to coagulation parameters, with the highest correlation between IL-6 and the International normalized ratio (INR) ($r2 = 0.444$, $P < 0.001$).
Conclusions Our results suggested that cytokines play an important role in the pathogenesis of COVID-19. In addition, IL-6 seems more relevant in the evaluation of the condition of COVID-19 patients.

PO-0208

Identification of novel serological autoantibodies in Takayasu arteritis patients using HuProt arrays

Xiaoting Wen
Peking Union Medical College Hospital

To identify novel autoantibodies of Takayasu arteritis (TAK) using HuProt array-based approach, a two-phase approach was adopted. In Phase I, serum samples collected from 40 TAK patients, 15 autoimmune disease patients, and 20 healthy subjects were screened to identify TAK-specific autoantibodies using human protein (HuProt) arrays. In phase II, the identified candidate autoantibodies were validated with TAK-focused arrays using an additional cohort comprised of 109 TAK patients, 110 autoimmune disease patients, and 96 healthy subjects. Subsequently, the TAK-specific autoantibodies validated in phase II were further confirmed using western blot analysis. We identified and validated eight autoantibodies as potential TAK-specific diagnostic biomarkers, including anti-SPATA7, -QDPR, -SLC25A2, -PRH2, -DIXDC1, -IL17RB, -ZFAND4, and -NOLC1 antibodies, with AUC of 0.803, 0.801, 0.780, 0.696, 0.695, 0.678, 0.635, and 0.613, respectively. SPATA7 could distinguish TAK from healthy and disease controls with 73.4% sensitivity at 85.4% specificity, while QDPR showed 71.6% sensitivity at 86.4% specificity. SLC25A22 showed the highest sensitivity of 80.7%, but at lower specificity of 67.0%. In addition, PRH2, IL17RB, and NOLC1 showed good specificities of 88.3%, 85.9%, and 86.9%, respectively, but at lower sensitivities (<50%). Finally, DIXDC1 and ZFAND4 showed moderate performance as compared with the other autoantibodies. Using a decision tree model, we could reach a specificity of 94.2% with AUC of 0.843, a significantly improved performance as compared with that by each individual biomarker. The performances of three autoantibodies, namely anti-SPATA7, -QDPR, and -PRH2, were successfully confirmed with western blot analysis. Using this two-phase strategy, we identified and validated eight novel autoantibodies as TAK-specific biomarker candidates, three of which could be readily adopted in a clinical setting.

PO-0209

Antiphospholipid Antibodies in Critically Ill Patients With COVID-19

Shulan Zhang
Peking Union Medical College Hospital

Objective Coagulopathy is one of the characteristics observed in critically ill patients with coronavirus disease 2019 (COVID-19). Antiphospholipid antibodies (aPLs) contribute to coagulopathy, though their role in COVID-19 remains unclear. This study was undertaken to determine the prevalence and characteristics of aPLs in patients with COVID-19.
Methods Sera collected from 66 COVID-19 patients who were critically ill and 13 COVID-19 patients who were not critically ill were tested by chemiluminescence immunoassay for anticardiolipin antibodies (aCLs), anti-β2 -glycoprotein I (anti-β2 GPI) (IgG, IgM, and IgA), and IgG anti-β2 GPI-domain 1 (anti-β2 GPI-D1) and IgM and IgG anti-phosphatidylserine/prothrombin (anti-PS/PT) antibodies were detected in the serum by enzyme-linked immunosorbent assay.

Results Of the 66 COVID-19 patients in critical condition, aPLs were detected in 31 (47%). Antiphospholipid antibodies were not present among COVID-19 patients who were not in critical condition. The IgA anti-β2 GPI antibody was the most commonly observed aPL in patients with COVID-19 and was present in 28.8% (19 of 66) of the critically ill patients, followed by IgA aCLs (17 of 66, or 25.8%) and IgG anti-β2 GPI (12 of 66, or 18.2%). For multiple aPLs, IgA anti-β2 GPI + IgA aCLs was the most common antibody profile observed (15 of 66, or 22.7%), followed by IgA anti-β2 GPI + IgA aCL + IgG anti-β2 GPI (10 of 66, or 15.2%). Antiphospholipid antibodies emerge ~35-39 days after disease onset. A dynamic analysis of aPLs revealed 4 patterns based on the persistence or transient appearance of the aPLs. Patients with multiple aPLs had a significantly higher incidence of cerebral infarction compared to patients who were negative for aPLs (P = 0.023).
Conclusion Antiphospholipid antibodies were common in critically ill patients with COVID-19. Repeated testing demonstrating medium to high titers of aPLs and the number of aPL types a patient is positive for may help in identifying patients who are at risk of developing cerebral infarction. Antiphospholipid antibodies may be transient and disappear within a few weeks, but in genetically predisposed patients, COVID-19 may trigger the development of an autoimmune condition similar to the antiphospholipid syndrome (APS), referred to as "COVID-19-induced APS-like syndrome." Long-term follow-up of COVID-19 patients who are positive for aPLs would be of great importance in understanding the pathogenesis of this novel coronavirus.

PO-0210

Association between genetic variants in the human leukocyte antigen-B/MICA and Takayasu arteritis in Chinese Han population

Xiaoting Wen
Peking Union Medical College Hospital

Aim Takayasu arteritis (TA) is a rare autoimmune disease with ethnic differences. Genome-wide association studies (GWAS) showed novel genetic variants in the human leukocyte antigen (HLA) region were associated with TA. The present study aimed to investigate the linkage between these single nucleotide polymorphisms (SNP) and TA in a Chinese Han population.
Methods Four hundred and twelve patients from multiple centers and 597 healthy controls were genotyped using the Sequenom MassArray iPLEX platform. The association between these SNPs and various clinical symptom of TA was also investigated.
Results Our study showed a higher risk allele frequency of rs12524487 in TA patients compared to healthy controls (26.6% vs. 21.7%, odds ratio [OR] 1.31, 95% CI 1.06-1.61). The other SNP rs9366782 in HLA-B/MICA (major histocompatibility complex class I polypeptide-related sequence A) showed association with TA ischemic brain disease (OR: 1.78, 95% CI: 1.16-2.73, Pc = 0.03). However, rs3763288 and rs114202986 in MICA were negatively related to TA either as a whole or in any clinical features. Meanwhile, ATGT(rs9366782, rs12524487, rs3763288 and rs114202986) were the risk haplotypes (Pc = 2.48 × 10-10).
Conclusions Our findings indicated that rs12524487 in HLA-B/MICA was a genetic risk factor for TA in a Chinese Han population and rs9366782 in this region was associated with ischemic brain disease in TA but not TA susceptibility.

PO-0211

Assessing serum IgG4 glycosylation profiles of IgG4-related disease using lectin microarray

Chaojun Hu
Peking Union Hospital

Objectives IgG4 related disease (IgG4-RD) is a multiorgan fibroinflammatory disorder. Lectin microarray is a high-throughput glycosylation analysis technology. The aim of our study was to investigate glycosylation profiling of serum IgG4 from IgG4-RD patients and controls.
Methods A large cohort of 167 IgG4-RD patients, 130 disease controls (DCs) and 86 healthy controls (HCs) were included in the current study. The glycan level of serum IgG4 of all participants was determined by lectin microarray. A verification assay of lectin microarray and lectin blot were used to clarify the relationship between the serum IgG4 and purified IgG4 glycosylation.
Results The results revealed that the glycan level of mannose (binding MNA-M, VVA mannose, ConA) was significantly increased and that the glycan level of fucose (binding LTL), GlcNAc (binding DSL), GalNAc (binding HPA) was significantly decreased in IgG4-RD patients compared to DCs and HCs. We further found that the glycan level of GlcNAc was positively correlated with that of complement 3 (C3), and that the reduced level of GlcNAc was associated with damage to multiple organs. In addition, the mannose level (binding MNA-M and VVA mannose) was negatively correlated with C3 and complement 4 (C4) levels.
Conclusions Serum IgG4 of IgG4-RD patients exhibits different glycosylation levels. This study demonstrated that there is important clinical value in identifying aberrant GlcNAc levels as a potential diagnostic index for multi-organ involvement. Furthermore, the mannose level of serum IgG4 may reflect the degree of inflammation of IgG4-RD.

PO-0212

Serum Protein Profiling Reveals a Landscape of Inflammation and Immune Signaling in Early-stage COVID-19 Infection

Xin Hou
Peking Union Medical College Hospital

Coronavirus disease 2019 (COVID-19) is a highly contagious infection and threating the human lives in the world. The elevation of cytokines in blood is crucial to induce cytokine storm and immunosuppression in the transition of severity in COVID-19 patients. However, the comprehensive changes of serum proteins in COVID-19 patients throughout the SARS-CoV-2 infection is unknown. In this work, we developed a high-density antibody microarray and performed an in-depth proteomics analysis of serum samples collected from early COVID-19 (n = 15) and influenza (n = 13) patients. We identified a large set of differentially expressed proteins (n = 132) that participate in a landscape of inflammation and immune signaling related to the SARS-CoV-2 infection. Furthermore, the significant correlations of neutrophil and lymphocyte with the CCL2 and CXCL10 mediated cytokine signaling pathways was identified. These information are valuable for the understanding of COVID-19 pathogenesis, identification of biomarkers and development of the optimal anti-inflammation therapy.

PO-0213

Metabolomic alterations associated with Kallmann syndrome

Ye Guo
Peking Union Medical College Hospital

Background This study was conducted to identify potential seminal plasma metabolic markers associated with disease activity in Kallmann syndrome (KS).
Methods We collected medical records and seminal plasma samples from 17 KS patients and 20 age-matched healthy controls (HC) and performed metabolomics analysis using the UPLC-QTOF-MS method.
Results Partial least squares discriminant analysis (PLS-DA) showed that the metabolomics profile of KS patients was clearly separated from HC. Statistical analysis of the data indicates that there are differential metabolites between KS patients and HC. The main metabolic pathways focus on linoleic acid (LA) metabolism, Glycerophospholipid metabolism.
Conclusions The seminal plasma metabolomics profile of KS patients has changed. Glycerophospholipids and LA are promising biomarkers for KS diagnosis.

PO-0214

Imbalance of the CD226/TIGIT Immune Checkpoint Is Involved in the Pathogenesis of Primary Biliary Cholangitis

Chuiwen Deng
Peking Union Medical College Hospital,

The relationship between the cluster of differentiation 226 (CD226)/T cell Ig and ITIM domain (TIGIT) immune checkpoint and primary biliary cholangitis (PBC) pathogenesis is unknown. Herein, PBC patients (n = 42) showed significantly higher proportions of peripheral CD8+ T and CD4+ T cells expressing either CD226 or TIGIT than disease (n = 25) and healthy (n = 30) controls. The percentage of CD8+TIGIT+ T cell was negatively associated with total bilirubin, direct bilirubin, total bile acid, γ-glutamyl transpeptidase, and alkaline phosphatase, but positively correlated with platelet count; alkaline phosphatase was positively associated with the frequency of CD8+CD226+ T cell; and the CD226/TIGIT ratio of CD8+ T cell was positively associated with total bilirubin, direct bilirubin, total bile acid, γ-glutamyl transpeptidase, alkaline phosphatase, and aspartate aminotransferase to platelet ratio, but negatively correlated with albumin and platelet count. The effector function of CD8+CD226+ T cells was more robust than the CD8+CD226- counterparts. CD226 blockade reduced CD107a+, IFN-γ+, and TNF-α+ proportions among CD8+CD226+ T cells, inhibiting CD8+ T cell proliferation. In conclusion, CD226/TIGIT immune checkpoint imbalance is involved in the pathogenesis of PBC. The CD226/TIGIT ratio of CD8+ T cell is a potential biomarker for evaluating the disease status and the prognosis of PBC patients. Moreover, CD8+CD226+ T cells represent a possible therapeutic target for PBC, and blocking CD226 could inhibit the activity of this cell subset in vitro.

PO-0215

Risk factors for mortality due to COVID-19 in intensive care units: a single-center study

Yu Chen
Peking Union Medical College Hospital

Background Many studies have revealed several risk factors associated with the prognosis of patients with coronavirus disease 2019 (COVID-19), but the risk factors associated with death in critically ill COVID-19 patients still needs to be fully elucidated. Therefore, we analyzed clinical characteristics and laboratory data of ICU patients to identify risk factors associated with COVID-19 death.
Methods Patients with COVID-19 from the ICU in the Sino-French New City Branch of Tongji Hospital Wuhan, China, between February 4 and February 29, 2020, were enrolled in this study. The final date of follow-up was April 4, 2020. Clinical manifestations, laboratory tests, treatment, and outcome of participants before and during the ICU stay were retrospectively collected and analyzed.
Results A total of 92 patients were admitted or transferred to the ICU from February 4 to February 29, 2020. Compared to survivors, the majority of non-survivors (73.8%) presented with dyspnea. A random forest classifier and ROC curve were used to develop a predictive model. IL-6, D-dimer, lymphocytes, and albumin achieved good performance with AUCs of 0.9476, 0.9165, 0.8994, and 0.9251, respectively, which were consistent with clinical observations, such as inflammation, lymphopenia, and coagulation dysfunction. Combining IL-6 and D-dimer improved the performance of this model with an excellent AUC (0.997).
Conclusions Mortality in COVID-19 was not rare in critically ill patients. The model that combined IL-6 and D-dimer was valuable for predicting the mortality of patients with COVID-19 with excellent performance. This model needs to be further optimized by adding more indicators and then evaluated with a multicenter study.

PO-0216

Association between the BANK1 rs3733197 polymorphism and polymyositis/dermatomyositis in a Chinese Han population

Si Chen
Department of Clinical Laboratory, Beijing Anzhen Hospital, Capital Medical University, Beijing, China.

The aim of our study was to investigate the association between single nucleotide polymorphisms (SNPs) in the BANK1 gene and polymyositis/dermatomyositis (PM/DM) in a Chinese Han population. In total, 363 PM patients, 654 DM patients, and 1280 healthy controls were recruited and genotyped using the Sequenom MassArray system. A significant allele association was observed in rs3733197 among the PM/DM patients (OR 0.81, 95%CI 0.70-0.94, Pc = 1.83 × 10-2). Notably, rs3733197 was associated with DM and PM/DM patients with ILD involvement (Pc = 0.026; Pc = 6.0 × 10-3, respectively). However, no statistically significant difference was observed in the allele or genotype frequencies of three SNPs (rs4522865, rs17266594, and rs10516487) among the DM, PM, and PM/DM patients and healthy controls (all Pc > 0.05). This study was the first to demonstrate that a BANK1 gene SNP (rs3733197) could confer genetic predisposition in PM/DM patients and PM/DM patients with ILD in a Chinese Han population.

PO-0217

The optimization of isolation and characterization method of exosomes based on ultracentrifugation

Zilong Yu[1]、Lifu Wang[2]、Xi Sun[2]
1. Guangdong second provincial general hospital
2. 中山大学中山医学院

Exosomes are small vesicles with diameter of 30-150 nm secreted by most cell types in vivo or in vitro and represent an important mode of intercellular communication by mediating cell signaling, immune response modulation, apoptosis induction. However, the lack of availability and purity of exosomes is an obstacle that seriously affects the follow-up research process currently and is a key factor that restricts the continuation of research. There is a need to determine a simple and reliable method for purifying exosomes. In this case, we optimize the traditional and commonly use ultracentrifugation (UC) extraction and perform a comparison to assess three protocols based on UC through negative-staining transmission electron microscopy, NanoSight, concentration and western blotting. Given that the third protocol (protocol 3) displays similar cup-shaped vesicles with diameters of 30-150 nm and express higher levels of exosomes protein, the third protocol outperforms the other two protocols. In summary, the optimized method can be effectively to harvest exosomes for downstream research and variety of immune study.

PO-0218

The expression and significance of TIPE2 in peripheral blood mononuclear cells from Children with Henoch-Schönlein purpura

Guang Shi
The first affiliated hospital of Zhengzhou University

Objective To explore the expression of TIPE2 and the relationship between TIPE2 and HSP related laboratory inflammatory parameters including blood WBC, serum IgA, complements C3 and C4, ESR, anti-streptolysin O, HSP symptom scores in peripheral blood mononuclear cells (PBMCs) from HSP patients.
Methods TIPE2 expression was detected in PBMCs from 40 HSP patients and 36 healthy individuals by western blotting. The correlation between TIPE2 and laboratory parameters including blood WBC, serum IgA, C3 and C4, ESR, anti-streptolysin O, HSP symptom scores was analyzed by Spearman's rank.
Results The TIPE2 expression level was significantly up-regulated in PBMCs from HSP patients compared with healthy individuals ($P < 0.01$). Furthermore, TIPE2 protein expression levels were positively correlated with IgA ($r = 0.3413$, $P = 0.0360$), complement C4 ($r = 0.5112$, $P = 0.0006$), ASO ($r = 0.6275$, $P < 0.0001$), clinical symptom scores ($r = 0.5134$, $P = 0.0010$). However, no statistically significant correlation was found between TIPE2 protein expression and ESR, WBC, C3 ($P > 0.05$, respectively).
Conclusion Increased expression of TIPE2 was correlated with IgA, complement C4 and ASO, but not with ESR, WBC, complement C3. TIPE2 may participate in the pathogenesis of children HSP. However, further studies are needed to definite the role of TIPE2 in the pathogenesis of HSP.

PO-0219

Combination of iron metabolism indexes and tuberculosis-specific antigen/phytohemagglutinin ratio for distinguishing active tuberculosis from latent tuberculosis infection

Ying Luo、Feng Wang、Ziyong Sun
Department of Laboratory Medicine, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Background Discriminating active tuberculosis (ATB) from latent tuberculosis infection (LTBI) remains challenging. The aim of this study was to investigate a diagnostic model based on the combination of iron metabolism and TB-specific antigen/phytohemagglutinin ratio (TBAg/PHA ratio) in T-SPOT.TB assay for differentiation between ATB and LTBI.
Methods A total of 345 participants with ATB (n = 191) and LTBI (n = 154) were recruited based on positive T-SPOT.TB results at Tongji hospital between January 2017 and January 2020. Iron metabolism analysis was performed simultaneously. Diagnostic model for distinguishing ATB from LTBI was established according to multivariate logistic regression.
Results TBAg/PHA ratio showed 64.00% sensitivity and 90.10% specificity in distinguishing ATB from LTBI when a threshold of 0.22 was used. All iron metabolism biomarkers in ATB group were significantly different from those in LTBI group. Specifically, serum ferritin and soluble transferrin receptor in ATB were significantly higher than LTBI. On the contrary, serum iron, transferrin, total iron binding capacity, and unsaturated iron binding capacity in ATB were significantly lower than LTBI. The combination of iron metabolism indicators accurately predicted 60.00% of ATB cases and 91.09% of LTBI subjects, respectively. Moreover, the combination of iron metabolism indexes and TBAg/PHA ratio resulted in a sensitivity of 88.80% and specificity of 90.10%, respectively. Furthermore, the performance of models established in Qiaokou cohort was confirmed in Caidian cohort.
Conclusions Our data suggest that the combination of iron metabolism indexes and TBAg/PHA ratio could serve as a biomarker to distinguish ATB from LTBI in T-SPOT-positive individuals.

PO-0220

Low-density granulocytes down regulate the positive rate of T-SPOT.TB assay via PD-L1/PD-1 pathway

Junming Li、Jiayue Rao、Rigu Su、Zikun Huang、Yang Guo、Qing Luo
the First Affiliated Hospital of Nanchang Universtiy

Background T-SPOT TB (T-SPOT) assay is the most commonly used clinical test worldwide for screening of MTB infection, which actually detects the quantity of IFN γ-secreting T cells in the condition of stimulation with MTB antigens. The purity and quality of PBMCs is one of the key factors impacting the detection of T-SPOT. However, high frequencies of low-density granulocytes (LDGs) were found recently in the peripheral blood of patients with tuberculosis and some other diseases at high risk of tuberculosis activation. These LDGs are located in PBMCs layer after density gradient centrifugation due to decreased density. Whether these LDGs in PBMCs will affect the detection of T-SPOT has not been investigated.
Objective To investigate the impact of LDGs on T-SPOT assay and related mechanism, and explore a method to improve the reliability of T-SPOT assay.
Methods T-SPOT assay and the frequencies of LDGs were detected with PBMCs collected from patients with tuberculosis, and the correlations between the frequencies of LDGs and the positive rate of T-SPOT assay and the amount of IFN γ-secreting cells (ISCs) represented by positive

spots in T-SPOT assay were analyzed. To explore the impact of LDGs on T-SPOT assay, LDGs in PBMCs was removed by immunomagnetic method, and purified LDGs was obtained from PBMCs by negative immunomagnetic sorting, followed by T-SPOT assay with LDGs removed PBMCs or PBMCs with exogenous addition of purified LDGs. Furthermore, the impact of LDGs on IFN-γ production in T cells was verified by FCM. The possible molecular mechanism of LDG's influence on T-SPOT assay was explored by detecting the levels of negative immune regulatory molecules expressed or secreted by LDG and confirmed by function blocking with neutralizing antibody against candidate target.
Results The positive rates of T-SPOT assay and ISCs in tuberculosis patients with low LDGs frequency were significantly higher than those with high LDGs frequency (100.00% vs 76.92%, P=0.015). After removing LDGs from PBMCs, the number of ISCs in the same number of PBMCs increased significantly, and the positive rate of T-SPOT assay also increased (from 77.78% to 94.44%，P=0.148), but the difference was not significant. After exogenous LDGs was added, the number of ISCS in the same number of PBMCs decreased significantly, and the positive rate of T-SPOT assay decreased significantly (from 100.00% to59.09%, P=0.0008). The results of flow cytometry showed that LDGs significantly suppressed the production of IFN-γ in T cells in response to MTB antigen stimulation. Further studies showed that the negative costimulatory molecule PD-L1 was highly expressed on the surface of LDGs. Compared with the untouched LDGs, the effect of LDGs pretreated with anti-PD-L1 McAb on T-SPOT assay significantly decrease. Treating PBMCs with anti-PD-L1 McAb during the T-SPOT assay can significantly increase the number of ISCs and the positive rate of T-SPOT, achieve the similar effect with LDG removal.
Conclusions LDGs can inhibit the production of IFN - γ in T cells and the positive rate of T-SPOT assay through PD-L1/PD-1 pathway. Blocking PD-L1 signal on LDGs can improve the positive rate of T-SPOT assay.

PO-0221

Tumor necrosis factor (TNF)-α and myoglobin (MYO) associated with long-term recovery time of coronary artery lesions in Kawasaki disease patients

Chaochao Tan
Hunan provincial hospital

Aim To assess the relationship between clinical parameters and long-term recovery time of Coronary artery lesions (CALs).
Methods In total, 344 KD patients were screened and 311 KD patients were included and followed-up for the next two years. Clinical records, clinical parameters and inflammatory biomarkers were collected for all subjects.
Results Results revealed that Tumor necrosis factor (TNF)-α and myoglobin (MYO) levels in patients without recovery from CALs were significantly higher than those without CALs and with recovery from CALs. Kaplan-Meier survival analysis showed that in the high-TNF-α group, the estimated median time to recovery (5.0 months, 95% CI 1.436–8.564) is significantly longer than the low-TNF-α group (2.00 months, 95% CI: 0.633–3.367, P = 0.044). Also, the estimated median time (5.0 months, 95% CI: 1.836–8.164) in the high-MYO group is significantly longer than the low-MYO group (2.00 months, 95% CI: 0.405–3.595, P = 0.002). Cox regression analysis showed independent factors for recovery of CALs included age, left coronary artery to aortic annulus ratio, TNF-α and MYO levels.
Conclusions These findings suggest that clinical parameters such as age, left coronary artery to aortic annulus ratio, TNF-α and MYO levels associate with long-term recovery time of CALs and could help in the design of a clinical strategy for the surveillance and prevention of late cardiovascular events.

PO-0222

新型冠状病毒 IgM 抗体阳性疑似病例的排查策略研究

高会霞、李雅楠、刘玉珍、黄颖、许怡、张志、戴二黑
石家庄市第五医院

目的 比较不同原理抗体检测试剂对新冠疑似病例诊断的准确性，对 IgM 抗体阳性疑似病例提出高效的排查方案，进一步为建立高风险人群的临床筛查路径提供科学依据。
方法 对 76 例由于 IgM 抗体初检阳性被转入定点医院隔离观察的新冠疑似病例，进行鼻咽拭子核酸检测，血清微量病毒中和抗体和三种市售不同原理抗体检测试剂检测，以及肺部 CT 检查，结合临床症状等信息，综合判断新冠确诊或排除情况，并将三种血清学抗体检测试剂与临床判断结果进行对比分析，比较三种检测方法结果的差异。
结果 通过综合判断，76 例疑似病例中有 3 例为确诊病例，73 例为排除病例。与临床确诊/排除结果比较，三种血清学抗体检测方法中，化学发光总抗体检测灵敏度 100%，特异性 97.26%，检测准确性高于化学发光法 IgM/IgG 和胶体金法 IgM/IgG 单独检测（入院第 1 天特异性均为 73.97%）。
结论 化学发光法检测新冠总抗体具有高灵敏度和高特异性，可以用于疑似病例抗体检测的初筛。针对重点人群筛查，应首先进行 2019-nCoV 核酸检测，若核酸检测阴性，则采用检测血清总抗体为主要指标的筛查路径。

PO-0223

Whole Exome Sequencing to Identify of Potential Rare Variants for Chinese Han Systemic Sclerosis

Chenxi Liu、yongzhe li
Peking Union Medical College Hospital

Objective Whole-exome sequencing (WES) studies in systemic sclerosis (SSc) patients of American ancestry have identified variants in the ATP8B4 gene and enrichment of variants in genes in the extracellular matrix (ECM)-related pathway increasing SSc susceptibility. Our goal was to evaluate the association of several genes of these two studies with SSc in a cohort of Chinese Han. And then to performed WES in Chinese Han SSc patients to identify rare variants predicted to be deleterious, and characterized their aggregate effects based on enrichment in specific genes and pathways.
Method Functional variants in genes reported in the two WES studies in American ancestry SSc were selected for gene association testing using the real-time PCR allelic discrimination technology. We performed whole-exome sequencing of 40 Chinese Han systemic sclerosis patients including 20 patients without scleroderma renal crisis (SSc-SRC-) and 20 patients with SRC (SSc-SRC+), and 20 healthy controls. Validation genotyping was performed in an independent sample of 363 controls.
Results We examined the association of individual genes that were previously reported in American systemic sclerosis, and none remained significant in Chinese Han SSc patients. Whole-exome sequencing and validation genotyping identified five variants in Chinese Han systemic sclerosis. The mutations in the genes CTDSP2, RPL23A, RGMA, ABCA3, and WRN were rare mutations that may potentially cause the onset of SSc. It is speculated that these genes mutations have a greater impact on gene function and can be used as important target genes for subsequent research.
Conclusion This study demonstrates the value of WES for the identification of novel gene variants and pathways that may contribute to scleroderma risk and/or severity. The candidate genes we discovered are potential targets for in-depth functional studies.

PO-0224

C60@PCN-224 给体-受体长程有序体系在脑损伤标志物检测中的应用研究

杨二利[1]、孙倩[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学附属中大医院临床检验医学中心
3. 东南大学江苏省重症医学重点实验室

光电化学（PEC）免疫分析法因具有背景信号低和灵敏度高等优点，在生物标志物检测领域受到人们的广泛关注。光电活性材料的光电转换效率对 PEC 免疫分析法的灵敏度具有至关重要的影响。C60 作为非金属半导体材料，具有独特的光电特性和电子结构，是潜在的新型光电活性材料。然而，C60 在生理水溶液体系较差的电子离域和积累能力以及生物结合界面的缺乏限制了其在 PEC 生物检测方面的应用。因此，本工作通过卟啉基金属-有机框架（PCN-224）与 C60 非共价偶联构成 C60@PCN-224 纳米复合物，改善了 C60 的光电化学性能和生物界面活性：PCN-224 的羧基末端为生物分子的高效结合提供了丰富的结合位点；PCN-224 与 C60 通过 p-p 相互作用构成了长程有序的电子供体-受体体系加快了光生电子的转移，协同提高了 PEC 生物传感的灵敏性，使 C60@PCN-224 在 PEC 生物传感方面表现出巨大潜力。此外，我们以 C60@PCN-224 为光电化学探针，纳米抗体为识别单元构建了 PEC 免疫传感器并成功用于脑损伤生物标志物 S100 钙结合蛋白 B（S100B）的检测，表现出较高的灵敏度、优异的选择性和良好的稳定性。这项工作可能为具有生物友好界面和高光电转换效率的 C60 基光电极在早期疾病诊断中的应用开辟新的道路。

PO-0225

Vitamin D Deficiency May Not Be an Independent Risk Factor for Peripheral Arterial Disease in Middle-Aged and Elderly Patients with Type 2 Diabetes in China

王彦[1]、张平[1]、冯同保[2]、周洪兴[2]、鲁科峰[2]
1. 南京医科大学附属常州第二人民医院
2. 南京医科大学附属常州第二人民医院

The purpose of our study was to explore the relationship between 25(OH)D levels and PAD in middle-aged and elderly type 2 diabetes mellitus (T2DM) patients in China. Pearson analysis and multivariable logistic regression analysis were used. The parameters including age, HbA1c, and disease duration between two groups showed significantly different. In addition, the frequency of smoking was significantly less and the frequency of well-controlled HbA1c was significantly higher. However, HbA1c significantly differed between groups with vitamin D deficiency and insufficiency in the T2DM patients with PAD. The findings demonstrate that the deficiency of vitamin D level is not related to PAD, but HbA1c may be linked to the presence of PAD in middle-aged and elderly patients with T2DM in China.

PO-0226

The mechanism of IL-17 in rats with acute gouty arthritis

Guozhen Wang、Yongtong Cao
China-Japan Friendship Hospital

Objective To investigate the role of IL-17 and its downstream inflammatory factors in the onset of gouty arthritis by using gouty arthritis rat model.
Methods Animal gouty arthritis model were used to explore the effect of IL-17 on the tissue damage of gouty arthritis. We injected purified IL-17, Urate crystal(MSU), MSU + IL-17 inhibitor or normal saline into the ankle joint of rats respectively, and observed the diameter of the joint, the inflammatory pathological changes of the soft tissue around the joint cavity, the pathological changes of the synovium and bone tissue, the main blood inflammatory and biochemical indexes, so as to clarify the role of IL-17 in the pathogenesis of gouty arthritis.
Results The results showed that the injection of purified monosodium urate (MSU) crystal or IL-17 into the ankle joint of rats could induce the local swelling of the joints, a large number of inflammatory cells infiltration, and the level of serum inflammatory factors significantly increased, which could be used to establish the gouty arthritis rat model. In the MSU + IL-17 inhibitor group, the local swelling of the joints of the rats was significantly reduced, the histopathology showed that the inflammatory response was lighter, and the levels of various inflammatory factors (such as PGE2, MPO, C-reactive protein, IL-6, IL-8 and TNF-α) were significantly lower than those in the MSU group alone ($P<0.05$). The inflammatory response of the rats injected with IL-6 inhibitor, IL-8 inhibitor or TNF-α inhibitor and IL-17 inhibitor were significantly weaker than that of the rats injected with IL-17 alone.
Conclusion IL-17 plays an important role in promoting the inflammation of gouty arthritis, and it may promote the expression and secretion of IL-6, IL-8, TNF - α and participate in the pathogenesis of gouty arthritis.

PO-0227

Circulating levels of IL-33 are elevated by obesity and positively correlated with metabolic disorders in Chinese adults

Haoneng Tang、Ning Liu、Xiaojing Feng、Yanyi Yang、Meilian Liu、Lingli Tang
Department of Laboratory Medicine，The Second Xiangya Hospital，Central South University

Background Interleukin-33 (IL-33) plays a pivotal role in regulating innate immune response and metabolic homeostasis. However, whether its circulating level is correlated with obesity and metabolic disorders in humans remains largely unknown. We aimed to address this gap by determining IL-33 serum level and its downstream type 2 inflammatory cytokines interleukin-5 (IL-5) and interleukin-13 (IL-13) in overweight/obese population, and analyzing the specific associations between IL-33 and obesity metabolic phenotypes.
Methods 217 subjects were enrolled and divided into three groups: healthy control (HC) subjects, metabolically healthy overweight/obese (MHOO) subjects and metabolically unhealthy overweight/obese (MUOO) subjects. Circulating levels of IL-33, IL-5 and IL-13 were measured using ELISA analyses. Multivariate regression analyses were further performed to determine the independent association between IL-33 and obesity metabolic phenotypes.
Results Circulating levels of IL-33 were significantly elevated in subjects of MUOO group compared with HC group and MHOO group, while no significant difference was observed between the latter two groups in IL-33 levels. Consistent with this, serum levels of IL-5/13 were higher in the MUOO group compared with HC and MHOO groups. In different multivariable models, MUOO phenotype was significantly associated with increased IL-33 serum levels

(OR=1.70; 95%CI: 1.09–2.64; p = 0.019). With the MHOO group as the reference population, higher circulating level of IL-33 was also positively associated with MUOO phenotype after adjusting for confounders (OR=1.50; 95%CI: 1.20–1.88; p =2.91E-4). However, there was no significant association between MHOO phenotype and IL-33 levels (p =0.942). Trend test further confirmed the positive correlation between MUOO phenotype and IL-33 level (p for trend =0.019). Additionally, IL-33 was significantly and positively correlated with diastolic blood pressure (DBP), total cholesterol (TC), alanine aminotransferase (ALT), aspartate aminotransferase (AST), white blood cell (WBC), neutrophil and IL-5 only in MUOO group, while inversely correlated with high density lipoprotein cholesterol (HDL-C) in MHOO subjects.
Conclusion Circulating levels of IL-33 were significantly elevated in overweight/obese Chinese adults with metabolic disorders. Increased levels of IL-33 were positively associated with metabolically unhealthy overweight/obese phenotype and several metabolic syndrome risk factors.

PO-0228

Establishment and clinical significance of T lymphocyte detection method

Chen Chen、Yanmei Liu、Shuxia Xuan、Weiguo Yin
The Sixth Affiliated Hospital of Guangzhou Medical University, Qingyuan People's Hospital

Objective Establish and verify the method for detecting the immune phenotype of peripheral blood T lymphocytes by cellular immune chip technology, analyze the cellular immune function of different populations in Qingyuan area, and discuss its clinical diagnostic value.
Methods First, select the samples for performance verification, use the cellular immune chip to detect peripheral blood T lymphocytes, and perform flow cytometry detection and verification; after the method is established, a total of 8389 cases of physical examination and inpatients from Qingyuan People's Hospital are selected, blood samples are collected, and cells are used. Immunochip technology detects the expression of T lymphocyte subsets CD3+, CD4+, CD8+ and CD4/CD8, and analyzes the differences in cellular immune function among people with physical examination, inflammation and cancer, as well as different cancer types and genders.
Results The cell immunochip method and flow cytometry method have the same accuracy and precision in detecting specimens; the CD3+, CD4+, and CD8+ T cell counts of inflammatory and cancer populations are significantly lower than those of the physical examination population, and the CD4/CD8 ratio is significantly higher than that of the physical examination population (P< 001), there is a statistical difference between inflammation and cancer (P＜0.001 or P＜0.01); there are statistics on the CD3+, CD4+, CD8+ T cell counts and the CD4/CD8 ratio of lung cancer, bowel cancer and liver cancer Differences in science (P<0.01 or P<0.05); there are certain differences in CD3+, CD4+, CD8+ T cell counts and CD4/CD8 ratios between male and female groups in physical examination, inflammation and cancer.
Conclusion The cellular immune chip method for T cell phenotype detection is simple and practical, and can be used for immune function monitoring and treatment prognosis evaluation of people with different diseases.

PO-0229

重组结核分枝杆菌 Hsp16.3 的纳米金免疫传感器检测 Hsp16.3 抗体

袁仕善[3]、贺靖[1]、郭婧玮[2]、谭云洪[2]
1. 湖南师范大学医学院医学检验系
2. 湖南省胸科医院检验科
3. 湖南师范大学医学院医学检验系

目的 结核分枝杆菌抗体检测是结核病诊断的有效辅助方法。热休克蛋白 16.3（Heat shock protein 16.3，Hsp16.3）在结核分枝杆菌感染早期大量分泌，其免疫原性强，能诱发机体产生特异性抗体，在结核病的诊断中具有一定价值。金纳米棒具有局部表面等离子体共振（LSPR）性质，将金纳米棒与 MTB 抗原连接后建立纳米金免疫传感器，通过检测金纳米棒纵向等离子体峰波长（LPW）的红移来反映抗原抗体的结合情况，可辅助诊断结核病。本文克隆和表达结核分枝杆菌热休克蛋白 16.3（Hsp16.3），建立 Hsp16.3 的纳米金免疫传感器检测结核病患者血清 Hsp16.3 抗体，为结核病诊断提供有益的参考。
方法 PCR 扩增 hsp16.3 基因，构建重组表达质粒 pQE30-hsp16.3，表达和纯化 Hsp16.3，Western blot 分析其反应原性；晶种生长法制备金纳米棒并连接 Hsp16.3，建立纳米金免疫传感器检测血清 Hsp16.3 抗体，接受者操作特性（ROC）曲线评价其灵敏度和特异性。
结果 成功构建重组表达质粒 pQE30-hsp16.3，纯化 Hsp16.3 具有良好的反应原性；Hsp16.3 的纳米金免疫传感器分别检测 50 例结核病患者、42 例非结核肺病患者和 50 例体检健康者血清，红移值大于 3.5 的例数分别为 42、7、1 例；ROC 曲线显示，曲线下面积 0.888（P<0.01），界值 3.5，灵敏度 82%，特异度 98%。
结论 Hsp16.3 的纳米金免疫传感器可用于检测结核病血清 Hsp16.3 抗体。

PO-0230

Plasma heat shock protein 90alpha as a biomarker for the diagnosis of liver cancer: in patients with different clinicopathologic characteristics

Yueting Han、Li Ren
Tianjin Medical University Cancer Institute and Hospital

Purposes The purposes of this study were to assess the correlation between the plasma level of Hsp90α and the clinicopathological characteristics of patients with liver cancer and compare the diagnostic efficacy of Hsp90α, AFP, CEA, and CA199 in HCC. Experimental design: A total of 200 individuals, including 140 patients with liver cancer or benign liver diseases and 60 healthy people, were enrolled for quantitative measurement of plasma Hsp90α by ELISA.
Results The plasma level of Hsp90α was significantly different between patients with liver cancer or benign liver diseases and healthy controls (P < 0.001). The sensitivity, specificity, and AUC (95% CI) of Hsp90α were 93.2%, 85.4%, and 0.931% (0.891–0.972%), respectively, when Hsp90α was applied to differentiate liver cancer patients and healthy controls. Significant positive correlations between the plasma Hsp90α level and clinicopathological characteristics such as the history of basic liver disease (P = 0.038), active stage of hepatitis (P = 0.039), Child-Pugh score (P < 0.001), size of focal liver lesions (P = 0.004), and extrahepatic metastasis (P < 0.001) were observed. AFP + Hsp90α was the best combination strategy for the auxiliary diagnosis of HCC, with a sensitivity of 95.7%, a specificity of 97.5%, and an AUC of 0.990 (0.976–1.000). The level of plasma Hsp90α decreased significantly (P < 0.001) after resection of tumor tissue.

Conclusions This study demonstrated that plasma Hsp90α levels are useful as a diagnostic biomarker in liver cancer and may predict the responses of patients with liver cancer to surgery. Some clinicopathological characteristics could affect the plasma Hsp90α levels.

PO-0231

Clinical characteristics of immune responce in severe and asymptomatic COVID-19 patients

Bin Liu[1]、feihu yan[2]
1. Second affiliated hospital of south China universit
2. 军事科学院长春研究所

The worldwide pandemic of coronavirus disease 2019 (COVID-19) is the prime challenge facing global public health. A comprehensive understanding of clinical characteristics in cellular and humoral immune responses against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the emerging virus causing COVID-19, is of great significance to the prophylactic and therapeutic countermeasures of COVID-19. Features of cytokine and antibody responses among COVID-19 patients has been reported but few consensus has been reached, especially the differences in patients with different severity as well as the relationship between these key indicators. Here, we investigated 29 individuals infected with SARS-CoV-2 in Hunan Province, China, including 12 asymptomatic carriers, and 17 severe COVID-19 patients based on nucleic acid test and clinical symptoms. Sera were collected from these people for cytokine and antibody responses based on RBD or N protein of SARS-CoV-2 respectively. Our retrospective observational study enriched and verified clinical characteristics of COVID-19. In terms of cytokine, difference are also observed between groups in our study. Virus-specific antibody is IgG1 baised in COVID-19 patients, IgG and IgG1 behaves the same tendency in both group. Dispite discrete, VNA titers of asymptomatic carriers is comparble to that of severe COVID-19 patients. The above information is of immediate relevance and would assist COVID-19 clinical diagnosis, prognosis and vaccine design.

PO-0232

液基细胞学技术的临床应用价值初探

文金润
昆明市中医医院

液基薄层细胞技术（(ThinPrep Cytology Test， TCT）是细胞工程专家推出的一种重大革新的细胞制片新技术，通过该技术去掉非诊断性杂质，制成观察清晰的薄层细胞片，克服了传统方法取材时细胞的丢失及涂片质量差的缺陷，薄层细胞经自动单片独立染色，使细胞学的诊断准确性明显提高。所有传统的涉及病理科细胞学的检测项目均适用于液基薄层细胞学检查。液基细胞学与 1996 年开始应用于临床，为临床细胞病理学诊断提供可靠参考。目前液基细胞学广泛应用于妇科宫颈癌筛查工作，但因其取材简单、制片简便、处理过程系统程序化，现在泌尿、呼吸、胃肠、外科等非妇科领域发挥重要作用[1]。

PO-0233

金标法与免疫比浊法检测 C 反应蛋白结果的可比性分析

田元琴
昆明市中医医院

目的 对本科室检测 C-反应蛋白（CRP）的金标法与胶乳免疫比浊法进行比较。
方法 采集 30 例门诊患者全血样本，并将其分为血浆组和全血组，每组均为 30 份。血浆组采用 AU5800 型全自动生化仪，全血组采用 FIA8600 免疫定量分析仪进行 CRP 的测定，对结果进行统计分析。 其检测结果金标法与免疫比浊法之间差异无显著性（P>0.05），且相关性好。
结论 金标法适用于单个样本快速检测，比浊法适用于批量检测。

PO-0234

IL-17 and IL-21 polymorphisms in relation to HBV related hepatocellular carcinoma in Chinese Han population

Wennan Wu、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Objective Inflammatory cytokine gene polymorphisms may influence the hepatic and extrahepatic HBV-related disease. In this study, we aimed to investigate the relationship between polymorphisms of IL-17, IL-21 gene and HBV related hepatocellular carcinoma in Chinese Han population.
Methods We performed a multi-center study comprised 866 HBV-related hepatocellular carcinoma (HCC) patients and 1086 unrelated patients with a diagnosis of chronic hepatitis B (CHB) as control to evaluate the effects of IL-17 (rs4711998), IL-21 SNPs (rs12508721, rs13143866 and rs2221903) and the susceptibility of HCC. MassARRAY technology was utilized to genotype. Enzyme-linked immunosorbent assay (ELISA) was used to detect the serum IL-17 and IL-21 level. Quantitative real time polymerase chain reaction (qRT-PCR) was used to analyze the serum viral loads.
Results In logistic regression analysis, our results showed the frequency of rs4711998 allele G in CHB group was significantly higher than that in HCC group (P = 0.042, 0.859(0.743-0.994)), and it is present only among females. Compared to HCC group, rs13143866 A allele was more likely to appear in HCC group (P = 0.015, 1.268 (1.049-1.532)). The frequency of AA also showed different between HCC group and CHB groups (P = 0.011, 3.135 (1.292-7.603)), which showed strong sex-specific relationships. ELISA showed a higher serum IL-17 and IL-21 expression in HCC patients compared to CHB patients (P all <0.05). Haplotype rs12508721C/rs13143866A/rs2221903T in male HCC group was statistically higher than in male CHB group(P = 0.013) but not in females (P > 0.05).
Conclusion We suggested rs4711998 allele A as risk factors for women to develop HBV related-HCC in Chinese Han population. rs13143866 allele A as risk factors to develop HBV related-HCC in Chinese male population. Male patients with haplotype rs12508721C/rs13143866A/rs2221903T may with 1.3-fold risk for HBV-related HCC.

PO-0235

构建 CHB 患者 IFN-α 疗效预测的列线图模型

荀振、欧启水
福建医科大学附属第一医院

目的 慢性乙型肝炎（CHB）患者干扰素-α（IFN-α）疗效预测问题一直困扰临床。本文旨在筛选预测 IFN-α 疗效的独立因素，运用 R 语言构建预测 IFN-α 疗效的列线图模型。
方法 首先收集 116 例经 IFN-α 治疗的 HBeAg 阳性 CHB 患者（包含经 IFN-α 治疗应答者和应答不佳者）详细的临床资料，包括患者基本信息如年龄、性别、用药情况，实验室指标如血常规、肝功能、血脂、HBV DNA、乙肝“两对半”等，以及影像学检查。其次采用 SPSS 22.0 软件，对每个临床变量进行单因素 logistic 回归分析，以筛出治疗反应的独立预测因子；利用 R 4.0.2 软件，将 logistic 回归分析得出的独立预测因子引入 R 代码，并因此应用 rms 包建立列线图预测模型；最后，利用受试者工作（ROC）曲线评估列线图模型的预后性能，并通过 Bootstrap 重抽样对模型进行内部验证。
结果 单因素 logistic 回归分析结果提示：HBV DNA、HBsAg、HBeAg、白蛋白、白蛋白-胆红素（ALBI）评分、ALT、AST、总胆汁酸（TBA）、总胆固醇与 CHB 患者 IFN-α 疗效相关（P<0.05）；以统计学上重要的影响因素作为自由变量进行单变量筛选，进行多因素 logistic 回归分析显示，HBeAg 和 TBA 是 CHB 患者 IFN-α 药效反应的独立风险因素；成功建立预测 CHB 患者 IFN-α 疗效的列线图模型，该预测模型的预测效能较好，其 ROC 曲线下面积 AUC 为 0.871（95%CI：0.795～0.926），在经过 1000 次 Bootstrap 重采样内部验证后，预测模型的一致性指数（C-index 值）为 0.839，校准曲线显示该列线图所预测的治疗应答率与实际观察情况具有很好的一致性。
结论 成功构建基于 HBeAg、ALBI、ALT、TBA 的可预测 IFN-α 疗效的列线图模型，该模型的指标易得、预测效能较好。

PO-0236

Taurocholic acid inhibits the response to interferon-α therapy in patients with HBeAg-positive chronic hepatitis B by impairing CD8+ T and NK cell function

Zhen Xun 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Pegylated interferon-alpha (PegIFNα) therapy has limited effectiveness in hepatitis B e antigen (HBeAg)-positive chronic hepatitis B (CHB) patients. However, the mechanism underpinning this failure is poorly understood. We aimed to investigate the influence of bile acids (BAs), especially taurocholic acid (TCA), on the response to PegIFNα therapy in CHB patients. Here, we used mass spectrometry to determine serum BA profiles in 110 patients with chronic HBV infection and 20 healthy controls (HCs). We found that serum BAs, especially TCA, were significantly elevated in HBeAg-positive CHB patients compared with HCs and patients in other phases of chronic HBV infection. Moreover, serum BAs, particularly TCA, inhibited the response to PegIFNα therapy in HBeAg-positive CHB patients. Mechanistically, expression levels of IFN-γ, TNF-α, granzyme B and perforin were measured using flow cytometry to assess the effector functions of immune cells in patients with low or high BA levels. We found that BAs reduced the number and proportion, and impaired the effector functions of CD3+CD8+ T cells and natural killer (NK) cells in HBeAg-positive CHB patients. TCA in particular reduced the frequency and impaired the effector functions of CD3+CD8+ T and NK cells in vitro and in vivo, and inhibited the immunoregulatory activity of IFN-α in vitro. Thus, our results show that BAs, especially TCA,

inhibit the response to PegIFNα therapy by impairing the effector functions of CD3+CD8+ T and NK cells in HBeAg-positive CHB patients. Our findings suggest that targeting TCA could be a promising approach for restoring IFN-α responsiveness during CHB treatment.

PO-0237

The Immune Imbalance of T-Lymphocyte Subsets：the key to the pathogenesis of unexplained recurrent spontaneous abortion

Yizhi Peng
Department of Laboratory Medicine, the Second Xiangya Hospital of Central South University

The etiologies of recurrent spontaneous abortion (RSA) were varied, but the etiology of 50% of patients with recurrent abortion was unknown, known as unexplained recurrent spontaneous abortion (URSA). The occurrence of URSA was related to maternal-fetal immune tolerance imbalance, especially the imbalance of various T-lymphocyte subsets, including Th1 cells, Th2 cells, Th17 cells, Treg cells and NKT cells. In this paper, the latest research progress of T-lymphocyte subsets and URSA occurrence in the world was reviewed, especially the research progress of T lymphocyte subsets in URSA occurrence in the aspects of immune mechanism, immune imbalance and the interaction between different subsets.

PO-0238

A new interpretation of TB-IGRAs quantifies peripheral blood IFN-γ in the progression of lung cancer

Yizhi Peng
Department of Laboratory Medicine, the Second Xiangya Hospital of Central South University

Objective To explore the value of TB-IGRAs quantification of peripheral blood IFN-γ in immune checkpoint inhibitors (ICI) resistance against various cancers and the progression of lung cancer.
Methods A total of 389 patients and 127 healthy volunteers admitted to the Second Xiangya Hospital from June 2018 to April 2021 were recruited, including 259 patients with lung cancer, 27 patients with liver cancer, and 103 patients with hematologic tumors. The TB-IGRAs test was performed within 24 hours after 10mL of heparin sodium was taken for anticoagulant vessels. SPSS version 26.0 software was used to analyze the results of each group.
Results The concentrations of IFN-γ in healthy control group, lung cancer group, liver cancer group and hematological malignancy patients were 517.91(352.83-750.75), 1022.61(253.41-2872.23), 2764.87(953.23-7084.61) and 11106.41(259.41-3326.28)pg/ mL, respectively, the ability of peripheral T cells to secrete IFN-γ in patients with lung cancer was higher than that in healthy control group, while the ability of peripheral T cells to secrete IFN-γ was lower in patients with liver cancer and hematologic tumor than that in healthy control group. The concentrations of IFN-γ in the non-metastatic group and the metastatic group were 2893.57(1092.94-7592.89) pg/mL and 1554.63(308.43-4927.04)pg/mL, respectively, the concentrations of IFN-γ in the non-metastatic group were higher than those in the metastatic group.
Conclusion The quantification of IFN-γ produced by peripheral T cells after stimulation with PHA by TB-IGRAs test may reflect the response of cancer to ICI, which may be closely related to the progress of lung cancer, and may reflect the immune status of patients to a certain extent. Monitoring lung cancer patients may help to judge whether they have a tendency to further metastasis.

PO-0239

The value of a new interpretation of the QFT-GIT test in the diagnosis of active and latent tuberculosis after clinical transplantation

Yizhi Peng
Department of Laboratory Medicine, the Second Xiangya Hospital of Central South University

Objective To evaluate the application and value of QFT-GIT test in the diagnosis of active and latent tuberculosis.
Methods 142 patients admitted to the Second Xiangya Hospital from July 2018 to April 2019 were collected, including 12 patients with Active Tuberculosis(ATB), 45 patients with Latent Tuberculous Infection(LTBI) and 85 patients without Tuberculosis (TB). The Quantiferon-TB Gold In-Tube Test(QFT-GIT) and T-Spot.TB Blood Test (T-SPOT) were performed within 24 hours after 10mL of heparin sodium was taken for anticoagulant vessels.
SPSS version 26.0 software was used to analyze the Results of each group, and the AUC and ROC of each variable were further calculated and analyzed.
Results The concentrations of IFN-γ in ATB group, LTBI group and control group were 68.45(7.77-425.53), 5.30(0-179.50) and 2.30 (0-17.94) pg/mL, respectively. The concentration of IFN-γ in TB group was higher than that in LTBI group and control group. When Cut-offIFN-γ was 15.205pg/ml, the specificity and negative predictive value of differentiating TB patients from other populations were 0.74 and 0.71, respectively. When Cut-offIFN-γ was 90.365pg/ml, the specificity and negative predictive value of differentiating LTBI from healthy population were 0.88 and 0.77, respectively.
Conclusion The quantitative determination of IFN-γ concentration in the QFT-GIT test can effectively determine the presence of Mycobacterium tuberculosis infection, and the new interpretation of the QFT-GIT test is expected to solve the problem of differential diagnosis of latent infection and active tuberculosis.

PO-0240

NKT-like 细胞在系统性硬化症患者中的意义

周新华[1]、李燕[2]、李英妮[3]
1. 南昌市第三医院
2. 晋中市第一人民医院
3. 北京大学人民医院

目的 研究外周血 NKT- like 细胞在系统硬化症（SSc）患者中的表达，探索 NKT-like 细胞与系统性硬化症实验室指标和临床指标之间的相关性，进而探讨 NKT-like 细胞在系统性硬化症疾病发生发展中的提示作用。
方法 选取 2018 年 12 月到 2019 年 12 月在北京大学人民医院风湿免疫科门诊和住院就诊的 46 例 SSC 患者（SSc 组），年龄性别与之匹配的 30 例健康体检者，作为健康对照组（HC 组）。采用流式细胞术收集 SSc 组和 HC 组外周血 NKT-like 细胞和其他淋巴细胞亚群的细胞数量和百分比。同时采用相应实验方法测定其他实验室指标。利用统计软件 SPSS24.0 对 NKT-like 细胞及其他临床和实验室指标进行相关统计分析。
结果 与 HC 组相比，SSc 组外周血中 NKT-like 细胞数量明显减少，差异具有统计学意义 (P<0.05)。相关性分析可见，NKT-like 细胞数目与总 T 淋巴细胞(r=0.562，P<0.0001)、CD4+T 细胞(r=0.418，P=0.004)、CD8+T 细胞(r=0.605，P<0.001)、B 淋巴细胞(r=0.503，P<0.0001)及 NK 细胞(r=0.332,P=0.024)存在明显正相关；NKT-like 细胞所占淋巴百分比与 CD8+T 细胞所占百分比呈明

显正相关(r=0.342，P=0.020)，与其他淋巴细胞百分比的相关性不明显(P>0.05)。NKT-like 细胞与血沉（ESR）具有明显负相关性(r=-0.344，P=0.019)。
结论 SSc 患者外周血 NKT-like 细胞存在数量和比例的明显减低，，与多种淋巴细胞正相关，而且与反映病情的 ESR 具有负相关关系。NKT-like 细胞可作为 SSC 患者病情评估的指标之一。

PO-0241

抗核抗体荧光核型在自身免疫性肝病筛查中的作用评估

张炜、王之青、郑冰
上海交通大学医学院附属仁济医院

目的 探讨 HEp-2 细胞为底物的间接免疫荧光法（IFA）荧光法检测抗核抗体（ANA）在自身免疫性肝病（ALD）筛查中的作用。
方法 分析国际抗核抗体荧光核型共识（ICAP）所定义的 30 种荧光核型在 6226 例 ALD 筛查人群，106 例原发性胆汁性肝硬化（PBC）和 138 例自身免疫性肝炎（AIH）患者中的检出率。比较抗线粒体抗体、AMA-M2 和 M2-3E 在胞浆网状/线粒体样型（AC-21）和其他胞浆颗粒型（AC-18/19/20）中检出率；抗 Sp100 和 PML 抗体在核多点型（AC-6）和核少点型（AC-7）中检出率；抗 gp210 抗体在点状核膜型(AC-12)和光滑核膜型（AC-11）中检出率以及抗平滑肌抗体、抗 F-肌动蛋白抗体在胞浆线性/肌动蛋白型（AC-15）和其他胞浆纤维型（AC-16/17）中检出率。
结果 ALD 筛查人群、PBC 和 AIH 患者荧光核型检出率最高的分别是：细颗粒型[16.4%（1023/6226）]、胞浆网状/线粒体样型[50.9%（54/106）]和细颗粒型[23.9%（33/138）]。抗线粒体抗体、AMA-M2 和 M2-3E 在 AC-21 中检出率分别为 80.7%（385/477）、72.8%（347/477）和 82.4%（393/477），明显高于其他胞浆颗粒型（AC-18/19/20）中检出率（7.5~23.1%）；抗 Sp100 和抗 PML 抗体在 AC-6 核型中检出率分别为 90.7%和 16.1%，明显高于其在 AC-7 中检出率 9.4%和 1.9%；抗 gp210 抗体在 AC-12 中检出率为 82.0%，在 AC-11 中检出率为 0%；抗 ASMA 和抗 F-肌动蛋白抗体在 AC-15 中检出率分别为 54.6%和 16.1%，明显高于其他胞浆纤维型中检出率。
结论 胞浆网状/线粒体样型、点状核膜型、核多点型和胞浆线性/肌动蛋白型荧光核型在 ALD 筛查中有重要意义，实验室应重视上述核型判读。

PO-0242

胃蛋白酶原、胃泌素-17、CA19-9、CA72-4 检测在不同类型胃炎及胃癌中的临床应用价值

杨淑娴、娄鉴芳
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨胃蛋白酶原、胃泌素 17、CA19-9、CA72-4 在胃部相关疾病中的临床应用价值。
方法 选取 2016 年 8 月至-2019 年 3 月在南京医科大学第一附属医院初次就诊并确诊为浅表性胃炎、萎缩性胃炎，胃癌的患者纳入研究。检测各组胃蛋白酶原、胃泌素 17、CA-199、CA72-4 水平，并进行比较。
结果 PGI 水平浅表性胃炎组（中位水平 122.4μg/L）显著高于胃癌组（中位水平 69.05 μg/L）和萎缩性胃炎组（中位水平 68 μg/L）。PGII 水平浅表性胃炎组（中位水平 13.9 μg/L）显著高于胃癌组（中位水平 9.2μg/L）和萎缩性胃炎组（中位水平 7.6μg/L），胃癌组显著高于萎缩性胃炎组。G-17 水平浅表性胃炎组（中位水平 3.7 pmol/L）、胃癌组（中位水平 3.5 pmol/L）、萎缩性胃炎组（中位水平 2.4 pmol/L）之间无显著差异。CA19-9 水平在胃癌组（36.93±17.84 U/mL）显著高于萎缩性胃炎组（22.04±14.33 U/mL）与浅表性胃炎组（18.87±11.36 U/mL），CA72-4 水平在胃

癌组（8.686±5.42 U/mL）显著高于萎缩性胃炎组（8.016±2.18 U/mL）与浅表性胃炎组（3.91±2.2 U/mL）。PGI 阳性率胃癌组显著高于浅表性胃炎组（P<0.05）而萎缩性胃炎组显著低于浅表性胃炎组（P<0.05）；PGII 阳性率胃癌组（P<0.05）、萎缩性胃炎组（P<0.05）显著低于浅表性胃炎组；CA19-9 阳性率胃癌组显著高于萎缩性胃炎组（P<0.05）和浅表性胃炎组（P < 0.05）。PGR、G-17、CA72-4 在三组之间无显著差异（P>0.05）。

结论 同时进行胃蛋白酶原、胃泌素-17、CA-199、CA72-4 多种指标的检测，可对胃部相关疾病的鉴别诊断提供帮助。

PO-0243

Immune cells and cytokines in patients with COVID-19 or cancer

Xiaojiao Zeng [2]、Xianghu Jiang[1]、Liu Yang[1]、Yunbao Pan[1]、Yirong Li[1]
1. Department of Laboratory Medicine, Zhongnan Hospital of Wuhan University
2. Zhongnan Hospital of Wuhan University

Objective This study explored the consistency and differences in the immune cells and cytokines between patients with COVID-19 or cancer. We further analyzed the influencing factors and correlations between the two types of inflammatory disease.

Methods This retrospective study involved 167 COVID-19 patients and 218 cancer patients. COVID-19 and cancer were each further divided into two subgroups. Quantitative and qualitative variables were measured by one-way ANOVA and chi-square test, respectively. Multivariate logistic regression analysis was used to explore the factors that influence various diseases. Herein, we carried out a correlation analysis between immune cells and cytokines, and used receiver operating characteristic (ROC) curves to discover the optimal diagnostic index.

Results COVID-19 and cancers were associated with lymphopenia and high levels of monocytes, neutrophils, IL-6, and IL-10. IL-2 was the optimal indicator to differentiate the two types of inflammation. Compared with respiratory cancer patients, COVID-19 patients had lower levels of IL-2 and higher levels of CD3+CD4+ T cells, 4/8 ratio, and CD19+ B cells, and there was no difference in IL-6 and IL-10 between the two groups. In the subgroup analysis, there was no significant difference in cytokines between severe and non-severe COVID-19 patients, while patients with severe COVID-19 had lower levels of lymphocyte subsets (CD3+ T cells, CD3+CD4+ T cells, CD3+CD8+ T cells, CD19+ B cells) and CD16+CD56+ NK cells and higher level of neutrophils. There were no significant differences in immune cells or cytokines between the metastatic and the non-metastatic cancer patients. Moreover, IL-6, CD3+CD8+ T cells, and lymphocytes were risk factors for severe COVID-19. Additionally, IL-6 was the optimal differential diagnostic parameter that had the ability to identify if COVID-19 patients would be severely affected. Age, CD16+CD56+ NK cells, and neutrophils were risk factors for distant metastases in cancer patients. There were higher correlations between IL-2 and IL-4, TNF-α and IL-2, TNF-α and IL-4, TNF-α and IFN-γ, and CD16+CD56+ NK cells and various subsets of T cells in COVID-19 patients. There was a higher correlation between CD3+CD4+ T cells and CD19+ B cells in cancer patients.

Conclusion As representatives of fatal acute and chronic inflammation, consistencies, differences, and satisfactory correlations were found to exist among immune cells and cytokines between patients with COVID-19 and those with cancers, and these inflammatory indexes played a crucial role in COVID-19 and cancers.

PO-0244

KLF4 乙酰化在系膜增生型 IgA 肾病炎性因子分泌中的作用机制及其临床应用初探

谢梦晓
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨 KLF4 乙酰化在系膜增生型 IgA 肾病炎性病变中的作用及其调控机制，并初步评估其在 IgA 肾病中的应用价值。
方法 1）复制大鼠 Thy-1 肾炎（Thy-1N）模型，或利用 C5b-9 刺激大鼠肾小球系膜细胞（GMC）。2）RNA、抗体芯片以及 IB 等进行分析并验证。3）ELISA 及报告基因等分析相应基因或蛋白对 IL-23/IL-36α 表达的影响与调控机制。4）免疫共沉淀及质谱等分析相应乙酰基转移酶乙酰化修饰转录因子对 IL-23/IL-36α 表达及其转录调控的作用。5）采用慢病毒肾动脉灌注的方式沉默上述基因以观察 Thy-1N 大鼠病变的改善。6）免疫组化检查 IgA 肾病患者及对照的肾组织中相应蛋白的表达水平。
结果 1）成功复制 Thy-1N 的动物与细胞模型。2）乙酰基转移酶 PCAF、转录因子 KLF4 以及炎症因子 IL-23/IL-36α 的表达显著升高。3）PCAF 和 KLF4 均能上调 IL-23/IL-36α 的表达，KLF4 能够直接结合于 IL-23/IL-36α 启动子区域，而该过程受 PCAF 影响。4）PCAF 乙酰化修饰 KLF4 赖氨酸 224 位点是促进其调控 IL-23/IL-36α 表达的关键位点。5）沉默上述基因能显著改善 Thy-1N 大鼠病变。6）PCAF、KLF4 和 IL-23/IL-36α 在系膜增生型 IgA 患者肾组织中的表达水平显著升高。
结论 C5b-9 能通过调控 PCAF 乙酰化修饰 KLF4 促进 IL-23/IL-36α 表达，进而导致系膜增生型 IgA 肾病炎性病变。PCAF、KLF4、和 IL-23/IL-36α 的表达在系膜增生型 IgA 患者的肾组织中显著升高，提示其在该疾病的诊断中具有潜在的应用价值。

PO-0245

系统性红斑狼疮患者外周血不同形式循环游离 DNA（cfDNA）的水平和免疫活性比较

黄建军、冯钢
皖南医学院弋矶山医院

目的 检测分析不同形式循环游离 DNA（cfDNA）在系统性红斑狼疮（SLE）患者外周血含量和对巨噬细胞和树突状细胞的刺激活性。
方法 58 例 SLE 患者、66 例非 SLE 病患者（non-SLE）和 60 例正常对照，提取血浆总 cfDNA、外泌体 cfDNA 和免疫复合物 cfDNA，检测 cfDNA 含量，cfDNA 总甲基化水平。体外诱导巨噬细胞和树突状细胞，分别与外泌体或免疫复合物共培养，检测巨噬细胞炎性蛋白 1a（MIP1a）、MIP-1b、白细胞介素 4（IL-4）、IL-1β、IL-2、白细胞介素 1 受体拮抗剂（IL-1ra）、单核细胞趋化蛋白 1(MCP-1)、IL-6、IL-9、IL-10、IL-12、IL-8、肿瘤坏死因子 α(TNF-α）、α 干扰素（IFN-α）和 IFN-γ 分泌以及细胞表面 CD40、CD80 和 CD86。
结果 SLE 组、non-SLE 组外泌体 cfDNA 和免疫复合物 cfDNA 水平显著增加，SLE 患者组也显著高于 non-SLE 组，单纯 cfDNA 在三组间无明显变化。SLE 患者 cfDNA 甲基化水平均显著低于 non-SLE 组和健康组。处理后的外泌体和免疫复合物刺激分泌的 MIP1a、MIP-1b、IL-4、IL-1β、IL-2、IL-1ra、MCP-1、IL-6、IL-9、IL-8、TNF-α 和 IFN-α 水平显著低于未经处理的刺激物，DNASE1L3 酶处理后的外泌体和免疫复合物刺激后分泌的细胞因子量也显著低于 IgG 酶消理后刺激物。与处理前相比经 DNASE1L3 酶处理后，对 CD80、CD86 和 CD40 在巨噬细胞和树突状细胞刺激反应性均降低（CD86 在巨噬细胞上的反应性无明显改变）；IgG 特异性降解酶降解处理前后的刺激对 CD80、CD86 和 CD40 在两种细胞的反应性表现不一，总体呈下降趋势。

结论 SLE 患者血浆外泌体和免疫复合物 cfDNA 水平显著升高，可刺激巨噬细胞和树突状细胞产生较强应答。

PO-0246

T3/rT3 对妊娠高血压类疾病的早期诊断价值研究

高谦、聂志文、段玉萍、洪茂、厉倩
上海市宝山区吴淞中心医院

目的 甲状腺功能障碍在生殖年龄相对常见，并与母亲和儿童的不良健康结果有关。探讨甲状腺功能相关指标与妊娠高血压类疾病诊断及严重程度的关系，为此类疾病早期诊断及预防提供参考。
方法 选取 2017 年 2 月至 2019 年 9 月来本院就诊的正常妊娠 85 例，妊娠高血压 87 例，轻度子痫 33 例，重度子痫 36 例，采用化学发光法检测四组在妊娠 12-16 周血清中的游离甲状腺素(FT4)、促甲状腺激素(TSH)、游离三碘甲腺原氨酸（FT3）、总三碘甲状腺原氨酸（TT3）、总甲状腺素（TT4）、抗甲状腺球蛋白抗体（TGAB）、抗甲状腺过氧化物酶抗体（TPOAB）、促甲状腺激素受体抗体（TRAb）和血清反三碘甲状腺原氨酸（rT3）水平；采用 ROC 曲线分析有差异指标对妊娠高血压类疾病的诊断价值，并与 24 小时蛋白尿，收缩压，舒张压进行相关性分析，logstic 二元回归分析妊娠高血压疾病发病的影响因素。
结果 正常妊娠组 rT3 水平显著低于其他三组（P＜0.01），T3/rT3 显著高于其他三组（P＜0.01）。 Pearson 相关分析结果显示，T3/rT3 与收缩压负相关（r＝0.278，P＜0.01），与舒张压负相关（r＝0.325，P＜0.01），与 24 蛋白尿无显著相关性。
ROC 曲线的评估结果显示，预测子痫前期 T3/rT3 的临界值为 2.416，曲线下面积 0.7200,敏感性 0.5652，特异性 0.8235；妊娠高血压预测 T3/rT3 的临界值为 2.625，曲线下面积：0.7393，敏感性 0.8721，特异性 0.5059。多因素 logistic 回归模型分析显示 T3/rT3 是妊娠高血压早期诊断的独立预测因子（Adjusted OR=0.077(0.007-0.89),P=0.04）。
结论 妊娠期妇女甲状腺功能指标 T3/rT3 可能是在妊娠高血压疾病早期诊断有价值的生物标志物。

PO-0247

青蒿琥酯对肺癌患者 CD8+T 细胞亚群免疫功能的影响

邢应如、胡东
安徽理工大学医学院

目的 研究青蒿琥酯对肺癌患者 T 淋巴细胞免疫功能的影响，探讨 ART 体内抗肿瘤的作用机制。
方法 采集肺癌患者和健康体检者外周血，分离 PBMC。确定 ART 的 IC50，检测 ART 刺激培养前后 CD8+ T 细胞的免疫治疗相关分子 CD39、CD279，活化相关分子 CD38，共刺激分子 CD28，细胞杀伤功能相关因子 GrzB 和 PerF，功能相关细胞因子 IFN-g 和 IL-2，以评价 T 细胞免疫功能变化情况。
结果 ART 的 IC50 浓度为 522μM；肺癌组 CD8+ T 细胞的 CD279 基线表达显著高于健康对照组；促进 ART 诱导 CD8+T 细胞 CD39 表达的临床因素有：未放疗；促进 ART 诱导 CD8+T 细胞 CD279 表达的因素有：年龄>60 岁、淋巴细胞数>1.26×109/L、NLR<5、放疗、0.29×109/L≤单核细胞数≤0.95×109/L，NLR 与淋巴细胞绝对值呈显著负相关。经 ART 刺激培养后，CD8+T 细胞的 CD38、CD28、IFN-g 和 PerF 等表达未见显著变化，IL-2 表达显著降低(P<0.05)，GrzB 表达显著增强(P<0.01)。
结论 肺癌患者 T 淋巴细胞 CD279 高表达可能与肿瘤免疫抑制相关，高剂量的 ART 诱导颗粒酶 B 表达上调，且不影响肺癌患者 CD8+T 细胞亚群的免疫活性， ART 可能增强肺癌患者 CD8+T 细胞亚群抗肿瘤的免疫功能。

PO-0248

miR-455 Inhibits the Viability and Invasion by Targeting RAB18 in Hepatocellular Carcinoma

Chenghong Wang
Department of Laboratory Medicine, Yantaishan Hospital, Yantai, Shandong

Aim Hepatocellular carcinoma (HCC) has been regarded as the fifth most common cancer worldwide with a low prognosis. miR-455 usually played the role of a tumor suppressor in multiple cancers. The aim of this study was to investigate the roles of miR-455 in HCC.
Materials and Methods Cell viability and invasion were measured by CCK8 and Transwell assays. Luciferase reporter assay was performed to verify that miR-455 directly binds to the 3′-noncoding region (UTR) of RAB18 mRNA in Huh7 cells.
Results The expression of miR-455 was lower in HCC tissues and cell lines than in nontumor tissues and normal cell line, and downregulation of miR-455 was connected with worse outcome of HCC patients. miR-455 suppressed cell proliferation in vitro and in vivo, and it inhibited the abilities of cell invasion and EMT in HCC. RAB18 was upregulated in HCC tissues and cell lines, and the expression of RAB18 was regulated by miR-455. RAB18 reversed partial roles of miR-455 on cell viability and invasion in HCC.
Conclusion miR-455 inhibited cell viability and invasion by directly targeting the 3′-UTR of RAB18 mRNA of hepatocellular carcinoma.

PO-0249

化学发光法检测 SARS-CoV-2 特异性 IgM、IgG 抗体的假阳性结果的分布特征分析

卢小岚、王强
川北医学院附属医院

目的 分析化学发光法检测 SARS-CoV-2 特异性 IgM、IgG 抗体假阳性结果的分布特征。
方法 应用 LIS 系统，计算机检索 2020 年 3 月至 2021 年 1 月川北医学院附属医院和南充市中心医院门诊及住院部进行 SARS-CoV-2 IgM、IgG 检测的病例，收集检测结果≥1.0 的病例，对 SARS-CoV-2 核酸检测结果及病人信息及进行回顾性分析。
结果 回顾性分析发现，单 SARS-CoV-2 IgM(+)的假阳性率最高，为 95.88%，明显高于单 SARS-CoV-2 IgG(+)的 67.50% ($\chi2$ =20.981, P<0.0001)、SARS-CoV-2 IgM & IgG(+)的 29.55% ($\chi2$ =71.368, P<0.0001)。单 SARS-CoV-2 IgM(+)、单 SARS-CoV-2 IgG(+)及 SARS-CoV-2 IgM & IgG(+)的假阳性结果在不同性别间比较差异无统计学意义(P>0.05)；在不同年龄段人群间比较无统计学差异(P>0.05)。单 SARS-CoV-2 IgM(+)的假阳性结果分布在 1.0~32.0 之间，多数结果集中在 1.0~3.0 之间；单 SARS-CoV-2 IgG(+)的假阳性结果分布在 1.0~40.0 之间，多数结果集中在 1.0~2.0 之间。SARS-CoV-2 特异性抗体动态监测发现，假阳性病例血清 SARS-CoV-2 IgM 抗体水平呈降低趋势，或者保持不变；SARS-CoV-2 IgG 抗体水平呈降低趋势。
结论 SARS-CoV-2 特异性抗体存在较高的假阳性，SARS-CoV-2 特异性 IgM、IgG 抗体假阳性结果的分布特征为临床医生鉴别真假性提供参考依据。

PO-0250

PDCD5 对子宫内膜癌的作用及其作用机制

高梦
山东大学第二医院

目的 子宫内膜癌是女性生殖系统最常见的恶性肿瘤之一。程序性细胞死亡 5 (PDCD5)是新近发现的与细胞凋亡相关的基因，在一些人类肿瘤的发生发展中发挥着重要作用。然而，PDCD5 对子宫内膜癌的作用及其机制尚未被研究。
方法 在本研究中，我们在体外分别过表达和干扰子宫内膜癌细胞中 PDCD5 的表达，检测子宫内膜癌细胞增殖、迁移、侵袭的变化。同时探究可能影响细胞增殖、迁移、侵袭的通路分子。同时通过体内动物实验验证体外的结果。
结果 PDCD5 过表达抑制子宫内膜癌细胞的增殖、迁移和侵袭，而其下调促进子宫内膜癌细胞的增殖、迁移和侵袭。同时，动物实验验证了我们的结果。
结论 我们的实验数据为 PDCD5 调控子宫内膜癌细胞生长提供了新的见解，并提示 PDCD5 可能是子宫内膜癌治疗中一个有吸引力的治疗靶点。

PO-0251

The role of procalcitonin dynamic monitoring in the early diagnosis of infection and prognostic evaluation after cardiac surgery

Qiang Miao[1]、Shengnan Chen[2]、Haojing Zhang[2]、Shan Huang[2]、Bei Cai[1]、Junlong Zhang[1]、Qian Niu[1]
1. West China Hospital, Sichuan University
2. 四川大学华西临床医学院

Objective To evaluate the usefulness of procalcitonin (PCT) levels and PCT clearance at different time points as biomarkers for the early diagnosis of postoperative infections and the short-term prognosis of patients through the dynamic monitoring of PCT levels after cardiac surgery.
Methods Include 210 adults and 42 children after cardiac surgery in West China Hospital of Sichuan University. They were divided into infection and non-infection groups, poor and good prognosis groups according to whether infection occurred after the operation and whether the hospital stay exceeded 28 days. The patient's serum PCT level was dynamically monitored on the first 1, 3, and 5 days after the operation, and the change value (△PCT) and clearance rate (△PCTc) of the patient's postoperative PCT were recorded. Compare the differences of PCT, △PCT, and △PCTc between the different groups of adult and pediatric patients on the first 1, 3, and 5 days after the operation, and use the ROC curve to analyze the PCT, △PCT, and △PCTC at different time points for the early diagnosis and short-term evaluation of postoperative infection Prognostic value.
Results The levels of PCT, △PCT, and △PCTc in the infected group of adult patients were significantly different from those in the non-infected group at 1, 3, and 5 days after surgery (P<0.05). The PCT level of children in the infected group was significantly higher than in the non-infected group only on the 3rd and fifth days after the operation (P<0.05). There was no significant difference between △PCT and △PCTC between the two groups (P<0.05). The PCT levels of the adult patients with poor prognosis were 7.31 (3.07, 23.14) ng/ml and 2.44 (0.82, 9.64) ng/ml on the 3rd and fifth day after the operation, and the levels of children were 47.98 (3.5, 79.02) ng/ml, 13.34 (1.41, 19.97) ng/ml was significantly higher than the good prognosis group (P<0.05). ROC curve analysis showed that the PCT level on the third day after surgery has the highest AUC of 0.806 and 0.804 for the diagnosis of early infection and poor prognosis in adults,

the threshold was 3.63 ng/ml and 2.28 ng/ml, the sensitivity was 73.17% and 93.33%, and the specificity was 81.66% and 58.97%. The highest diagnostic value for early infection and poor prognosis in children is the PCT level on the 5th day after surgery, and the threshold for both was 10.2 ng/ml. The AUC, sensitivity and specificity were 0.756, 61.11%, 91.67% and 0.721, 66.67%, 88.89%, respectively.
Conclusion This study shows that dynamic monitoring of PCT levels after cardiac surgery can be an effective clinical means for early diagnosis of postoperative infection and short-term prognosis evaluation. The PCT level on POD 3 in adult patients has the highest clinical value for postoperative infection and short-term prognosis evaluation. In contrast, the PCT level on POD 5 has the highest clinical value in minor patients.

PO-0252

Epac1 下调在体内和体外通过抑制 AKT/CyclinD1/CDK4 信号通路抑制卵巢癌细胞增殖

高梦
山东大学第二医院

目的 卵巢癌是妇科恶性肿瘤中最主要的死亡原因，高级别浆液性卵巢癌是最常见和最具侵袭性的亚型。最近的研究表明，cAMP 通过 Epac (cAMP 直接活化的交换蛋白)蛋白介导蛋白激酶 A 非依赖性途径。Epac 蛋白，包括 Epac1 和 Epac2，涉及多种不同的细胞作用，如胰岛素分泌、胞吐、细胞钙处理和细胞间连接的形成。有多篇报道表明，Epac1 在促进某些癌细胞的增殖、侵袭和迁移方面具有重要作用。然而，Epac1 在卵巢癌中的表达水平和作用尚未被研究。
方法 在本研究中，我们检测了 Epac1 mRNA 和蛋白在 SKOV3、OVCAR3 和 CAOV3 3 种卵巢癌细胞中的表达水平。此外，我们还在体内外研究了下调 Epac1 对 SKOV3 和 OVCAR3 细胞增殖和凋亡的影响。
结果 Epac1 mRNA 和蛋白在 SKOV3 和 OVCAR3 细胞中表达较高。在体外和体内，Epac1 表达下调抑制 SKOV3 和 OVCAR3 细胞的增殖。细胞增殖抑制可能是由于 AKT/CyclinD1/CDK4 信号通路失活导致 Epac1 下调诱导的 G1 期阻滞，而不是由于 MAPK 通路或细胞凋亡的改变。
结论 我们的实验数据为 Epac1 调控卵巢癌细胞生长提供了新的见解，并提示 Epac1 可能是卵巢癌治疗中一个有吸引力的治疗靶点。

PO-0253

NT-proBNP、sST2 在心力衰竭诊断中的价值研究

彭亮、黄路遥、王京京、侯彦强
上海市松江区中心医院

目的 探讨血清 NT-proBNP、sST2 水平在心力衰竭诊断中价值，为提高临床诊疗水平提供参考依据。
方法 选取 2020 年 1 月至 2020 年 12 月年在上海市松江区中心医院住院治疗心衰患者 111 例作为观察组，另随机选取 20 例同一时期收住心内科无心衰患者作为对照组。检测血清 NT-proBNP、sST2 和常规生化指标，比较两组血清 NT-proBNP、sST2、临床资料及常规生化指标的差异，绘制 ROC 曲线分析血清 NT-proBNP、sST2 水平对心衰的诊断价值，比较心衰患者不同 NYHA 心功能分级 NT-proBNP、sST2 水平。
结果 观察组 NT-proBNP、sST2、BUN、Cr 水平高于对照组（$p<0.05$）；血清 NT-proBNP、sST2 水平诊断心衰 ROC 曲线分析显示曲线下面积(AUC)分别是 0.973、0.744($P<0.05$)；心衰组患者 NT-proBNP、sST2 水平在不同 NYHA 心功能级别中比较差异有统计学意义（$p<0.05$）。

结论 血清 NT-proBNP、sST2 水平对诊断心衰有一定价值，两者浓度均随着心功能分级的升高而升高，能够反应患者病情的严重程度。在心衰诊断方面 sST2 的应用价值虽然不如 NT-proBNP，但由于心衰患者易合并肾功能异常，而 sST2 具备不受肾功能的影响的特性，可以为临床提供更多有用的信息。

PO-0254

人补体因子 H 相关蛋白（BTA）在膀胱癌的诊断、病理分级及临床分期中的应用价值

刘杨、张志平、彭道荣、邢瑞青、李静、赵媛、刘家云
空军军医大学西京医院

目的 探讨尿液中人补体因子 H 相关蛋白（BTA）在膀胱癌的诊断、病理分级和临床分期中的应用价值。
方法 回顾性分析 2020 年 4 至 12 月我院收治的 69 例膀胱癌患者、30 例泌尿系良性病变患者及 30 例体检健康者，采用微孔板化学发光法检测各组尿液 BTA 水平。分析其与膀胱癌各临床病理参数的关系，ROC 曲线分析其诊断膀胱癌的临床价值。
结果 膀胱癌组、良性疾病组及健康人对照组尿液 BTA 中位浓度及阳性率逐渐下降，差异有统计学意义（H=73.17，P<0.001；c2=60.14.0，P<0.001）。BTA 水平及阳性率随着膀胱癌患者的 WHO 病理组织学分级，TNM 分期及肿瘤大小的升高而升高（P<0.01）。尿液 BTA 诊断膀胱癌的 ROC 曲线下面积（AUCROC）为 0.922，cut-off 值为 89.03 U/mL，敏感性为 76.80%，特异性为 95.00%。
结论 尿液 BTA 可用于膀胱癌的早期筛查，其水平与疾病的严重程度密切相关，具有较高的临床诊断价值。

PO-0255

多巴胺通过 DRD5 受体抑制金黄色葡萄球菌感染引起的巨噬细胞炎症反应作用研究

吴昱青[1]、胡颖超[1]、王冰微[2]、李晟[1]、马春梅[1]、刘雪[1]、Paul N. Moynagh[3]、周嘉伟[4]、杨硕[1]
1. 南京医科大学
2. 南京中医药大学
3. 爱尔兰梅尔努斯大学
4. 中国科学院脑科学与智能技术卓越创新中心

目的 DA（Dopamine，多巴胺）是一种重要的儿茶酚胺类神经递质，其缺失与帕金森氏病发生密切相关，此外，在调节机体免疫功能中 DA 也发挥着重要的作用。然而，目前 DA 在调控免疫炎症反应中的具体作用机制尚不明确。本研究旨在探索 DA 在控制金黄色葡萄球菌感染引起的炎症反应中的作用及分子机制，为临床脓毒症、脑膜炎等感染性炎症疾病防治提供新的线索。
方法 1）用模拟金黄色葡萄球菌病原分子的 TLR2（Toll-like receptor 2，Toll 样受体 2）受体配体 Pam3（Pam3CSK4，三酰脂肽）和金黄色葡萄球菌刺激小鼠 BMDMs（Bone marrow derived-macrophages，骨髓来源的巨噬细胞）细胞，检测 DA 处理后炎症因子的表达情况。2）用 RNA 测序分析 Pam3 和 DA 刺激后 BMDMs 细胞内与炎症相关通路的变化，并通过 Western blot 验证相关通路变化。3）通过体内脓毒症和脑膜炎小鼠模型检测相关多巴胺信号通路分子在感染性炎症反应中的作用。
结果 1）DA 处理后 Pam3 和金黄色葡萄球菌感染激活的炎症因子表达降低。2）RNA 测序结果提示主要通过抑制 NFkB（Nuclear transcription factor-kB，核转录因子 kB）信号通路来抑制炎症反

应。3）DRD5（Dopamine receptor 5，多巴胺受体 5）敲除后，DA 抑制炎症作用消失，表明 DA 通过其受体 DRD5 发挥抑制炎症作用。
结论 DA 激活 DRD5 后，通过 DRD5 受体 EFD 和 IYX(X)I/L 结构基序将负调节蛋白 ARRB2/ PP2A 招募入 TLR2 信号中的 TRAF6-IKK 复合物中，进而控制 NFkB 炎症信号，抑制金黄色葡萄球菌引起的脓毒症和脑膜炎。因此，本研究结果提示 DA-DRD5 信号轴可作为今后相关炎症疾病的潜在干预靶标。

PO-0256

炎症性肠病中 EB 病毒感染的价值分析

陈健康
空军军医大学西京医院

目的 探讨 EB 病毒感染在炎症性肠病的表达分析。
方法 回顾性分析我院收治的 628 例炎症性肠病患者临床资料，利用酶联免疫试剂盒检测分析患者的 EB 病毒抗体谱指标（抗 EBV 衣壳抗体 IgM、抗 EBV 早期抗体 IgG、抗 EBV 衣壳抗体 IgG、抗 EBV 核抗体 IgG）的表达水平。
结果 共收集的 628 例炎症性肠病患者中，EBV-CAIgM 的阳性率为 16.7%（105/628）；在 CD 组中 EBV-CAIgM 的阳性率为 22.2% (55/247)；在 UC 组中 EBV-CAIgM 的阳性率为 13.1% (50/381)，两者差异具有统计学意义（c2= 8.99，P =0.003）。在不同性别间比较中， UC 组男性 EBV-CAIgM 阳性率为 9.9%（23/232），女性 EBV-CAIgM 阳性率为 18.1%（27/149）。男女性别间 EBV-CAIgM 阳性率有统计学差异（c2= 5.36，P =0.021）。在本研究中，患者中既往感染占比最大，抗体表达谱（EBV-CAIgG、EBNA-IgG 均阳性）占比为 71.9%（452/628）；现症感染中抗体谱 EBV-CAIgM、EBV-CAIgG、EBNA-IgG 均阳性占比次之（22.2%）。
结论 炎症性肠病患者中 EB 病毒感染率明显高于正常人群，具有高的既往感染率以及现症感染率，临床应加强对炎症性肠病患者中 EB 病毒感染的筛查和监测，为炎症性肠病的诊疗提供有价值的思路。

PO-0257

Serum Macrophage Inhibitory Cytokine-1 Serves as a Novel Diagnostic Biomarker of Early-Stage Colorectal Cancer

戴春阳、李明、马艳玲、陈兆武、陈少华、张扬
中国科学技术大学附属第一医院（安徽省立医院）西区

Patients with colorectal cancer usually have a poor prognosis because of the absence of suitable biomarkers for asymptomatic patients. We screened 2759 subjects with risk factors. Endoscopic and histopathological analyses revealed that 19 and 47 subjects had CRC or precancerous lesions. We randomly selected 24 subjects with normal colonoscopies as healthy controls. The optimal thresholds of MIC-1 levels with precancerous lesions or CRC were 314.12 pg/mL and 357.64 pg/mL. Moreover, MIC-1 levels distinguished precancerous lesions better than CEA, CA19-9, or CA24-2 (AUC: 0.760 vs 0.529, 0.624, and 0.585) or CRC (AUCs: 0.821 vs 0.743, 0.657, and 0.688) from the healthy controls. Serum MIC-1 levels increased the sensitivity of detection CRC and can be used to improve screening.

PO-0258

Tripartite Motif-Containing 22 Genotype is Correlated with the IFN-α Therapy Response in Hepatitis B e Antigen-Positive Chronic Hepatitis B

long wang、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Background Interferon-α (IFN-α) plays an important role in the treatment of chronic hepatitis B (CHB), but its limited response rate and side effects limit its clinical application. We intend to explain the factors affecting the efficacy of IFN-α from the perspective of host SNPs and clarify the relevant mechanism.
Methods One hundred and twenty-four patients diagnosed CHB was enrolled in this study. Patients received IFN-α for 48 weeks. Response was defined as an HBV DNA <500 IU/mL at 12 months post-treatment. DNA samples are genotyped by Asian Screening Array (ASA) chip.
Results CHB patients were genotype into 483500 loci with ASA chip, of which we focused on TRIM family including TRIM15, TRIM22, TRIM26, TRIM31, TRIM38, TRIM39. Among them, we found that the expression of TRIM22 mRNA in patients with rs10838543 CT and CC genotypes was significantly higher than that in patients with TRIM22 rs10838543 TT genotypes, while other TRIM SNPs did not show significant statistical difference. During the 48-week follow-up, there was no significant difference in the distribution of different TRIM22 rs10838543 genotypes in the decrease of HBV DNA and HBsAg. However, the genotype of TRIM22 rs10838543 TT was positively correlated with the negative conversion of HBeAg. In vitro experiments showed that TRIM22 was one of the significantly upregulated TRIM members and HBV inhibits the expression of TRIM22 after IFN-α treatment. The level of HBV-related serological markers in the supernatant of HepAD38 cell lines overexpressing TRIM22 was consistent with that of microarray and in vitro experiments.
Conclusion TRIM22 involves in the anti-HBV of IFN-α and its polymorphism rs10838543 may affect the therapeutic responses to chronic HBV infection. These findings may provide new insight into choosing the optimal candidates and improving the therapeutic effect for anti-HBV treatment with IFN-α.

PO-0259

慢性乙型肝炎患者外周血 T 淋巴细胞 HLA-DQ 表达变化及其临床意义

曾星月[1]、阿衣包它[1]、布丽地尔新[1]、刘天赐[1]、郑墨涵[2]、陆松松[1]、宋英[1]、刘忱[1]
1. 北京大学人民医院
2. 北京大学医学部基础医学院

背景 人类白细胞抗原-DQ（HLA-DQ）和颗粒溶素（Granulysin，GNLY）的单核苷酸多态性被报道会影响 CHB 的发生和 HBV 的清除，然而它们在 CHB 患者外周血 T 细胞的表达和意义尚不明确。本研究旨在研究 T 细胞 HLA-DQ 和颗粒溶素表达和功能，分析他它们在 HBV 感染中的临床意义。
方法 收取 25 例 CHB 患者，21 例 HBV 非活动性携带者和 25 例健康对照者外周血，分析 Treg, Tfh, Tfr, Tfc 等 T 细胞亚群中 HLA-DQ 和颗粒溶素的表达。功能方面，通过体外培养检测 HLA-DQ+和 HLA-DQ-的 T 细胞分泌 IFN-γ 以及 Treg 细胞分泌 IL-10 的能力，通过 CD45RA 和 CCR7 的表达，将 T 细胞分为 Tnaive，Teff，Tcm 和 Tem，将 Treg 细胞分为 CD45RA-FoxP3hi 活化型 Treg，CD45RA+FoxP3lo 静息型 Treg 等亚群，再分别检测 HLA-DQ+和 HLA-DQ-细胞中上述各个亚群的比例差异。在此基础上分析各细胞亚群和 HBV 感染指标的相关性。

结果 CHB 患者 T 细胞 HLA-DQ 表达上调，而颗粒溶素则表达下降。CHB 患者 Tfh、Tfr 和 Tfc 中 HLA-DQ+的比例上调，但 Treg 中 HLA-DQ+ 比例下调。HLA-DQ+的 CD4+T 细胞分泌 IFN-γ 增加，HLA-DQ+ Treg 细胞分泌 IL-10 增加。HLA-DQ+T 细胞中 CD4+Teff, CD4+Tnaive, CD4+Tem, CD8+Tem 和 CD8+Tcm 显著升高，HLA-DQ+Treg 中 CD45RA-FoxP3hi 活化型 Treg 比例显著升高。HLA-DQ+的 CD4+T 细胞与感染指标正相关，而 HLA-DQ+ Treg 细胞与感染指标负相关。
结论 HLA-DQ 表征抑制能力，而颗粒溶素则表征较强的抗病毒免疫能力。HLA-DQ 和颗粒溶素对 CHB 患者的免疫状态评估具有潜在应用价值。

PO-0260

TCF1 通过对线粒体的适应性的调节影响 HIV 感染者的 T 细胞的功能

蔡红娇[1]、石珏[1]、殷林波[2]、郑杰夫[1]、张子宁[1]
1. 中国医科大学附属第一医院
2. 辽宁省人民医院

目的 分析 TCF1 在健康人群及 HIV 感染者中的表达情况， 及其与疾病进展的关系，并探讨其影响疾病的进展的可能机制。
方法 选取 HIV 感染未治疗者（包括快速进展者，长期不进展者），抗逆转录治疗者（ART）及 HIV 阴性对照者分离 PBMC，CD4+T 细胞，CD8+T 细胞进行 TCF1 mRNA 的检测，并分析其与疾病进展的关系。同时应用流式细胞仪对三组人群细胞中的 TCF1 表达情况进行分析，明确 TCF1 表达的特点。最后，应用 si-RNA 技术，下调细胞中 TCF1 的表达情况，并分析其对细胞功能的影响极其可能原因。
结果 与 HIV 阴性对照组相比，TCF1 在 HIV 感染者中的表达明显降低，且与 CD4 计数成正相关(r2=0.381，P=0.043)，与病毒载量呈负相关(r2=0.541，P=0.010)。流式结果显示，TCF1 在 NAIVE 及 TCM 细胞中的表达高于 TEM 及 TEMRA,此表达特点无人群特异性，但与 HIV 阴性人群相比，TCF1 在 HIV 感染者中的表达下调，且该下调在 CD4+T 细胞中主要集中在 TCM,TEM 及 TEMRA 中，而在 CD8+T 细胞中，该下调主要发生于 NAÏVE,TCM 和 TEM 细胞亚群中 。通过 si-RNA 技术下调 TCF1 后，可看到细胞分泌的效应因子 IL2 的水平明显下降，增殖能力明显降低。同时线粒体染色的结果表明，下调 TCF1 后，线粒体膜电位下降，去极化线粒体水平明显升高，线粒体功能受损。
结论 TCF1 在 HIV 感染者中表达下调，影响线粒体的适应性，进而影响了 HIV 感染者中 T 细胞的功能。

PO-0261

Toll-like receptors, long non-coding RNA NEAT1, and RIG-I expression are associated with HBeAg-positive chronic hepatitis B patients in the active phase.

Yongbin Zeng 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

Background Innate immunity plays a crucial role in host-virus interactions and greatly influences viral replication including HBV infection. However, few studies have investigated the possible antiviral immune roles played by TLRs, RIG-I, and long no-coding RNA NEAT1 in chronic HBV infection (CHB) patients in clinical samples and their relationships among immune responses. In

this study, we sought to investigate the mRNA expression levels of TLR1-10, RIG-I, and NEAT1 expression in HBeAg-positive CHB treatment-naïve patients with the active phase.
Methods The expression levels of TLR1-10, RIG-I, and NEAT1 of CHB patients with the active phase and healthy controls were measured by qPCR. Serum HBV DNA and routine liver biochemistry including ALT, etc were also measured to evaluate the impaired physiological function of the liver affected by CHB.
Results The expression levels of TLR1 and TLR6 in CHB with active phase were remarkably lower than that in healthy controls. The levels of TLR3 in CHB patients with active phase were remarkably higher than that in healthy controls. The total NEAT1 expression was abnormally decreased in CHB patients as compared with healthy controls. The levels of RIG-I were significantly decreased in CHB patients in the active phase when compared to healthy controls. The expression of TLR6 and RIG-I was closely correlated with NEAT1 expression. TLR6 level was positively correlated with RIG-I level.
Conclusion Chronic HBV infection can alter the innate immune response by downregulating functional expression of TLR1, TLR6, NEAT1.

PO-0262

Serum Cyr61 is Associated With Clinical Disease Activity and Inflammation in Patients With Systemic Lupus Erythematosus

Jinpiao Lin、Qishui Ou
the First Affiliated Hospital of Fujian Medical University

Our previous studies have shown that secreted extracellular matrix-associated protein Cysteine rich angiogenic inducer 61 (Cyr61), a novel proinflammatory factor, is involved in the pathogenesis of rheumatoid arthritis (RA). However, whether Cyr61 has any effect in systemic lupus erythematosus (SLE) remains unknown. This study aims to assess the level of serum Cyr61 and to investigate the association of serum Cyr61 and clinical disease activity in SLE. We found the level of serum Cyr61 in patients with SLE was significantly higher than healthy controls ($P < 0.001$), and Cyr61 was high expressed in renal tubule of lupus nephritis compared to control. The sensitivity of Cyr61 in diagnosis of SLE was 47.3%. In receiver operating characteristic (ROC) curve analysis, the area under the curve (AUC) was 0.830, with a 95% confidence interval (CI) from 0.776 to 0.885. Cyr61 was present in 60.0%, 54.5%, and 41.5% of anti-double stranded DNA (dsDNA), anti-antinuclear antibodies (ANA), and anti-Sm negative SLE patients, respectively. Serum Cyr61 levels were significantly higher in high systemic lupus erythematosus disease activity index (SLEDAI) group than that in low SLEDAI group ($P = 0.003$). Correlation analyzes showed a significant negative correlation between serum Cyr61 and complements (C3) ($P = 0.015$), C4 ($P = 0.04$). Moreover, increased Cyr61 level in SLE was associated with serum level of TNF-α, interleukin 6 (IL-6), and IL-17. In conclusion, serum Cyr61 was increased in patients with SLE which was associated with clinical disease activity and inflammation in SLE, suggesting Cyr61 may be a novel potential auxiliary marker for the diagnosis of SLE.

PO-0263

T 细胞活化、分化、记忆及耗竭检测指标参考区间的建立及其临床意义

王悦、熊璇、唐甜、付帅、张子宁
中国医科大学附属第一医院

目的 建立辽宁地区健康成人外周血 T 淋巴细胞表面活化、分化记忆、耗竭相关分子的参考区间，分析两性别间是否有差异，相关指标随年龄变化趋势及两主流仪器平台结果是否有差异，判断是否需按性别、年龄、仪器单独建立参考区间。
方法 选择 70 例健康成人，用流式细胞仪检测 $CD4^+$、$CD8^+$T 细胞表面活化、分化记忆、耗竭相关分子表达水平；分析上述指标在不同年龄、性别及仪器平台间差异。
结果 1）研究对象分为三组。青年组（24～30 周岁）10 例，年龄 28±2 周岁，中年组（31～49 周岁）34 例，年龄 41±6 周岁，老年组（50～86 周岁）26 例，年龄 62±11 周岁；男女各 35 例，采用 robust method 建立上述 14 项指标的参考区间；
2）在 BD FACSCanto Ⅱ上测得 $CD4^+PD\text{-}1^+$、$CD8^+CD38^+$T 细胞百分比在性别间差异有统计学意义；在 Beckman Navios 上测得 $CD8^+CD28^-CD57^+$、$CD8^+CD38^+$T 细胞百分比在性别间差异有统计学意义；
3）在两平台分析中 $CD8^+CD38^+$T 细胞百分比均随年龄增长而降低；$CD4^+CD38^+$T 细胞百分比在老年组略低于中年组；$CD4^+HLA\text{-}DR^+$T 细胞百分比随年龄增长而增加；
4）$CD4^+PD\text{-}1^+$、$CD8^+PD\text{-}1^+$、$CD4^+CD45RA^-RO^+$、$CD4^+CD45RA^+RO^-$、$CD4^+CD38^+$T 细胞的百分比在两个平台间差异有统计学意义。
结论 1、本研究首次建立了 T 细胞表面耗竭相关分子 PD-1 的参考区间。2、首次建立适用于辽宁地区和其他具有相似人口统计学特征的健康成年人群的临床常用的外周血 T 淋巴细胞 $CD4^+$、$CD8^+$T 细胞表面活化分子 HLA-DR、CD38，分化及记忆相关分子 CD45RA、CD45RO、CD28、CD57 的参考区间。3、首次对 BD FACSCanto Ⅱ、Beckman Navios 两平台上测定的 T 细胞相关指标进行对比。

PO-0264

Correlation between albumin to fibrinogen ratio, C-reactive protein to albumin ratio and Th17 cells in patients with rheumatoid arthritis

Yujue He、Jinpiao Lin
the First Affiliated Hospital of Fujian Medical University

Background The albumin to fibrinogen ratio (AFR) and the C-reactive protein to albumin ratio (CAR) have been served as inflammatory markers. However, their roles in RA remain unclear. We investigated the association of AFR/CAR with the concentration of autoantibodies and Th17 cells in RA.
Methods A total of 196 RA patients, 200 patients with systemic lupus erythematosus (SLE), and 200 healthy donors (HD) who were admitted to the First Affiliated Hospital of Fujian Medical University were enrolled. The results of FIB, ALB, CRP, anti-cyclic citrullinated peptide antibodies (anti-CCP), rheumatoid factor (RF) and erythrocyte sedimentation rate (ESR) from RA patients and SLE patients were retrospectively analyzed. The percentage of Th17 cells in peripheral blood of RA patients was detected by flow cytometry, and the relative expression of TNF-α, IL-6 and IL-17A was detected by RT-qPCR. Correlation analysis of AFR/CAR and Th17 cells, CRP, ESR, TNF-α, IL-6 and IL-17A in RA was conducted.

Results Compared with SLE patients and healthy donors (HD), AFR concentration was significantly lower (P < 0.01) in RA patients, while CAR concentration was significantly increased (P < 0.01) in RA patients. AFR showed negative correlation with CRP (r = -0.7103), ESR (r = -0.6542), RF (-0.2219), Th17 cells (r = -0.5952) and IL-17A (r = -0.4681). CAR was positively correlated with CRP (r = 0.9899), ESR (r = 0.605), RF (0.1867), Th17 cells (r = 0.6818), TNF-α (r = 0.3388), and IL-17A (r = 0.2046).
Conclusions The concentration of AFR in RA patients was reduced, while CAR concentration was increased. AFR and CAR are associated with CRP, ESR, RF, and Th17 cell ratios in RA patients, which can be used as potential indicators for determining RA inflammation.

PO-0265

一种新型的超高灵敏度的免疫检测技术的分析探讨

代艳文、吴大富
三峡大学附属仁和医院

目的 通过阐述免疫检测技术的发生发展，比较分析各种检测的优缺点以及临床应用情况，以期为进一步开发超高灵敏度免疫诊断检测方法及其临床应用提供理论基础。
方法 回顾性分析免疫检测技术从放射免疫、酶联免疫、免疫胶体金到化学发光、流式荧光技术，再到单分子免疫检测技术等各种检测的优缺点以及临床应用情况，并着重比较分析目前市场主导技术化学发光技术和拥有超高免疫检测灵敏度的单分子免疫检测技术。
结果 化学发光具有自动化程度高、灵敏度高、准确率高、特异性好、精密度好，检测时间短等优势，因此在临床上迅速推广，市场占有率超过 70%。但在快速的发展过程中，其检测原理却始终利用的是抗原抗体结合后的发光反应，然后将待测样本的发光强度与标准曲线比较进而实现定量分析。在当今设备高度自动化前提下，其检测灵敏度已达到理论上的极限。而单分子免疫检测则是通过免疫标记的方法，利用抗体捕获和识别抗原，进行信号分子标记或是酶联标记的形式，通过单分子荧光信号检测或单分子酶促反应实现的单分子级别蛋白分子的检测，是一种新型的超高灵敏度的检测技术。经过十几年的发展，其可在极小体积内（10-21L）对待测分子信号进行检测，是传统免疫检测技术检测灵敏度的数万倍，从而能在更早期识别蛋白分子，满足大部分标志物检测的需求。
结论 虽然化学发光检测灵敏度理论上已达到极限，但是就现有的检测技术来讲，其临床诊断市场在很长时间内都无法被取代。单分子免疫检测技术作为一种新型的超高灵敏度的检测技术，但其检测操作流程繁琐复杂，耗时长，成本高，这些因素很大程度的限制了其临床推广和使用。因此研发成本低，操作简单，更加高效和成熟的单分子免疫检测平台，将有助于推动单分子免疫检测技术的临床应用，为临床疾病早诊断，早发现，早治疗提供新的手段。

PO-0266

A novel diagnostic model in early hepatitis B virus related hepatocellular carcinoma diagnosis

Qiang Wang
Affiliated Hospital of North Sichuan Medical college

Objectives We used protein induced by vitamin K absence or antagonist-II (PIVKA-II) and alpha-fetoprotein (AFP) combined with aspartate aminotransferase (AST), alanine aminotransferase (ALT), and total bilirubin (T-Bil) to establish a novel diagnostic model for early-stage hepatitis B virus (HBV)-related HCC.
Methods The serum levels of PIVKA-II, AFP, AST, ALT, and T-Bil were measured in 148 patients with early-stage HBV-related HCC and 940 patients with chronic hepatitis B. The receiver

operating characteristic (ROC) curves were used to verify the diagnostic efficacy of the novel diagnostic model in early-stage HBV-related HCC diagnosis.
Results The mathematical model of [1.5 × PIVKA-II / (AST × T-Bil) + AFP / (ALT × T-Bil)] was selected as the novel diagnostic model. The areas under ROC curves (AUROCs) of the novel diagnostic model in detection of early-stage HBV-related HCC were significantly higher than those of PIVKA-II, AFP, and PIVKA-II combined with AFP (HCC ≤ 5cm: 0.925 vs 0.826, 0.666, and 0.821; HCC < 3cm: 0.896 vs 0.741, 0.651, and 0.765, respectively) (all P < 0.001). The novel diagnostic model had the highest AUROC values of 0.960 (HCC ≤ 5cm, 89 cases) and 0.933 (HCC < 3cm, 40 cases) in diagnosis of early-stage HBV-related HCC with serum level of AFP > 20 ng / ml; the sensitivity were 83.15% and 77.50%, respectively, while the specificity were 95.34% and 90.69%.
Conclusion The novel diagnostic model is superior to PIVKA-II and AFP in the diagnosis of early-stage HBV-related HCC, especially for early-stage HBV-related HCC with abnormal serum result of AFP.

PO-0267

Longitudinal single-cell immune profiling reveals distinct immune response in asymptomatic COVID-19 patients

Erhei Dai
The Fifth Hospital of Shijiazhuang,

While some individuals infected by SARS-CoV-2 present mild to severe disease, many SARS-CoV-2-infected individuals are asymptomatic. We sought to identify the distinction of immune response between asymptomatic and moderate patients. We performed single-cell transcriptome and T-cell/B-cell receptor (TCR/BCR) sequencing in 38 longitudinal collected peripheral blood mononuclear cells from asymptomatic, moderate, and severe patients with healthy controls. Asymptomatic patients displayed increased CD56briCD16– natural killer (NK) cells and upregulation of IFNG in effector T cells and NK cells. They showed robust TCR clonal expansion but did not have strong BCR clonal expansion. Moderate patients display robust TCR clonal expansion and moderate BCR expansion and they declined with disease progression. Moderate patients also showed higher expression of the interferon-stimulated gene across multiple cell populations compared to asymptomatic patients but lower than in a severe patient. Our data suggest that early activation of NK cells and type I immunity may contribute to the asymptomatic infection.

PO-0268

Distribution of Serum Thrombospondin-2, a Novel Tumor Marker , in General Population and Cancer Patients in China

seyin zou[1]、jinhong xu[2]、donglin cao[1]
1. Guangdong Second Provincial General Hospital
2. 广东医科大学

Purpose Distribution of serum thrombospondin-2 in general population and cancer patients in China have not been reported. Methods. This study evaluated the expression level of serum thrombospondin-2 in general population and various cancer patients, the 95% confidence interval was used for the derivation of reference range.
The comparison of the expression levels in controls for age and gender was performed. The associations between candidate biomarkers (thrombospondin-2 [THBS2]) expression and tumor

metastasis status were also explored. Results.125 healthy controls and 193 various cancer patients were enrolled. The mean ± SD in serum THBS2 levels in general population was 42.37±12.24ng/ml, there was no significant sex and age difference, the reference range is 18.37-66.36ng/ml. Most cancer patients present a decreased serum THBS2 level except hepatoma and lymphoma which most patients showed a relatively high level of THBS2. There was no statistical difference of serum THBS2 level between metastasis and non-metastasis group in breast, lung, cervical, colorectal cancer, nasopharyngeal carcinoma and hepatoma (P >0.05) while a significant negative correlation was observed in ovarian cancer (P = 0.0209).
Conclusions The distribution of serum THBS2 displayed an obvious heterogeneity among various cancers comparing to health controls, ovarian cancer patients detected with low THBS2 expression may be more prone to develop metastasis in China.

PO-0269

Efficacy and safety of pregnant women with chronic hepatitis B receiving nucleos(t)ide analogs therapy: a network meta-analysis

Bo Zhu、Erhei Dai
The Fifth Hospital of shijiazhuang, Shijiazhuang, China

Objective Reducing mother-to-child transmission (MTCT) of hepatitis B virus(HBV) is one of the key ways to eliminate hepatitis B. Although many studies have proved that nucleos(t)ide analogs(NAs) were more effective and safer than no treatment, there is still a lack of comparison between drugs.The network meta-analysis aims to comprehensively compare and summarize the efficacy and safety of the three drugs (Lamivudine(LAM), Telbivudine(TBV) and Tenofovir(TDF)), providing a basis for drug selection.
Methods A comprehensive search of studies published by PubMed (Medline), Web of Science, Cochrane Library, EMBASE, CNKI and SinoMed as of December 2019 on oral NAs for pregnant women with high HBV DNA road to prevent HBV MTCT .We performed pair-wise meta-analysis and Bayesian network meta-analysis to compare the efficacy and safety of LAM , TDF and TBV.
Results A total of 35 studies with involving a total of 6,109 pregnant women who infencted HBV were selected. The results of traditional meta analysis show that , the HBsAg positive rate and HBV DNA positive rate of newborns and infants from 6 ~12 months in the LAM group, TBV group and TDF group were lower than those of the control group, and the differences were statistically significant（$p<0.05$）. The HBV DNA levels of the three groups of pregnant women at delivery were lower than those of the control group, the differences were statistically significant ($p<0.05$).The cesarean section rate, postpartum hemorrhage rate and CK increase rate of the three groups of pregnant women, as well as the infant's birth weight, birth length and Apar score were not statistically different from those of the control group ($p>0.05$).The results of the network meta-analysis show that the HBsAg positive rates of infants aged 6 ~12 months in the LAM, TBV and TDF groups were lower than that of the control group, and the differences were statistically significant. However, the pairwise comparison did not show statistical differences. The probability of the three drugs in reducing the positive rate was ranked from low to high as LAM<TBV<TDF, and the probability of being in this ranking is 72%、42% and 47%.
Conclusion Pregnant women who infected HBV with high viral load （HBV DNA≥2×105IU/mL） taking LAM, TBV and TDF during pregnancy can effectively prevent HBV MTCT and reduce the level of HBV DNA at delivery. Their safety is good. LAM may be the drug with the worst effect in reducing the positive rate of infants aged 6~12 months, and TDF may be the drug with the best effect.

PO-0270

探讨 CA125 在慢性心衰患者中危险评估的价值

胡广梅
中山大学孙逸仙纪念医院

目的 研究血清 CA125 水平对慢性心衰患者的危险评估价值。
方法 收集 2014.1~2018.7 医院收治的慢性心衰患者 284 例，记录各患者半年内再入院次数和原因、本次入院天数、血清 CA125、Nt-proBNP、肌酐和心动图参数。
结果 NYHA III/IV 级患者 CA125 浓度以及阳性率显著高于 NYHA I/II 级；CA125 异常升高组相较于 CA125、Nt-proBNP 正常组以及单独 Nt-proBNP 异常升高组，其住院天数、LA、RVDd 和 LVDd 明显增高，而 EF%明显降低，同时患者表现出更高的半年内再入院风险（因心脏疾病）。胸腹水或心包积液阳性的患者 CA125 浓度显著高于阴性者，P<0.05。
讨论与结论 慢性心衰患者中，CA-125 异常升高表明更严重的心肌重塑状态，更低 EF%，较差的心功能代偿，预示更长的住院天数以及高风险的半年内再入院概率（因心脏疾病），比单独 Nt-proBNP 更有利于临床对慢性心衰进行危险分级以及预后风险评估。

PO-0271

血清 ProGRP、HE4、NSE 在肺癌中诊断价值

徐少华
四川省三台县人民医院

目的 探究胃泌素释放肽前体（ProGRP）、人附睾蛋白 4（HE4）、神经元特异性烯醇化酶（NSE）在肺癌中的诊断价值。
方法 选择 39 例肺癌患者、7 例肺部良性肿瘤患者和 100 例健康体检者，分别作为肺癌组、肺部良性肿瘤组及健康对照组，检测各组研究对象的血清 ProGRP、HE4、NSE 水平；比较肺癌组中小细胞癌、腺癌、鳞状细胞癌等不同病理类型患者的 ProGRP、HE4、NSE 水平。绘制受试者工作特征（ROC）曲线，分析血清 ProGRP、HE4、NSE 单项检测和联合检测在肺癌中的诊断价值。
结果 肺癌组患者的血清 ProGRP、HE4、NSE 水平均高于肺部良性肿瘤组和健康对照组，差异均有统计学意义（P < 0.05）；肺部良性肿瘤组和健康对照组的血清 ProGRP、HE4、NSE 水平比较，差异均无统计学意义（P > 0.05）；小细胞癌患者的血清 ProGRP 水平高于腺癌和鳞状细胞癌患者（P < 0.05）。ROC 曲线分析结果显示，血清 ProGRP、HE4、NSE 单独检测诊断肺癌的曲线下面积（AUC）分别为 0.817、0.705 及 0.871，均低于三者联合诊断的 0.893。
结论 血清 ProGRP、HE4、NSE 联合检测利于肺癌的早期筛查及诊疗；高水平的 ProGRP 和 HE4 与肺癌的不良表型有关，可以作为肺癌的生物标志因子。

PO-0272

Caspase 依赖的氧化应激对脓毒症肾小管上皮细胞损伤的作用机制研究

孙林春
南京市儿童医院（南京医科大学附属儿童医院）

目的 氧化应激是脓毒症肾损伤的重要机制，而 ROS 爆发可能涉及线粒体 Caspase 途径的细胞凋亡，但氧化应激和 Caspase 途径细胞凋亡与脓毒症肾细胞损伤的研究较少。本研究利用免疫印记技术、流式细胞术、MTT 法酶联免疫检测等免疫检验技术，观察 Caspase 依赖的氧化应激对肾小

管上皮细胞损伤的调节作用，研究氧化应激通过线粒体 Caspase 途径参与脓毒症肾小管上皮损伤的机制。

方法 LPS 处理 HK-2 细胞建立脓毒症细胞模型，用 H_2O_2 和 Caspase 3 抑制剂单独或联合干预细胞，随机分为 H_2O_2 组、Caspase 抑制剂组、Caspase 抑制剂+H_2O_2 组、阴性对照组和空白对照组。免疫印记技术检测 Cleaved-Caspase 3 和 Cleaved-PARP 蛋白表达，MTT 法检测细胞增殖，流式细胞术检测细胞 ROS 水平、细胞凋亡和细胞周期。

结果 H_2O_2 组 Cleaved-Caspase 3 和 Cleaved-PARP 蛋白较阴性对照组和空白对照组升高（$p<0.05$）。和空白对照组相比，脓毒症组细胞 ROS 升高，增殖率降低，凋亡率升高，G1 期细胞所占比例升高（p 均<0.05）。和阴性对照组相比，H_2O_2 组 ROS 升高，增殖率降低，凋亡率升高，处于 G1 周期的细胞比例升高（p 均<0.05）。Caspase 抑制剂+ H_2O_2 组 ROS 较 H_2O_2 组降低（$p<0.05$），但仍高于阴性对照组（$p<0.05$）。Caspase 抑制剂+H_2O_2 组增殖率较 H_2O_2 组升高（$p<0.05$），凋亡率降低（$p<0.05$），处于 G1 周期细胞比例减少（$p<0.05$）。

结论 脓毒症肾小管上皮细胞存在异常升高的氧化应激反应，氧化应激产生的大量 ROS 通过线粒体-Caspase 凋亡途径，抑制细胞增殖、促进细胞凋亡和引起细胞 G1 期阻滞。抑制 Caspase 对 ROS 引起的脓毒症肾小管上皮细胞损伤有保护作用。

PO-0273

Antiphospholipid Antibodies in Critically Ill Patients With COVID-19

Meng Xiao、Yan Zhang、Shulan Zhang、Xuzhen Qin、Yongzhe Li、Shuyang Zhang
Peking Union Medical College Hospital

Objective Coagulopathy is one of the characteristics observed in critically ill patients with coronavirus disease 2019 (COVID-19). Antiphospholipid antibodies (aPLs) contribute to coagulopathy, though their role in COVID-19 remains unclear. This study was undertaken to determine the prevalence and characteristics of aPLs in patients with COVID-19.

Methods Sera collected from 66 COVID-19 patients who were critically ill and 13 COVID-19 patients who were not critically ill were tested by chemiluminescence immunoassay for anticardiolipin antibodies (aCLs), anti–β2-glycoprotein I (anti-β2GPI) (IgG, IgM, and IgA), and IgG anti-β2GPI–domain 1 (anti-β2GPI–D1). IgM and IgG anti–phosphatidylserine/prothrombin (anti-PS/PT) antibodies were detected in the serum by enzyme-linked immunosorbent assay.

Results Of the 66 COVID-19 patients in critical condition, aPLs were detected in 31 (47%). Antiphospholipid antibodies were not present among COVID-19 patients who were not in critical condition. The IgA anti-β2GPI antibody was the most commonly observed aPL in patients with COVID-19 and was present in 28.8% (19 of 66) of the critically ill patients, followed by IgA aCLs (17 of 66, or 25.8%) and IgG anti-β2GPI (12 of 66, or 18.2%). For multiple aPLs, IgA anti-β2GPI + IgA aCLs was the most common antibody profile observed (15 of 66, or 22.7%), followed by IgA anti-β2GPI + IgA aCL + IgG anti-β2GPI (10 of 66, or 15.2%). Antiphospholipid antibodies emerged ~35–39 days after disease onset. A dynamic analysis of aPLs revealed 4 patterns based on the persistence or transient appearance of the aPLs. Patients with multiple aPLs had a significantly higher incidence of cerebral infarction compared to patients
who were negative for aPLs ($P = 0.023$).

Conclusion Antiphospholipid antibodies were common in critically ill patients with COVID-19. Repeated testing demonstrating medium to high titers of aPLs and the number of aPL types a patient is positive for may help in identifying patients who are at risk of developing cerebral infarction. Antiphospholipid antibodies may be transient and disappear within a few weeks, but in genetically predisposed patients, COVID-19 may trigger the development of an autoimmune condition similar to the antiphospholipid syndrome (APS), referred to as “COVID-19–induced APS-like syndrome.” Long-term follow-up of COVID-19 patients who are positive for aPLs is of great importance in understanding the pathogenesis of this novel coronavirus.

PO-0274

NSun2 regulates aneurysm formation by promoting autotaxin expression and T cell recruitment

Yang Zhao、Li-yan Cui
Department of Laboratory Medicine, Peking University Third Hospital

Abdominal aortic aneurysm (AAA) is characterized by inflammatory cell infiltration and aggravated by hyperhomocysteinemia (HHcy). It is unknown whether the homocysteine (Hcy)-activated RNA methyltransferase NOP2/Sun domain family member 2 (NSun2) is associated with AAA. Here, we found that NSun2 deficiency significantly attenuated elastase-induced and HHcy-aggravated murine AAA with decreased T cell infiltration in the vessel walls. T cell labeling and adoptive transfer experiments confirmed that NSun2 deficiency inhibited the chemotaxis of vessels to T cells. RNA sequencing of endothelial cells showed that Hcy induced the accumulation of various metabolic enzymes of the phospholipid PC-LPC-LPA metabolic pathway, especially autotaxin (ATX). In the elastase-induced mouse model of AAA, ATX was specifically expressed in the endothelium and the plasma ATX concentration was upregulated and even higher in the HHcy group, which were decreaseddramatically by NSun2 knockdown. In vitro Transwell experiments showed that ATX dose-dependently promoted T cell migration. HHcy may upregulate endothelial ATX expression and secretion and in turn recruit T cells into the vessel walls to induce vascular inflammation and consequently accelerate the pathogenesis of AAA. Mechanistically, secreted ATX interacted with T cells by binding to integrin α4, which subsequently activated downstream FAK/Src-RhoA signaling pathways and then induced T cell chemokinesis and adhesion. ATX overexpression in the vessel walls reversed the inhibited development of AAA in the NSun2-defcient mice. Therefore, NSun2 mediates the development of HHcy-aggravated AAA primarily by increasing endothelial ATX expression, secretion and T cell migration, which is a novel mechanism for HHcy aggravated vascular inflammation and pathogenesis of AAA

PO-0275

化学发光免疫法快速监测新冠疫苗接种后及 COVID-19 康复者血清抗体谱

李敏[2]、豆小文[1]、王恩运[1]、姜瑞伟[1]、熊丹[1]、张秀明[1]
1. 深圳市罗湖医院集团医学检验实验室
2. 深圳市罗湖医院集团医学检验实验室

目的 探讨新冠疫苗接种者和康复者体内随接种和康复时间不同血清抗体的变化规律，辅助免疫应答效果评价。

方法 招募疫苗接种志愿者 195 例（其中男 86 例，女 109 例，平均 39 岁。完成 2 个月随访的志愿者 37 例），完成灭活疫苗接种程序（0，28 天）以及新冠康复期患者 10 例。研究采取单中心、随机、双盲试验，在受试者接种首剂疫苗前、接种后 14 天和 28 天、接种第二次后 7 天、14 天和 28 天分别采集静脉血（3mL）编码处理。分离血清，采用化学发光法测定 SARS-CoV-2 中和抗体、SARS-CoV-2 RBD IgG 抗体、SARS-CoV-2 RBD 总抗。计算不同采血点的抗体阳转率，考察不同时间、抗体和配对样本的结果差异及相关分析。

结果 中和抗体与 RBD IgG 诊断结果无差异（P＞0.05），中和抗体、RBD IgG 与 RBD 总抗诊断结果存在差异（P＜0.05）；化学发光法 CLIA 定量检测中和抗体、RBD IgG 和 RBD 总抗抗体水平相关系数 R＞0.90；与 cPass ELISA 法测定的中和抗体水平 R＞0.60。疫苗接种后抗体水平呈现“S 型”变化，第一次接种后 14 天三种抗体阳转率≤11.1%，第二次接种后 7 天各抗体阳转率剧增至 81%以上，完成接种程序后中和抗体阳转率稳定在 91%。相比基础值 1.272AU/mL（95%CI：

0.832~1.712AU/mL），接种完 14 天抗体水平最高升至 104.1AU/mL（95%CI：76.54~131.6AU/mL），升高达 81 倍。疫苗诱导的中和抗体水平是新冠康复者的中和抗体水平的 0.2 倍。

结论 采用 CLIA 可快速评估疫苗接种者和康复者的体液免疫应答产物中和抗体、RBD IgG 与 RBD 总抗变化规律，持续性抗体水平的动态监测将有助于评价体液免疫的保护作用。

PO-0276

血清 PlGF 联合多普勒超声在预测子痫前期的价值分析

刘文渊、周碧华、杨秀萍
宁波市妇女儿童医院

目的 研究孕妇血清 PlGF 联合多普勒超声在预测子痫前期中的价值。

方法 选择 2019 年 7 月至 2020 年 4 月在宁波市妇女儿童医院行常规产前检查并确诊妊娠期高血压疾病的孕妇，分为子痫前期组 82 例、妊娠高血压组 85 例、对照组 170 例。于 15～20 周、24～28 周采用免疫荧光分析法检测 PlGF 水平，孕 20～24 周行子宫动脉多普勒超声，获得子宫动脉搏动指数 PI、阻力指数 RI。计算血清指标和超声指标及其并联和串联组合对子痫前期的敏感度和特异度。

结果 孕 15～20 周血清 PlGF，子痫前期组（132±78μg/L）、妊娠高血压组（146±65μg/L）与对照组（76±59μg/L）比较，差异均无统计学意义（P>0.05）。孕 24～28 周血清 PlGF，子痫前期组（42±23μg/L）、妊娠高血压组（355±87μg/L）与对照组（454±90μg/L）比较，差异均有统计学意义（P<0.05）。孕 20～24 周子宫动脉搏动指数 PI、阻力指数 RI，子痫前期组（1.5±0.4，0.7±0.1）、妊娠高血压组（1.2±0.3，0.6±0.1）、 对照组（0.7±0.2，0.5±0.1）三组差异有统计学意义。PlGF 截断值选择 256 μg/L 时，预测子痫前期的灵敏度和特异度分别为 80.3%和 90.2%；子宫动脉搏动指数 PI 截断值选择 0.710 时，灵敏度和特异度分别为 71.3%和 89.2%。子宫动脉阻力指数 RI 截断值选择 1.39 时，灵敏度和特异度分别为 76.3%和 91.2%。PlGF、子宫动脉搏动指数及阻力指数并联预测子痫前期的灵敏度为 94.3%，特异度为 63.4%，串联灵敏度为 62.1%，特异度为 95.8%。

结论 孕妇血清 PlGF 联合多普勒超声在预测子痫前期中具有较好的临床价值。

PO-0277

A novel autoantibody specific for the Annexin A2 on podocyte in primary nephrotic syndrome

qing ye
The Children's Hospital, Zhejiang University School of Medicine

In recent years, it has been found that B-cell dysfunction plays an important role in the pathogenesis of primary nephrotic syndrome (PNS). B cells play a pathogenic role by secreting antibodies against their target antigens after transforming into plasma cells. Therefore, this study aims to screen the autoantibodies caused PNS and to explore their pathogenic mechanisms. Western blotting and mass spectrometry were employed to screen and identify the autoantibody against podocytes of PNS children. Then, both animal experiments and cell experiments were used to study its pathogenic mechanism. This finding was also confirmed in a large multicenter clinical study in children. We found that Annexin A2 autoantibody is highly expressed in PNS children with a pathological type of minimal change disease (MCD) or focal segmental glomerulosclerosis (FSGS) without genetic factors. The mouse model demonstrated that anti-annexin A2 antibody could induce proteinuria in vivo. The research on mechanism showed that the effect of Annexin A2 antibody on Rho signaling pathway was realized by promoting Tyr24

phosphorylation of Annexin A2 on podocytes by reducing its binding to Protein Tyrosine Phosatase 1B (PTP1B), which then led to the cytoskeleton rearrangement and damage to podocytes, and eventually caused proteinuria and PNS. In conclusion, Annexin A2 autoantibody may be responsible for some PNS children with MCD/FSGS.

PO-0278

基于大数据探讨 MMP11 在肿瘤的诊断及预后中的价值

钱凯、高峰
江苏省中医院

目的 基于大数据分析基质金属蛋白酶 11（MMP11）在肿瘤的诊断及预后中的作用。
方法 运用 TIMER2.0、GEPIA 2、UALCAN 分析 MMP11 在肿瘤及周围正常组织中的表达水平，运用 GEPIA 2 的生存分析模块分析不同 MMP11 水平的肿瘤患者生存期差异。
结果 1.使用基于 TGCA 数据库的 TIMER2.0 分析发现膀胱尿路上皮癌、乳腺浸润癌、宫颈鳞癌和腺癌、胆管癌、结肠癌、食管癌、多形性胶质瘤、头颈鳞状细胞癌、肾透明细胞癌、肾乳头状细胞癌、肝细胞肝癌、肺腺癌、肺鳞癌、嗜铬细胞瘤和副神经节瘤、前列腺癌、直肠腺癌、胃癌、甲状腺癌、子宫内膜样腺癌中 MMP11 基因表达水平明显高于正常组织（p＜0.05）；使用基于 TCGA 和 GTEx 数据库的 GEPIA 2 分析发现肾上腺皮质癌、弥漫性大 B 细胞淋巴瘤、卵巢浆液性囊腺癌、胸腺癌、子宫癌肉瘤基因表达明显高于正常组织（p＜0.05）。2.UALCAN 分析发现 MMP11 蛋白表达在子宫内膜样腺癌、肺腺癌中明显高于正常组织（p＜0.05）。3. GEPIA 2 生存分析发现肾嫌色细胞癌、脑低级别胶质瘤、葡萄膜黑色素瘤 MMP11 高表达组的总生存期和无病生存期均较低表达组短（p＜0.05）；多形性胶质瘤、间皮瘤、胰腺癌高表达组较低表达组总生存期短（p＜0.05）；前列腺癌高表达组较低表达组无病生存期短（p＜0.05）；子宫内膜样腺癌高表达组较低表达组无病生存期长（p＜0.05）。
结论 基于大数据分析发现 MMP11 在多种肿瘤中均高表达，且其表达水平与患者预后明显相关，可作为肿瘤筛查和预后判断的分子标志物。

PO-0279

Matrix metalloproteinase 3: a novel effective biomarker for predicting the mortality and the severity of pneumonia

Shuo Yang、Fei Wang、Chong Liu、Zhen Xu、Keke Jia、Jiansuo Zhou、Liyan Cui
Peking University Third Hospital

BACKGROUND Matrix metalloproteinase 3 (MMP3) is known as an inflammatory factor, however, the effectiveness of MMP3 for diagnosis of pneumonia and predicting outcomes is unclear. We evaluated the diagnostic and prognostic value of serum MMP3 in patients with pneumonia.
METHODS 185 patients with pneumonia and 52 healthy controls were enrolled. Serum MMP3, neutrophil gelatinase-associated lipocalin (NGAL), interleukin 6 (IL-6), procalcitonin (PCT), C-reactive protein (CRP) concentrations at admission were measured. The patients were followed up for 90 days.
RESULTS Compared with healthy controls, the concentrations of MMP3, NGAL and IL-6 at admission were significantly higher in patients with pneumonia (P<0.05). The median concentrations of MMP3, NGAL and IL-6 were significantly higher in the patients with severe pneumonia than the group of non-severe pneumonia (P<0.05). Compared with PCT (AUC=0.778), CRP (AUC=0.719), and IL-6 (AUC=0.726), MMP3 (AUC=0.846) and NGAL (AUC=0.826) had significantly higher AUC value for distinguishing the severity of pneumonia. The ROC of the combination of MMP3, neutrophil to lymphocyte ratio (NLR), and D-dimer showed the best

performance of predicting pneumonia severity, which gave an AUC of 0.956. The AUC of MMP3 (0.950) for predicting mortality was highest, followed by NLR (AUC=0.945), D-dimer (AUC=0.938) and NGAL (AUC=0.913). Multivariable logistic regression analysis showed MMP3, D-dimer and NLR were the independent predictors of hospital mortality in patients with pneumonia. Patients with MMP3 concentration >124.3 ng/mL had a significantly higher risk of mortality (P<0.05).
CONCLUSIONS MMP3 is a valuable biomarker in assessment of the severity and prediction of mortality in patients with pneumonia.

PO-0280

血清半胱氨酸蛋白酶抑制剂 1 的检测及其对食管鳞状细胞癌早期诊断的价值

王建伟[1,3]、余丽丽[2,3]、章良铭[2,3]、黄毅[2,3]
1. 福建省立金山医院
2. 福建省立医院
3. 福建医科大学省立临床医学院

目的 血清半胱氨酸蛋白酶抑制剂 1（CST1）与恶性肿瘤的相关性近来引起关注，我们通过免疫组织化学技术（IHC）的检测发现 CST1 蛋白在食管鳞状细胞癌（ESCC）早期患者癌组织中存在异常高表达。在此基础上，我们拟构建用于血清 CST1 检测的化学发光免疫分析（CLIA）法，并进行系统的方法学评价；基于 CLIA 法检测 CST1 在 ESCC 早期患者血清的表达水平，探讨血清 CST1 检测对 ESCC 的早期诊断价值。
方法 构建用于血清 CST1 检测的 CLIA 法，并通过线性范围、最低检出限、准确度、精密度、干扰实验、样本稳定性、试剂稳定性，评价其对血清 CST1 的检测性能。采用构建的 CLIA 法检测 112 例 ESCC 早期患者、107 例食管良性病变（EBL）及 151 例健康对照（HC）的血清 CST1 水平，评价血清 CST1 检测对 ESCC 早期患者的诊断性能。
结果 构建的 CLIA 法检测血清 CST1 的线性范围为 6.25~400 Pg/ml；最低检出限 1.35 Pg/ml；平均回收率 102.65％；本方法的低、高水平批内精密度分别为 4.43％、1.94％，均<1/4TEa；批间精密度分别为 1.39％、1.90％，均<1/3TEa；血红蛋白、类风湿因子对本方法无显著干扰，重度脂血和黄疸对低浓度 CST1 的检测存在一定的干扰；样本的 4℃保存稳定性良好；试剂的 25℃、37℃热稳定性与 4℃效期稳定性良好。以 68.33 Pg/ml 为 cutoff 值，CLIA 法的检测结果显示，ESCC 早期患者组血清 CST1 的水平与阳性率均明显高于 EBL、HC 组（P<0.05）；血清 CST1 检测对 ESCC 早期患者的诊断敏感性 31.25%（特异性 92.64%），AUC 达 0.654。
结论 构建的 CLIA 法具有良好的检测线性、灵敏度、准确度、精密度、特异性与稳定性，对血清 CST1 的检测性能良好；血清 CST1 检测对 ESCC 具有理想的早期诊断价值。

PO-0281

血清白细胞介素-26 水平与肝功能指标相关指标对慢性丙型肝炎预后相关性分析

朱建光
咸宁市中心医院

目的 通过检测慢性丙型肝炎患者血清中白细胞介素-26（IL-26）、C-反应蛋白（CRP）、总胆红素（TBIL）、谷丙转氨酶（ALT)、天冬氨酸氨基转移酶（AST）等水平，探讨血清 IL-26 与肝功能相关指标对慢性丙型肝炎预后的相关性和存在的潜在意义。

方法 选取 2018 年 1 月-2019 年 12 月于本院就诊的慢性丙型肝炎患者 140 例，其中高病毒载量慢性丙型肝炎患者 68 例（高病毒组），低病毒载量慢性丙型肝炎患者 72 例（低病毒组）；慢性丙型肝炎患者进展为肝硬化、失代偿肝硬化、肝衰竭或肝癌的患者 55 例为不良预后组，未发生进展的患者 85 例非不良预后组。另随机选取同期于本院进行体检的健康人群 140 例为对照组。采用全自动生化分析仪检测血清天冬氨酸氨基转移酶（AST）、丙氨酸转氨酶（ALT）及总胆红素（TBIL）水平；采用免疫比浊法测定 CRP 水平；采用酶联免疫吸附（ELISA）法检测血清 IL-26 水平；采用 Logistic 回归分析影响慢性丙型肝炎患者发生不良预后的危险因素。
结果 高病毒组与低病毒组慢性丙型肝炎患者血清 IL-26 水平均显著高于对照组，且高病毒组显著高于低病毒组（P＜0.05）；不良预后组血清 CRP、TBIL、ALT、AST 及 IL-26 水平均显著高于非不良预后组（P＜0.05）；Logistic 回归分析结果显示，血清 CRP、ALT、AST 及 IL-26 水平均是影响慢性丙型肝炎患者发生不良预后的独立危险因素（P＜0.05）。
结论 慢性丙型肝炎患者血清 IL-26 水平升高，且随患者病毒载量升高而升高，血清 CRP、ALT、AST 及 IL-26 均与患者预后存在一定相关性，可能是评估慢性丙型肝炎患者预后的潜在参考指标。

PO-0282

糖尿病合并肾病患者的尿脂联素、炎症因子与血脂水平变化与临床分期相关性

冯奕习、陈日寿、李汉秋
广州中医药大学东莞医院

目的 探讨糖尿病肾病患者的血液和尿液生物标志物在临床上的应用价值。
方法 纳入健康对照、单纯 2 型糖尿病正常蛋白尿、2 型糖尿病合并微量白蛋白尿及 2 型糖尿病合并大量白蛋白尿病人各 30 例，检测研究对象的血糖、及血液、尿液生物标志物。
结果 随着疾病病情加重，炎症因子的检出水平逐渐升高，尿液的生物标志物水平逐渐升高（所有 P 值均<0.05）。其中估算的肾小球滤过率（eGFR）随着病情加重逐渐下降，血肌酐、血同型半胱氨酸、血胱抑素 C 和 24 小时微量白蛋白尿检出水平逐渐升高（所有 P 值均<0.05）。尿脂联素水平在正常对照组和白蛋白尿组水平逐渐下降，但在微量和大量白蛋白尿组突然增高（P<0.001）。Logistic 回归分析结果显示，高血压、白细胞计数、中性粒细胞、淋巴细胞比率、单核细胞计数、血清淀粉样蛋白 A 水平、甘油三酯水平以及同型半胱氨酸水平异常增高，高密度脂蛋白胆固醇水平降低等均是糖尿病肾病的独立危险因素（所有 P 值均<0.05）。与正常的糖化血红蛋白相比，水平在 6.5%-7.5%之间的患者其糖尿病肾病的危险程度增加（P 值均<0.05）。进一步分析尿脂联素水平与糖尿病肾病的相关性，显示脂联素的四分位数间距水平与 eGFR、24 小时微量白蛋白尿、血肌酐和胱抑素 C 的水平间均存在显著性差异（所有 P 值均<0.001）。
结论 炎症因子及尿脂联素水平在糖尿病各亚组间的分布存在差异性，血液增高的新型生物标志物单核细胞计数/高密度脂蛋白胆固醇、尿液高脂联素水平的患者患有更严重的蛋白尿和肾脏功能不全，提示血液单核细胞计数/高密度脂蛋白胆固醇以及尿液脂联素可作为糖尿病肾病风险及预示临床分期的替代指标。

PO-0283

E3 泛素连接酶 CBL，CBL-B 和 CBL-C 在乳腺癌发生发展中的作用及其分子机制的初步研究

宋筱羽、肖斌、李林海
广州医科大学附属第六医院，清远市人民医院检验医学部

目的 探讨 E3 泛素连接酶 CBL，CBL-B，CBL-C 对乳腺癌细胞增殖和转移的影响，高通量筛选其相互作用蛋白，初步研究其介导相互作用蛋白泛素降解的分子机制。
方法 通过免疫组化染色观察 CBL，CBL-B，CBL-C 在乳腺癌及癌旁组织中的表达水平；构建稳定过表达 CBL，CBL-B，CBL-C 细胞株并进行细胞表型相关实验，观察它们过表达对乳腺癌细胞增殖、迁移和侵袭能力的影响；通过免疫沉淀结合质谱分析筛选 CBL，CBL-B，CBL-C 的相互作用蛋白，利用免疫共沉淀、免疫荧光共定位实验鉴定它们与各自候选蛋白的相互作用；通过 qPCR、Western-blot 实验检测过表达 CBL，CBL-B，CBL-C 对各自相互作用蛋白表达的影响；通过稳定性和泛素化实验验证过表达 CBL，CBL-B，CBL-C 对各自相互作用蛋白的稳定性及泛素化降解的影响。
结果（1）乳腺癌组织中 CBL，CBL-B，CBL-C mRNA 表达水平显著低于癌旁组织（P <0.05）；（2）细胞表型实验结果显示过表达 CBL，CBL-B，CBL-C 均明显抑制了乳腺癌细胞的增殖、迁移及侵袭能力；（3）通过 COIP、免疫共沉淀和激光共聚焦技术、稳定性和泛素化实验证实了 CBL 可促进 NCK2 的泛素化降解、 CBL-B 可促进 SNX-18 的泛素化降解、CBL-C 可促进 CTTN 的泛素化降解。
结论 CBL，CBL-B，CBL-C 均为乳腺癌的抑癌基因，在乳腺癌组织中低表达且与预后密切相关。CBL，CBL-B，CBL-C 的过表达均抑制乳腺癌细胞的增殖，迁移和侵袭。 CBL，CBL-B，CBL-C 可能分别通过促进 NCK2、SNX-18、CTTN 蛋白的泛素化降解而在乳腺癌中发挥抑制作用，这些研究为乳腺癌患者的治疗和预后评估提供了新的治疗靶点。

PO-0284

CXCL13/CXCR5 在食管癌中的表达及其意义

龙思琪、郭晓兰、祝静、刘文、李英、唐茜
川北医学院附属医院

目的 探讨食管癌患者手术前后外周血趋化因子 CXCL13 及其受体 CXCR5 水平的变化及意义。
方法 收集食管癌患者 50 例（其中食管癌术前患者 29 例，食管癌术后患者 21 例）、健康对照 24 例，采用流式细胞术检测研究对象外周血中 CXCR5+ 细胞、CD4+CXCR5+T 细胞、CD19+CXCR5+T 细胞、CD4+CD25+CD127lowTreg 及 Treg+CXCR5+T 细胞水平，酶联免疫吸附试验（ELISA）检测研究对象血浆中 CXCL13 水平，并将各指标进行统计学分析。
结果 食管癌患者 CD4+CXCR5+T 细胞、Treg 细胞及 CXCL13 水平均明显高于健康对照组（P<0.05，P<0.05，P<0.01）；食管癌术后患者 CD4+CXCR5+T 细胞、Treg+CXCR5+T 及 Treg 细胞水平较食管癌术前患者显著降低（P<0.05，P<0.01，P<0.01），而血浆 CXCL13 水平在食管癌患者手术前后变化无统计学意义。
结论 食管癌患者免疫功能可能处于抑制状态；CXCL13 可能通过与 CD4+T 细胞表面 CXCR5 作用参与了食管癌的发病。

PO-0285

全血抗病毒蛋白 MxA 在儿童呼吸道感染鉴别诊断的临床应用研究

叶辉铭[1]、陈自敏[2]、杨智过[3]、宋浏伟[2]、朱敏[1]、葛胜祥[3,4]
1. 厦门市妇幼保健院（厦门大学附属妇女儿童医院）
2. 厦门万泰凯瑞生物技术有限公司
3. 厦门大学公共卫生学院实验医学系
4. 国家传染病诊断试剂与疫苗工程技术研究中心（厦门大学）

目的 评估全血抗病毒蛋白 MxA 在儿童呼吸道细菌、病毒、肺炎支原体及其混合感染的鉴别诊断价值。
方法 应用自主研发的全血抗病毒蛋白 MxA 酶联免疫检测试剂盒检测 215 例儿童呼吸道感染患儿及 168 例健康体检儿童的全血 MxA 蛋白水平，比较呼吸道病毒、细菌、肺炎支原体及混合感染患儿全血 MxA 水平，受试者工作曲线分析评价全血 MxA 与 C 反应蛋白、白细胞计数等传统感染指标对呼吸道病毒感染和细菌感染的诊断效率。
结果 呼吸道病毒、细菌、混合感染和肺炎支原体感染患儿全血 MxA 水平的中位数分别是结果分别为 17.09ng/ml、1.51ng/ml、10.24ng/ml 和 8.76ng/ml，健康体检儿童全血 MxA 水平的中位数为 0.74ng/ml。病毒感染 、混合感染和肺炎支原体感染患儿全血 MxA 蛋白与健康体检儿童之间的差异具有统计学意义（P<0.0001），细菌感染患儿与健康体检儿童全血 MxA 无统计学差异（P=0.0912）。 ROC 曲线分析了全血 MxA、 C 反应蛋白、白细胞数、淋巴细胞数、中性粒细胞数、淋巴细胞比率、中性粒细胞比率对于儿童呼吸道病毒感染诊断价值， 其中 MxA 指标的 AUC 为 0.9562，说明对于病毒感染鉴别诊断效果最佳。
结论 全血 MxA 蛋白对于儿童呼吸道感染的病因具有良好的鉴别诊断价值，对于抗生素合理使用具有一定的指导价值。

PO-0286

原发免疫性血小板减少症患者血清细胞因子水平变化与血小板参数的相关性研究

李傲航
首都医科大学附属北京友谊医院

目的 探讨原发免疫性血小板减少症（ITP）患者血清细胞因子水平变化与血小板参数的相关性。
方法 选取 2018 年 10 月至 2019 年 10 月我院收治的 ITP 患者（60 例）为研究组，并选取同一时期的健康人（60 例）为对照组。比较两组患者血清中白介素-33（IL-33）、白介素-9（IL-9）、γ 干扰素（IFN-γ）、转化生长因子-β（TGF-β）的水平；比较两组血小板参数：血小板计数（PLT）、血小板比积（PCT）；采用 Pearson 法分析 ITP 患者血清细胞因子水平变化与血小板参数的相关性。
结果 研究组 IL-33、IL-9、IFN-γ 水平均明显高于对照组（P<0.05），研究组 TGF-β 水平明显低于对照组（P<0.05）；研究组 PLT、PCT 均明显低于对照组（P<0.05）；Pearson 及多重性回归分析表明 ITP 患者 IL-33、IL-9、IFN-γ 水平与 PLT 及 PCT 呈负相关（P<0.05），TGF-β 水平与 PLT 及 PCT 呈正相关（P<0.05）。
结论 ITP 患者 IL-33、IFN-γ、IL-9 水平升高，而 TGF-β 水平降低，ITP 患者机体内 IL-33、IFN-γ、IL-9、TGF-β 水平与血小板参 数密切相关。

PO-0287

Ureaplasma urealyticum Cysteine Desulfurase Promotes Th1-Biased T Cell Immune Response via TLR4-Mediated Activation of Dendritic Cells

Fangyi Guo[1,2]、Guozhi Dai[1,2]
1. The First People's Hospital of Chenzhou
2. 南华大学附属郴州医院

Ureaplasma urealyticum(U.urealyticum, Uu), the motive agent of a sexually transmitted illness, is a very successful microorganism with a complex ability to regulate the host immune response. Insights into the U.urealyticum factors modulating host response are needed to get vaccine antigen targets and higher perceived dynamic interactions between microorganism and host cells. Iron-sulfur [Fe-S] cluster are one of the foremost ancient and versatile inorganic cofactors because of their intrinsic chemical properties in biology. In prokaryotes, [Fe–S] clusters are protein cofactors. They are needed for crucial biological processes such as catalyst activity, leptontransfer, organic process, substrate binding/activation, iron/sulfur storage, organic phenomenon regulation, and chemical action. Cysteine desulfurase could be a scaffold supermolecule of the [Fe-S] cluster that is important for changing sulfur into biomolecules, together with [Fe-S] clusters and changed nucleotides. We have got shown that the U.urealyticum cysteine desulfurase(Uu-IscS) will induce each body substance and cellular immunologic response once intramuscular injection into BALB/c mice. Uu-IscS-immunized mice made a T-lymphocyte response once re-stimulation with immunogen Uu-IscS in vitro, which showed a Th1-biased cytokine spectrum with high levels of IFN-γ. A powerful body substance immune response was additionally detected within the immunized mice with high titers of specific serum IgG antibodies at an equivalent time. However, the direct result of Uu-IscS on antigen-presenting cells, which are essential for t cell activation, is not apparent. In this study, we tend to exploit the useful role of Uu-IscS in promoting naïve $CD4^+$/$CD8^+$ T cell differentiation toward Th1-type T-cell immunity through an interaction with dendritic cells (DCs). Uu-IscS functionally induced DC maturation by up-regulating the expression of cell surface molecules (CD40, CD80, CD86, and MHC class I and II) and production of many pro-inflammatory cytokines (IL-12p70, TNF-α, IL-1β and IL-6) in DCs. These effects of Uu-IscS in DC activation were initiated upon binding to Toll-like receptor 4 (TLR4) followed by activation of downstream MyD88-, MAPK-, and NF-κB-dependent signalling pathways. Uu-IscS-activated DCs displayed a superb capability to effectively polarise naïve $CD4^+$and $CD8^+$ T cells toward Th1-type T-cell immunity with the dose-dependent secretion of IFN-γ and IL-2 at the side of increased levels of CXCR3 expression. Notably, Uu-IscS-stimulated DCs induced the proliferation of Ag-specific Th1-type effector/memory $CD44^{high}CD62L^{low}$ T cells from the spleen Uu-infected mice in a TLR4-dependent manner. Conjointly, these results demonstrate that Uu-IscS is an immune matter that interacts with DCs, specifically via TLR4, to get Th1-biased memory T cells in an antigen-specific manner. Uu-IscS could contribute to the improved understanding of host-pathogen interactions and supply a rational basis for the invention to develop an efficient U.urealyticum vaccine.

PO-0288

全光谱流式细胞术检测 T 淋巴细胞亚群百分比和绝对计数的结果分析

张静文[1,2]、潘建华[1,2]、兰山卉[1]、郑倩[1]、李明敏[1]
1. 广州金域医学检验中心有限公司
2. 广州医科大学金域检验学院

目的 探讨全光谱流式细胞仪体积法和微球法检测 T 淋巴细胞百分比和绝对值结果与传统流式检测结果的差异。
方法 应用全光谱流式细胞仪体积法和微球法对 25 例外周血样本进行 T 淋巴细胞亚群绝对计数，分析全光谱流式细胞仪体积法和微球法检测结果与传统流式微球法检测 CD3+，CD3+CD4+,CD3+CD8+细胞百分比和绝对计数的结果差异，并用 t 检验，比较全光谱流式细胞仪两种方法和传统流式微球法间结果是否具有统计学差异。
结果 与传统流式细胞仪单平台法检测 T 淋巴细胞亚群绝对计数结果相比，光谱流式细胞仪体积法检测结果偏低，CD3+，CD3+CD4+,CD3+CD8+绝对计数平均偏差分别为-22.60%、-24.83%、-20.57%；光谱流式细胞仪微球法检测结果偏高，CD3+，CD3+CD4+,CD3+CD8+绝对计数平均偏差分别为 9.54%、7.77%、13.51%；其中体积法检测 CD3+，CD3+CD4+绝对计数结果与传统流式微球法检测结果具有统计学差异（P<0.05）。光谱流式仪检测 T 淋巴细胞亚群百分比结果均低于传统流式仪，CD3+，CD3+CD4+,CD3+CD8+百分比平均偏差分别为-3.20%、-3.48%、0.00%，无统计学差异（P>0.05）。
结论 使用全光谱流式细胞术检测 T 淋巴细胞亚群，百分比检测结果与传统流式细胞检测结果较一致；如进行绝对计数检测，建议使用微球法。光谱流式仪使用体积法进行绝对计数检测，需重新建立参考区间。

PO-0289

铁死亡在肝癌中的调控因素及潜在应用

潘亚芳、郭玮
复旦大学附属中山医院

目的 研究铁死亡在肝癌中的调控因素及潜在应用。
方法 通过查阅铁死亡参与肝癌进展的相关文献进行综述。
结果 各项研究表明铁死亡影响肝癌的发生发展，并已知肝癌中参与铁死亡调控的相关因素：P62-Keap1-NRF2 通路的激活抑制肝癌细胞中铁死亡的发生；Sigma-1 受体对肝癌细胞铁死亡有保护作用；MicroRNA-214-3p 通过靶向肝癌细胞中的 ATF4 增强 erastin 诱导的铁死亡；LncRNA-GABPB1-AS1 和 GABPB1 在 erastin 诱导 HepG2 肝癌细胞铁死亡过程中调节氧化应激。此外，在肝癌的治疗上研究显示可通过内、外源性途径诱导肝癌细胞铁死亡从而辅助治疗。
结论 铁死亡是诱导肝癌细胞死亡的有效机制，对肝癌中铁死亡的理解可以为我们改善肝癌的治疗和发展带来新希望。

PO-0290

Research Progress in Prognostic Factors and Biomarkers of Ovarian Cancer

Shuna Liu、Ming Wu、Xin Fu、Fang Wang
南京医科大学第一附属医院（江苏省人民医院）

Purposes Ovarian cancer is the most fatal gynecological tumor, its incidence is next to cervical cancer and endometrial cancer, but its mortality rate is the first among reproductive system malignancies. Compared with other gynecological tumors, ovarian cancer has complex pathological types, high recurrence rate and poor prognosis. Patients with distant metastasis due to delayed medical treatment and tolerance to chemotherapy have worse prognosis. Therefore, the identification of effective clinical prognostic factors and biomarkers is crucial to improve the prognosis of ovarian cancer patients.

Methods Based on the topics discussed in this review, we systematically searched the recent medical literature on novel prognostic biomarkers of ovarian cancer in PubMed and PMC databases by using our search strategy. All the literature included in the study were published between February 1, 2015 and February 1, 2021. After excluding the duplicated literature in the two databases, a total of 1,923 literature met the restriction conditions. Then the retrieved literature were imported into the literature management software Endnote. Preliminary screening was performed by reading the titles and abstracts of the literature to exclude irrelevant studies, and then the full text of the included literature was evaluated. In order to ensure the reliability of the research results, we only selected studies with more than 50 patients with ovarian cancer, and the biomarkers studied in the literature were consistent with the clinical results. The inclusion and exclusion criteria and search strategy are provided in the appendix. Finally, a manual search was conducted in major journals and the reference lists of the selected papers to find other relevant citations that were missing by the electronic search.

Results A total of 297 different novel prognostic biomarkers were reported in 296 studies that met the inclusion criteria. These prognostic biomarkers were classified according to the purpose of the study, there were 45 studies on biomarkers in the blood of ovarian cancer patients and 251 studies on biomarkers in tumor tissues. The 41 novel prognostic biomarkers provided by 45 studies can be classified by biological function, including cell proliferation and invasion, inflammatory response, angiogenesis, antioxidant, immune response, chemotherapeutic sensitivity, mitosis process, EMT (epithelial-to-mesenchymal transformation) and metastasis, deregulation of the cellular transport and apoptosis process. The selected tissue prognostic biomarkers can be divided into immunohistochemical biomarkers (68.77%), DNA biomarkers (3.95%) and RNA biomarkers (27.28%). These markers are classified according to their biological functions, mainly including such functional pathways as EMT and metastasis, inflammation and immunity, antioxidant, angiogenesis, cell proliferation, migration and invasion, chemotherapeutic sensitivity and cell cycle regulation.

Conclusions Ovarian cancer is the most fatal gynecological malignancy with high incidence and low survival rate. By exploring the prognostic biomarkers associated with ovarian cancer recurrence and progression, independent risk factors affecting patient prognosis were identified, which laid a solid foundation for the development of novel treatment strategies and the improvement of patient treatment outcomes. This review searched the literature and database for the relevant reports on prognostic biomarkers of ovarian cancer, reviewed the classic clinical prognostic biomarkers, and focused on the recently discovered various prognostic markers. The prognostic value of a variety of novel biomarkers was evaluated by integrating genomic, proteomic and metabolomic data and clinical information with a multivariate analysis model. The effectiveness of these novel prognostic biomarkers still needs to be further validated in large clinical trials. By studying the functional pathways of regulation of these molecular markers, the potential molecular mechanisms are revealed, so as to identify new therapeutic targets. This is a high-precision medical method, which may promote personalized treatment of ovarian cancer patients and improve their prognosis.

PO-0291

A multivariate diagnostic model based on urinary EpCAM-CD9 positive extracellular vesicles for resectable prostate cancer diagnosis

Yibei Dai[1]、Yiyun Wang[2]、Lingyu Zhang[1]、Zhenping Liu[3]、Pan Yu[1]、Ying Cao[1]、Ying Ping[1]、Danhua Wang[1]、Gong Zhang[1]、Yiwen Sang[1]、Xuchu Wang[1]、Zhihua Tao[1]
1. The Second Affiliated Hospital Zhejiang University School of Medicine
2. 浙江大学医学院
3. 杭州师范学院附属余杭医院杭州市余杭区第一人民医院

Prostate cancer (PCa) is one of the most frequently diagnosed cancers and the leading cause of cancer death in males worldwide. However, current biomarkers used in the clinic such as prostate-specific antigen (PSA) are not satisfied for the resectable PCa due to its low specificity, unclear benefits for reducing PCa deaths and the harms of overdiagnosing indolent disease. In this study, we aimed to investigate the performance of urinary EpCAM-CD9 positive EVs ($uEV_{EpCAM-CD9}$) for the diagnosis of prostate cancer using a newly laboratory-developed chemiluminescent immunoassay. Results showed that the $uEV_{EpCAM-CD9}$ were able to distinguish PCa from controls and significant decrease of $uEV_{EpCAM-CD9}$ were observed after prostatectomy. We further constructed an exclusive multivariate diagnostic model based on $uEV_{EpCAM-CD9}$, PSA and other clinical parameters, which showed an enhanced diagnostic sensitivity without substantially decreasing specificity and performed excellently to diagnose resectable prostate cancer (AUC = 0.953, P<0.0001). Moreover, this diagnostic model also exhibited a superior diagnostic performance (AUC = 0.921, P<0.0001) over PSA (AUC = 0.712, P=0.0018) at the PSA gray zone. Overall, the multivariate diagnostic model is a promising tool in the field of resectable PCa diagnosis.

PO-0292

Changes of serum IL-10, IL-1β, IL-6, MCP-1, TNF-α, IP-10 and IL-4 in COVID-19 patients

Qingqing Lu[1]、Zhenhua Zhu[2]、Chaochao Tan[3]、Hui Zhou[2]、Yan Hu[2]、Ge Shen[4]、Pan Zhu[4]、Gang Yang[4]、Xiaobing Xie[2]
1. Hunan University of Chinese Medicine
2. 湖南中医药大学第一附属医院
3. 湖南省第一人民医院
4. 娄底市疾控中心

Background and purpose Studies have shown that some cytokines in COVID-19 patients were elevated. This study aims to assess whether IL-10, IL-1β, IL-6, MCP-1, TNF-α, IP-10 and IL-4 serve as potential diagnostic biomarkers of COVID-19.
Methods The above serum cytokines in COVID-19 patients and non COVID-19 patients were detected by ELISA, SARS-CoV-2 IgM and IgG were detected by chemiluminescence method. Independent-samples Mann-Whitney U-test was utilized to compare cytokines levels in different groups and course, Levene T-test, T'-test were utilized to compare they in different genders, and Spearman Correlation test was utilized to analyze the correlation between the cytokines levels with ages, SARS-CoV-2 IgG and IgM.
Results Serum levels of IL-10, IL-1β, MCP-1, TNF-α and IL-4 in COVID-19 patients were significantly higher than those in non-COVID-19 patients, while IL-6 were only significantly higher than in healthy people, IP-10 were significantly lower than in other diseases patients. AUCs of COVID-19 diagnosed by IL-10, IL-1β, IL-6, MCP-1, TNF-α, IP-10 and IL-4 were 0.735, 0.775, 0.595, 0.821, 0.848, 0.387 and 0.682, respectively. In COVID-19 patients' serum, the levels of IL-

10 and MCP-1 of male had noticeably higher than those of female, and all cytokines were significantly positively correlated with age, IL-1β and IL-4 were significantly negatively correlated with SARS-CoV-2 IgM, while IL-10, IL-1β, IL-6, TNF-α and IP-10 were significantly negatively correlated with SARS-CoV-2 IgG. IL-10 on 43-56 days were significantly lower than at 29-42 days, TNF-α at 15-42 days were significantly higher than at 0-14 days, IP-10 at 0-14 days were the highest, IL-4 at 29-42 days were significant higher than on 0-14 days.
Conclusions The detection of IL-10, IL-1 β, IL-6, MCP-1, TNF-α and IL-4 would assist the clinical study of COVID-19, and IP-10 may be the cytokine `of early elevation in COVID-19 patients.

PO-0293

IL-1B 及 IL-1RN intron2 基因多态性与大肠癌关系的研究

邢培祥、杨发林、阚世锋
山东大学齐鲁医院

目的 探讨白介素-1B（IL-1B）及白介素-1RN（IL-1RN）基因多态性与中国山东地区汉族人大肠癌的关系。
方法 用基因芯片检测 IL-1B–31/-511 位点单核苷酸多态性（SNP）；以凝胶电泳检测 IL-1RNintron2 基因多态性(VNTR)；以 ELISA 测定 IL-1b/-1ra 血清水平。以其它 3 类大肠相关疾病及健康体检者为对照，以病例-对照研究方法分析 490 例大肠癌与 IL-1B–31/-511 SNP 及 IL-1RNVNTR 的关系。用 χ^2、*t* 检验行相关指标的比较。以比值比(OR)及其 95％可信区间(95％CI)估计相对风险。
结果 （**1**）大肠癌组 IL-1ra /-1b 比值显著低于对照组（u =-23，*P*<0.01）； IL-1B-511TT 及 T 频率均显著高于对照组[（χ^2 =5.22，*P*<0.05）vs（χ^2 =4.59，*P*<0.05）]。（2）直肠癌及管状腺癌组-511TT/T 频率均显著高于对照组，其 OR(95％CI)分别为,TT: 1.59（1.03～2.45）及 1.74（1.19～2.55）； T: 1.39（1.04～1.86）及 1.42（1.10～1.83）。低分化管状腺癌组-511TT 频率（61.90%）显著高于对照组；而其 CT 频率（19.05%）显著低于对照组，其 OR(95％CI)分别为,TT: 4.57（1.96～10.65）及 CT:0.23（0.08～0.64）；中及低分化管状腺癌组-511T 频率均显著高于对照组，其 OR(95％CI)分别为： 5.80（1.24～27.08）及 2.35（1.24～4.59）。
结论 IL-1B/T SNP 与山东地区汉族人大肠癌相关。

PO-0294

Cyr61 Mediates Oxaliplatin Resistance in Colorectal Cancer Cells by Regulating Bcl-XL Expression

Yanfang Song
Peoples Hospital Affiliated to Fujian University of Traditional Chinese Medicine

Even though the clinical application of oxaliplatin (L-OHP) has brought improvements in the survival of colorectal cancer (CRC) patients, about half of patients with CRC fail to acquire good clinical outcomes, indicating resistance to L-OHP therapy. Cysteine-rich protein 61 (Cyr61), as a multifunctional extracellular matrix protein, is highly expressed in a variety of tumors, and increased Cyr61 is known to be closely involved in chemotherapeutic resistance of many tumors, but its role in the L-OHP resistance of CRC cells has not been studied. In this study, we aimed to investigate the role of Cyr61 on L-OHP resistance of CRC cells and mechanism underlying. Our findings showed that the mRNA and protein level of Cyr61 in L-OHP-resistant cells were significantly increased compare with those in the non-resistant cells. Knockdown of Cyr61 enhanced chemosensitivity of L-OHP-resistant cells. Mechanistically, we found that overexpression of Cyr61 decreased the L-OHP-induced apoptosis in the drug-resistant of CRC

cells through the regulation of Bcl-xL. Collectively, our results revealed for the first time Cyr61 displays a crucial role in the CRC cell resistance to L-OHP, and targeting Cyr61 may be a promising therapeutic strategy to overcome L-OHP resistance in CRC.

PO-0295

High Performance of SARS-Cov-2 N Protein Antigen Chemiluminescence Immunoassay as Frontline Testing for Acute Phagse COVID-19 Diagnosis：A Retrospective Cohort Study

Qiaoling Deng[1]、Guangming Ye[1]、Yunbao Pan[1]、Wen Xie[1]、Gui Yang[1]、Zhiqiang Li[2]、Yirong Li[3,4]
1. Department of Laboratory Medicine, Zhongnan Hospital of Wuhan University
2. Department of Neurosurgery, Zhongnan Hospital, Wuhan University
3. Department of Laboratory Medicine, Zhongnan Hospital of Wuhan University
4. Wuhan Research Center for Infectious Diseases and Cancer, Chinese Academy of Medical Sciences

Objectives Disease COVID-19 emerged and rapidly spread throughout the world. Testing strategies focus on patients with COVID-19 requires assays that are high-throughput, low-risk of infection and small sample volumes. Antigen surveillance can be used to identify exposure to pathogens and measure acute infections.
Methods A total of 914 serum samples collected from 309 currently infected COVID-19 patients, 48 recovered ones and 410 non-COVID-19 patients were used to measure N protein antigen by an chemilumineseent immunoassay. Diagnostic performances were analyzed in different periods after onset.
Results There was a high level of N protein antigen in COVID-19 patients (0.56 COI), comparing to the recovered patients (0.12 COI) and controls (0.19 COI). In receiver-operating characteristic curve analysis, area under the curve of serum N protein antigen was 0.911 in the first week after onset. In this period, Sensitivity and specificity of serologic N protein antigen testing was 76.27% and 98.78%. Diagnosis performance of specific antibodies became better from third week after onset. Subgroup analysis suggested that severe patients had higher levels of antigens than mild patients.
Conclusions High level of serum antigen suggested early infection and seriously ill. Serum N protein antigen testing by chemiluminescence immunoassay is considered as a viable assay used to improve diagnostic sensitivity for currently patients.

PO-0296

Study of risk factor of urinary calculi according to the association between stone composition with urine component

Pan Wang、Jiansuo Zhou、Chong Liu、Boxin Yang、Liyan Cui
Peking University Third Hospital

Urolithiasis is a common urinary disease with high recurrence. The risk factor for the recurrence of calculi is not very clear. The object of the present study was to evaluate the association between calculi composition and urine component and analyse the risk factor for the recurrence of urolithiasis. In this study, a total of 223 patients with calculi and healthy control were enrolled, and the components of the calculi and urina sanguinis collected before surgery were analysed. Of the 223 patients, 157 were males and 66 were females. According to the stone composition, the case group was subdivided into three groups. 129 patients had single calcium

oxalate stones, 72 had calcium oxalate stones mixed with other stones and 22 had other type of stones excluding calcium oxalate stones. Urine biochemicals were analysed and the associations were found between the chemicals in each group. Multivariate logistic analysis demonstrated that reduced urinary magnesium and uric oxalic acid were independent risk factors when comparing all cases with normal controls. Only decreased urinary magnesium was found to be a risk factor comparing the single calcium oxalate group with normal control group. Low level of urinary magnesium and uric oxalic acid were found to be risk factors comparing the mixed calcium oxalate group with normal control group. No risk factor was found comparing the other stone group with normal control group. In conclusion, there were clear relationships between stone components and urine chemicals. Urine chemicals might be risk factors to predicate the occurrence of urolithiasis.

PO-0297

抗肾小球基底膜抗体（ELISA 法）与肾穿刺活检不符一例

杨静、周佳烨、邵文琦、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 本研究报道 1 例患者因血尿 2 周入院，于肾炎类型的鉴别过程中发现 ELISA 法检测抗肾小球基底膜（GBM）抗体阳性而肾穿刺活检结果为阴性，针对两种检查方法的结果差异，我们进行了原因分析。

方法 通过文献复习，结合患者临床症状和其他辅助检查等，依据患者 ELISA 法检测抗 GBM 抗体与病理结果不一致的可能原因进行分析。

结果 我们通过（1）更换不同品牌的 ELISA 检测试剂盒进行检测，该患者的血清抗 GBM 抗体检测结果为阴性；（2）使用 ANCA 六基质（包括 GBM 抗原点）和 GBM 猴肾组织片的荧光法检测，结果均为阴性。结果不符的可能原因：（1）肾小球严重破坏的情况下，荧光可能会产生假阴性结果；（2）患者体内有其他自身抗体共存的情况下，免疫球蛋白和/或补体成分的其他沉积可能会模糊图像导致假阴性结果。（3）ELISA 检测方法中常见的非特异性结合导致假阳性结果。

结论 通过更换不同的检测平台进行抗 GBM 抗体检测，结合患者临床症状和其他辅助检查，本实验室采用的 ELISA 试剂盒检测抗 GBM 抗体阳性的原因可能是由于患者体内的其他抗体与微孔板包被的 GBM 产生了非特异性反应导致的假阳性。

PO-0298

前列腺特异性抗原同源异构体 p2PSA 的稳定性研究

周佳烨、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 鉴于大量研究发现，p2PSA 的加入对于提高辅助诊断前列腺癌的正确性，区别癌症的侵袭性以及病理性升级有重大价值。在具有一定的临床价值的背景下，探究 p2PSA 的稳定性因素对临床开展的影响。

方法 PSA 范围在 4-10ng/ml 并接受直肠超声引导前列腺穿刺活检的 100 名男性患者采集血清标本，通过模拟临床实际可能会遇到的影响血样检测结果的前处理因素，包括时间、温度、添加剂、反复冻融，检测总 PSA、游离 PSA、游离 PSA 百分比、p2PSA 以及其衍生指标 Phi 的，判断是否产生临床可接受的偏倚。

结果 在常温 31℃条件下且未离心情况下，血液需在 2h 内完成检测，大于 2h 后检测 p2PSA 均产生明显偏倚；离心后的血清置于 4℃条件下且 6h 内完成检测，p2PSA 结果与立即检测时一致。将

血清分离后 4℃保存可稳定 24h，-20℃或-70℃条件下保存可稳定 6 个月，-70℃的条件比-20℃保存效果好，偏倚更小。
结论 本研究显示不管在何种条件下，血清 p2PSA 水平均随着时间的延长而升高的趋势，在未离心、常温放置的情况下结果升高最为明显，将血清分离保存的情况下 p2PSA 水平是随时间的延长呈现下降的趋势。

PO-0299

新冠肺炎康复者恢复期血浆治疗 COVID-19 患者体内抗体含量和核酸基因 ORF1ab 与 N 清除研究

段丽[1]、林国跃[1]、秦莹[1]、李明[1]、宋玉霞[1]、李剑平[2]、蔺志强[1]、孙贤礼[1]、李远达[1]、张弛[1]、屈晓娟[1]
1. 新疆医科大学第八附属医院（新疆新冠肺炎医疗救治定点医院）
2. 辽宁省血液中心沈阳中心血站

目的 探讨康复者恢复期血浆治疗 COVID-19 患者后体内抗体 IgM、IgG 产生和核酸基因 ORF1ab、N 清除效果。
方法 检测 COVID-19 患者治疗前后抗体 IgM、IgG ct 值和核酸基因 ORF1ab、N 变化，并统计比对分析。
结果（1）有 99 例快速发展型、重型和危重症 COVID-19 患者接受康复者恢复期血浆治疗，总有效率 100%，治愈率 100%，总输血率达 9.31%（99/1064），无严重输血不良反应。（2）康复者恢复期血浆 229 袋每袋 200ml 平均含有抗体量 IgG ct 值 31.61±23.28（1:64），IgM 为 7.19±11.94（1:8）。（3）输注康复者冰冻血浆患者体内抗体 IgG 和 IgM ct 值（68.70±69.14 和 47.89±64.63）分别显著高于输注血浆前（4.46±13.99 和 4.55±11.02）含量，与未输注血浆组（43.41±35.61 和 17.33±16.26）比较明显的增高（p＜0.05）；重型和危重型患者入院时抗体 IgG 含量明显高于快速发展型（P＜0.05）；IgM 抗体重型和危重型差异大，危重型 IgM 显著下降（P＜0.05）。输血组重型患者出院时 IgG 和 IgM 抗体含量均明显高未输血组（P＜0.05）。（4）未输血组入院或出院时抗体 IgG 含量重型低于快速发展型（P＜0.05），快速发展型出院时 IgG 含量比入院时明显的高（P＜0.05）；重型患者入院时 Ig M 含量明显高于快速发展型（P＜0.05）。（5）输血组病毒核酸基因 ORF1ab、N 转阴率（63.89%）明显高于未输血组（26.50%）（p＜0.005）。（6）快速发展型和重型患者住院天数输血组均较未输血组患者明显缩短（P＜0.05）。
结论 应用康复者恢复期血浆治疗 COVID-19 患者可大幅提高重型和危重型住院患者抗体含量、加快病毒清除及促进核酸转阴效果。

PO-0300

肌钙蛋白大数据回顾分析

周佳烨、林依婷、周琰、王蓓丽、郭玮
复旦大学附属中山医院

目的 心肌肌钙蛋白是诊断急性心肌梗死的重要生物标志物。本研究的目的是评估生物学和时间因素与血浆心肌肌钙蛋白 T（cTnT）浓度的相关性，并探讨哪个因素（性别，年龄，血样采集时间和季节）对血浆 cTnT 水平的影响最大。
方法 本研究选取了 2019 年上海市中山医院 3519 名急诊胸痛中心患者，收集了患者的基础资料及血浆 cTnT 检测结果。在进行数据分析之前，使用 Tukey 检验严格排除检测结果中的异常值。Kolmogorov-Smirnov（K-S）检验用于估计数据分布，非正态分布的数据表示为中位数（Q1，

Q3）。 使用 Mann-Whitney U 检验比较男性与女性之间的 cTnT 水平，Kruskal-Wallis 检验比较各性别组之间的 cTnT 水平，分析各个因素与血浆心肌肌钙蛋白 T（cTnT）浓度的相关性。
结果 在 70 岁以上的人群中，男性和女性的 cTnT 水平均随着年龄的增长而逐渐升高。 cTnT 在 80 岁以上的个体中达到最高水平（男性为 0.019μg/ L，女性为 0.016μg/ L）。不同血液采样时间的个体之间的 cTnT 浓度不同。在男性和女性中，cTnT 浓度分别在 8：00 和 13：00 达到最大值（分别为 0.013μg/ L 和 0.012μg/ L）。此外，在春季和冬季，cTnT 水平通常高于夏、秋两季。
结论 血浆 cTnT 水平受性别，年龄，采血时间和一年中的季节的影响很大。因此，为避免错误地将 cTnT 值识别为异常，应考虑个体的性别和年龄，一天中的采血时间以及一年中的季节，并建立不同的参考区间。

PO-0301

高血压性脑出血患者血清胶质纤维酸性蛋白水平变化及意义

王虹霏、史清海
新疆军区总医院

目的 胶质纤维酸性蛋白(GFAP)特异性表达于中枢神经系统星形胶质细胞，本研究通过观测高血压性脑出血患者血清中 GFAP 的浓度变化，探讨其可否作为诊断脑出血及评估患者病情和预后的标志物。
方法 选取 55 例高血压性脑出血患者和 55 例健康体检者进行临床观察。病例组分别在脑出血发病后 12 小时内和入院后 10 天内连续采集静脉血。根据头颅 CT 资料诊断及评估疾病，用格拉斯哥昏迷评分对患者临床状况进行评估，采用酶联免疫吸附法进行分析血清中 GFAP 的浓度。统计分析上述资料。
结果 55 例患者男性 42 例，女性 13 例，平均年龄 52 岁。超过半数(43%)患者表现为中重度脑出血，平均血清 GFAP 水平为 0.034 ng/mL。55 例健康体检者男性 35 例，女性 20 例，平均年纪 47 岁，平均血清 GFAP 水平为 0.012ng/ml。入院时精神表现正常患者组（格拉斯哥昏迷评分 15 分）与健康体检者相比，血清中 GFAP 显著升高，平均血清 GFAP 水平为 0.045ng/ml。GFAP 诊断脑出血的截止值为 0.03g/L，敏感性为 77.8%，特异性为 94.2%[曲线下 ROC 分析面积 0.972 (95% CI，0.802-1)，p＜0.001]。与格拉斯哥昏迷评分相比，患者发病 12h 内血清中 GFAP 的浓度与其并无显著相关性。与手术后患者的颅内压进行比较，发现在术后十天内，患者的颅内压如果一直高于正常，GFAP 的水平也会明显升高。与不同部位的脑出血体积相比较，呈正相关（相关系数 0.55，p＜0.05）。
结论 研究表明 GFAP 是诊断脑出血疾病的敏感和特异性的生物标志物，可能作为临床诊疗高血压性脑出血疾病的一种有价值的工具。

PO-0302

Hs-CRP、PCT、IL-6 和 NLR 对细菌感染和肺炎支原体感染的早期诊断价值比较

刘伟平[1]、毛小倩[2]
1. 自贡市第一人民医院
2. 天津医科大学临床医学院

目的 比较超敏 C 反应蛋白（hs-CRP）、降钙素原（PCT）、白介素 6（IL-6）、中性粒细胞与淋巴细胞比值（NLR）对细菌感染和肺炎支原体感染的早期诊断价值。
方法 收集自贡市第一人民医院 2020 年 12 月至 2021 年 2 月的初诊入院的肺部感染性疾病患者 131 例，其中细菌感染组 72 例、肺炎支原体感染组 59 例。收集两组患者的一般临床资料，对所有

受试者进行血常规、IL-6、hs-CRP、PCT 检测。利用 SPSS 26.0 软件对所有数据进行统计学分析，比较 hs-CRP、PCT、白介素 6（IL-6）和 NLR 对细菌感染和肺炎支原体感染的鉴别诊断价值。
结果 细菌感染组 hs-CRP、PCT、IL-6 和 NLR 值均高于肺炎支原体感染组，差异有统计学意义（P＜0.05）；细菌感染组和肺炎支原体感染组比较，PCT、hs-CRP、IL-6、NLR 的 ROC 曲线下面积（AUROC)分别为 0.971、0.859、0.831、0.858。诊断切点分别为 0.49 ng/mL、38.33mg/L、19.50 pg/mL、4.82；PCT 的诊断灵敏度为 100%、特异度为 93.2%、约登指数为 0.93；hs-CRP 的诊断灵敏度 75.0%、特异度 84.7%、约登指数为 0.60；IL-6 的诊断灵敏度 73.6%、特异度 81.4%、约登指数为 0.55；NLR 的诊断灵敏度 79.2%、特异度 79.7%、约登指数为 0.59。
结论 血液 PCT、IL-6、NLR、hs-CRP 测定对于鉴别诊断细菌性感染和肺炎支原体感染有较高的临床价值，PCT 的诊断价值最高。

PO-0303

新型心肌标志物血清可溶性生长刺激表达基因 2(sST2) 蛋白在血液透析患者中的应用价值

漆星
四川大学华西医院资阳医院·资阳市第一人民医院

目的 探讨血清可溶性生长刺激表达基因 2(sST2) 蛋白血清水平在维持性血液透析（MHD）患者发生心血管疾病（CE）的价值。
方法 收集四川大学华西医院·资阳医院 2019 年 1 月 1 日至 2019 年 12 月 31 日，血液透析中心患者 205 例，其中男性 108 例，女性 97 例，平均年龄（57.02±15.03）岁，将患者分为 MHD 并发 CE 组 113 人和 MHD 未并发 CE 组 92 人，采用高灵敏度双抗体夹心法检测 sST2，以及采用罗氏 cobas e602 电化学发光法测定血清 NT-proBNP、TNT 和 MYO，分析在 MHD 患者中心血管疾病的风险预测模型比较。
结果 MHD 并发 CE 组 113 人和 MHD 未并发 CE 组 92 人作为对照组，MHD 并发 CE 组年龄，伴糖尿病的风险构成统计学差异，NT-proBNP、sST2、TNT 值更高均构成构成统计学差异；通过 Logistic 多因素回归分析，sST2 是 MHD 并发 CE 的独立危险因素；绘制 ROC 曲线表明 NT-proBNP、sST2、TNT 对 CE 具有较好的独立预测能力；采用 R 语言运算随机森林 sST2 与 NT-proBNP、TNT 相比，sST2 是最重要的变量，其平均下降精度和平均递减 Gini 明显高于 NT-proBNP 和 TNT；再次建立三个预测模型，TNT 和 NT-proBNP 为Ⅰ，TNT、NT-proBNP、sST2 为Ⅱ，NT-proBNP、TNT、MYO 为Ⅲ，通过 R 语言得出Ⅰ与Ⅱ的 NRI：0.2083,Ⅱ比Ⅰ准确度增加了 20.83%，IDI 值: 0.0411 P= 0.00473，表明Ⅱ相对Ⅰ预测风险在新模型中提高了 4.11%。Cox 回归分析 sST2 是其死亡的独立预测因子。
结论 sST2 作为 MHD 患者新型标志物，相对其他心肌生物标记物有干预能力小，预测性能高，利用 R 语言随机森林对多种生物标记物的评估及风险预测模型建立，也是我们今后为患者全面评估风险预测体系的探索方向

PO-0304

The role of TPS, CA125, CA15-3 and CEA in prediction of distant metastasis of breast cancer

Jingya Zhang、Li Ren
天津市肿瘤医院(天津医科大学肿瘤医院)

Objective To explore the application value of breast cancer tumor markers TPS, CA125, CA15-3 and CEA detection alone and in combination for the monitoring of distant metastasis of breast cancer.
Method The clinical data of 389 female breast cancer patients admitted to Tianjin cancer hospital from January 2016 to March 2017 were retrospectively analyzed. Serum levels of TPS, CA125, CA15-3 and CEA were compared to analyze their significance in monitoring distant metastasis of breast cancer. The patients were divided into the distant metastatic group and the non-metastatic group according to whether the patients had distant metastasis. The non-metastatic group was divided into control group and distant recurrent group according to whether distant metastases occurred within 3 years after treatment.
Result The level of serum tumor markers of distant metastatic group and recurrence group were higher than those of non-metastatic group and non-recurrence group and the level of serum tumor markers of distant recurrent group were higher than those of control group. The receiver operating characteristic curve analysis revealed the four markers had diagnostic value in distant metastasis of breast cancer (AUCTPS=0.754, AUC15-3=0.821, AUCCEA=0.755, AUCCA125=0.651) and in distant recurrence in 3 years of breast cancer (AUCTPS=0.751, AUC15-3=0.744, AUCCEA=0.725, AUCCA125=0.661). TPS, CA15-3, CEA show similar performance in diagnosis of metastasis of breast cancer. TPS, CA15-3, CEA and CA125 show comparable performance in diagnosis of distant metastasis in 3 years of breast cancer.
To estimate whether the discrimination ability could be improved by marker panels, we established marker panels composed of TPS, CA125, CA15-3 and CEA didnot significantly improve AUCs than a single marker in the analysis groups (non-distant metastasis vs. metastasis in three years). To discriminate distant metastasis from non-distant metastasis, no significant improvements were shown in AUC compared with single marker. However, the sensitivity of all the markers were improved when the marker-panels were used.
Conclusion All tumor markers can be used effectively in monitoring distant metastasis of breast cancer. Different combination of serum TPS, CA125, CA15-3 and CEA is more valuable than using the tumor marker singly in terms of improving sensitivity.

PO-0305

胸苷激酶 1 检测在肝癌诊断及预后中的价值研究

胡涛、卢仁泉、郭林
复旦大学附属肿瘤医院

目的 研究胸苷激酶-1（TK-1）在肝细胞肝癌（HCC）中的诊断及预后价值。
方法 总共收集了 123 名 HCC 初诊患者的血清标本，以及 80 名肝良性病变患者和 98 名健康人群对照标本，检测并比较了不同人群的血清 TK-1（sTK-1）的水平，分析 TK-1 在肿瘤诊断中的特异性和敏感性；结合 HCC 患者的 AFP，CA19-9 等数据，使用 ROC 曲线建立模型，分析 sTK-1 在 HCC 中的诊断价值；检测 HCC 患者术前、术后、术后 1 个月、3 个月、6 个月的 sTK-1 水平，并随访术后 12 个月肿瘤复发情况，分析 sTK-1 在 HCC 患者手术疗效评价和预后管理中的作用。
结果 HCC 患者 sTK-1 中位水平为 2.38 pM，阳性率为 55.3%，显著高于肝良性病变患者的中位水平 1.50 pM 和和健康人群的 1.32 pM（P 均<0.001）；TMN III-IV 期 HCC 患者 sTK-1 中位水平 2.93 pM，高于 I-II 期患者的 1.94 pM（P=0.019）；HCC 患者 sTK-1 的 AUC 为 0.7983，联合

AFP 诊断的 AUC 为 0.9221；术前 sTK-1 阴性患者的无进展生存期（PFS）显著高于 sTK-1 阳性患者（P<0.001）；在 HCC 患者 sTK-1 水平动态监测中，肝癌患者术后 sTK-1 水平比术前有明显的下降（P<0.001），术后复发或转移患者的 sTK-1 水平在术后 6 个月内显著高于术后无进展患者（P 均<0.001）。

结论 sTK-1 能够辅助诊断 HCC，sTK-1 联合 AFP 检测可以进一步提高 HCC 诊断的特异性及敏感性。术前 sTK-1 是独立的 HCC 复发风险预测指标。术后半年内 sTK-1 水平的动态变化能够帮助肝癌患者评价手术疗效和进行预后分层。

PO-0306

拉萨地区 1196 例藏族儿童维生素 D 营养状态分析

尼玛顿珠[1]、边珍[1]、秦绪珍[2]
1. 西藏自治区人民医院
2. 中国医学科学院北京协和医院

目的 分析西藏拉萨地区 0-12 岁儿童维生素 D 浓度分布，观察地域、性别、年龄、季节对儿童维生素 D 营养状态的影响。

方法 纳入在西藏自治区人民医院门诊就诊的 1196 例 0-12 岁儿童，排除明确诊断患儿，采用索霖化学发光法检测血清 25-(OH)D 水平，收集性别、年龄、检测日期等相关信息，并进行统计分析。

结果 本地区 0-12 岁儿童血清 25-(OH)D 总体水平为 19.7（10.2，27.9）ng/mL。1196 例儿童中维生素 D 严重缺乏、缺乏、不足、充足、过量组患儿分别占 24.33%、26.92%、27.17%、21.32%、0.25%。不同年龄、性别 25-(OH)D 水平比较差异有统计学意义（P<0.05），学龄前组浓度最高，幼儿组、婴儿组和学龄组依次降低。随着儿童年龄增长，VD 充足率逐渐降低，1 岁以上儿童 VD 充足率不足 20%，男童高于女童。夏、秋季儿童 25-(OH)D 水平平均浓度高于春季，春季高于冬季。冬季维生素 D 缺乏、不足率明显高于其他 3 组（P<0.05）。

结论 拉萨市 0-12 岁儿童普遍存在维生素 D 缺乏和不足的现象，应改善饮食习惯，摄入 VD 含量较高的食物，根据不同地区、季节进行户外运动，增加皮肤暴露面积。孕妇及不同年龄阶段儿童补充 VD，定期监测血清 25-(OH)D 浓度水平，做到“因时、因地、因人而异”，并进行广泛的宣传教育。

PO-0307

1056 例抗中性粒细胞胞浆抗体的临床分布

姜茜
中国医科大学附属盛京医院

目的 通过对抗中性粒细胞胞浆抗体（ANCA）检测结果的分析，了解 ANCA 在就诊患者中的检出率及其分布特征，为临床疾病诊断提够帮助。

方法 使用 IIF 法判读 ANCA 荧光核型，同时使用 CLIA 法定量检测 ANCA 靶抗体。对 25822 例样本 ANCA 的检测结果进行分析，统计 ANCA 的阳性率、荧光核型及临床分布。

结果 共检出 1056 例阳性，ANCA 的阳性率为 4.09%，其中男性阳性率为 3.67%，女性阳性率为 4.38%，两组差异有统计学意义（P＜0.05）；阳性样本中，以 61 岁以上组别人数最多，占 45.27%，41-60 岁组别次之，占 27.37%，20 岁以下年龄组占 16.95%，位列第三，21-40 岁组别人数占比最少，占 10.42%。各年龄组中女性比例均高于男性，依次为 56.1%、74.4%、60.3%、73.6%。男性与女性的年龄构成差异有统计学意义（P＜0.01）；荧光核型以 pANCA 阳性率最高，为 51.14%，靶抗体以 MPO 为主（70.56%），aANCA 占 36.46%，cANCA 占 12.41%；荧光模型不同靶抗体的分布有统计学差异（P＜0.01）；临床诊断，23.30%为 ANCA 相关性血管炎，14.11%为类风湿性关节炎，10.42%为系统性红斑狼疮，8.43%为慢性肾病，6.16%为发热。

结论 ANCA 在不同年龄、性别、疾病中的检出率有所不同，ANCA 的检测不仅对 AAV 的诊断及治疗有帮助，对其他自身免疫性疾病的鉴别诊断亦有重要意义。

PO-0308

Combination of Alpha-fetoprotein, Des-gamma Carboxyprothrombin, and Lectin-Bound Alpha-fetoprotein in Detecting Early Hepatocellular Carcinoma

Yuan Liao、Yaqiong Chen
Third Affiliated Hospital of Sun Yat-sen University

Alpha-fetoprotein (AFP) is widely used as a surveillance test for Hepatocellular carcinoma (HCC) among patients with cirrhosis. Des-gamma carboxy-prothrombin (DCP), lectin-bound AFP (AFP-L3) and Golgi protein-73 (GP73) are potential surveillance tests for HCC. The aims of this study were to determine performance of AFP, DCP, AFP-L3 and GP73 and their combinations for the diagnosis of HCC. A total of 578 patients were enrolled, including 303 HCC patients, 104 patients with liver cirrhosis (LC), 101 patients with chronic hepatitis (CH) and 70 healthy volunteers. The serum levels of AFP, DCP, AFP-L3 and GP73 were quantified and the relationship between histological staging and serum markers were systematically analyzed. AFP had the best area under the curve (AUC = 0.850) followed by DCP (0.775) and AFP-L3 (0.763) for predicting HCC, while GP73 had low diagnostic value (0.549). The combination of AFP, DCP and AFP-L3 significantly improved diagnostic performance (AUC = 0.895). In addition, the combined index also achieved excellent diagnostic accuracy (AUC = 0.855) in early HCC. In conclusion, AFP was more sensitive than DCP and AFP-L3 for the diagnosis HCC. The combined index may be a strong indicator for discriminating HCC from non-malignant chronic liver diseases.

PO-0309

慢性肾脏病患者肺癌相关血清肿瘤标志物水平的改变及临床价值分析

苗强[1]、成渠霞[2]、牛倩[1]、蔡蓓[1]、张君龙[1]
1. 四川大学华西医院
2. 四川省广安市岳池县中医医院

目的 探讨肺癌相关血清肿瘤标志物在慢性肾脏病（CKD）患者中的表达变化及临床诊断价值，并初步估计参考范围。
方法 选取 2020 年 3 月-2020 年 9 月四川大学华西医院 729 例 CKD 患者为病例组， 94 例健康体检者为对照组；检测血清中 CA125、CYFRA21-1、SCC、NSE、ProGRP 的水平，比较各指标在两组间差异及不同 CKD 分期中水平的变化，对 CKD 各期患者肺癌相关肿瘤标志物阳性率进行比较分析并应用 ROC 曲线对其临床诊断价值进行评价；采用非参数法初步估计 CKD3~5 期肺癌相关指标的 95%参考范围。
结果 CKD 患者肺癌相关肿瘤标志物水平除 NSE 外均明显高于健康对照组（P<0.05），其中 CYFRA21-1、ProGRP 水平在 CKD2~5 期患者中均明显高于对照组（P<0.01），SCC 在 CKD3~5 期、CA125 在 CKD4~5 期患者中明显升高（P<0.01）。CYFRA21-1、ProGRP 在 CKD3~5 期患者中阳性率均大于 60%明显高于对照组（P<0.001）。在 ROC 曲线分析中，ProGRP、CYFRA21-1、SCC 对 CKD 诊断的灵敏度分别为 83.3%、90.9%、75.9%，曲线下的面积分别为 0.933、0.928、0.789。ProGRP 在 CKD3、4、5 期患者中的 95%参考范围上限分别为

148.5 pg/ml、225.9 pg/ml、375.5 pg/ml；CYFRA21-1、SCC 在 CKD3 和 CKD4~5 期患者中的的 95%参考范围上限分别为 7.56 ng/ml、11.27 ng/ml 和 4.52 ng/ml、8.92 ng/ml。
结论 血清 ProGRP、CYFRA21-1、SCC、CA125 的水平随着 CKD 分期的递增而显著增高，NSE 水平不受影响， 建议 CKD 患者联合检测肺癌相关血清肿瘤标志物并采用恰当的参考限值进行结果解释。

PO-0310

Association of Genetic Variants in TPMT, ITPA, and NUDT15 With Azathioprine-Induced Myelosuppression in Southwest China patients with Autoimmune Hepatitis

Qiang Miao、Lin Yan、Yanhong Zhou、Yi Li、Yuangao Zou、Lanlan Wang、Yangjuan Bai、Junlong Zhang
West China Hospital, Sichuan University

Aims This study aimed to investigate the influence of *TPMT*3C, ITPA, NUDT15*, and 6-thioguanine nucleotides (6-TGN) on azathioprine (AZA)-induced myelosuppression in Southwest China patients with autoimmune hepatitis (AIH).
Methods A total of 113 Chinese patients with AIH receiving AZA maintenance treatment were evaluated. The relevant clinical data of the patients were collected from the hospital information system. Genotyping of *TPMT*3C(rs1142345), ITPA (rs1127354) and NUDT15(rs116855232)* was conducted using a TaqMan double fluorescent probe. The concentration of 6-TGN was determined using UPLC-MS/MS.
Results Among AIH patients treated with AZA, 40 (35.4%) exhibited different degrees of myelosuppression. The *NUDT15* variant was associated with leukopenia (*P*=8.26X10-7; OR=7.5; 95% CI, 3.08–18.3) and neutropenia (*P*=3.54X10-6; OR=8.05; 95% CI, 2.96–21.9); however, no significant association with myelosuppression was observed for *TPMT*3C* and *ITPA* variants (*P*>0.05). There was no significant difference in 6-TGN concentration between AIH patients with or without myelosuppression (*P*= 0.556), nor was there a significant difference between patients with variant alleles of TPMT*3C, ITPA, or NUDT15 and wild-type patients (*P*>0.05). Interestingly, it was found that patients with a lower BMI had higher adjusted 6-TGN levels and a higher incidence of myelosuppression. (*P*=0.026 and 0.003).
Conclusion This study confirmed that *NUDT15* variants are a potential independent risk predictor for AZA-induced leukopenia and neutropenia. BMI may be a crucial non-genetic factor that affects the concentration of AZA metabolites and myelosuppression. In addition, the 6-TGN concentration in red blood cells does not reflect the toxicity of AZA treatment, and new biomarkers for AZA therapeutic drug monitoring need further research.

PO-0311

尘螨过敏原组分 Der p1、Der p2 特异性 IgE 纳米磁微粒化学发光免疫学检测方法的建立及其性能评估

韩菲菲、崔玉宝
无锡市人民医院

目的 采用纳米磁微粒化学发光免疫学建立快速定量检测尘螨过敏原主要组分 Der p1、Der p2 特异性免疫球蛋白 E（sIgE）的方法。
方法 利用本实验室培养的尘螨获得主要过敏原 Der p1、Der p2 的单组份重组蛋白制品。基于常规化学发光平台，优化试剂组份和反应模式，评估纳米磁微粒化学发光免疫技术检测尘螨过敏原主要

组分 sIgE 的各项性能指标。同时以该方法检测 50 例疑似尘螨过敏患者血清 Der p1、Der p2 sIgE 水平，并参照美国赛默飞 Phadia（Immuno CAP 系统）对两种方法学进行比对及符合率统计分析。
结果 建立的纳米磁微粒化学发光免疫学检测体系最低检出限（LoD）小于 0.01 U/mL，线性范围为 0.2～100 U/mL，批内精密度小于 5%，交叉污染率小于 0.1%。与 Phadia 相比，尘螨过敏原组分 Der p1 阳性符合率为 78%，阴性符合率为 100%，χ2＝19.51,P＜0.001；Der p2 阳性符合率为 93.3%，阴性符合率为 85%，χ2＝31.25,P＜0.001，表明本研究建立的组分分辨诊断法与 Phadia 有良好的相关性，用于检测尘螨有显著意义。
结论 利用纳米磁微粒化学发光免疫法检测尘螨过敏原组分 Der p1、Der p2 sIgE，成功建立了组分分辨诊断技术平台,其 LoD、线性范围、批内精密度、交叉污染率等性能指标良好，与 Phadia 有较好的一致性，可成为尘螨过敏原主要组分 sIgE 临床检测的推荐方法。

PO-0312

血清 N-MID 在原发性肺癌患者骨转移辅助诊断和疗效监测中的应用分析

陆立、卢仁泉
复旦大学附属肿瘤医院

背景与目的 目前临床上用于原发性肺癌患者骨转移辅助诊断的血清学标志物相对缺乏，该研究旨在探讨血清中骨钙素 N 端中分子片段（N-MID）的表达水平在肺癌患者骨转移辅助诊断和疗效监测中的作用。
方法 选取 2017 年 3 月至 2018 年 1 月在复旦大学附属肿瘤医院诊断为原发性肺癌的 231 例患者作为实验组，其中包括 97 例肺癌合并骨转移患者以及 134 例未骨转移肺癌患者，选取 69 例同期健康体检人员为健康对照组。利用 Logistic 多因素回归模型分析血清 N-MID、癌胚抗原（CEA）、神经元特异性烯醇化酶（NSE）、细胞角蛋白 19 片段（CYFRA21-1）、碱性磷酸酶（ALP）等在肺癌骨转移中的相关性。
结果 治疗前骨转移组血清 N-MID 水平明显高于无骨转移组与健康对照组（P 均<0.001）。Logistic 多因素分析显示，血清 N-MID（OR=9.265）和 NSE 水平（OR=2.688）是肺癌患者发生骨转移的危险因素。通过受试者工作特征（ROC）曲线确定血清 N-MID 的 Cut-off 值为 14.96ng/mL，并将实验组分为 N-MID >14.96ng/mL 组和 N-MID≤14.96ng/mL 组。治疗前，血清 N-MID >14.96ng/mL 组肺癌患者的无进展生存期（PFS）明显低于 N-MID≤14.96ng/mL 组患者（HR=2.040）。在肺癌合并骨转移患者中，治疗前后血清 N-MID 水平降低提示病情缓解（P<0.001）。
结论 血清 N-MID 水平与肺癌合并骨转移存在相关性，检测治疗前后的血清 N-MID 浓度可用于肺癌患者骨转移的辅助诊断和疗效监测。

PO-0313

Cyr61 decreases Cytarabine chemosensitivity in acute lymphoblastic leukemia cells via NF-κB pathway activation

Xianjin Zhu
Fujian Medical University Union Hospital

Objective To investigate the role of Cyr61 in regulating ALL cell chemosensitivity to Cytosine arabinoside (Ara-C).
Methods Cyr61 levels in plasma and bone marrow (BM) from ALL patients were determined by enzyme-linked immunosorbent assay. The expression of Cyr61 in Jurkat (T ALL cell lines), Nalm-6 (B ALL cell lines), and bone marrow mononuclear cells from ALL patients were measured by

real-time PCR and western blotting. Cell apoptosis was analyzed using an Annexin V-FITC and PI Double-Staining Kit. Activation of signal transduction pathways was determined by western blotting. Bcl-2 expression was analyzed by real-time PCR and western blotting.
Results Cyr61 was increased in plasma, bone marrow (BM), and bone marrow mononuclear cells from ALL patients as compared with samples from normal controls. Furthermore, we observed that increased Cyr61 effectively decreased Ara-C-induced apoptosis of ALL cells, and its function was blocked by the use of the anti-Cyr61 monoclonal antibody 093G9. Furthermore, Cyr61 increased the level of Bcl-2 in Ara-C-treated ALL cells. Mechanistically, it was shown that Cyr61 affected ALL cell resistance to Ara-C partially via the NF-κB pathway.
Conclusion Our findings support a functional role for Cyr61 in promoting chemotherapy resistance and suggest that targeting Cyr61 directly or its relevant effectors pathways may improve clinical responses in ALL.

PO-0314

探究单克隆免疫球蛋白（M 蛋白）对 CysC 检测的影响

刘杭敏
福建医科大学附属协和医院

目的 探究单克隆球蛋白（M 蛋白）对 CysC 检测的影响。
方法 对 58 例 M 蛋白阳性的血清样本和 5 例 M 蛋白阴性的血清样本分别检测原倍和 1:3 稀释血清及消除了 M 蛋白的血清 CysC 值，去除 M 蛋白使用聚乙二醇 PEG6000 蛋白沉淀法［1］［2］［3］，所有的 CysC 值均由罗氏 cobas8000（c702）测得，计算回收率，以小于、等于和大于正常回收率（90%～110%）的 M 蛋白阳性的血清样本中对应的免疫球蛋白浓度作均数加减标准差（X±S）和作图等统计学方法，分析 M 蛋白对 CysC 检测是否产生影响，以及产生的具体影响。
结果 M 蛋白阳性的血清样本中，对应的免疫球蛋白浓度值越大，对 CysC 测量值的影响越大，消除了 M 蛋白的血清样本的回收率越偏离正常回收率，1:3 生理盐水稀释无法判断 M 蛋白对 CysC 检测的干扰。
结论 单克隆球蛋白（M 蛋白）对 CysC 的检测存在干扰。准确可靠的 CysC 的检测对检测产生 M 蛋白的这类疾病如多发性骨髓瘤等引发肾功能损害有参考价值

PO-0315

Bioinformatics analyses reveal that SCARA5 is a novel biomarker in colorectal cancer

刘锦
福建医科大学附属协和医院

Objective we evaluated SCARA5 expression levels in CRC and its potential value as a diagnostic biomarker for CRC.
Methods Data were downloaded from the TCGA, GEO, and Oncomine databases to evaluate SCARA5 mRNA expression levels. The prognosis value was assessed using the online tool Cutoff Finder. Immunohistochemistry was performed to analyze expression levels.
Results SCARA5 mRNA levels were downregulated in CRC tissues compared with normal tissues. Survival analysis showed that low SCARA5 expression was associated with poor prognosis. These results were validated in clinical specimens, wherein the SCARA5 protein levels were significantly downregulated in CRC tissues compared with para-carcinoma tissues.
Conclusions SCARA5 may act as a human cancer suppressor gene in CRC.

PO-0316

新生儿败血症中血清细胞因子谱的表达

谢奇朋、陈碎朋
温州医科大学附属第二医院、育英儿童医院

目的 败血症仍然是新生儿死亡的主要原因，但对其潜在的病理机制了解甚少。为了解细胞因子在新生儿败血症中的作用，特做此课题研究。
方法 我们招募了 40 名患有败血症的足月新生儿和 26 名无感染的新生儿作为对照。使用 Luminex Bead 免疫分析系统分析了血清中的四十种细胞因子/趋化因子。使用酶联免疫吸附测定法测量血清 IL-17。
结果 我们的结果显示血清 IL-6，IL-8，TNF-α，IL-1β，MIF，CXCL13，CXCL1，CXCL2，CXCL5，CXCL6，CXCL16，CCL27，CCL2，CCL8，CCL3，CCL20，CCL23，CCL27 和 CX3CL1 水平与对照组相比，新生儿败血症患者中显着增加（所有 $p < 0.05$）。迟发性败血症（LOS）的血清 CXCL6，CXCL1，IL-6，CXCL10，CXCL11，CCL20 和 IL-17 的水平高于早发败血症（EOS）（所有 $p < 0.05$）。相反，LOS 中的血清 IL-16，CXCL16 和 CCL22 低于 EOS（所有 $p < 0.05$）。CX3CL1，CXCL2，CCL8 和 TNF-α 的水平均与 SOFA 得分呈正相关。
结论 我们的发现表明，新生儿败血症可能与过量的促炎细胞因子有关。此外，趋化因子显着增加感染后免疫细胞的募集，以参与新生儿的抗感染防御，但这反而可能导致损害。

PO-0317

The Diagnostic Value of Serum Tumor-associated Autoantibodies in Esophageal Cancer

kangjia xiao、Renquan Lu、Lin Guo
Department of Clinical Laboratory, Fudan University Shanghai Cancer Center

Objective To explore the application value of serum autoantibodies in the early diagnosis of esophageal cancer.
Methods In total, 130 patients with esophageal cancer and 110 controls (25 benign controls + 85 healthy participants) were included. Enzyme-linked immunosorbent assay (ELISA) was used to quantitatively detect autoantibodies in esophageal cancer and control serum samples, and the results were used to analyze the relationship with clinicopathological parameters. Then, the sensitivity and specificity of autoantibody combinations were obtained after screening.
Results There were significant differences between the autoantibody test results of the esophageal cancer patient group and the control group. As a result, anti-CAGE, anti-CTAG2, anti-MAGE-A4, anti-Trim21 and anti-RalA were selected in combination. In the esophageal cancer patient group, the CUTOFF value of each serum autoantibody concentration was calculated according to the ROC curve, and the total sensitivity of the autoantibody combination was calculated, with a positive judgment standard of 83.08%, total specificity of 72.73%, and accuracy of 78.33%. A nomogram was established based on the positive judgment standard, and the area under the ROC curve was calculated to be 0.880 after verification with the calibration curve. Two-week follow-up analysis found that compared with the preoperative control, the postoperative model integral value will significantly decrease.
Conclusion The determination of serum autoantibodies has certain clinical application value in the early diagnosis of esophageal cancer and can be used as an auxiliary index for early diagnosis. The combination of serum autoantibody groups can effectively improve the specificity and sensitivity for early diagnosis.

PO-0318

非小细胞肺癌患者血清 POSTN 的表达与预后研究

贾丽
天津医科大学肿瘤医院

目的 分析骨膜蛋白（POSTN）在非小细胞肺癌中的表达情况，探讨非小细胞肺癌中 POSTN 蛋白的表达与临床各病理参数及预后的相关性。POSTN 在非小细胞肺癌患者血清中的表达是否增高；POSTN 在不同年龄、肿瘤大小、TNM 分期、是否有淋巴结转移、远处转移患者中的表达是否有差异，POSTN 检测能否提高非小细胞肺癌的检出率，尤其是对早期非小细胞肺癌的诊断；术后患者血清 POSTN 表达是否降低；POSTN 的血清学检测能否作为手术治疗效果的评价指标。
方法 收集天津医科大学肿瘤医院 2019 年 6 月-2020 年 1 月天津肿瘤医院有完整病理资料非小细胞肺癌患者 165 例，其中 8 例同时收集到术前术后血清，并收集 62 例健康体检者作为对照组。查阅整理病人的病理资料包括年龄、肿瘤大小、是否淋巴结转移、是否远处组织转移。采用酶联免疫吸附法（ELISA）测定样本血清中的 POSTN 的含量，运用 SPSS 统计软件进行统计分析，同时用 graphpad prism6.0 软件进行作图。
结果 POSTN 在非小细胞肺癌患者中的表达明显高于正常对照组； POSTN 在非小细胞肺癌中其表达在不同年龄患者中无统计学意义，与其肿瘤大小、TNM 分期、淋巴结转移、远处转移均差异具有统计学意义；POSTN 在非小细胞肺癌诊断中优于传统非小细胞肺癌标志物；多项标志物联合检测可增高其敏感性、特异性等诊断能力；术后患者血清 POSTN 表达明显降低。

PO-0319

血清羧肽酶 N1 在浸润性乳腺癌化疗监测中的临床检测价值

崔冉亮、任丽、李悦国
天津医科大学肿瘤医院

目的 浸润性乳腺癌的发病率和死亡率逐年上升，提高治愈率，选择准确监测疗效标志物格外重要，故本研究探讨血清 CPN1 是否可作为潜在标志物连续监测浸润性乳腺癌疗效在临床应用价值。
方法 收集浸润性乳腺癌的患者 34 例连续 5 次化疗血清，随机分组其中 15 例为训练组，19 例为验证组，利用电化学发光法测定血清 CA153 和 CEA 表达，并用 ELISA 法测定血清 CPN1 浓度，分析 CPN1 下降率在浸润性乳腺癌监测效能。
结果 患者血清 CPN1 水平整体呈现下降趋势，分析治疗前后血清的变化，。II 周期化疗前后血清 CPN1 水平变化（训练集：21.8±13.13 VS 13.69±4.56、验证集： 31.68±12.70 VS 18.83±9.65）与浸润性乳腺癌患者化疗预后有相关性（P＜0.05）；分析连续两次化疗周期前后下降比率绘制 CPN1、CA153、CEA 的 ROC 特征曲线，比较 AUC 结果，II vs III ：训练集：AUCCPN1=0.833 vs AUCCA153=0.742 vs AUCCEA=0.667；验证集 AUCCPN1=0.7766 vs AUCCA153=0.7701 vs AUCCEA=7340；III vs IV：AUCCPN1=0.899 vs AUCCA153=0.799 vs AUCCEA=0.681；验证集：AUCCPN1=0.7855 vs AUCCA153=0.7717 vs AUCCEA=0.7510；血清 CPN1 水平与肿瘤直径、淋巴结转移、CA153 相关（P＜0.05），对比影像学与血清 CPN1 变化一致。
结论 血清 CPN1 水平可作为化疗监测标志物评价疗效以及指导临床化疗用药。

PO-0320

1728 例皮肌炎患者抗特异性肌炎谱抗体结果分析

谢曙光、李玲
广州金域医学检验中心

目的 探讨抗特异性肌炎谱抗体在特发性炎性肌病中的临床意义，为临床提供辅助诊断依据。
方法 免疫印记法测定临床诊断为皮肌炎患者血清中抗肌炎谱抗体抗 EJ 抗体、抗 Fibrillarin 抗体、抗 KU 抗体、抗 MDA5 抗体等抗体并分析结果。
结果 （1）抗特异性肌炎谱抗体在 1728 例患者检测结果总阳性人数 907 例，总阳性率为 52.49%。不同年龄组之间，41～50 岁组阳性率最高，比例为 62.58%；其次是 61～70 岁组，比例为 57.80%；<18 岁组最低，为 30.82%；<18 岁组与 40 岁以上各年龄组阳性率比较，组间差异显著，P<0.05，具有统计学意义。（2）特异性肌炎谱抗体在男性组阳性率为 42.58%，女性组阳性率为 58.93%，组间差异显著，P<0.05，具有统计学意义。（3）不同特异性肌炎谱抗体在男性组及女性组阳性率占比情况：各抗体总阳性率与在男性组、女性组分布一致；抗 Ro-52 抗体总阳性率为 24.83%，女性阳性率为 18.17%，男性阳性率为 6.66%；抗 JO-1 抗体总阳性率为 7.29%，女性阳性率为 5.27%，男性阳性率为 2.03%；抗 RNA-PⅢ抗体总阳性率为 6.25%，女性阳性率为 4.34%，男性阳性率为 1.91%；男女组阳性率组间比较差异非常显著，P<0.05，具有统计学意义。（4）不同模式组合阳性率及占总阳性率的比例：907 例阳性结果出现了 195 种抗体组合模式，不同模式中 Q 模式（抗 Ro-52 抗体）阳性例数最高，共 121 例，阳性占比 13.34%；其次是 DQ 模式（抗 JO-1 抗体+抗 Ro-52 抗体），阳性例数为 64 例，阳性占比 7.06%；第三是 U 模式（抗 SRP 抗体）阳性例数为 39 例，阳性占比 4.30%。（5）单独 1 种抗体阳性率最多，共 475 例（58.59%）；其次是 2 种抗体阳性模式，共 323 例（35.61%）；第三是 3 种抗体阳性模式，共 80 例（8.82%）。

PO-0321

基于人工神经网络的抗核抗体荧光核型智能判读

任茂源、夏玲芝
南京金域医学检验所有限公司

目的 评价在使用 Helios 全自动间接免疫荧光分析仪自动对焦拍照的基础上使用 YOLOv4 目标检测网络模型在判读 ANA 荧光核型上的应用价值。
方法 从南京金域检验所有限公司自免室 ANA 荧光图片数据库中随机选取 12000 张荧光图片（均质型、颗粒型、着丝点型、核仁型、胞浆颗粒型、阴性各占 1/6）。其中 6000 张荧光图片作为训练集，剩下的 6000 张图片作为测试集（训练集和测试集中每个核型的数量都一致）。构建 YOLO v4 的目标检测网络，并通过水平镜像，垂直镜像，90°旋转，180°旋转把训练集中的数据进行数据增强，将训练集中的数据扩增到 24000 张。之后用 Kappa 检验分析神经网络判读和人工判读之间的一致性，K<0.4 为一致性较低的标准，0.4≤K≤0.75 为一致性适中的标准，K>0.75 为一致性较高的标准。
结果 模型的判读结果的总体一致率为 95.06%，Kappa 值为 0.94。不同核型的一致率从高到低为胞浆颗粒（98.5%）、着丝点型（96.4%）、均质型（95.7%）、核仁型（95.1%）、核颗粒型（93.5%）、阴性（91.2%）。
结论 和传统的人工判读相比，基于 Helios 的自动对焦功能，利用深度学习建立 YOLOv4 目标检测网络模型来通过图片预测 ANA 核型更加高效，也能够较好的满足临床需求，为未来 ANA 荧光核型检测的标准化打下基础。

PO-0322

利巴韦林在 HCV 患者 RNA 定量检测中的影响研究

王倩[1]、赵秋剑[1]、杨鹏[2]
1. 宝鸡市中心医院
2. 宝鸡市妇幼保健院

目的 丙型病毒性肝炎(hepatitis C virus,HCV)是全球性的传染性疾病，而我国更是 HCV 患者基数最多的国家，其防治迫在眉睫。核酸检测是临床上诊断 HCV 及评估 HCV 药物治疗效果的重要手段。然而 PCR 反应容易受逆转录抑制剂药物的影响从而影响结果的准确性，本研究从 HCV 的治疗药物利巴韦林入手，研究不同提取方法对 PCR 结果的影响，同时研究使用精胺（Seprmine）解除逆转录抑制后，HCV 在血液中的表达水平差异来为后续的优化 HCV 检测提供新的思路和研究基础。
方法 对比磁珠法和 Trizol 法提取病毒 RNA 的含量，分析不同提取方法对 RNA 纯度和 PCR 定量结果的影响；利用精胺解除逆转录抑制，分析利巴韦林对 PCR 结果的影响。
结果 磁珠法提取 HCV 患者血清 RNA 的纯度优于 Trizol 法，同时 PCR 定量结果中，磁珠法也高于 Trizol 法；加入精胺后，两种方法的 PCR 检出含量均有所提高，同时加入精胺后 Trizol 法的 PCR 结果高于磁珠法未加精胺的 PCR 结果。
结论 HCV 患者在接受干扰素和利巴韦林的治疗后，HCV 含量检测应优先选择磁珠法或去除利巴韦林影响的提取方法，这样可以有效的减少利巴韦林对逆转录反应的抑制，从而更好的反应血液中 HCV RNA 的实际含量，为临床的治疗提供更准确的检测结果。

PO-0323

隐源性机化性肺炎患者 T 淋巴细胞亚群分析临床意义

薛占成、刘锦、巩庚、周秀、鲍布和、庞伟
武警特色医学中心

目的 检测隐源性机化性肺炎患者支气管肺泡灌洗液（bronchoalveolar lavage fluid，BALF）及外周血（peripheral blood，PB）中 T 淋巴细胞亚群，探讨其在隐源性机化性肺炎诊断中的价值。
方法 选取 45 例隐源性机化性肺炎患者（观察组）及 30 例健康体检者（对照组）为研究对象，应用流式细胞仪检测其 BALF 及 PB 中 T 细胞亚群，并比较其差异性。
结果 观察组 BALF 和 PB 中 CD3+CD4+及 CD4+/CD8+比值低于对照组（P<0.05）， CD3+CD8+高于对照组（P<0.05）;观察组 BALF 中 CD3+和 CD3+CD8+显著高于 PB（P<0.05）绘制 ROC 曲线比较显示，BALF 中 T 淋巴细胞亚群检测价值高于 PB，差异具有统计学意义（P<0.05）。
结论 BALF 及 PB 中 T 淋巴细胞亚群检测有助于隐源性机化性肺炎的诊断。

PO-0324

A novel diagnostic predictive index combining TK1, HE4 and CA125 shows better performance than the risk of ovarian malignancy algorithm (ROMA) for premenopausal women with a pelvic mass

Cheng Zhu[2]、Renquan Lu[1,2]、Lin Guo[1,2]、Ailing Zhong[2]、Kangjia Xiao[2]
1. 复旦大学上海医学院肿瘤学系
2. 复旦大学附属肿瘤医院检验科

Objective The purpose of this study was to create a new diagnostic index ROMI (Risk of Ovarian Malignancy Index) developed from Risk of Ovarian Malignancy Algorithm (ROMA) by combing thymidine kinase 1 (TK1), HE4 and CA125, and to explore whether it presented stronger diagnostic capabilities in distinguishing malignant ovarian tumors from benign masses than ROMA.
Methods A total of 385 patients with a pelvic mass on imaging and 46 healthy controls were enrolled in analysis. ROMI was set up according to backward stepwise conditional logistic regression with univariate and multivariate analysis. Serum TK1, HE4 and CA125 were measured on preoperative samples. ROMI, ROMA, TK1, HE4 and CA125 were evaluated for sensitivity, specificity, accuracy, positive predictive value and negative predictive value. TK1 was analyzed in the cohort for all, pre- and postmenopausal women. For continues variables, the significance of differences was tested by Mann-Whitney U test or Wilcoxon signed-rank test according to comparison of independent samples or paired samples. The Fisher's exact test was used to compare decline rates of TK1 before and after surgery. The McNemar test was utilized for comparing sensitivity, specificity and accuracy of tumor markers. The diagnostic performances of ROMI, ROMA, TK1, HE4 and CA125 were evaluated by the receiver operating characteristic (ROC) curve and the area under the ROC curve (AUC) with 95% confidence intervals (95%CI). When p values were <0.05, the differences among various groups or AUCs were considered as statistically significant.
Results The levels of TK1 in benign masses were significantly higher for premenopausal women than for postmenopausal women (1.23 vs 1.11, p<0.001). For premenopausal women, ROMI had better specificity (0.939 vs 0.816, p=0.002) and accuracy (0.894 vs 0.825, p=0.013) than ROMA and comparable sensitivity (0.846 vs 0.835, p=1.000). Besides, at a set specificity of 0.800, ROMI had better sensitivity (0.901 vs 0.835, p=0.031) than ROMA; For postmenopausal women, ROMI had comparable sensitivity, specificity and accuracy with ROMA. The cut-off values of TK1 were 2.35 pmol/L and 1.27 pmol/L for pre- and postmenopausal women with a pelvic mass, respectively. For all, TK1 was elevated in malignant ovarian tumor group comparing to that in groups of healthy control and benign mass. The preoperative serum level of TK1 reduced significantly after surgery for all (p<0.001), pre- (p<0.001) and postmenopausal (p<0.001) women. Among 106 patients, a total of 31 cases accounting for 93.9% of tested premenopausal patients and 69 cases accounting for 94.5% of tested postmenopausal patients showed a downward trend for TK1 levels when compared to the preoperative levels. The decline rates between pre- and postmenopausal women showed no significant difference (p=1.000). The expression of TK1 was found to be positively correlated with the presence of intrapelvic metastasis (p<0.001), lymphatic metastasis (p<0.001) and distant metastasis (p<0.001). And there was a significant difference of serum levels of TK1 between stage I+II and stage III+IV patients (3.23 vs 13.53, p<0.001).
Conclusions ROMI shows better diagnostic performance than ROMA in distinguishing benign masses and malignant ovarian tumors for premenopausal women. The cut-off values of TK1 differ for pre- and postmenopausal women with a pelvic mass.

PO-0325

外泌体与自身免疫性疾病的发展现状与研究进展

袁成良、曹维维
德阳市人民医院

外泌体作为由细胞膜分泌的细胞外小泡的一种，可被多种免疫以及非免疫细胞分泌。由于其可传递多种来自源细胞的蛋白质，核酸和脂类等，在细胞间的局部和系统的信息交流中起到重要作用。外泌体涉及多种生理过程，广泛地参与到炎症、自身免疫性疾病和肿瘤的发生和发展中。对于外泌体的深入研究有助于我们更完整和系统地了解炎症和免疫反应的发生机制，并在作为疾病的检测和治疗中体现了巨大的潜力。本文主要从外泌体参与免疫反应的过程以及与自身免疫性疾病的关系方面进行探讨。

PO-0326

血清磷脂酰肌醇蛋白聚糖 3 在 HBV 相关 HCC 早诊中价值

刘秀红、姜菲菲、李鑫、李宁、娄金丽
首都医科大学附属北京佑安医院

目的 组织磷脂酰肌醇蛋白聚糖 3（GPC3）表达在 HCC 诊断中起重要作用，但因有创性受到限制。血清 GPC3 在 HCC 早期诊断中的效能，因入组患者、所用试剂和方法等不同而不同。本研究用有望上市的试剂对临床上诊治的患者分层研究，其目的是要明确血清 GPC3 在 HBV 相关 HCC 中早诊价值，为临床诊断提供数据。
方法 收集 2010 年 1 月至 2020 年 9 月，在北京佑安医院就诊的有 HBV 感染的 561 例患者和 154 例健康对照者的血清，其中慢乙肝 75 例、肝硬化 94 例、初治的肝癌患者 392 例，按巴塞罗纳分期分为极早期 69 例、早期 77 例、进展期 182 例、晚期 64 例。AFP 检测是用电化学发光法（Cobase601，德国罗氏，正常值<7ng/mL)；DCP 检测用化学发光酶免疫法（Cobase601，日本富士必欧，正常值<40ng/mL)；使用酶免疫试剂盒（CanAg-Glypican-3 EIA，FUJIREBIO，Diagnostics，Inc.）测定 GPC3。应用受试者操作特征（ROC）曲线分析 AFP、DCP 和 GPC3 的单独和联合诊断 HCC 能力。
结果 当 HCC 和非 HCC 比较时，DCP 的 AUC 为（0.850，95%CI:（0.821-0.879））高于 AFP 和 GPC3；当比较早期 HCC 和非 HCC 时，GPC3 的 AUC 为（0.822，95%CI:（0.759-0.886））高于 AFP 和 DCP。在 HCC、早期 HCC 以及非常早期 HCC 与非 HCC 相比时，AFP+DCP+GPC3 的 AUC 分别为（0.907，95%CI:（0.886-0.929））,（0.822，95%CI:0.781-0.863）和（0.768，95%CI:0.710-0.827），高于任何二者的联合。
结论 GPC3 无论单独还是联合均有从非肝细胞癌中诊断出极早期肝细胞癌的价值。

PO-0327

Decreased peripheral blood ALKBH5 correlates with markers of autoimmune response in systemic lupus erythematosus

罗清、黄自坤、李俊明
南昌大学第一附属医院

Although it has been proved that the epigenetic modification is involved in the pathogenesis of SLE, there is no study to explore whether the modification of m6A in RNA is involved. In this

study, the levels of m6A writers, erasers and readers in peripheral blood were determined by qRT-PCR. The results demonstrated that the levels of METTL3, WTAP, FTO, ALKBH5 and YTHDF2 in peripheral blood from SLE patients were significantly decreased. The levels of ALKBH5 in SLE patients were associated with anti-dsDNA, anti-nucleosome, rash and ulceration. Multivariate logistic regression analysis showed that the level of ALKBH5 is a risk factor of SLE. This study suggests that the mRNA level of ALKBH5 in peripheral blood may involve in pathogenesis of SLE.

PO-0328

Serum exosomal EphA2 is a prognostic biomarker in patients with pancreatic cancer

Qian Wei
Tianjin Medical University Cancer Institute and Hospital

Background Pancreatic cancer (PC) has one of the worst prognoses of malignant diseases. It is of great significance to identify biomarkers with predictive clinical value for its prognosis and recurrence.
Methods In our study, enzyme-linked immunosorbent assays (ELISA) were used to detect the expression of Exo-EphA2 in the serum of PC patients and controls. Kaplan-Meier curve and Cox regression analyses were used to evaluate the prognostic value of Exo-EphA2 expression in patients with primary and recurrent PC.
Results The level of serum Exo-EphA2 was significantly higher in the PC group than in the control group. High expression of Exo-EphA2 in PC was associated with shorter overall survival (OS), and proved to be a significant negative prognostic factor in the multivariate analysis (HR = 1.04, 95%CI: 1.00-1.09, P <0.001). Additionally, we found that the level of serum Exo-EphA2 in recurrent PC patients (first recurrence < 12 months) was positively correlated with the level of Exo-EphA2 at primary diagnosis. Multivariate analysis showed that a high expression of Exo-EphA2 in recurrent PC was associated with shorter recurrence-free survival (RFS) (HR = 1.41, 95% CI: 1.10-1.70, P < 0.001).
Conclusion High expression of serum Exo-EphA2 represents a biomarker of poor prognosis in pancreatic cancer patients.

PO-0329

Prognostic values of tumor immune microenvironment related genes in Ovarian Cancer:A gene expression-based study

Ze Li[1]、jing tian[2]、li ren[1]
1. Tianjin medical university cancer institute and hospital
2. 天津医科大学肿瘤医院妇科肿瘤科

Ovarian cancer is the most common malignant diseases in women and the leading cause of cancer-related death. The high mortality rate of ovarian cancer stems from a variety of factors, such as difficulty in screening, delayed diagnosis and limited treatment options. In The Cancer Genome Atlas (TCGA) ovarian cancer cohort, based on the tumor microenvironment cell infiltration level and immune-related genes, we tried to systematically determine predictive molecular networks and key genes as prognostic markers. We identified 13 nodes(hub-genes) in ovarian cancer, functional annotations indicated that the 13 hub-genes were mostly involved in Cell adhesion molecules (CAMs) , Natural killer cell mediated cytotoxicity， Leukocyte trans endothelial migration , TNF signaling pathway ,Phagosome ,etc.

Kaplan-Meier method indicated that expression of C3AR1, CD86, CXCL10 and FN1 significantly correlated with favorable outcome for OS (p<0.001). Moreover, we found that these genes also correlation with level of immune infiltrates (Macrophages, NK cells, Neutrophils). C3AR1, CD86, CXCL10 were significantly positive correlation with several immune checkpoint genes(PDCD1, PDCD1LG2, CTLA4, CD80)（average correlation coefficient was 0.71）. In summary, we identified genes that are potentially associated with prognosis, while also being correlated with immune checkpoint expression. So, whether it can be used as an evaluation indicator for immunotherapy needs further study.

PO-0330

The Roles of Host Noncoding RNAs in Mycobacterium tuberculosis Infection

Li Wei、Haixin Dong、Qingli Bie、Bin Zhang
Department of Laboratory Medicine, Affiliated Hospital of Jining Medical University, Jining Medical University

Tuberculosis (TB), which is caused by the intracellular pathogen Mycobacterium tuberculosis (M. tuberculosis), remains the leading cause of death from a single infectious agent (ranking higher than HIV/AIDS). Tuberculosis remains a major health problem. Mycobacterium tuberculosis, the causative agent of tuberculosis, can replicate and persist in host cells. Noncoding RNAs (ncRNAs) widely participate in various biological processes, including Mycobacterium tuberculosis infection, and play critical roles in gene regulation. In this review, we summarize the latest reports on ncRNAs (microRNAs, piRNAs, circRNAs and lncRNAs) that regulate the host response against Mycobacterium tuberculosis infection. In the context of host-Mycobacterium tuberculosis interactions, a broad and in-depth understanding of host ncRNA regulatory mechanisms may lead to potential clinical prospects for tuberculosis diagnosis and the development of new antituberculosis therapies.

PO-0331

新型冠状病毒 S 蛋白全长及受体结合区单克隆抗体的制备、鉴定和应用

范笑地、陈满君、余楠、温坤
南方医科大学珠江医院

目的 2019 年 12 月，湖北武汉爆发了由新型冠状病毒（nCoV-19）引起的新冠肺炎（COVID-19）疫情，已在全世界迅速蔓延，对人类的生命健康产生了严重的威胁。新型病毒可藉由刺突蛋白（S）的受体结合区（RBD）与人类细胞膜表面的血管紧张素转化酶 2（ACE2）受体的特异性结合而进入细胞，可诱导中和性抗体的产生。并且 S 蛋白是病毒最大的主要结构蛋白，具有很好的抗原性，有望成为检测 nCoV-19 的重要抗原靶标。因此，制备识别 S 蛋白的单克隆抗体，筛选高中和活性抗体，将成为研究 S 蛋白的结构和功能、发病机制等的重要工具。
方法 采用真核表达具备天然结构的三聚体 S 蛋白和 RBD 区免疫或加强免疫 BALB/c 小鼠，采用传统的杂交瘤细胞融合技术和 ELISA 的方法进行杂交瘤的制备和克隆筛选。进一步采用间接 ELISA、免疫印迹、生物膜层干涉技术（BLI）、细胞实验对抗体的效价、亲和力、识别位点及中和活性进行测定。最后，使用识别不同表位的 S 单抗，尝试各种组合配对，初步建立了双抗体夹心 ELISA 方法检测 nCoV-19 的 S 抗原。
结果 获得 19 株针对 nCoV-19 S 蛋白的单克隆抗体，其中 12 株结合 S 蛋白的 RBD 区，均具有不同程度的中和活性，5 株在体外细胞中和实验中表现出较高中和滴度（>1:320）。IgG 亚类鉴定显示：19 株抗体中，10 株为 IgG1，5 株为 IgG2a，4 株为 IgG2b。18 株 S 蛋白单抗至少识别 4 个以

上抗原位点。10 种优化配对组合检测 S 蛋白灵敏度均达 3.125ng/ml，其中仅 G1 和 G3 两个组合可检测到病毒培养上清液中的病毒抗原，灵敏度可达 10 TCID50/ml。
结论 获得了 nCoV-19 S 蛋白特异性单克隆抗体和具有较高中和活性的抗体，为进一步研究 S 蛋白的结构和功能、开发疫苗和药物等奠定基础。双抗体夹心 ELISA 法检测 S 抗原可做为感染早期诊断方法的一种补充，但其灵敏度仍有待提高。

PO-0332

Serum Nitrotyrosine and Occludin as Biomarkers for Predicting Severity, Hemorrhagic Transformation, and Patient Prognosis in Acute Ischemic Stroke Treated with t-PA Thrombolysis

Bin Wang
Affiliated Hospital of Xuzhou Medical University
徐州医科大学

Background and purpose Acute ischemic stroke (AIS) accounts for 80% to 90% of the total incidence of stroke. The overall prognosis and treatment of ischemia stroke are still unsatisfactory, as t-PA is the only FDA-approved drug, with a narrow treatment time window (4.5hrs). The blood-brain barrier (BBB) damage plays an essential role in cerebral injury and hemorrhagic transformation (HT)after AIS. We investigated the potential role of serum nitrotyrosine and occludin in predicting the severity of AIS, HT (HT), and patient prognosis.
Methods We conducted a correlation analysis study between serum nitrotyrosine and occludin and multiple factors of cerebral injury after t-PA thrombolysis for ischemic stroke in the Affiliated Hospital of Xuzhou Medical University between 2018 and 2020.
The main inclusion criteria in brief: adults, with AIS, receiving t-PA thrombolytic reperfusion therapy. In patients with AIS, serum nitrotyrosine and occludin levels were measured by enzyme-linked immunosorbent assay 24h after t-PA thrombolysis, and the presence and grading of cerebral edema（CED）was assessed by computed tomography, and the presence and grading of HT was assessed by cranial CT or MIR. Clinical outcomes included early neurological function NIHSS (NIH Stroke Scale) and neurological function status at three months. Ordinal regression models and logistic regression models were obtained with adjusted odds ratios and 95% CI(confidence intervals). Receiver operating characteristics analysis in the training cohort was used to define the optimal cutoff values and validated on an independent dataset.
Results We included a total of 594 patients in this research. Serum nitrotyrosine and occludin levels and cerebral injury (CED) adjusted odds ratios were 1.61 [1.34 to 1.93], (P<0.05) and 1.92 [1.61 to 2.43], (P<0.05), respectively; early neurological deterioration (NIHSS) adjusted odds ratios were 1.64 [1.33~1.94], (P<0.05) and 1.95 [1.58~2.24], (P<0.05); adjusted odds ratios for HT were 1.95 [1.58~2.64], (P<0.01) and 1.42 [1.13~1.73], (P<0.05); adjusted odds ratios for 90d functional status were 1.32 [1.01 to 1.53], (P<0.05) and 1.43 [1.18 to 1.74], (P<0.05), respectively. Serum nitrotyrosine and occludin levels were the best predictors of t-PA thrombolysis for AIS, with the area under the curve for nitrotyrosine and occludin being approximately 0.7 and 0.9, respectively.
Conclusions Serum nitrotyrosine and occludin levels in patients with AIS after t-PA thrombolytic reperfusion therapy can be used for the assessment of cerebral injury and HT and to predict the severity of AIS and prognosis after a short period.

PO-0333

Soluble Tim-3/Gal-9 as predictors of adverse outcomes after kidney transplantation: a cohort study

Yan Yang[1]、Lin Yan[2]、Yamei Li[2]、Yi Li[2]
1. West China Clinical Medical College, Sichuan University
2. 四川大学华西医院

Purpose T cell immunoglobulin and mucin domain-3 (Tim-3) and its ligand, galectin-9 (Gal-9), play an important role in immune regulation. Serum soluble Tim-3 (sTim-3) and Gal-9 (sGal-9) were observed to be correlated with renal function after kidney transplantation in our previous study, but whether these two could predict the adverse outcomes after transplantation is unknown.
Methods 91 recipients receiving kidney transplantation were enrolled in this cohort study. The expressions of sTim-3 and sGal-9 before and one month after transplantation were measured by ELISA. 20 of all recipients suffered adverse outcomes (consists of biopsy-proven rejection, graft loss, death and clinical rejection) within two years after kidney transplantation. 71 recipients had stable renal function during this period.
Results The level of sTim-3 before transplantation was significantly higher in recipients with stable renal function than adverse outcomes [Median (range), 2275 (840-4236) pg/mL vs 1589 (353-3094) pg/mL, P=0.002]. The level of sGal-9 after transplantation was significantly lower in stable group than adverse outcome group [Median (range), 4869: (1418-13080) pg/mL vs 6852: (4128-10760) pg/mL, P=0.003]. Area under curve (AUC) of sTim-3 before transplantation was 0.737 (P=0.002) through the analysis of receiver operating characteristic curve (ROC curve). AUC of sGal-9 after transplantation was 0.751 (P=0.003). After survival analysis, the percentage of recipients free from adverse outcomes was significantly lower in patients with low level of sTim-3 than high sTim3 (P<0.0001), so was in patients with high sGal-9 than low sGal-9 (P=0.0004). Post-eGFR had greater diagnosis sensitivity on adverse outcomes than pre-Tim-3 (85.0% vs 71.0%) and had lower sensitivity with post-Gal-9 (85.0% vs 92.9%). While pre-Tim-3 and post-Gal-9 had greater specificity compared with post-eGFR (83.3% vs 43.7% and 59.4% vs 43.7%).
Conclusion Serum sTim-3 and sGal-9 could predict the adverse outcomes within two years after kidney transplantation.

PO-0334

一种位于登革病毒特异性表位多肽筛选及其应用

林亚英
南方医科大学珠江医院

目的 鉴定 I 型登革病毒（denguevirus，DENV）感染病人中 NS1 蛋白 B 细胞表位，并以鉴定得到的 DENV 特异性表位建立一种 IgM 检测方法，探索这种方法在登革热诊断的应用价值。
方法 采用 10 名 2006 年广州地区 1 登革病毒感染病人血清和 1 组覆盖 DENV-1NS1 的重叠多肽（20 肽）反应来定位 I 型登革病毒非结构蛋白 1 上 B 细胞表位。根据筛选结果对阳性多肽进行进一步的生物信息学分析和多肽分析，筛选出具有 DENV 特异性的多肽片段。构建高反应性多肽三聚体-pBVIL1 质粒，在大肠杆菌表达系统制备的重组全长三聚体蛋白，以该重组蛋白作为抗原，建立 DENV IgM 抗体间接 ELISA。用这种方法检测来自同一组 80 例 2014 年 DENV-1 感染患者血清标本和 100 名健康人体检血清标本，并将其检测的敏感性与商品化的 Panbio DENV IgM 抗体捕获 ELISA 试剂盒进行对比.
结果 筛选得到 DENV 保守肽段 269-HLGKLELDF-277 能够识别 DENV 阳性血清。构建该多肽三聚体--pBVIL1 质粒，表达纯化重组蛋白构建间接 ELISA 试剂盒同 2014 年 DENV-1 感染病人血清反应。本研究所提供的 NS269 三聚体抗原能与 2014 年广州登革热疫情中 80 份 DENV-RNA 阳性患者血清（发病后 3-5 天血清）中 68 份发生阳性反应，检出率为 85%，上述 80 份样品采用澳大利

亚 panbio 公司登革热 IgM 捕获试剂盒检测，65 份样品阳性，其中 64 份同本发明提供的 NS269 三聚体抗原检测结果一致，同 panbio 公司登革热 IgM 捕获试剂盒检测结果无差异（P<0.01）。NS269 三聚体抗原与 100 份健康人血清无交叉反应特异性为 100%。

结论 NS269 抗原具有 DENV 特异性的免疫学活性，其检测结果同国外同类产品具有较好的一致性，可用于检测 DENV IgM 抗体，在 DENV 诊断试剂研究中具有一定的应用价值。

PO-0335

Tim-3 on NK Cells Associated with Disease Activity in SLE

Di Zhao
qilu hospital of shandong university

T cell immunoglobulin and mucin domain-containing molecule-3(Tim-3) has been found to play important roles in systemic lupus erythematosus(SLE), but whether Tim-3 is involved in depletion of NK cells in SLE pathogenesis remains unknown. In this study, we firstly observed a decreased proportion of CD3−CD56+ NK cells and an increased proportion of AnnexinV+NKcells in SLE patients. The proportion of AnnexinV+NKcells was positively correlated with anti-dsDNA and SLEDIA. Tim-3 expression on NK cells was up-regulated in SLE patients. Further analysis showed that Tim-3 expression on NK cells was negatively correlated with the proportion of AnnexinV+NKcells, anti-dsDNA and SLEDIA, while positively correlated with the proportion of NK cells.The present results suggest that Tim-3 might participate in the progression of SLE by protecting NK cells from apoptosis and Tim-3 might serve as a potential target for the treatment of SLE.

PO-0336

TIPE2 对肝细胞肝癌生长转移的影响和机制研究

曹雪蕾
山东大学齐鲁医院

目的 肝细胞肝癌是最常见的人类恶性肿瘤之一，其显著特点是容易发生侵袭和转移。因此，寻找能抑制肝癌生长和转移的分子，对肝癌的治疗具有十分重要的价值。TIPE2 是最近新发现的免疫负调控分子，前期研究发现 TIPE2 在人肝细胞肝癌组织中表达下调或缺失，为了明确 TIPE2 在肝细胞肝癌中的作用并阐明其作用机制，我们进行了如下研究。

方法 1. 免疫组化方法检测肝癌组织中 TIPE2 表达，并且分析其与临床病理特征之间的相关性。

2. 将 TIPE2 过表达载体转染入肝癌细胞系，检测细胞增殖、克隆形成以及细胞迁移和侵袭。

3. 建立裸鼠皮下和原位肝癌移植瘤模型，给与 TIPE2 质粒治疗，绘制肿瘤生长曲线，测量肿瘤体积和重量，观察肺转移情况。

4. 免疫共沉淀方法检测 TIPE2 能否与 Rac1 结合，并构建了 TIPE2 突变载体。进行免疫共沉淀并检测 Rac1 的活性。

5. 转染突变载体检测细胞迁移和侵袭，观察细胞骨架以及基质蛋白水解酶的表达。

结果 1. TIPE2 表达与 TNM 分期有显著相关性，TIPE2 表达降低或缺失与肝癌的侵袭转移有关。

2. 转染 TIPE2 后细胞生长明显减缓，克隆形成数明显减少，细胞迁移和侵袭的数量均明显降低。

3. TIPE2 组皮下瘤以及原位肿瘤相比于对照组明显减小，并且发生肺转移的比例降低。

4. 内源性 TIPE2 能够与 Rac1 结合，并且野生型 TIPE2 与 Rac1 的结合会降低
Rac1 的活性，而突变的 TIPE2 与 Rac1 的结合能力降低，并且能逆转其抑制效应。

6. 野生型 TIPE2 能够减少微丝的聚合，并且降低了 MMP9 和 uPA 水平，而突变载体的抑制作用消失。

结论 通过以上实验我们可以得出以下结论，TIPE2 通过 Rac1 通路抑制细胞骨架的聚合以及 MMP9 和 uPA 表达，进而抑制肝癌细胞的转移。

PO-0337

IL-2/4/6 通过自噬调节非对称氨基酸甲基化 90kDa 核蛋白的表达

曹雪蕾
山东大学齐鲁医院

目的 蛋白精氨酸甲基化修饰介导产生非对称性二甲基精氨酸（aDMA）和对称性二甲基精氨酸（sDMA）。目前，肿瘤微环境中低氧、饥饿或细胞因子是否调节 aDMA 或 sDMA 尚未得知。
方法 Western Blot 检测肿瘤细胞中内源性以及应用白介素和（或）雷帕霉素刺激的 aDMA 和 sDMA 修饰蛋白的表达及核定位或自噬关键分子 LC3 的表达。应用甲基化转移酶抑制剂 AdOx 后，Western Blot 检测经白介素处理的乳腺癌细胞中 p90aDMA 和 p70aDMA 的表达。应用自噬抑制剂 3-MA 或自噬相关基因 ATG5 的小干扰后，Western Blot 检测经雷帕霉素处理的乳腺癌细胞中 p90aDMA 和 p70aDMA 的表达。
结果 我们发现 aDMA 或 sDMA 修饰的分子量 70 或 90 kDa 的蛋白 p90aDMA、p70aDMA 和 p90sDMA 广泛表达于乳腺癌细胞系中。值得关注的是白介素 IL-2、IL-4 和 IL-6 而非 IL-8 促进 p90aDMA 而非 p90sDMA 在核中积聚；并且上述效应受到 AdOx 的抑制。这表明肿瘤细胞中内源性蛋白受到 aDMA 的修饰作用。而且，乳腺癌和宫颈癌细胞对低氧、饥饿和雷帕霉素发生应激，导致内源性 aDMA 修饰的蛋白的降解。然而，IL-2/4/6/8 对乳腺癌细胞中基础水平和雷帕霉素诱导的自噬无显著影响。但阻断自噬能逆转雷帕霉素诱导乳腺癌细胞中 p90aDMA 和 p70aDMA 蛋白降解。与之相反，雷帕霉素诱导乳腺癌细胞中 p90sDMA 的聚集。
结论 我们的研究加深了在不同应激反应中精氨酸甲基化调节网络复杂性的认识，并且首次证实了 aDMA 作为选择性自噬降解底物的特异性信号。

PO-0338

Effect of miRNA-200b on the proliferation and apoptosis of cervical cancer cells by targeting RhoA

Lijie He
Tianjin Fifth Central Hospital

Objective The paper aims to investigate the effect of miRNA-200b on the proliferation and apoptosis of cervical cancer cells by targeting RhoA.
Methods HeLa cells of cervical cancer were divided into five groups: blank control group, negative control group (miRNA-200b mimic NC), miRNA-200b mimic group, RhoA negative control group, and RhoA overexpression group. Cells were collected 48 hours after transfection. The expression levels of miRNA-200b were detected by RT-PCR. Target relationship between miRNA-200b and RhoA was verified by dual-luciferase reporter assay. RhoA mRNA and protein expression were detected by Western blot and RT-PCR methods. Flow cytometry was used to detect the apoptosis of cells in each group, and CCK8 method was used to detect the proliferation of cells in each group. The mRNA and protein expression of Bax and cyclin D1 were detected by RT-PCR and Western blot.
Results The results of dual-luciferase reporter assay showed that RhoA was the target gene of microRNA 200b. Compared with the blank control group and the miRNA-200b mimic-NC group, the proportion of apoptotic cells increased significantly in the miRNA-200b mimic group, and the proliferation of cells was inhibited ($P<0.05$). After overexpression of RhoA, the percentage of apoptotic cells decreased and the ability of cell proliferation increased significantly ($P<0.05$).

Conclusion miRNA-200b can inhibit the proliferation and promote the apoptosis of cervical cancer cells by targeting RhoA gene.

PO-0339

Preliminary study of serum Cripto-1 in early diagnosis and therapeutic evaluation of gastric cancer

Xin Zhang
Qilu Hospital of Shandong University

Objective To discuss the application value of serum Cripto-1 in the diagnosis and therapeutic evaluation of gastric cancer, which providing reference for clinics.
Methods From January to June 2018, serum specimens of 79 patients with gastric cancer (gastric cancer group), 42 patients with chronic atrophic gastritis (chronic atrophic gastritis group) and 30 healthy subjects (healthy control group) were collected in Qilu Hospital of Shandong University. Cripto-1 was detected by enzyme-linked immunosorbent assay, and carcinoembryonic antigen (CEA) and sugar chain antigen 724 (CA724) were determined by electrochemical immunoluminescence.
Results Levels of serum Cripto-1 in gastric cancer group, chronic atrophic gastritis group and healthy control group were [3.76（1.42-9.73）]μg/L, [0.71（0.34-0.86）] μg/L and [0.36（0.285-0.515）] μg/L, and a significant difference was observed among 3 groups（P<0.001）. Among them, levels of serum Cripto-1 in gastric cancer group were significantly higher than those in chronic atrophic gastritis group and healthy control group（all P<0.05）; levels in chronic atrophic gastritis group were significantly higher than those in healthy control group（P<0.05）. Levels of serum CEA [3.46（2.15-4.59）] U/L and CA724 [3.45（2.44-4.75）] U/L were only significantly increased in gastric cancer group. The area under the receiver operating characteristic curve for gastritis group diagnosis was 0.818（95%CI：0.747～0.876）, significantly higher than CEA and CA724（all P<0.05）. For gastric cancer patients, serum Cripto-1 were significantly decreased after operation when compared with levels in pre operation （P <0.05）.
Conclusion Serum Cripto-1 is increased in patients with gastric cancer, then declined after operation, with higher diagnostic value than CEA and CA724, which is a potential index for the diagnosis and therapeutic evaluation of gastric cancer.

PO-0340

B7-H3 在习惯性流产患者外周血中的表达探讨

冯萍
苏州大学附属第二医院

目的 通过检测习惯性流产患者外周血单核细胞 B7-H3 的表达，分析 B7-H3 在习惯性流产中的作用，为习惯性流产患者的临床治疗提供理论依据。
方法 采用流式细胞仪检测习惯性流产患者外周血单核细胞 B7-H3，采用酶联免疫吸附实验检测习惯性流产患者血清可溶性 B7-H3（sB7-H3），采用 CBA 方法检测习惯性流产患者血清 Th1/Th2 细胞因子，包括 Th1 型（IL-2、IFN-γ 和 TNF-α）、Th2 型（IL-4、IL-6 和 IL-10）。
结果 （1）习惯性流产患者外周血 CD14+单核细胞比例分别低于正常组、妊娠组和流产且妊娠组，均有显著差异（P＜0.05）；习惯性流产患者外周血 CD14+单核细胞 B7-H3 的表达水平分别明显高于正常组、妊娠组和流产且妊娠组，均有显著差异（P＜0.05）。妊娠女性孕周 3 个月、6 个月、9 个月分别按孕周、年龄分组，B7-H3 的表达水平没有显著差异。习惯性流产组血清 sB7-H3 水平和妊娠组均高于正常组和流产且妊娠组，均有显著差异（P＜0.05）。

（2）流产且妊娠组血清细胞因子 IL-2 分别高于正常组、妊娠组、习惯性流产组，均有显著差异（P＜0.05）；习惯性流产组、流产且妊娠组和妊娠组血清细胞因子 IL-4 均分别低于正常组，有显著差异（P＜0.05）；流产且妊娠组血清细胞因子 IL-6 分别高于正常组、妊娠组、习惯性流产组，均有显著差异（P＜0.05）；流产且妊娠组血清细胞因子 IL-10 分别高于正常组、妊娠组、习惯性流产组，均有显著差异（P＜0.05）。

结论 习惯性流产患者外周血单核细胞 B7-H3 高表达且存在 Th1/Th2 失衡现象，同时 B7-H3 与 IL-4 呈正相关，B7-H3 可能参与了习惯性流产的发病机制。

PO-0341

快速量子点荧光免疫层析法白介素 6 试剂盒的研发

唐劲松
东莞市大朗医院

目的 研发出快速检测白介素 6（IL-6）的量子点荧光免疫层析法试剂盒。

方法 通过量子点荧光材料标记 IL-6 抗体，研发出一种能快速定量检测 IL-6 浓度的量子点免疫荧光层析法试剂盒,通过对不同浓度标准品测量，绘制出标准曲线，计算剂盒的线性检测范围，并验证其灵敏度、回收试验、精密度、特异性、稳定性及与贝克曼 IL-6 发光试剂盒的相关性。

结果 试剂盒线性范围为 10-4000pg/mL，在此线性范围内，试剂盒线性相关系数 r≥0.950；灵敏度≥2pg/mL；在 50pg/mL 浓度的回收率在 90.5%-111.8%，变异系数为 8.57%，在 2500 pg/mL 浓度的回收率在 84.5%-110%，变异系数为 6.99%，在 5000pg/mL 浓度的回收率在 93.5%-106.3%，变异系数为 4.76%； 批内精密度其变异系数（CV）2.2%-3.9%，批间精密度其变异系数（CV）2.4%-5.3%；特异性实验中白介素-4、干扰素 γ 在实验中并未检测到；白介素-1α、白介素-1β、白介素-2、白介素-8 的交叉反应率均小于 0.1%；稳定性试验中试剂卡放在 50℃烘箱中加速破坏 1 周、2 周、3 周、4 周后与常温保存的试剂卡在低、中、高浓度的荧光信号 T/C 值基本没变化；本试剂盒与贝克曼发光法 IL-6 检测试剂盒进行 200 例临床样本检测比对，结果基本一致，回归方程为 y = 0.9894x+2.9985，R2 =0.9971，相关性良好。

结论 本试剂盒灵敏度、准确性、精密度、特异性及稳定性都较好，能够准确、快速的完成临床样品 IL-6 浓度的定量检测。

PO-0342

中国人群类风湿关节炎相关 TGIF rs73620203 基因多态性研究

谭慧玲、张丽静、任如钰、赖红历、王雪安、王莉、杨滨
四川大学华西医院

目的 本研究旨在全面探讨 TGIF 基因多态性（SNPs）与血清骨代谢指标和 RA 易感性的关系。

方法 在本项病例对照研究中，我们通过高分辨率熔解（HRM）分析对 155 例 RA 患者和 168 例健康对照者的 TGIF 基因中的 3 个 SNP 进行基因分型，用电化学发光法检测了 108 名随机选择的 RA 患者的血清骨钙素、骨碱性磷酸酶（BALP）和 βI 型胶原交联的 C 端肽（β-CTX）的含量。

结果 基因型和等位基因频率分析表明，rs73620203 与 RA 骨侵蚀有关（分别为 P = 0.012，P = 0.003），携带 rs73620203 的 T 等位基因的个体显示 RA 风险降低（OR = 0.59，95％CI = 0.42-0.84；P = 0.003）。在针对性别的分析中，rs73620203 多态性与女性 RA 患者的骨侵蚀有关（分别为 P = 0.022，P = 0.006）。 此外，rs73620203 基因座处为 TT 基因型的 RA 患者的血清骨钙素和 BALP 显著低于 CC 和 CT 基因型 RA 患者（分别为 P = 0.006，P = 0.037）。单倍型分析表明，RA 组单倍体 ATG，GCA 频率明显降低（分别为 P = 0.036，OR = 0.693；P = 0.002，OR = 0.189），而单倍体 ACA 频率升高（P = 1.70×10-6，OR = 5.058）。

结论 我们的研究首次表明 rs73620203 基因多态性与 RA 的骨侵蚀有关，并为了解不同性别的 RA 患者 TGIF 基因中的三个 SNP 与骨代谢调节之间的关系提供了新的见解，我们需要扩大样本量并进行进一步的功能实验验证我们的实验结果。

PO-0343

Expression and clinical significance of CXCL10 and CXCL11 in primary biliary cholangitis

Yan Liang[1]、Lin Zhou[1]、Hong Shi[1]、Zhong Renqian[1]、Zaixing Yang[2]
1. Department of Laboratory Diagnostics, Changzheng Hospital, Naval Medical University, Shanghai, China
2. 浙江台州第一人民医院

Objective To determine serum chemokine CXCL10 and CXCL11 and to explore the association with development and progression of PBC.
Methods Sixty PBC patients and thirty healthy controls (HC) were enrolled. The sera were detected for CXCL10 and CXCL11 using multiplex immunoassay. The expression of CD3 in portal areas of liver tissues was determined by immunohistochemistry in 6 PBC patients.
Results Serum concentrations of CXCL10 and CXCL11 were higher in PBC patients than HC (P<0.05). PBC stage and bilirubin were correlated inversely with CXCL11(r=-0.262, -0.315, P=0.043, 0.014). There were significant correlations between serum levels of CXCL10 (r=0.971, P=0.001) and CXCL11 (r=0.883, P=0.020) and CD3 expression within portal areas. In PBC patients, there were significant correlations between CXCL10 and CXCL11(r=0.744, P<0.01).
Conclusion Serum levels of CXCL10 and CXCL11 are increased in PBC patients, which are correlated with infiltration of CD3+T lymphocytes.

PO-0344

应用新型纳米探针检测 α 肿瘤坏死因子的光电化学免疫测定方法

张明明
东南大学附属中大医院

目的 肿瘤坏死因子-α（TNF-α）是一种细胞因子，主要是由单核细胞和巨噬细胞产生，是引发炎症和先天免疫的关键蛋白之一。 TNF-α 是许多疾病的潜在生物标志物，例如类风湿性关节炎、神经变性疾病、肺癌和卵巢癌等，因此 TNF-α 的检测具有非常重要的临床意义。本研究将开发一种高灵敏度高特异性的新方法用以 TNF-α 的检测。
方法 首先，我们选用芘四甲酸二酐衍生物（PTCNH2）作为光活性的光电化学免疫测定探针。 为提高光电化学免疫传感器的性能，氧化石墨烯（GO）被用作纳米载体和电子介体，与 PTCNH2（GO-PTCNH2）形成纳米杂化物，由于此纳米杂化物具有大的表面积，良好的电子传导性和丰富的羧基，故被用于衔接后续的生物分子。在通过其固定在电极上的抗体（抗-TNF-α）捕获 TNF-α 后，由于抗原蛋白的空间位阻和绝缘性，源自 GO-PTCNH2 的光电流强度将降低，由此构建出基于 GO-PTCNH2 的 PEC 免疫传感器。
结果 通过实验数据，我们统计出线性检测范围为 10pg / mL-100ng / mL，检测限（LOD）为 3.33pg / mL。 该方法还成功应用于人血清中 TNF-α 的检测，回收率为 92.5％~96.6％，相对标准偏差小于 9.99％。
结论 本研究开发了一种检测 TNF-α 的简单且经济有效的新方法。PTCNH2 作为主要光电流源，而 GO 通过增加生物分子负载和光电流强度而充当有效的纳米载体和电子介体。实验证明此方法具有显著的可靠性和实用性，可用于实际样品的检测。这种具有高灵敏度和高选择性的光电化学免疫传感器为疾病的早期筛查和诊断提供了希望。

PO-0345

NF-κB 参与细菌感染诱导的 DcR3 表达升高

陈洪卫
上海市松江区中心医院

目的 利用体外细胞实验研究细菌感染诱导 DcR3 表达升高的信号转导机制。
方法 流式细胞术检测细胞表面 Toll 样受体 2（TLR2）和 Toll 样受体 4（TLR4）的表达，脂多糖（LPS）、脂磷壁酸（LTA）以及酵母聚糖（zymosan）刺激细胞以及采用特异性抑制剂阻断 NF-κB 和 MAPK 信号通路后，ELISA 法检测细胞培养上清中 DcR3 的表达，Real-time PCR 法检测细胞内 DcR3 mRNA 表达水平，Western-blot 法检测细胞内 DcR3 蛋白的表达。
结果 HUVEC 细胞表面既表面 TLR2，也表达 TLR4 受体；中，高浓度的 LPS、LTA 以及 zymosan 刺激细胞 24 后，细胞培养上清中 DcR3 的表达较未刺激组明显升高（P<0.05）。细胞内 DcR3 mRNA 和蛋白的表达随刺激时间的延长和浓度的升高也明显升高（P<0.05）。通过阻断 NF-κB 通路，细胞以及上清液中 DcR3 表达较刺激组均明显下降（P<0.05），而阻断 P38 MAPK 通路对细胞及上清液中 DcR3 表达无明显影响。
结论 LPS、LTA 以及 zymosan 通过激活 NF-κB 信号通路诱导 HUVEC 表达 DcR3。

PO-0346

妊娠糖尿病(GDM)患者血清羟自由基（·OH）、谷胱甘肽过氧化物酶(GSH-PX)的变化

徐敏
昆明市延安医院

目的 通过测定正常妊娠妇女和妊娠糖尿病妇女体内羟自由基（·OH）、谷胱甘肽过氧化物酶(GSH-PX)的含量，探究其与氧化应激的关系及在妊娠糖尿病发病中作用。
方法 选取 2017 年 8 月～2018 年 2 月来我院诊治的 GDM 患者 20 例作为实验组，正常孕妇 20 例作为对照组，分别应用分光光度法测定每组抑制羟自由基(·OH)能力和 GSH-PX 的活力。
结果 实验组抑制羟自由基能力较对照组显著升高（P<0．05)、GSH-PX 活力较对照组显著下降（P<0．05)
结论 OH 含量升高，GSH-PX 含量的下降影响着机体的氧化应激状况，对妊娠糖尿病的发生具有重要作用。

PO-0347

血清血脂指标在糖尿病视网膜病变患者中的变化及影响因素

刘真真、邵明希、李圣杰、曹文俊
复旦大学附属眼耳鼻喉科医院

目的 探究血清血脂指标在糖尿病视网膜病变（DR）患者中的变化及影响因素。
方法 采用回顾性病例研究。纳入 2018 年 1 月至 2020 年 12 月在我院眼科确诊的糖尿病视网膜病变患者 146 例（糖网组），同期进行健康体检的年龄、性别匹配的健康体检者 189 例（对照组）。检测两组研究对象外周静脉血清甘油三酯（TG）、总胆固醇（TC）、脂蛋白 A（ApoA）、脂蛋白 B（ApoB）、高密度脂蛋白胆固醇（HDL）、低密度脂蛋白胆固醇（LDL）。两独立样本 t 检验比较两组血脂水平的差异，血脂指标与其他指标的相关性采用 Pearson 相关分析法，多因素 Logistic 回归分析筛选 DR 患者发病的危险因素。

结果 糖网组 TC、ApoA、ApoB、HDL 和 LDL 与对照组相比，均存在显著统计学差异（P<0.05），血清 TG 水平与正常对照组相比无显著统计学差异。Logistic 回归分析提示，ApoA（OR=0.095）、LDL（OR=0.589）、HbA1c（OR=9.234）均是糖尿病性视网膜病变的发病的独立危险因素（P<0.05）。

结论 血脂代谢异常是糖尿病视网膜病变发病的影响因素，加强血脂管理对糖尿病性视网膜病变患者的发病和治疗均有重要的临床意义。

PO-0348

ADAM10-cleaved ephrin-A5 contributes to prostate cancer metastasis

Shibao Li、Chenchen Cai
The Affiliated Hospital of Xuzhou Medical University

ADAM10 promotes the metastasis of prostate cancer, but the specific mechanism is indistinct. In this study, a DU145 cell line with stable overexpression and knockdown of ADAM10 was constructed. Overexpression of ADAM10 significantly promotes cell proliferation, migration, invasion and inhibits apoptosis. At the same time, it is found that ADAM10 can specifically hydrolyze ephrin-A5 and release it outside the cell. Meanwhile, immunofluorescence and immunoprecipitation techniques found that it interacted with EphA3 and ephrin-A5. After overexpression of EphA3, it exerts opposite effects in DU145 (ephrin-A5+) and PC-3 (ephrin-A5±) cell lines. The exogenous ephrin-A5-Fc treatment can reverse its cancer-promoting effect on PC-3 cells and increase the phosphorylation level of EphA3. Tumor-bearing experiments in nude mice showed that, compared with the control group, overexpression of ADAM10 resulted in accelerated growth of the primary tumor in nude mice. The content of ephrin-A5 in the tumor tissue decreased, but increased in the peripheral blood; accompanied by an increase in the expression of CD31 and VEGF in the tissue. Finally, Enzyme-linked immunosorbent assay (ELISA) results indicated that the serum ephrin-A5 content of patients with metastatic prostate cancer was significantly higher than that of the non-metastatic group (P<0.05). ROC curve showed that the AUC of serum ephrin-A5 as a marker for identifying prostate cancer metastasis was 0.843, with a sensitivity of 93.5% and a specificity of 75%. The above results indicate that in the progression of prostate cancer, ADAM10 can cleave ephrin-A5 to promote prostate cancer metastasis, and ephrin-A5 released into the blood can be used as a new biomarker for prostate cancer metastasis.

PO-0349

Dysregulated expression of long noncoding RNA KIAA1586-2:1 serves as a diagnostic biomarkers of gastric cancer

Haoliang Zhang
Affiliated Hospital of Xuzhou Medical University

Object Detect the expression level of exosomal long non-coding RNA lnc-KIAA1586-2:1 in the plasma of gastric cancer patients and evaluate its diagnostic value as a marker.

Methods In this study, HiPure Exosome RNA kits was used to extract plasma exosomes, and then extracted total exosome RNA, following we used western blotting and particle size analysis to identify exosomes. The expression of lnc-KIAA1586-2:1 in plasma exosomes of 29 healthy people and 63 gastric cancer patients was first detected by real-time quantitative reverse transcription PCR (qRT-PCR), and the relationship between the expression level and

clinicopathological parameters was analyzed .Finally, a receiver operating characteristic curves（ROC curve）was used to evaluate the clinical value of lnc-KIAA1586-2:1 as a diagnostic marker for gastric cancer.
Results Western blotting and particle size analysis showed successful separation of plasma exosomes. qRT-PCR results revealed that compared with the healthy control group, lnc-KIAA1586-2:1expression level in plasma exosomes of gastric cancer patients was significantly down-regulated(P<0.05), and the area under the ROC curve (AUC) was up to 0.710. lnc-KIAA1586-2:1 expression level was not correlated with age (P=0.7848), gender(P=0.3211), or lymphatic metastasis(P=0.4879), but with tumor size(P=0.0189), TNM stage(P=0.0056), and venous invasion (P=0.0367).
Conclusions Our experimental data suggest that lnc-KIAA1586-2:1 may performs a vital role in the progression of gastric cancer and is expected to be used as an assistant marker for early diagnosis of gastric cancer.

PO-0350

慢性非传染性疾病中 DAMPs 的表达及免疫状态研究

杨欢[1,2]、陈星[1,2]、李思进[1]、李慧洋[1]、任碧琼[1,2]
1. 湖南中医药大学临床医学院
2. 湖南省脑科医院

目的 探讨损伤相关分子模式（DAMPs）分子在慢性非传染性疾病（NCD）中的表达水平，同时分析各 NCD 组中 Th1、Th2 及 Th17 分泌的相关细胞因子 IFN-γ、TNF-α、IL-4、IL-6、IL-10、IL-17 表达水平并探讨 DAMPs 水平与细胞因子表达的关系，分析 DAMP 分子在疾病中激活机体免疫类型，为慢性病的预防和治疗及延缓衰老方面提供新思路。
方法 选择 2019 年 1 月至 2020 年 12 月湖南省第二人民医院明确诊断的 NCD 患者 101 名，包括 2 型糖尿病 30 名，H 型高血压 27 名，阿尔茨海默病 21 名，帕金森病 23 名，同期健康对照组 23 名。采用化学发光、免疫比浊、免疫增强比浊方法分别检测血清 S100、CRP、SAA 及 UA 水平，采用流式细胞术检测细胞因子 IFN-γ、TNF-α、IL-4、IL-6、IL-10、IL-17 水平。
结果 1. 2 型糖尿病组与 H 型高血压组血清 CRP、SAA 及 UA 水平均高于健康组，而血清 S100 水平无显著性差异。阿尔茨海默病组与帕金森病组血清 SAA 水平高于健康组，血清 S100、CRP、UA 水平无显著性差异。2. 2 型糖尿病组血清 IL-17 水平高于健康对照组，血清 IL-6、IL-10、IFN-γ 及 IL-4 无差异。H 型高血压组血清 IL-6、IL-10、IFN-γ 及 IL-17 均高于健康对照组(P< 0.05），血清 IL-4 差异无统计学意义。阿尔茨海默病组血清 IL-6、IL-10、IFN-γ、IL-17 及 IL-4 均高于健康组。帕金森病组血清 IL-6 及 IL-17 均高于健康组，血清 IL-10、IFN-γ 及 IL-4 水平差异无统计学意义。2 型糖尿病组中血清 SAA 与 IL-17、UA 与 IL-17、UA 与 IFN-γ 呈正相关；H 型高血压病组中血清 UA 与 IFN-γ 呈正相关；阿尔茨海默病组血清 CRP 与 IL-6 呈正相关关系；帕金森病组中血清 CRP 与 IL-6、CRP 与 IL-17 呈正相关，血清 SAA 与 IL-10 呈正相关关系，其余各指标之间无相关性。
结论 DAMPs 分子 S100、CRP、SAA 及 UA 在 NCD 中均有一定程度的升高；各 NCD 组的免疫激活类型不同，2 型糖尿病仅细胞因子 IL-17 水平升高；H 型高血压中 IFN-γ、IL-6、IL-10 及 IL-17 升高，阿尔茨海默病中 IFN-γ、IL-4、IL-6、IL-10 及 IL-17 均升高，Th1、Th2 及 Th17 细胞均被激活；帕金森病中 IL-6 及 IL-17 升高，Th2 及 Th17 细胞被激活，但未见 Th1 细胞激活的依据；DAMPs 分子介导的慢性炎症反应参与年龄相关疾病的发生发展，调控机体慢性炎症，本研究为 NCD 的防治及延缓衰老提供新思路。

PO-0351

基于数据挖掘研究血小板数量对血清钾的影响及解决方案

张好良[1]、夏良裕[2]
1. 徐州医科大学附属医院
2. 中国医学科学院北京协和医院

目的 为探究血小板数量对血清钾的影响并提供血清钾报告审核的解决方案。
方法 将同时送检血常规和血清生化或血浆生化的患者数据进行于大数据挖掘。利用决策树模型对血小板血清钾或血浆钾和进行分析，进一步根据血小板数量分为 A 组≤100×109/L、B 组（101-350）×109/L、C 组（351-500）×109/L、D 组>500×109/L 进行血清和血浆钾的验证，分别研究血清钾和血浆钾与血小板的关系。在实验室信息系统中将血小板数量与血清钾或血浆钾进行关联。
结果 决策树模型显示，血清钾随着血小板数量的增加显著升高（P<0.001），而血浆钾无明显增减。血清钾与血浆钾组间比较有统计学意义（P<0.001）。A、B、C、D 分组血清钾分别是（4.06±0.45）mmol/L、（4.19±0.35）mmol/L、（4.33±0.37）mmol/L、（4.54±0.46）mmol/L，组间相比 P 均<0.001，血浆钾分别是（3.86±0.50）mmol/L、（3.87±0.41）mmol/L、（3.81±0.41）mmol/L、（3.83±0.53）mmol/L，组间比较无统计学意义。血清钾与血小板数量呈（r=0.381）、血小板压积（r=0.384）正相关，与血小板其他参数不相关。血清钾与血小板数量的回归方程为 y=0.001x+4.06。报告审核时实验室信息系统对血小板>500×109/L 的血清钾结果进行拦截并添加备注。
结论 血小板增多症对血清钾有正干扰。血清钾和血浆钾应分别设置参考区间。实验室信息系统可即时拦截血清钾的报告审核并增加检验备注或通知临床医生进行血浆钾或血气钾的检测，避免假性高钾报告的发出。

PO-0352

乳胶增强免疫比浊法检测血清脂联素的性能评价

王黎[1]、蒋慧[1,2,3]、胡帅[1]、何仁栋[1,2,3]、郭斌[1,2,3]、雷燕[1,2,3]
1. 川北医学院附属医院检验科
2. 川北医学院医学检验系
3. 川北医学院转化医学研究中心

目的 脂联素（Adiponectin, ADPN）是脂肪细胞分泌的一种蛋白质激素，通过调控葡萄糖和脂质代谢来参与代谢过程，具有多种生理功能，包括抗炎症、抗动脉粥样硬化、调节胰岛素敏感性，在肥胖、胰岛素抵抗、心血管疾病、糖尿病、代谢综合征、骨关节炎、类风湿性关节炎等疾病中发挥重要作用。本文对乳胶增强免疫比浊法定量检测血清 ADPN 进行方法学评价，判断其是否满足临床检测需要。
方法 参考相关标准评价方法对免疫比浊法检测血清 ADPN 的精密度、正确度、回收实验、线性范围、临床可报告范围、干扰实验、生物参考区间进行评价。
结果 乳胶增强免疫比浊法测定血清 ADPN 的低水平质控品批内和批间变异系数分别为 3.36%和 4.55%，高水平质控品批内和批间变异系数分别为 3.39%和 5.46%，精密度良好；不同批号校准品相对偏差均在<10%可接受范围内，正确度验证通过；回收率为 96.17%~104.04%；血清 ADPN 水平在 1.12-40ug/mL，回归方程 Y=1.0058X-0.5043，r2=0.9987，符合厂家要求，检测线性良好；临床可报告范围上限为 400ug/mL，最大稀释倍数为 10 倍；当样本中胆红素≤40mg/dL、甘油三脂≤1000mg/dL、血红蛋白≤1000mg/dL 时对该方法检测血清 ADPN 无干扰；血清 ADPN 生物参考区间（女姓≥5 ug/mL；男性≥4 ug/mL）验证通过。
结论 乳胶增强免疫比浊法测定血清 ADPN，精密度良好，检测线性范围宽，干扰因素较小，满足临床实验室的基本要求，可为临床提供可靠检测结果。

PO-0353

Lp-PLA2 和 D-二聚体在急性非 ST 段抬高型心肌梗死患者中的表达

石秀芳、敖家富
亳州市人民医院

目的 分析急性非 ST 段抬高型心肌梗死（NSTEMI）患者中血清脂蛋白相关磷脂酶 A2（Lp-PLA2）和血浆 D-二聚体的表达变化及意义。
方法 收集 2019 年 5 月至 2020 年 4 月亳州市人民医院心内科确诊冠心病的 94 例患者，其中急性非 ST 段抬高型心肌梗死（NSTEMI）患者 32 例，急性 ST 段抬高型心肌梗死（STEMI）患者 32 例，不稳定型心绞痛（UAP）患者 30 例。收集一般资料及相关检查结果，并进行血清低密度脂蛋白胆固醇(LDL)、血清脂蛋白相关磷脂酶 A2（Lp-PLA2）和 D-二聚体检测，并对检测数据进行统计分析。
结果 NSTEMI 组、STEMI 组和 UAP 组的 Lp-PLA2 和 D-二聚体水平组间比较，差异均具有统计学意义（ P＜0.05 ），血清 LDL 在三组间表达水平差异无统计学意义(P＞0. 05)；冠状动脉病变支数一支病变组、二支病变组、多支病变组间比较，血清 LDL，Lp-PLA2 和 D-二聚体水平组间差异均无统计学意义(P＞0. 05)。
结论 Lp-PLA2 和 D-二聚体表达水平在三组间的明显差异，结合传统的生物学标志物，有助于 NSTEMI 患者预防和诊疗，但与冠状动脉狭窄程度没有相关性。

PO-0354

血液灌流联合高通量血液透析对不同年龄阶段尿毒症患者钙磷代谢和肾功能的影响

谌亚星
四川省人民医院

目的 血液透析是临床治疗肾衰竭的重要方法之一，本研究旨在探讨血液灌流联合高通量血液透析对不同年龄阶段尿毒症患者钙磷代谢和肾功能的影响。
方法 纳入 2020 年 3 月至 2021 年 3 月于四川省人民医院进行进行血液灌流联合高通量血液透析治疗超过 3 个月以上，每周 2-3 次患者，四个年龄阶段（<30 岁，30-40 岁，40-50 岁，>50 岁）各 80 例为研究对象,划分比较不同年龄阶段患者透析前后肾功能指标和钙磷代谢指标变化情况。入选的所有患者在入选后进行透析前后分别使用全自动生化分析仪检测血清钙、血清磷、血清尿素氮、血清肌酐及血清胱抑素 C。
结果 血液灌流联合高通量血液透析治疗前后患者血尿素氮、血清肌酐、血清磷、血清钙水平比较差异具有统计学意义（均 P<0.05）,血清胱抑素 C 水平比较差异无统计学意义。且在不同年龄差异更明显，年龄越小低透析治疗前后患者血尿素氮、血清肌酐、血清磷、血清钙水平比较差异越大，透析效果越好。
结论 血液灌流联合高通量血液透析对年级越小的尿毒症患者治疗效果较好,且能调节患者钙磷代谢,保护肾功能。

PO-0355

脂代谢在过敏性紫癜患儿疾病进展中的意义研究

张益多
四川大学华西第二医院

目的 研究血清中脂类物质代谢在过敏性紫癜患儿疾病进展中的变化，分析脂类物质检测在过敏性紫癜疾病进展过程中的临床应用价值。
方法 选取 2018 年 1 月至 2019 年 12 月，在我院就诊的过敏性紫癜患儿 32 例，过敏性紫癜康复患儿 26 例，同时选取紫癜性肾炎（HSPN）患儿 12 例，分别对血清中高密度脂蛋白胆固醇（HDL-C）、低密度脂蛋白胆固醇（LDL-C）、总胆固醇（TC）、甘油三酯（TG）、载脂蛋白 AI（Apo AI）、载脂蛋白 B（Apo B）以及甘油三酯-空腹血糖指数（TyG）进行检测，比较不同组之间血清中脂类代谢物质含量的差异，同时对脂类物质在过敏性紫癜疾病进展中的诊断价值进行分析。
结果 三组受试者在年龄、性别组成中不存在明显差异（P>0.05）。HSPN 组患儿血清中 HDL-C、LDL-C、TC、Apo A1、Apo B 以及 TyG 明显高于过敏性紫癜组以及过敏性紫癜恢复组，具有显著差异(P<0.05)。HSPN 组患儿血清中 TG 与过敏性紫癜组以及过敏性紫癜恢复组不存在明显变化（P>0.05）。过敏性紫癜组相比较过敏性紫癜恢复组血清中脂类物质水平均没有明显差异（P>0.05）。HDL-C、LDL-C、TC、Apo AI、Apo B 以及 TyG ROC 曲线下面积（AUC）分别为 0.667，0.614，0.690，0.680，0.631，0.644，cut-off 值分别为 1.495mmol/L，4.48mmol/L，5.375 mmol/L，1.495 g/L，1.18 g/L，8.77。
结论 血清中脂类物质代谢和过敏性紫癜进展过程密切相关，HDL-C、LDL-C、TC、Apo A1、Apo B 以及 TyG 对于紫癜性肾炎的诊断以及鉴别诊断具有较好临床意义，可以用于临床对于过敏性紫癜疾病进展情况的判断和治疗预后分析。

PO-0356

Simple and efficient methods for simultaneous extraction and determination of 11 water-soluble vitamins in plasma by LS/MS

Weikang Li
Guangdong Provincial Chinese medicine hospital

Purpose Targeted metabolic profiling characterized by complementary platforms, multiplexing, and low volume consumption is increasingly used for studies using biobank material. Using liquid-liquid extraction, we developed a sample workup suitable for quantification of 11 water-soluble vitamins simultaneously.
Method 200µL plasma was mixed with 1ml ethyl acetate after adding corresponding internal standard. After some process and removing the upper layer, the remaining aqueous fraction was mixed with 500µl MeOH:AcN(v:v=50:50) and go through the same process followed by evaporating by nitrogen flow with the upper layer liquid. Afte dissolved with 500µL 1% FA water and filtered with a 0.22µm water filtration membrane, the sample was injected using an autosampler, and the injection volume was 5µL. Isotope-labeled internal standards were used for all analytes. Chromatographic run times for the LC-MS/MS were 6 minutes.
Results The linear range for Thiamine Hydrochloride, Riboflavin, Nicotinic acid, Nicotinamide, Pyridoxine hydrochloride, D-Biotin, Folic acid and Cyanocobalamin were 0.1-50ng/ml; D-Pantothenic acid hemicalcium salt and Pyridoxamine dihydrochloride were 1-200ng/ml; L-Ascorbic acid was 0.1-100µg/ml. The lower limits of quantification and detection were lower than endogenous concentrations. Recoveries rate ranged from 25.81 - 134.72% of all analytes. The CV of inter-day precision and intra-day precision were 0.66 - 8.27%, 0.28 - 6.12 respectively. No significant evidence of potential carry-over effect and matrix effect was observed.

Conclusion This low-volume, high-throughput multianalyte assay shows good performance and convenience, and currently use in our laboratory for the quantification of 11 water-soluble vitamins in plasma to provide supplementary advice for clinic diagnosis.

PO-0357

识别 HDL 亚类的 ApoA1 单抗对冠心病的辅助诊断价值

丁慧、王寅
上海市交通大学医学院附属同仁医院

目的 探讨能识别高密度脂蛋白（HDL）亚类的载脂蛋白 A1（ApoA1）单抗对冠心病的辅助诊断价值及与冠心病的关联性。
方法 检测 180 例经冠脉造影确诊的冠心病患者和 199 例体检健康者（正常对照组）血清 ApoA1 单抗和多抗水平。采用 t 检验比较 ApoA1 单抗和多抗检测结果在组间的差异。采用 Pearson's 相关系数分析 ApoA1 单抗和多抗检测结果与冠心病的相关性。使用受试者工作特征（ROC）曲线评价二者对冠心病的辅助诊断价值。根据得出的最佳临界值比较 ApoA1 单抗和多抗的敏感性和特异性。引入常规危险因素（年龄、性别、糖尿病、高血压、血脂异常、吸烟）进行校正，采用非条件 Logistic 回归分析评估 ApoA1 单抗作为冠心病危险因素的价值及与冠心病的关联强度。
结果 筛选出一株组间检测结果具有显著性差异的 ApoA1 单抗（P＜0.001）。冠心病组 ApoA1 单抗检测结果明显高于对照组（P＜0.001），与冠心病显著正相关（r=0.229, P<0.001）；而 ApoA1 多抗检测结果明显低于对照组（P＜0.001），与冠心病显著负相关（r=-0.344, P<0.001）。ApoA1 单抗和多抗检测结果的 ROC 曲线下面积分别为 0.729 和 0.624，且单抗检测结果的灵敏度和特异性均优于多抗检测结果（0.696>0.563，0.634>0.558)。非条件 Logistic 回归分析显示 ApoA1 单抗和多抗检测的比值比（OR）分别为 3.25 和 0.245，95%可信区间（CI）为 1.75-6.05 和 0.028-2.160。
结论 ApoA1 单抗可甄别与冠心病正相关的 HDL 亚类，对冠心病有一定的辅助诊断价值，是冠心病的危险因素。

PO-0358

Serum microRNA expression patterns in subjects after five kilometers' exercise are strongly associated with cardiovascular adaptation

Dandan Li
Department of Clinical Laboratory, Jinling hospital, Nanjing University School of Medicine, 1Nanjing, China

Emerging evidence indicate that circulating microRNAs (miRNAs) are dysregulated during exercise. However, the changes of specific serum miRNAs during Five kilometers' run test and their association with traditional cardiovascular related indicators have not been well-characterized. A total of 240 venous blood samples were collected before and after the five kilometers' run test from 120 young subjects. The serum levels of miR-1, miR-21, miR-146a, miR-155, miR-181 and miR-210 were detected by reverse transcription-quantitative PCR (RT-qPCR). Besides, the levels of cardiac Troponin I (cTNI), myoglobin (Myo), creatine kinase (CK), creatine isoenzyme (CK-MB), aspartate aminotransferase (AST), lactate dehydrogenase (LDH), ischemic modified albumin (IMA), interleukin-6 (IL-6), and C-reactive protein (CRP) were also determined by automatic biochemistry analyzer. The correlation between serum miRNAs' levels and biochemical parameters were also analyzed. The levels of miR-1, miR-146a, miR-155, miR-181 and miR-210 were significantly increased in the serum of the subjects after five kilometers' run test as compared with resting state. Serum levels of miR-146a, miR-155 and miR-210 after five

kilometers' run test were positively correlated with Myo, CK-MB and LDH respectively, while miR-1, miR-146a, miR-181 and miR-155 were positively correlated with the levels of IL-6. Additionally, all the 5 miRNAs were negatively correlated with IMA levels. Multivariate logistic regression analysis showed that high levels of miR-146a, AST, LDH and IL-6 in serum were risk factors, while low IMA contents was a protective factor for cardiovascular adaptation during exercise. In conclusion, the dynamic changes of miRNAs under the condition of high intensity training contribute to the adaptive regulation of the body's cardiovascular function.

PO-0359

Covid-19 无症状感染者与症状前感染者实验室指标特征分析及风险分层模型的建立

李卫巍、夏欣一
中国人民解放军东部战区总医院

目的 区分 COVID-19 无症状感染者、非重症症状前患者和重症症状前患者有助于优化临床风险分层管理，改善预后。目前尚未有报道利用常规实验室指标对无症状和症状前 COVID-19 患者进行分层研究。
方法 收集 2020 年 2 月 4 日至 2020 年 4 月 10 日在武汉火神山医院住院的 COVID-19 患者。回顾性分析病例资料，对患者进行分类，所有患者被分为无症状、症状前感染或有症状。一共纳入 39 例无症状患者，34 例症状前患者，最终进展为非重症 9 例和重症 25 例，25 例中 ICU 入住率和死亡率分别为 8.3%和 3%，2907 个有症状（非重症 n=1385；重症 n=1522）的病人。用 63 个实验室指标构建风险分层模型。无症状患者疾病进展是由入院时的风险分层定义。
结果 根据实验室指标分析得出非重症症状前患者与重症症状前患者具有系统差异。因此，我们构造了二步法风险分层模型。第一步，区分症状前患者和无症状患者的 ROC 曲线平均 AUC=0.89（95%可信区间 0.81 ~ 0.98），所用实验室指标贡献度前 5（脑利钠肽 BNP、IgG、IgM、葡萄糖、D 二聚体）。第二部，对重症和非重症症状前患者进行临床预后进一步分层（曲线下面积 0.82），所用指标贡献度前 5（脑利钠肽 BNP、IgG、IgM、降钙素原、白/球蛋白比）。结果提示，应用实验室指标对无症状和症状前的 COVID-19 患者进行分层是可行的，该风险分层模型可用于筛查入院时的非重症和重症症状前患者。
结论 本研究建立的两步风险分层模型，以 10 项实验室指标为基础，对症状前患者和无症状患者进行初步区分，并进一步根据疾病严重程度对患者进行分层。该模型有助于尽早识别无症状 COVID-19 患者，并预测疾病严重程度，进行适当的临床管理。

PO-0360

比较不同高敏肌钙蛋白作为健康人群选择标准对 NT-proBNP 参考范围的影响

李阳、蔺亚惠、周洲
中国医学科学院阜外医院

目的 比较将高敏肌钙蛋白 I（hs-cTnI）和 T（hs-cTnT）高于第 99 百分位参考上限（99th URL）单独和联合作为健康人群选择标准时对 NT-proBNP 参考范围的影响。
方法 收集 1578 例院内健康管理中心表观健康人，依据 AACC 与 IFCC 联合共识中关于建立 NT-proBNP 参考区间的纳入排除条件剔除不符合条件样本后，最终纳入 1222 例。年龄 21-85 岁，男性 860 例，女性 362 例。按年龄分为 5 组（21-40 岁、41-50 岁、51-60 岁、61-70 岁、＞70 岁）。

用罗氏 Cobas E602 测定 NT-proBNP 和 hs-cTnT 的浓度，用雅培 i2000 检测 hs-cTnI 的浓度。按照 WS/T 402-2012 要求统计结果。
结果 将 hs-cTnI≥99th URL 作为健康人排除标准时男、女性 NT-proBNP 参考区间分别为 2.5-315.0ng/ml 和 2.5-469.5ng/ml，将 hs-cTnT≥99th URL 纳入后分别为 2.5-196.8ng/ml 和 2.5-337.9ng/ml，而不用 hs-cTn 排除时参考区间上限较高，分别为 2.5-351.1ng/ml 和 2.5-468.1ng/ml。若将 hs-cTnI 和 T 均纳入后参考区间上限无显著变化，分别为 2.5-197.6ng/ml 和 2.5-344.0ng/ml。按照年龄分组后，不考虑 hs-cTn 作为入选标准，年龄从小到大各组参考区间分别为 2.5-91.2ng/ml、2.5-154.9ng/ml、2.5-385.9ng/ml、5.0-327.5ng/ml 和 30.2-2150.8ng/ml。考虑 hs-cTnI 作为入选标准时，分别为 2.5-91.2ng/ml、2.5-154.7ng/ml、2.5-350.8ng/ml、4.8-327.6ng/ml 和 30.2-2150.8ng/ml；考虑 hs-cTnT 作为入选标准时，分别为 2.5-91.3ng/ml、2.5-141.1ng/ml、2.5-262.0ng/ml、4.6-327.8ng/ml 和 29.5-1525.3ng/ml；考虑 hs-cTnI 和 T 同时作为入选标准时，分别为 2.5-91.3ng/ml、2.5-137.3ng/ml、2.5-264.5ng/ml、4.5-327.8 ng/ml 和 29.5-1525.3ng/ml。
结论 将 hs-cTnI 和 T≥99th URL 单独和联合作为健康人群选择标准时显著影响 NT-proBNP 参考范围，纳入后总体、男性和女性的参考上限均逐渐降低，尤其对于 41-50 岁和 51-60 岁两组的参考上限降低更为明显。同时结果显示 hs-cTnT 的影响更为显著。

PO-0361

New biomarker LncRNA AL355711 promotes atherosclerosis

Chunmin Kang、Xianzhang Huang
The Second Affiliated Hospital of Guangzhou University of Chinese Medicine

Background and aims Atherosclerosis and related cardiovascular diseases are the greatest threats to human health worldwide. Vascular smooth muscle cells (VSMCs) contribute at least 50% of atheroma foam cells, and the first step is migration in human atherosclerotic lesions. Long noncoding RNAs (lncRNAs) have emerged as significant players in almost every diverse biological process. This study aimed to investigate the role of lncRNA in VSMCs.
Methods The expression of lncRNA or mRNA was detected using real-time quantitative fluorescence polymerase chain reaction. The Gene Expression Omnibus (GEO) DataSets in the NCBI portal were searched using the key words of “Atherosclerosis AND tissue AND and Homo sapiens” and datasets GSE12288, which measured the gene expressions from circulating leukocytes identifies patients with coronary artery disease or controls, was used to analysis the correlation coefficient and the expression profile. The protein level of ABCG1 and matrix metalloproteinase (MMP)3 was determined by immunohistochemistry and western blot analysis. The analysis of mouse aortic roots was performed using Masson stain and oil red O stain.
Results The expression of lncRNA AL355711, ABCG1 and MMP3 was higher in human atherosclerotic plaques or atherosclerotic coronary artery disease (CAD). Correlation analysis revealed that ABCG1 may be involved in the regulation between lncRNA AL355711 and MMP3 in atherosclerotic CAD. Knockdown of lncRNA AL355711 inhibited ABCG1 transcription and smooth muscle cell migration. In addition lncRNA AL355711 was found to regulate MMP3 expression through the ABCG1 pathway. The expression of ABCG1 and MMP3 was high in an animal model of atherosclerosis.
Conclusions The results indicated that lncRNA AL355711 promoted VSMC migration and atherosclerosis via the ABCG1/MMP3 pathway. The inhibition of lncRNA AL355711 might serve as a novel therapeutic target for atherosclerosis and lncRNA AL355711 in circulating leukocytes may be a new biomarker for atherosclerotic CVD.

PO-0362

中国南部地区脂蛋白相关磷脂酶 A2 水平及与经典心血管疾病标志物相关性初探

赵晶晶、张鹏、郑磊
南方医科大学南方医院

目的 探究中国南部地区多中心及不同性别、不同年龄段间脂蛋白相关磷脂酶 A2（Lipoprotein associated phospholipase A2，Lp-PLA2）水平差异，以及 Lp-PLA2 与常用的心血管标志物低密度脂蛋白胆固醇（Low density lipoprotein cholesterol，LDL-C）、超敏 C 反应蛋白（Hypersensitive C-reactive protein，hs-CRP）的相关性。

方法 纳入八所中国南部地区一线三甲医院健康人群的血清标本 2318 例，检测 Lp-PLA2 水平，对不同性别、年龄及不同中心的结果进行分析，并将 LP-PLA2 结果与经典心血管风险标志物 LDL-C（血脂水平）和 hs-CRP 的结果相关性进行分析。

结果 中国南部地区 2318 例健康志愿者 Lp-PLA2 平均值为 145.84ng/mL，参考区间上限为 217.93ng/mL，其中男性（1205 例）平均值为 152.13ng/mL，女性（1113 例）平均值为 139.03ng/mL，差异有统计学意义（$p<0.05$）；50 岁以下年龄组与 50-59 岁、60-69 岁及 70-79 岁三个年龄分组间差异有统计学意义（$p<0.05$），与 80 岁以上年龄段之间无明显差异，但无需根据年龄和性别设立独立的参考区间。各中心 Lp-PLA2 均值水平有所差异，其中海南省人民医院 Lp-PLA2 均值水平最高（157.67 ng/mL），福建医科大学附属协和医院 Lp-PLA2 均值水平最低（135.21 ng/mL）。相关性采分析结果提示 Lp-PLA2 和 LDL-C 以及 hs-CRP 分别都具有显著相关性。

结论 本课题对健康人群中研究通过大数据调查分析建立了中国南部地区健康人群 Lp-PLA2 水平 95% 参考区间，对 Lp-PLA2 与血脂和 Hs-CRP 相关性进行了初步探讨。

PO-0363

不同保存时间的脑脊液中外泌体生物学特性的对比

朱迎星
徐州医科大学附属医院

目的 脑脊液外泌体对于神经系统疾病的诊断和治疗具有不可比拟的优势,但其保存**方法** 、保存时间、保存效果的评估研究较少.文章旨在观察不同保存时间的脑脊液中外泌体的大小、密度、形态、总 RNA 量及标志蛋白表达有无改变。

方法 使用 Exoquick 试剂盒分别提取新鲜及保存在-80℃冰箱 1 年、3 年、5 年的脑脊液中的外泌体;使用纳米粒度颗粒跟踪分析仪对提取的外泌体进行粒径分析;使用透射电镜对提取的外泌体的形态进行观察;试剂盒提取脑脊液外泌体总 RNA,使用 NanoDrop ND-1000 对 total RNA 质量进行检测;Western blot 检测外泌体标志物 TSG101 和 CD63 的表达改变。

结果 保存时间达 5 年的脑脊液中的外泌体粒径较大(40～220 nm);电镜下不同保存时间的脑脊液中外泌体形态变化不明显;随着保存时间的延长,脑脊液中外泌体总 RNA 量降低，同时蛋白 TSG101 及 CD63 含量也发生降低,其中 CD63 降低尤其明显。

结论 不同保存时间的脑脊液中外泌体粒径及形态变化差异不大,但其内含 RNA 及蛋白标志物随着时间延长发生明显减少,因此进行外泌体 RNA 及蛋白的相关研究时推荐新鲜提取立即实验。

PO-0364

Corin 在顺铂引起肾脏毒性中的作用研究

薛美婷
天津医科大学肿瘤医院

顺铂是一种用于化疗的抗肿瘤药物，它对多种癌症有效。但由于顺铂引起的以肾毒性为首的毒性作用，其临床应用受到了很大限制。然而，顺铂引起肾脏毒性的具体机制，目前尚不完全清楚。因此研究顺铂引起肾脏毒性具体机制并且找到有效预防手段迫在眉睫。Corin 是一种 II 型跨膜丝氨酸蛋白酶，主要表达在心脏，在肾脏的表达仅次于心脏。Corin 的生物学功能是将 pro-ANP 转化成具有生物学活性的 ANP。我们之前的研究发现 Corin 参与了肾脏疾病发病以及进展，Corin 通过 MAPK 和 eNOS 信号通路在糖尿病肾病内皮功能障碍中起保护作用，因此 Corin 可能作为肾脏疾病的生物标志物。研究表明顺铂通过亚硝化应激、氧化应激、炎症、凋亡、调节内皮功能等途径引起肾脏毒性，并且 Corin-proANP 活化途径与这些信号通路有一定的相关性。我们通过诱导 Corin 敲除小鼠模型、HK-2 细胞 Corin 减少模型以及顺铂模型，运用 Western blot、real-time PCR、IHC、IF 等分子生物学技术研究 Corin 在顺铂引起的肾脏毒性中的具体保护性机制，以期为顺铂引起肾脏毒性提供新的治疗靶点。本研究课题在我们课题组之前的研究结果以及国内外学者的研究基础上，首次探索 Corin 在顺铂引起肾脏毒性中的保护性作用，具有一定的先进性和首创性，并且我们会在当前设想的基础上，随着研究深入分子机制的研究，力求发现更多原创性成果。

PO-0365

血清 Aβ40 与 Aβ42 在糖尿病肾病检测中的临床价值分析

杨海玉
泰州市中医院

前言 β 淀粉样蛋白（Aβ）是一种氨基酸片段，且主要由脑组织合成，其中 Aβ40 和 Aβ42 含量较多。近年来，Aβ40 和 Aβ42 越来越成为研究阿尔兹海默病的重要生物标记物。而在其他疾病中，Aβ40 和 Aβ42 却很少被关注。本研究通过分析糖尿病肾病患者血浆 Aβ40 和 Aβ42 的水平变化，旨在指导糖尿病肾病的早期诊断与预后评估。
目的 探讨血清 Aβ40 与 Aβ42 水平在糖尿病肾病中的表达和诊断意义。
方法 收集 2018 年 1 月至 2020 年 1 月糖尿病肾病患者 87 例作为观察组，并将同期 78 例健康受试者作为对照组，对比研究两组间 Aβ40 与 Aβ42 和基线资料的差异。将纳入的 87 例糖尿病肾病患者按 CKD 分期分为五组，对比组间血清 Aβ40 与 Aβ42 水平和基线资料差异，探讨 Aβ40 与 Aβ42 水平与糖尿病肾病肾功能损伤程度的差异。通过 ROC（受试者工作特征曲线）评估 Aβ40 与 Aβ42 水平对糖尿病肾病肾功能损伤的诊断价值。
结果 糖尿病肾病患者血清中 Aβ40 与 Aβ42 水平高于对照组（$P<0.05$），非参数秩和检验和 Pearson 积矩相关分析提示，血清 Aβ40 与 Aβ42 水平与糖尿病肾病患者肾功能损伤程度成正相关。通过血清 Aβ40 与 Aβ42 诊断糖尿病肾病的 ROC 曲线可知，Aβ40 的阈值为 121ng/ml,曲线下面积为 0.94；血清 Aβ42 的阈值为 113ng/ml,曲线下面积为 0.88。
结论 Aβ40 与 Aβ42 水平在糖尿病肾病患者血清中表达水平升高，且与患者肾功能损伤程度呈正相关。血清 Aβ40 与 Aβ42 水平在糖尿病肾病的临床诊断上具有较高的应用价值，同时对糖尿病肾病的临床治疗起到指导作用。

PO-0366

小而密低密度脂蛋白与 2 型糖尿病的 相关性分析

李珊珊、荣嵘
北京大学人民医院

目的 探讨小而密低密度脂蛋白与 2 型糖尿病的相关性及其 cutoff 值。
方法 收集北京大学人民医院内分泌科收治的 725 例 T2DM 患者的临床资料，纳入病例组。选取同期 822 例体检正常者纳入对照组。检测 LDL-C、 HDL-C、CHO、TG、GLU、CRP 及 sdLDL 水平，分析小而密低密度脂蛋白水平与 T2DM 的关系。
结果 sd LDL 在 2 型糖尿病组明显高于正常对照组（1.25±0.019 mmol/L，0.95±0.016 mmol/L，p<0.05），差异有统计学意义；根据病例颈动脉斑块情况，将其分为三组，sd LDL 在无斑块组，稳定斑块组及不稳定斑块组是依次递增的（1.04±0.01，1.23±0.04，1.29±0.04，p<0.05）有统计学意义；在校正了其他血脂成分的影响后，CHO,CRP,GLU 等是造成患 T2DM 的危险因素，血脂 sdLDL 与 T2DM 的发生密切相关（OR=89.335，95%CI:29.305-272.458，P<0.001）；根据是否患有 T2DM 对 sdLDL 进行 ROC 工作曲线分析，sdLDL 预测 T2DM 的最佳界值为 1.12mmol/L，AUC 为 0.775 （95%CI：0.748-0.802，p<0.05），诊断效能较高。
结论 sd LDL 在 2 型糖尿病患者中显著升高，可能是 2 型糖尿病的危险因子。当 sd LDL 为 1.12 mmol/L 时，需积极治疗，警惕 2 型糖尿病的发生。

PO-0367

健康体检人群代谢综合症与冠脉病变程度相关性分析

杨璐、卢英
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨健康体检人群代谢综合症与冠脉病变程度的相关性。
方法 收集 2018 年 1 月～2019 年 1 月在本院体检中心行冠状动脉 CT 检查的 178 例体检者的相关临床资料，包括体检者的年龄、性别、身高、体重、血压、相关生化结果等，将所有受检者分为 MS 组和非 MS 组，比较两组间冠脉疾病的发生率，对代谢综合症与冠脉病变病情严重程度进行相关性分析。
结果 178 例体检者中，MS 组 65 例，非 MS 组 113 例，MS 组与非 MS 组相比，年龄、收缩压、舒张压差异无统计学意义，均 P＞0.05；而性别、BMI 指数、空腹血糖、TG、HDL-C 差异有统计学意义，均 P＜0.05；MS 组的冠脉疾病检出率高于非 MS 组，差异有统计学意义（P＜0.05）；BMI 指数、血压、TG 水平、代谢紊乱评分与冠状动脉病变积分呈正相关（P＜0.05）；多元回归分析显示，TG、高血压、3 项或 3 项以上的代谢紊乱是冠脉病变的危险因素。
结论 可以通过对体检人群代谢综合症患病情况的评估，筛查出冠心病发病潜在人群，开展相应的影像学检查，以期能够早期发现 CHD 疾病，为临床诊疗提供参考。

PO-0368

革兰阴性脓毒症患者血清 apoE、LDLR、LRP、PCSK9 检测的临床价值

祝青、郭琪、吴颖、吴圆圆、邹国英
湖南省脑科医院检验科

目的 探讨载脂蛋白 E(apoE)、低密度蛋白受体(LDLR)、低密度脂蛋白受体相关蛋白(LRP)、前蛋白转化酶枯草溶菌素 9(PCSK9）对革兰阴性（G-）脓毒症患者早期诊断、病情严重程度和预后的评估价值。
方法 选取湖南省脑科医院收治的 90 例革兰阴性脓毒症患者、40 例单纯全身炎症反应综合征（SIRS）患者、38 例革兰阳性（G+）脓毒症患者和 40 例健康体检人员为研究对象。采用 ELISA 法检测所有研究对象血清 apoE、LDLR、LRP、PCSK9 水平，收集其他实验室指标。采用 Mann-Whitney U 检验比较各组血清 apoE、LDLR、LRP、PCSK9 水平差异，采用受试者工作曲线（ROC 曲线）及曲下面积（AUC）分析各指标预测疾病发生、判断病情严重程度及评估预后价值。
结果 与健康对照组、SIRS 组、G+脓毒症组相比，G-脓毒症组患者血清 apoE、PCSK9 水平明显升高，而 LDLR、LRP 水平明显降低（P<0.05）；患者入住 ICU 后第 1、3、5 天血清 apoE 水平呈持续下降趋势（P<0.05），随着 G-脓毒症患者病情加重，apoE、PCSK9 水平明显升高，LDLR、LRP 水平明显降低（P<0.05）；死亡组患者较存活组患者血清 apoE、PCSK9 水平明显升高，而 LDLR、LRP 水平明显（P<0.05）；ROC 曲线分析结果显示 apoE、LDLR、LRP、PCSK9 早期诊断 G-脓毒症的曲线下面积分别为 0.900、0.840、0.932、0.897，判断病情严重程度的 AUC 分别为 0.810、0.772、0.720 和 0.764，而 apoE 联合 LRP 预测预后的 AUC、灵敏性和特异性分别为 0.97、95.24%、89.88%高于 apoE(0.71、66.18%、65.86%)、LRP(0.78、66.67%、78.26%)。
结论 血清 apoE、LDLR、LRP、PCSK9 可用于 G-脓毒症的早期诊断、病情严重程度的判断；apoE 与 LRP 联合应用提高预后评估的敏感性和特异性。

PO-0369

9 例细胞色素 P450 氧化还原酶缺乏症初诊患者血浆 19 项类固醇激素结果异常变化的研究

孙慧颖、侯生根、孔许净、樊晓敏、郑燕华、陈宝荣
北京金域医学检验实验室有限公司

目的 寻找并确定细胞色素 P450 氧化还原酶缺乏症诊断的异常血浆类固醇激素标志物。
方法 研究类固醇激素代谢路径，基于 LC-MS/MS 技术平台进行临床正常参考人群和患者血浆样本中 19 种类固醇激素的测量；以临床确诊的 9 例（男 3 例，女 6 例）细胞色素 P450 氧化还原酶缺乏症患者初诊时血浆中孕烯醇酮等 19 种类固醇激素的测量结果为研究对象，采用 R 4.0.1 软件绘制患者与正常参考人群组血浆孕烯醇酮等 19 种类固醇激素及睾酮/双氢睾酮比值结果的 box-plot 及散点图，分析 9 例细胞色素 P450 氧化还原酶缺乏症确诊患者与正常参考人群血浆类固醇激素结果数据分布的差异并进行 Wilcoxon 检验验证。
结果 9 例细胞色素 P450 氧化还原酶缺乏症患者初诊时血浆中孕烯醇酮等 19 种类固醇激素与正常参考人群比较结果呈现三种变化：孕烯醇酮、17-羟孕酮、皮质酮、11 脱氧皮质酮、11-脱氧皮质醇、21 脱氧皮质醇 6 种激素浓度明显增加，且与参考人群结果有显著差异（P<0.001，Wilcoxon 检验）；脱氢表雄酮、孕酮、雌酮、雌三醇、皮质醇、可的松 6 种激素浓度变化无明显规律，与参考人群结果无显著差异（P>0.05，Wilcoxon 检验）；17-羟孕烯醇酮、醛固酮 2 种激素浓度增加，但与参考人群结果差异不显著（0.001<P<0.05，Wilcoxon 检验）；男性细胞色素 P450 氧化还原酶缺乏症患者雄烯二酮、睾酮、双氢睾酮、硫酸脱氢表雄酮、雌二醇浓度明显降低，且与参考人群

结果有显著差异（P<0.001，Wilcoxon 检验）；女性细胞色素 P450 氧化还原酶缺乏症患者双氢睾酮、硫酸脱氢表雄酮 2 种激素浓度浓度降低，与参考人群结果有显著差异（P<0.001，Wilcoxon 检验），雄烯二酮、睾酮、雌二醇与参考人群结果无显著差异（P>0.05，Wilcoxon 检验）；男性细胞色素 P450 氧化还原酶缺乏症患者睾酮/双氢睾酮比值明显降低，且与参考人群结果有显著差异（P<0.001，Wilcoxon 检验）。女性细胞色素 P450 氧化还原酶缺乏症患者睾酮/双氢睾酮比值轻度增加，与参考人群结果无显著差异（P>0.05，Wilcoxon 检验）。

结论 孕烯醇酮、17-羟孕酮、皮质酮、11 脱氧皮质酮、11-脱氧皮质醇、21 脱氧皮质醇 6 种激素是细胞色素 P450 氧化还原酶缺乏症诊断的重要血清标志物；对于男性患者雄烯二酮、睾酮、双氢睾酮、硫酸脱氢表雄酮、雌二醇、睾酮/双氢睾酮比值也可作为细胞色素 P450 氧化还原酶缺乏症诊断的重要参照血清标志物。

PO-0370

尿 RBP、TRF 及 NGAL 在 2 型糖尿病肾病早期诊断中的应用分析

宋涛
湖北省襄阳市第一人民医院

目的 探讨尿视黄醇结合蛋白（RBP）、转铁蛋白（TRF）及中性粒细胞明胶酶相关载脂蛋白（NGAL）水平对 2 型糖尿病肾病（DN）早期诊断的临床意义。

方法 将 2019 年 1 月至 2020 年 12 月湖北省襄阳市第一人民医院内分泌科和肾病内科收治的 180 例 2 型糖尿病患者纳入研究组。根据患者 24 小时尿蛋白排泄率（UAER）水平将其分为三组，即正常白蛋白尿组 60 例（UAER<30mg/24h）、微量白蛋白尿组 60 例（UAER 30-300mg/24h）和大量白蛋白尿组 60 例（UAER>300mg/24h），选择同期 60 例健康体检者作为对照组，检测各组对象清晨尿液 RBP、TRF 及 NGAL 水平，并对结果进行统计学分析。分析检测结果与 UAER 的相关性，采用受试者工作曲线（ROC）评价 3 项指标对 DN 的诊断效率。

结果 正常白蛋白尿组 RBP、TRF 及 NGAL 水平与对照组比较差异无统计学意义（p>0.05）。微量白蛋白尿组及大量白蛋白尿组 RBP、TRF 及 NGAL 水平均高于正常对照组及正常白蛋白尿组，差异有统计学意义（p<0.05）。2 型糖尿病患者尿液 RBP、TRF 及 NGAL 水平与 UAER 结果呈正相关（r=0.778,0.645,0.693），尿 RBP、TRF 及 NGAL 诊断糖尿病肾病的 ROC 曲线下面积（AUC）分别为 0.895、0.833 和 0.714，敏感度分别为 81.7%、68.3%及 55.0%，特异度分别为 95.0%、94.2%及 89.2%。

结论 尿液 RBP、TRF 及 NGAL 可作为 2 型糖尿病肾病早期诊断指标，三者联合检测可提高疾病诊断的敏感度和特异度。

PO-0371

2 型糖尿病患者血清脂蛋白(a)水平与冠状动脉粥样硬化性心脏病发生风险及严重程度相关研究

顾俊旭、邢垚、苏明、贾玫、王春燕
北京大学人民医院

目的 探讨脂蛋白(a) [lipoprotein(a), Lp(a)]在 2 型糖尿病(Type 2 diabetes mellitus, T2DM)患者中与冠状动脉粥样硬化性心脏病(Coronary atherosclerotic heart disease, CAHD)发生风险及严重程度关系。

方法 对 2017 年 1 月至 2019 年 12 月在北京大学人民医院就诊的 T2DM 患者 1228 例（男性 717 例，女性 511 例）。根据冠状动脉造影(coronary angiography，CAG)结果分为 CAHD 组和 non-CAHD 组。糖尿病合并 CAHD 患者按照堵塞支数分为单支病变组、双支病变组和多支病变组；并根据 GS(Gensini score, GS)分为低 GS 组（GS ≤ 25）、中 GS 组（GS:26～40）、高 GS 组（GS≥41）。采用二元 Logistics 逐步回归方程评估 Lp(a)与 CAHD 发生风险及严重程度关系。
结果 CAHD 组血清 Lp(a)水平明显高于 non-CAHD 组[39.82 (48.06) nmol/L vs 38.27 (33.64) nmol/L，Z=-2.595, p= 0.006]。多支血管疾病组 Lp(a)水平显著升高[32.81 (40.73) nmol/L vs. 39.47 (45.54) nmol/L vs. 43.51 (49.94) nmol/L，H=18.440, p < 0.001]，高 GS 组血清 Lp(a)水平显著高于其他两组[33.74 (40.75) nmol/L vs. 39.57 (45.63) nmol/L vs. 46.21 (52.75)，H=20.548, p<0.001]。根据 Mantel-Haenszel 线性趋势检验分析得出，随着血清 Lp(a)水平的升高，冠状动脉阻塞程度加重（p<0.001）。经过 logistics 二元逐步回归方程分析得到 Lp(a)水平仍然与 CAHD 发生风险及其严重程度独立相关(CAHD 组 vs. non-CAHD: OR = 2.207, 95% CI: 1.790 – 5.060, p = 0.026; 多支病变组 vs. 单支病变组: OR = 3.288, 95% CI: 1.871 – 7.278, p = 0.035; 高 GS 组 vs. 低 GS 组: OR = 2.556, 95% CI: 2.046 – 5.378, p = 0.023)。
结论 在 T2DM 患者中，Lp(a)升高是 CAHD 的独立风险因素并于与 CAHD 的严重程度相关。

PO-0372

长链非编码 RNA SNHG1 在三阴乳腺癌中的生物学功能及其分子机制研究

汪桂华、鞠少卿
南通大学附属医院

目的 探讨 lncRNA SNHG1 在三阴乳腺癌（TNBC）的生物学功能及参与 TNBC 恶性进展的分子机制。
方法 检测 SNHG1 在乳腺癌患者癌组织和细胞中的表达，并分析其与临床病理参数之间的相关性；构建 shRNA 干扰载体检测 SNHG1 干扰对 TNBC 细胞增殖、周期、迁移与侵袭能力的改变。建立 SNHG1 干扰的稳转及对照株，构建裸鼠乳腺原位移植瘤模型，分析 SNHG1 的表达对 TNBC 原位移植瘤生长的影响。shSNHG1 转染 MDA-MB-231 细胞，转录组测序分析 SNHG1 参与的信号通路；RNA pull-down 联合质谱技术寻找与 SNHG1 相结合的蛋白；RIP 验证 SNHG1 与蛋白的结合；免疫组化法检测互作蛋白的表达；细胞功能试验分析 SNHG1 是否通过与此蛋白作用而影响 TNBC 的生物学功能。
结果 SNHG1 在 TNBC 组织的表达量显著高于其他类型乳腺癌及乳腺良性疾病，SNHG1 的高表达与肿瘤 TNM 分期显著相关。TNBC 细胞株中 SNHG1 的表达显著增高，主要定位于胞核部位。干扰 SNHG1 后，TNBC 细胞增殖明显减慢，细胞的迁移与侵袭能力明显减弱。shSNHG1 组瘤块体积和重量均小于对照组。干扰 SNHG1 表达后，差异基因富集的信号通路主要有 TNF-α 信号通路、细胞因子受体信号通路、NF-κB 信号通路等。RNA pull-down 筛选出可能与 SNHG1 相互作用的蛋白分子 NPM1，RIP 验证 SNHG1 与 NPM1 蛋白能够结合。TNBC 组织样本中 NPM1 蛋白及 mRNA 的表达水平显著高于其他类型乳腺癌；NPM1 蛋白在 TNBC 细胞中的表达高于其他类型乳腺癌细胞；NPM1 蛋白主要定位于胞核的核仁部位。TNBC 细胞中干扰 SNHG1 后 NPM1 蛋白表达下降，原位移植瘤 shSNHG1 组 NPM1 蛋白表达显著降低；而干扰 NPM1 表达对 SNHG1 无影响。以上说明 SNHG1 与 NPM1 结合后可调控 NPM1 蛋白的变化。NPM1 细胞生物学功能的影响：干扰 NPM1 后，可抑制 TNBC 细胞的增殖、侵袭和迁移，同时过表达 SNHG1 不能恢复干扰 NPM1 对细胞功能的影响。测序提示 SNHG1 可调节 NF-κB 信号通路。荧光素酶报告试验显示 SNHG1、NPM1 干扰均抑制 NF-κB 通路的活化。
结论 SNHG1 在 TNBC 中高表达，主要定位于胞核。干扰 TNBC 细胞 SNHG1 的表达可抑制细胞的增殖、侵袭和迁移，体内可抑制原位移植瘤的生长。SNHG1 与 NPM1 蛋白结合，调控其蛋白表

达增加，增加的 NPM1 可作为伴侣分子促进 NF-κB 靶基因的转录。SNHG1 参与三阴乳腺癌恶性进展，可能成为 TNBC 诊疗的潜在靶标。

PO-0373

Pre-albumin is a strong prognostic marker in elderly intensive care unit patients

Min Wang
Jiangsu Province Hospital

Aims There are many indicators that can be used to evaluate the association between nutrition status and in-hospital mortality. This will prompt us to think which one of these indicators is best. However, there is no literature to do this and make a comparison in a study.
Methods We operated a retrospective study including 145 patients admitted to our institution's elderly intensive care unit (ICU) from January, 2017 to December, 2019. Admission laboratory results were collected. Regression analysis and receiver operating curve were analyzed to explore the performance of different nutrition indexes.
Results Pre-albumin (PAB) was significantly different between survivor and non-survivor group (p =0.001). Univariate analysis showed nutrition indexes (lymphocytes, albumin, BMI, GNRI, PNI and PAB) were associated with in-hospital mortality (all P＜0.1). Following adjustment for age, platelets and creatinine (CREA), only BMI and PAB remained statistically significant (BMI: HR 2.799, 95% CI 1.167-6.715, p = 0.021; PAB: HR 6.329, 95% CI 2.660-15.151, p<0.001). In addition, PAB had the highest area under the curve (AUC) for predicting in-hospital mortality (AUC = 0.696) followed by BMI (AUC = 0.561) and other factors.
Conclusion PAB is a better predictor of in-hospital mortality than other nutrition indexes in elderly ICUs patients.

PO-0374

体液与细胞免疫检测应用在脓毒症患者诊断中的作用探讨

杨艳茹
陆军军医大学第一附属医院（西南医院）

目的 分析体液检测和细胞免疫检测用于脓毒症患者诊断中的价值。
方法 本次研究开始的时间为 2019 年 11 月，结束的时间为 2020 年 12 月，在此期间选取 90 例脓毒症患者作为研究对象，其中 48 例脓毒症患者和 41 例脓毒症休克患者分别纳入脓毒症组和脓毒症休克组，再选取同期于我院进行健康体检的人员 40 名作为对照组。所有研究对象均进行体液检测和细胞免疫检测，对检测结果进行分析和对比。
结果 脓毒症组患者的 IgG、IgM 和 IgA 水平分别为（3.54±0.44）mg/dL、（1049.78±27.71）mg/dL 和（3.52±0.61）mg/dL，脓毒症休克组患者的 IgG、IgM 和 IgA 水平分别为（3.50±0.42）mg/dL、（1074.19±28.16）mg/dL 和（2.91±0.53）mg/dL，对照组的 IgG、IgM 和 IgA 水平分别为（8.25±0.61）mg/dL、（1248.54±38.64）mg/dL 和（7.60±0.73）mg/dL，统计学分析后，脓毒症组和脓毒症休克组患者的 IgG、IgM 和 IgA 水平均显著低于对照组，且脓毒症休克组患者的 IgG 水平明显高于脓毒症组，IgM 水平明显低于脓毒症组，P＜0.05。脓毒症组患者的 CD3+、CD4+、CD8+水平分别为（72.51±7.52）、（46.67±3.48）、（30.57±3.36），脓毒症休克组患者的 CD3+、CD4+、CD8+水平分别为（37.27±4.18）、（24.41±1.92）、（12.63±2.13），对照组的 CD3+、CD4+、CD8+水平分别为（65.31±7.17）、（57.54±3.52）、（30.49±3.42），统计学分析后，脓毒症组的 CD3+水平明显高于脓毒症休克组和对照组，且脓毒症休克组的 CD3+水平明显低于对照组，P＜0.05；脓毒症组和脓毒症休克组的 CD4+水平均低于对照组，且脓毒症休克组的

CD4+水平低于脓毒症组，P＜0.05；脓毒症休克组患者的 CD8+水平明显低于脓毒症组和对照组，脓毒症组和对照组的 CD8+水平无显著统计学意义（P＞0.05）。
结论 体液检测和细胞免疫检测用于脓毒症患者的诊断中均具有较高的价值。

PO-0375

Association Between Serum Lipid Levels and Patients With Primary Angle-Closure Glaucoma in China: A Cross Sectional, Case-Control Study

Mingxi Shao、wenjun cao
EENT Hospital

Objective To evaluate the serum lipid levels of patients with primary angle-closure glaucoma (PACG) and to investigate the relationship between serum lipid levels and PACG.
Methods In this cross-sectional, case-control study, a total of 320 PACG subjects and 242 age- and sex-matched control subjects were recruited. Serum high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C), small dense LDL-C (SDLDL-C), triglyceride (TRIG), and cholesterol (CHOL) levels were measured using enzymatic colorimetry. Serum apolipoprotein A (APOA), apolipoprotein B (APOB), apolipoprotein E (APOE), and lipoprotein(a) (LPa) levels were measured by immunoturbidimetry.
Results The serum LDL-C, TRIG, HDL-C, APOE, LPa, CHOL, APOB, and APOA levels were significantly higher ($p < 0.05$) in the PACG group than in the control group. Multiple liner regression analyses revealed that there was a statistically correlation between HDL-C levels and mean deviation MD (B = 0.389, P = 0.002, 95% confidence interval [CI] = -1.249 to -0.624); LDL-C levels and MD (B = 0.190, P = 0.019, 95% CI = -5.632 to -1.306); and CHOL levels and MD (B = 0.364, P = 0.27, 95% CI = -7.727 to -1.839). Logistic regression analyses showed that high serum HDL-C (odds ratio [OR] = 11.01, 95% CI = 5.616-21.587), LDL-C (OR = 1.330, 95% CI = 1.079-1.640), SDLDL-C (OR = 1.007, 95% CI = 1.005-1.008), APOA (OR = 13.621, 95% CI = 7.251-25.591), APOB (OR = 2.243, 95% CI = 1.060-4.732), LPa (OR = 0.999, 95% CI = 0.998-1.00), and CHOL (OR = 1.131, 95% CI = 1.005-1.326) levels were significantly associated with PACG.
Conclusions High serum HDL-C, LDL-C, APOA, APOB, LPa, and CHOL levels were associated with PACG.

PO-0376

图文并茂的免疫固定电泳结果检验报告单的设计与应用

王金行[1]、张玉辉[2]、王希超[1]
1. 中国医科大学附属第一医院
2. 柏彬医疗器械

目的 将免疫固定电泳常规图片与 IgD 的图片合拼成一张图谱导入文字报告单中建立图文报告。
方法 免疫固定电泳：采用美国 Helena 公司的 Spife3000 或 Spife TOUCH 电泳仪及配套试剂进行免疫固定电泳测定，每个标本分别在琼脂糖凝胶 SP、IgG、IgA、IgM、κ、λ 泳道加对应的固定剂及抗血清，由于 IgD 型多发性骨髓瘤少见，海伦娜胶片没有预留 IgD 泳道位置，将一个单独检验位作为 IgD 泳道加抗 IgD 血清。图文报告设计：报告单模版，结合本单位的原有常规化验单样式，根据报告纸张大小将需要的各项目、信息（患者信息：病案号、年龄、性别、科室等和检验信息：标本类型、检验结果、审核医师、检验医师、回报日期等）的位置及高度、宽度进行固定，预留出检验结果图片大小的位置。将染色处理完的琼脂糖凝胶片通过扫描仪，把每个样本转换成图像并保存。

图像合并与传输，采用北京柏彬软件工程师制作的处理程序，将免疫固定电泳常规图片与 IgD 的图片合拼成一张图片。通过信息监听程序，将生成的图片和对应样本信息等抓取并传输到院内的 lis 系统中。

结果 免疫 固定电泳 SP 参考泳道及对应的 IgG、IgA、IgM、κ、λ 与 IgD 泳道显示有无异常浓集区带，即特异性的抗原抗体沉淀带。同时加 IgD 泳道，避免将 IgD 型 MM 误诊为轻链型 MM 及轻链缺失的 IgD 型 MM 的漏诊。

结论 智能化和规范化图文报告有利于提高医疗诊断水平,方便临床会诊。给人的良好直观视觉感并增强其可信性。其广泛应用对提高实验室科技内涵和对实验室认知程度具有极其深远的意义。

PO-0377

三种 CKMB 活性试剂抗溶血干扰能力的比较

陈若虹
中南大学湘雅二医院

目的 通过对三种不同品牌的 CKMB 活性检测试剂进行比对及溶血干扰实验，寻找有较强抗溶血干扰能力的试剂。

方法 依据 EP9-A2 文件，收集 40 例血清样本用三种试剂检测 CKMB 活性，比较不同品牌之间的结果差异；人为对样本造成溶血后，再一次检测 CKMB 活性，比较同一试剂溶血前及溶血后结果的差异。依据 EP7-A2 文件，收集 CKMB 活性接近医学决定水平的高值和低值两份混合血清样本，在样本中加入用由红细胞制成的溶血干扰物作为干扰高值样本，加入等量的去离子水作为干扰低值样本，两份样本按 L、3L+1H、2L+2H、1L+3H、H 的比例混合，配置成不同浓度梯度的干扰样本，用血细胞分析仪检测干扰样本中的血红蛋白浓度，用三种试剂检测干扰样本中的 CKMB 活性，计算干扰样本与零干扰样本中结果的偏差。

结果 美康、关东、罗氏试剂检测 40 例样本的 CKMB 活性的均值为分别为：27.8±27.4U/L、23.7±26.0 U/L、35.7±29.5 U/L，关东与美康的平均偏差为 14.7%，罗氏与美康的偏差为 28.4%，关东与罗氏的偏差为 33.6%。三种试剂检测 CKMB 活性的两两比对线性回归方程在医学决定水平处的偏差均超过了设定的 12.5%的允许偏差。美康、关东、罗氏试剂溶血前后的 CKMB 活性均值的偏差分别为 109.6%、0.1%、160.6%。将溶血前后的检测结果作线性回归，计算在医学决定水平 25U/L、90U/L 处的偏差，美康试剂偏差分别为 202.9%、115.1%；关东试剂的偏差分别为 0.4%、5.6%；罗氏试剂的偏差为 197.8%、108.0%。5 个干扰样本中血红蛋白浓度分别为 0、125、250、375、500 mg/dL；美康试剂零干扰低值和高值样本 CKMB 活性均值分别为 34.7、92.8U/L，干扰样本的偏差分别为 69.5%、144.4%、225.7%、292.0%以及 8.7%、24.5%、36.8%、51.6%；关东试剂零干扰低值和高值样本 CKMB 活性均值分别为 28.5、85.3U/L，干扰样本的偏差分别为-4.8%、-9.5%、-10.9%、-14.1%以及 0.6%、1.4%、2.5%、5.0%；罗氏试剂零干扰低值和高值样本 CKMB 活性均值分别为 34、109.2U/L，干扰样本的偏差分别为 62.1%、132.8%、202.4%、282.4%以及 11.6%、22.0%、35.9%、53.2%。

结论 美康、关东及罗氏三种 CKMB 活性检测试剂之间的可比性较差。美康及罗氏试剂受溶血干扰影响较大，在样本溶血时结果假性升高，关东试剂有较强的抗溶血干扰能力，更适用于临床诊断与监测。

PO-0378

血 CEA、CA125、纤维蛋白原联合预测结直肠癌肝肺转移的价值探讨

吴虹铮、钟白云
中南大学湘雅医院

目的 初步探讨 CEA、CA125、纤维蛋白原联合检测对结直肠癌患者发生肝、肺转移的预测价值。
方法 选取 2015 年 1 月至 2021 年 1 月在中南大学湘雅医院确诊住院的 356 例结直肠癌患者为研究对象，其中结直肠癌伴肝或肺转移的患者 178 例作为实验组，并按照性别、确诊年龄、原发肿瘤部位匹配结直肠癌不伴肝及肺转移的患者 178 例作为对照组。收集所有患者第一次入院时癌胚抗原（CEA）、糖类抗原 125（CA125）与纤维蛋白原（Fg）的检测数据以及相关病例资料，采用单因素及多因素分析研究以上血指标单独或联合检测对结直肠癌肝、肺转移的预测价值。
结果 单因素及多因素回归分析结果表明结直肠癌伴肝或肺转移患者血 CEA、CA125 与纤维蛋白原水平显著高于结直肠癌不伴有肝及肺转移患者（P<0.05），ROC 曲线分析及约登指数进一步确定 CEA、CA125 与纤维蛋白原的临床诊断阈值分别为 10.05ng/ml、10.19KU/L、3.82g/L，且曲线结果表明 CEA、CA125、纤维蛋白原单独诊断 CRC 患者肝、肺转移的灵敏度分别为 61.2%、48.9%、65.2%，特异性分别为 87.1%、83.7%、77.0%，诊断准确性相对有限。但 CEA、CA125 联合纤维蛋白原检测时预测结直肠癌患者肝、肺转移的准确性较高（AUC=0.811，P<0.001），灵敏度和特异性分别为 79.8%、73.0%。
结论 血 CEA、CA125 及纤维蛋白原均为结直肠癌肝肺转移的独立预测因素，且 CEA、CA125 联合纤维蛋白原检测对结直肠癌肝、肺转移的预测价值优于单一或任意两种指标联合检测，灵敏度和特异性均较高，可作为结直肠癌肝肺转移预测模型的参考指标。

PO-0379

探讨血清蛋白电泳联合胱抑素 C 在 2 型糖尿病肾病辅助诊断中的应用

王丽馨
陆军特色医学中心（大坪医院）

目的 探讨血清蛋白电泳以及胱抑素 C 检测在 2 型糖尿病肾病辅助诊断中的临床应用价值。
方法 选择陆军特色医院中心 2017 年 01 月至 2021 年 04 月收治的 2 型糖尿病患者 160 例，经临床诊断分为糖尿病组 50 例，2 型糖尿病肾脏组 110 例 ，并按照《中华糖尿病杂志<中国糖尿病肾脏疾病防治临床指南（2019 年）>》对糖尿病肾病组分为 5 期，同时选取 50 例健康体检者作对照。用毛细管电泳法对所有样本进行血清蛋白电泳检测，透射比浊法检测血清中胱抑素 C（Cys-C）含量。
结果 血清蛋白电泳结果显示 β1-球蛋白随着疾病发展先代偿性升高后呈降低趋势，其余较大分子蛋白在病情发展过程中均呈现代偿性升高趋势。糖尿病肾病组与对照组相比，血清蛋白电泳中较多指标在 2 期时表现出显著性差异（P＜0.05），胱抑素 C 随着病情的发展一直呈升高趋势，对照组与糖尿病肾病组各期间均有显著性差异,其中(α+β2)/Alb、Cys-C、(α+β2)/Alb+Cys-C 的 ROC 曲线下 AUC 面积分别为 0.793、0.756、0.767，除 γ-球蛋白外，其余血清蛋白电泳指标 AUC 皆高于 Cys-C。
结论 2 型糖尿病肾病患者的血清蛋白电泳在 2 期时开始出现明显改变，(α+β2)/Alb 的比值联合胱抑素 C 对 2 型糖尿病肾病的辅助诊断有临床价值。由此可见，血清蛋白电泳可反映糖尿病肾脏疾病患者血清中蛋白的变化趋势，联合胱抑素 C 检测可为 2 型糖尿病肾病早期的诊断及患者的预后提供参考依据。

PO-0380

基于 MALDI-TOF 质谱技术快速筛选血清 M 蛋白方法的建立

崔瑞芳[1]、张瑞[2]、张顺利[2]、王清涛[2]
1. 长治医学院附属和平医院
2. 首都医科大学附属北京朝阳医院

目的 M 蛋白检测是多发性骨髓瘤(MM)的重要诊断标准。目前，血清蛋白电泳(PEL)和免疫固定电泳(IFE)是鉴定或排除 M 蛋白的常规方法。然而，现有的检测技术由于在灵敏度和/或特异性方面的缺陷，不能完全满足临床需要。本研究旨在建立一种基于 MALDI-TOF 质谱技术的灵敏、快速、特异的血清 M 蛋白检测方法。
方法 对样品前处理条件和 MALDI-TOF MS 条件进行优化。将 23 份 M 蛋白阳性样品分别进行原倍、10 倍、100 倍和 200 倍稀释后，使用 IFE 和 MALDI-TOF MS 方法进行检测，比较两种方法的灵敏度。采用 PEL、IFE 和 MALDI-TOF MS 对 712 份样品进行测定，以 IFE 为金标准，进行灵敏度、特异性和符合率评价。根据 M 蛋白不同分型，比较 PEL 和 MALDI-TOF MS 对 M 蛋白的检测能力。
结果 采用 MALDI - TOF MS 检测 M 蛋白的质荷比，通过还原将轻链与免疫球蛋白重链解离。以健康样本谱图为背景，对 MM 样本进行分析，从多克隆的背景中筛选出单克隆 M 蛋白。23 个 M 蛋白阳性样本分别进行原倍、10 倍、100 倍、200 倍稀释。10 倍稀释后，MALDI-TOF MS 的检出率为 100%，IFE 为 96%。当稀释 100 和 200 倍时，IFE 的检出率分别占 MALDI-TOF MS 的 28%和 23%。以 IFE 为金标准，在 712 份样品中，PEL 和 MALDI-TOF MS 的符合率分别为 85.9%和 92.3%。对于 IFE 阳性样本，PEL 和 MALDI-TOF MS 的符合率分别为 72.8%和 99.7%。在 M 蛋白不同亚型中，MALDI-TOF-MS 和 IFE 对 IgA、IgD、IgM、游离轻链和双克隆型的符合率达到 100%，而 PEL 对 IgM、IgA 和游离轻链样本的检出率分别只有 66.7%、58%和 19.5%。
结论 建立了一种快速筛查 M 蛋白的定性方法，该法简便、快速、高通量、价格低廉、特异性强、易于解读，可以满足大规模筛查实验的要求。MALDI-TOF MS 检测灵敏度高于常规的 M 蛋白检测技术，有望在多发性骨髓瘤的筛查、诊断、预后及微小残留病检测方面发挥重要作用。

PO-0381

4 例多发性骨髓瘤尿蛋白电泳 λ 轻链多聚体分析

陈欢欢、张炳峰、赵中建
江苏省人民医院（南京医科大学第一附属医院）

目的 分析多发性骨髓瘤（λ 轻链型）患者的非浓缩尿蛋白 SDS 电泳异常图谱，解决尿轻链多聚体对尿蛋白电泳检测的干扰。
方法 收集 2017 年 8 月至 2018 年 4 月江苏省人民医院检验学部发现的 4 例多发性骨髓瘤（λ 轻链型）患者尿液样本，用 5% β 巯基乙醇解聚，将未经解聚和解聚后的尿液同时行 SDS 电泳。
结果 4 例未经解聚样本电泳后都出现了异常条带，一例样本异常条带位于 IgM 所在的区域，3 例样本异常条带位于加样点附近，提示出现大分子蛋白；解聚后的 4 例样本电泳后，原有的异常条带消失，并且在轻链条带所在区域出现浓染条带，提示存在轻链多聚体。值得注意的是，原有的白蛋白条带区域出现大幅度减弱。4 例样本解聚前的电泳结果与解聚后的电泳结果均有显著差别，其中白蛋白比例分别为 74% vs 3.8%，77.2% vs 27%，61.5% vs 21.4%，61.2% vs 7.3%；游离轻链比例分别为 15% vs 91.3%，5.8% vs 70.3%，2.6% vs 75.4%，3.9% vs 87.5%。
结论 多发性骨髓瘤（λ 轻链型）患者尿液样本中出现了大量的轻链多聚体，严重干扰 SDS 电泳结果的准确性，错误的结果可能使临床对患者蛋白尿类型的作出错误判断，而准确的结果更有利于判断患者的预后。

PO-0382

TNF-α 在肺癌患者血清中的浓度和意义

李德涛
重庆医科大学附属第一医院

目的 探讨肺癌患者血清中 TNF-α 的浓度及其检测的临床意义。
方法 分别检测 63 例肺癌患者和 15 例肺良性疾病患者以及 39 例健康对照血清 TNF-α 的浓度，同时检测血清中其他常见肺癌肿瘤标志物（NSE、proGRP、CYFRA21-1）的浓度，比较各组血清 TNF-α 浓度的差异；分析血清中 TNF-α 浓度与肺癌患者临床病理特征的关系。
结果 肺癌患者血清 TNF-α 浓度显著高于肺良性疾病组和健康对照组{10.8（8.31，18.1）pg/ml vs 7.46（6.5，12.1）pg/ml，P=0.021；10.8（8.31，18.1）pg/ml vs 6.49（4.49，7.69）pg/ml，P＜0.01}；肿瘤直径＞3cm 组肺癌患者血清中 TNF-α 浓度显著高于直径≤3cm 肺癌患者组（P=0.0317）；发生淋巴结转移肺癌患者血清中 TNF-α 浓度同肺癌患者显著高于未发生淋巴结转移肺癌组（P=0.025）；肺癌患者血清中 TNF-α 浓度与肺部肿瘤的组织病理学类型、病理分期以及患者的吸烟状况、性别、年龄等无显著关系。通过绘制 ROC 曲线，当取 Cut-off 值为 8.665 ng/ml 时，血清 TNF-α 对肺癌的诊断价值最大，曲线下面积为 0.808（95% CI：0.727-0.889），敏感性为 73.0%，特异性为 80.9%，通过分析血清 TNF-α 水平与现有临床肺肿瘤标志物（NSE、proGRP、CYFRA21-1）的相关性，同血清 TNF-α 联合后，敏感性分别从 66.7%、40.5%、76.2%提高到 83.7%、83.9%和 93.6%，但是特异性由 94.9%、87.2%、92.3%降低到 76.8、70.5%、74.7。
结论 血清 TNF-α 浓度与肺癌肿瘤大小，淋巴结转移状态高度相关，值得进一步扩大样本量进行研究。

PO-0383

The molecular mechanism of TAT-P in reducing the damage of blood-brain barrier after ischemic stroke by inhibiting TRPV1 phosphorylation

Qian Feng[1,2]、jinjin song[2]、jia liang[2]、yuanjian song[2,3]、zhen zhang[2]
1. Affiliated Hospital of Xuzhou Medical University
2. 徐州医科大学
3. 徐州市医学遗传与转化工程中心

Objective To demonstrate the role of TAT-P in reducing blood-brain barrier damage after ischemic stroke and clarify the molecular mechanism of TAT-P in reducing blood-brain barrier damage after ischemic stroke.
Methods In this study, a mouse middle cerebral artery occlusion (MCAO) model was constructed by the intraluminal filament. Capsazepine (CPZ, 7.5ug/3uL /mice) was injected into the lateral ventricle 30 minutes before MCAO, TAT-P (12.5ug /uL /mice), and TAT-PS (12.5ug /uL /mice) were injected into the cortex and hippocampus. In our study, the motor function of mice was detected by the open field test and the rotarod test; the learning and memory function of the mice was detected by the water maze experiment; the cerebral infarct volume of the mice was detected by the TTC staining; the nerve function damage of mice was evaluated by mNSS score: the pathological damage of mice wad detected by HE staining: blood-brain barrier permeability of mice was detected by Evans Blue staining: the cerebral vascular damage and MMP9 expression in mice was detected by immunofluorescence staining; the interaction between PKA and AKAP150 was detected by Co-immunoprecipitation; the expression of pTRPV1, iNOS, NOX2、MMP9, Claudin5, Occludin, IL-IB, Cleaved-caspase3 protein level was detected by western blot.
Results Compared with the I/R group, the total distance, the total number of crossing and the latency in the middle area of mice in the IR+CPZ group and I/R+TAT-P group for the open field

were significantly increased (P<0.05) ; the latency of mice in the IR+CPZ group and I/R+TAT-P group were significantly prolonged in the rotarod experiment (P<0.05); the latency of the mice to reach the platform, the percentage of distance in the target quadrant and the percentage of time to total distance and total time and the number of crossing to the platform in the I/R+CPZ group and I/R+TAT-P group in the water maze experiment increased significantly (P<0.05).
(2) Compared with the I/R group, the cerebral infarction volume of the mice in the IR+CPZ group and IR+TAT-P group was significantly reduced (P<0.05); in the mNSS score, compared with the IR group, I/R +CPZ group, and I/R+TAT-P group mice nerve function damage scores were significantly reduced (P<0.05); in the HE staining experiment, compared with I/R group, /R+CPZ group and I/R+TAT-P group mice nucleus pyknosis was reduced, and cell edema was reduced
(3) Compared with the IR group, the amount of Evans blue penetrating the brainparenchyma in the I/R+CPZ group and I/R+TAT-P group were significantly reduced (P<0.05); in the immunofluorescence staining experiment, compared with the IR group, the fluorescence intensity of Claudin5 in the I/R+CPZ group and I/R+TAT-P group increased; in the western blot experiment, compared with the I/R group, the Claudin5. Occludin protein levels increased significantly (P<0.05).
(4) Compared with the I/R group, the MMP9 fluorescence intensity of mice in the I/R+CPZ group and I/R+TAT-P group were reduced; in the western blot experiment, compared with the IR group, the protein levels of iNOS. NOX2. and MMP9 in the I/R+CPZ group and I/R+TAT-P group were significantly reduced (P<0.05)
(5) Co-immunoprecipitation results showed that compared with the 1/R group, the combination of AKAP150 and PKA in the I/R+TAT-P group was reduced; the western blot results showed that compared with the I/R group, the protein level of pTRPVI in the I/R+TAT-P group was significantly reduced (P<0.05).
Conclusion TAT-P might reduce TRPV1 phosphorylation by inhibiting the combination of AKAP150 and PKA, thereby reducing blood-brain barrier damage after ischemic stroke.

PO-0384

LC-MS/MS 法测定肺栓塞患者血浆中利伐沙班的浓度

陆秋涯
上海交通大学医学院附属瑞金医院

目的 用 LC-MS/MS 法检测肺栓塞患者血浆中利伐沙班血药浓度，与常规凝血指标联合检测，评估患者疗效和凝血平衡。
方法 55 例肺栓塞患者（25 例男性），年龄 27~91 岁（均值 69.9 岁），服用利伐沙班剂量 15mg bid 或 20mg qd，其中 17 例测谷浓度，38 例测峰浓度。采样时，同步检测利伐沙班血药浓度、常规凝血 5 项和抗 Xa 活性。用 LC-MS/MS 法测定利伐沙班血药浓度，Sysmex C5100 测定凝血 5 项和 ACL-TOP 测定抗 Xa 活性。
结果 利伐沙班血药谷浓度中位数 49.7ng/ml（6.1~94.3ng/ml），峰浓度中位数 219.5 ng/ml（106.3~415.1ng/ml）。利伐沙班谷浓度与 APTT 和抗 Xa 活性有良好的相关性（p<0.05），而峰浓度与 PT、APTT 和抗 Xa 活性均有良好的相关性（p<0.05）。
结论 肺栓塞患者因服药剂量和个体代谢的差异，体内利伐沙班血药浓度存在很大差异。常规 PT 试验对于利伐沙班谷浓度不敏感。LC-MS/MS 法测定利伐沙班血药浓度与常规凝血 5 项、抗 Xa 活性联合检测，有利于患者药效和凝血平衡的评估。

PO-0385

20 例血红蛋白变异体不同检测系统结果分析

黄勤烽
联勤保障部队第九〇〇医院

目的 血红蛋白变异体在不同糖化血红蛋白检测系统中的图谱分析。
方法 1.20 例血红蛋白变异体样本，在 ARKRAY HA8180V、ARKRAY The lab 001、BIO-RAD VARIANT II 系统中分别检测。2.分析血红蛋白变异体的图谱及电泳特性。3.对 ARKRAY The lab 001、BIO-RAD VARIANT II 两个检测系统的检测结果进行对比分析，以平均血糖值（eAG）表示，换算公式 eAG(mmol/L)=1.59×HbA1c-2.59。
结果 1.ARKRAY HA8180V，序号 1 为 HbF，3、9、14、17 均有 HbA1c 检测结果，其余序号均无结果，无阴影无峰面积数据，图谱图形异常；2.BIO-RAD VARIANT II，序号 1 为 HbF，所有序号均可得到 HbA1c 结果，并分离出异常峰。3.ARKRAY The lab 001，序号 1 为 HbF，序号 3 为 HbS，序号 14、17 无 HbA1c 检测结果、无阴影、无峰面积数据、图谱图形异常，其余序号均可得到 HbA1c 检测结果，但未能分离出变异峰。4.BIO-RAD VARIANT II 的 HbA1c（5.19±0.46）低于 ARKRAY The lab 001 的检测结果（5.83±0.14），差异均有统计学意义（t=-3.597,P<0.05）；ARKRAY VARIANT II eAG 结果（5.67±0.73）同样低于 ARKRAY The lab 001（6.68±0.94），差异均有统计学意义（t=-3.594,P<0.05）。
结论 血红蛋白变异体对不同检测系统具有显著干扰，但是这种干扰通常取决于方法学、仪器的高分辨率，目前现有的血红蛋白检测系统，对于常见的 HbF、HbS，已能实现检测，对于罕见的血红蛋白变异体，仅能做到提示作用，进一步的确诊有待于基因测序。实验室在进行 HbA1c 检测时，应注意识别血红蛋白变异体，以防止对结果测定的影响。

PO-0386

降钙素原等生物标记物检测对呼吸机相关性肺炎患者的意义

王晓磊[1]、杨笑礼[2]
1. 杭州市第一人民医院
2. 浙江中医药大学医学技术学院

目的 研究机械通气合并呼吸机相关性肺炎(VAP)患者白细胞（WBC）、超敏 C-反应蛋白（hs-CRP）、降钙素原（PCT）和 PCT 清除率（PCTc）的水平及其临床意义。
方法 选择本院重症监护室 74 例机械通气患者，根据是否发生 VAP 分为 VAP 组和非 VAP 组，VAP 组根据预后情况分为恶化组和转归组。比较 VAP 组与非 VAP 组患者气管插管后第 1、3、5、7、9 天血液中 PCT、WBC 计数和 hs-CRP 浓度，比较恶化组和转归组患者血清中的 PCT 和 PCT 清除率的水平。应用受试者工作曲线(ROC)评价四项指标单独和联合诊断 VAP 的诊断效能(包括诊断准确率、灵敏度、特异度、阳性预测值和阴性预测值等) 以及 PCT 和 PCT 清除率对预后情况判断的价值 。
结果 VAP 组患者第 7 天的 PCT 结果以及第 9 天的 PCT 和 hs-CRP 结果显著高于非 VAP 组(P＜0.05)。ROC 曲线显示，在插管后第 7 天应用 PCT、hs-CRP 、WBC 单独和联合预测 VAP 的 AUC 分别为 0.764、0.645、0.559、0.735，其最佳截点分别为 PCT ≥0.33μg/L 、 hs-CRP≥128.5mg/L、 WBC≥15.3×109/L；插管后第 9 天应用 PCT、hs-CRP 、WBC 单独和联合预测 VAP 的 AUC 分别为 0.908、0.712、0.556、0.897，其最佳截点分别为 PCT ≥0.25μg/L 、 hs-CRP≥12.8mg/L、 WBC≥12.95×109/L。VAP 患者恶化组和转归组的 PCT 清除率在第 7 天和第 9 天的结果有明显差异(P＜0.05)，并且 ROC 曲线显示，PCT 清除率第 7 天和第 9 天的 AUC 分别为 0.773 和 0.777，约登指数分别为 0.433 和 0.522。而 VAP 组与非 VAP 组的白细胞浓度并无统计学差异（P>0.05）

结论 机械通气并发 VAP 患者 WBC 、hs-CRP、 PCT 水平明显升高，PCT 和 hs-CRP 对于 VAP 的诊断具有一定的临床价值。 PCT 清除率对 VAP 的预后判断有较高预测价值。

PO-0387

酶法测定尿液草酸和枸橼酸的方法学性能验证及分析前影响因素研究

秦东芳[1]、龚珂[1]、王学晶[1]、张曼[2]
1. 民航总医院
2. 首都医科大学附属北京世纪坛医院

目的 对酶法检测尿液草酸和枸橼酸试剂盒进行方法学性能验证，并对尿液保存方法进行探究，目的是用于泌尿系结石患者代谢评估的临床实践。
方法 参考美国临床和实验室标准协会（CLSI）文件和国内行业标准对草酸和枸橼酸酶法试剂盒进行性能验证，评价其精密度、正确度及线性范围。收集 2020 年 4 月北京大学民航临床医学院门诊 10 例尿液标本，分装后分别于室温、4℃和-20℃保存。在 0、2、4、8、24h 各测量一次草酸和枸橼酸浓度， 比较尿液草酸和枸橼酸浓度在不同温度下放置的变化情况。收集 20 例无结石对照和 20 例泌尿系结石患者的随机尿液标本，每例分为 4 组（A-D），分别按 100:1（即刻）、50:1（即刻）、100:1（24h 后）和 50:1（24h 后）加入 6mol/L 的 HCl 酸化。比较不同比例和时机加入浓 HCl 对草酸和枸橼酸浓度的影响。
结果 精密度和正确度验证分为低浓度和高浓度。在低浓度下，草酸的批内不精密度为 0.92%，批间不精密度为 1.63%，偏倚为-2.05%；枸橼酸的批内不精密度为 1.41%，批间不精密度为偏倚为 1.32%，偏倚为-3.36%；在高浓度下，草酸的批内不精密度为 0.32%，批间不精密度为 1.18%，偏倚为-0.93%；枸橼酸的批内不精密度为 0.91%，批间不精密度为 3.05%，偏倚为-4.62%。精密度和正确度良好。草酸在 1.65～210.71mg/L 范围内线性良好（Y=0.993X-0.216，R2=0.999）。枸橼酸在 0.19～17.85mmol/L 范围内线性良好（Y=0.953X+0.044，R2=0.999）。不加任何防腐剂，尿液在室温、4℃及-20℃保存后，草酸浓度显著降低，枸橼酸浓度较稳定。在尿液收集后即刻和收集后 24h，按照 50:1 的体积比例加入 6 mol/L 的 HCl，草酸和枸橼酸浓度没有差别（P＞0.05）。
结论 酶法尿液草酸和枸橼酸检测试剂盒的性能良好，可用于临床检测。尿液收集后 24h 加入浓 HCl 可保持草酸和枸橼酸稳定。

PO-0388

可溶性肿瘤生成抑制因子 2、平均血小板体积和同型半胱氨酸与慢性心力衰竭患者病变程度的相关性研究

蔡玉婵
上海市杨浦区中心医院

目的 探讨可溶性肿瘤生成抑制因子 2（soluble suppression of tumorigenicity 2，sST2）、平均血小板体积（MPV）、同型半胱氨酸（homocysteine,Hcy）与慢性心力衰竭（chronic heart failure,CHF)及其左心室射血分数和纽约心脏学会（NYHA）心功能分级之间的关系。
方法 选取 2019 年 9 月至 2021 年 4 月于杨浦区中心医院收治的 133 例慢性心衰患者为心衰组，另选取同期健康体检的 106 名心功能正常者作为对照组。检测所有研究对象 sST2、MPV 和 Hcy 浓度，分析三种生物标志物在不同 LVEF 和 NYHA 分级中的差异，并评估 sST2 与 MPV、Hcy 的相关性。

结果 与对照组相比，CHF 组 sST2、MPV 和 Hcy 浓度明显升高，差异均有统计学意义（P＜0.05）；随着 LVEF 的降低和 NYHA 分级的增加，患者 sST2、MPV 和 Hcy 水平逐渐升高，差异具有统计学意义（P＜0.05）；sST2 与 MPV、Hcy 浓度存在线性关系(r＝0.4581，P＜0.05；r＝0.5193，P＜0.05)。

结论 sST2、MPV 和 Hcy 浓度水平与 CHF 及其病变程度有关，联合检测 3 项指标可为 CHF 的严重程度及其预后评估提供重要参考价值。

PO-0389

基于血清直接胆红素的结肠癌根治术后患者生存期预测模型构建与验证

陆丽
上海交通大学医学院附属仁济医院(东院)

目的 探讨血清直接胆红素水平与Ⅱ、Ⅲ期结肠癌根治术后预后的关系。

方法 回顾性分析 567 例Ⅱ、Ⅲ期结肠癌根治术后患者的临床资料；单因素 Cox 回归分析血清总胆红素、直接胆红素及间接胆红素水平与Ⅱ、Ⅲ期结肠癌根治术后总生存期（OS）及无病生存期（DFS）的关系；X-tile 确定结肠癌患者 OS 和 DFS 的直接胆红素水平的 cut-off 值；选择影响结肠癌患者生存期的多个独立危险因素，采用多元 Cox 回归模型绘制预测结肠癌的 OS 及 DFS 的 Nomograms。

结果 单因素 Cox 回归分析确定直接胆红素为结肠癌 OS 及 DFS 的重要预后因素。X-tile 确定结肠癌 OS 和 DFS 的直接胆红素的 cut-off 值均为 3.1 μmol/L。多因素分析结果显示直接胆红素（P = 0.001）、年龄（P = 0.018）、低分化结肠癌（P < 0.02），T3 和 T4 期（P < 0.001），N 期（P < 0.001），具有淋巴血管侵犯（P < 0.001）是影响Ⅱ、Ⅲ期结肠癌根治术后 5 年总生存期的重要危险因素。单变量对数秩检验分析结合多元 Cox 回归分析显示直接胆红素高水平是Ⅱ、Ⅲ 期结肠癌根治术后患者预后的独立危险因素。

结论 直接胆红素可用于Ⅱ、Ⅲ期结肠癌根治术后患者的预后预测。

PO-0390

Trimetallic AuPtCo nanozyme for efficient catalysing the outstanding chemiluminescence based on biofunctionalization

Xiaoyan Zhou
Department of Clinical Laboratory, The Affiliated Hospital of Medical College, Qingdao University, Qingdao 266101, China

Chemiluminescence (CL) system with stable and glowing light emission is great significance for accurate CL quantitative of biomarkers. And catalysts harbor high catalytic activity that are effective for catalyzing the intensive chemiluminescence with improved analytical performance. In this work, trimetallic AuPtCo nanopolyhedrons possess the intrinsic peroxidase-like and catalase-like activities are synthesized through a facile strategy. The AuPtCo nanozyme can catalyze an intensive flash-type CL emission when reacts with chemiluminescent substrates of ABEI and H2O2. Interestingly, biofunctionalization on the surface of AuPtCo (AuPtCo@Bio) endows the slow-diffusion effect on the catalytic interface, thereby prolonging the emission for a glow-type CL. On the basis, the different biofunctionalized AuPtCo nanocomposites are versatilely adopted to

develop two CL assays, including AuPtCo@Cys-ABEI CL reaction and AuPtCo@AbLp-PLA2-based CL immunosensor for sensitive and selective detection of H2O2 and Lp-PLA2, respectively. Moreover, the application of these two CL assays in female vaginal discharge samples for H2O2 and human serum samples for Lp-PLA2 all exhibit good correlation with clinical results, demonstrating their excellent analytical performance. Overall, the trimetallic AuPtCo nanopolyhedrons and its biofunctionalized nanocomposites can be served as promising catalyst in the field of enzymatic bioanalysis, especially the chemiluminescent assays.

PO-0391

Clinical haematological nomograms for prediction of lymph node metastasis and prognosis in resectable esophagogastric junction adenocarcinoma

Can-Tong Liu、Yi-Wei Xu、Yu-Hui Peng
Shantou University Medical College Cancer Hospital

Background Esophagogastric junction adenocarcinoma (EJA) lacks blood-based predictive indicators for lymph node status and prognosis. We aimed to build nomograms with the preoperative haematological parameters to predict lymph node metastasis (LNM) and prognosis in resectable EJA.
Methods The training cohort consisted of resectable EJA patients from December 2003 to December 2010, and patients in the validation cohort were collected from January 2011 to December 2017. 52 candidate indicators for nomogram construction included sociodemographic data and preoperative clinical laboratory haematological baseline data. Lasso regression was used to build LNM prediction nomogram (H-score nomogram). Univariate and multivariate Cox regression analysis was applied to select factors for overall survival prediction nomogram (OS nomogram).
Findings 465 resectable EJA patients were appointed to the training cohort, and the validation cohort was comprised of 289 patients. For predicting LNM, the H-score nomogram containing seven indicators showed good discrimination and calibration ability, with C-indexes of 0·684 and 0·630 in the training and validation cohorts, respectively. Moreover, the OS nomogram for survival prediction composed of 12 factors yielded C-indexes of 0·652 and 0·613 in the training and validation cohorts, respectively. Kaplan-Meier survival analysis showed patients with high OS nomogram scores had worse 5-year OS than those with low scores (training cohort: 59·6% vs. 26·2%; validation cohort: 58·6% vs. 38·6%; all $p < 0·0001$).
Interpretations Nomograms constructed based on the clinical laboratory haematological indicators are potential prediction models for lymph node status and survival of resectable EJA.

PO-0392

GO-PTCNH2 纳米杂化物作为光电化学活性探针检测 TNF-α

陈梦园[1]、尹斐[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学中大医院，临床检验医学中心
3. 东南大学江苏省重症重点实验室

肿瘤坏死因子-α(TNF-α)作为一种细胞因子，是肺癌等多种疾病的潜在生物标志物，开发出即时有效的检测方法将提高相关疾病诊断的准确性和有效性。为此，我们课题组开发了一种简单快速的光电化学（PEC）免疫分析方法用于有效检测 TNF-α。此法通过简单研磨和超声处理，得到了具有优异光电性能和快速电子传递动力的多层氧化石墨烯/氨基端基苊衍生物（GO/$PTCNH_2$）组装。

其作为光电化学活性探针，一方面具备优异的光电化学活性；另一方面，能够提供大的表面积，快速的电子转移动力学和丰富的活性位点用于生物分子连接。首先通过简单的滴涂法将 GO-PTCNH$_2$ 组装在电极上，然后将抗 TNF-α 与 GO-PTCNH$_2$ 偶联，并对目标蛋白 TNF-α 进行捕获，能够使得传感器 PEC 信号的下降值与目标物含量呈现线性关系，从而制备出了一种用于检测 TNF-α 的“signal-off”型 PEC 免疫分析法。此检测法具有 10 pg/mL - 100 ng/mL 的检测范围且具备 3.33 pg/mL 的检测限。另外，该方法并成功运用在人血清中 TNF-α 的检测，回收率在 92.5%~ 96.6%之间，相对标准偏差小于 9.99%。这是首次利用 PTCNH2 作为光电化学活性探针来检测肿瘤生物标志物，具有显著的可靠性和简单性，可用于实际样品的检测。总之，这种高灵敏度和高选择性的 PEC 免疫传感器为癌症的早期筛查和诊断提供了前景。

PO-0393

血尿酸水平与尿路结石患者肾功能的相关性分析

赖晓霏
重庆医科大学附属第一医院

目的 探究和分析血清尿酸水平对尿路结石患者肾脏功能的临床评价预防诊断中的应用价值。
方法 选择我院 2019 年 4-5 月信息完整的尿路结石患者共 51 例作为阳性组，20 例健康体检人群作为阴性对照组。分别收集 24 小时尿液和血清标本，对 24 小时尿液进行尿草酸、尿尿酸、尿枸橼酸、尿钙、尿镁、尿磷的检测，对血清进行血尿酸检测，并对检测结果进行统计学分析。
结果 1.尿尿酸、尿钙、尿枸橼酸的检测值在尿路结石组和健康对照组有明显统计学差异（p<0.05）,尿路结石患者以高尿酸尿、高钙尿、低枸橼酸尿为主要特征。2.在结石患者中，尿尿酸和尿钙的检测值在男性尿路结石和女性尿路结石患者中有明显统计学差异（p<0.05）,尿草酸和尿钙的检测值在较大结石（直径>10mm）和较小结石（直径小于 10mm）患者中有明显统计学差异（P<0.05）， 尿尿酸和尿磷的检测值在尿路结石初发和复发患者中有明显的统计学差异（p<0.05）,尿钙和尿镁的检测值在尿路结石患者排石治疗和外科治疗中有明显统计学差异（p<0.05）。尿液中的某些成分与结石患者的部分临床表现有相关性。3.在结石患者中，血尿酸与尿枸橼酸成明显负相关，相关系数 r 为-0.341（P<0.05）；血尿酸与尿尿酸成极其显著的正相关，相关系数 r 为 0.471（P<0.001）。高尿酸血症是导致尿路结石的高危风险因素。4.在结石患者中，血尿酸水平跟胱抑素 C 水平成明显正相关，跟血肌酐水平成极其显著正相关，跟 eGFR 成明显负相关，相关系数 r 分别为 oo（P 小于 0.05），oo（P 小于 0.001），-00（P 小于 0.05）。且血尿酸与 eGFR 在尿酸结石组（R 平方=0.290）的负相关性要高于非尿酸结石组（R 平方=0.077）和对照组（R 平方=0.043）。
结论 1.上尿路结石患者以高钙尿、高尿酸尿、低枸橼酸尿为特征 2.尿液中成分跟结石患者的部分临床特征有相关性 3.高尿酸血症是致尿路结石的危险代谢因素 4.高尿酸血症是结石患者肾功能下降的危险因素。

PO-0394

甲状腺癌患者血清 IGF-1 检测的临床意义

侯玉磊
重庆医科大学附属第一医院

目的 探究血清类胰岛素生长因子 1 （Insulin-like Growth Factor 1，IGF-1）在甲状腺癌患者中的临床意义。

方法 采集所有研究对象空腹静脉血 5 ml，3000 r / min，离心 6 min，分离血清，西门子 Immulite1000 化学发光仪检测血清 IGF-1 浓度。IGF-1 测定试剂盒（化学发光法）由西门子公司提供。
结果 中晚期甲状腺癌患者血清 IGF-1 浓度显著高于早期甲状腺癌患者血清 IGF-1 浓度（Z=-2.186，P=0.029）；单发结节患者血清 IGF-1 水平显著高于多发结节患者（Z=-2.024，P=0.043）；淋巴结转移的甲状腺癌患者 IGF-1 浓度显著高于未发生淋巴结转移的甲状腺癌患者（Z=-2.356, P=0.018）；结节大小>1cm 的甲状腺癌患者血清 IGF-1 浓度高于结节大小≤1cm 的患者（Z=-2.160，P=0.031），IGF-1 浓度与结节个数呈负相关（Z=-2.024，P=0.043）
结论 甲状腺癌患者血清 IGF-1 浓度与肿瘤分期、结节个数相关，其作为甲状腺癌新的标志物具有广泛的临床应用前景。

PO-0395

基于胸水生物标志物和 CT 征象的肺癌风险模型的建立与验证

毕小云
重庆医科大学附属第一医院

目的 利用生物标志物与 CT 征象建立肺癌风险模型，以期为伴有胸水的肺部良恶性病变的诊断提供依据。
方法 纳入 594 例胸水患者，其中训练集 460 例，验证集 134 例，根据临床-放射学及实验室参数纳入 20 个危险因素。通过多因素 Logistic 回归分析建立两个列线图模型（模型 1、模型 2），并对模型进行外部验证。用曲线下面积（AUC）来量化模型预测区分能力，以 Delong 检验进行 AUC 的比较，并通过校准曲线和决策曲线分析评价模型及其临床应用价值。
结果 通过多因素 Logistic 回归分析，5 年前胸外肿瘤病史、胸水癌胚抗原（CEA）、细胞角蛋白 19 片段（CYFRA21-1）、白球比（A/G）、肿块直径、空气支气管征、分叶征和血管集束征为肺癌的危险因素。模型 1 与模型 2 在训练集中 AUC 分别为 0.979（95% CI：0.968～0.991）和 0.932（95% CI：0.909～0.955），P<0.001。在验证集中 AUC 分别为 0.911（95% CI：0.861～0.961）和 0.846（95% CI：0.776～0.917），P=0.009。在诊断分类表中两个模型的正确分类比例分别为 86.6%和 82.1%。决策曲线分析表明在 50%的阈值概率下模型 1 的净效益为 45.0%，模型 2 为 39.8%，并且在校准曲线中前者的预测值与实际值显示了更好的一致性。
结论 通过验证，胸水生物标志物和 CT 征象结合构建的模型可用于评估伴有胸水的肺部病变的癌症风险。

PO-0396

AIS 患者血清 IMA 水平及其他血液学特征与 MCA 重度狭窄/闭塞的关系研究

陈星[3,4]、杨欢[1]、李思进[1]、李慧洋[1]、任碧琼[2,4]
1. 湖南中医药大学临床医学院检验医学系
2. 湖南中医药大学临床医学院检验医学系
3. 湖南中医药大学临床医学院检验医学系
4. 湖南省第二人民医院检验科

目的 探讨急性缺血性脑卒中(AIS)患者血清缺血性修饰白蛋白(IMA)水平以及其他血液学特征与大脑中动脉(MCA)重度狭窄/闭塞的关系，为 MCA 重度狭窄/闭塞性 AIS 患者提供辅助诊断依据。
方法 纳入 2019 年 1 月至 2020 年 12 月我院卒中救治中心收治的 AIS 患者 169 例，根据 MRA 确定颅内大动脉是否重度狭窄/闭塞分为非重度狭窄/闭塞和重度狭窄/闭塞两组。再次将重度狭窄/闭塞

按是否 MCA 重度狭窄/闭塞分为 MCA 重度狭窄/闭塞和其它血管重度狭窄/闭塞两组。纳入健康人 29 例为对照组。测定患者的血清 IMA 及白蛋白（ALB）水平，计算 IMA 与白蛋白比值(IMAR)、经白蛋白调整的缺血性修饰白蛋白指数(IMA index)，同时检测血清超敏 C 反应蛋白（Hs-CRP）、血清淀粉样蛋白 A(SAA)、尿酸（UA） 、小而密低密度脂蛋白（sdLDL-c）、血脂、胆碱酯酶酶（CHE）、血常规、凝血常规等，结合患者一般资料进行综合分析。

结果 研究结果显示，重度狭窄/闭塞组血液 IMA、IMAR 水平、白细胞(WBC)、中性粒细胞值(NUT) 、INR、FDP、DD 显著高于非重度狭窄/闭塞组，而 TG、C/H、CHE 水平显著低于另外一组；MCA 重度狭窄/闭塞组的血液 IMA、IMAR 水平、INR、TT 显著高于其它血管重度狭窄/闭塞组，而 IMA index、ALB、CHE 水平显著低于另外一组；各组之间 sdLDL-c、Hs-CRP、SAA 等指标无统计学差异。多重线性回归分析表明，IMA 与白蛋白呈明显负相关。联合诊断 ROC 曲线分析表明，在 AIS 患者中，判断 AIS 患者患有颅内大动脉重度狭窄/闭塞的最佳组合为入院 NIHSS 评分+ CHE (AUC=0.783)。判断 AIS 患者患有 MCA 重度狭窄或闭塞最佳组合为 IMAR 联合入院 NIHSS 评分及 CHE(AUC=0.827)。

结论 MCA 重度狭窄/闭塞患者的 IMA、IMAR 水平明显增高， ALB、IMA index、CHE 水平显著降低。IMA、IMAR 及 IMA index 同时使用，对 MCA 重度狭窄/闭塞型 AIS 患者有一定的辅助诊断价值，并且 IMAR 联合入院 NIHSS 评分及 CHE 是判断 AIS 患者为 MCA 重度狭窄或闭塞性的最佳组合。

PO-0397

LC-MS/MS 法检测 24 小时尿液游离皮质醇的内标选择和评价

赵蓓蓓[1,2]、李冰玲[1]、袁楚茹[1]、董衡[1,2]、林清娜[1]、佘旭辉[1,2]、李卓阳[1,2]
1. 广州金域医学检验中心有限公司
2. 广州医科大学金域检验学院

目的 评估 LC-MS/MS 法检测 24 小时尿液游离皮质醇的方法中，不同氘代标记的同位素内标，对临床样品检测结果的影响。

方法 建立 LC-MS/MS 法检测 24 小时尿液游离皮质醇的方法，选择皮质醇-D4（9,11,12,12-D4）、皮质醇-D6（2,2,6,6,21,21-D6）作为同位素标记内标，评估了方法的基质特异性、基质效应、准确度、精密度、干扰实验等。将所建立方法应用于实际样品检测中，评估不同同位素标记内标对尿液样品检测结果的影响。

结果 分别采用皮质醇-D4、皮质醇-D6 作为内标，方法的基质特异性、基质效应、准确度、精密度、干扰实验等评估均满足要求。但在实际样本检测中，部分尿液样本中能检出皮质醇-D4，比较了选用皮质醇-D4 和皮质醇-D6 作为内标，建立的 LC-MS/MS 定量的检测结果存在显著差异，最高差异可达 41.7%。

结论 尿液基质中可能存在自然界同位素标记物皮质醇-d4 或皮质醇-d4 同分异构体等干扰物，虽然 LC-MS/MS 方法验证通过，但在大批量临床样本检测过程中发现干扰，可更换氘代标记数量更多的皮质醇-D6，减少对临床样品检测结果的影响。

PO-0398

Establishment of Sex-and Age-Specific Reference Intervals for High-sensitivity Cardiac Troponin I in Healthy Adults of Jilin Province Aged 20~≤95 years

bing he
First Hospital of Jilin University

Objective Cardiovascular disease was the leading cause of morbidity and mortality worldwide. Cardiac troponin (cTn), especially high-sensitivity cardiac troponin (hs-cTn), was the preferred biomarker for the diagnosis of MI. At present, there was no uniform standard for the reference interval of hs-cTnI in Chinese population. The aim of our study was to establish the 99th percentile gender-and age-related reference interval for hs-cTnI in healthy adults of Jilin Province, and to analyze the relationship between hs-cTnI and other laboratory findings.
Methods The serum specimen from recruited healthy adults (n=2183, 20~≤95 years old) were collected from the First Hospital of Jilin University. Due to the unknown interception point, we continued collecting samples from March to June 2020 to try for more than 120 individuals at every 10 years of age and each sex. The serum hs-cTnI concentration was measured on the VITROS 5600 Integrated System. For each group, the Dixon test was used to identify outliers, which were removed. Distribution and scatter plots were visually inspected to determine sex and age partitions. One sample Kolmogorov–Smirnov test was used to decide whether a random sample follows a Gaussian distribution. Differences were tested using Harris and Boyd's z-test after achieving normality. Ninety percent confidence intervals were computed for the upper limits of each reference interval. Reference interval was established by Medcalc according to the EP28-A3c guidelines issued by the Clinical and Laboratory Standards Institute. Correlation analysis was used by Spearman method.
Results The 99th percentile URL hs-cTnI concentration was 11.1 ng/L (90% CI 10.3–12.9 ng/L) for all healthy participants according to the non-parametric method. The 99th percentile URL was significantly higher in men (12.5 ng/L, 90% CI 11.1–13.8 ng/L) than in women (9.6 ng/L, 90% CI 7.6–10.9 ng/L). The 99th percentile URL of ≥55 years old group (12.6 ng/L, 90% CI 11.1–13.8 ng/L) was higher than in the < 55 years old group (8.0 ng/L, 90% CI 5.0–10.3 ng/L). The males 99th percentile URL for hs-cTnI concentration were 10.3 ng/L for <55 years old group and 13.7 ng/L for ≥55 years old group. In females, the 99th percentile URL for hs-cTnI concentration were 5.3 ng/L for <55 years old group and 10.6 ng/L for ≥55 years old group. The gender difference in the serum hs-cTnI concentration was more significant for the <55 years old group. Hs-cTnI values were significantly associated with age ($r = 0.57$, $p < 0.001$). Except for age, the strongest correlation was shown between hs-cTnI and NT-proBNP ($r = 0.44$, $p < 0.001$). Additionally, the correlation between hs-cTnI and sex ($r = 0.14$, $p < 0.001$) was lower than that between hs-cTnI and age.
Conclusion There were gender- and age-specific differences in the hs-cTnI reference intervals in healthy adult of Jilin province, China. We first established the reference intervals of hs-cTnI in Chinese adults and the validation of the reference intervals should be tested in future.

PO-0399

P2PSA 及其衍生指标对前列腺癌诊断和治疗的应用价值

陈晓婷
江苏省人民医院（南京医科大学第一附属医院）

前列腺癌是欧美国家男性最高发的肿瘤，近年来，在我国的发病率也逐年上升。相对于发达国家，我国患者的前列腺癌病死率更高。前列腺特异抗原（PSA）已广泛应用于前列腺癌的筛查和治

疗监测，但是，PSA 特异性不高，会造成 PSA 灰区患者的过度筛查与诊断。proPSA 分为 4 种亚型，其中[-2]proPSA（P2PSA）最稳定且最具癌症特异性，成为比 PSA 更为特异的标志物。而由 P2PSA 计算的衍生指标前列腺健康指数（PHI，[(p2PSA/fPSA)×√tPSA]）和%p2PSA[(p2PSA/fPSA)×10 0]，在预测高分级前列腺癌，提升前列腺癌预测模型效能等方面都有较高价值，可减少不必要的前列腺穿刺活检。本文就 P2PSA 及其衍生指标 PHI 和%p2PSA 在前列腺癌诊断和治疗中的应用价值作一综述。

PO-0400

Relationship between Oxidative Stress Biomarkers and Visual Field Progression in Patients with Primary Angle Closure Glaucoma

Shengjie Li、wenjun cao
Eye & ENT Hospital, Shanghai Medical College, Fudan University

Purpose To investigate the serum changes of oxidative stress markers and the relationship between these factors and visual field (VF) progression in patients with primary angle closure glaucoma (PACG).
Methods A case-control and a prospective cohort study. A total of 94 patients with PACG and 89 normal controls were enrolled. Furthermore, 94 PACG subjects were followed up for at least two years (once every six months). All participants were evaluated for serum levels of superoxide dismutase (SOD), total antioxidant status (TAS), hydrogen peroxide (H2O2), malondialdehyde (MDA), glutathione peroxidase, glutathione reductase, and detailed eye and systematic examination. Binary logistic regression analysis and Cox regression analysis were performed.
Results The serum levels of SOD and TAS in the PACG group were significantly lower than those in the control group ($p < 0.001$). Meanwhile, PACG subjects had significantly higher levels of MDA and H2O2 than the normal control subjects ($p < 0.001$). Serum levels of TAS (OR = 0.773, 95%CI = 0.349 − 0.714, $p < 0.001$), SOD (OR = 0.975, 95%CI = 0.955 − 0.995, $p < 0.001$), MDA (OR = 1.155, 95%CI = 1.080 − 1.235, $p < 0.001$), and H2O2 (OR = 1.216, 95%CI = 1.142 − 1.295, $p < 0.001$) were independent risk/protective factors for PACG. TAS levels (HR = 0:041, 95%CI = 0.008 – 0.218, $p < 0.001$), SOD levels (HR = 0:983, 95%CI = 0.971 – 0.994, $p = 0.003$), and MDA levels (HR = 1.010, 95%CI = 1.001 – 1.018, $p = 0.015$) at baseline were associated with visual field progression. Kaplan–Meier curves reveal that patients with TAS < 0.95/SOD < 143/ MDA > 12 had a significantly higher percentage of PACG progression ($p < 0.05$).
Conclusions Decreased levels of TAS and SOD as well as increased levels of MDA at baseline were associated with VF progression in patients with PACG. These findings suggest that oxidative stress was involved in the onset and development of PACG.

PO-0401

Gd-BOPTA-enhanced MRI in the hepatobiliary phase: Evaluate liver function with the Degree of Biliary System Visualization

min huang
Shandong Provincial Hospital Affiliated to Shandong First Medical University

Background Assessment of preoperative hepatic function is very important in surgical planning for avoiding post-hepatectomy liver failure. The Child-Pugh classification system is commonly

used for evaluation of liver function. However, it has limitation in quantitatively evaluating liver function.
Purpose To evaluate liver function according to the degree of biliary system visualization of Gd-BOPTA-enhanced MRI.
Results The RE were associated with total bilirubin (r = -0.542, P < 0.01), prothrombin time (r = -0.520, P < 0.01), albumin (r = 0.555, P < 0.01) and liver parenchyma enhancement (r=0.457, P<0.001). The RE was significantly higher for NLF group than LCA (P < 0.001), LCB (P < 0.001), and LCC (P < 0.001) groups. The RE was significantly higher for LCA group than LCB (P < 0.001), and LCC (P < 0.001) groups. ROC curves revealed a cut-off value ≥2.695 (sensitivity 0.81, specificity 0.93, AUC 0.793) for NLF group, and ≥ 2.305 (sensitivity 0.83, specificity 0.92, AUC 0.954) for LCA group.
Conclusions The degree of biliary system visualization of Gd-BOPTA-enhanced MRI may be used as an imaging-based, quantifiable metric to estimate liver function.

PO-0402

慢性肾功能不全患者中血清脂肪酶升高的临床研究及相关性分析

黄少铃、何奥玉、李卫滨、张胜行
中国人民解放军联勤保障部队第 900 医院

目的 研究慢性肾功能不全（Chronic renal failure，CRF）患者血清脂肪酶（Lipase，LIPA）水平与病情严重程度之间的关系，探究 CRF 患者血清 LIPA 升高的原因。
方法 选取联勤保障部队第九〇〇医院 2021 年收治的慢性肾功能不全住院患者共 110 例，用回顾性分析方法收集资料，比较血清 LIPA 在 CRF 不同阶段患者中的表达水平及 30 例健康对照者之间的差异，分析血清 LIPA 升高与肾小球滤过率（Estimated Glomerular filtration rate，eGFR）、尿素（Urea）、胱抑素 C（Cystain C，CYS-C）、血肌酐（Serum creatinine，Scr）、淀粉酶（Amylase，AMY）、全段甲状旁腺素（Intact parathyroid hormone，iPTH）、甘油三酯（Triglycerides，TG）之间是否存在相关性。
结果 1.110 例 CRF 患者中，共有 45 例发生血清 LIPA 水平增高，占比 40.9%，其中 CKD5 期 48.1%、CKD4 期 42.9%、CKD3 期 28%、CKD2 期 20%。所有病例均未出现 LIPA 超出上限三倍及以上的情况，AMY 均在正常范围内。正常体检组未出现 LIPA 增高超出上限的情况。2.CRF 患者血清 LIPA 水平为 258.5（173.75~389）U/L，正常体检者为 96(82~107)U/L，差异有统计学意义（P＜0.05）。3.CKD2 期患者血清 LIPA 水平为 122.5(113.5~531.25)U/L，CKD3 期患者为 177(148~291)U/L，CKD4 期患者为 272.5(146.25~433.75)U/L，CKD5 期患者为 280.5(222~462.5)U/L。其中正常体检组与 CKD3、CKD4 期、CKD5 期差异有统计学意义（P＜0.05），CKD3 期与 CKD5 期差异有统计学意义（P＜0.05）。4.CRF 患者的血清 LIPA 与 AMY（r=0.37,P＜0.05）、P（r=0.35,P＜0.05）呈正相关。与 iPTH、TG 的相关性无统计学意义。
结论 慢性肾功能不全患者血清脂肪酶相较正常人升高，升高幅度在参考区间上限的三倍之内，从 CKD3 期开始，随 CKD 的进展而增加。LIPA 水平与肾功能、血清淀粉酶水平密切相关，其升高的原因可能是 CRF 时清除率的下降或产生亚临床胰腺损伤。诊断急性胰腺炎时，应考虑到慢性肾功能不全导致血清 LIPA 升高的可能；对 CRF 患者动态检测血清脂肪酶对判断 CRF 分期及严重程度、指导治疗、判断预后有一定临床价值。

PO-0403

二甲双胍减轻铁代谢及脂质代谢紊乱机制的研究

贾佳
南京大学医学院附属鼓楼医院

目的 近十几年的研究发现二甲双胍不仅是降糖首选药，而且具有良好的降脂减肥作用，但是又有研究表明，长期服用二甲双胍会导致不同程度的贫血，原因尚未明确。
方法 铁作为机体必须的微量元素之一，以多种存在形式参与脂质代谢的过程。铁与脂质两种代谢途径在体内许多场所相互作用，铁可通过参与脂质代谢的酶和转运蛋白的组成，直接影响脂质的分布、转归和分泌，也可通过亚铁形式的铁诱导氧化应激和炎症间接影响脂质代谢；而脂质代谢也不同程度影响铁的吸收和分布。本研究旨在用高脂喂养的脂肪肝小鼠模型探讨二甲双胍的降脂作用与铁代谢通路改变的影响。
结果 二甲双胍灌胃脂肪肝小鼠模型相较于未用二甲双胍灌胃小鼠肝细胞死亡及肝纤维化程度均减轻。
结论 二甲双胍通过对机体脂代谢的影响，降低机体铁死亡，对于伴有血脂紊乱相关疾病的预防和治疗有重要意义。

PO-0404

五种项目在乳腺癌患者中的变化及临床意义

赵宗晨
山东第一医科大学附属省立医院

目的 乳腺癌患者外周血红细胞分布宽度（RDW-CV）、中性粒细胞与淋巴细胞比值（NLR）、血小板分布宽度（PDW）、白蛋白（ALB）及血红蛋白与红细胞分布宽度的比值（HGB/RDW-CV）的变化及临床意义。
方法 收集 2010 年 7 月至 2012 年 2 月山东大学附属省立医院乳腺癌住院患者 400 例为研究组，体检健康志愿者 300 例为健康对照组。比较两组 RDW-CV、NLR、PDW、ALB 及 HGB/RDW-CV 比值的结果及与其他病理参数的关系。
结果 乳腺癌患者组的 RDW-CV、NLR、PDW、ALB、HGB/RDW-CV 比值均显著高于对健康照组，差异有统计学意义（P<0.05）。绘制 ROC 曲线，RDW-CV 曲线下面积为 0.333，确定最佳截点后，将 400 例乳腺癌患者组分为低 RDW-CV（≤12.55，146 例）组和高 RDW-CV（>12.55，254 例）组。NLR 曲线下面积为 0.446，分为低 NLR（≤2.37，301 例）组和高 NLR（>2.37，99 例）组。PDW 曲线下面积为 0.652，分为低 PDW（≤12.15，211 例）组和高 PDW（>12.15，189 例）组。ALB 曲线下面积为 0.951，分为低 ALB（≤44.65，334 例）组和高 ALB（>44.65，66 例）组。HGB/RDW-CV 曲线下面积为 0.749，分为低 HGB/RDW-CV（≤10.78，253 例）组和高 HGB/RDW-CV（>10.78，147 例）组。高低组 RDW-CV、NLR、PDW、ALB 在病理分级中均无统计学意义（P>0.05），高低组 HGB/RDW-CV 在病理分级分级中有统计学意义（P<0.05）。高低组 RDW-CV、NLR、PDW、ALB 在 TNM 分级中无统计学意义（P>0.05），高低组 HGB/RDW-CV 在 TNM 分级中有统计学意义（P<0.05）。
结论 NLR、RDW-CV、PDW、ALB 及 HGB/RDW-CV 在乳腺癌诊断提供了重要的参考价值，且 HGB/RDW-CV 与乳腺癌的恶性程度有关。

PO-0405

新疆生产建设兵团某师 30 岁以上常住居民血脂异常随机抽样调查

查贺飞、刘春燕、张新
新疆生产建设兵团医院

目的 探讨新疆生产建设兵团(以下简称兵团)某师常住居民血脂异常的患病率及影响因素，为预防血脂异常提供依据。
方法 选取 2014 年 11 月至 2015 年 3 月兵团第四师≥30 岁的常住居民(居住时间＞6 个月)，采用多阶段分层随机抽样的方法，最终纳入 4624 人为调查对象。比较男女的血脂水平及血脂异常患病率差异；分析不同年龄组男女血脂异常患病率差异；比较血脂正常组和血脂异常组合并超重和肥胖、糖尿病、高血压、慢性肾病患病率；采用多因素 Logistic 回归分析兵团第四师居民血脂异常的影响因素。
结果 女性 TC 和 LDL-C 水平高于男性，TG 水平和血脂异常患病率低于男性，差异有统计学意义(*P*<0.05)。调查对象＜60 岁时，相同年龄段中男性血脂异常的患病率均高于女性，调查对象≥60 岁时，男性血脂异常的患病率低于女性，差异有统计学意义(*P*<0.05)。血脂异常组合并超重和肥胖、糖尿病、高血压、慢性肾病的患病率均高于血脂正常组，差异有统计学意义(*P*<0.05)。性别(男性)、超重和肥胖、糖尿病、高血压和慢性肾病均是调查对象发生血脂异常的独立危险因素(*P*<0.05)。
结论 中青年男性和更年期后女性是兵团第四师居民血脂异常的防控重点，应加强血糖和血压的检测，并通过改善不良的生活习惯降低该地区血脂异常的患病率。

PO-0406

高尿酸血症伴高血压患者认知功能障碍的横断面研究

冯双亮
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 高尿酸血症和高血压是认知功能障碍的独立因素。然而，这两个因素的结合与认知功能障碍之间的关系尚不清楚。本研究旨在探讨高尿酸血症合并高血压与认知功能障碍风险的关系。
方法 本研究于 2018 年对 2963 名 45 岁及以上的参与者进行了横断面调查。自报高血压及血压≥140/90mmhg 者为高血压。以空腹静脉血尿酸水平测定高尿酸血症。采用简易精神状态检查（MMSE）探讨认知障碍。采用多变量 logistic 回归模型分析不同人群组合与认知功能障碍的关系。
结果 健康 1724 例（58.2%），高尿酸血症伴高血压 57 例（1.9%），单纯高尿酸血症 45 例（1.5%），单纯高血压 1137 例（38.4%）。高尿酸血症合并高血压组 MMSE 评分（26.8±3.4）明显低于正常对照组（28.1±1.9；P<0.001）。高尿酸血症合并高血压组认知功能障碍的患病率明显高于其他组（17.5%）。认知功能障碍与高尿酸血症合并高血压（校正比值比[OR]：3.04；95%可信区间[CI]：1.30-7.24）、单纯性高尿酸血症（校正比值比[OR]：0.44；95%可信区间[CI]：0.05-3.55）、单纯性高血压（校正比值比[OR]：1.26）显著相关；95%置信区间[CI]：0.79-1.99）。女性单纯性高血压、单纯高尿酸血症、高尿酸血症合并高血压有相关性，有统计学意义，男性无相关性。
结论 高尿酸血症合并高血压与认知功能障碍风险增加有关，尤其是女性。为早期预防认知障碍和痴呆提供临床依据。

PO-0407

全自动生化分析仪生化检验指标在肝硬化疾病诊断中的应用价值评估

付舒婷
吉林大学第一医院

目的 利用全自动生化分析仪生化检验指标在肝硬化疾病诊断中的应用价值评估。
方法 选取我院 2019 年 11 月～2021 年 3 月收治的 80 例肝硬化患者作为研究对象分为研究组，同时选取同期 80 例健康体检者作为参照组，两组人员均在空腹状态下抽取 5ml 静脉血液，离心机调至 3500 r/min，5min 进行血清分离，通过全自动生化分析仪对血液标本进行生化指标检验，然后借助两点终点法、速率法、酶法等对肝功能指标包括丙氨酸氨基转移酶（ALT）、门冬氨酸氨基转移酶（AST）、碱性磷酸酶（ALP）、γ-谷氨酰转肽酶（γ-GT）、总蛋白（TP）、白蛋白（ALB)、总胆红素(TBIL)、直接胆红素(DBIL)、胆碱酯酶(CHE）等进行检测，对比两组人员肝脏的生化指标。
结果 研究组门冬氨酸氨基转移酶（AST）、丙氨酸氨基转移酶（ALT）、γ-谷氨酰转肽酶（γ-GT）、碱性磷酸酶（ALP）、总胆红素(TBIL)、直接胆红素(DBIL)水平均明显高于参照组，研究组总蛋白（TP）、白蛋白（ALB)、胆碱酯酶(CHE）水平均明显低于常规组，差异有统计学意义（P<0.05）。
结论 生化检验指标在肝硬化疾病诊断中的临床应用价值高，临床上可依据生化检验指标判断肝硬化患者的肝脏病变程度，从而为疾病的临床诊断提供指导意见和诊断依据，对早期的诊断具有重要意义。

PO-0408

98 例维持性血液透析患者透析充分性的实验室指标评价

刘春燕、李晓苗、葛若卿、梁梦洁、张新
新疆生产建设兵团医院

目的 采用实验室指标对 98 例维持性血液透析(maintenance hemodialysis, MHD)患者透析充分性进行评价，为 MHD 患者诊疗方案的持续改进提供实验室基础。
方法 选取 2017 年 10 月至 2019 年 08 月在新疆生产建设兵团医院血液净化中心接受透析龄 3 个月以上的 98 例 MHD 患者（男 50 例，女 48 例），参照《中国血液透析充分性临床实践指南》对 MHD 患者透析充分性的评价标准，采用非参数检验、c2 检验对 MHD 患者透析前的单室尿素清除率（spKt/V）、酸碱平衡、营养状况及骨矿物质代谢等实验室指标进行统计分析。
结果 66.3%的 MHD 患者 spKt/V≥1.4，女性组 spKt/V≥1.4 的患者数量多于男性组（P<0.05）。62.2%患者存在不同程度的酸中毒，女性组血清碳酸氢盐<20.0mmol/L 的患者数量多于男性组（P<0.05）。17.3%患者血清白蛋白（Alb）未达到 35 g/L，Alb 浓度达到 35～40.0 g/L 的患者为 59.2%，仅有 23.5%患者控制较好（≥40 g/L），且女性低蛋白血症患者数量明显多于男性（P<0.05）。33.7%的患者存在不同程度贫血，其中女性贫血患者高达 47.9%，女性贫血患者数量显著多于男性（P<0.05）。43.9%的患者呈现低钙血症状态，男性校正血钙<2.10 mmol/L 的患者数量多于女性（P<0.05）。另外，55.1%的患者甲状旁腺激素≥300 pg/mL，甲状旁腺激素的浓度从 1.23 到 1914 pg/mL。
结论 98 例 MHD 患者实验室指标基本能达到《中国血液透析充分性临床实践指南》的标准，但女性更易发生营养不良、酸碱平衡紊乱等临床表现，男性更易发生骨矿物质代谢紊乱，临床应制定精细化、个体化 MHD 患者透析治疗和生活指导方案，以期更好延长患者生存期。

PO-0409

Optilite 特定蛋白分析仪尿液 Lambda 游离轻链参考区间的建立

张玲、潘建华、周锐雄
广州金域医学检验中心

目的 初步建立 Optilite 特定蛋白分析仪尿液 Lambda 游离轻链参考区间。
方法 选取广州金域体检中心健康者 150 名，男女各 75 人，男女性平均年龄 43 岁，按年龄段分为 5 组选样，为 20～30 岁选 20 人、31～40 岁组选 50 人、41～50 岁组选 40 人、51～60 岁组选 30 人、≥60 岁组选 10 人。留取肉眼可见的澄清尿液样本，立即送检，并参考血液检测的相关项目指标正常，该组人群血液酶法检测尿素(UREA)平均值为 4.72mmol/L、肌酐(Cr)均值为 81U、γ-谷氨酰转肽酶(GGT)均值为 26U/L，血常规 31 项结果无异常，同时采用 Optilite 特定蛋白分析仪（免疫比浊法）检测 Lambda 游离轻链。依据我国卫生行业标准 WS/T 402—2012《临床实验室检验项目参考区间的制定》CLISI C28 建立 Lambda Freelite 的参考区间，采用 EP Evaluator 软件进行统计。
结果 测得尿液 Lambda Freelite 均值 4.182mg/L、标准差 3.72mg/L、检测结果范围 0.67-20.61mg/L、最小值 0.67mg/L、最大值 44.58mg/L、次大值 20.61mg/L、极差 43.91mg/L、1/3 极差为 14.64mg/L、离群值验证 23.97mg/L。剔除离群值 44.58mg/L 后验证极差为 19.94mg/L，1/3 极差为 6.65mg/L，离群验证值为 4.49mg/L，小于 1/3 极差 6.65mg/L，验证通过，本室验证 Optilite 特定蛋白分析仪检测 Lambda Freelite 的参考区间为 0-15.42mg/L，与 Optilite Lambda Freelite 厂家说明书提供的参考范围 0-3.79mg/L，比值相差 4.07 倍。
结论 临床实验室应该根据中国人群建立 Optilite 特定蛋白分析仪尿液 Lambda 游离轻链参考区间来对检测结果进行判断，为临床提供可靠客观的诊断依据。

PO-0410

同位素稀释液相色谱串联质谱技术在定量血清载脂蛋白 C-Ⅰ、C-Ⅱ和 C-Ⅲ上的应用

李卿、居漪、孙贺伟、虞科颖
上海市临床检验中心

目的 载脂蛋白 C 家族在血脂异常方面有重要临床意义。目前 apo C 项目尚未广泛开展。在临床质谱领域上，罕见蛋白类项目。本研究使用同位素稀释液相色谱串联质谱技术（ID-LC-MS）定量检测载脂蛋白 C-Ⅰ、C-Ⅱ和 C-Ⅲ，为建立基于质谱平台的蛋白类多项目联合检测提供方法支持。
方法 采用“自下而上”的蛋白定量思路。选择代表性定量肽段，对样品与同位素标记的肽段同步进行变性、还原、烷基化等前处理，经胰蛋白酶酶解，用液相色谱串联质谱定量检测目标肽段，峰面积与内标比和浓度构建校准方程，换算出待测物的载脂蛋白 C-Ⅰ、C-Ⅱ和 C-Ⅲ的含量，并与定值血清的靶值比较。
结果 肽段 TP（apo C-Ⅰ）、TY（apo C-Ⅱ）和 GW（apo C-Ⅲ）响应最高，被选择为定量肽段。使用校准品的定量肽段与同位素标记肽段的峰面积比与校准品浓度建立校准方程，三个蛋白的校准方程相关系数 R>0.95。ID-LC-MS 检测定值血清样品，与靶值的相对偏移分别为-1.5%（apo C-Ⅰ）、-5.2%（apo C-Ⅱ）和-5.4%（apo C-Ⅲ）。
结论 ID-LC-MS 可用于定量检测人血清 apo C-Ⅰ、apo C-Ⅱ和 apo C-Ⅲ。apo C-Ⅰ的定量结果并不包括截短的 apo C-I 亚型，apo C-Ⅱ和 apo C-Ⅲ的定量结果为血清中总的组分。清晰明确的靶向定量，不仅为临床的应用转化提供了借鉴方案，也推动了方法的标准化和溯源。

PO-0411

新生儿高胆红素血症凝血功能回顾性分析

谢珊辉
中国医科大学附属盛京医院

目的 探讨新生儿高血清胆红素血症与凝血功能异常的相关性。
方法 收集盛京医院于 2018 年 1 月至 2021 年 4 月分娩的 138 例新生儿为研究对象，将临床上诊断为高胆红素血症的 97 例患儿为病例组，包括生理性黄疸组和病理性黄疸组，将同期出生的 41 例正常足月儿为对照组。检测并比较各组新生儿凝血功能相关指标包括活化部分凝血活酶时间（APTT）、凝血酶原时间（PT）、血浆纤维蛋白原降解产物（FDP）、凝血酶时间（TT）、血浆纤维蛋白原（FIB）、抗凝血酶活性测定（AT）、总胆红素（Tbil）、直接胆红素（Dbil）。
结果 病例组和对照组相比，FDP、Tbil、Dbil 水平升高，APTT 延长，TT 缩短、AT 水平降低，差异具有统计学意义(P<0.05)，而病理性黄疸组和生理性黄疸组相比，AT 水平升高，Tbil 水平降低，APTT、PT 缩短，差异具有统计学意义(P<0.05)。logistics 回归分析结果显示病例组 Tbil，FDP 水平均高于对照组，TT 延长(P<0.05),而生理性黄疸组 FDP 水平高于病理性黄疸组，Tbil 水平低于病理性黄疸组(P<0.05)。
结论 新生儿高胆红素血症可影响凝血功能，在新生儿儿科临床中应加强对凝血指标的监控。

PO-0412

肝酶、平均血小板体积和红细胞分布宽度值对预测妊娠期糖尿病发生发展的临床应用价值

缪淑贤
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨测定肝酶、红细胞分布宽度(RDW)和平均血小板体积(MPV)数值对于预测妊娠期糖尿病(GDM)发生发展的临床应用价值。
方法 收集 368 例 2019 年 1 月至 2019 年 12 月在江苏省妇幼保健院确诊为妊娠期糖尿病孕妇的病例资料，记录相关实验室检查参数结果。同时收集同期 368 例健康体检者作为对照组，比较不同组间所有参数差异。
结果 在所有参数中，GDM 组的血小板分布宽度(PDW)、转氨酶(ALT)和 γ-glutamyl 转移酶（GGT）明显高于健康对照组（P＜0.05）；GDM 组的血小板压积 (PCT)水平显著降低(P＜0.01)；而在平均血小板体积（MPV）、红细胞分布宽度（RDW）、血小板计数（PLT）和天冬氨酸转氨酶（AST）水平上，组间无显著差异。
结论 我们的研究结果表明，ALT、GGT、PCT 和 PDW 可以作为预测 GDM 发展的预测指标，为临床诊断妊娠期糖尿病开拓了新的思路。

PO-0413

四川省学龄前儿童全血微量元素检测结果分析

李清春、丁玲
四川金域医学检验中心有限公司

目的 微量元素在人体内含量虽然微乎其微，但却能在生理代谢过程中发挥着不可或缺的作用，对维持机体的正常生理功能和生长发育具有十分重要的意义，其含量在人体内处于动态平衡，缺乏或过量均会对人体产生不良的影响，尤其是学龄前儿童微量元素的缺乏对儿童的生长发育有较大影响。

通过对四川省 18439 人次（共 129073 例数据）学龄前儿童全血微量元素镁、钙、锰、铁、铜、锌、铅 7 种元素进行结果分析，了解四川省学龄前儿童（0~7 岁）微量元素含量水平。
方法 采用电感耦合等离子质谱（ICP-MS）技术对 18439 人次（共 129073 例数据）学龄前儿童全血进行微量元素检测，并按不同性别、年龄、项目对检测结果进行统计、比较、分析。
结果 检测结果显示，在检测的 7 种元素中，缺乏人数最多的是锌，锌缺乏者 3540 人（19.20%）；其次是铁，缺乏者 629 人（3.41%）；过量人数最多的元素是铜，过量者 1267 人（6.87%）；其次为锰，过量者 122 人（0.66%）。同时，锌、铁的缺乏及铜、锰的过量在 0~2 岁年龄段时人数最多，随年龄增长，缺乏或过量人数皆逐渐降低，直至 6~7 岁阶段人数有所回升。学龄前儿童中，铁、铜、锰、锌的缺乏及镁、铜、锰、钙的过量人数在 0~2 岁阶段远高于 3~7 岁的儿童。
结论 锌元素的缺乏和铜元素的过量在四川省学龄前儿童中是非常多见的，是这个年龄段儿童全血微量元素异常普查的主要方向，而 0~2 岁年龄段则是学龄前儿童全血微量元素异常的主要年龄段。建议儿童应注意微量元素的普查，在医师的指导下及时全面的进行膳食营养调节。同时，根据儿童不同年龄阶段，医师应针对相应最容易发生异常的元素进行着重监测和调节，以保障儿童微量元素在体内含量不失衡，从而减少微量元素异常对儿童生长发育的影响。

PO-0414

一氧化氮、胱抑素 C 和同型半胱氨酸联合检测对脑梗死辅助诊断价值

刘园
南京大学医学院附属鼓楼医院

目的 评价血清一氧化氮（NO）、胱抑素 C（Cys C）及同型半胱氨酸（Hcy）联合检测对脑梗死的诊断价值。
方法 选取 2019 年 1 月至 2019 年 6 月在南京大学医学院附属鼓楼医院就诊的 60 例脑梗死患者为观察组，30 名同期健康体检者作为健康对照组。采用间接比色法进行 NO 检测，采用免疫比浊法进行 CysC 检测，采用酶循环法进行 Hcy 检测。检测观察组和对照组血清 NO、CysC 及 Hcy 水平，并对两组检测结果进行比较分析。绘制受试者工作特征（ROC）曲线并计算及比较曲线下面积，评价 3 指标单项及联合检测的诊断价值。
结果 观察组血清 NO、CysC 和 Hcy 水平分别为：42.05(32.70~53.30) μmo/L、1.20(0.88~1.59) mg/L、19.80(14.93~22.65) μmo/L，均明显高于对照组（均 P<0.05）。单项指标检测诊断脑梗死时，Hcy 的敏感度最高（78.33%），CysC 的特异度最高（96.67%）。3 项联合检测时，敏感度高达 90.00%，特异度为 90.00%。血清 NO、CysC、Hcy 诊断脑梗死的最佳诊断临界值分别为 40.30μmo/L、1.05mg/L、14.50μmo/L，ROC 曲线下面积分别为 0.657、0.831、0.829。 3 项联合检测 ROC 曲线下面积为 0.942，高于 NO、CysC、Hcy 单指标检测，差异有统计学意义（Z=5.011、3.038、2.768，均 P<0.05）。
结论 血清 NO、CysC 及 Hcy 在脑梗死辅助诊断中具有一定价值，3 项联合检测相比于单项检测效能具有明显的优势，有更好的临床价值。

PO-0415

安徽地区非孕期健康女性抗苗勒氏管激素医学参考值建立

王波、张明亮
合肥金域医学检验实验室有限公司

目的 分析安徽地区非孕期健康女性抗苗勒氏管激素（AMH）情况，建立安徽地区抗苗勒氏管激素（AMH）医学参考值。

方法 选取 2020 年 1 月-2020 年 12 月送检合肥金域医学检验实验室有限公司抗苗勒氏管激素（AMH）样本 4019 例，按年龄段分为 5 组，20~24 岁（422 例）、25~29 岁（853 例）、30~34 岁（945 例）、35~39 岁（730 例）、40 岁以上（1069 例），抗苗勒氏管激素（AMH）采用 Roche cobas e602 全自动电化学发光免疫分析仪检测（该项目参加安徽省及卫生部临床检验中心室间质评，成绩优秀）。分析不同年龄段抗苗勒氏管激素（AMH）结果差异，参考值范围用（P50）及双侧限值（P2.5，P7.5）表示。

结果 5 组 AMH 检测结果差异具有统计学意义（$p<0.05$），抗苗勒氏管激素（AMH）在 20~24 岁参考值为（1.650-9.590）ng/ml、25~29 岁参考值为（1.080-9.260）ng/ml、30~34 岁参考值为（0.572-7.450）ng/ml、35~39 岁参考值为（0.677-5.140）ng/ml、40 岁以上参考值为（0.046-2.060 ng/ml）。

结论 本次回顾性分析发现抗苗勒氏管激素（AMH）随着年龄不断增长，AMH 结果有下降趋势，存在地区特异性，因此建立各地区抗苗勒氏管激素（AMH）医学参考值及其重要。

PO-0416

Performance evaluation of ICP-MS in detecting eight nutrient elements

Fang Luan
Shandong Provincial Hospital

Objective To evaluate the performance of ICP-MS in detecting eight nutrient elements.

Method Nutrient elements in whole blood were determined within one week using Agilent 7900 Inductively Coupled Plasma Mass spectrometry (ICP-MS) (Agilent, Tokyo, Japan). The ultrapure water (≥18.0MΩ.cm, 25℃) used in the experiment was prepared by Milli-Q ultrapure water meter (Millipore Corporation, USA). Whole blood element testing kit was used for measurement (LOT: WL191102; Baichen, Hangzhou, China). The performance evaluation is as follows: The matching calibrator (LOT: 20011401) were tested for 3 times for assessing the linearity. In accordance with the Clinical and Laboratory Standards Institute (CLSI) 15A-3, within-run Coefficient of variations (CVs) and total CVs were calculated in four replicates of two concentrations quality control products (LOT:2001140) every day for five consecutive days. Trace Elements Whole Blood L-2 RUO (LOT: 1702825; Seronor™, Norway), which have been analyzed in independent laboratories (ALS Scandinavia AB, Luleå, Sweden), was determined for estimation of bias. The internal standard recovery was within 80-120%.

Result Limit of detection (LOD), and limit of quantification (LOQ). The LOD and LOQ were determined through detection of reagent blank for at least 10 times for each analyte and calculate the standard deviation (SD). The LOD was defined as three times of SD while the LOQ was defined as ten times of SD. The LODs of Mg, Ca and Fe were 0.003, 0, and 0.006 mmol/L, Cu and Zn were 0 and 0 μmol/L, Mn, Se and Sr were 1.366, 0.695, and 0 μg/L; LOQs, 0.009, 0, and 0.021 mmol/L, 0 and 0 μmol/L, 4.552, 2.316, and 0 μg/L, respectively.

Linearity. Linearity was evaluated via linear regression of the calibrator concentrations on the theoretical concentrations. The correlation coefficients (r2) of linearity for Mg, Ca, Fe, Cu, Zn, Mn, Se and Sr were >0.999.

Precision Precisions of Mg, Ca, Fe, Cu, Zn, Mn, Se and Sr were evaluated using two concentrations of quality controls. The within-run CVs and totle CVs for eight nutrient elements were shown in Supplemental table 2 respectively.

Estimation of bia. Comparing with the analytical data of Seronorm™ Trace Elements Whole Blood L-2 RUO, bias of Mg, Ca, Fe, Cu, Zn, Mn, Se and Sr were all within 10%.

Conclusion ICP-MS behaves well in accuracy, repeatability, linear range in detecting elements in whole blood.

PO-0417

难治性继发性甲状旁腺功能亢进中脂肪因子的变化研究

周允、曹永彤
中日友好医院

目的 对难治性 SHPT 患者血清全段甲状旁腺激素（intact parathyroid hormone, iPTH）和脂肪因子水平进行相关性分析。
方法 选取拟行甲状旁腺切除术（parathyroidectomy, PTX）治疗的终末期肾病患者 70 例，收集患者临床资料，ELISA 测定血清 TNF-a、IL-6、总脂联素（total adiponectin, APN）和高分子量脂联素（high molecular weight adiponectin, HMW APN）、Chemerin 和 Adipsin 水平，采用 Pearson 法对其相关性进行分析。
结果 70 例患者中，男性 40 例，女性 30 例，平均年龄 47.5 ± 12.5 岁（24～69 岁）；PTX 前血清 iPTH 1212 ± 709 ng/L（328～3585 ng/L），WBC 计数 6.27 ± 1.57 109/L（3.75 ～9.96 109/L），SOD 149 ± 29 U/ml（86～215 U/ml），TNF-a 115 ± 75 pg/ml （2～397 pg/ml），IL-6 35 ± 22 pg/ml （2～181 pg/ml），APN 15.1 ± 9.6 μg/ml （1.6～43 μg/ml），HMW APN 4.9 ± 3.7 μg/ml （0.2～20 μg/ml），Chemerin 210 ± 42 ng/ml （135～307 ng/ml），Adipsin 16.8 ± 0.5 μg/ml （15.2～17.7 μg/ml）。Pearson 相关分析表明，SHPT 患者血清 iPTH 水平与年龄、WBC 计数、TNF-a、APN、HMW APN 无显著相关性，与 SOD （p=0.005）、Chemerin （p=0.002）呈显著正相关，与 IL-6 （p=0.048）、Adipsin （p=0.000）及 HMW APN/APN 比值（p=0.046）呈显著负相关。
结论 难治性 SHPT 患者 PTX 前血清 iPTH 水平与血清 SOD 和脂肪因子 Chemerin、IL-6、Adipsin 水平以及 HMW APN/APN 比值密切相关，提示脂肪因子家族可能参与了 SHPT 患者内环境稳态的调控。这将为阐明 SHPT 患者的微炎症状态提供新认识，为 SHPT 并发症的防治提供新见解，而其内在机制也值得进一步探讨。

PO-0418

同型半胱氨酸及血脂相关指标在糖尿病合并冠心病中的应用研究

王堃[1]、师悦杰[2]
1. 中南大学湘雅医院
2. 中南大学湘雅医学院

目的 研究同型半胱氨酸、高密度脂蛋白、低密度脂蛋白、载脂蛋白 A1、载脂蛋白 B 等血脂相关指标在糖尿病合并冠心病患者中的独立相关性、预测价值和对于疾病预后的作用。
方法 收取符合收入标准的非合并糖尿病冠心病患者 145 例，合并糖尿病冠心病患者 28 例，健康体检受试者 59 例，三者分别定为疾病对照组、疾病观察组、健康对照组，采用回顾性分析的方法研究 HCY 及血脂相关指标与冠心病患病情况的关系。
结果 采用 t 检验分析同型半胱氨酸及其他血脂相关指标。其中观察组（冠心病）HCY 水平显著高于健康对照组（15.44±7.66vs10.96±1.77，P<0.05，有统计学意义)。疾病观察组与疾病对照组相比，甘油三酯、HCY 显著升高，有统计学意义（HCY：21.48±6.12vs13.84±2.21，P<0.05，有统计学意义；TG：1.76±0.49vs1.08±0.38，P<0.05,有统计学意义）。对 55 岁以下人群估计 HCY 参考区间（<14.24umol/L）。对 HCY 与冠心病患病情况在控制其他血脂指标的前提下进行偏相关分析。
结论 TG、HCY 是冠心病发病的独立危险因素，且 HCY 与冠心病发病具有较稳定的相关性，即使控制了其他血脂指标，相关性仍然显著。55 岁以下糖尿病合并冠心病患者的 HCY 参考区间为（<14.24umol/L)。

PO-0419

常规检验项目在多发性骨髓瘤及相关浆细胞疾病预测中的应用

梁珊珊、贾成瑶
四川大学华西医院实验医学科

目的 多发性骨髓瘤及相关浆细胞疾病临床表现不特异，临床容易漏诊、忽视，而影响患者的早期诊断和治疗，拟利用常规检验项目，建立浆细胞疾病诊断的预测模型，在临床诊疗工作中起到提示作用。
方法 回顾性分析 2012 年-2019 年在四川大学华西医院诊断为多发性骨髓瘤(MM)及相关浆细胞疾病且进行血清蛋白电泳检查患者的完整初诊数据，M 蛋白结果为阳性的人群为病例组，以血清蛋白电泳阴性人群为对照组。采用二元 logisitic 分析 MM 及相关浆细胞疾病的独立危险因素，并建立包含多个指标的概率预测模型，采用受试者工作曲线 ROC 对该模型进行评估，并验证模型准确性。
结果 共纳入实验组 743 例，对照组 3532 例，性别（SEX）、年龄（AGEclasss）、骨损情况（BONE IMPAIR）、血红蛋白（HB）、球蛋白（GLB）、白球比（A/G）、肾小球滤过率（eGFR）、校正钙（CA）比较，差异均有统计学意义（P<0.05）。建立回归预测模型，ROC 曲线下面积为 0.743，约登指数为 0.381，灵敏度 0.623，特异性 0.758。
结论 预测模型预测效果较好，但仍需不断完善。临床医生可利用此预测模型，通过常规的检验项目结果，尽早对可疑浆细胞相关疾病的人群开展血清蛋白电泳筛查。

PO-0420

TG/HDL-C 比值可作为预测 2 型糖尿病发生发展的新型标志物

童玲[1,2]、梁如意[2]、杨舒羽[2]、陈奕君[2]、干伟（通讯作者）[2]
1. 自贡市第三人民医院检验科
2. 四川大学华西医院实验医学科

目的 研究甘油三酯与高密度脂蛋白胆固醇比值（TG/HDL-C）与 2 型糖尿病发生发展的关系，评估其作为 T2DM 早期标志物的可行性。
方法 根据 1999 年 WHO 糖尿病诊断和分型标准，纳入 2015 年 1 月至 2021 年 1 月在四川大学华西医院内分泌科就诊的 553 名住院患者，根据葡萄糖耐量试验（OGTT）和临床检查结果，将其分为正常糖耐量组（NGT），空腹血糖受损组（IFG），糖耐量异常组（IGT），2 型糖尿病组（T2DM）以及 2 型糖尿病伴并发症组。对各组患者临床资料与实验室指标进行统计分析，采用单因素回归分析筛选与 T2DM 发生发展的相关指标，通过多因素回归分析逐步调整年龄、性别、吸烟、饮酒等指标，探讨 TG/HDL-C 是否是糖尿病发生发展的独立危险因素。
结果 TG/HDL-C 在各组之间的趋势如下：NGT 组 0.91（0.62-1.54），IFG 组 1.32（0.89-2.00），IGT 组 1.33（0.81-2.43），T2DM 组 1.68（1.08-3.27）以及 T2DM 伴并发症组 1.67（1.00-2.61）。在 TG/HDL-C 与 HOMA-IR 的受试者工作曲线（ROC）中，得到其 AUC 面积 为 0.707，当 TG/HDL-C 比值大于 1.272 时，预测胰岛素抵抗发生的灵敏度为 0.684，特异性为 0.651。在校正了年龄、性别、吸烟、饮酒、BMI 后，TG/HDL-C 仍然有统计意义，其 P 值如下：IFG 组（P=0.004），IGT 组（P=0.006），T2DM 组（P＜0.001）以及 T2DM 伴并发症组（P=0.001），其 OR 值分别为 IFG 组 1.347(1.100-1.648)，IGT 组 1.313(1.081-1.594) ，T2DM 组 1.456(1.207-1.751)和 T2DM 伴并发症组 1.404(1.159-1.700)。
结论 TG/HDL-C 是 2 型糖尿病发生发展的独立危险因素，相比于 OGTT，检测更为简单，可作为预测 T2DM 的早期标志物。

PO-0421

还原氧化石墨烯场效应晶体管生物传感器高灵敏免标记检测外泌体

喻轶、张国军
湖北中医药大学

外泌体是一种粒径在 50-150 nm 左右的微小囊泡，其中包含具有多种功能活性的生物分子如蛋白质，核酸等。由于与其来源细胞具有高度的同源性，广泛存在于各类体液中（如：血液，尿液，唾液等）可反应疾病的进程和状态，因此在临床诊断上具有重要的意义。目前，定量生物体液中低浓度的癌源性的外泌体仍然是一个巨大的挑战。场效应晶体管生物传感器由于在检测中具有灵敏度高，特异性高，高度集成化的特点被广泛的应用于各类生物分子的检测中。在本研究中，我们探索了一种基于还原氧化石墨烯场效应晶体管生物传感器高灵敏，免标记的方法来直接检测外泌体。在传感区域修饰了可特异性识别外泌体的 CD63 抗体，用于免标记的对外泌体进行定量检测，该传感器检测外泌体灵敏度为 33 particles/μL,且具有较高的特异性，与现有的检测方法相比灵敏度较高，此外该生物传感器可以用于检测临床血清样本中的外泌体，结果显示外泌体含量在在健康人群中和前列腺癌患者中存在显著的差异。与其他技术不同的是本研究提供了一种独特的方法，无需标记即可直接定量外泌体，表明了该传感器在临床癌症早期诊断中的潜力。

PO-0422

不同公式估算的肾小球滤过率与尿微量白蛋白/肌酐在糖尿病肾病中的应用

李强、 达娃顿珠
中国医科大学附属盛京医院

目的 通过分析糖尿病肾病患者和健康人肾小球滤过率和尿微量白蛋白/肌酐比值的情况，以进一步了解肾小球滤过率和尿微量白蛋白/肌酐与糖尿病肾病患者发病的关系，同时应用不同公式（CKD-EPI 2009 Cr 公式和 CKD-EPI 2012 CysC-Cr 联合公式）估算肾小球滤过率，为更好地防治和诊断上述疾病提供参考依据。
方法 比较糖尿病肾病患者公式（CKD-EPI 2009 Cr 公式和 CKD-EPI 2012 CysC-Cr 联合公式)估算的肾小球滤过率和尿微量白蛋白/肌酐水平，探究各项指标与糖尿病肾病各分期的相关性。
结果 在 DN 的各阶段 CKD-EPI2009Crea 公式较 CKD-EPI2012Crea-CYSc 公式得出的值更高，在 DN 二期时两种公式的标准偏差较小且两种公式间相差小。在 DN 三期时 CKD-EPI2012Crea-CYSc 公式得出的标准偏差较大，DN 四、五期时 CKD-EPI2009Crea 公式得出的标准偏差较大，且在 DN 五期两种公式得出的标准偏差间存在更明显的差异。
结论 用肌酐和胱抑素 C 联合使用计算的 CKD-EPI2012Crea-CYSc 公式有较好的一致性，用肌酐和胱抑素 C 联计算的 CKD-EPI2012Crea-CYSc 公式与单独用肌酐计算的 CKD-EPI2009Crea 公式有一定差异。CKD-EPI2012Crea-CYSc 公式的准确度较高是更适合临床评价肾小球功能的 eGFR 公式。

PO-0423

变构探针触发的双信号循环为基础的 CRISPR-Cas12a 系统用于免水洗胞外囊泡分析

赵贤贤[1,2]、罗阳[1,2]
1. 重庆大学医学院智慧检验与分子医学中心
2. 重庆大学医学院公共实验中心

Extracellular vesicles (EVs) are emerging as promising biomarkers for cancer diagnosis and therapy. Recognizing low abundance EVs from clinical samples in an easy-to-operate way is highly desired but remains a challenge. Herein, we established an allosteric probe-initiated dual cycle amplification-assisted CRISPR-Cas12a (AID-Cas) platform for sensitive detection of EVs in a wash-free way. In AID-Cas, the allosteric probe can specifically recognize and bind with target EVs and thus initiate the following dual-cycle amplification. Subsequently, the amplified products were transcribed to generate numerous single-stranded RNAs, which could work as crRNA to trigger the trans_x0002_cleavage of CRISPR-Cas12a. Consequently, the proposed approach achieved a good linear response to extracted EVs in a concentration range from 102 to 106 particles/μL. Because of its high sensitivity,together with its wash-free convenience, the proposed strategy could have promising clinical potentials for early diagnosis of cancers.

PO-0424

液相色谱串联质谱技术在 17-羟化酶缺乏症诊断中的应用

孔许净、郑燕华、樊晓敏、姚珺、孙慧颖、陈宝荣
北京金域医学检验实验室有限公司

背景 液相色谱串联质谱（LC-MS/MS）技术在临床检验中应用逐渐深入，尤其在内分泌领域逐步发挥重要作用，如儿茶酚胺及其代谢物、神经递质和类固醇激素的检测等。其中类固醇激素其含量低且化合物间结构类似，因免疫技术检测原理的限制难以实现其准确可靠地检测。目前越来越多的国内实验室建立多种类固醇激素的检测，可以提高检测的灵敏和准确度，从而更好地为临床服务。
目的 在 Waters TQ-S IVD 检测系统上建立一种高灵敏高特异性的液相串联质谱方法，检测肾上腺皮质代谢路径中的 19 种主要类固醇激素，应用于先天性肾上腺皮质增生症（CAH）中 17-羟化酶缺乏症（17-OHD）的筛查及鉴别诊断。
方法 采用固相萃取法进行标本前处理，在 Waters TQ-S IVD 检测系统上进行检测。液相**方法** 色谱柱为 C8 色谱柱，流动相 A 为 0.5mmol/L 氟化铵水溶液，流动相 B 为纯甲醇，采用梯度洗脱；质谱**方法** 采用多反应监测模式。本研究纳入 67 例血浆标本进行临床验证，其中包含 18 例 17-OHD 患者，49 例正常人。产生的数据通过 MassLynx 软件进行处理，以中位数表示，采用 t'检验进行统计学分析。
结果 17-OHD 患者血浆中孕烯醇酮（7033pg/mL）、孕酮（1ng/mL）、11-脱氧皮质酮（674.6pg/mL）和皮质酮（43.34ng/mL）在的含量均高于正常人（941.7pg/mL，0.06ng/mL，25.14pg/mL，1.8ng/mL），其他指标均出现不同程度的降低，且女性患者降低幅度明显高于男性患者。17-OHD 患者的类固醇激素异常主要体现在孕烯醇酮、孕酮、11-脱氧皮质酮和皮质酮升高及皮质醇、可的松、脱氢表雄酮、硫酸脱氢表雄酮、雄烯二酮、睾酮和双氢睾酮降低，其余指标无明显差异。
结论 本研究所建立的 LC-MS/MS 方法检测 19 种类固醇激素，可准确定位肾上腺皮质代谢路径中某一个酶的缺乏，对 CAH 中 17-OHD 的诊断具有重要价值。

PO-0425

HBV 相关肝硬化进展为肝癌的预测模型建立

冯永辉[1]、赵可馨[2]
1. The First Hospital of China Medical University
2. 中国医科大学附属第一医院

目的 肝癌是我国第二大致死原因，五年生存率低于 5%，预后极差。有效的早期筛查指标进行早期预测，对提高肝细胞癌的整体诊治水平至关重要。本研究纳入 HBV 相关肝硬化及肝癌患者的实验室检测指标作为预测因子，旨在建立有效的诊断预测模型；
方法 收集中国医科大学附属第一医院就诊的乙肝肝硬化 661 例和乙肝肝癌患者 696 例，选取相关实验室指标并对其数据进行 Logistic 回归，分析所选指标与 HCC 发病风险的相关性。选取肝癌发病风险高相关性指标（P < 0.05）构建列线图预测模型，并且通过 ROC 曲线及校准曲线对模型进行验证。
结果 对两组数据采用 Logistic 回归进行单因素分析，结果表明 24 个指标是肝硬化进展到肝癌的危险因素（P< 0.05）；使用方差膨胀因子进行多重共线性检验并采用向后逐步回归法进行多因素分析，结果表明 Ca、HBV-cAb、AFP、Fbg 均为肝癌的高风险因素（P< 0.05），将此 4 个指标构建列线图预测模型，ROC 曲线显示模型的 AUC=0.761（95% CI: 0.731-0.791），Hosmer-Lemeshow 拟合优度检验 P=0.19。验证组 ROC 曲线显示模型的 AUC=0.768（95% CI: 0.723-0.814），Hosmer-Lemeshow 拟合优度检验 P=0.91。
结论 基于 Ca、HBV-cAb、AFP、Fbg 建立了一个 HBV 相关肝硬化进展为 HCC 的预测模型，该模型具有良好的区分度和校准度，能够对患者 HBV 相关 HCC 发病风险的预测提供帮助。

PO-0426

公式法计算离子钙结果可靠性评估

林炜炜、张乐乐、沈盈、彭凤、李敏
上海交通大学医学院附属仁济医院

目的 比较离子选择电极法与 4 种公式法计算离子钙（iCa）结果的差异，评估公式法与离子选择电极法的相关性，对公式法计算离子钙结果的可靠性进行评价。
方法 回顾统计了 2020 年 7 月至 2020 年 12 月的 6147 例门诊及住院患者，其中男性 3591 例，女性 2556 例，平均年龄 57.89 岁（9 个月到 95 岁间），均有测定总钙、离子钙、总二氧化碳、碳酸氢根离子、总蛋白、白蛋白、氯离子等项目。以离子选择电极法为参考方法，计算法为实验方法，计算相关系数及回归方程；并以离子钙测定值为参考值，计算不同公式与直接测定值符合率。
结 果 公式法与选择电极法相关性由高到低依次为自建公式 2：（iCa=0.330×tCa-0.007[AG]+0.006×[Cl-]+0.003×[HCO3-]-0.001×ALB-0.158 ）；自建公式 1（iCa=0.327×tCa+0.006×[Cl-]+0.003×[HCO3-]-0.006×[AG]-0.108）；Forster 1985 公式；Nordin 1989 公式相关系数依次为：0.659,0.657,0.477,0.222。6147 例标本中离子选择电极法 iCa 浓度分布 0.23-1.70mmol/L，以离子选择电极法 iCa 浓度为对照组，以百分偏差小于 10%为要求，公式法符合率由高到低依次为：自建公式 2、Forster 1985 公式、自建公式 1、Nordin 1989 公式；符合率依次 92.19%、87.59%、82.11%、51.47；当离子选择电极法 iCa 浓度在 0.99-1.40mmol/L 之间时符合率最高,依次为 95.52%、90.78%、86%、52.92%；当离子选择电极法 iCa 浓度≤0.98 或≥1.41mmol/l 时，公式法结果符合率均下降，尤以离子选择电极法 iCa 浓度≤0.98mmol/L 更明显，符合率均降至 40%以下。此外自动线性建模（公式 2）结果显示，预测离子选择电极法 iCa 结果按重要性高低依次为 tCa(0.208)、Cl-（0.164）、AG(0.160)、HCO3-(0.157)、ALB(0.155)、TCO2(0.155)。

结论 离子选择电极法 iCa 浓度在 0.99-1.40mmol/L 时与公式法有很高的符合率，特别是公式 2，符合率 95.52%；离子选择电极法 iCa 浓度在≤0.98mmol/L 时，所有计算公式结果均明显高于实际测定值，用计算公式可能会高估 iCa 的浓度；离子选择电极法 iCa 浓度在≥1.41mmol/L 时，所有计算公式结果均明显低于实际测定值，用计算公式会低估 iCa 的浓度

PO-0427

高密度脂蛋白及其受体在革兰阴性脓毒症发生发展中的应用研究

邹国英、祝青
湖南省第二人民医院

目的 探讨革兰阴性菌脓毒症（G-脓毒症）患者血清高密度脂蛋白(HDL）、B 类 I 型清道夫受体(SR-BI）、载脂蛋白 M(apoM)、载脂蛋白 C(apoC)的水平，探讨其对 G-脓毒症的诊断、病情严重程度及预后的评估价值。
方法 选取湖南省第二人民医院 2019 年 9 月至 2020 年 9 月收治的 128 例脓毒症患者、40 例单纯全身炎症反应综合征患者，40 例健康人员作为研究对象。根据血培养及革兰染色结果分为 90 例 G-脓毒症患者和 38 例革兰阳性脓毒症患者；按病情严重程度分为一般组（53 例）和休克组（37 例）；按 28 天病情转归分为存活组（69 例）和死亡组（21 例）。采用酶联吸附法检测研究对象血清中 SR-BI、apoM 和 apoC 水平，并动态监测上述指标在患者入住 ICU 后第 1、3、5 天的水平变化。分析 HDL 及其受体与 SOFA、APACHEⅡ评分相关性，并绘制 ROC 曲线分析 HDL 及其受体对 G-脓毒症的诊断、病情严重程度及预后评估价值。
结果 1.早期诊断：SIRS 组、G+脓毒症组及 G-脓毒症组较健康对照组相比，患者血清 HDL-C、apoC、apoM 和 SR-BI 水平均有明显降低，ROC 曲线分析结果显示 SR-BI、HDL-C、apoM 和 apoC 诊断 G-脓毒症的敏感性分别为 97.78%、85.56%、93.33%和 73.03%，特异性分别为 82.50%、95.00%、61.54%和 82.50%。
2.判断病情严重程度：休克组较一般组患者血清 HDL-C、apoC、apoM、SR-BI 水平均明显降低；监测结果提示患者血清 SR-BI、apoC 水平呈上升趋势；SR-BI、apoC 水平改变程度达到 3 倍；SR-BI、apoC、apoM 与 SOFA 评分、APACHEⅡ评分存在负相关。进一步采用 ROC 曲线分析结果显示其诊断 G-脓毒症休克的敏感性分别为 32.43%、43.24%、65.75%、72.97%，特异性分别为 94.34%、86.79%、83.07%、81.13%。
3.预后评估：死亡组较存活组患者血清 HDL-C、apoC、apoM 和 SR-BI 水平明显降低；ROC 曲线结果显示 SR-BI 的的预测效能最好，apoM 联合 SR-BI 的 AUC、灵敏性和特异性分别为 0.977、95.24%、89.88%，高于 apoM 和 SR-BI。
结论 HDL 及其受体与细菌感染类型相关，患者血清 HDL-C、apoC、apoM 和 SR-BI 的水平可以作为 G-脓毒症早期诊断的潜在生物标志物，且其血清水平降低时，提示病情加重，尤其是 SR-BI 和 apoC 的监测有利于及时发现病情的改变。血清 apoM 与 SR-BI 联合应用提高预后评估的敏感性和特异性。

PO-0428

异常血红蛋白电泳原因分析

庞雪利
成都医学院第一附属医院

目的 地中海贫血是一组常见的危害较大的遗传性溶血性贫血疾病。它是由于基因缺陷或者点突变致使血红蛋白中一种或一种以上珠蛋白链合成缺如或不足所导致的贫血或病理状态，呈小细胞低色

素性贫血。血红蛋白电泳检测是地中海贫血的筛查试验，但血红蛋白电泳结果异常并非一定就是地中海贫血，本研究旨在探讨血红蛋白电泳结果异常的可能原因。
方法 收集 2018 年 9 月至 2021 年 3 月在成都医学院第一附属医院检测了血红蛋白电泳的 3666 名患者的结果并进行分析。同时分析了有异常电泳结果患者的血常规，铁蛋白和地中海贫血基因检测结果。其中，血常规主要分析了血红蛋白(Hb)，平均红细胞体积（MCV），平均红细胞血红蛋白含量(MCH)和红细胞体积分布宽度的变异系数（RDW-CV）。
结果 检测了血红蛋白电泳的 3666 名患者中，有 233 名患者的结果出现了异常，约占总数的 6.36%。在这 233 名患者中，检出地中海贫血基因阳性 128 例，为血红蛋白电泳异常总人数的 54.9%，为血红蛋白电泳筛检总人数的 3.49%。其中 α 地中海贫血 12 例，为地贫患者总人数的 9.37%。β 地中海贫血基因的阳性例数为 116 例，为地贫患者总人数的 90.63%。在 HbA2 升高的病例当中，80.03%为 β 地中海贫血；在 HbA2 降低的病例当中，18.37%为 α 地中海贫血，48.98%为缺铁性贫血，6.12%为 β 地中海贫血；HbA2、HbF 均升高的病例中，90.00%为 β 地中海贫血。可能为异常血红蛋白病的有 5 例。
结论 血红蛋白电泳的异常结果大部分是由于贫血导致，地中海贫血是导致出现异常结果的主要原因。而其他贫血疾病如缺铁性贫血也是导致出现异常血红蛋白电泳的重要原因。

PO-0429

Fitted serum ALT, AST, and AFP values in the short-term prognosis of chronic viral hepatitis

Jiexin Zhang、Lei Huang、Mengyao Yu、Shichang Zhang
Department of Laboratory Medicine, The First Affiliated Hospital of Nanjing Medical University

Purpose Chronic viral hepatitis (CVH) is a prior stage of cirrhosis, acute-on-chronic liver failure and primary cancer, which causes significant morbidity and mortality in liver-related diseases. Standard protocols of CVH monitor and assessment are of great significance for precise treatment and better prognosis during the long follow-up period. Our study aimed to analyze multiple serum indexes in CVH patients and compare their clinical prediction value of short-term curative effect.
Methods We enrolled 55 CVH patients who were first diagnosed in our hospital from July 2015 to June 2016 by necessary criteria. With the complete collection of their clinical as well as laboratory data up to now, we divided them into the effective treatment group (33 patients) and the ineffective treatment group (22 patients) according to clinical outcomes at discharge. The generalized models of each serum index were respectively constructed by R language to predict the fluctuation trend of each index in time-dependent manner and to observe the time-dependent relationship among these indicators.
Results Serum virus copy numbers, liver enzymes, and blood coagulation indexes were significantly decreased after standardized interferon therapy in the effective treatment group ($p<0.005$). Their serum alpha-fetoprotein (AFP) level was 29.80 (9.80, 158.90) ng/mL characterized by a sharp increase in less than 4 months followed by a rapid decrease to the baseline. We combined serum AFP with Alanine aminotransferase (ALT) and Aspartate aminotransferase (AST) of all patients to establish generalized additive models and found: 1) AFP secretion in the effective treatment group was upregulated in response to increased ALT and AST levels; 2) ALT and AST levels alleviated by liver cell regeneration; 3) AFP level gradually dropped as liver function restored. Overall, the dynamic changes of serum ALT, AST and AFP in CVH patients exhibited an intersecting nested bell-shaped diagram during five-year follow-up. Nevertheless, serum AFP level was 4.00 (2.40, 5.65) ng/mL in the ineffective treatment group, and it had no correlation with neither ALT nor AST.
Conclusion Serum AFP is a promising index of CVH short-term prognosis which predicts effective liver regeneration and recovery. The measurement of serum AFP, ALT and AST at

monthly interval will help to optimize the anti-virus therapy and may guide other interference protocols to prolong disease-free survival.

PO-0430

建立 LC-MS/MS 法测定血浆中利伐沙班的浓度

陆秋涯
上海交通大学医学院附属瑞金医院

目的 建立 LC-MS/MS 法检测血浆中利伐沙班血药浓度，用于患者服药后疗效和出血风险评估。
方法 血浆样品经含内标利伐沙班-d4 乙腈沉淀蛋白，使用色谱柱为 Phenomenex Kinetex F5 柱（3.0 × 100 mm, 2.6 μm），流动相为 5mM 醋酸铵水溶液（A）：甲醇（B），采用梯度洗脱分离，流速 0.5 mL·min-1，柱温为 40℃。 采用电喷雾离子化电离源（ESI），正离子方式检测，利伐沙班和内标的离子对分别为 m/z 436.0→m/z 145.1 和 m/z 440.1→m/z 145.1。
结果 血浆中利伐沙班在 2~500 ng·mL-1 范围内线性关系良好（r =0.9995）。 最低检测浓度为 2 ng·mL-1，提取回收率与基质效应分别为 97.5%~111.3%和 94.2%~102.8%。 质控样本日内和日间准确度分别为 95.0%~110.8%和 99.7%~112.9%，相对标准差（RSD）均<10%。 样本稳定性符合要求。
结论 本研究建立的方法快速且准确，适用于血浆利伐沙班的血药浓度检测,可用于药效和出血风险评估。

PO-0431

同型半胱氨酸、血清淀粉样蛋白 A、 脂蛋白相关磷脂酶 A2 在早期糖尿病足中的诊断价值

肖曦
湖南省

目的 探讨同型半胱氨酸（Hcy）、血清淀粉样蛋白 A（SAA）、 脂蛋白相关磷脂酶 A2（Lp-PLA2）在早期糖尿病足中的诊断价值。
方法 收集 252 例 wagenr 分级 1、2 级糖尿病足患者（观察组）和 175 例 2 型糖尿病无并发症患者（对照组），分别采用循环酶分析法、免疫透射比浊法和速率法检测两组血清 Hcy、SAA、 Lp-PLA2 的水平并比较，分析其在早期糖尿病足中的诊断价值。
结果 观察组 Hcy、Lp-PLA2、SAA 水平显著高于对照组，差异具有统计学意义（P<0.05）；Hcy、SAA、Lp-PLA2 均为早期糖尿病足的危险因素（β 值分别为 0.448、0.206、0.044）并具有统计学意义（P<0.001）；ROC 曲线结果显示，Hcy、SAA、Lp-PLA 曲线下面积（AUC）分别为 0.918、0.892、0.967，三者联合为 0.99。
结论 T2DM 早期糖尿病足患者体内 Hcy 和 Lp-PLA2 水平高于 T2DM 无并发症患者；Hcy、Lp-PLA2 和 SAA 为 T2DM 早期糖尿病足的相关危险因素，联合检测对早期糖尿病足的诊断具有重要意义。

PO-0432

Correlation of Krebs von den Lungen-6 and fibronectin with pulmonary fibrosis in coronavirus disease 2019

Dinghui Peng[1]、Yi Luo[1]、Li jun Huang[2]、Fan lu Liao[1]、Yan yuan Liu[1]、Peng Tang[1]、Han ning Hu[1]、Wei Chen[1]
1. Zhongnan Hospital of Wuhan University
2. Department of Clinical Laboratory, Huangzhou District People's Hospital

Objective Coronavirus Disease 2019 (COVID-19) caused by a novel severe acute respiratory syndrome corona_x0002_virus 2 (SARS-CoV-2), is still spreading worldwide, which may progress to pulmonary fibrosis (PF), leading to the worsen outcome. As the markers of lung injury, the correlation of Krebs von den Lungen-6 (KL-6) and fibronectin (Fn) with pulmonary fibrosis in COVID-19 was still unclear.
Methods 113 patients diagnosed as COVID-19 were enrolled in this retrospective study, and divided into three categories as mild, moderate and severe cases. The concentrations of serum KL-6 and Fn at hospital admission were tested using the method of latex agglutination assay and immunoturbidimetic assay, respectively.
Results Compared with that in the non-severe COVID-19 cases and normal control subjects, serum KL-6 con_x0002_centration on admission was significantly higher in the severe group, which was positively correlated with Creactive protein, and negatively correlated with lymphocytes count. Whereas, no obvious elevation in serum Fn concentration was investigated in COVID-19 patients with the different phenotypes. The severe cases displayed the higher incident rate of pulmonary fibrosis at hospital discharge. Compared with non-PF patients, the COVID- 19 cases with PF had the higher serum KL-6 values.
Conclusion Serum KL-6 concentration was significantly elevated in severe COVID-19 patients, which may be useful for evaluating the disease severity. For early prevention of the development of pulmonary fibrosis, high concentrations of serum KL-6 in the early stage of COVID-19 should be paid close attention.

PO-0433

铁蛋白用于化疗诱导的心脏毒性的诊断价值评估

张芳芳、任丽
天津医科大学肿瘤医院

目的 肿瘤患者在接受化疗期间或者化疗后短期或长期发生的心脏功能障碍称为化疗诱导的心脏毒性（CIC）。随着肿瘤患者生存期的不断延长，CIC 已成为导致肿瘤患者死亡的主要原因之一。近年来，越来越多的研究工作表明铁死亡过程在化疗诱导的 CIC 中起到了非常重要的作用。铁死亡是一种细胞内铁离子代谢紊乱并以 ROS 堆积和脂质过氧化为主要特点的细胞程序性死亡事件。目前对铁死亡机制的研究主要集中在细胞内的铁离子代谢变化，而 CIC 患者体内的总体铁含量是否会随之发生变化还不清楚。铁蛋白是反应人体铁含量相对稳定的一个指标，本研究旨在评价铁蛋白是否可用于 CIC 患者的早期预测及长期动态监测，为临床医生治疗方案的及时调整和改善肿瘤患者预后提供重要参考价值。
方法 单点采集样品随机选取天津市肿瘤医院 2020 年 10 月 1 日至 10 月 15 日接受化学治疗的 150 名患者和没有接受化疗的 100 名患者的血清样品，并对其中二十位接受化疗的患者的血清样本进行连续跟踪收集。针对所有样品的 B 型钠尿肽（BNP）、肌钙蛋白 I（TnI）和铁蛋白（Ferr）含量进行检测。结合患者病历资料，使用 Graphpad Prism 软件进行统计分析。
结果 1.单次检测患者血清铁蛋白含量我们发现铁蛋白在化疗患者血清中显著升高，但相关性分析结果显示无论在化疗组还是非化疗组，血清铁蛋白含量与传统心脏标志物（BNP,TnI）的相关性都不高，提示单次检测血清铁蛋白的含量对于评价化疗患者是否会发生心脏毒性意义不大。2.对铁蛋白

和 BNP、TnI 进行连续监测的结果显示，在出现心脏毒性的患者血清中，铁蛋白的异常升高均早于或伴随着传统心脏标志物的异常，提示连续监测血清铁蛋白可能具有化疗诱导的心脏毒性的早期预测价值及较高的诊断敏感性。
结论 连续监测血清铁蛋白含量有助于对化疗诱导的心脏毒性的早期诊断。

PO-0434

沈阳地区 13610 例维生素 D 结果分析及与 2 型糖尿病的关系

杨梅
中国医科大学附属盛京医院

目的 了解沈阳地区不同年龄、性别、季节人群维生素 D 的水平，探究维生素 D 水平与 2 型糖尿病（T2DM）的关系。
方法 选取 13610 例健康查体者，检测血清总 25-羟维生素 D 水平，比较不同年龄、性别、季节维生素 D 水平；选取 200 例 T2DM 患者为 T2DM 组，同期 200 例健康体检者为对照组，检测血清总 25-羟维生素 D 水平，采用二元 Logistic 回归分析对不同维生素 D 水平的 T2DM 比值比（OR）进行分析。
结果 受检者 13610 例中维生素 D 缺乏者占 21.53%，不足者 28.06%，正常者 50.41%；年龄分组中，婴儿组维生素 D 水平显著高于其他各组(P<0.05)，其次幼儿组，随着年龄增加，维生素 D 水平逐渐减低；按性别分组，男性维生素 D 水平显著高于女性(P<0.05)；按季节分组，夏季维生素 D 水平显著高于冬季(P<0.05)；T2DM 组维生素 D 水平显著低于健康对照组（P<0.05），维生素 D 不足人群较正常人群患 T2DM 的风险增加（OR=2.86,95%CI 为 1.39-6.11），维生素 D 缺乏人群较正常人患 T2DM 的风险则明显增加（OR=4.08,95%CI 为 1.20-8.33）。
结论 加强沈阳地区儿童及以上年龄段人群维生素 D 的补充，加强冬季维生素 D 的补充与监测。维生素 D 不足或缺乏人群患 T2DM 的风险明显增加。

PO-0435

血清 LDH,CA153,FA 和 Hcy 水平检测在 MA 和 MDS 临床鉴别诊断中的作用研究

岳虹
西安市第一医院

目的 探讨血清乳酸脱氢酶(LDH)、糖类抗原 153(CA153)、叶酸(FA)和同型半胱氨酸(Hcy)水平检测在巨幼细胞性贫血(MA)、骨髓增生异常综合征(MDS)临床鉴别诊断中的作用效果。
方法 选择 2018 年 5 月至 2019 年 8 月 MA/MDS 患者 98 例作为对象,设为观察组,根据疾病类型分为 MA 组和 MDS 组,选择同期体检健康者 54 例,设为对照组。检测各组 LDH、CA153、FA 及 Hcy 水平;绘制受试者工作特征曲线(ROC 曲线),分析 LDH、CA153、FA 及 Hcy 在 MA、MDS 中鉴别诊断效能。
结果 观察组 LDH、CA153 及 Hcy 水平均高于对照组(P<0.05),FA 水平低于对照组(P<0.05);MA 组 LDH、CA153、FA 及 Hcy 水平均高于 MDS 组(P<0.05);ROC 曲线分析结果表明,LDH、CA153、FA 联合 Hcy 检测在 MA、MDS 中鉴别诊断灵敏度、特异度均高于 LDH、CA153、FA、Hcy 单独检测(P<0.05)。
结论 LDH、CA153、FA 及 Hcy 在 MA、MDS 患者中表达异常,联合检测能实现 MA、MDS 的诊断、鉴别,能为临床诊疗提供依据和参考。

PO-0436

Down-regulation of USP8 Inhibits Cholangiocarcinoma Cell Proliferation and Invasion

xu jing
The Second Hospital of Shandong University

Objective Cholangiocarcinoma is the second most common primary hepatobiliary malignancy with high incidence and recurrence rate. Ubiquitin-specific protease 8 (USP8) is recently reported to be involved in tumor progression. Herein, we aimed to investigate the effects of USP8 on the growth and metastasis abilities of cholangiocarcinoma cells.
Methods The siRNA interference was used to knock down USP8 in cholangiocarcinoma cell lines QBC939 and RBE; Hucct-1 cells were transfected with pcDNA3.1-USP8 to upregulate its expression. The effects of USP8 on cholangiocarcinoma were detected by cell function assays. We analyzed the expressions of USP8, Bcl2, Bax, cleaved caspase-3, cleaved caspase-9, Akt, p-Akt, Cyclin D1 and P70S6K by Western blot analysis.
Results We demonstrated that knockdown of USP8 significantly inhibited the proliferation, migration and invasion of QBC939 and RBE cells in vitro, while USP8 overexpression showed significant promoting effects on Hucct-1 cells. Moreover, silencing of USP8 also promoted apoptosis in cholangiocarcinoma cells by regulating the Bcl-2/Bax axis and Caspase cascade; up-regulation of USP8 decreased apoptosis in Hucct-1 cells. Importantly, knockdown of USP8 inhibited activation of the Akt signaling pathway by decreasing the phosphorylation level of Akt and up-regulated p53 expression, while USP8 overexpression increased activation of the Akt signaling pathway in Hucct-1 cells. Further, IGF-1 could reverse the inhibitory effects of USP8 knockdown on the Akt signaling pathway and the proliferation of QBC939 and RBE cells.
Conclusion Taken together, our findings suggest that USP8 exerts an oncogenic role in the progression of cholangiocarcinoma and may be a potential therapeutic target for cholangiocarcinoma treatment.

PO-0437

ISG15 通过 NF-κB 通路调控细胞衰老和影响动脉粥样硬化的机制研究

李雪蘅
南方医科大学南方医院

背景 动脉粥样硬化（AS）是一种与年龄相关的慢性炎症疾病，其好发于中老年人，发病率与死亡率位居多种疾病的首位。细胞衰老在动脉粥样硬化不同阶段起着关键作用，内皮细胞衰老是动脉粥样硬化始动因素。本研 究通过芯片检测衰老内皮细胞中差异表达 mRNA，发现 ISG15 高表达。因此本研究通过探究 ISG15 对细胞衰老和 AS 的影响及具体机制，为调控细胞衰老和 AS 防治提供科学依据。
方法 分离新鲜的人原代脐静脉内皮细胞（HUVEC），利用过氧化氢刺激 HUVEC 构建细胞衰老模型进行基因芯片分析，采用免疫印迹实验检测人 AS 斑块组织和 AS 模型小鼠主动脉窦斑块组织中 ISG15 的表达水平，酶联免疫实验检测 ISG15 在不同年龄表观健康人群和对应年龄 AS 患者血清中的表达水平；构建 ISG15 小干扰片段转染 HUVEC， 通过 β 半乳糖苷酶染色、细胞周期 PI 染色、Edu 细胞增殖实验、单核巨噬细胞 黏附实验、一氧化氮检测、活性氧检测观察 ISG15 对复制性细胞衰老及应激性衰老的影响。
结果 1.进行基因芯片发现 ISG15 的 mRNA 水平上调； 2. AS 斑块和 ApoE-/-小鼠主动脉斑块组织中 ISG15 的表达水平 升高； 3. ＞60 岁的冠心病患者与对应年龄表观健康人相比，其血清中 ISG15 的表 达水平升高。同时＞60 岁的冠心病患者血清中的 ISG15 浓度较 20-45 岁的冠心病患者

升高； 4. 敲减 ISG15 能促进内皮细胞增殖和细胞周期转换，减少 β 半乳糖苷酶衰老细胞数量，增加一氧化氮表达并减少活性氧的产生和单核巨噬细胞的黏附； 5. 敲减 ISG15 可降低磷酸化 p65、磷酸化 IκBα、衰老标志物 p16 蛋白的水平，而过表达 p65 则作用相反。
结论 1.ISG15 在人和 ApoE-/-小鼠的动脉粥样硬化斑块组织中表达上调。 2.ISG15 在老年冠心病患者血清中表达升高。 3.ISG15 通过 NF-κB 通路调控内皮细胞衰老。

PO-0438

Volatile rganic compounds in urine for noninvasive diagnosis of hepatocellular carcinoma: a pilot study

Fangbo Xia、Hongwei Zhou
Zhujiang Hospital of Southern Medical University

Hepatocellular carcinoma is the sixth most prevalent cancer and the third most frequent cause of cancer-related death. In this study, firstly, the parameters of headspace solid-phase microextraction gas chromatography mass spectrometry (HS-SPME-GC-MS) method were optimized with univariate experimental design and central composite design. And then, a total of 95 urine samples divided into discovery phase and validation phase were collected and their urinary VOMs were analyzed with this method. Principal component analysis (PCA) in terms of VOM profiles demonstrated that HCC patients could be significantly distinguished from healthy controls. Partial least squares discriminant analysis (PLS-DA) based on the discovery phase showed 14 metabolites, including deoxyguanosine, pelargonic acid, undecanoic acid and others exerted higher contribution to the difference. ROC analysis showed these biomarkers possessed excellent performance to diagnose HCC patients in both discovery and validation phases. In conclusion, the analysis of VOMs in urine could distinguish HCC patients and this method might supply support for the detection of HCC.

PO-0439

Reference intervals for lipid-related parameters in healthy adults of Southwest China and its usefulness in assessing carotid atherosclerosis

Ruyi Liang[1]、Shuyu Yang[1]、Ling Tong[1,2]、Yijun Chen[1]、He Zhang[1]、Xiaolin Li[1]、Shanshan Liang[1]、Wei Gan[1]
1. West China Hospital, Sichuan University
2. 自贡市第三人民医院

Background Cardiovascular disease has become the first leading cause of death worldwide in recent years. Recent studies showed that combined lipid parameters were more powerful in predicting ASCVD. For example, it has been reported that TC/HDL-c and LDL-c/HDL-c ratio had a higher predictive value for atherosclerosis progression, than any single lipid parameter. Some studies have suggested that Non-high-density lipoprotein cholesterol (non-HDL-c) level is a better predictor of carotid IMT than lipid parameters alone, even than TC/HDL-c. Howeve, the comparison among the capabilities of lipid-related parameters for assessing atherosclerosis is still limited, and there were no specific reference intervals for Southwest Chinese.
Objective The study aims to build reference intervals of various lipid-related parameters for our laboratory, and to investigate the role of 4 traditional lipid indicators and 7 calculated lipid parameters in carotid plaque formation and progression.
Methods For building reference intervals, 777,5 participants (males, 38.8%) were eventually enrolled. The establishment of reference intervals were performed according to the EP28-A3C guideline on Defining, Establishing, and Verifying Reference Intervals. Outliers were identified

using Dixon-Reed's outlier test or method proposed by Tukey (1977). Method cited by the EP28-A3C guideline was used to judge whether partitioning of reference intervals was necessary. The 2.5th and 97.5th percentiles values of the distribution were defined as the lower and upper reference limits. The relationship between age/sex and lipid-related parameters were explored. For exploring its usefulness in assessing carotid atherosclerosis, 759 subjects (males, 50.1%) were selected. Linear and logistic regression analysis were used to evaluate the relationship between various lipid-related parameters and carotid intima-media thickness and carotid plaque.
Results Sex and age-specific reference intervals of lipid-related parameters were established. The multiple linear regression analysis demonstrated that TC/HDL-c (sβ: 0.136, p < 0.001)，LDL-c/HDL-c (sβ: 0.134, p < 0.001)，mono/HDL-c (sβ: 0.131, p < 0.001) and non-HDL-c/HDL-c (sβ: 0.136, p < 0.001) were independent risk factors for IMT, a model for predicting IMT was established. Age (sβ: 0.325, p＜0.001), SBP(sβ: 0.081, p: 0.014), smoking(sβ: 0.144, p＜0.001), eGFR (sβ: -0.107, p: 0.005), LDL-c/HDL-c (sβ: 0.121, p＜0.001), and mono/HDL-c (sβ: 0.116, p: 0.001) were enrolled in the model. And the multiple logistic regression analysis revealed that non-HDL-c/HDL-c (OR: 1.449, p < 0. 001), RC (OR: 3.357, p < 0. 001), and TC/HDL-c (OR: 1.449, p < 0. 001) were independent parameters, a model for predicting plaque was established. Age (OR =1.093, 95% CI: 1.076 – 1.111, p ＜0.001), SBP (OR: 1.013, 95% CI: 1.004-1.022, p: 0.006), smoking (OR: 2.976, 95% CI: 1.903 - 4.655, p ＜0.001), TG (OR: 1.565, 95% CI: 1.206 – 2.029 , p: 0.001), and LDL-c/HDL-c (OR: 1.327, 95% CI: 1.053 – 1.673, p: 0.017) were enrolled in the model.
Conclusion Sex and age-specific reference intervals of lipid-related parameters in Southwest China were established. It needed to be mention that while most laboratories currently applied the one-side reference range of HDL, but some recent studies showed that HDL-c is not the higher, the better, so we finally adopt the two-side reference range. TC/HDL-c, non-HDL-c/HDL-c and LDL-c/HDL-c were excellent indicators for carotid atherosclerosis. Models using routine clinical information and lipid-related parameters for predicting IMT and plaque were established and can be used in clinical practices.

PO-0440

血清 HMGB1、sRAGE 在初诊 MM 中的研究价值

李红梅
新疆生产建设兵团第六师医院

目的 评估血清高迁移率族蛋白 B1,可溶性晚期糖基化终末产物受体对初诊 MM 的诊断、疗效监测及预后价值。
方法 采用 ELISA 检测 2018 年 10 月至 2020 年 5 月收治的 50 例初诊 MM 患者化疗前后及 50 例血液科门诊就诊者的血清 HMGB1、sRAGE 水平，用 ROC 进一步分析血清 HMGB1、sRAGE 水平对 MM 诊断的效能；比较化疗前后血清 HMGB1、sRAGE 水平，分析其在 MM 患者疗效评估中的价值，根据血清 HMGB1、sRAGE 水平的均值进行分组，对所有患者进行跟踪，比较患者临床特点及生存状况。
结果 MM 组患者血清 HMGB1 水平高于对照组，sRAGE 水平低于对照组（P＜0.05）；分别单独应用血清 HMGB1、sRAGE 水平检测诊断ＭＭ的 AUC 为 0.955、0.811。经 3 个疗程化疗后，CR 组患者的 HMGB1 水平较化疗前低，PD 组患者的 HMGB1 水平较化疗前明显升高，PR 组患者的 sRAGE 水平较化疗前明显升高（P<0.05）；HMGB1 低表达组（25 例）和 HMGB1 高表达组（25 例）的患者相比，在 R-ISS 分期、HGB、CRP、ESR、CD56、CD117、D13S319 缺失等方面均有统计学差异；sRAGE 低表达组（28 例）和 sRAGE 高表达组（22 例）的患者相比，在 ISS 分期、CRP、CD56 等方面均有统计学差异；Kaplan-Meier 生存分析：HMGB1 低表达组的存活状况更好：其中 PFS:T 低表达组＞T 高表达组，OS:T 低表达组＞T 高表达组。sRAGE 高表达组的存活状况更

好：其中 PFS:T 低表达组＜T 高表达组，OS:T 低表达组＜T 高表达组。Cox 分析：LDH、HMGB1 均影响患者预后，其中两者均影响患者的 PFS。 另外 HMGB1 影响患者的 OS。
结论 初诊 MM 患者经化疗后血清 HMGB1、sRAGE 水平均发生改变，且初诊时 HMGB1 高表达组患者生存期更短，预后更差。

PO-0441

UBQLN4 is an ATM substrate that stabilizes the anti-apoptotic proteins BCL2A1 and BCL2L10 in mesothelioma

刘芳[1]、潘润桑[2]、丁宏宇[3]、古丽玲[1]、杨云[1]、李传银[3]、许永杰[4]、胡荣贵[3]、陈辉[4]、张湘燕[4]、聂瑛洁[4]
1. 贵州大学
2. 贵阳妇幼保健院
3. 中国科学院上海生命科学研究院
4. 贵州省人民医院

Objective DNA is the main carrier of biological genetic information, and its stability is of vital significance for maintaining the health of organisms. Its abnormal function and damage can cause a variety of human diseases. Among all types of chromosomal damage, DNA double strand breaks have the most serious consequences. Inaccurate repairs can cause local DNA sequence changes and even chromosome rearrangements. The repair of DNA double-strand breaks involves multiple signal transduction pathways. As one of the most upstream signaling molecules, the ataxia telangiectasia mutated (ATM) gene plays a crucial role in the DNA damage response and ATM mainly plays a role by phosphorylating downstream proteins. This study mainly screened and suggested batches of potential ATM substrates through novel functional genetics methods, and initially explored the role of one of the ATM substrates, ubiquilin4 (UBQLN4), in the process of mesothelioma development.
Methods 1. Screen and prompt batches of potential ATM substrates using drug screening methods based on the GFP competition assay system. 2. By immunoprecipitation, Western blot and other methods to further confirm whether UBQLN4 is an ATM substrate. 3. To explore the expression level of UBQLN4 in mesothelioma through bioinformatics analysis and immunohistochemistry experiments. 4. To explore the effect of UBQLN4 on the formation, apoptosis and cycle of mesothelioma cells by cloning, CCK8 and flow analysis. 5. Explore the interaction between UBQLN4 and the BCL2 protein family through immunoprecipitation and IF. 6. Explore the expression levels of Bcl-2-related protein A (BCL2A1) and Bcl-2-like protein 10 (BCL2L10) in mesothelioma tissues by immunohistochemistry.
Results 1. Screened and suggested 51 potential ATM substrates, and confirmed that UBQLN4 was an ATM phosphorylated substrate. 2. UBQLN4 is highly expressed in mesothelioma tissue and significantly affects the prognosis of patients. 3. After knocking down UBQLN4, it was found that under the condition of inducing DNA damage, it can significantly enhance the apoptosis of mesothelioma cells, reduce the semi-lethal concentration of DNA damage drugs, and have no significant effect on the cycle of mesothelioma cells. 4. UBQLN4 interacts with members of the anti-apoptotic protein family BCL2A1 and BCL2L10 to enhance its stability and thereby regulate the apoptosis of mesothelioma cells. 5. UBQLN4, BCL2A1 and BCL2L10 are highly expressed in mesothelioma tissues, and the expression levels of BCL2A1, BCL2L10 and UBQLN4 are positively correlated.
Conclusions 1. Screen and suggest 51 potential ATM substrates, and confirm UBQLN4 as ATM substrate by biochemical methods. 2. UBQLN4 is highly expressed in mesothelioma tissues and significantly affects the survival and prognosis of patients. 3. UBQLN4 enhances its stability by interacting with anti-apoptotic proteins BCL2A1 and BCL2L10, thereby regulating the apoptosis of mesothelioma cells

PO-0442

Combined application of untargeted metabolomics analysis and gene expression profiling find a new glucose metabolism regulator C19orf12

Meng Zhao
Tianjin Medical University Cancer Institute and Hospital

Background and Aim Life is the interplay between energy and structure. Aberrant mitochondrial biogenesis and quality control are found in a variety of malignant diseases and may be the underlying cause of cancer. Thus, identifying new mitochondrial regulators could provide important insight into the contribution of altered metabolism to tumorigenesis. C19orf12 codes for a transmembrane glycine zipper-containing mitochondrial protein. Mutations in this gene are a cause of neurodegeneration with brain iron accumulation-4 (NBIA4), but the specific function of the encoded protein is unknown. It has been reported that genes downregulated in neurodegenerative disorders are often upregulated in cancer and vice versa. Thus, we carried out this study to evaluate the potential role of C19orf12 in cancer progression and explore the mechanism behind it using NSCLC as a model system.
Methods Untargeted mass spectrometry-based metabolomics was utilized to identify differences in the levels of functionally relevant intracellular metabolites. RNA-seq analysis was performed to find C19orf12 downstream targets. TCGA data and clinical samples analysis were utilized to examine clinical revavence of C19orf12. In vivo and In vitro NSCLC models was used to detect C19orf12 specific function in NSCLC progression.
Results TCGA data and clinical sample analysis indicates that C19orf12 is upregulated and correlated with poor prognosis in a wide range of malignant diseases, especially in NSCLC. High expression of C9orf12 was observed in NSCLC tissue compared to adjacent normal tissue. Experimental data demonstrate that C19orf12 promotes invasion, migration and resistance to anoikis in vitro and metastatic potential in vivo, but has no impact on cell proliferation and apoptosis. RNA-seq results combined with GO and GSEA analysis indicate C19orf12 regulates key factors in oxidative phosphorylation, cell adhesion, migration and actin cytoskeleton. Metabolomics analysis indicates aberrent glucose and lipid metabolism. Oncogenic pathway such as PI3K-AKT, ERK and JNK was activated after C19orf12 overexpression. Furthermore, loss of C19orf12 enhances H2O2-induced ROS accumulation and overexpression of C19orf12 reverses the effect. Fragmented mitochondrial network and decreased mitochondrial membrane potential was observed in C19orf12 depletion cells which indicates impaired mitochondria quality.
Conclusion Taken together, our findings identify C19orf12 as metastatic promoter in NSCLC, uncover the role of C19orf12 in mitochondria quality control and glucose and lipid metabolism, and provide a resource of potential NSCLC biomarkers and therapeutic targets

PO-0443

miR-494-3p 通过靶向调控 PRR14 表达参与食管鳞状细胞癌发生发展的分子机制

王成[1]、钟錦莎[1]、丁梦[1]、顾万建[2]、汪俊军[1]、张春妮[1]
1. 中国人民解放军东部战区总医院
2. 江苏省中医院

目的 探讨 miR-494-3p 通过调控 PRR14 (proline rich 14)蛋白表达参与食管鳞状细胞癌（ESCC）发生发展的分子机制。
方法 收集 ESCC 组织及癌旁正常组织 20 对，Western blot 和免疫组化检测组织中 PRR14 蛋白表达变化情况； qRT-PCR 检测 PRR14 信使 RNA（mRNA）表达水平；生物信息学方法预测可调控

PRR14 表达的 miRNA，分析 PRR14 蛋白和 mRNA 水平与 miRNA 表达相关性，荧光素报告试验证实 miRNA 与 PRR14 调控关系； RNAi 技术敲除 ESCC 细胞株（TE-10 和 ECA109）PRR14 基因表达后，利用 CCK8、EDU、克隆形成实验检测细胞的增殖能力，利用 Trans well，划痕实验和流式细胞术检测 PRR14 对细胞侵袭和凋亡的影响；进一步通过瞬时转染或慢病毒稳转过表达或抑制 miRNA、miRNA 过表达同时靶基因功能回复实验（ORF 过表达）重复上述检测指标。
结果 Western blot 和免疫组化结果显示，与癌旁正常组织相比，PRR14 蛋白在 ESCC 组织中显著高表达（$P < 0.05$）；qRT-PCR 显示，PRR14 mRNA 水平在 ESCC 组织中表达升高（$P < 0.05$）；生物信息学分析结果表明，miR-494-3p 可调控 PRR14 表达，且 miR-494-3p 在 ESCC 组织中表达显著降低，与 PRR14 蛋白和 mRNA 水平呈显著负相关（$P < 0.05$）；荧光素报告试验证实 miR-494-3p 可与 PRR14 3'UTR 结合并调控其表达；RNA 干扰、miRNA 过表达及回复实验显示，敲除 PRR14 或过表达 miR-494-3p 可抑制 TE-10、ECA109 细胞增殖，侵袭能力，并促进细胞凋亡。
结论 miR-494-3p 可通过调控 PRR14 蛋白表达抑制 ESCC 增殖、侵袭能力和促进细胞凋亡，与 ESCC 的发生发展密切相关。

PO-0444

2 型糖尿病患者 25-羟基维生素 D 缺乏与糖尿病并发症的关系

刘宁阳、张晋、秦晓松
中国医科大学附属盛京医院

目的 评价 2 型糖尿病(T2DM)患者血清 25-羟基维生素 D 水平与糖尿病并发症的关系。
方法 随机 2019 年 1 月至 2020 年 6 月住院患者 292 例 T2DM 病患者（其中无并发症组 46 例，糖尿病肾病组 33 例，糖尿病神经病变组 33 例，糖尿病视网膜病变组 18 例，合并两种以上糖尿病微血管并发症组 48 例，糖尿大血管并发症组 28 例，糖尿病微血管合并大血管并发症组 86 例）归为实验组，选择同期 118 例健康体检者为对照组。收集各组研究对象的一般资料，并比较各组患者的 FBG、TG、TC、HDL、LDL、Cr、CYSC、UA、Ca、P、HbA1c、25(OH)D3 对比实验组以及对照组的 25-羟基维生素 D 水平以及 25-羟基维生素 D 缺乏的下降率，对比实验组内各分组的临床指标。
结果 实验组患者的血清 25(OH)D3 水平均明显低于对照组($p < 0.05$)。糖尿病微动脉并发症组、糖尿病大血管并发症组和糖尿病微血管合并大血管并发症组在 BMI、TC、HDL、LDL、Cr、UA、Ca、P 等一般资料比较，差异无统计学意义（$P>0.05$），其中糖尿病微动脉并发症组中病程、HA1c、FBG 明显高于无并发症组，25(OH)D3 明显低于无并发症组；糖尿病大血管并发症组的病程明显高于无并发症组，25(OH)D3 明显低于无并发症组；糖尿病微血管合并大血管并发症组 CYSC 明显高于无并发症组和糖尿病微血管并发症组。单纯肾病组、单纯周围神经病变组以及合并三种微血管并发症组的 25(OH)D3 下降率明显高于无并发症组。相关性分析显示，在微血管并发症组和微血管合并大血管并发症组中 25(OH)D3 与 CYSC 呈负相关（分别为 $r=-0.178$，$P<0.05$ 和 $r=-2.61$，$P<0.05$）。
结论 糖尿病患者血清 25(OH)D3 水平与糖尿病及其并发症的发展有关。血清 25(OH)D3 水平低可能是糖尿病代谢控制更差的结果。

PO-0445

Serum Metabolites as Potential Diagnostic Biomarkers in Patients with AFP-negative Hepatocellular Carcinoma.

Duo Zuo 、Haohua An、Li Ren
Tianjin Medical University Cancer Institute and Hospital

PURPOSE Primary liver cancer (PLC) is the fourth most common malignancy in China. The lack of effective diagnostic methods has led to the failure of patients with PLC to receive timely and effective diagnosis and treatment. Hepatocellular carcinoma (HCC) is the most common liver malignancy, and it accounts for more than 90% of primary liver cancer. In this study, we applied nuclear magnetic resonance hydrogen spectroscopy (1H-NMR) high-throughput platform to detect small-molecule metabolites in serum of HCC patients, patients with benign liver disease (BLD) and healthy subjects, and explored the application of serum metabolites as potential diagnostic biomarkers for primary hepatocellular carcinoma with alpha-fetoprotein (AFP) negativity.

METHODS A total of 61 preoperative serum samples from HCC patients with negative serum AFP expression (AFP < 20 ng/ml) were collected from the Department of Hepatobiliary Oncology, Tianjin Medical University Cancer Institute and Hospital, along with 50 patients with hepatitis and cirrhosis (benign liver disease, BLD), and 59 healthy controls (HCs). Serum metabolites were detected by 1H-NMR platform and screened by multivariate analysis and univariate analysis to identify serum metabolite indicators that could be used as potential diagnostic markers for AFP-negative primary HCC.

RESULTS A total of 39 serum small molecule metabolites were obtained by 1H-NMR detection of serum samples. Through metabolomics data analysis methods and model validation, we found that 1H-NMR serum metabolic profile can distinguish patients with HCC from those with BLD, and HCs. Variable influence on projection (VIP) values > 1.0 and Mann-Whitney U test p-values < 0.05 were used as judgment criteria for the OPLS-DA model. Six metabolites, namely Glucose, Alanine, Glutamic acid, Glutamine, Glycerol, and Proline, were initially selected for the next step of analysis of HCC versus HCs. Six metabolites, namely Glucose, Glutamic acid, Glutamine, Lactic acid, 3-Hydroxybutyric acid, and Proline, were initially selected for the next step of analysis of HCC versus BLD. Moreover, Receiver operating characteristic curve (ROC) analysis showed that the combined diagnosis of glucose, glutamate and proline had good diagnostic performance in differentiating HCC patients with serum AFP-negative expression from HCs, and the area under curve (AUC) in the training set and the validation set were 0.941 [95% confidence intervals (CI): 0.890-0.993, training set] and 0.902 (95%CI: 0.767-0.973, validation set), respectively. Meanwhile, the combined diagnosis of glucose, glutamate, 3-hydroxybutyric acid, and proline in differentiating AFP-negative HCC patients from AFP-negative BLD patients was 0.886 (95% CI: 0.813-0.959, training set) and 0.705 (95% CI: 0.530-0.880, validation set), respectively.

CONCLUSION In this study, it was preliminarily found that the combined diagnosis of serum glucose, glutamate, 3-hydroxybutyric acid and proline could be used as potential diagnostic markers in discriminating between HCC patients with serum AFP-negative expression and BLD patients with serum AFP-negative expression, suggesting that the serum metabolomics study may provide a new idea for the development of clinical diagnostic markers in HCC patients.

PO-0446

2020 年某实验室全血微量元素不合格样本分析

张敏
西安金域检验所有限公司

目的 样本合格率是实验室分析前质量控制的重要组成部分，决定着检测结果的准确性，同时采集合格的临床样本，还可提升临床服务能力，改善医患关系。本研究通过分析微量元素不合格样本，指导分析前样本采集，提升送检样本质量。
方法 对 2020 年某实验室送检的微量元素不合格样本统计，样本类型为静脉全血和末梢血，抗凝剂选择为肝素抗凝。并对不合格样本进行分类分析。
结果 本次统计微量元素样本为 42660 例，不合格样本总数为 81 例，占总样本量的 0.19%。对不合格样本进行分类统计：样本凝固 41 例，占比为 50.6%；样本量不足 21 例，占比为 25.9%；样本类型不符 9 例，占比为 11.1%；样本采集容器错误 4 例，占比为 4.9%；其他原因 6 例，占比为 7.4%。
结论 样本是否合格决定着检测的成败和检测结果的质量。通过本次研究发现，不合格样本产生于采样过程中。加强采样人员培训和教育，提高样本采集人员的能力，同时实验室应加强分析前样本采集环节质量控制，提高样本合格率，对提升实验室的临床服务能力和促进实验室质量管理体系健康、有效运行至关重要。

PO-0447

Analysis of electrophoresis detection of 47940 cases in a tertiary academic China hospital: a 6-year retrospective audit and briefly review

Lujiang Yi
Department of Laboratory Medicine, The First Affiliated Hospital of Nanjing Medical University

Background This audit provides baseline data on the prevalence, testing pattern and yield of electrophoresis tests performed over a 6-year period in a tertiary academic China hospital.
Methods This was a retrospective audit of all SPE, UPE and IFE tests performed on new and follow-up adult patients (aged ≥18 years) from 2014 to 2019, using data from the Department of Laboratory Science of Jiangsu Province Hospital laboratory information system database.
Results A total of 47,940 cases of electrophoresis, there are 15,473 cases SPE tests (of which 25.6% were follow-up tests); have 12,531 cases UPE tests (10.2% of the tests were follow-up tests); have 19,327 cases SIFE tests (31.6% of which were follow-up tests). Hematology was the highest rate of submission and positive. SPE testing before IFE tests can effectively increase the positive rate of IFE.
Conclusion This audit provides baseline data on the prevalence of test requests, their source and the yield of electrophoresis testing in our laboratory. An increasing trend in SIFE and UIFE was evident.

PO-0448

生物合成 Au@Ag 双金属纳米颗粒用于快速比色检测 H2O2

蒋兴禄[1,2]、吴国球[2]
1. 东南大学医学院
2. 东南大学附属中大医院检验科

双金属纳米颗粒的性能取决于其组成、大小和形状，因此其合成方法和技术应用得到了许多研究人员的关注。然而，双金属纳米颗粒在化学合成过程中往往需要严格的反应条件和有毒的化学品。我们开发了一种生物合成的方法，即在室温下，没有稳定剂或表面活性剂的条件下成功制备 Au@Ag 双金属纳米颗粒。TEM 结果显示均匀圆形的双金属 Au@Ag 纳米颗粒，直径约为 14-18 nm，在核中间有 1 - 2 个金纳米颗粒，外层环绕 1-2 nm 大小的银纳米颗粒，X 射线衍射能谱结果进一步证明 TEM 图像中纳米颗粒含有 Au 和 Ag 元素，粒径结果和 TEM 的结果一致（约为 23.01 nm）。Au@Ag NPs 在 360 nm 处得到的强吸收峰，但在 H2O2 存在时，吸收峰发生红移至 426 nm，且吸收明显增强并和峰值的大小和 H2O2 的浓度有相关性(R2 = 0.9806，范围为 5 to 300 μM）。 在短短的两分钟内吸收峰值到达最大值。 通过研究发现这是由于局域表面等离子共振，它可以在不需要 3,3 ‘、5,5 ‘ -四甲基联苯胺(TMB)和过氧化物酶的情况下实现对 H2O2 的快速比色检测。

PO-0449

牛磺酸在结肠癌发展及预后中的作用研究

李琼[1]、赵新宇[1]、吕亚平[1]、张道祥[2]、李敏[1]
1. 上海交通大学医学院附属仁济医院
2. 安徽医科大学生命科学学院

目的 代谢组学研究表明，代谢物与肿瘤的生物学行为密切相关，但牛磺酸及其前体亚牛磺酸在结肠癌发展及预后中的作用尚且未知。本研究拟采用体外实验探讨牛磺酸在结肠癌发展及预后中的作用，最后采用血清标本对实验结果进行进一步验证。
方法 首先采用 GC-MS 分析结肠癌肿瘤组织与正常组织代谢产物的表达差异。接下来采用细胞增殖实验、克隆形成实验、细胞凋亡及迁移侵袭实验确定牛磺酸对亚牛磺酸诱导的结肠癌进展的影响。进一步采用 qRT-PCR 检测 EMT 相关标志物表达，Western blot 检测 ERK 信号蛋白的表达，确定牛磺酸调控结肠癌的进展是否与 EMT 及 ERK 通路密切相关。采用 LC-MS/MS 分析结肠癌细胞中牛磺酸及亚牛磺酸表达的相互影响，确定血清牛磺酸水平与结肠癌预后的相关性。
结果 与正常组织相比，结肠癌组织的代谢产物存在着显著差异，亚牛磺酸显著增加，牛磺酸明显减少（P<0.01）。体外实验均表明，牛磺酸可明显阻断亚牛磺酸诱导的结肠癌进展及转移（P<0.01）。并且 qRT-PCR 结果显示，牛磺酸可明显增加 CDH1，降低 Snail 的表达（P<0.01）。Western blot 结果表明，牛磺酸可明显降低 ERK 和 RSK 的磷酸化水平。代谢组学结果显示，结肠癌细胞中牛磺酸可显著降低亚牛磺酸的水平，而亚牛磺酸水平对牛磺酸并无显著影响（P<0.01）。LC-MS/MS 结果也证实，血清牛磺酸水平降低，预示着结肠癌患者的预后较差（P<0.01）。
结论 牛磺酸可通过 EMT 及 ERK 信号通路，也可通过对亚牛磺酸含量的调节，参与结肠癌发生发展的调控。并且，血清牛磺酸水平可作为结肠癌患者预后的潜在生物学标志物，具有潜在的临床应用前景。

PO-0450

环磷酰胺与他克莫司治疗特发性膜性肾病的效果比较分析

于瑶、吴丽娜
中国医科大学附属盛京医院

目的 特发性膜性肾病（Idiopathic membranous nephropathy）发病率较高，2020 年 KDIGO 临床实践指南提出经观察评估存在进展风险的 IMN 患者推荐应用免疫抑制治疗。为评估环磷酰胺和他克莫司治疗 IMN 的效果，寻找能够影响治疗效果的影响因素，尝试为最佳诊疗方案的制定提供依据。
方法 本实验选取 2015 年 6 月至 2020 年 2 月于中国医大学附属盛京医院肾脏内科就诊，诊断为 IMN 的患者共 176 例，对所有患者进行规律随访，收集用药前、治疗后 3、6、12 个月的临床资料，分析研究对象的临床资料、缓解情况，建立 COX 回归模型探寻 IMN 患者疗效影响因素。
结果 治疗前激素联合环磷酰胺和激素联合他克莫司两组 IMN 患者临床资料无统计学差异（P＞0.05），治疗后第 3 个月两治疗组间 Alb、TP、HDL-C、尿酸水平有显著差异（P＜0.05）。治疗 6 个月后两治疗组患者的 Alb 水平与治疗后第 3 个月和基线的 Alb 水平相比有统计学差异（P＜0.05）。治疗 12 个月后两组患者 Alb、TP 水平较前三个观察点有显著差异（P＜0.05）。治疗后第 6、12 个月不同治疗组 Alb、TP、尿酸水平差异有统计学意义（P＜0.05）。COX 回归模型显示治疗方案（以激素联合他克莫司治疗作为对照组，HR=2.243，95%CI 1.014-4.960，P<0.05）,治疗后第 3 个月 Alb 水平（HR=1.104，95%CI 1.044-1.168，P＜0.05）,与治疗后第 3 个月 24h 尿蛋白定量水平（HR=0.902，95%CI 0.814-1.000，P＜0.05）能够影响 IMN 患者治疗结局。
结论 在 12 个月治疗期内激素联合环磷酰胺方案治疗 IMN 的效果优于激素联合他克莫司。Alb 和 24h 尿蛋白定量是反映治疗效果比较理想的指标，治疗后第 3 个月的 Alb 和 24h 尿蛋白定量水平可以用来预测治疗结局。

PO-0451

Polyethylene glycol-6000 pretreatment method was used to obtain the accurate clinical chemical test results for lipemic serum samples

Wenhui Yang、Yulin Yuan
The People’s Hospital of Guangxi Zhuang Autonomous Region

Objective To obtain the accurate clinical chemical test results in lipemic serum samples. **Methods** Five simulated lipemic serum samples with different concentration gradients were prepared by fat emulsion for clinical chemical testing. Use 20% polyethylene glycol-6000 (PEG-6000) and 10000rpm low-temperature high-speed centrifugation to pre-treat the lipemic serum samples, and then the clinical chemistry tests were performed to compare the applicability of the two pretreatment methods. For different clinical chemistry testing items, select 20 samples with different concentration ranges and use the PEG-6000 pretreatment method as the experimental method to establish the linear regression equation. Finally, statistical analysis was conducted to determine whether the deviation was acceptable according to 1 / 2 of the allowable error of Health industry standard of the people’s Republic ofChinaand the EQA.
Results Use these two methods to pretreat the lipemic serum samples can help us get the correct test results when testing AFU, ALB, APO-A1, CEA, CHE, CL, GLU, CO2, PA, TBA, ALP, CREA, CA, FPSA, Fe, LPS, Mg, Na, P, T-Bil and TPSA. The PEG-6000 pretreatment method is better than high speed centrifugation method in the detection of ALP, CREA, CA, FPSA, Fe, LPS, Mg, Na, P, T-Bil and TPSA. In particular, we can only use the PEG-6000 pretreatment method instead of high-speed centrifugation method when testing TG item in lipemic serum samples.

Conclusion By using the PEG-6000 pretreatment method to establish the linear regression equation, more accurate clinical chemistry test results of lipemic serum samples can be obtained.

PO-0452

Early Systemic Inflammatory Response Syndrome Duration and Infectious Pancreatic Necrosis

Chaochao Tan
Hunan provincial hospital

BACKGROUND AND AIMS Infectious pancreatic necrosis (IPN) remains a major challenge for AP management and SIRS is associated with the severity of AP, but the relation with IPN remains unclear. In this study, we aimed to evaluate the correlation between SIRS and infectious pancreatic necrosis (IPN), and the application of SIRS duration to predict IPN in a prospective cohort of patients with AP.
METHODS Acute physiology and chronic health evaluation II (APACHE II) scoring system and CT severity index (CTSI) scores were calculated within the first 48 h after admission in 2130 patients with AP between January 2012 and October 2017 in Hunan Provincial People's Hospital. The SIRS duration of the first week, demographic, radiology, and all clinical laboratory data were prospectively collected. Univariate and multivariate logistic regression analyses were performed to evaluate the relationship between clinical parameters and IPN. The predictive accuracy of clinical parameters was measured using area under the receiver-operating curve (ROC).
RESULTS A significant upward tendency of IPN incidence was observed with increased SIRS duration. The AUC of SIRS duration to predict pancreatic infection was 0.92 [95% confidence interval (CI): 0.91-0.94], which was even moderately higher than the AUC of APACHE II and CTSI scores. A SIRS duration of ≥48h (persistent SIRS) had a sensitivity of 99.18%, specificity of 80.88%, and nearly 389.36 (95% CI 54.54, 2779.55) times more likely to develop IPN than those with duration of <48h ($P < 0.0001$).
CONCLUSION Early SIRS duration was strongly associated with IPN and could serve as an easy bedside indicator to predict pancreatic infection.

PO-0453

液相色谱串联质谱与均相酶免疫法检测甘胆酸在妊娠期肝内胆汁淤积症诊断价值中的比较

赵峰峰
东南大学附属中大医院

目的 比较液相色谱串联质谱与均相酶免疫法检测甘胆酸在诊断 ICP 中的应用价值；
方法 搜集 2020 年 11 月 1 日至 2021 年 4 月 30 日在东南大学附属中大医院产检的 396 名孕妇，产检检测甘胆酸的同时加做质谱法。比较二者阳性率及其在 ICP 诊断中的价值；
结果 396 名孕妇中有 48 名孕妇最终诊断为 ICP，其中液相色谱串联质谱阳性率为 100%，阴性率为 100%，均相酶免疫法阳性率为 87%，阴性率为 100%。
结论 液相色谱串联质谱检测甘胆酸在诊断 ICP 中具有明显的优势，建议推广。

PO-0454

脂蛋白相关磷脂酶 A2 对急性缺血性脑卒中早期神经功能恶化的预测诊断价值

杨丽华
陆军军医大学第一附属医院（西南医院）

目的 探讨急性缺血性脑卒中患者的血清脂蛋白相关磷脂酶 A2（Lp-PLA2）水平对早期神经功能恶化的预测诊断价值。
方法 选取 2020 年 3 月至 2020 年 12 月在我院收治经颈动脉彩超、头颅 CT、头颅 MRI 等检查确诊为急性缺血性脑卒中 100 例患者作为研究对象，进行分型和神经功能缺损程度(NIHSS 评分). 同时选取我院收治的非脑血管病人 100 例作为对照对象，比较 2 患者血清 Lp-PLA2 水平与急性脑梗死不同临床类型的相关性和神经功能损伤程度的关系。
结果 观察组 Lp-PLA2 水平明显高于对照组，组间差异显著（P<0.05）。通过 Lp-PLA2 水平与早期神经功能缺损程度的 Spearman 相关性分析，结果显示 Spearman 相关系数 0.58（P<0.05），中等程度相关性。
结论 Lp-PLA2 浓度与早期疾病严重程度呈正相关，能够作为评价病情严重程度的参考，且对神经功能的恶化具有警示作用。

PO-0455

The significance of KL-6 as prognosis monitoring biomarker in patients with severe COVID-19 from stabilized stage toward convalescence

Long He、Lie Ying Fan
East hospital, Shanghai

Background This study aims to identify some biomarkers for monitoring the recovery of lung injury in severe COVID-19 patients from stabilized stage toward convalescence.
Methods We enrolled participants who diagnosed with severe COVID-19 (n = 28) and health volunteers (n = 25) from Taikang Tongji (Wuhan) Hospital. The patients were in a stabilized stage and had a course of 48.1±12.8 days. We followed these patients for 90 days. The blood routine, cytokines (IL-1β, Il-2, IL-4, IL-5, IL-6, IL-10, IL-12p70, IL-17A, TNF-α, IFN-α, IFN-γ), type II alveolar epithelium injury indicators (Surfactant protein A (SP-A), Krebs von den Lungen-6 (KL-6)) and chest CT were tested on the 1, 30, 60, and 90 days after enrollment.
Results In stabilized stage, the parameters of blood routine and some cytokines (IL-1β, IL-2, IL-4, IL-12p70, TNF-α) had bounced back to normal (p>0.05). Some cytokines (IL-5, IL-6, IL-10, IL-17A, IFN-α, IFN-γ) and type II alveolar epithelium injury indicators (SP-A and KL-6) were still higher than normal (p<0.05). During the stabilized stage to convalescence, in spite of the variation of monocyte count, monocyte/lymphocyte ratio, IL-5, IL-10, IL-12p70, IL-17A, IFN-γ, IFN-α, SP-A and KL-6 were downward trend (p<0.05), only KL-6 level (p<0.05) could simultaneously reflect the lung injury volume which be measured by CT.
Conclusions Our preliminary data indicated that KL-6 could be an effective prognostic biomarker for monitoring the recovery of lung function in patients with severe COVID-19 from stabilized stage toward convalescence.

PO-0456

A candidate reference method using standards addition for lithium in human serum by ICP-MS

Xiaoyu Fan [1]、Qing Li[1]、Ping Lin[2]、Zhonggan Jin[1]、Meizi Chen[2]、Yi Ju[1]
1. Shanghai Center for Clinical Laboratory
2. 上海市精神卫生中心

Objective Therapeutic monitoring of lithium (Li) is important because of its narrow therapeutic range and therapeutic index. Standardization of the measurement of Li concentration in serum is of considerable interest for quality assurance in patient care. Here, the authors present the evaluation of a new inductively coupled plasma mass spectrometry (ICP-MS) method for the determination of lithium in serum.
Methods Serum samples were diluted 100 × by 0.3% ultrapure nitric acid, and used germanium (Ge) as an internal standard. Lithium calibration solutions with different concentrations were added to serum matrix solutions. The serum lithium concentration was calculated according to the standards addition method.
Results The validation of the method, as well as a comparison with other lithium method, was investigated. The correlation coefficients (r) between the measured Li/Ge ratios and the analyte concentration ratios were all > 0.9999. The measurement range from 0.10mmol/L to 4.45mmol/L . The expanded combined measurement uncertainties for the determination of the new method values were estimated as ≥ 1.0% (k = 2) for each measurand. The coefficients of variation (CV) were 1.11% and 0.49% for the two serum samples. Excellent trueness was found testing certified Standard Reference Materials from NIST: SRM956d Level I, Level II and Level III. Comparison with international inter-laboratory comparisons and the ion selective electrode routine method gave satisfied results.
Conclusions This new ICP-MS method is an attractive alternative for lithium measurement and may be used as a candidate reference method for setting target values in the standardization of serum lithium measurements.

PO-0457

血清 IgG/C3 比值在 IgAN 诊断预测中的作用

罗厚龙、夏勇、纪玲
北京大学深圳医院检验科

目的 探讨血清 IgG、C3 及其比值在 IgA 肾病（IgAN）诊断预测中的作用。
方法 收集自 2019 年 1 月~2020 年 12 月于北京大学深圳医院行肾穿刺活检诊断的原发性肾小球疾病患者 431 例，其中 IgAN 患者 243 例，其他肾小球疾病患者 188 例。在患者行肾穿刺前使用免疫比浊法检测患者血清中 IgG、C3 水平，并计算 IgG/C3 比值。通过绘制受试者工作特征曲线（ROC 曲线），计算曲线下面积（AUC），评价血清 IgG、C3 及其比值在 IgAN 诊断预测中的价值。
结果 IgAN 患者组血清 IgG 水平及血清 IgG/C3 比值明显高于其他肾小球疾病患者组，而其血清 C3 水平明显低于其他肾小球疾病患者组。其 AUC 分别为 0.703（IgG）、0.716（IgG/C3 比值）和 0.629（C3）。
结论 血清 IgG/C3 比值在原发性肾小球疾病中对 IgAN 的诊断具有一定的价值，且优于血清 IgG 和 C3。在未开展肾穿刺活检的医院或不同意行肾穿刺活检的患者中血清 IgG/C3 比值对 IgAN 诊断具有一定的辅助价值。

PO-0458

液相色谱-串联质谱联用检测血清油酸的建立及其在代谢相关脂肪性肝病分级中的应用

叶致含、马萌萌、陆柳、谢丽鸿、余明、宗明、范列英
上海市东方医院（同济大学附属东方医院）

目的 建立液相色谱-串联质谱联用技术（LC-MS/MS）检测血清油酸（OA）的方法，分析 OA 在代谢相关脂肪性肝病（MAFLD）分级中的作用。
方法 使用 OA-[13C5]作为同位素内标物，OA 和 OA-[13C5]的离子对分别为 281.3/281.3 和 286.3/286.3。ZORBAX SB-Aq C18 反相色谱柱，流动相 A 为超纯水，流动相 B 为甲醇：乙腈（1:1，v/v），进行梯度洗脱，流速 0.3 mL/min。考察精密度、线性、稳定性、携带污染率等性能以评价该方法的可靠性。选取体检 B 超和临床表现诊断 MAFLD 者 180 名及健康体检者 60 名，采用 LC-MS/MS 检测 OA，B 超评价 MAFLD 分级程度。最后进行综合分析，评价 OA 与脂肪肝分级的相关性。组间比较使用单因素方差分析，相关分析采用 Spearman 分析。
结果 所建立的 OA LC-MS/MS 方法特异性好，在 10~1000 μmol/L 范围内线性关系良好，y=0.00737x+0.00673，r=0.9994，定量限（LLOQ）为 10 μmol/L，批内精密度（CV）≤ 0.88%，实验室内总 CV≤ 1.41%，方法精密度较好，适合临床血清样本的测定。与对照组（200.53±67.45, μmol/L）相比，MAFLD 组血清 OA 含量（337.81±141.84, μmol/L）显著升高，且 OA 水平与 MAFLD 分级程度正相关。
结论 所建立的 LC-MS/MS 检测方法能够科学、高效定量血清中 OA 的含量，为动态监测代谢性疾病人群 OA 含量的变化提供可靠的方法。

PO-0459

血清脂类指标对视神经脊髓炎谱系疾病的诊断价值分析

王进洋[1,3]、王佳楠[2]、李芮冰*[3]、王成彬*[1,3]
1. 潍坊医学院医学检验学院
2. 解放军医学院
3. 中国人民解放军总医院第一医学中心检验科

目的 探讨视神经脊髓炎谱系疾病(NMOSD)患者血清脂类指标的诊断价值，并分析其与 NMOSD 临床特征的关系。
方法 回顾性分析 2018 年 1 月－2020 年 7 月于解放军总医院第一医学中心神经内科和眼科确诊的 324 例 NMOSD 患者(NMOSD 组)、147 例多发性硬化(MS)患者(MS 组)，以及 252 名无神经系统受累者(健康对照组)的临床及实验室诊断相关信息。采用 logistic 回归控制年龄、性别、病程、病变部位、各血清脂类指标间的相互作用，分析三组 研究对象的血清总胆固醇(TC)、三酰甘油(TG)、载脂蛋白 A1(ApoA1)、载脂蛋白 B(ApoB)、高密度脂蛋白(HDL)和低 密度脂蛋白(LDL)水平，以及各指标在 NMOSD 急性期、复发期、缓解期中的水平差异。根据 AQP4 抗体效价高低、受累部位不同等 NMOSD 临床特征进一步分组，分析各指标在不同亚组间的水平差异。
结果 NMOSD 患者中位病程为 20 个月，MRI 显示受累部位主要为视神经(198/324，61.1%)；MS 患者中位病程较长(48 个月)，呈多部位受累(56/147，38.1%)。NMOSD 组与 MS 组、健康对照组 TC、ApoA1、LDL、ApoB 水平差异有统计学意义(P<0.05)。亚组分析结果显 示，NMOSD 急性期、复发期、缓解期三个亚组中，仅急性期与复发期 Apo B 水平差异有统计学意义(P<0.05)；NMOSD 不同主要受累部位 TC、ApoA1、ApoB、HDL、LDL 水平差异有统计学意义(P<0.05)。ROC 曲线分析显示，联合血清 TC、Apo A1、Apo B、LDL 预测 NMOSD 的 AUC 为 0.732，敏感度为 57.86%，特异度为 81.15%。

结论 联合血清 TC、ApoA1、ApoB、LDL 能较好地特异性诊断 NMOSD，且 ApoA1 和 ApoB 可分别作为提示受累部位和 NMOSD 疾病活动程度的 指标。

PO-0460

血清 KL-6 在肺癌术后辅助治疗性肺损伤应用价值的探索

吴丽娜、陈晓卉、高弋、刘勇、秦晓松
中国医科大学附属盛京医院

目的 探讨血清涎液化糖链抗原-6（ KL-6）在非小细胞肺癌（NSCLC）术后辅助治疗性肺损伤中的诊断价值。
方法 本研究共分为三组，NSCLC 术后辅助治疗组（肺损伤亚组、无肺损伤亚组）、NSCLC 手术组（术前亚组、术后亚组）及健康对照组，其中 NSCLC 术后辅助治疗性肺损伤亚组以药物诱导性肺损伤（DILI）、放射性肺损伤（RILI）的诊断标准作为入组的金标准，比较各组血清 KL-6 水平的差异；并以 NSCLC 术后辅助治疗无肺损伤亚组为基准，初步建立血清 KL-6 用于 NSCLC 术后辅助治疗性肺损伤的诊断界值。
结果 NSCLC 术后辅助治疗肺损伤亚组患者血清 KL-6 水平[512.40 U/mL（322.30 ~ 819.20 U/mL）]显著高于无肺损伤亚组[147.80 U/mL（114.25 ~ 229.80 U/mL），P < 0.001）、NSCLC 术后亚组[143.80 U/mL（111.90 ~ 247.80 U/mL），P < 0.001）、NSCLC 术前亚组[204.40 U/mL（162.70 ~ 283.20 U/mL），P < 0.001）及健康对照组[177.70 U/mL（154.20 ~ 206.40 U/mL），P < 0.001）；血清 KL-6 为 310.15 U/mL 用于 NSCLC 术后辅助治疗性肺损伤的诊断界值，其灵敏度、特异性、阳性似然比、阴性似然比分别为 86.3%（95%可信限[confidence interval，CI]，0.73 ~ 0.94），96.2%（95% CI，0.86 ~ 0.99），22.43（95% CI，5.74 ~ 87.69），0.14（95% CI，0.07 ~ 0.28）。
结论 血清 KL-6 在 NSCLC 术后辅助治疗性肺损伤的诊断中具有良好的应用前景。

PO-0461

The relationship between serum trace elements and oxidative stress of patients with different types of cancer

Yuwei Yang、Chunmei Dai、Xiaohong Chen、Jiafu Feng
电子科技大学医学院附属绵阳市中心医院

Objective Many studies have identified a causal and promotive roles of oxidative stress (OxS) and oxidative damage caused by OxS in the occurrence and progression of cancer. Many biomarkers in the blood circulation of patients may change correspondingly with the development of tumors. This study aims to investigate the correlation between OxS and serum trace element (TE) levels of patients with different types of cancer.
Methods 1143 different types of cancer patients and 178 healthy controls from Mar. 2018 to Aug. 2020 in Mianyang Central Hospital were involved in this study. Their levels of OxS parameters (including total oxidant status (TOS), total antioxidant status (TAS) and oxidant stress index (OSI)) and the concentrations of serum TEs (including Cu, Zn, Fe and Se) were determined.
Results Compared with healthy controls, all types of cancer patients have higher TOS level (z = 4.976 ~ 9.245, all P < 0.001) and OSI level (z= 6.228 ~ 9.909, all P < 0.001), and lower TAS level (z= -8.517 ~ -3.994, all P < 0.001). But among patients with different types of cancer, there is no statistical difference in OSI ($\chi2$ = 14.072, P = 0.080) level, while statistically significant difference in TOS ($\chi2$ = 35.862, P < 0.001) and TAS ($\chi2$ = 45.593, P < 0.001) levels (Shown in Figure-1). This indicates that OxS is common in cancer patients, but the degrees of OxS may be different in patients with different types of cancer.

Many cancer patients have an increase in the Cu (z = 3.441 ~ 11.473, all P < 0.05) and a decrease in Se (z= -9.746 ~ -3.996, all P < 0.01). The decrease in Zn is observed only in breast cancer patients (z= -6.356, P < 0.001). The change of Fe varies among different types of cancer patients (Shown in Figure-2).
Multinomial logistic regression shows that the risks of different tumors are related to the level change of multiple TEs and OxS parameters (all P <0.05) (Shown in Table-1). And the more significant the changes of TES and OXS parameters in multiple tumors, the higher the risk of tumors, include the highest ORs (OR= 2.82 and 1.44, P <0.001 and =0.003) with the highest levels of TOS and Cu in cancer, The lowest level of FE in colorectal cancer, the lowest ORs (OR= 0.68 and 0.22, P <0.001) with the lowest levels of FE and SE in brain cancer, the lowest OR (OR= 0.81, P <0.001) with the lowest levels of Zn in breast cancer.
The correlation analysis of TEs and OxS parameters shows Cu (|r|= 0.297 ~ 0.795, all P <0.001) with mild-to-strong correlation in all types of cancer patients, Zn(|r|= 0.200 ~ 0.521, all P <0.05) with mild-to-moderate correlation except in brain cancer patients, Fe(|r| = 0.214 ~ 0.760, all P <0.05) with mild-to-strong correlation (except in brain and kidney cancer patients), and Se(|r|= 0.187 ~ 0.408, all P <0.05) with weak-to-moderate correlation (only in breast, lung, esophageal and kidney cancer patients). There were no correlations of TEs and OxS parameters in healthy control subgroup (all P >0.05).
Conclusions Tumorigenesis is often accompanied by OxS occurrence, which is a certain correlation with the change of TEs. In order to evaluate OxS correctly, TAS, TOS and their ratio OSI should be detected. In the specific cancer types, some TEs and OxS parameters change significantly, therefore, it can be potential marker for this cancer type.

PO-0462

AFP 联合 GGT/AST 检测对 HBV 相关肝细胞癌的诊断价值

蔡馨
武汉大学人民医院

目的 探讨 AFP 联合 GGT/AST 在 HBV 相关肝细胞癌（HCC）中的临床诊断价值。
方法 选取 2019 年 1 月 15 日—2019 年 6 月 15 日于武汉大学人民医院诊治的慢性乙型肝炎患者（CHB 组）、乙型肝炎肝硬化患者（LC 组）、HBV 相关 HCC 患者（HCC 组）和健康体检者（HC 组）共 352 例，其中 HC 组 86 例，CHB 组 68 例，LC 组 69 例，HCC 组 129 例，回顾性分析所有研究对象血清学检测数据。计算出预测变量，并绘制 AFP、GGT/AST 以及预测变量单独或联合检测的受试者工作特征曲线（ROC 曲线），计算曲线下面积（AUC）及敏感度、特异度。
结果 HCC 组 GGT/AST 和 AFP 水平显著高于其他组，组间差异均有统计学意义（P<0.05）。ROC 曲线结果显示，在 HCC 组分别与 HC 组，CHB 组，LC 组区别诊断中，联合指标的 AUC 将 AFP 单独诊断的 AUC 分别从 0.921，0.803，0.760 提升至 0.948，0.846，0.802。在 BCLC 分期的 A 期分别与 B 期、C 期的区别诊断中，AFP 单独诊断的 AUC 在联合 GGT/AST 后分别从 0.715，0.737 提升至 0.800，0.759。并且在 AFP 阴性的 HCC 患者中 GGT/AST 单独检测 AUC 均达到 0.7 以上。
结论 AFP 联合 GGT/AST 能提高 HBV 相关 HCC 的临床诊断性能，具有一定诊断价值。

PO-0463

先兆子痫早期预测 nomogram 标准图的建立与验证

岳朝艳、应春妹
复旦大学附属妇产科医院

目的 为了对先兆子痫进行早期预测，我们开发并验证了一种用于中国孕妇先兆子痫早期预测的新型列线图。
方法 采用逐步回归模型进行特征选择。多变量逻辑回归分析用于开发预测模型。我们纳入了 BMI、血压、子宫动脉超声参数和血清学指标危险因素，并用列线图表示。列线图的性能根据其校准、辨别力和临床实用性进行评估。
结果 由 11 个选定特征组成的特征与发育数据集的先兆子痫状态 (P <0.1) 相关。个性化预测列线图中包含的预测因子包括 BMI、血压、子宫动脉超声参数和血清学指标水平。该模型显示出良好的辨别力，ROC 曲线下面积为 0.8563（95% CI：0.8364-0.8761）且校准良好。当应用于验证数据集时，列线图仍然具有良好的辨别力和良好的校准（ROC 曲线下面积为 0.8324，95% CI：0.7873-0.8775）。决策曲线分析表明列线图在临床决策中是有效的。
结论 本研究提出的列线图综合了 BMI、血压、子宫动脉超声参数和血清学指标，可以方便地用于子痫前期的个体化预测。

PO-0464

血清中糖化白蛋白候选参考测量程序的建立及性能评估

张素洁、居漪、李卿、金中淦
上海市临床检验中心

目的 建立一种基于液相色谱串联质谱（ID-LC/MS/MS）技术的血清糖化白蛋白候选参考测量程序并对其进行评价。
方法 基于日本临床化学学会（JSCC）推荐的同位素稀释色谱串联质谱法，加入 ^{13}C 及氘同位素标记的糖化赖氨酸及赖氨酸内标，通过负离子交换柱从血清中分离白蛋白，加入盐酸将纯化的白蛋白分解为氨基酸片段,以赖氨酸（Lys）及糖化赖氨酸（DOF-Lys）纯品作标准品,优化液相和质谱条件,根据标准品和同位素峰面积比分别计算样本中赖氨酸和糖化赖氨酸的含量。采用日本临床化学标准参考物质研究所（ReCCS）糖化白蛋白标准参考物质 JCCRM611-1H 验证参考方法正确性；糖化白蛋白质控品（旭化成制药株式会社）高低两个浓度血清样本测定三个批次，评价本方法精密度。
结果 Lys 和 DOF-Lys 线性标准曲线 R^2 范围分别为 0.9959-0.9999 和 0.9959-0.9979。ReCCS 标准参考物质 JCCRM611-1H 的批内不精密度为 0.5%-3.7%，批间不精密度为 2.8%，与靶值偏移为 -0.72%。两个不同浓度血清样本批内不精密度为 0.4%-5.6%，批间不精密度为 3.1%-5.4%。
结论 建立了一种基于液相色谱串联质谱法检测血清糖化白蛋白的方法，该方法精密度高，正确性好，可作为我国测定糖化白蛋白的候选参考测量程序。

PO-0465

Anterior Gradient 2 Increases Long-chain Fatty Acid Uptake via Stabilizing FABP1 and Facilitates Lipid Accumulation

Yunqiu Wang
the Second Hospital， Shandong University

Anterior gradient 2 (AGR2), a protein disulfide isomerase (PDI), is a well-established oncogene. Here, we found that Agr2−/− mice had a decreased fat mass and hepatic and serum lipid levels compared with their wild-type littermates after fasting, and exhibited reduced high-fat diet (HFD)-induced fat accumulation. Transgenic mice overexpressing AGR2 (Agr2/Tg) readily gained fat weight on a HFD but not a normal diet. Proteomic analysis of hepatic samples from Agr2−/− mice revealed that depletion of AGR2 impaired long-chain fatty acid uptake and activation but did not affect de novo hepatic lipogenesis. Further investigations led to the identification of several effector substrates, particularly fatty acid binding protein-1 (FABP1) as essential for the AGR2-mediated effects. AGR2 was coexpressed with FABP1, and knockdown of AGR2 resulted in a reduction in FABP1 stability. Physical interactions of AGR2 and FABP1 depended on the PDI motif in AGR2 and the formation of a disulfide bond between these two proteins. Overexpression of AGR2 but not a mutant AGR2 protein lacking PDI activity suppressed lipid accumulation in cells lacking FABP1. Moreover, AGR2 deficiency significantly reduced fatty acid absorption in the intestine, which might be resulted from decreased fatty acid transporter CD36 in mice. These findings demonstrated a novel role of AGR2 in fatty-acid uptake and activation in both the liver and intestine, which contributed to the AGR2-mediated lipid accumulation, suggesting that AGR2 is an important regulator of whole-body lipid metabolism and down-regulation of AGR2 may antagonize the development of obesity.

PO-0466

脂代谢与肝纤维化的研究进展

吴逢曦
中南大学湘雅二医院

肝纤维化是肝脏病变的一个慢性过程，其引起的慢性门静脉高压会引起多种临床并发症，包括水肿、失代偿、出血事件以及肝性脑病。因此，肝纤维化的发展决定了患者生活质量以及预后。肝纤维化涉及细胞外基质成分的过度积累，其过程主要由非实质细胞的协同作用介导，特别是肝星状细胞、巨噬细胞（包括枯否细胞）和内皮细胞，肝星状细胞的激活在其中占主导作用。脂质是细胞膜的基本结构成分，在不同的代谢途径和细胞功能中起着至关重要的作用。肝脏是脂质稳态的中枢，肝脏脂质代谢由不同的核受体、转录因子共同调节，主要受到甾醇调节元件 1c、过氧化物酶增殖物激活受体、肝脏 X 受体、法呢样 X 受体等调控，共同维持肝内脂质稳态。脂代谢的紊乱会引发炎症、缺氧等一系列反应，进而调控肝纤维化。近年来，各种脂代谢相关分子都被证明与肝纤维化息息相关，与甘油三酯代谢相关的如前粒蛋白、与磷脂代谢相关的如鞘氨醇 1-磷酸和血小板活化因子、与胆固醇代谢相关的如 SREBP 切割激活蛋白和缺氧诱导因子 1α，以及一些脂蛋白如 vLDL、ApoA1、rHDL 等均在肝纤维化的发生发展中起着调控作用。因此，对脂代谢调控纤维化机制的深入研究，可能有助于肝纤维化的诊断和治疗

PO-0467

分析阿尔茨海默病相关非编码 RNA 调控网络及寻找潜在生物标志物的研究

郭瑞
山东省千佛山医院

阿尔茨海默病（AD）发病机制目前尚不明确，缺乏有效的生物指标和治疗措施。非编码 RNA 已被证实与多种疾病密切相关，但目前关于 AD 非编码 RNA 调控网络的研究还很少。申请人前期已利用测序技术在血清中发现 9 种 AD 相关 miRNAs，其中 miR-22-3p 差异最显著，经数据库预测得到 lncRNA(RP11-145M9.4)—miR-22-3p—ERBB3—circRNA1814 调控通路。本课题将进一步对 AD 血清 lncRNA、circRNA 和 mRNA 进行表达谱分析，应用生物信息学分析技术，构建 AD 相关 miRNA-lncRNA-circRNA-mRNA 调控网络。并以前期预测的调控通路为例，应用质粒构建、共转染、细胞模型构建等技术，建立体外实验验证流程，研究非编码 RNA 间的相互作用及对靶基因的调控作用，阐明非编码 RNA 调控网络在 AD 发病过程中的作用，为 AD 的诊治提供新的生物标志物和治疗靶点。

PO-0468

温和还原反应介导的电化学适配体传感方法用于蛋白标志物检测

李玲玲
上海交通大学医学院附属第九人民医院
上海大学

目的 机体细胞内各种蛋白的表达水平在病理状态下会发生一定改变，因此检测蛋白表达谱的改变可以快速且准确地诊断相关疾病。
方法 在本研究中，以肝癌相关蛋白质标志物-甲胎蛋白（AFP）作为研究对象，设计了温和还原反应介导的杂交链式信号放大策略用于蛋白质类疾病标志物检测的通用电化学适体传感方法。具体而言，含有二硫键的目的蛋白经电极表面固定化适配体捕获后，通过温和还原反应可以暴露出活性巯基，而蛋白表面的活性巯基通过巯基-马来酰亚胺反应偶联探针 DNA，并由此引发杂交链式反应，因此大量的电化学信号分子聚集在链式反应的长链产物上因而可得到放大的电化学信号响应。
结果 研究结果表明，温和还原反应介导的电化学适配体传感方法用于肝癌标志蛋白甲胎蛋白检测可以获得较宽的线性范围（1×10-4 ~ 100 ng/mL）和低的检出限（0.041 pg/mL）。
结论 进一步研究表明证实了该方法对蛋白识别的高选择性，也体现了其在蛋白检测中的普适性，可以通过改变相应的适配体来实现不同蛋白标志物的检测需求。因此，该方法为实现高通量、自动化的临床蛋白标志物分析奠定了基础。

PO-0469

CRP、CK、CK-MB、LDH 及 NSE 在新生儿缺氧缺血性脑病中的临床价值

乔正梅
宝鸡高新医院

目的 探讨 CRP、CK、CK-MB、LDH 及 NSE 在新生儿缺氧缺血性脑病中的相关变化及临床价值。
方法 选择 45 例缺氧缺血性脑病新生儿为患儿组，40 例健康新生儿作为对照组。按病情严重程度

将患儿组分为轻度组、中度组和重度组，根据病程检测各组出生后 3 小时（h）、3 天（d）、7d、14d 时间点的 CRP、CK、CK-MB、LDH 及 NSE 水平变化。病情严重程度、病程多个时间节点的多组间上述数据比较运用方差分析，病情严重程度的组间比较运用独立样本 t 检验，病程多个时间节点的组间比较运用配对 t 检验。

结果 患儿组 CRP、CK、CK-MB、LDH 及 NSE 水平均高于对照组，差异有统计学意义（P＜0.001）；轻度、中度和重度组随着病情程度的加重，其 CRP、CK、CK-MB、LDH 及 NSE 水平越高，差异有统计学意义（P＜0.05）。HIE 组于出生后 3h、3d、7d 的血清 CRP、CK、CK-MB、LDH 及 NSE 水平差异有统计学意义（P＜0.05），出生后第 3d 达到高峰，第 7d 明显下降，出生后第 7d 上述数据低于出生后 3h、3d，但明显高于对照组（P＜0.05）。经 14d 治疗后，HIE 治疗有效组的 CRP、CK、CK-MB、LDH 及 NSE 水平低于无效组（P＜0.05）。

结论 CRP、CK、CK-MB、LDH 及 NSE 水平能较好地反映新生儿 HIE 的病情严重程度和病程变化，随着脑损伤程度越重，CRP、CK、CK-MB、LDH 及 NSE 水平越高，并随病情好转进行性降低，因此检测 CRP、CK、CK-MB、LDH 及 NSE 水平变化有利于新生儿缺氧缺血性脑病的诊治。

PO-0470

纤溶酶原激活物抑制剂-1(4G/5G)基因多态性与深静脉血栓事件的风险

张莹、程晓东、胡玉皎、王昊、周铁成、郝晓柯、刘家云
空军军医大学西京医院

目的 分析我国西北地区纤溶酶原激活物抑制剂-1(PAI-1) (4G/5G)基因在不同人群中的分布情况，以及不同基因型患者血栓事件的发生率，为携带 PAI-1(4G/5G)基因 4G 型的手术患者提供数据支持和用药指导。

方法 收集 1 494 例人群血液样本，使用荧光探针原位杂交技术检测 PAI-1(4G/5G) 基因位点，分析我国西北地区 PAI-1(4G/5G)基因在体检健康者、剖腹产患者、烧伤患者、心脑血管疾病患者之间 4G 基因的差异性。

结果 336 例体检健康者中 5G5G（野生型）78 例（23.21%），4G5G（杂合突变型）152 例（45.24%），4G4G（纯合突变型）106 例（31.55%）。401 例剖腹产患者中 5G5G（野生型）60 例（14.96%），4G5G（杂合突变型）195 例（48.63%），4G4G（纯合突变型）146 例（36.41%）。603 例烧伤患者中 5G5G（野生型）100 例（16.58%），4G5G（杂合突变型）295 例（48.93%），4G4G（纯合突变型）208 例（34.49%）。154 例心脑血管疾病患者中 5G5G（野生型）21 例（13.64%），4G5G（杂合突变型）81 例（52.59%），4G4G（纯合突变型）52 例（33.77%）。PAI-1(4G/5G)4G 型基因携带率在剖腹产患者、烧伤患者、心脑血管疾病患者与健康体检人群间均差异有统计学意义（P<0.05）。200 例烧伤手术患者患病后 2 个月内深静脉血栓事件追踪结果表明，4G4G 基因型血栓事件为 86.49%，4G5G 基因型血栓事件为 65.00%，5G5G 基因型血栓事件为 50.00%，不同的基因型间差异有统计学意义（P<0.01）。

PO-0471

脑脊液常规、脑脊液糖/乳酸、脑脊液糖/血糖比值对颅内感染诊断的意义

余罗莉、江丽
福建医科大学附属第一医院

目的 分析颅内感染患者脑脊液常规、CSF 糖/血糖和 CSF 糖/CSF 乳酸比值变化的临床意义。
方法 收集我院 2016 年 5 月—2017 年 5 月进行脑脊液细菌培养的 72 例患者作为观察对象。其中 40 例培养出致病菌并有脑膜炎刺激症,将其作为感染组;32 例培养阴性的癫痫患者作为阴性对照组。对所有对象进行脑脊液常规检测（颜色、潘氏试验、白细胞计数及分类）和脑脊液生化检查（本文只做 CSF 乳酸、CSF 糖）,同时对 CSF 糖与血糖的比值以及 CSF 糖与乳酸的比值进一步分析。
结果 感染组患者脑脊液常规的白细胞总数显著高于对照组,其中细菌性脑膜炎患者多个核细胞明显多于单个核细胞;感染组 CSF 糖/血糖的值均<0.4,对照组 CSF 糖/血糖的值均>0.4,组间差异有统计学意义（P<0.05）;感染组 CSF 糖/CSF 乳酸的值均<1.00,而对照组 CSF 糖/CSF 乳酸的值均>1.00,组间差异有统计学意义（P<0.05）。
结论 脑脊液常规检查的变化,通过联合应用 CSF 糖与血糖的比值以及 CSF 糖与乳酸的比值的检测,可提高对细菌性脑膜炎的诊断和可信度,帮助患者早期确诊,更好地为临床早期治疗提供依据。

PO-0472

基于随机森林算法的肾移植术后 DSA 风险预测模型构建

周晓涵[1]、巫丽娟[2]、周娟[2]、陆小军[2]
1. 四川大学华西临床医学院
2. 四川大学华西医院

目的 肾移植后供者特异性抗体（donor specific antibody, DSA）是引起排斥的主要原因，排斥反应会导致移植物失功，早期预测或诊断 DSA 有助于对患者进行早期干预，改善患者预后。但目前尚无满足临床需求的移植后 DSA 预测手段，本研究全面探讨了肾移植术后发生排斥反应的相关因素，构建了基于随机森林算法的肾移植术后 DSA 风险预测模型，利用大数据建模的手段提高了肾移植术后发生排斥反应的预测效能。
方法 纳入四川大学华西医院 2009 年 1 月至 2019 年 12 月 4629 例肾移植术后受者，回顾性分析受者的人口学基本特征、流行病学资料及肾移植术后受者的临床特征、生化、免疫和血常规检测结果等 40 指标。经过筛选的病例按照 8:2 的比例随机划分为训练集和测试集，基于训练集使用随机森林算法建立肾移植术后 DSA 风险预测模型，并进一步评估模型预测效能及探索 DSA 影响因素的重要性。
结果 42.86%（1984/4629）患者产生术后 DSA，基于随机森林的 DSA 风险预测模型的训练集判对率为 86.1%，测试集为 87.0%；模型的特异性、灵敏度和 AUC 分别为 0.9209、0.7946 和 0.91。同时进行 DSA 影响因素重要性探索，发现最重要的预测因素前五位依次为年龄、eGFR(估算肾小球滤过率)、MCV（平均红细胞体积）、CREA（肌酐）和 SYS-C（胱抑素 C）。
结论 随机森林算法在肾移植术后 DSA 风险预测模型中有较好的应用，该模型可以很好预测肾移植术后 DSA 的发生风险。同时应当特别关注受者年龄、eGFR、MCV、CREA 和 SYS-C 五项指标的变化情况。

PO-0473

Urinary peptidomics analysis reveals proteases involved in idiopathic membranous nephropathy

Baoxu Lin 、Xiaosong Qin
Shengjing Hospital of China Medical University

Background Idiopathic membranous nephropathy (IMN) is a cause of nephrotic syndrome with increasingly incidence and lack of clear pathogenesis. Urine peptidomics is a promising technology to elucidate the molecular mechanism of diseases. Dysregulation of the proteolytic system is implicated in various diseases. Here, we aimed to conduct urinary peptidomics analysis and predict proteases may related to IMN.
Methods Naturally produced peptides in the urine of 20 heathy individuals, 22 patients with IMN, and 15 patients with other kidney diseases were extracted with weak cation magnetic bead (WC-MB), peptides fingerprint and proteomics profile were analyzed by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) and data-independent acquisition mass spectrometry (DIA-MS), respectively. Proteins matched with peptides that were differentially expressed in IMN patients were identified. Proteasix database was used to predict the proteases that involved in peptide production, iProX and Gene Expression Omnibus (GEO) databases were used to validate the proteins and proteases corresponding to each peptide. Finally, western blot analysis was used to validate the expression of the key proteases .
Results Peptides fingerprints indicated there were differences in urine peptides components among heathy individuals, patients with IMN and other kidney diseases. In total, 1080 peptide-matched proteins were identified, 279 proteins differentially expressed in the urine of IMN patients were screened, and 32 proteases were predicted; 55 of the matched proteins were also differentially expressed in the kidney tissue of IMN patients, and these were mainly involved in the regulation of proteasome-, lysosome-, and actin cytoskeleton-related signaling pathways. The 32 predicted proteases showed abnormal expression in the glomerulus of IMN patients. Western blot revealed that the expression of calpain the CAPN1, matrix metalloproteinase MMP14, and cathepsin S (CTSS) was increased in the kidney tissue of IMN patients.
Conclusions Collectively, these results shown the calpain, matrix metalloproteinase and cathepsin axis may be dysregulated in IMN.

PO-0474

HYDRASHIFT 2/4 daratumumab 检测在消除达雷妥尤单抗对血清免疫固定电泳干扰的应用

徐双
北京大学人民医院

背景 达雷妥尤单抗是一种用于治疗浆细胞疾病的单克隆抗体，使用该药物治疗后免疫固定电泳会出现此种药源性 IgG-κ 型单克隆条带，进而导致免疫固定电泳结果出现假阳性，使临床医生对患者治疗疗效做出错误的分类。HYDRASHIFT 2/4 daratumumab 检测可以消除达雷妥尤单抗对血清免疫固定电泳结果的干扰。
方法 收集使用达雷妥尤单抗进行治疗的 8 名浆细胞疾病患者的血清样本（T0,T1（C2D1），T2（C3D1）），分别进行标准的免疫固定电泳检测及 HYDRASHIFT 2/4 daratumumab 检测。
结果 单抗治疗后，81.3%（13/16）的样本出现药物性单克隆条带（IgGκ 型），未出现药物性单克隆条带的样本考虑与个体差异、给药间隔时间有关。出现 IgGκ 型单克隆条带的样本中 76.9%

（10/13）可通过免疫固定电泳直接区分其为内源性或外源性单克隆条带，余 3 份样本（3/13），需要使用 HYDRASHIFT 2/4 daratumumab 检测进行区分。
结论 使用达雷妥尤单抗治疗后 81.3%（13/16）的样本出现药物性单克隆条带，其中 3 份样本（3/13）不能区分其为内源性或外源性单克隆条带，使用 HYDRASHIFT 2/4 daratumumab 检测可以去除达雷妥尤单抗对免疫固定电泳结果的干扰，辅助疗效评判。

PO-0475

血清 25 羟维生素 D 候选参考方法的建立

龙琪琛[1,2]、张天娇[1,2]、张莉[1,2]、曾庆璋[1,2]、周伟燕[1]、曾洁[1]、张江涛[1]、张传宝[1]
1. 北京医院 国家老年医学中心 国家卫生健康委临床检验中心 北京市临床检验工程技术研究中心 中国医学科学院老年医学研究院
2. 中国医学科学院北京协和医学院

目的 25 羟维生素 D（25-hydroxyvitamin D，25OHD）是反映体内维生素 D 缺乏状态的重要指标，检测 25 羟维生素 D 的临床需求日益增长。为确保常规检测的准确可比，推动 25 羟维生素 D 检测的标准化至关重要。本研究拟建立血清 25 羟维生素 D 候选参考方法，并对该候选参考方法进行全面的性能确认。
方法 使用 25 羟维生素 D3 和 25 羟维生素 D2 的标准溶液对质谱条件和色谱条件进行摸索和确认。比较不同类型的前处理方式，并对选择的样本制备方案进行优化。选择 14 种 25 羟维生素 D 的结构类似物进行干扰分离，并对方法的精密度、正确度和检测限等进行了性能确认。
结果 该方法使用的色谱柱为 Shimadzu Shim-pack Velox PFPP（2.1×100mm，1.8 μm），前处理方式使用蛋白沉淀和液液萃取一步处理法。该方法检测 25 羟维生素 D3 的不精密度为 0.97% ~ 1.25%，25 羟维生素 D2 不精密度为 1.24% ~ 2.77%。测定 25 羟维生素 D3 和 25 羟维生素 D2 的加标回收率及变异系数为 100.8% ± 0.8％ ~ 101.0% ± 0.6％和 99.9% ± 1.2％ ~ 101.0% ± 1.5％，且测定国际标准物质 NIST 972a 的相对偏倚均在不确定度范围内。方法的检测限和定量限分别为 0.002 ng 和 0.005 ng（25 羟维生素 D3）以及 0.004 ng 和 0.012 ng（25 羟维生素 D2）。
结论 本研究开发了基于同位素稀释液相色谱串联质谱法的血清 25 羟维生素 D 的检测方法。该方法准确精密灵敏，特异性高，分析时间短，有望作为 25 羟维生素 D 参考方法。

PO-0476

A nomogram for predicting metabolic steatohepatitis: the combination of NAMPT, RALGDS, GADD45B, FOSL2, RTP3, and RASD1

Shenling Liao 、He He、Yuping Zeng、Lidan Yang、Zhi Liu、Zhenmei An、Mei Zhang
West China Hospital, Sichuan University

Objective The gold standard for diagnosing MASH is the biopsy, but the biopsy is an invasive and costly method that is not easy to be accepted by patients. Therefore, developing new, non-invasive, and reliable biomarkers is undergoing. Our study aims to identify differentially expressed and clinically significant mRNAs and construct a potential prediction model for metabolic steatohepatitis (MASH).
Methods We downloaded four microarray datasets， GSE89632, GSE24807, GSE63067, GSE48452 from the Gene Expression Omnibus database. GSE63067, GSE24807, and GSE89632 were used to identify DEGs. GSE89632 was analyzed with the weighted gene co-expression network. The online analysis platform GEO2R (https://www.ncbi.nlm.nih.gov/geo/geo2r/) was employed to compare two groups of samples to

identify differentially expressed genes. With weighted gene co-expression network analysis (WGCNA) R package, clusters (modules) of highly correlated genes were found and the correlation between modules external sample traits was constructed for GSE89632. The differentially expressed genes analysis and weighted gene co-expression network analysis were performed to screen significant genes. Finally, we constructed a nomogram of six hub genes in predicting MASH and assessed it through receiver operating characteristic (ROC) curve， calibration plot and decision curve analysis (DCA). In addition, qRT-PCR was used for relative quantitative detection of RNA in QSG-7011 cells to further verify the expression of the selected mRNA in fatty liver cells.
Results The GEO2R and limma R package were applied to analyze differentially expressed genes. 296 DEGs were screened in GSE89632 (p-value < 0.05, log FC absolute value > 1.2). 83 DEGs were screened in GSE63067 (p-value < 0.05, log FC absolute value > 1.2). 1643 DEGs were screened in GSE24807 (p-value < 0.05, log FC absolute value > 2). There were 14 modules in the weighted gene co-expression network analysis, and brown module and yellow module had a negative and positive relation to disease respectively. GO and KEGG pathway analyses for genes in the two modules were performed, and these genes highlight inflammation and inflammatory cytokines. Based on common DEGs and brown and yellow modules, 7 hub genes were identified, which were NAMPT, PHLDA1, RALGDS, GADD45B, FOSL2, RTP3, RASD1. After logistic regression analysis, six hub genes were used to establish the nomogram, which were NAMPT, RALGDS, GADD45B, FOSL2, RTP3, RASD1. The area under the ROC of the nomogram was 0.897. The DCA showed when the threshold probability of MASH was 0-0.8, the prediction model was valuable to GSE48452. In QSG-7011 fatty liver model cells, the relative expression levels of NAMPT, GADD45B, FOSL2, RTP3, RASD1 and RALGDS were lower than the control group.
Conclusion We identified seven hub genes NAMPT, PHLDA1, RALGDS, GADD45B, FOSL2, RTP3, RASD1. The nomogram showed good performance in the prediction of MASH and it had clinical utility in distinguishing MASH from simple steatosis.

PO-0477

血清游离轻链、比值及差值在肾脏受累的系统性轻链型淀粉样变性病中的临床价值

胡娟娟
空军军医大学西京医院

目的 分析血清游离轻链、比值及差值在肾脏受累的系统性轻链（AL）型淀粉样变性病中的临床价值。
方法 对空军军医大学附属第一医院西京医院肾内科住院的新确诊为肾脏受累的 AL 型淀粉样变性患者 222 例进行血清游离轻链（sFLc）水平、sFLCκ/λ 比值、差值（dsFLC）进行回顾性分析，评估此检测在肾脏受累的系统性轻链（AL）型淀粉样变性病中诊断，治疗和预后的影响。
结果 肾脏受累的 AL 型淀粉样变性患者血 β2 微球蛋白和骨髓浆细胞比例与 sFLC 有相关性(P＜0.05)，血肌酐、24 小时尿蛋白定量与 sFLC-λ 有相关性(P＜0.05)。肾脏受累的 AL 型淀粉样变性研究组患者 sFLCκ/λ＜0．26 或＞1．65 的比例为 80.2%高于对照组患者，差异有统计学意义（χ^2=18.342，P＜0.05)。不同化疗疗程前后患者轻链差值变化结果显示，化疗一个周期后，dsFLC 达到缓解程度无反应性占比例大，为 47.3%，随着化疗次数的增加，无反应性比例减少，dsFLC 达到完全缓解比例从 8.15%到 35.1%，dsFLC 达到血液学有反应性比例从 52.3%到 81.9%。结果表明轻链差值（dsFLC）变化可以明确的反应血液学缓解程度。
结论 血清游离轻链水平、比值在肾脏受累的系统性轻链（AL）型淀粉样变性病的诊断中提供重要依据。sFLCκ/λ 比值、差值与患者临床预后密切相关，可作为预后评估监测的理想指标。

PO-0478

糖化白蛋白、尿蛋白以及空腹血糖检测对糖尿病肾病患者的临床评估

虢瑾、张莹、童开、肖鹏涛
空军军医大学西京医院

目的 探讨糖化白蛋白、尿蛋白以及空腹血糖检测对糖尿病肾病患者的临床评估。
方法 以我院 2019 年 1 月到 2020 年 12 月确诊为糖尿病的患者 289 例为研究组。根据其是否患糖尿病肾病将其分为肾病组（ n=90 ）和非肾病组（ n=199 ）。对照组为同一时间段在我院体检的健康者 80 名。对两组研究参与者均进行糖化白蛋白、尿蛋白以及空腹血糖的检测， 就检测结果进行组间及组内的数据对比分析。
结果 研究组患者的糖化白蛋白、尿蛋白以及空腹血糖水平均高于对照组，且差异有统计学意义（ P＜0.05 ）；肾病组患者的糖化白蛋白、尿蛋白以及空腹血糖水平均高于非肾病组（ P＜0.05 ），可知其水平与疾病严重程度正相关； 3 项联合检测、糖化白蛋白和空腹血糖联合检测、尿蛋白单一检测对糖尿病肾病的阳性率分别为 85.11％ 、 64.72％ 、 21.22％ ， 3 项联合检测的阳性率最高（ P＜0.05 ）。
结论 糖化白蛋白、尿蛋白以及空腹血糖水平对糖尿病肾病患者的诊断及疾病严重程度判断有重要临床意义，联合检测可显著提高诊断准确率。

PO-0479

分析儿童全血部分常量和微量元素含量的年龄差异

韩旭
山东省千佛山医院

目的 探讨儿童全血常量元素（钙、镁）和微量元素（铁、锌、铜）含量的年龄差异，并建立临床正常参考范围。
方法 以 20 946 例健康查体的儿童（男 12 447 例，女 8 499 例）为对象 按照年岭分为四组(<1 岁，1 岁～，3 岁～，>6 岁)。采用原子吸收光谱法测定末梢血钙、镁、铁、锌、铜元素的含量。计算出各年龄组、各元素含量第 3，10，25，50，75，90，97 百分位的相应数值。
结果 不同年龄组之间血钙、镁、铁、锌、铜的含量有显著性差异（P< 0.05），且随年龄的变化而变化。便于临床应用，取第 25-75 百分位的相应数值作为正常参考范围。
结论 判断 5 种元素含量是否正常应考虑年龄因素，各年龄组需分别参考其相应的正常范围。

PO-0480

Uridine Diphosphate Promotes Rheumatoid Arthritis Through P2Y6 Activation.

Hongxing Wang
Qilu Hospital, Shandong University

BACKGROUND Uridine diphosphate (UDP) is an extracellular nucleotide signaling molecule implicated in diverse biological processes via specific activation of pyrimidinergic receptor P2Y, G Protein-Coupled, 6 (P2Y6). There is very little knowledge about the function and mechanism of UDP in rheumatoid arthritis (RA).

METHODS This study used a quasi-targeted liquid chromatography-mass spectrometry (LC-MS) approach to investigate the unique expression of metabolites in RA synovial fluids (SF) (n = 10) with samples from osteoarthritis (OA) as controls (n = 10). RA fibroblast-like synoviocytes (FLSs) were collected from synovial tissues (n = 5) and cultured with UDP or MRS2578, a P2Y6 antagonist, and FLSs from OA were used as controls (n = 5). Rats with collagen-induced arthritis (CIA) were injected with UDP, MRS2578 or both (n = 9 for each group). P2Y6 expression was examined using real-time PCR, Western blotting and immunohistochemistry. Cell proliferation, apoptosis and migration of RA FLSs were measured using CCK-8 assay, real-time cell analysis, flow cytometry, wound healing assay and Transwell assay, respectively. The UDP levels in the culture medium, synovial fluid (n = 36) and peripheral blood (n = 36) of RA and CIA rats were measured using a Transcreener UDP Assay. Levels of proinflammatory cytokines were measured using a flow assay. Interleukin-6 (IL-6) levels were measured using ELISA and flow.
RESULTS LC-MS analysis detected significantly increased UDP levels in RA SF compared with OA SF, and the level was positively correlated with anticyclic citrullinated peptide (anti-CCP) and rheumatoid factor (RF)levels in RA. The increased UDP concentration was verified in the blood and synovial fluids of RA patients compared with samples from OA patients and healthy volunteers, respectively. UDP stimulated cell proliferation, migration and IL-6 secretion in RA FLSs and inhibited their apoptosis in culture, and MRS2578 inhibited these effects of UDP. UDP injection accelerated CIA and stimulated IL-6 production rather than other proinflammatory cytokines in the rat model, but simultaneous injection of MRS2578 suppressed these effects and alleviated CIA. P2Y6 expression was increased in RA and CIA synovial tissues.
CONCLUSION These results suggest that UDP is highly expressed in RA and stimulates RA pathogenesis by promoting P2Y6 activities to increase IL-6 production.

PO-0481

CircRNA 在代谢性疾病中的研究进展及前景

石盛洁、谢小兵
湖南中医药大学第一附属医院

代谢性疾病是影响世界公共卫生健康的主要原因之一，造成了大量人员死亡。早期诊断和预后判断是治疗、减少并发症以及降低死亡率的关键。环状 RNA（Circular RNA, circRNA）在机体的生理和病理过程中起重要作用，参与许多疾病的发生发展。保守性、稳定性、特异性、普遍性等优良特性使得 circRNA 有望成为新的潜在生物标志，但其作为检测指标应用于临床要需要迎接一定的挑战。

PO-0482

Albumin-bilirubin score is associated with response to pegylated interferon and nucleos(t)ide analogues in chronic hepatitis B patients

Zhen Xun 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Background and Aim Recently, the role of albumin-bilirubin (ALBI) score in chronic hepatitis B (CHB) has not been well-understood. We aimed to investigate the association of ALBI score with natural history of chronic HBV infection and treatment response of CHB patients.
Methods The ALBI score in a cohort of 849 individuals including 721 chronic HBV-infected patients naïve to anti-HBV treatment in different phases and 128 healthy controls were estimated. Additionally, the dynamic changes of ALBI score of 243 hepatitis B e antigen (HBeAg)-positive

CHB patients treated with pegylated interferon-alpha (PEG-IFN-α) or nucleos(t)ide analogues (NAs) were tested for 72 weeks.
Results ALBI score differed among phases, with the highest score in HBeAg-positive CHB patients, followed by HBeAg-negative CHB patients, HBeAg-positive chronic HBV infection, and HBeAg-negative chronic HBV infection. Besides, CHB patients harbouring high baseline ALBI score exhibited a relatively stronger therapeutic response to PEG-IFN-α or NAs. Moreover, the rate of HBeAg and HBsAg loss in patients with ALBI grade 2 was persistently higher than that in patients with ALBI grade 1 throughout the course of treatment. Furthermore,
ALBI score was an independent predictor of sustained response achievement. The combined use of ALBI score, HBeAg and ALT could enhance the predictive value of treatment response.
Conclusions ALBI score differed significantly across the natural course of chronic HBV infection and was correlated with PEG-IFN-α and NAs treatment response in HBeAg-positive CHB patients, which suggested that ALBI score could be useful as an auxiliary clinical factor to determine the initiation of therapy and predict stronger
antiviral treatment response.

PO-0483

Effect of Addition of WZB117 as an Inhibitor of Glucose Transporter 1 for Venous Blood Glucose Determination

lei zhang[1]、 Yaqiong Ran[2]、 Yan Zhu[2]、 Qianna Zhen[2]
1. 1 Clinical Laboratory, the First Affiliated Hospital of Chongqing Medical University
2. Clinical Laboratory, the First Affiliated Hospital of Chongqing Medical University

Objective Sodium fluoride (NaF) has been applied to inhibit glycolysis in venous specimens for decades. However, it has had little effect on the rate of glycolysis in the first 1 to 2 hours, resulting in a decrease of glucose, so a more efficient method is needed. Recently, we discovered that WZB117, a specific Glut1 inhibitor, restricts glycolysis by inhibiting the passive sugar transport of human red blood cells and cancer cells. The purpose of this study was to evaluate the results of intravenous blood glucose determination after the addition of WZB117.
Methods Venous specimens from 40 pairs of healthy volunteers were collected for several days and placed in tubes containing NaF plus EDTA-disodium (Na2) without WZB117 (the A group); citric acid, trisodium citrate, and EDTA-Na2 without WZB117 (B group); and NaF plus EDTA-Na2 with WZB117 (C group). The glucose concentration was measured after venipuncture and compared with test tubes treated for 1 hour, 2 hours, and 3 hours before centrifugation. Glucose level was determined by the hexokinase method. The paired t-test was used to examine differences in glucose values at baseline and at different time points. The number of misdiagnoses and the misdiagnosis rate were calculated at 2 diagnostic stages: high risk of diabetes (glucose level of 6.1 mmol/L) and diagnosis of diabetes (glucose level of 7.0 mmol/L).
Results Glucose levels decreased by 1.0% at 1 hour and by 2.1% at 3 hours in the C group tubes and simultaneously decreased by 1.7% at 1 hour and by 2.5% at 3 hours in the B group tubes. In contrast, glucose levels decreased by 4.1% at 1 hour and by 6.3% at 3 hours in the A group tubes. There was a statistically significant difference in glucose levels measured in the A group tubes and B group tubes at 1 hour, 2 hours, and 3 hours. The misdiagnosis rate of clinical diagnosis in diabetes was highest in the A group tubes (7.0‰ at 1 hour, 0.1‰ at 3 hours at 7.0 mmol/L point; 14.6‰ at 1 hour, 0.4‰ at 3 hours at 6.1 mmol/L point) and lowest in the C group tubes (2.95‰ at 1 hour, 0‰ at 3 hours at 7.0 mmol/L point; 4.8‰ at 1 hour, 0.1‰ at 3 hours at 6.1 mmol/L point).
Conclusion The tube addition of WZB117 is more suitable for minimizing glycolysis and has no effect on glucose levels even if specimens are left uncentrifuged for up to 3 hours.

PO-0484

Development of Potential Diagnostic Biomarkers for HBV-Related Hepatocellular Carcinoma with BCLC Stage 0-A by 1H-NMR-based Lipidomic Analysis.

HaoHua An、Li Ren
Tianjin Medical University Cancer Institute and Hospital

Background Early diagnosis is essential for improving the prognosis and survival of patients with hepatocellular carcinoma (HCC). However, due to the lack of ideal biomarkers with satisfactory sensitivity and specificity, the diagnosis of HCC has been challenging to date. This study aims to explore the clinical value of 1H-nuclear magnetic resonance (1H-NMR)-based lipoprotein subfraction assays in the diagnosis of hepatitis B virus (HBV)-related HCC.
Methods A total of 196 serum samples were detected by 1H-NMR spectroscopy. Eight pairs of cancerous and paracancerous tissue samples were detected by LC-MS/MS. Orthogonal partial least-squares discriminant analysis (OPLS-DA) and backward stepwise logistic regression were performed to classify distinct serum profiles and construct a prediction model for HCC diagnosis. Furthermore, the overall and disease-free survival rates were estimated by Kaplan–Meier survival analysis.
Results The diagnostic panel constructed from apolipoprotein-A1 (Apo-A1) and the number of very-low-density lipoprotein (VLDL), intermediate-density lipoprotein (IDL) and low-density lipoprotein (LDL-1, LDL-2, LDL-4 and LDL-5) particles achieved higher diagnostic accuracy (AUC: 0.891; 95% CI: 0.807-0.948) than that constructed from serum alpha-fetoprotein alone (AUC: 0.831; 95% CI: 0.736-0.902). In addition, Apo-A2, high-density lipoprotein (HDL) and HDL-3 Apo-A2, IDL and HDL-3 phospholipids, VLDL-4 cholesterol, and HDL-3 and HDL-4 free cholesterol were significantly decreased after surgical treatment. We also found that the expression of proteins involved in lipid metabolism was significantly changed in HBV-related HCC tissues and significantly associated with a poor HCC prognosis.
Conclusion Our research focused on an innovative combination of lipid profile alterations in HCC patients and 1H-NMR-based lipidomics research, which provided new insight for the development of diagnostic biomarkers for HCC. Moreover, LC-MS/MS analysis indicated that abnormal lipid metabolism may be an important factor in promoting HCC development.

PO-0485

四种不同方法的可溶性生长刺激表达基因 2 蛋白试剂的性能评价

莘琳琳、范雪松、袁慧
首都医科大学附属北京安贞医院

目的 对四种不同检测方法（分别用 A、X、J、L 表示）的可溶性生长刺激表达基因 2 蛋白（sST2）检测试剂盒进行性能验证，为后续临床实验室应用该指标提供参考。
方法 对四种不同方法学试剂的基本性能进行验证和方法学比对。收集 2021 年 1 月至 3 月首都医科大学附属北京安贞医院 120 例患者和 40 名表观健康人剩余血清，参考 CLSI 文件和行业标准要求对免疫层析(A)、增强免疫荧光（X）、乳胶免疫比浊（J）和磁微粒化学发光(L)的 sST2 检测试剂盒分别进行性能评价；并且以美国 Presage 生产的 ELISA 检测试剂盒作为参比试剂，进行临床样本比对和医学决定水平处的偏差的计算。
结果 四种检测方法试剂的批内精密度分别为 6.26%~9.14%、5%~5.88%、0.88%~1.42%、0.72%~0.8%；都有不少于 90%的表观健康人落入生物参考区间；线性验证均验证通过；但 A 试剂批间精密度为 CV%=18%，A 和 J 厂家的正确度验证未通过；J 试剂对类风湿因子的抗干扰能力与说明书标注的范围不符。X、J、L 试剂分别可进行 10 倍，20 倍和 50 倍的稀释比例，可报告范围

达到 10000ng/ml、8000ng/ml 和 15000ng/ml。四种试剂与美国 Presage 生产的酶联免疫吸附法试剂之间相关性 R2 分别为 0.8032、0.9569、0.9404、0.9064；在医学决定水平处的平均预期偏差分别为 45.19%、64.07%、59.12%、53.84%。

结论 四种不同方法学的 sST2 试剂的批内精密度、线性和生物参考区间均符合说明书标注的检测范围，但部分厂家的正确度和抗干扰能力以及试剂之间的一致性有待提高。

PO-0486

环状 RNA hsa_circ_0000745 与冠心病的相关性研究

苏明、张登伟、李珊珊、曹珍菊、贾玫
北京大学人民医院

目的 近年来，环状 RNA（circRNA）在冠心病中的作用越来越引起重视，探索新的 circRNA 对于揭示冠心病的发病机制有重要意义。为发现新的冠心病相关 circRNA，通过表达谱芯片进行了筛选发现新的 circRNA hsa_circ_0000745 在冠心病患者中表达上调。由此提示，该 circRNA 可能是潜在的冠心病相关基因。本研究以 hsa_circ_0000745 为研究对象，探讨其表达与冠心病之间的关系，旨在为冠心病的发病机制研究提供实验依据。

方法 分离经冠脉造影确诊的 200 例冠心病患者及 35 例非冠心病对照的外周血单个核细胞（PBMC），提取 RNA 使用随机引物逆转录成 cDNA，采用实时荧光定量 PCR 技术检测 hsa_circ_0000745 在冠心病及对照人群中的表达水平。采用 2-ΔΔCt 法标准化后利用非参数检验及 logistic 回归分析 hsa_circ_0000745 的表达差异性与临床表型之间的关联。

结果 与对照组相比，冠心病患者的 hsa_circ_0000745 表达上调（$p<0.05$），ROC 曲线下面积 0.657。单因素二元 logistic 回归显示冠心病发生与 hsa_circ_0000745 表达水平上调显著相关。此外，单因素二元 logistic 回归分析和多因素二元 logistic 回归分析显示，相对于心绞痛患者，急性心肌梗死患者 hsa_circ_0000745 表达显著上调。

结论 冠心病患者外周血单个核细胞中 hsa_circ_0000745 表达水平上调，可能是一种新的冠心病相关生物标志物。

PO-0487

Relationship Between Apolipoprotein E Genotype and Lipoprotein Particles in Patients with Coronary Heart Disease

Qiong Yang、Zhaohui Liu、Yahui Lin、Zhou Zhou
Fuwai Hospital, Chinese Academy of Medical Sciences

Background Recent studies have indicated that as the main therapeutic target for reducing cardiovascular risk, LDL-C cannot explain all cardiovascular risks. Intervention studies on cholesterol-lowering therapy shows that even after reaching the optimal cholesterol concentration, the residual risk still exists. These clinical evidences have led to further research on lipoproteins, making people aware of the atherogenic effects of lipoprotein particles themselves rather than their cholesterol content. The new cardiovascular risk factor LDL particles (LDL-P) can better indicate the risk of CHD than low-density lipoprotein cholesterol (LDL-C). Previous researches have shown that the concentration and subclass distribution of lipoprotein particles differ with APOE genotypes. Our study aims to cross-sectionally analyze the relationship among APOE genotype, lipoprotein particles and disease severity in patients with coronary heart disease treated with statins, so as to provide more accurate evidence for clinical cholesterol-lowering therapy.

Methods Blood samples were collected from 360 patients with coronary heart disease treated with statins within 24 hours after admission. Lipoprotein particle parameters including VLDL, IDL, LDL, Small-LDL, Medium-LDL, Large-LDL concentration and LDL size were measured by NMR spectrometer. The NMR spectroscopy (NMRS) can provide a quick measurement to distinguish and quantify lipoprotein subclasses. When exposed to magnetic field, different lipoprotein particles will emit a unique signal, which is proportional to their concentration. APOE alleles were determined based on SNPs rs7412 and rs429358 haplotypes. Genotyping was performed by using TaqMan SNP genotyping assays with genomic DNA extracted from peripheral blood leukocytes. The severity of coronary artery disease was indicated by Gensini score and the number of diseased coronary artery branches.
Results In order to facilitate statistical comparison, 360 patients were divided into three groups according to the carrying of three alleles of APOE: 47 patients in ε2+ group (ε2/ε2 and ε2/ε3), 252 patients in ε3 group (ε3/ε3 and ε2/ε4) and 61 patients in ε4+ group (ε3/ε4 and ε4/ε4). The comparison of clinical baseline of each group showed no statistically significant difference in age, BMI, HbA1c, hs-CRP, ALT, Cr, TC, TG, HDL-C, LDL-C, Lp(a) and the proportion of males and diabetes among the ε2+, ε3 and ε4+ groups in patients with coronary heart disease already treated with statin. However, compared with ε3 group, ε2+ group showed lower concentrations of total LDL, S-LDL and M-LDL particles and larger LDL size, which indicated cardiovascular protective effect. ε4 + group showed higher concentrations of total LDL, S-LDL particles and smaller LDL size, which indicated the residual risk of cardiovascular disease($P<0.05$). After adjusting for male, age, diabetes, BMI, HbA1c, hs-CRP, ALT and Cr, ε2+ genotype could independently increase the concentration of VLDL, L-LDL and LDL size, while decrease the concentration of LDL, S-LDL and M-LDL. ε4 + genotype could independently increase the concentration of LDL and S-LDL. The atherogenic S-LDL accounted for about 50% of total LDL particle concentration. The increase of S-LDL concentration was associated with high Gensini score ($B=0.058$, $P=0.024$). Compared with ε3 group, the risk of increased branch lesions in the ε2+ group was lower ($OR=0.416$, $P=0.027$).
Conclusions APOE genotype can affect the severity of coronary artery disease by affecting lipoprotein particle profile such as S-LDL concentration and LDL size. Individualized cholesterol-lowering therapy should be carried out for ε4 allele carriers. In addition to statins, they should further reduce the additional cardiovascular risks caused by increased LDL particle concentration.

PO-0488

基于危险因素和常规实验室指标的子痫前期风险预测模型研究

邓兴宇、杨楠、薛宇廷、张华、贾珂珂
北京大学第三医院

目的 构建妊娠早期子痫前期（preeclampsia, PE）风险预测模型，比较 Logistic 回归模型和极端梯度提升(extreme gradient boosting, XGBoost)模型的预测能力。
方法 回顾性分析 2015 年 1 月至 2020 年 8 月北京大学第三医院 925 例 PE 患者和 7613 例正常对照组的 6-10 周的一般资料、PE 发病危险因素和 27 项常规实验室指标，采用秩和检验、Logistic 回归、XGBoost 等统计学方法进行数据分析，分别建立预测模型，绘制受试者工作特征曲线，计算曲线下面积、灵敏度、特异度。并用 XGBoost 绘制特征重要性条形图。
结果（1）两组孕妇是否患血栓性疾病、阻塞性睡眠呼吸暂停以及是否采用辅助生殖技术的比例无统计学差异（$P>0.05$），是否患糖尿病、APS、SLE、肾性疾病以及是否为初产妇、是否有 PE 史的比例有统计学差异（$P<0.05$）。（2）27 个常规实验室指标中，两组除 PLT/LYM 的水平不存在统计学差异（$P>0.05$）外，其余指标均具有统计学差异（$P<0.05$）。（3）仅纳入危险因素建立 Logistic 回归模型 AUC=0.621（95%CI 0.601-0.640，敏感度=34.8%，特异度=81.5%），低于危险因素联合实验室指标预测 Logistic 模型 AUC=0.752（0.735-0.769，64.2%，76.0%），低于

XGBoost 模型 AUC=0.867（0.839-0.896，73.0%，82.3%）。XGBoost 筛选出重要性排在前三的指标依次为 TG、Lp(a)、C1q。
结论 PE 发病危险因素联合常规实验室指标预测妊娠早期 PE 发病风险的效果，优于单独使用 PE 发病危险因素。XGBoost 模型早期预测 PE 发病的性能优于 Logistic 回归模型。TG、Lp(a)、C1q 是用 XGBoost 模型早期预测 PE 发病的重要变量。

PO-0489

胃泌素释放肽的表达与胃癌的关系

李礼
滨海县人民医院

Purpose This study was to assess the diagnostic and prognostic value of ProGRP in gastric cancer (GC)patients.
Methods 150 patients with GC, 50 healthy controls and 66 patients with benign gastric diseases were recruited.The levels of serum ProGRP, CEA and CA72-4 were measured.
Results ProGRP in GC were significantly higher compared to controls, and ProGRP was significantly correlated with tumor size, TNM stage, differentiation, invasion depth and lymph node metastasis.ProGRP were significantly decreased after chemotherapy. ProGRP were significantly positively correlated with CA-724 and CEA respectively. With combined detection of ProGRP, CEA and CA72-4 have better diagnostic power for GC.
Conclusion ProGRP could be useful as a potential biomarker for GC diagnosis and therapy.

PO-0490

TC、TG 对 TBA 检测的交叉污染

刘道林、李丹
隆回县人民医院

发现问题：连续发现三例总胆汁酸异常升高，复查后均正常的标本。
提出质疑：1.仪器清洗工作站漏液？2.会不会是交叉污染？3.哪个部位的交叉污染？ 4.是比色杯污染？5.是搅拌棒污染？
查找原因：1.仔细检测仪器运转良好，无漏液等现象，2.再次排查比色杯清洗不干净引起的交叉污染，发现其对 TBA 检测无明显的污染。3.查找三个标本第一次检测所用到的 R1、样本、R2 搅拌棒均为 2，3，2 号搅拌棒。再查找这三个搅拌棒之前所检测的项目均为总胆固醇。做总胆固醇的交叉污染排除实验，确定 TC 对总胆汁酸的检测存在交叉污染。4.排除其他检测项目是否也存在对 TBA 有明显交叉污染。发现 TG 的 R1 试剂对 TBA 的检测也存在明显的交叉污染现象。
解决方法 贝克曼 AU5800 生化仪有内外两圈比色杯与搅拌棒，我们只需把 TBA 与 TC、TG、HDL、LDL、APA 这些项目不放同一圈检测就可以防止交叉污染的发生。

PO-0491

Analytical and clinical performance of a liquid chromatography–tandem mass spectrometry method for measuring gastrin subtypes G34 and G17 in serum (This manuscript has been accepted by Clinical Chemistry)

Songlin Yu
Peking Union Medical College Hospital

Background Two major forms of gastrin, gastrin-17 (G17) and gastrin-34 (G34), exist in blood. However, conventional immunoassay methods can only quantify total gastrin or G17 alone. Here, we aimed to establish a liquid chromatography–tandem mass spectrometry (LC-MS/MS) method to quantify G17 and G34 simultaneously.
Methods Serum samples were prepared by anion-exchange solid-phase extraction. The analytical performance of the LC-MS/MS method was validated and the method was compared to chemiluminescence immunoassay (CLIA) and radioimmunoassay (RIA). The G17 and G34 concentrations in 245 serum samples from healthy controls, individuals with gastrinoma, and individuals with other diseases were analyzed.
Results The total runtime of the LC-MS/MS method was 6 min. No substantial matrix effect was observed with internal standard correction. The intra-assay coefficients of variation (CVs) for G17 and G34 were 4%–14.2% and 4.4%–10.4%, respectively, and total CVs were 5.2%–14.1% and 4.6%–12.4%, respectively. The correlation coefficient between LC-MS/MS and CLIA was 0.87, and between LC-MS/MS and RIA was 0.84. The G17+G34 concentrations for 87.5% of individuals with gastrinoma were higher than the 95th percentile of healthy controls (18.1 pg/mL), whereas the concentrations for individuals with other diseases and GA overlapped. Based on the Youden indices calculated for G17+G34, G34, and G17, the most specific biomarker was G17 (96.9% clinical specificity at 209.8 pg/mL).
Conclusions This method should aid in the diagnosis of diseases associated with increased gastrin concentrations.

PO-0492

基于多中心研究建立中国男性性激素和性激素结合球蛋白年龄特异性的参考区间模型

马超超、邱玲
中国医学科学院北京协和医院

背景 卵泡刺激素(FSH)、促黄体生成素(LH)、催乳素(PRL)、雌激素(E2)、总睾酮(TT)、游离睾酮(FT)、生物可利用睾酮(BAT)和性激素结合球蛋白(SHBG)水平受年龄影响。本研究的目的是建立性激素和 SHBG 的年龄相关参考区间模型，并呈现男性性激素和 SHBG 随年龄的波动规律。
方法 基于全国多中心研究纳入 1043 名男性。采用 Tukey 方法识别异常值。基于 Altman 理论，采用加权多项式回归建立均值模型和标准差模型。95%年龄相关参考区间模型用均值模型±1.96 × SD 模型表示。采用 z 分数图来评价模型的拟合效果。
结果 中国成年男性性激素和 SHBG 呈右偏态分布。性激素和 SHBG 模型主要涉及 5 项，分别为常数项、Age-2、 Age-1 、Age 以及 Age3。所有性激素和 SHGB 的 z-score 图点均分布在 0 线上。所有性激素和 SHGB 的 Z-score 均满足正态分布。性激素以及激素结合球蛋白随年龄变化的模式各异。

结论 性激素和 SHBG 的分布向右侧倾斜。男性性激素和 SHBG 的年龄特异性参考区间模型随着年龄的增长呈现不同的模式。我们提供了计算男性性激素和 SHBG 年龄特定参考区间的工具。只需将年龄带入模型，即可计算出对应年龄下的参考区间。

PO-0493

谷氨酰胺肠外营养液对肝细胞短时急性损伤的临床研究

张洁心、衣鲁江、张炳峰
江苏省人民医院（南京医科大学第一附属医院）

目的 谷氨酰胺肠外营养液是重症患者补充谷氨酰胺的重要途径。该药广泛应用于营养支持治疗，使用前需评估患者肝肾功能，然而在给药过程中以及使用后其对肝细胞的作用影响尚无研究数据。
方法 我们招募 30 例经临床评估需输注谷氨酰胺肠外营养液的 45 至 65 岁重症患者（伦审号：2020-SR-487）。根据其病史及肝功分为三组：肝功正常且无肝原发病，有非肝癌的肝脏原发病且肝功正常，有非肝癌的肝脏原发病且肝功异常。在静脉滴注谷氨酰胺肠外营养液前、滴注完毕、滴注后 24 小时和滴注后 48 小时共计四个时间点分别收集患者血清标本进行肝功能评价。体外肝细胞系实验中，我们使用两种不同剂型谷氨酰胺肠外营养液以及其分解代谢产物谷氨酰胺、丙氨酸，分别按照浓度梯度、时间梯度刺激细胞，检测培养上清中各酶学指标的变化情况。使用流式细胞术检测细胞凋亡比例。
结果 我们首次观察到在肝功正常且无肝原发病组，多个肝脏酶学指标在使用该药后的短时间内（24 至 48 小时）出现大幅升高再逐渐恢复的现象。肝细胞培养上清中天冬氨酸氨基转移酶（AST）、乳酸脱氢酶（LDH）和 α-羟丁酸脱氢酶（HBDH）的活性在营养液刺激下呈剂量及时间依赖性大幅增加，且以谷氨酰胺单剂作用最为显著。进一步实验表明，在谷氨酰胺肠外营养液的推荐使用浓度范围内，肝细胞出现明显凋亡。
结论 以谷氨酰胺为核心成分的肠外营养液在短期内对患者肝细胞功能造成损伤，蓄积的代谢产物如谷氨酰胺更可导致细胞死亡。本研究结果提示临床，在该药使用过程中应密切关注其作为重症患者营养支持的科学性与适时性。

PO-0494

Metabolic characterization of hepatic disease patients with hepatitis B virus DNA replication by untargeted metabolomics

Lin Yu、Qian Zhou、Bei Xu、Jiafu Feng
Mianyang Central Hospital

Background and aims Until now, the metabolic effects of HBV DNA replication (active HBV) on the progress of hepatic diseases (hepatitis, cirrhosis, and liver cancer) and liver functions remain unexplored. Thus, the main aim of our study was to determine the serum metabolic characteristics of hepatic disease patients with active HBV.
Methods A total of 199 hepatic diseases patients with active and inactive HBV were enrolled to explore the serum metabolic characterizations via untargeted metabolomics. Multiple analysis including principal component analysis (PCA), partial least squares discriminant analysis (PLS-DA), volcano plot and pathway analysis were used for metabolic data analysis. Additionally, differential metabolites were analyzed by commercial databases. All samples were also analyzed for liver function tests.
Results Our data indicated that most of the altered metabolic pathways was D-Glutamine and D-glutamate metabolism, indicating a strong link to HBV replication ($p < 0.05$). In addition, alanine

transaminase (ALT) was increased concomitant to the progression of hepatic disease with HBV DNA replication, and the levels of L-lactate dehydrogenase (LDH-L), alkaline phosphatase (ALP), aspartate transaminase (AST) and gamma-glutamyl transferase (GGT) were statistical different between cirrhosis patients with the inactive and active HBV ($p < 0.05$).
Conclusions Thus, the metabolomic profiles demonstrated that there may be a relationship between D-Glutamine and D-glutamate metabolism and HBV DNA replication. Besides, there did have an influence of HBV DNA replication on liver functions. And L-Glutamic acid, D-Glutamine and D-Glutamate and ALT may be candidate biomarkers for monitoring hepatic disease prognosis, diagnosis and treatment efficacy.

PO-0495

妊娠期糖尿病患者多项生化指标检验分析

王维
成都市龙泉驿区妇幼保健院

目的 探讨妊娠期糖尿病(gestational diabetes mellitus，GDM)患者多项生化指标检验的结果及血糖干预价值。
方法 于本院 2018 年 9 月～2019 年 9 月期间内接收的 GDM 患者中随机选取 72 例作为研究对象，纳入观察组，另选取同期来本院进行健康体检的 OGTT 试验耐糖量正常的 67 例孕妇纳入对照组。对两组研究对象进行生化指标检验，对比入院时及干预后各项指标水平变化情况。
结果 观察组入院时 FBG、PBG、HbA1c 水平、TC、TG 水平、Scr、BUN、24h 尿蛋白定量水平均高于对照组，P＜0.05。经干预后 FBG、PBG、HbA1c 水平、TC、TG 水平、Scr、BUN、24h 尿蛋白定量水平较对照组稍高，但比较 P＞0.05。观察组总并发症发生率较对照组稍高，但比较 P＞0.05。证实糖尿病组经干预后预后较好。
结论 GDM 患者多项生化指标检验可帮助早诊断、早治疗疾病，对于改善预后来说意义重大。

PO-0496

Logistic 回归和 Fisher 判别分析模型在冠心病鉴别诊断中的临床价值

王潇、段勇、黄本林
昆明医科大学第一附属医院

目的 探讨基于常规实验室检查建立的 Logistic 回归和 Fisher 线性判别分析模型在冠状动脉粥样硬化性心脏病鉴别诊断中的临床价值。
方法 选取我院 2018 年 3 月—2019 年 2 月以胸闷胸痛为主诉就诊的 178 例患者为对象，根据冠状动脉造影结果分为冠心病组和非冠心病组，回顾性分析这些患者的常规实验室指标，建立诊断冠心病的 Logistic 回归和 Fisher 判别分析模型，并验证模型诊断和预测的准确率，进一步评价其在临床中的实际意义。
结果 建立的 Logistic 回归方程为：Logit((P)= -24.641+0.105×年龄+1.520×糖尿病+0.286×BMI+1.209×LDL-C+0.614×PDW+4.131×(Mono/HDL-C)；建立的 Fisher 分类判别分析函数为：f1（冠心病）= -69.314+0.629×年龄+2.378×BMI+1.985×PDW+5.123×LDL-C+0.304×Ln（TG）+1.972×Ln（HDL-C），f2（非冠心病）= -52.184+0.527×年龄+2.164×BMI+1.660×PDW+4.104×LDL-C-0.149×Ln（TG）+3.818×Ln（HDL-C）。Logistic 回归模型对冠心病和非冠心病的诊断准确率分别为 93.0%和 84.0%，预测准确率分别为 91.4%和 70.0%；回顾法、留一法交叉验证及外部数据验证法检验 Fisher 判别函数的判别正确率分别为 82.0%、81.5%、81.3%。

结论 Logistic 回归和 Fisher 线性判别分析模型在冠心病鉴别诊断中均具有较好的鉴别和预测价值。

PO-0497

冠心病患者血清总同型半胱氨酸（tHcy）升高与颈动脉斑块的关系探讨

方欢英
上海市东方医院（同济大学附属东方医院）南院检验科

目的 探讨冠心病患者血清总同型半胱氨酸（tHcy）升高与颈动脉斑块的关系。
方法 共纳入 283 例冠心病患者。超声检查评估颈动脉斑块。酶循环法测定血清 tHcy 浓度。
结果 颈动脉斑块患者血清 tHcy 水平明显升高且与年龄、收缩压、高敏心肌肌钙蛋白 T 水平呈正相关。校正年龄、收缩压后，logistic 回归分析显示血清 tHcy 水平是一个冠心病患者颈动脉斑块有无的影响因素（p=0.033），但暂未发现 tHcy 水平与颈动脉斑块是单侧还是双侧存在、以及是在左侧颈动脉还是在右侧颈动脉有关（p>0.05)。ROC 曲线分析显示血清 tHcy 判断颈动脉出现的 AUC 为 0.726(95%CI:0.664-0.789；P=0.000），其最佳截断水平为 13.6μmol/L。
结论 血清 tHcy 水平升高与颈动脉斑块出现有关，但与颈动脉斑块位置关系不大。

PO-0498

α1-酸性糖蛋白在肺炎支原体感染所致的支气管肺炎患儿中的临床意义

方欢英
上海市东方医院（同济大学附属东方医院）南院检验科

目的 探讨 α1-酸性糖蛋白（α1-AGP）在肺炎支原体（MP）感染所致的支气管肺炎中的临床意义。
方法 收集 2018 年 1 月-12 月我院儿科住院的肺炎支原体肺炎（MPP）患儿（87 例）和非 MPP 支气管肺炎患儿（181 例）的血液样本进行检测，比较两组 α1-AGP、降钙素原（PCT）等指标差异，并通过 Logistic 多因素回归进一步分析筛选 MPP 的主要相关因素，通过受试者工作特征曲线（ROC）及曲线下面积[AUC（95%CI）]评价不同指标对支气管肺炎和 MPP 的鉴别能力。
结果 MPP 患儿 AGP 水平显著高于对照组，差异有统计学意义（ (136.06±46.37 vs. 122.29±44.21, P= 0.020)。Logistic 多因素分析发现校正年龄后仅 α1-AGP 为 MPP 患儿的危险因素，其 ROC 曲线曲线下面积 0.703(95% CI: 0.634-0.772;P≤0.001)。联合 α1-AGP 与 PCT，可使 AUC（95%CI）略提升至 0.732 (95% CI: 0.666-0.797, P≤0.001)。
结论 α1-AGP 对 MPP 有一定诊断价值，入院初期检测患儿血液 α1-AGP，可助益于鉴别 MPP 和其他支气管肺炎，辅助临床及早进一步诊治。

PO-0499

血清 Lp（a）与心绞痛的相关性研究

何挚、束国防、芦慧霞
东南大学附属中大医院

目的 本研究通过观察 Lp（a）与心绞痛（AP）的相关性，探讨 Lp（a）对于 AP 的诊断和预测价值，为冠心病的预防提供帮助。

方法 选择本院心内科住院的 1336 名患者为研究对象，采集临床资料，检测 Lp（a）、TC、TG、HDL、LDL 等指标。根据研究对象 Lp（a）水平的四分位值分为 A、B、C、D 四组：A 组 Lp（a）≤159mg/L，共计 336 人；B 组，159mg/L<Lp（a）≤305mg/L，共计 332 人；C 组，305mg/L<Lp（a）≤562mg/L，共计 334 人；D 组，Lp（a）>562mg/L，共计 334 人。比较各组 AP 患病率，探讨 Lp（a）与 AP 发病的关系。
结果 各组 AP 患病率比较，A 组和 B 组差异无统计学意义（P＞0.05）；C 组显著高于 A、B 组（P<0.001）；D 组显著高于 A、B、C 组(P<0.001）。
结论 随着 Lp（a）水平的升高，AP 的患病率逐渐升高，且体内高水平的 Lp（a）浓度对于冠心病患者 AP 的发生具有一定的提示及鉴别作用。

PO-0500

急性心肌梗死患者的临床危险因素分析

何挚、束国防、芦慧霞
东南大学附属中大医院

目的 对临床急性心肌梗死（AMI）发生的危险因素进行调查分析，为此类疾病的预防提供循证依据。
方法 选择本院 880 名住院患者为研究对象，采集详细病史资料，检测 Lp（a）、TC、TG、HDL、LDL 等指标。按研究对象的临床诊断标准，分为 AMI 组，共 352 例；经冠脉造影检查确诊无上述疾病者为对照组，共 528 例。
结果 糖尿病不是 AMI 的危险因素，性别（P=0.663）、吸烟（P=0.068）不是其独立危险因素，年龄、TC、LDL、TG、高血压、Lp（a）为独立危险因素，HDL 为保护因素（P<0.001，OR=0.114）。
结论 AMI 发病有多个危险因素，其中年龄、高血压、TC、Lp（a）是独立的的危险因素，且 Lp（a）具有最好的风险评估作用，HDL 为保护因素。

PO-0501

Incidence rate of hemolysis, lipemia, icterus and influence factors: A single center retrospective study of 501, 612 fasting serum specimens

Gang Tian、Zhangrui Zeng、Xinrui Jin、Guangrong Li、Jinbo Liu
Affiliated Hospital of Southwest Medical University

Objective The aim of the study was to assess the incidence rate of hemolysis, lipemia and icterus and influence factors based on serum biochemical specimens in order to reduce laboratory turnaround time, specimen re-collection and re-test, as well as the preanalytical interference for clinical chemistry results.
Methods A single center retrospective study was conducted to analyze the incidence rate of hemolysis, lipemia and icterus and influence factors based on the hemolysis-, lipemia- and icterus- (HLI) index of 501,612 fasting serum specimens in a teaching hospital in the Southwest China from January 1, 2017 to May 31, 2018.
Results Among 501,612 specimens, the total incidence rate (IR) of hemolysis, lipemia and icterus was 3.84%, 0.53% and 6.12%, respectively. Compared with female, male has higher IR of hemolysis (4.13% vs 3.54%), lipemia (0.67% vs 0.38%) and icterus (6.95% vs 5.43%), all *P*<0.001. Specimens with longer transfer time or detection time had higher IR of hemolysis, lipemia and icterus (all *P*<0.001). Compared with specimens from outpatients, hospitalized patients had higher IR of hemolysis (4.03% vs. 3.54%), lipemia (0.63% vs. 0.36%) and icterus

(7.10% vs. 4.75%), all *P*<0.001. The medical department of pediatrics had the highest IR of hemolysis (16.2%) in 26 included departments with odds ratio (OR) 5.06, [95% confidence interval (*CI*), 4.72–5.43, *P*<0.001)] and adjusted OR (AOR) 4.93 (95% *CI*, 4.59–5.29, *P*<0.001) by year, gender, transfer time and detection time of specimens. The neonatology department had the highest IR of lipemia (3.82%) with OR 4.62 (95% *CI*, 3.72–5.73, *P*<0.001) and AOR 1.17 (95% *CI*, 0.91–1.51, *P*<0.001), and highest IR of icterus (30.1%) with OR 6.71(95% *CI*, 6.26–7.20, *P*<0.001) and AOR 4.93 (95% *CI*, 4.59–5.29, *P*<0.001). The pooled ratio risk (RR) of the top ten departments for hemolysis, lipemia and icterus was 1.12 (95%*CI*, 1.04–1.21), 1.05 (95%*CI*, 0.92–1.19) and 1.26 (95%*CI*, 1.11–1.43). There was higher IR of hemolysis and icterus for children under 1 year or adults aged more than 40 years.
Conclusion The HIL-index provides an effective screening tool for evaluating IR of hemolysis, lipemia and icterus. Strictly control pre-analytical factors related to hemolysis, lipemia and icterus are important to ensure the quality of the specimens and provide accurate, high-quality results.

PO-0502

Matrix metalloproteinase 3 as a valuable marker for patients with COVID-19

石盛洁
湖南中医药大学第一附属医院

The situation of the coronavirus disease 2019 (COVID‐19) continues to evolve, our studyexplored the significance of serum levels of matrix metalloproteinase 3 (MMP3) as amarker for patients with COVID‐19. Sixty‐two COVID‐19 patients in the First Hospital ofHunan University of Chinese Medicine and Loudi Center for Diseases Prevention andControl, from January to March 2020, were sampled as the novel coronavirus pneumoniainfected group.

PO-0503

Improvements of an autoverification system for clinical chemistry test results using a combined strategy of knowledge-based rule selection and historical data percentile-based range determining

Jing Zhu、HAO WANG、WEI GUO、BAI-SHEN PAN、BEI-LI WANG
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University

Objectives The knowledge-based only autoverification has shown shortages and an improvement is necessary.
Methods The original autoverification system had no priority and the range of each rule was determined by knowledge. In the improved system, new types of rules, extreme value and consistency check, were added and the autoverification workflow was rearranged, to construct the framework. The ranges of extreme value rules, limit check rules, consistency check rules and delta check rules were determined by analysis of historical data from Zhongshan laboratory, generating the criteria. The effectiveness of the improved system was evaluated using pooled data of 20 centers
and the improvement of efficiency was assessed by a multicenter process.
Results The evaluation of effectiveness included true positive rate, true negative rate and overall consistency rate, compared to manual verification. The system had a true positive rate of 77.55%

and a true negative rate of 78.53%. The overall consistency rate was 78.3%, compared to 56.2% of the original system. Pass rates, an indicator of efficiency, of the improved system among hospitals were 43% - 93%, consistently higher than those of the original system, which were 36% - 81%. The customization of the improved system using individualized data further increased the lowest pass rate from 43% to 54%.
Conclusions The improved system showed a comparable effectiveness with the original system, while the efficiency was markedly increased. The customization trial suggested that the improved system could be popularized via utilizing the historical data of each individual hospital.

PO-0504

The role of prognostic nutritional index as an indicator of the severity and complications of silicosis

Lagu He、yuan huamin
Hunan Prevention and Treatment Institute for Occupational Diseases

Objective To evaluate prognostic nutritional index (PNI) for predicting the the severity and complications of silicosis.
Methods 166 cases silicosis patients were collected in Hunan Prevention and Treatment Center for Occupational Diseases (HPTCOD) from January 2020 to December 2020. The value of PNI and neutrophil/lymphocyte ratio (NLR) for prediting the prognosis of silicosis were evaluated by ROC and the relationship between the PNI , PLR, NLR , forced vital capacity(FVC) and forced expiratory flow in 1 s/forced vital capacity (FEV1/FVC) of silicosis patients were analyzed.
Results Silicosis patients exhibited higher PLR, NLR and lower PNI compared with the control groups (P<0.05). The calculated PNI was negatively correlated with NLR and PLR in the silicosis groups (r=-0.339, P <0.01; r=-0.542, P <0.01,respectively), In addition, PNI was positively correlated with FEV1/FVC in the silicosis groups (r=0.352, P <0.01).The areas under the ROC curves of NLR and PNI were0.866(95% CI 0.811 -0.922,P = 0.000) and 0.908 (95% CI 0.865▪0.951,P = 0.000). The median cut-off PNI score for the prediction of postoperative OS was 51.81. Based on this cut-off value, PNI-low (<51.81) group is more likely to get complications.
Conclusion PNI can be used as indicators of state and severity in clinical prognosis of patients with silicosis. PNI is more sensitive to assessing disease activity compared with NLR.

PO-0505

缺血修饰蛋白在急性冠状动脉综合征早期诊断中的研究

李建花
潍坊医学院附属医院

目的 通过观察急性冠状动脉综合征（ACS）患者血清中缺血修饰白蛋白（IMA）水平的变化，探讨 IMA 在 ACS 早期诊断中的价值。
方法 连续动态监测 115 例 ACS 患者［包括急性心肌梗死（AMI）52 例、不稳定型心绞痛（UAP）63 例］急性胸痛发作后 2、6、12、24、48 h 血清 IMA 水平的变化，并与 49 例疑似 ACS 最终确诊排除的患者（对照组）比较；评价 IMA 在 ACS 早期诊断中的应用价值。
结果 UAP 及 AMI 患者发病后 2h 血清 IMA 水平明显高于对照组（P＜0.05），AMI 患者发病 12 h 时达高峰，24 h 时下降到和对照组水平基本持平。受试者工作特征（ROC）曲线显示 AMI 患者发病 2 h 时，IMA 诊断 AMI 的曲线下面积（AUC）为 0.801。
结论 心肌缺血是 ACS 最常见的发病机制，IMA 可作为 ACS 心肌缺血的敏感指标，可用于早期诊断 AMI。IMA 无论对 UAP 患者的早期心肌缺血还是对 AMI 患者早期诊断及疗效监测均具有较高的应用价值，是对 ACS 预防、诊断、监测的一个较好的心肌标志物。

PO-0506

血清 AFP 的 O-GlcNAc 修饰在肝癌患者预后判断中的价值

吴昊、王蓓丽、郭玮
复旦大学附属中山医院

目的 本研究旨在探讨血清中 AFP 蛋白的 O-GlcNAc 糖基化修饰对肝癌患者预后评估的价值。
方法 收集复旦大学附属中山医院 100 名肝癌患者的血清标及病理资料。离心超滤管浓缩血清总蛋白后沉淀血清蛋白中的 AFP，WB 实验使用识别 O-GlcNAc 糖基化的特异性抗体检测血清 AFP 的 O-糖基化水平。结果量化后与肝癌患者的肿瘤大小、TNM 分期等病理因素行卡方检验。同时通过 Kaplan-Meier 法分析血清 AFP 的 O-糖基化水平与患者总体生存及无进展生存的关系。使用 COX 回归分析 AFP 的 O 糖基化水平是否可作为肝癌患者的独立预后因子。通过 LC-MS/MS 检测血清 AFP 发生 O-糖基化的关键位点，分析特定位点的糖基化水平与肝癌患者预后的关系。
结果 肝癌患者血清 AFP 的 O-GlcNAc 修饰水平与患者肿瘤大小、肿瘤结节数量、T 分期呈正相关。AFP 的 O-糖基化处于高水平的肝癌患者总体生存期及无进展生存期比低水平患者显著减短。TNM I-II 期患者，AFP 高水平 O-糖基化意味着总生存期及无进展生存期更短； III-IV 期患者，O-糖基化的差异与生存期的关系则无统计学意义。COX 回归分析得出 AFP 的 O-GlcNAc 水平可作为评估肝癌患者总体生存及无进展生存的独立预后因子。通过质谱技术鉴定出血清 AFP 的 O-GlcNAc 修饰关键位点为 Ser286，通过对 Ser286 有无糖基化修饰的患者生存期进行分析显示发生糖基化修饰与患者更短的总体生存及无进展生存显著相关。
结论 血清 AFP 的 O-GlcNAc 修饰可作为评估患者不良预后的独立指标，并对 TNM I-II 期患者的预后判断能力更强。Ser286 位点的 O-GlcNAc 修饰对判断患者预后有重要价值。

PO-0507

Noninvasive detection of human dehydroepiandrosterone, progesterone and testosterone using LC-MS/MS revealed effects of birth control pills/devices and body weight on ovulatory prediction

Liqiao Han
Guangdong Provincial Hospital OF Chinese Medicine

Liquid chromatography-tandem mass spectrometry (LC-MS/MS) has been increasingly used to measure steroids in human saliva. We studied the performance of a conventional LC-MS/MS for measuring dehydroepiandrosterone (DHEA), testosterone and progesterone in human saliva. These three steroids were co-extracted by liquid-liquid extraction and derivatized. Derivatives were resolved on a C18 column and quantified using an LC-MS/MS (AB Sciex API 2000) instrument. The assay's limits of quantification were 0.03 ng/mL for all three steroids. Inter-assay coefficients of variation were 16.6–18.8% (DHEA), 12.0–15.8% (testosterone), and 12.7–19.3% (progesterone). Assay linearity analysis showed R2 of 0.9926, 0.9750 and 0.9949 for DHEA, testosterone and progesterone, respectively. No carry-over between samplings was observed. An ion-enhancement effect of 11.6% for DHEA determination and ion-suppression effects of 13.9% and 20.7% for analysis of progesterone and testosterone, respectively, were determined. No interferences by 9 steroid analogs were detected. Spiked recoveries were 85.5% (DHEA), 86.5% (testosterone), and 92.6% (progesterone). Comparison with laboratory developed test (LDT)-LC-MS/MS methods by other New York State Department of Health certified laboratories revealed R2 = 0.9425 (DHEA, LC-MS/MS = 1.0267 LDT + 21.989), R2 = 0.9849 (testosterone, LC-MS/MS = 0.9447 LDT + 9.8037), and R2 = 0.9736 (progesterone, LC-MS/MS = 1.1196 LDT + 0.0985). Reference intervals for the 3 steroids in saliva for young males and females were estimated.

Results of intra-individual salivary progesterone analysis indicated that caution should be exercised when using progesterone concentrations in predicting ovulation for females who are under treatment with birth control pills/devices or has body a weight of > 90 kg.

PO-0508

Choosing an appropriate glomerular filtration rate estimating equation: Role of Body Mass Index

Jiayong Li
Clinical Laboratory Medicine Center, Shanghai General Hospital Affiliated to Shanghai Jiao Tong University

Background We aimed to investigate the accuracy of different equations in evaluating estimated glomerular filtration rate (eGFR) in a Chinese population with different BMI levels.
Methods A total of 837 Chinese patients were enrolled, and the eGFRs were calculated by three Chronic Kidney Disease Epidemiology Collaboration (CKD-EPI) equations, three full-age spectrum (FAS) equations and two Modification of Diet in Renal Disease (MDRD) equations. Results of measured GFR (mGFR) by the 99Tcm-diathylenetriamine pentaacetic acid (99Tcm-DTPA) renal dynamic imaging method were the reference standards. According to BMI distribution, the patients were divided into three intervals: below 25th（BMI_{P25}), 25th to 75th（BMI_{P25-75}) and over 75th percentiles（BMI_{P75}).
Results The medium BMI of the three BMI intervals were 20.9, 24.8 and 28.9 kg/m2, respectively. All deviations from mGFR (eGFR) were correlated with BMI ($p<0.05$). The percentage of cases in which eGFR was within mGFR ± 30% (P30) was used to represent the accuracy of each equation. Overall, $eGFR_{FAS\_Cr\_CysC}$ and $eGFR_{EPI\_Cr\_2009}$ performed similarly, showing the best agreement with mGFR among the eight equations in Bland-Altman analysis (biases: 4.1 and -4.2 mL/min/1.73m2, respectively). In BMI_{P25} interval, $eGFR_{FAS\_Cr}$ got -0.7 of the biases with 74.2% of P30, the kappa value was 0.422 in classification of CKD stages and the AUC_{60} was 0.928 in predicting renal insufficiency, and $eGFR_{EPI\_Cr\_2009}$ got 2.3 of the biases with 71.8% of P30, the kappa value was 0.418 in classification of CKD stages and the AUC60 was 0.920 in predicting renal insufficiency. In BMI_{P25-75} interval, the bias of $eGFR_{FAS\_Cr\_CysC}$ was 4.0 with 85.0% of P30, the kappa value was 0.501 and the AUC_{60} was 0.941, and $eGFR_{FAS\_Cr\_CysC}$ showed balanced recognition ability of each stage of CKD (62.3%, 63.7%, 68.0%, 71.4% and 83.3% respectively). In BMI_{P75} interval, the bias of $eGFR_{EPI\_Cr\_CysC\_2012}$ was 3.8 with 78.9% of P30, the kappa value was 0.484 the AUC_{60} was 0.919, and $eGFR_{EPI\_Cr\_CysC\_2012}$ equation showed balanced and accurate recognition ability of each stage (60.5%, 60.0%, 71.4%, 57.1% and 100% respectively). In BMI_{P75} interval, the bias of $eGFR_{FAS\_Cr\_CysC}$ was -1.8 with 78.5% of P30, the kappa value was 0.485, the AUC_{60} was 0.922. However, the recognition ability of each stage of $eGFR_{FAS\_Cr\_CysC}$ equation(71.1%, 61.2%, 70.0%, 42.9% and 50.0% respectively) was not as good as $GFR_{EPI\_Cr\_CysC\_2012}$ equation.
Conclusion For a Chinese population, we tend to recommend choosing $eGFR_{FAS\_Cr}$ and $eGFR_{EPI\_Cr\_2009}$ when BMI was around 20.9, $eGFR_{FAS\_Cr\_CysC}$ when BMI was near 24.8, and $eGFR_{EPI\_Cr\_CysC\_2012}$ when BMI was about 28.9.

PO-0509

广东省 11820 例儿童血清 25-羟基维生素 D 水平调查分析

李云珍、张玲、李玲、姚少濠、苏坤华、黄献中
广州金域医学检验中心

目的 了解广东省儿童血清 25-羟基维生素[25（OH）D]的水平状态，为 1～14 岁儿童合理补充维生素 D 提供科学依据。

方法 选取 2019 年 1 月~2020 年 12 月送检本检验中心常规体检的≤14 岁儿童 11820 例，其中男童 6787 例，女童 5033 例，通过采集静脉血进行血清 25（OH）D 检测。

结果 （1）广东省 11820 例≤14 岁儿童血清 25（OH）D 均值为（37.54±15.13）ng/mL，男、女童血清 25（OH）D 均值分别为（37.71±14.82）和（37.31±15.52）ng/mL 差异无有统计学意义（P=0.16）。学龄期组男童 25（OH）D 水平高于女童，比较有统计学意义（P<0.05）（2）婴儿组、幼儿组、学龄前组和学龄期组血清 25（OH）D 均值分别为（50.56±14.18）ng/mL、（42.26±12.85）ng/mL、（30.85±8.97）ng/mL、（25.349±8.09）ng/mL，血清 25（OH）D 水平婴儿组＞幼儿组＞学龄前组＞学龄期组，各组比较差异均有统计学意义（均为 P<0.01）。（3）25（OH）D 水平比较秋冬季高于春夏季，除春夏两季比较、秋冬两季比较，均无统计学意义（P＞0.05），其他季节组间比较均有统计学意义（P<0.05）。不同季节间 25（OH）D 不足及缺乏率比较，春季（11.87%）＞夏季（9.69%）＞冬季（9.26%）＞秋季（8.20%）。春季不足及缺乏率最高，较其他三季节比较均有显著差异（P<0.01）。夏秋两季比较有统计学意义（P=0.03），夏冬两季、秋冬两季比较无差异（P＞0.05）。

结论 广东省儿童血清 25（OH）D 总体平均水平达标，但是维生素 D 缺乏情况仍需重视，应依据季节、年龄特点行针对性补充维生素 D 措施。

PO-0510

Hb G-Coushatta 变异体对毛细管电泳法检测 HbA1c 的影响

刘瑜[1]、郭晓燕[2]、牛文彦[1,3]
1. 天津医科大学朱宪彝纪念医院
2. 天津医科大学临床医学院
3. 天津医科大学

目的 糖化血红蛋白（HbA_{1c}）是临床上常用的血糖监测指标。近年来研究发现，血红蛋白（Hb）变异体会导致 HbA_{1c} 电泳图谱中异常峰的产生，干扰 HbA_{1c} 检测结果的准确性，导致结果假性升高或降低。本文以血红蛋白 β 链变异体 Hb G-Coushatta 为主要研究对象，探讨其对毛细管电泳法检测 HbA_{1c} 的影响，为糖尿病的诊疗提供有益的参考。

方法 从 2020 年 6 月 1 日至 2021 年 3 月 17 日共收集天津医科大学朱宪彝纪念医院 HbA_{1c} 电泳图谱存在异常峰的标本 265 例，对这些标本经过 DNA 提取、PCR、胶回收及测序等，筛选存在 Hb G-Coushatta 变异体（HBB: c.68A>C）的标本 71 例作为实验组；另取 80 例 HbA_{1c} 电泳图谱无异常峰的标本（Hb AA）作为对照组。收集两组患者的性别、年龄、MCV、MCH、MCHC、RDWSD、FBG、HbA_{1c} 等参数，用 SPSS 25.0 进行统计分析。

结果 经分析发现，Hb G-Coushatta 组与对照组相比，二者的 MCH、MCHC、RDWSD、HbA_{1c} 均无明显差异(P>0.05)，而 Hb G-Coushatta 组的 MCV（87.2±4.0 fL）和 FBG（7.8 mmol/L）低于 Hb AA 组的 MCV（89.0±4.2 fL）和 FBG（9.1 mmol/L）(P<0.05)； 进一步对 HbA1c 分段处理后发现，当 HbA_{1c}≥10.0 %时，Hb G-Coushatta 组的 FBG 低于 Hb AA 组 (P<0.05)。

结论 Hb G-Coushatta 变异体的 MCV 低于对照组，这说明 Hb β 链第 22 位 Glu 变为 Ala 时，可能会影响红细胞的体积，导致其变小。另外，对于存在 Hb G-Coushatta 变异体的糖尿病患者来说，当其 HbA_{1c}≥10.0 %时，毛细管电泳法检测的 HbA1c 结果可能不能很好的反映其血糖水平。

PO-0511

Triptolide 通过靶向 P62/keap1 促进卵巢癌化疗敏感性的分子机制研究

麦佳
四川大学华西第二医院

目的 化疗耐药是卵巢癌患者疗效不佳的关键原因之一。包括顺铂、紫杉醇在内的多种化疗药物通过诱导大量的活性氧（ROS）应激杀伤肿瘤细胞，而氧化还原基因的异常表达是化疗耐药的重要机制。P62-Keap1-Nrf2 信号通路是调节氧化还原系统的重要信号通路，Nrf2 作为转录因子，直接参与抗氧化基因的转录调节，p62、Keap1 则可以通过相互作用调控 Nrf2 的蛋白表达水平。为了探索氧化还原调节在卵巢癌发生发展及治疗的应用，我们将深入探讨 P62/keap1 促进卵巢癌化疗敏感性的分子机制。

方法 本课题通过生物信息学分析，初步探讨 P62、Keap1、Nrf2 在卵巢癌中的作用，并建立了 p62-Keap1 的 BiFC 筛药模型，使用高内涵进行天然产物小分子药物库的高通量药物筛选。收集晚期卵巢癌患者化疗前后血清，进行 ROS 检测，明确氧化还原调节参与卵巢癌继发耐药；采用 WB、RT-PCR、IP、pull-down 实验进一步验证 Triptolide 抑制 P62-Keap1 相互作用的分子机制；将在卵巢癌耐药细胞的细胞实验和动物实验中联合使用 Triptolide 和化疗药物，观察 Triptolide 在化疗耐药卵巢癌治疗过程中的作用。

结果 公共数据库生存分析显示，P62、KEAP1 与卵巢癌病人预后密切相关；生物信息学分析结果显示 P62 在卵巢癌中参与氧化还原调节、MAPK 信号通路、细胞程序性死亡、蛋白翻译后修饰、蛋白磷酸化等生物学过程；高通量药物筛选发现 Triptolide 可以抑制 p62-Keap1 相互作用，体内、外实验证明 Triptolide 可以降低抗氧化基因表达，促进细胞凋亡。

结论 本课题将通过临床资料分析，体内、外功能评价，分子机制探索揭示了 Triptolide 通过调控氧化还原水平，促进卵巢癌化疗敏感性的作用及分子机制，为逆转卵巢癌化疗耐药策略提供了新的理论依据，对卵巢癌病人的治疗具有重要的意义。

PO-0512

Expression of IL-1β, TNF-α and IL-6 and correlation analysis with hs-CRP and ESR in knee osteoarthritis patients

Hongmei Ding
Tianjin Hospital

Objective To investigate the expression of interleukin (IL)-1β, tumor necrosis factor (TNF)-α and IL-6 and their correlation with high sensitivity C-reactive protein (hs-CRP) and erythrocyte sedimentation rate (ESR) in patients with knee osteoarthritis (KOA).

Methods Serum samples were obtained from 85 patients with KOA and 80 healthy controls (HC). Joint fluid samples were obtained from 25 patients with KOA. The levels of IL-1β, TNF-α and IL-6 in serum and joint fluid were measured by enzyme-linked immnuosorbent assay (ELISA). The levels of hs-CRP in serum were measured by Latex immunoturbidimetry assay. Serum levels of ESR were measured by automatic ESR monitor. The correlations between IL-1β, TNF-α, IL-6 and hs-CRP, ESR were evaluated using Pearson correlation test.

Results Serum levels of IL-1β, TNF-α and IL-6 in KOA patients were significantly higher compared with HC (all $P<0.01$). Moreover, the levels of IL-1β, TNF-α and IL-6 increased with the increase of clinical severity. The levels of IL-1β, TNF-α and IL-6 in joint fluid were higher than that in serum (all $P<0.05$). The levels of hs-CRP and ESR in patients with KOA were higher than HC (all $P<0.01$). The serum levels of IL-1β, TNF-α and IL-6 were positively correlated with hs-CRP (r

was 0.489，0.426，0.389，respectively) and ESR (r was 0.348，0.423，0.394，respectively). The levels of IL-1β, TNF-α and IL-6 in joint fluid were positively correlated with hs-CRP (r was 0.547，0.644，0.511，respectively) and ESR (r was 0.564，0.579，0.589，respectively).
Conclusion Our data showed that detection of inflammatory cytokines and hs-CRP, ESR may be used as potential biomarkers for assisting early diagnosis，disease evaluation and prognosis assessment of KOA.

PO-0513

新型电化学免疫传感器的制备及其在骨髓间充质干细胞成骨分化标志物检测中的应用研究

王婷
江苏省人民医院

间充质干细胞向骨细胞的分化是骨组织再生过程中最重要的环节，但易受生理微环境的影响。因此，通过实时监测细胞分泌的生物标记物来系统地评估骨移植物的有效性和安全性以提高疗效是未来组织工程进展的基本要求之一。目前常规技术手段如表面等离子体共振（SPR）和酶联免疫吸附试验（ELISA）存在一定的不足，例如所需样本量大、对检测背景要求高、特异性和灵敏度较低等。为了解决这些技术难题，亟需开发新的用于细胞行为分析的生物传感平台。在本研究中，我们设计了一种基于电化学阻抗谱（EIS）技术的免疫传感器，用于监测间充质干细胞的成骨分化过程中最主要的生物标志物——骨桥蛋白（OPN）的浓度变化。我们采用亲和素-生物素-OPN 特异性抗体对微电极表面进行功能化并用电化学工作站收集信号。在体外诱导间充质干细胞的成骨分化并收集不同时间点的细胞上清。随后使用传感器和 ELISA 检测上清中 OPN 的浓度并对两种方法的结果进行比较来评估免疫传感器的性能。同时对诱导的成骨细胞进行 OPN 和 OCN 的 PCR、ALP 活性、茜素红染色等其他骨分化评价检测。结果表明，该电化学免疫传感器对 OPN 具有媲美 ELISA 的检测性能，具有较高的灵敏度和特异性。相较 ELISA，该电化学免疫传感器以其定量检测的操作快速、简单、所需样本量小和超低检测限必将具有更广阔的临床应用价值。

PO-0514

Quantitative Assessment of Serum Amino Acids and Association with Early-onset Coronary Artery Disease.

Chao Xuan[1]、Hui Li[1]、Qing-Wu Tian[1]、Jun-Jie Guo[1]、Guo-Wei He[2]、Li-Min Lun[1]、Qing Wang[1]
1. Department of Clinical Laboratory, The Affiliated Hospital of Qingdao University, Qingdao, China.
2. 天津医科大学心血管病临床学院泰达国际心血管病医院

Background Cardiovascular disease (CVD) is a leading global cause of death. Early-onset coronary artery disease (EOCAD) is a CVD type, defined by the patient's age (<50 years old) when the initial diagnosis of coronary heart disease (CAD) is made. The majority of patients are male. EOCAD patients have a poor long-term prognosis, meaning that identifying risk factors is critical for disease diagnosis and control. Amino acids play essential roles in protein construction and metabolism. Our study aims to provide a profile of amino acid changes in the serum of patients with EOCAD and identify potential disease biomarkers. These biomarkers may help understand the pathophysiological process of EOCAD and may have special significance for the disease risk assessment and prediction.
Methods A total of 128 CAD patients (mean age 44.27 ± 5.26 years) and 64 controls (mean age 44.82 ± 5.12 years) were recruited from the Affiliated Hospital of Qingdao University between September 2019 and July 2020. Serum activity/concentrations of fasting blood glucose (FBG), triglycerides (TG), total cholesterol (TC), serum creatinine (SCr), high-density lipoprotein

cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C), and lipoprotein(a) were determined using an automatic biochemistry analyzer (Hitachi HCP-7600, Hitachi, Japan). Ultra-performance liquid chromatography multiple reaction monitoring multistage/mass spectrometry (UPLC-MRM-MS/MS) was used to determine the amino acid profile of patients with EOCAD in sample pools. UHPLC separation was performed using an Agilent 1290 Infinity II series UHPLC System (Agilent Technologies), equipped with a Waters ACQUITY UPLC BEH Amide column (100 × 2.1 mm, 1.7 μm). An Agilent 6460 triple quadrupole mass spectrometry (Agilent Technologies, USA) with an electrospray interface and multiple reaction monitoring (MRM) modes was used for the quantitative analysis. The study was divided into two stages. In the first stage, 200 μL serum was taken from each sample and mixed into a sample pool with 8 other samples from the group. There were 8 sample pools in the CAD with MI group, 8 in the CAD without MI group, and 8 in the control group. UHPLC-MRM-MS/MS was used to analyze the levels of 25 serum amino acids and screen for potential differences between groups. In the second stage, UHPLC-MRM-MS/MS was used to verify the screened differential amino acids of interest in each sample and study their relationship with CAD.

Results In the first stage, every eight serum samples were combined into a single sample pool. The study included CAD with and without myocardial infarction (MI) groups, and control group, with each group containing 8 sample pools. Of the 25 amino acids examined, differences in serum levels between groups of eight were seen (One-way ANOVA, $p < 0.05$). Compared with the control group, serum levels of seven amino acids (L-Arginine, L-Methionine, L-Tyrosine, L-Serine, L-Aspartic acid, L-Phenylalanine, and L-Glutamic acid) increased and one (4-Hydroxyproline) decreased in the patient group. Results from the validation stage demonstrate that serum levels of 4-Hydroxyproline were significantly lower in MI patients (9.889 ± 3.635 μg/ml) than those in the controls (16.433 ± 4.562 μmol/L, $p < 0.001$). Elevated serum 4-Hydroxyproline levels were shown to be an independent protective factor for MI (OR = 0.863, 95% CI: 0.822-0.901). The significant negative correlation was seen between serum 4-Hydroxyproline levels and cardiac troponin I ($r = -0.667$) in MI patients.

Conclusion We initially quantified serum levels of 25 amino acids levels in EOCAD patients and identified eight amino acids associated with disease status. Compared to the control group, serum levels of L-Arginine, L-Methionine, L-Tyrosine, L-Serine, L-Aspartic acid, L-Phenylalanine, and L-Glutamic acid were higher in the EOCAD group, and 4-Hydroxyproline levels were lower. 4-Hydroxyproline appears to be a promising amino acid for further biomarker studies of predicting fibrosis and ventricular remodeling after MI.

PO-0515

Associations of serum amyloid A and 25-hydroxyvitamin D with diabetic nephropathy: a cross-sectional study

Fumeng Yang、Qian Liu
The Second People's Hospital of Lianyungang

Background Previous studies have separately reported that serum amyloid A (SAA) has a potential relationship with diabetic nephropathy (DN) and that 25-hydroxyvitamin D (25(OH)VD) is potentially linked to the occurrence and progression of DN. The aim of this study was to provide potential evidence for the prevention and management of DN by investigating the relationships between SAA, 25(OH)VD and DN.

Methods A total of 182 patients with type 2 diabetes mellitus (T2DM) were enrolled in this study. Conventional characteristics were measured and collected. Receiver operating characteristic (ROC) curve analysis was applied for the combined measurement of SAA and 25(OH)VD, and risk factors for DN were evaluated using binary logistic regression analysis.

Results The levels of SAA in T2DM patients were significantly higher than those in healthy subjects, and the level significantly increased with the progression of DN ($P<0.05$). In contrast, the level of 25(OH)VD in T2DM patients was significantly lower than that in healthy subjects, and

the level significantly decreased with the progression of DN (P<0.05). In addition, the combined measurement of SAA and 25(OH)VD could distinguish DN patients from T2DM patients better than the measurement of SAA or 25(OH)VD alone (P<0.05). In addition, the SAA level was an independent risk factor for DN, but the level of 25(OH)VD was an independent protective factor for DN.
Conclusion SAA and 25(OH)VD could be used as additional indicators to help distinguish patients with DN from those with T2DM, and might provide a potential basis for monitoring the occurrence of DN.

PO-0516

糖化血红蛋白在 4 种检测系统间结果的比较

单汉明、李晓博、谢轩波、刘洋洋
杭州迪安医学检验中心有限公司

目的 探讨不同检测仪器对糖化血红蛋白（HbA1c）检测结果的比对及偏倚评估。
方法 分别使用东曹 G11、惠中 MQ-6000、迈克 G01 及罗氏 Cobas c513 全自动糖化血红蛋白分析仪对 58 例患者的全血样本进行检测，记录相关数据并进行统计学分析。
结果 以东曹 HLC-723 G11 全自动糖化血红蛋白分析仪作为参比仪器,将惠中 MQ-6000、迈克 G01、罗氏 c513 全自动糖化血红蛋白分析仪与其进行比对并进行相关性分析。迈克 G01：y = 1.0891x - 0.0127，R^2 = 0.999；惠中 MQ6000：y = 1.1059x - 0.7626，R^2 = 0.9973；罗氏 c513：y = 1.0594x - 0.3043，R^2 = 0.9993。偏倚分析：迈克 G01 检测结果普通偏高，正偏倚明显；惠中 MQ-6000 和罗氏 c513 检测结果在 6%以上的，也明显存在正偏倚情况。
结论 糖化血红蛋白在不同仪器的检测值上具有一定的差异性，但相关性均较好，能提供可靠的检验数据。

PO-0517

Causal relationships between body fat percentage and non-alcoholic fatty liver disease: a Mendelian randomization study

yuping zeng、He He、Mei Zhang、Zhenmei An
Sichuan University, West China hospital

Background Several observational studies have revealed the positive correlation between body fat percentage and non-alcoholic fatty liver disease (NAFLD). However, the association might be biased by confounding factors (such as obesity, type 2 diabetes, and hyperlipidemia) and reverse causality (NAFLD causes abnormal body fat percentage). This study aimed to investigate the causal relationships between body fat percentage and NAFLD by two-sample Mendelian randomization (MR) analysis, to determine the potential causes and carry out risk stratification for NAFLD patients.
Methods Single-nucleotide polymorphisms significantly associated with exposures (body fat percentage and body fat mass) were extracted from the Neale Lab Consortium ($P < 5.0\times10^{-8}$). Genome-wide association studies (GWAS) summary data for outcomes (NAFLD, NAFLD-related risk factors, and disorders) were extracted from the MR-Base database. We used the inverse-variance weighted method to assess the causal association between exposures and outcomes. We also performed the sensitivity analysis by weighted median and MR-Egger regression. The strength and interpretability of instrumental variables and the statistical power of MR analysis were assessed. All analyses were conducted using the R packages “TwoSampleMR”.

Results Genetically predicted higher body fat percentage was causally associated with higher NAFLD risks (odds ratio (OR): 5.07, 95% confidence interval (CI): 1.99-12.92, P: 6.6×10-4). Body fat mass was also causally associated with higher NAFLD risks (OR: 3.95, 95% CI: 2.07-7.57, P: 3.3×10-5). Besides, genetically predicted 1-SD increased body fat percentage was associated with reduced total cholesterol (coef = -0.13) and high density lipoprotein cholesterol (coef = -0.23), increased fasting insulin (coef = 0.13), HOMA-IR (coef = 0.13), HOMA-B (coef = 0.07), systolic pressure (coef = 0.17) and diastolic pressure (coef = 0.24) with all P less than 4.2×10-3. Strong causal effects were seen for body fat percentage and type 2 diabetes (OR: 2.53, 95% CI = 2.04-3.13), high blood pressure (OR: 1.13, 95% CI = 1.11-1.16), and gout (OR: 1.72, 95% CI = 1.19-2.49) with P less than 5.0×10-3. Body fat percentage also significantly increased the risks of cardiovascular disease (OR: 1.66, 95% CI = 1.44-1.91), coronary heart disease (OR: 1.53, 95% CI = 1.34-1.75), myocardial infarction (OR: 1.55, 95% CI = 1.35-1.78), stroke (OR: 1.20, 95% CI = 1.08-1.33), and ischemic stroke (OR: 1.24, 95% CI = 1.12-1.36). Sensitivity analyzes supported the robustness of the causal estimates. The statistical power for MR analysis was more than 80%, suggesting a sufficient power to detect the observed ORs.
Conclusions Our study revealed a strong causal effect of body fat percentage on the increased NAFLD risks. We also observed the causal association between body fat percentage and NAFLD-related risk factors and cardiometabolic diseases. Further studies are needed to elucidate the specific mechanism.

PO-0518

“图灵图案”和纳米颗粒协同作用的智能水凝胶微流体界面的构建用于捕获、培养和分析活的循环肿瘤细胞

陈东亮、杨大伟
聊城市人民医院

从患者外周血中高效捕获活体循环肿瘤细胞(CTCs)并建立稳定传代的细胞株是生物学研究的难点。基于微流体界面具有体积小、处理速度快、多路复用能力和大比表面积的特点为 CTCs 高效捕获提供了可能。本文构建“图灵图案”和纳米颗粒协同作用的智能水凝胶微流体界面用于高效捕获、培养和临床药物分析活体循环肿瘤细胞。通过调控“图灵图案”中峰-谷相对高度、峰-峰宽度以及表面粗糙度探究其结构尺度与 CTCs 捕获效率和培养稳定传代的细胞株之间的关系。并建立对乳腺癌、肝癌、食道癌动物和患者外周血中 CTCs 的捕获和培养进行生物学研究（细胞计数、细胞迁移、细胞侵袭、细胞状态、细胞蛋白分泌含量）和临床药敏性分析，探讨疾病状态下 CTCs 与实体瘤各种临床指标及疾病转归的关系，可对病人进行个体化的治疗提供理论依据。

PO-0519

一种用于嗜铬细胞瘤诊断的磁性分子印迹聚合物的制备

王浩然[1,2]、张连杰[1]、徐成钰[1]
1. 苏州市独墅湖医院
2. 重庆医科大学

目的 嗜铬细胞瘤是起源于肾上腺髓质嗜铬细胞的神经内分泌肿瘤，大量分泌儿茶酚胺类物质，如果不加治疗容易导致患者死亡。采用高效液相色谱-荧光法检测随机尿样本中的甲氧基去甲肾上腺素(NMN)、甲氧基肾上腺素(MN)、 3-甲氧酪胺(3-MT)，可用于嗜铬细胞瘤(PPGLs)的诊断。为此，拟制备一种磁性分子印迹聚合物(MMIP)用于快速、简便地富集随机尿样本中的 NMN, MN 和 3-MT。
方法 采用多巴胺(DA)和 MN 为双模板分子，甲基丙烯酸为功能单体，二甲基丙烯酸乙二醇酯为交联剂，偶氮二异丁腈为引发剂合成 MMIP。在 500 μL 随机尿样本中加入 2.5 mL 磷酸盐缓冲液后，

再加入 40 mg MMIP，室温振荡 30 s 混匀，吸附 8.0 min 后磁分离。加入 1.0 mL 超纯水清洗后弃上清，再用 200 μL 2.0%醋酸溶液洗脱 7.5 min，磁分离后取上清液 50 μL 进行高效液相色谱-荧光法检测。

结果 1、采用 DA 和 MN 双模板，模板分子、功能单体和交联剂的比例为 1:20:20，合成的 MMIP 粒径较为均一，表面为空洞疏松的结构，对于 NMN, MN 和 3-MT 标准品的吸附效率均高于 89.0%。2、采用 MMIP 对随机尿样品进行预处理耗时 20 min。MMIP 处理随机尿样本批内变异系数均 ≤4.9%，批间变异系数均 ≤6.3%，结果见表 1；平均回收率为 93.2%-112.8%，结果见表 2，可重复使用 14 次。分别采用 MMIP 和固相萃取法对正常对照组和 PPGLs 组各 10 例随机尿样本预处理后检测，其结果有较好的相关性 (相关系数 ≥0.7)。

结论 合成的 MMIP 可以用于富集正常人和 PPGLs 患者随机尿中的 NMN, MN 和 3-MT，重复性好，样品预处理耗时短，为快速及时地诊断 PPGLs 奠定基础，有利于在临床中推广，3-MT 对于良性嗜铬细胞瘤的诊断效能仍需进一步探索。

PO-0520

UPLC-MS/MS based plasma lipidomics reveal a distinctive signature in systemic lupus erythematosus patients

Jiaxi Chen
Enze Hospital of Enze medical center group

Global lipidomics are of considerable utility for exploring altered lipid profiles and unique diagnostic biomarkers in diseases recently. We aim to apply ultra performance UPLC-MS/MS to characterize the lipidomics profile in systemic lupus erythematosus (SLE) patients and explore the underlying pathogenic pathways using lipidomics approach. Plasma samples from 18 SLE patients, 20 rheumatoid arthritis (RA) patients, and 20 healthy controls (HC) were collected. A total of 467 lipids molecular features were extracted from each sample. OPLS-DA, K-mean clustering analysis and KEGG pathway analysis indicated disrupted lipid metabolism in SLE patients, especially in phospholipid, glycerol and sphingolipid metabolism. AUC of lipid metabolism biomarkers were better than SLE inflammation markers that ordinarily used in the clinic. Proposed model of MG(16:0/0:0/0:0), MG(18:0/0:0/0:0), PE(18:3/16:0), PE(16:0/20:4) and PC(O-16:2/18:3) yielded AUC 1.000 (95% CI, 1.000-1.000), specificity 100% and sensitivity 100% in the diagnosis of SLE from HC. A panel of three lipids molecular PC(18:3/18:1), PE(20:3/18:0), PE(16:0/20:4) permitted to accurately diagnosis of SLE from RA, with AUC 0.921 (95% CI, 0.828-1.000), 70% specificity and 100% sensitivity. The plasma lipidomics signatures could serve as an efficient and accurate tool for early diagnosis and provide unprecedented insight into the pathogenesis of SLE.

PO-0521

基于人群的糖尿病预测模型的建立及验证

李迪
武汉大学人民医院

目的 构建并验证糖尿病预测模型。

方法 收集信息化数据库中空腹血糖小于 7.00 mmol/L 的患者，排除信息不全或 BMI 极度异常 (BMI<15 kg/m2 或 >55 kg/m2) 的患者。最终纳入训练集 9045 例，同时纳入临床特征与之匹配的验证集 3562 例。用随机森林在训练集数据中对变量进行重要性排序，筛选变量并构建糖尿病预测模型同时进行验证。

结果 训练集与验证集的临床特征中各个变量均匹配良好（P>0.05）。训练集中，随访时间跨度为2.00-5.71 年，随访期间糖尿病共发生 61 例（6.74‰）；验证集中，随访时间跨度为 2.00-5.65 年，随访期间糖尿病共发生 20 例(5.61‰)。根据平均准确度下降程度（Mean Decrease Accuracy）对自变量重要性进行排序，用赤池信息量(AIC)准则和贝叶斯信息量(BIC)准则对模型进行筛选得出模型包含是 Change in FPG, FPG 和 Age 三个变量。在内部验证中，模型的 C 指数为 0.921，Brier Score 为 0.006，十折交叉验证平均 AUC 为 0.915；在外部验证中，模型总 C 指数为 0.921，按照预测概率分组后随着样本量下降 C 指数有所降低，但总体上仍较高。模型的 Brier Score 为 0.005。十折交叉验证平均 AUC 为 0.960。反应了本研究模型有极高的准确性。
结论 本研究建立的预测模型对糖尿病患病风险有很好的预测能力。

PO-0522

赖氨酸羟化酶 JMJD6 作为黑色素瘤预后标志物的潜在价值研究

司文喆、崔丽艳
北京大学第三医院

背景 黑色素瘤起源于上皮组织基膜上的黑素细胞，是最具侵袭性的皮肤癌，占皮肤癌相关死亡的75%。尽管 BRAF 突变和丝裂原活化蛋白激酶（MAPK）通路在黑色素瘤的发病机制中起着重要作用，但 MAPK 信号在黑色素瘤发生发展中的调控机制仍不完全清楚。
方法 我们采用免疫组化方法检测黑色素瘤组织中 JMJD6 的表达。使用人黑色素瘤细胞系进行体外增殖和侵袭实验，并使用小鼠黑色素瘤 B16F10 细胞通过生物发光成像进行异种移植小鼠体内肿瘤生长和肺转移评估。通过内皮管形成实验、鸡卵黄囊膜实验和基质凝胶栓实验，研究了 JMJD6 对血管生成的影响。
结果 我们报道了羟化酶 JMJD6 在黑色素瘤中显著上调。我们发现 JMJD6 的高表达与黑色素瘤的临床病理分期、侵袭性和预后不良密切相关。RNA-seq 显示 JMJD6 的敲除影响一组转录物的选择性剪接，包括编码 MAPK 信号通路的关键成分 PAK1 的转录物。我们证明 JMJD6 增强 MAPK 信号传导并促进多种细胞过程，包括黑色素瘤细胞的黑素生成、增殖、侵袭和血管生成。
结论 我们的研究结果表明 JMJD6 与黑色素瘤的发生密切相关，支持 JMJD6 作为黑色素瘤侵袭性的潜在生物标志物和黑色素瘤干预的靶点。

PO-0523

The variation of serum adiponectin and the relationship with nesfatin-1, IL-6 and TNF-αin prediabetes

Kangkang Huang、Yunlai Liang、Yating Ma、Jiahui Wu、Huidan Luo、Bin Yi
Xiangya Hospital of Central South University

Aim Prediabetes may not clear symptoms until it has progressed to type 2 diabetes mellitus(T2DM). The variation and correlation among adiponectin, nesfatin-1, TNF-α and IL-6, which involve diabetes development, have not been elucidated. This study aims to investigate the roles of these factors in the process of prediabetes developing into diabetes.
Methods In total, 72 T2DM, 75 prediabetes and 72 age-sex-matched healthy individuals were enrolled in this study and their serum levels of adiponectin, nesfatin-1, TNF-α and IL-6 were tested with appropriate methods.
Results Results showed that serum levels of each factor in prediabetes were between in T2DM and the healthy group, and significant differences were found among them. Both nesfatin-1 and TNF-α levels in T2DM had obvious variation compared to those in prediabetes or in healthy, while no significant difference of nesfatin-1 or TNF-α levels was observed between the two groups;

both adiponectin and IL-6 levels in the healthy group were significantly changed in contrast to those in prediabetes or in T2DM, while between them there was no distinct difference of adiponectin or IL-6 levels. Further correlation analysis found that in prediabetes, serum adiponectin concentration was positively correlated with TNF-α (R=0.2939, P=0.0105) and IL-6 (R=0.3918, P=0.0005), and the relationship between them was greatly strengthened when prediabetes accompanied by insulin resistant (TNF-α: R=0.7732, P<0.0001, IL-6: R=0.6663, P=0.0005). In addition, we demonstrated that declined levels of adiponectin (OR=6.238, P=0.019) and nesfatin-1 (OR=2.812, P=0.01) as well as elevated TNF-α (OR=5.541, P=0.001) levels were risk factors for prediabetes towards diabetes.
Conclusion Conclusively, this research proved significant variations of adiponectin, nesfatin-1, IL-6 and TNF-α levels in the healthy, prediabetes and T2DM, suggesting a significant but slow and gradual change during the progression of healthy condition toward diabetes via prediabetes.

PO-0524

Clinical and diagnostic value of the combination of lymphocyte count and creatine kinase in the detection of coronavirus 2019

Yanqing Du
Tianjin Haihe Hospital

The current study aimed to investigate the diagnostic efficiency of absolute number of lymphocytes (LYM#) and creatine kinase (CK) levels in the diagnosis of coronavirus disease 2019 (COVID-19). Therefore, the clinical data from 84 patients with COVID-19 admitted to the Tianjin Haihe Hospital between January and February 2020 were collected. The patients were divided into the following groups: The common COVID-19 group (n=61); and severe COVID-19 group (n=23). In addition, 30 healthy subjects were included as the control group. The results demonstrated that the percentage of neutrophils (NEU%) was significant increased, while the absolute number of white blood cells (WBC), LYM# and the percentage of lymphocytes (LYM%) were significantly decreased in patients with COVID-19. Furthermore, in the severe group, the absolute number of red blood cells (RBC) in female patients, the percentage of neutrophils (NEU%), the neutrophil-to-lymphocyte ratio (NLR) and the serum levels of interleukin 6 (IL-6) and C-reactive protein (CRP) were notably elevated, while those of LYM# and LYM% were significantly decreased (all P<0.05). Additionally, in the receiver operating characteristics curve analysis for the combination of LYM# + CK, the area under the curve values were 0.9645 and 1, with sensitivity of 95.08 and 100%, specificity of 86.67 and 100% and cut-off values of 0.4188 and 0.5, for the common and severe COVID-19 group, respectively. This finding indicated that the diagnostic efficiency of LYM# + CK was higher than when a single factor was analyzed. Finally, a moderate correlation was obtained between lactate dehydrogenase (LDH) with CRP and NLR (r=0.492 and 0.433, respectively; all P<0.05). Overall, the results of the present study suggested that the values of LYM# and CK were associated with COVID-19 progression, suggesting that the combination of both factors could exert a clinical diagnostic value for COVID-19.

PO-0525

脂蛋白相关磷脂酶 A2、同型半胱氨酸、抗凝血酶Ⅲ与冠脉病变程度的关系

王贝
东南大学附属中大医院

目的 研究脂蛋白相关磷脂酶 A2（LP-PLA2）、同型半胱氨酸(HCY) 、抗凝血酶Ⅲ（AT-Ⅲ）与冠状动脉病变程度的关系。

方法 选取拟行冠脉造影检查的患者 292 例，根据冠脉造影结果分为冠心病组 175 例、对照组（非冠心病组）117 例。冠心病组根据检查结果对冠脉病变程度进行 Gensini 积分，分为第 1 组（n = 45）、第 2 组（n = 43）、第 3 组（n = 43）、第 4 组（n = 44）。测定患者血浆 LP-PLA2、HCY、AT-Ⅲ水平，比较两组 LP-PLA2、HCY、AT-Ⅲ的差异，并分析与冠状动脉病变严重程度的关系。

结果（1）冠心病组 LP-PLA2 高于对照组，HCY 高于对照组，AT-Ⅲ水平低于对照组，差异有统计学意义（P<0.05）；（2）在 Gensini 积分四分位分组中，随积分的增加，LP-PLA2、HCY 呈升高趋势,AT-Ⅲ呈下降趋势，差异有统计学意义（P<0.05）；（3）Logistic 回归分析：冠心病的危险性因素 LP-PLA2 （OR：1.08，95% CI：1.05 ~ 1.11，P <0.01），HCY（OR：0.89，95% CI：0.93 ~ 0.98，P<0.01）；AT-Ⅲ是冠心病的保护性因素（OR：0.95，95%CI：0.93 ~ 0.98，P < 0.01）；（4）相关性分析显示：LP-PLA2 ,HCY 与 Gensini 积分呈明显正相关（r = 0.48，r = 0.56,P < 0.01），AT-Ⅲ与 Gensini 积分呈明显负相关（r = -0.24，P < 0.01）。

结论 冠心病组 LP-PLA2,HCY 高于对照组，且与冠脉病变呈明显正相关；AT-Ⅲ低于对照组，与冠状动脉病变程度呈明显负相关，可作为预测冠状动脉病变严重程度的指标，具有临床指导意义。

PO-0526

粪便性状及分析前标本处理方式对钙卫蛋白检测结果影响探讨

曾俊祥
上海交通大学医学院附属新华医院

目的 探讨采样方式、离心条件等相关分析前因素对不同性状粪便的钙卫蛋白(fecal calprotectin, FC)检测结果的影响，从而进一步优化粪便钙卫蛋白检测流程。

方法 收集在上海交通大学医学院附属新华医院进行粪便钙卫蛋白项目检测的的粪便标本 357 例，按照布里斯托大便分类量表进行性状评估。选取不同性状的粪便标本同时进行称量法和 2 种商品化采样装置采样操作，比较不同采样方式、离心条件，以及离心对不同性状、对不同区间段 FC 值结果的影响。

结果 1）采样方式：商品化采样装置与称量法结果均存在一定偏差，在水样便和坚硬便的标本中尤甚，其中装置 A 所得结果较称量法所得结果平均偏移度为 27.2%，装置 B 则达到 57.5%。2）离心条件：离心前后 FC 结果差异有统计学意义（P<0.05），而离心的转数与离心时间对结果没有明显影响。离心后 FC 结果较离心前降低，其中坚硬的粪便样本最明显，离心前后水样便 FC 结果差异无统计学意义（P>0.05），而其他性状的粪便结果差异则有统计学意义（P<0.05）。离心后的结果更加接近称重法的结果。

结论 采样是 FC 检测分析前最重要也是最容易忽视的环节，对不同性状的粪便样本，采样装置的使用应有区别，液态稀便应使用定量移液管，而坚硬粪便应先用锉刀进行样本均质操作后再进行采样操作。在用采样装置采样后，除了液态便外其他性状的粪便均应常规进行离心操作。

PO-0527

Correlation of sperm DNA fragmentation index with seminal plasma biochemical index and semen parameters in infertile men

Kangsheng Liu
Department of Clinical Laboratory, Women's Hospital of Nanjing Medical University，Nanjing Maternity and Child Health Care Hospital, Nanjing, Jiangsu 210029, China.

In general, routine semen analysis makes only limited predictions about a man's reproductive potential and is not always able to explain why he is infertile. In fact, many male infertility cases are caused by sperm DNA defects ,which routine semen quality analyses fail to detect. The relationship between sperm DFI , sperm parameters and their diagnostic value were analyzed and evaluated by observing the seminal parameters of infertile patients without accessory gonadal infection. Specimens of 151 cases were collected from infertile patients who visited the male department of STD and reproductive specialty clinic of our hospital from August 2018 to September 2019. SCD test was performed to measure the DNA fragmentation in native. The routine semen analysis was performed with a semen quality detection system (CFT-920, Jiangsu Ruiqi Life Science & Tech Dev .Co.Ltd) and supporting reagents. Seminal plasma malondialdehyde (MDA), and total antioxidant capacity (TAC) were assessed. Fructose(Fru) 、a-glucosidase (a-glu), and zinc (Zn) levels are quantitatively detected by kehua-310, a fully automated biochemical tester provided by Nanjing Xindibio. According to DFI level, there were 31 cases in group I (DFI≤15%), 81 cases in group II (15% < DFI < 30%), and 39 cases in group III (DFI≥30%). Compared with group II, there were significant differences in sperm survival rate, PR% and Fru by non-parametric test (Z = -2.16 -2. 43. - 2. 20,respectively,P < 0. 05). There were significant differences in sperm survival rate and PR% between group I and group III (t = 4. 32, 4.25, respectively, P< 0.01). Compared with group III, there were significant differences in sperm survival rate and PR% by non-parametric test (Z= -3. 26, -3. 50, respectively).Sperm DFI was negatively correlated with sperm survival rate and PR%(R=-0.56,-0.46,P<0.01). DFI was positively correlated with MDA content (R=0.42, P<0.01) and negatively correlated with TAC (r=-0.40, P<0.01).There was no correlation with age ,abstinence days, semen volume, sperm concentration, percentage of normal form sperm, Fru, a-Glu, Zn (R= 0. 15, 0. 05,0.03,-0.03, -0.2, -0.16,- 0.20, 0.03, 0.15, p > 0.05).The survival rate and PR% of sperm decreased significantly with the increase of DFI level, antioxidant can decrease the rate of DNA fragmentation, antioxidant can decrease the rate of DNA fragmentation. Semen volume and sperm concentration were mainly related to the secretion volume of accessory gonads and total sperm count, but no correlation was found between them and DFI.

PO-0528

Sp17 抗体在肿瘤诊断中的初步探讨

高骞
中南大学湘雅医院

背景 肿瘤的发生发展是一个多因素、多步骤、多基因共同作用的综合病变过程。肿瘤的转移性以及早、中期无症状的特征使得在肿瘤的防治过程中，早期发现、早期诊断、早期治疗尤为重要。相较于肿瘤相关抗原(tumor-associated antigen, TAA)的升高出现于癌症晚期，肿瘤相关自身抗体(TAAbs)被发现在癌症早期阶段表现出升高的水平，且半衰期可能比抗原更长，更容易被检测到，有可能成为有价值的诊断标记物。

目的 初步探讨精子蛋白 17（Sperm protein 17，Sp17）抗体在肿瘤诊断中的价值。

方法 收集 2019 年 1 月至 2019 年 4 月期间,于中南大学湘雅医院确诊的未经治疗的肿瘤患者的血清，同时收集同期在该院体检的正常人血清，所有血清保存于-20℃至使用，采用 ELISA 检测血清中 Sp17 抗体浓度。GraphPad prism 7.01 作图软件帮助数据分析。
结果 本研究成功检测血清中 Sp17 抗体浓度，其中恶性黑色素瘤患者 Sp17 抗体浓度普遍较高。
结论 提示 Sp17 抗体在恶性黑色素瘤中可能有更多研究价值。

PO-0529

Data Mining: Biological and temporal factors associated with blood parathyroid hormone, vitamin D, and calcium concentrations in the Southwestern Chinese population

Fei Ding、li guixing
Department of Laboratory Medicine, West China Hospital, Sichuan University

Background Parathyroid hormone (PTH) and vitamin D plays a major role in calcium (Ca) homeostasis and bone turnover. The purpose of this study was to assess which factors (sex, age, time of blood sampling, season of the year, temperature and sunshine hours (SHH)) had the greatest impact on plasma PTH, 25-OH-VitD, and Ca levels, and then whether these effects were clinically acceptable in a large number of Southwestern Chinese subjects.
Method The data was from West China Hospital Health Examination Center, Sichuan University from April 1, 2018 to June 30, 2019. A total of 18,664 physical examination subjects were included. PTH and 25-OH-VitD were measured by a Roche Cobas e 601, and Ca was measured by a Roche Cobas 8000. Linear regression models were used to assess correlations between PTH, 25-OH-VitD, Ca and the above factors.
Results The concentrations of serum PTH in females were significantly higher than those in males, while the 25-OH-VitD and Ca were opposite. The concentration of PTH in data collection decreased in summer and increased in spring. The concentration of 25-OH-VitD decreases in spring and increases in autumn. PTH concentrations were negatively correlated with last month temperature and SHH, while 25-OH-VitD were opposite. Linear regression showed that season may be the main factor affecting serum PTH and 25-OH-VitD levels, and these effects were not clinically acceptable.
Conclusion In order to avoid influencing clinicians' investigation of suspected hyperparathyroidism and hypovitaminosis, reference intervals for PTH, 25-OH-VitD, and Ca should be established, taking into account sex, age and the season.

PO-0530

Fasting plasma lactate: A diagnosis and staging biomarker with superior performance in adult nonalcoholic fatty liver disease

Xin Nie[1]、Jianfei E[2]、He He[1]、Fei Ding[1]、Haolan Song[1]、Yong He[1]、Guixing Li[1]
1. Department of Laboratory Medicine, West China Hospital, Sichuan University, Chengdu 610041, P.R. China
2. Department of Laboratory Medicine, People's Hospital of Deyang City, Deyang, 618000, P.R. China

Purpose For the assessment and staging of metabolic diseases such as obesity and type 2 diabetes mellitus (T2DM), fasting plasma lactate (FPL) has been a useful marker. However, it has never been used to evaluate nonalcoholic fatty liver disease (NAFLD). Since NAFLD is one of the significant metabolic syndromes, we investigated whether FPL can be used as a biomarker for diagnosing and staging NAFLD.

Methods A total of 102 patients who were diagnosed with NAFLD and 100 healthy control between October 2018 and September 2019 were enrolled in our study. We determined the levels of FPL, total cholesterol (TC), triglycerides (TG), high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C), alanine aminotransferase (ALT), aspartate aminotransferase (AST), fasting plasma glucose (FPG), fasting insulin (FINS), and homeostasis model assessment of insulin resistance (HOMA-IR). We performed receiver operating characteristic (ROC) analysis to evaluate their diagnostic performance.
Results In NAFLD patients, we found FPL, ALT, AST, TG, FPG, FINS, and HOMA-IR levels to be elevated while HDL-C level was reduced ($P < 0.05$). FPL, FPG, FINS, and HOMA-IR levels were higher in mild NAFLD patients than moderate to severe ones ($P < 0.05$). For NAFLD diagnosis and staging, the areas under the ROC curve (AUC) of FPL were 0.973 and 0.999, making it clearly ($P < 0.05$) superior to other biomarkers. For diagnosing and staging NAFLD, the cutoff value of 1.285 mmol/L and 2.370 mmol/L for FPL had the highest validity, respectively. The sensitivity, specificity, negative likelihood ratio (LR-), and positive likelihood ratio (LR+) were 87.25%, 98.00%, 0.13, and 43.63 for the diagnosis cutoff value and. 92.19%, 97.37%, 0.08, and 35.05 for staging, respectively. In addition, for NAFLD patients, FPL positively correlated with TG, FPG, FINS, and HOMA-IR ($P < 0.05$).
Conclusion Thus, in adult NAFLD, FPL can be used as a diagnosis and staging biomarker with superior performance.

PO-0531

Associations of urinary metabolites of polycyclic aromatic hydrocarbons with diabetes mellitus complicated with proteinuria in U.S. adults, NHANES 2003–2014

Jiang Li
Chian-Japan Friendship Hospital

Background Increasing concentrations of air pollution have been shown to be a risk factor for many diseases. Polycyclic aromatic hydrocarbon (PAH) exposure has been shown to be associated with diabetes mellitus (DM) and kidney disease. But studies on the correlation between urinary PAHs and DM complicated with proteinuria are limited. This study will explore the association between urinary PAHs and DM complicated with proteinuria based on a national representative sample from the general U.S. population.
Method Data utilized were extracted from the 2003-2014 National Health and Nutrition Examination Survey (NHANES). Eight urinary PAHs were detected as PAH metabolites (OH-PAHs). Multivariable logistic regression analyses were used to examine the association of OH-PAHs with DM and albuminuria. All of models were adjusted for confounding factors.
Result A total of 6,997 NHANES (2003-2014) participants with complete data were eligible. In the quartile analyses, 2-NAP was positive associated with the risk of DM and albuminuria in DM without albuminuria group [OR (95% CI), 1.54 (1.16-2.05), P<0.001], DM with albuminuria group [OR (95% CI), 1.70 (1.19-2.45), P<0.001] and albuminuria without DM group [OR (95% CI), 1.68 (1.30-2.17), P<0.001], 2-FLU was positive associated with the risk of albuminuria in DM with albuminuria group [OR (95% CI), 1.48 (1.03-2.13), P<0.05] and albuminuria without DM group [OR (95% CI), 1.50 (1.15-1.95), P<0.001], but 1-NAP was only positive associated with the risk of albuminuria in albuminuria without DM group [OR (95% CI), 1.47 (1.13-1.91), P<0.001] in the fully adjusted model.
Conclusion 1-NAP, 2-NAP, 2-FLU were positively associated with the risk of albuminuria in pure albuminuria group, but only 2-NAP was positively associated with the risk of DM in pure DM group. PAH exposure may be more closely associated with proteinuria. Prospective studies, including cohort studies and experimental studies, are needed to investigate the effects of OH-PAHs on kidney function impairment.

PO-0532

中国西部地区妊娠妇女特异性促甲状腺激素参考区间的建立

郭英
四川大学华西第二医院

目的 探讨中国西部地区妊娠期妇女特异性促甲状腺激素的正常参考区间。
方法 收集 2015 年 1 月 1 日至 2020 年 12 月 30 日期间到四川大学华西第二医院产科或妇科门诊就诊孕妇的促甲状腺激素（TSH）检测结果。排除有甲状腺疾病个人病史、接受影响甲状腺功能的药物治疗、多胎妊娠或超声检查发现相关异常的孕妇，以及 TSH <0.001mIU/L 或高于一般人群参考值的孕期妇女。建立参考区间的所有过程均参照临床实验室标准协会发布的文件 CLSI EP28-A3。根据抗甲状腺过氧化物酶抗体（TPOAb）是否阳性分组，建立以第 2.5 百分位数～第 97.5 百分位数（P2.5~P97.5）表示的参考区间。
结果 共纳入符合标准的 TPOAb 阴性组孕妇 14332 例，TPOAb 阳性组孕妇 10254 例。两组孕妇均孕早期 TSH 水平最低，孕晚期最高，孕中期处于两者之间，趋势一致。抗体阳性组中各孕期之间 TSH 水平比较和相同孕期中抗体阳性和阴性组之间 TSH 差异均有统计学意义。根据 CLSI EP28-A3 文件我们建立的 TPOAb 阴性组孕早期、孕中期和孕晚期 TSH 参考区间分别为 0.02-5.23mIU/L, 0.03-5.24mIU/L, 0.37-5.68mIU/L; TPOAb 阳性组孕早期、孕中期和孕晚期 TSH 参考区间分别为 0.23-4.73 mIU/L，0.35-4.67 mIU/L，0.43-4.75 mIU/L。
结论 妊娠期血清 TSH 水平不同于非孕正常妇女，且妊娠不同时期、TPOAb 阴性和阳性的参考区间亦不相同。建立特异性妊娠早、中、晚期血清 TSH 的参考区间非常必要，对 TPOAb 阳性的孕妇应全程监测甲状腺激素变化。

PO-0533

子痫前期患者检测孕中期 β-HCG 与孕后期 D-二聚体的临床意义

倪艳丽
南方医科大学珠江医院

目的 探讨子痫前期孕妇孕中期 β-HCG、孕后期 D-二聚体水平与疾病的发生及轻重程度的关系。
方法 回顾性分析 2015.1-2016.12 在南方医科大学珠江医院接受孕中期筛查并成功随访直至分娩的 54 例单胎孕妇孕中期血清学筛查 β-HCG MoM 值和孕后期血浆 D-二聚体结果与孕妇发生子痫前期及其轻重的情况。
结果 在 54 例患者资料中，39 例为正常孕妇，15 例经诊断为子痫前期患者，两组比较，孕中期 β-HCG MoM 值差异不显著；孕后期血浆 D-二聚体水平具有显著差异（P＜0.001）。患者组按轻重程度分组，重度组与正常组、轻度组具有显著性差异（P＜0.001、P＜0.01）。
结论 孕中期血清学筛查 β-HCG 对孕妇患子痫前期的预测意义不明显；孕后期血浆 D-二聚体水平对判断子痫前期孕妇的严重程度有显著的意义。

PO-0534

Transiently elevated TC and sdLDL-C levels and falsely low LDL-C levels in patients with extrahepatic cholangiocarcinoma

Yi Guo、Yong-Gen Zhang、Hong-Chun Li、Yin-Hai Xu
The Affiliated Hospital of Xuzhou Medical University

Purpose Most patients diagnosed with extrahepatic cholangiocarcinoma (ECCA) exhibit cholestasis caused by obstruction of the bile duct. Cholestasis has been shown to be associated with lipid metabolic disorders, but studies focused on the changing lipid parameters in ECCA patients have not been found. Here, we aim to observe lipid profiles in ECCA patients, and to investigate whether cholestasis relief corrects the dyslipidemia.

Methods We consecutively included patients admitted in the hepatobiliary surgery department from October 2019 to May 2020. The patients were presumedly divided into an ECCA group or a non-ECCA group base on the disease assessment. Patients who were histologically confirmed were finally included into the ECCA group. Blood samples were collected on admission and five days after treatment. Automatic biochemistry analyzer (Roche Cobas 8000) was used to test liver function and to measure serum lipid levels by spectrophotometry. Serum lipoprotein electrophoresis was performed using barbitone sodium buffer and Sudan black B. Statistical analysis was carried out using SPSS (version 23.0, SPSS Inc., Chicago, IL, USA). Continuous variables with normal distribution were expressed as mean ± standard deviation and analyzed using independent samples t-test, while those with skewed distribution were shown as median (Q1, Q3) and analyzed using Mann-Whitney U test.

Results One hundred and eighty patients met the inclusion criteria and were finally enrolled in the study. A total of 76 patients were diagnosed with ECCA after histological evaluation. Among these patients, 41 (54.0%) were diagnosed to have proximal cholangiocarcinoma, 9 (11.8%) had middle cholangiocarcinoma, and 26 (34.2%) had distant cholangiocarcinoma. In the ECCA group, 69 patients underwent radical resection, including 1(1.3%) in stage 0, 6 (7.9%) in stage I, 11 (14.5%) in stage II and 51(67.1%) in stage III. The other 7 patients were in stage IV, and underwent percutaneous transhepatic biliary drainage and stenting for palliative treatment. A total of 104 patients were enrolled in the non-ECCA group. Among these patients, 37 as diagnosed as choledocholithiasis, 3 as cholangitis, 53 as cholecystolithiasis, 9 as cholecystitis, and 2 as cholecystic polypus. In the non-ECCA group, 64 patients underwent cholecystectomy, and 40 underwent common bile duct exploration and T-tube drainage. Three hundred and sixty blood samples were collected, including 180 samples before treatment and 180 samples after treatment. Before treatment, TC levels were significantly elevated in the ECCA group compared to the non-ECCA group (5.70 [4.82, 7.40] mmol/L vs. 4.17 [3.53, 5.06] mmol/L, P <0.01). Correspondingly, the ECCA group showed significantly higher levels of sdLDL-C compared with the non-ECCA group (1.633 [1.043, 3.072] mmol/L vs. 0.980 [0.641, 1.329] mmol/L, P <0.01). Unexpectedly, the levels of LDL-C were slightly lower in the ECCA group compared with in the non-ECCA group. (1.97 [0.92, 2.84] mmol/L vs. 2.13 [1.69, 2.85] mmol/L, P = 0.04). Serum lipoprotein electrophoresis showed serum samples in the ECCA group were detained in the sample wells and lipoproteins failed to be separated.

The levels of TC and sdLDL-C were significantly decreased after treatment in the ECCA group. Most ECCA patients showed normal levels of TC and sdLDL-C after they received treatment, and there were no significant differences in TC and sdLDL-C levels between the ECCA and the non-ECCA groups after treatment (P>0.05). Lipoprotein electrophoresis results revealed that ECCA patients who had serum LDL particles that were not able to be separated showed a normal lipoprotein pattern after treatment

Conclusion ECCA patients exhibited transiently elevated TC and sdLDL-C levels and falsely low LDL-C results. TC, sdLDL-C, and LDL-C levels could return to the normal levels after cholestasis relief.

PO-0535

衰老标志物在细胞衰老及个体老化中的研究进展

韦钊
山东大学齐鲁医院

目的 随年龄增加，老年性疾病的发病率显著增加。细胞衰老一方面是机体防御肿瘤发生的重要屏障，另一方面在个体老化中起重要作用，并可通过 SASP 而促进肿瘤。预防和尽早发现是减少或延缓疾病发生的关键，而衰老标志物的发现则可以帮助我们解决这一问题。
方法 构建细胞衰老模型并进行基因芯片检测。通过生物信息学分析，找出衰老细胞相对于正常细胞表达上调的基因，与 GEO 数据库中人类胚胎干细胞和诱导性干细胞基因表达谱数据进行比对，找出同时在干细胞中表达下调的基因。对筛选到的基因在六种细胞衰老模式中的表达进行检测验证。
结果 我们发现有 41 个基因在复制衰老和氧化损伤诱导的细胞衰老中均上调显著。其中 11 个基因同时在人类胚胎干细胞和诱导性干细胞中表达下调。我们对这 11 个基因在六种细胞衰老模式中的表达进行了 PCR 验证，结果表明有 4 个基因在 5 种以上的细胞衰老类型中普遍上调。且不同年龄人类皮肤和皮下脂肪组织 RNA-Seq 数据表明这些基因确实存在指示衰老进程的潜力。
结论 通过基因表达谱筛选和在细胞衰老模型中的验证发现了 4 个可作为细胞衰老潜在标志物的基因。进一步明确多种细胞类型及多种衰老模式中这些衰老基因作为衰老标志物的潜在价值，将为衰老相关研究提供更多的检测手段及理论基础，研究这些基因指示个体老化及器官老化的能力，将为老年型疾病提供早期检测的理论基础，从而为衰老相关疾病的检测和治疗提供新的思路和依据。

PO-0536

基于数据挖掘分析 OGG1 在肝细胞癌组织中的表达及临床意义

张禾
四川大学华西医院

肝细胞癌是全球范围内最常见的成人原发性肝癌,也是中国癌症死亡的主要原因之一。肝细胞癌缺乏早期诊断标志物，预后较差。本文通过数据挖掘分析肝细胞癌中核酸修复蛋白 OGG1 的表达并探讨其临床意义。利用 TCGA 和 GEO 数据库分析肝细胞癌患者肿瘤组织和癌旁组织中 OGG1 基因表达差异和甲基化程度分析；使用 GEPIA 在线分析工具和 Kaplan-Meier Plotter 分析 OGG1 基因表达与患者生存时间的相关性；最后应用 STRING 数据库分析与 OGG1 相互作用的蛋白。OGG1 在肝细胞癌患者肿瘤组织中表达显著高于癌旁组织（$P<0.05$）；肝细胞癌肿瘤组织中 OGG1 基因的甲基化水平显著低于癌旁组织（$P<0.05$）；高表达 OGG1 的肝细胞癌患者生存时间更短（$P=0.01$）。STRING 数据库分析及功能富集显示 OGG1 与碱基切除修复、DNA-N 端糖苷化酶激活、DNA 分解代谢过程和脱氧核糖核酸分解代谢过程等发挥作用。通过对 TCGA 和 GEO 数据库中信息的深入挖掘和分析，发现 OGG1 在肝细胞癌中高表达且与患者预后密切相关，OGG1 可能成为评估肝细胞癌预后的指标和一个潜在的肝细胞癌治疗靶点。

PO-0537

两种糖化血红蛋白检测系统的方法学评价研究

宋佳、姚瀚鑫
吉林大学第一医院

目的 分别采用 TOSOH G8 离子交换高效液相色谱法检测系统和 Premier 亲和层析高效液相色谱法检测系统对 708 个糖化血红蛋白标本进行检测，在精密度，准确度，线性范围方面进行比较，然后

再选取常规标本和异常标本留样再测，异常标本包括肾病和贫血患者，比较相对于靶机相对偏倚小于 5%的标本数量，靶机为美国 Bio-Rad Vatiant Ⅱ。

方法 精密度：每日连续测定 5 次低值，高值室内质控，连续测定 3 天。批内 CV(%)≤1/4 TEa 临床允许误差；总 CV(%)≤1/3 TEa 临床允许误差。准确度：选取美国 CAP 糖化血红蛋白 2 支留样标本(1 号和 4 号)，2020 年卫生部室间质评糖化血红蛋白第一次 2 支留样标本（编号为 2 号和 3 号），2 支 Bio-Rad 定值校准品（编号为 5-6），作准确度标本。线性范围验证：取评价项目的高、低值病人标本各一份，（高值标本为接近线性范围上限或高于线性上限 10%-15%的标本，低值标本为接近线性范围下限的标本）。低值标本为 1 号，高值标本为 6 号，低高值标本 4：1 混和为 2 号，3：2 混和为 3 号，2：3 混和为 4 号，1：4 混和为 5 号。每个编号标本重复测定 2 次，记录结果。标本留样再测：比对 5 天，共检测留样再测标本 708 份，其中大于 6 的标本 328 份，留样再测标准相对于靶机相对偏倚小于 5%，1/2TEa。

结果 精密度结论两种检测系统均符合设定的精密度批内 CV 及总 CV 要求。正确度结论两种检测系统结果均在允许范围内。线性范围结论两种检测系统 R 值均大于 0.975，符合要求。常规标本留样再测结果为：亲和层析高效液相色谱法检测系统大于 5%的标本为 258 个，即 36.4%的标本与靶机相对偏倚超过 5%。离子交换高效液相色谱法系统大于 5%的标本为 84 个，即 11.8%的标本与靶机相对偏倚超过 5%。异常标本（肾病和贫血患者）留样再测结果亲和层析法检测系统与靶机相对偏倚超过 5%的标本数量最少。

结论 两种检测系统在精密度，准确度，线性范围方面均符合要求，对于常规标本，离子高效液相色谱法检测系统与 Bio-Rad 靶机比对相对偏倚超过 5%的标本数量最少，优于亲和层析法检测系统。对于肾病和贫血患者的标本，亲和层析法检测系统要优于离子交换层析法检测系统。

PO-0538

脊柱退行性病变老年女性定量 CT 骨密度与血清总胆红素和 AST/ALT 比值的相关性探讨

刘武征、徐东江
北京积水潭医院

目的 研究罹患脊柱退行性病变的老年女性定量 CT 骨密度（bone mineral density，BMD）与血清总胆红素（total bilirubin，TBIL）、天门冬氨酸氨基转移酶（Aspartate aminotransferase，AST），丙氨酸氨基转移酶（Alanine aminotransferase，ALT）的相关性。

方法 病例对照研究，回顾性分析 2019 年 7 月～ 2019 年 12 月期间在我院脊柱外科诊断为脊柱退行性病变并做定量 CT 的老年女性人群 555 例，根据中国老年骨质疏松症诊疗指南（2018）将入组人群分为骨质疏松组 277 例、低骨量组 211 例、骨密度正常组 67 例，分析三组人群体重指数（BMI）、总胆红素（TBIL）、天门冬氨酸氨基转移酶（AST）、丙氨酸氨基转移酶（ALT）及 AST/ALT 比值与骨密度的关系。以单因素方差分析研究各组差异，Person 相关分析不同指标间相关性，p<0.05 为具有显著性水平。

结果 经单因素方差分析，骨密度正常、骨密度减低、骨质疏松三组年龄分别为（58.67±9.23 岁、63.45±6.58 岁、69.28±7.75 岁），差异有统计学意义 (P<0．05)；腰椎 BMD 分别为（154.25±20.75 mg／cm3、102.77±10.35 mg／cm3、67.15±10.98 mg／cm3），差异有统计学意义 (P<0．05)；BMI 分别为（24.91±2.55 kg/m2、23.99±2.69 kg/m2、22.77±2.33 kg/m2），差异有统计学意义 (P<0．05)；TBIL 分别为（15.27±5.67μmol／L、15.24±6.79μmol／L、13.85±4.99μmol／L），差异有统计学意义 (P<0．05)；ALT 分别为（23.98±17.36IU/L、23.14±16.96 IU/L、18.15±9.10 IU/L、），差异有统计学意义 (P<0．05)；AST 分别为骨密度正常组（20.39±7.35 IU/L）、骨密度减低组（21.17±9.15 IU/L）、骨质疏松组（20.04±8.17 IU/L）三组间比较，差异无统计学意义；AST/ALT 分别为（0.98±0.29、1.06±0.39、1.23±0.43），差异有统计学意义 (P<0．05)。

结论 脊柱退行性病变的老年女性患者血清中 TBIL、AST/ALT 与骨密度有显著相关性，骨质疏松症诊断时起到辅助诊断意义。

PO-0539

血清可溶性甘露糖受体在肝癌患者中的表达及其临床意义

黄程荣
安徽医科大学第二附属医院

目的 探讨肝癌（HCC）患者体内可溶性甘露糖受体（sMR）的表达水平及其临床意义。
方法 采用酶联免疫吸附实验分别检测肝癌患者、慢性乙型肝炎（CHB）患者及健康对照（HC）血清 sMR 水平，统计分析一般资料，比较不同分期及病理特征患者血清 sMR 水平，并通过绘制 ROC 曲线评价 sMR 及 AFP 对肝癌的诊断效能。
结果 肝癌患者血清 sMR 水平高于慢性乙型肝炎及健康对照者，根据巴塞罗那临床肝癌分期分类标准将 HCC 患者的疾病严重程度分为巴塞罗那 A、B、C、D 期（早、中、晚、终末期），其中 A 期 27 例，B 期 39 例，C 期 42 例，D 期 21 例。结果提示随着疾病进展，肝癌患者体内 sMR 水平升高，同时发现 HCC 患者血清中 sMR 水平在肝癌组肿瘤直径＞5 cm 及多发结节组中均升高但 AFP 水平与肿瘤数目及肿瘤大小差异无显著性。进一步以不同研究对象作为对照组绘制 ROC 曲线评估 sMR 及 AFP 对 HCC 患者的诊断效能，研究发现以 HC 组或非肝癌患者为对照组 sMR 曲线下面积（0.992 和 0.864）均高于 AFP（0.848 和 0.761），且当 AFP 与 sMR 联合检测时，ROC 曲线下面积（0.996 和 0.909）均高于单个指标。说明 AFP+sMR 是 HCC 患者诊断的良好预测指标。以非肝癌组为对照组，AFP 阴性 HCC 患者（49 例）作为病例组，ROC 曲线下面积为 0.854（0.783~0.909），当 sMR 截断值为 110pg/ml 时，敏感性和特异性分别为 79.59%、80.0%，表明 sMR 对于 AFP 阴性的 HCC 患者也有一定的补充诊断价值。
结论 血清 sMR 水平在肝癌患者中升高，其表达水平与肿瘤分期、大小及数目有关，同时发现血清 sMR 及 AFP 联合检测对于肝癌的诊断水平高于单个指标对肝癌诊断具有重要临床意义和应用价值。

PO-0540

MicroRNA-210 did not change expression of TET2 and interleukin-6 in trophoblasts

Qian Li [2]、Yuping Duan[1]、Leiming Cai[1]
1. Wusong branch，Zhongshan hospital，Fudan university
2. 复旦大学附属中山医院吴淞医院

Recent studies have found that in the blood of patients with advanced pre-eclampsia (PE), the levels of hypoxia-related microRNA-210 (miR-210) and pro-inflammatory factor Interleukin-6 (IL-6) are significantly increased and positively correlated. Through bioinformatics analysis, we found that ten-eleven translocation enzyme 2 (Tet2) is the target gene of miR-210, while Tet2 is reported as atranscription repressor of IL-6. Here we detected expression of Tet2 and IL-6 in placenta from PE patients and analyzed the effect of miR-210 on IL-6 and Tet2 in primary trophoblast cells and HTR8/SVneo. We found that placental IL-6 expression was increased and Tet2 expression was down-regulated in PE. But Tet2 is not a direct target gene of miR-210. The mechanism of the decrease of Tet2 and the increase of IL-6 in PE placenta needs further exploration.

PO-0541

Inhibition of LDHA suppresses cell proliferation and increases apoptosis in cervical cancer cells

Wenjing Zhang、Liang Ming
The First Affiliated Hospital of Zhengzhou University

Propose Warburg effect or aerobic glycolysis has become a hallmark of cancer. Lactate dehydrogenase (LDH), which catalyzes pyruvate into lactate, plays a critical role during Warburg effect. It has been reported that LDHA is up-regulated in many cancers and plays a vital role in tumor growth and progression. However, its expression and function in cervical cancer (CC) has not been characterized thoroughly. Therefore, we undertook experiments in an attempt to elucidate the underlying roles and mechanism of LDHA in cervical cancer.
Methods To explore the gene expression of LDHA in human tumors and normal samples, we used web-based data to analyze The Cancer Genome Atlas (TCGA) datasets via Gene Expression Profiling Interactive Analysis(GEPIA) dateset. To examine the LDHA inhibition effect in CESC cells, oxamate was used. Meanwhile, we constructed stable LDHA-depeleted CESC cell lines. Moreover, we detected glucose consumption, lactate production and ATP level after inhibition of LDHA by shRNA or oxamate in both Hela and Siha cells. Furtheremore, we detected the effect of LDHA inhibiton on the cell proliferation, cell cycle and apoptosis.
Results We evaluated LDHA expression in TCGA database and found that LDHA was upregulated in cervical cancer compared to normal tissues and LDHA overexpression was remarkably correlated with shorter overall survival in cervical cancer patients. Moreover, we documented that inhibition of LDHA by oxamate, a small-molecule inhibitor of LDHA, disturbed energy metabolism by greatly decreasing glucose consumption, lactate production and ATP level in both Hela and Siha cells. Similarly, knockdown of LDHA in CESC cells also decreased the glucose utilization, and lactate production and ATP levels. LDHA inhibition by oxamate or shRNA in Hela and Siha cells inhibited the cell growth. Furthermore, we detected the effect of LDHA inhibiton on the cell cycle and found that knockdown LDHA or oxamate treatment led to G2/M cell cycle arrest. We detected the effect of LDHA inhibiton on the cell apoptosis and found that knockdown LDHA or oxamate treatment led to increased apoptosis and activated mitochondrial apoptosis pathway.
Conclusion LDHA inhibition decreased the glucose utilization, and lactate production and ATP levels, ultimately lead to disturb energy metabolism and repress the Warburg effect in CESC cells. LDHA deficiency resulted in increased apoptosis and G2/M cell cycle arrest. Collectively, these results indicate that LDHA is pivotal in CC pathogenesis and may be a promising therapeutic target for CC treatment.

PO-0542

IGF2BP1 基因在食管鳞癌中的表达水平及风险模型构建

韩博成、王敏、阴晟
中南大学湘雅二医院

目的 利用生物信息学手段探究 21 种 m6A 调节基因在食管鳞癌中的表达水平以及对患者的预后影响。主要解决两个问题，哪些基因表达量显著差异并且对患者预后显著影响的基因,基于显著基因构建的风险模型性能如何。
方法 利用肿瘤信息数据库 TCGA 和 GTEX 的 RNA-seq 数据分析 m6A 调节蛋白在食管鳞癌和正常组织中的表达差异；通过生存分析统计方法 Cox 回归筛选对患者预后有影响的蛋白；使用免疫组化方法从蛋白质水平验证 IGF2BP1 表达量；将 96 例食管癌患者分为训练集（60 例）和验证集

（36 例）；训练集通过 Lasso 回归方法构建风险模型，利用验证集验证模型性能，模型性能用 ROC 曲线反映。

结果 基于肿瘤信息数据库 TCGA-ESCA 和 GTEx 数据集分析结果发现 IGF2BP1 基因在食管鳞癌中高表达，而在正常食管中低表达。并且 IGF2BP1 基因高表达对食管鳞癌患者生存期延长有益(HR=0.478，95%CI=0.284-0.803，P<0.05)。免疫组化研究表明食管鳞癌中 IGF2BP1 蛋白的表达量高于其癌旁组织。本文利用与 IGF2BP1 相关的 55 种 RNA 的表达量构建风险模型，模型对患者一年期生存率具有一般的预测性能（最佳 cutoff=0.9858，AUC=0.65），对二年期生存率具有较高的预测性能（最佳 cutoff=1.128，AUC=0.83）。

结论 IGF2BP1 基因在食管鳞癌中高表达，且该基因对延长患者生存期有益；基于 IGF2BP1 相关 RNA 构建的风险模型对患者两年期生存率具有较好预测性能。

PO-0543

BATF2 抑制 GBM 中髓源性抑制细胞作用机制研究

张鑫
南方医科大学南方医院
四川大学华西医院

碱性亮氨酸拉链 atf 样转录因子 2 (BATF2)与炎症反应和抗肿瘤作用有关。然而，关于它在维持非支持性癌症微环境中的细胞外作用，我们知之甚少。在这里，我们发现 BATF2 可以抑制胶质瘤的生长和骨髓源性抑制细胞(MDSCs)的募集。有趣的是，过表达 batf2 的胶质瘤细胞系来源外泌体在体外抑制了 MDSCs 的趋化。此外，BATF2 抑制细胞内 SDF-1α，并有助于降低 SDF-1α。在 AMD3100 处理下，通过阻断 SDF-1α/ CXCR4 信号通路，可逆转 BATF2 下调诱导的 MDSCs 募集。通过对 24 对胶质瘤和健康供体不同阶段 EV 的检测，发现血浆中大量的 BATF2 阳性 EV 可以区分 III-IV 期胶质瘤、I-II 期胶质瘤和健康人。综上所述，我们的研究发现 BATF2 在调节 MDSCs 招募方面的新调控功能，为胶质瘤 BATF2+ plEVs 提供了预后价值。

PO-0544

Making Aggregation-Induced Emission Luminogen More Valuable by Gold: Enhancing Anticancer Efficacy by Suppressing Thioredoxin Reductase Activity

Hang Zou 、Jing Zhang、Lei Zheng
Nanfang Hospital, Southern Medical University

Gold complexes have been recognized as potential anticancer agents against various kinds of diseases due to their inherent suppressions of antioxidant thioredoxin reductase (TrxR) activity. Herein, a powerful aggregationinduced emission luminogen (AIEgen), TBP-Au, was designed and synthesized by integrating an anticancer Au(I) moiety with an AIE-active photosensitizer (TBP), in which both the production and consumption routes of reactive oxygen species (ROS) were elaborately considered simultaneously to boost the anticancer efficacy. It has been demonstrated that TBP-Au could realize superior two-photon fluorescence imaging in tumor tissues with high resolution and deep penetration as well as long-term imaging in live animals due to its AIE property. In addition, the introduction of a special Au(I) moiety could tune the organelle specificity and efficiently facilitate the ROS-determined photodynamic therapy (PDT). More impressively, TBPAu could efficiently eliminate cancer cells under light irradiation through the preconceived synergetic approaches from the PDT and the effective suppression of TrxR, demonstrating that TBP-Au holds great potential for precise cancer theranostics.

PO-0545

Identification of prognosis-related genes in the tumor microenvironment of stomach adenocarcinoma by TCGA and GEO datasets

Na renna
General Hospital of Northern Theatre Command
解放军总医院

Object Identification of prognosis-related genes in the tumor microenvironment of stomach adenocarcinoma by TCGA and GEO datasets。
Methods we used gene expression data of STAD avail- able from TCGA and GEO datasets to infer tumor purity using ESTIMATE algorithms, and predicted the associations between tumor purity and clinical features and clinical outcomes. Next, we calculated the differentially expressed genes (DEGs) from the comparisons of immune and stromal scores, and postulated key biological processes and pathways that the DEGs mainly involved in. Then, we analyzed the prognostic values of DEGs in TCGA dataset, and validated the results by GEO dataset. Finally, we used CIBERSORT computational algorithm to estimate the 22 tumor infiltrating immune cells (TIICs) subsets in STAD tissues.
Results stromal and immune scores were significantly correlated with STAD subtypes, clinical stages, Helicobacter polyri infection, and stromal scores could predict the clinical outcomes in STAD patients.We screened 307 common DEGs in TCGA and GSE51105 datasets. In the prognosis analyses, we only found OGN, JAM2, RERG, OLFML2B, and ADAMTS1 genes were significantly associated with overall survival in TCGA and GSE84437 datasets, and these genes were correlated with the fractions of T cells, B cells, macrophages, monocytes, NK cells and DC cells, respectively
Conclusions Our comprehensive analyses for transcriptional data not only improved the understanding of characteristics of TME, but also provided the targets for individual therapy in STAD.

PO-0546

miR-519d-3p/HIF-2α axis increases the chemosensitivity of human cervical cancer cells to cisplatin via inactivation of PI3K/AKT signaling

lixia jiang[1]、SHAOHUA SHI[1]、FENG LI[1]、QIAOFA SHI[2]、TIANYU ZHONG[1]、HUIJUAN ZHANG[1]、YU XIA[1]
1. Department of Laboratory Medicine,First Affiliated Hospital of Gannan Medical University
2. Department of Immunology, Medical College of Nanchang University

Cisplatin (DDP)-based chemotherapy is a standard treatment for cervical cancer, although chemotherapy resis- tance remains a major concern. Hypoxia-inducible factor-2 α (HIF-2α) plays an important role in chemotherapy resistance. MicroRNAs (miRs) can inhibit gene expression by binding to the 3'-untranslated region of the target gene. The authors' previous study showed that miR-519d-3p plays an important role in the regulation of HIF-2α expression under hypoxic conditions in cervical cancer. However, the function and regulatory mechanisms of the miR-519d-3p/HIF-2α axis in DDP-resistance in cervical cancer are not fully understood. Therefore, the aim of the present study was to investigate whether the miR-519d-3p/HIF-2α axis increased DDP resistance by regulating the PI3K/AKT signaling pathway. It was found that the expression of miR-519d-3p was lower in DDP-resistant cervical cancer cells (CaSki/DDP and HeLa/DDP) compared with CaSki and HeLa cells under hypoxic conditions. Additionally, miR-519d-3p overexpres- sion decreased the IC50 value in CaSki/DDP and HeLa/DDP cells, and inhibited

HIF-2α protein expression and the PI3K/AKT signaling pathway under hypoxic conditions. Furthermore, it was demonstrated that HIF-2α overexpres- sion reduced the effect of miR-519d-3p overexpression on HeLa/DDP and CaSki/DDP cells. Moreover, the present results suggested that HIF-2α overexpression increased the IC50 value in CaSki/DDP and HeLa/DDP cells. It was also found that HIF-2α overexpression reduced the effect of miR-519d-3p overexpression on the PI3K/AKT signaling pathway. Therefore, the present results indicated that the miR-519d-3p/HIF-2α axis increased DDP resistance of cervical cancer cells by suppressing the PI3K/AKT signaling pathway under hypoxic conditions.

PO-0547

炎症通过上调前列腺六次跨膜上皮抗原 4 促进肺铜摄取

薛明慧[1]、蔡刚[1]、江岑[1]、聂小蒙[2]、何思炜[1]
1. 上海交通大学医学院附属瑞金医院
2. 第二军医大学附属长海医院

目的 评估炎症对肺部铜代谢的影响，探究调节肺部铜吸收的机制。
方法 收集 19 名 ILD 患者，21 名支气管扩张患者，20 名符合全球哮喘倡议(GINA)指南的重度哮喘患者，22 名 COPD 患者和 24 名健康对照者的痰液，使用原子吸收分光光度计测定痰液中铜离子水平。使用香烟烟雾、脂多糖和硫酸铜构建小鼠慢性肺部炎症模型，对左肺进行 HE 染色分析和组织病理学评价；获取小鼠肺泡灌洗液，离心后涂片染色，进行白细胞分类计数；提取小鼠右肺组织 RNA，通过 RT-PCR 的方法检测 Steap4 基因表达水平；使用过氧化氢/过氧化物酶检测试剂盒检测组织匀浆中的 O2-水平；使用荧光染色的方法评估 DNA 降解水平。培养小鼠来源的原代支气管肺泡上皮细胞，PBS 处理作为对照组，分别给予 IL-17、TNF-α、IL-1、IL6、IL-4、IL-13 刺激。建立 Steap4-/- MLE-12 细胞系，与野生型 MLE-12 细胞分别通过炎症因子刺激后分析胞内铜离子水平，ROS 产生的水平和 TUNEL 染色阳性细胞的比率。
结果 严重哮喘或慢性阻塞性肺病患者的痰液铜离子水平显著高于正常对照组(P＜0.05)。间质性肺病和支气管扩张症患者痰铜水平也有升高，但与健康对照者相比差异无显著性意义(P>0.05)。动物实验中，组织学分析显示 CS/LPS+CuSO4 炎症模型小鼠血管及支气管周围炎性细胞浸润增加；与 CS/LPS 处理的小鼠相比，支气管肺泡灌洗液中细胞水平显著升高（P＜0.05），Cu-CS/LPS 处理的小鼠的中性粒细胞募集显著增加（P＜0.05），但嗜酸性粒细胞募集不明显（P＞0.05）；CS/LPS+CuSO4 处理的小鼠的 ROS 水平明显高于 CS/LPS 处理的小鼠（P＜0.05）；与对照组小鼠肺组织相比，CS/LPS 和 Cu-CS/LPS 组小鼠肺组织中 Steap4 mRNA 表达均显著上调（P＜0.05），且 Cu-CS/LPS 组小鼠肺组织中 Steap4 mRNA 表达高于 CS/LPS 组小鼠，但差异不具统计学意义（P＞0.05）。IL-17 和 TNF-α 可显著诱导 Steap4 在气道上皮细胞中表达，其他细胞因子如 IL-1、IL6、IL-4、IL-13 的诱导作用不明显（P＞0.05）。经炎症因子刺激后，Steap4-/-细胞的 ROS 生成和 TUNEL 染色阳性细胞的比率相较 Steap4+/+细胞明显减少（P＜0.05），胞内铜离子水平在两组之间没有显著差异（P＞0.05）。
结论 STEAP4 在气道上皮细胞的表达可以同时受到炎症因子 IL-17 和 TNF-α 的调控，且铜摄取中具有重要作用。

PO-0548

非痰液标本分离阴沟肠杆菌整合子分布及其耐药情况

朱玉、朱雯雯、王童、魏取好
上海市奉贤区中心医院

目的 了解非痰液阴沟肠杆菌的临床分布和耐药情况，为临床治疗阴沟肠杆菌感染抗菌药物的使用提供参考依据。
方法 收集 63 株 2016-2019 年非重复分离自非痰液标本的阴沟肠杆菌，运用聚合酶链反应（PCR）筛查第 1、2、3 类整合酶基因，对整合酶阳性菌株采用长片段 PCR 扩增整合子可变区，通过测序确定可变区基因盒种类。
结果 63 株分离自非痰液标本的阴沟肠杆菌中，21 株第 1 类整合酶阳性，未检出第 2、3 类整合酶基因。21 株第 1 类整合酶阳性菌株中，有 18 株成功扩增处可变区，其中 7 株可变区是 aadA2， 2 株是 aacA4，2 株是 aac（6’）-II-△ereA2-IS1247-aacA3-arr-△ereA2， dfA15， dfrA17，dfrA17-aadA5，aacA4-blaoxA-10-aacA1，aacA27-△ereA2-IS1247-△ereA2，aacA4，aadB-aadA2 各 1 株。其中基因盒组合 aac（6’）-II-△ereA2-IS1247-aacA3-arr-△ereA2 和 aacA27-△ereA2-IS1247-△ereA2 为阴沟肠杆菌中首次报道。
结论 非痰液标本分离阴沟肠杆菌菌株整合子携带率低于其他肠杆菌科细菌，其可变区耐药基因盒种类多样，首次在阴沟肠杆菌临床分离菌株中发现基因盒组合 aac（6’）-II-△ereA2-IS1247-aacA3-arr-△ereA2 和 aacA27-△ereA2-IS1247-△ereA2。

PO-0549

门诊采血自助排号和条码自动切割一体化方案的建立

王左
四川省肿瘤医院

背景 目前智能化采血系统已广泛应用于各大医院，极大的提高了门诊采血效率，减少了患者等待时间。但部分医院受制于采血场地及布局不易更改等原因，不能运用智能采血系统。故在既有条件下，对采血流程和方案进行优化，以缓解门诊采血负荷，具有现实意义。
目的 本研究设计并运用门诊检验患者采血自助排号和检验条码自动切割一体化方案，从而使患者自助采血排号和条码打印一次性解决。
方法 首先，优化实验室信息管理系统，并整合信息发布与自助机信息平台，实现三大平台智能互联互通。其次，将采血排队号、检验条码及患者回执单集成在一段条码纸上。然后，在条码打印机上安装条码切割机，编写切割程序，并按设计的规则自动触发切割条码。最后，将排队信息放大发布到电子屏幕上，语音播报采血患者。
结果 三大平台智能互联互通，实现了检验医嘱智能判断，排除并提示不符合采血者。集成打印条码，实现了门诊就诊患者刷一次电子就诊卡，就能完成自助采血报道，获取采血排队号、采血条码以及取报告回执单等四个要素。条码按规则自动切割，解决了患者拉拽条码打印机等不能分割条码，而导致的条码打印故障等问题。
结论 门诊采血自助排号和条码打印一体化方法的建立，实现了患者刷一次电子就诊卡完成四个采血要素的目标，优化了采血流程，减少了抽血者甄别医嘱和打印条码的时间，缩短了病人采血窗口处等待时间，提高了工作效率。

PO-0550

提升医学实验中专利技术的产出

谢盼盼
黑龙江金域医学检验实验室有限公司

目的 从事基础检验工作的技术人员，很多只关注自己本岗位职责或是实验相关基本工作，认为实用新型、发明专利距离自己很遥远，从未想过要参与其中。本文旨在帮助从事基层检验工作的人员，挖掘专利点，提升检验人员的创新意识和能力，增加实验室专利成果输出数量和质量。
方法 为了提升实验室员工发现专利点以及撰写专利的能力，采取以下几点措施：1.设置专职/兼职创新管理人员，每月定期统一收集各科室、各岗位实验操作或流程的痛点；2.定期交流，组织员工们对各类痛点进行改进的创新想法碰撞，包括结构类器具或检测方法，创新管理人员可做适当的指导；3.培训书写能力，将创新的想法书写成专利的稿件，此环节可以借助专业的第三方机构或人员的帮助；4.领导带头作用。各小组长/主管等领导身先士卒，带头参与，并带动员工参与。5.奖励制度。为了激励员工参与，设置合理的奖励措施；6.每季度公示发表的专利或获奖名单，营造良好的竞争氛围。
结果 本实验室在 2020 年实现了授权实用新型 11 件，受理发明 2 件（自主发明专利零突破）和实用新型 13 件，以及其他创新性的改进。
结论 通过以上措施的有效执行，加强了实验室的创新氛围，员工参与度从 0 提升至 40%，专利距离大家不再遥远。在输出专利的过程中，大家发现创新、写作能力和创新思维得到提升，输出的创新成果质量更是逐年提升，既提升了员工的综合素质，又提升了公司的知识产权核心竞争力，为公司的建设添砖加瓦。

PO-0551

Labeling and Tracking of Bacteria Outer Membrane Vesicles using an Aggregationinduced Emission Fluorogen

Zihao Ou
Nanfang hospital, Southern medical university

Visualizing the intracellular behaviors and the in vivo distribution of bacteria outer membrane vesicles (OMVs) is of great value to obtain knowledge about their roles in cross-species information communication between bacteria and their host, but ideal probes are currently lacking. In this work, an aggregation-induced emission (AIE) fluorogen, namely DPASP, was reported for OMV labeling and tracking with excellent performance. DPASP exhibits low background in aqueous solution, high affinity and strongly fluorescent response to OMVs, enabling it to achieve OMV labeling with high signal-to-noise ratio as well as superior labeling efficiency. Importantly, the excellent photostability of DPASP allows the intracellular movements of OMVs to be continuously visualized in real-time. Moreover, its capability of mapping the in vivo distribution of OMVs is also successfully demonstrated. All these advantages make DPASP a useful tool for studying behaviors and functions of bacteria OMVs in many physiological and pathological processes of human bodies

PO-0552

基于生物信息学方法构建类风湿性关节炎 miRNA-mRNA 调控网络

曹维维、袁成良
德阳市人民医院

目的 基于生物信息学方法构建类风湿性关节炎核心 miRNA-mRNA 调控网络并筛选相关核心基因，探索其在类风湿性关节炎疾病中的分子调控机制。
方法 从 GEO 数据库下载 miRNA 和 mRNA 基因表达谱芯片 GSE72564 和 GSE55235。采用 GEO2R 分析工具筛选差异表达的 miRNA 和 mRNA，应用 miRNet 在线数据库分析预测 miRNA 差异表达的靶基因并与 mRNA 数据集筛选出的差异基因进行交叉匹配，获得 miRNA-mRNA 相互作用关系对。使用 ClusterProfiler 包对 miRNA-mRNA 的差异基因进行 GO 和 KEGG 分析。应用 Cytoscape 软件绘制 miRNA-mRNA 调节网络图。
结果 共筛选出差异 miRNA23 个。筛选到差异基因 1038 个。交叉匹配后获得 143 个差异基因，GO 注释分析表明其主要位于细胞外基质等部位，参与细胞对氧含量降低的反应、细胞生长调节等生物过程。KEGG 分析表明其主要富集与 PI3K-AKT 等信号通路。成功构建 miRNA-mRNA 调控网络，筛选出 8 个 DE-miRNA,其中 hsa-mir-218-5p、has-mir-30c-3p、hsa-mir-1305、hsa-mir-708-5p 表达下调，而 hsa-mir-496、hsa-mir-346、hsa-mir-2276-3p、hsa-mir-4263 表达为上调，。KLHL21、HSPG2 等关键基因在互作网络中发挥重要作用。
结论 通过数据挖掘和芯片分析方法成功构建类风湿关节炎 miRNA-mRNA 调控网络，为进一步研究 RA 发生和发展的分子机制提供了有价值的线索。

PO-0553

实验室检验数据实时监控

白岩
吉林大学第一医院

建立完整的检验信息系统，构建高效的数据统计平台，实时显示是检验质量实时监控的条件；提升医院检验的科学管理效能，是提高医疗质量实时监控的目的。检验系统质量控制实时监控的应用：医疗基本统计信息；建立质控平台，加强检验的科学管理；完善检验质量实时监控，建立医疗检验质量指标警示系统。实时监控的方式是监控检验效果的决定因素。检验质量管理是医院的核心和精髓，

PO-0554

LINC00665/miR-9-5p/ATF1 信号通路在结直肠癌中的调控作用

赵旭鸿[1]、翁文浩[1]、龙吟[1]、潘伟洁[1]、李智[1]、孙奋勇[2]
1. 上海市杨浦区中心医院（同济大学附属杨浦医院）
2. 上海市第十人民医院（同济大学附属第十人民医院）

目的 了解长非编码 RNA00665（LINC00665）在结肠直肠癌(CRC)及其调控机制中的作用。
方法 采用实时聚合酶链反应(RT-PCR)来检测 LINC00665、miR-9-5p 和激活转录因子 1(ATF1) mRNA 在 CRC 组织中的表达。同时，采用免疫组织化学和免疫印迹试验（Western blot）对 CRC 组织中 ATF1 的表达进行检测。并采用 CCK-8 和菌落形成试验检测细胞增殖、流式细胞术检测分

析细胞周期和细胞凋亡、划痕愈合实验和 Transwell 实验检测细胞迁移和侵袭、双荧光素酶报告基因分析进行验证 LINC00665 与 miR-9-5p、miR-9-5p 和 ATF1 的靶向关系。
结果 LINC00665 在结直肠癌组织中显著过表达，并与 miR-9-5p 的表达呈负相关、与 ATF1 的表达呈正相关。LINC00665 通过分泌 miR-9-5p 促进结直肠癌细胞的增殖、迁移和侵袭，并抑制细胞凋亡。ATF1 被证实是 miR-9-5p 的下游靶点，并受 LINC00665 间接调控。
结论 LINC00665 通过调节 miR-9-5p/ATF1 轴参与了结直肠癌的进展。

PO-0555

白藜芦醇改善高糖诱导肾脏细胞损伤的作用机制研究

王琳
天津医科大学

目的 糖尿病肾病（diabetic nephropathy，DN）是以渐进性肾功能损伤为特征的一种微血管病性合并症。与单纯糖尿病相比，其死亡风险高 3–12 倍。新近研究表明炎症反应以及肾脏细胞发生的程序性死亡（programmed cell death，PCD）是 DN 进展的主要原因之一。我们前期研究发现在 DN 中，Gasdermin E（GSDME）可介导肾脏细胞发生焦亡。白藜芦醇（resveratrol，RSV）作为一种天然多酚类物质可降低多种疾病中的炎症反应，但其在 DN 中的作用机制尚不明确。因此，我们进一步探究白藜芦醇（RSV）对体外高糖刺激引起肾脏细胞损伤的潜在分子保护机制。
方法 取处于对数生长期的 RGMCs、HK2，分为甘露醇高渗透压对照组（OC）、正常对照组（NG）、高糖组（HG）以及高糖 RSV 处理组，分别处理 24、48h。LDH 试剂盒检测不同时间各组细胞上清液中 LDH 的水平；Western blot 检测不同时间各组凋亡相关蛋白 Bcl-2、Bax、caspase-1、p20（caspase-1 活性片段）、GSDME（Gasdermin E）、GSDME-N（GSDME 活性片段）、caspase-3、p17（caspase-3 活性片段）、炎性因子 IL-1β 及其活化形式 mIL-1β 的表达；ELISA 检测不同时间各组细胞培养上清 IL-1β 的水平。
结果 LDH 结果显示 RSV 可降低高糖刺激 48h 后细胞的死亡率。Western blot 结果显示 RSV 处理 24h 后，Bax 表达较 HG 组显著降低，同时伴随 Bcl-2 表达升高；RSV 处理 24h 后 HG 组 p20、mIL-1β 表达降低； RSV 处理 48h 后 p17、GSDME-N 的表达较 HG 组明显下降，同时 ELISA 结果显示，RSV 处理 48h 后 HG 组 IL-1β 的释放率显著降低。
结论 RSV 通过抑制高糖刺激引起的早期凋亡以及晚期 GSDME 介导的细胞焦亡，并减少炎症因子的产生来改善高糖引起的肾脏细胞损伤。

PO-0556

The association between chronic obstructive pulmonary disease and dietary inflammatory index

Haiyue Liu[1,2]、Xiaobo Ma[1,2]、Yanqing Zheng[1,2]、Bo Zhu[1,2]、Gangsen Zheng[1,2]、Lili Fang[1,2]、Guolin Hong[1,2]
1. 厦门大学附属第一医院检验科
2. 厦门市基因检测重点实验室

Background Chronic obstructive pulmonary disease (COPD) is characterized as an inflammatory disease with irreversible and progressive airflow limitation and has become a major public health problem throughout the world due to its high morbidity and mortality. The role of dietary in inflammatory lung diseases is depicted in previous studies. Nevertheless, little is known about diet-related inflammation in COPD. In this study, we aimed to explore the association between COPD and dietary inflammatory index (DII) scores in adults over 40-year-old.
Methods Data were obtained from the 2013-2018 National Health and Nutrition Examination Survey (NHANES). In the present study, 9929 participants were included and analyzed. The DII

score was calculated and divided into tertiles. Logistic regression analysis was performed to determine the odds ratios of DII tertiles.
Results Participants were categorized into COPD (565, 5.69%) and non-COPD groups (9364, 94.31%) according to interview information. COPD individuals had higher DII scores than non-COPD individuals (0.429 ± 1.809 vs. -0.191 ± 1.791, $p < 0.001$). The highest DII score tertile included 46.55% of COPD individuals and was associated with lower family incomes and education and a higher smoking rate ($p < 0.01$). The odds ratios (95% CIs) of COPD according to logistic regression were 0.709 (0.512-0.982) for T1 and 0.645 (0.475-0.877) for T2 of the DII score ($p = 0.011$).
Conclusion Higher DII scores were positively correlated with COPD in participants over 40 years old. These results further support that diet can be used as an intervention strategy for COPD management.

PO-0557

通过体外培养探索中药单体苦参碱对肠道菌群的影响

刘海月[1,2]、马晓波[1,2]、郑燕青[1,2]、朱波[1,2]、郑港森[1,2]、房丽丽[1,2]、洪国焌[1,2]
1. 厦门大学附属第一医院检验科
2. 厦门市基因检测重点实验室

背景与目的 中药的治病机理复杂，较难用现代科学的理论解释。近年来的研究表明，中药可能对肠道菌群肠道产生影响，进而发挥治病作用。肠道菌群被认为是人类的第二基因库。肠道菌群的紊乱会导致多种疾病的发生与，包括了肥胖、糖尿病、冠心病、高血压、自闭症、抑郁以及炎症性肠病等等。诸多的研究已经表明通过粪菌移植的方式能够通过改善肠道菌群而达到治疗疾病的作用。葛根素又被成为葛黄素，它是从中药葛根中分离提存的一种异黄酮衍生物，既往的研究认为它具有治疗冠心病、扩张冠状动脉的作用。近年来的研究表明心脑血管疾病与肠道菌群密切相关，因此，葛根素也有可能通过影响肠道菌群来发挥作用。本研究拟通过体外培养结合 16S 测序的方法，探索葛根素对肠道微生物的影响。
方法与结果 搜集心脑血管疾病患者粪便标本共 9 例。进而配置培养液，其中培养液包括 PBS 培养液以及富营养培养液，根据是否添加苦参碱（10mg 配置于 500mL 培养液中）分为 4 组，分别是 PBS 组、富营养培养液组、PBS+苦参碱组、富营养培养液+苦参碱组。每一份样品取 1g 粪便，并加入 9ml 生理盐水稀释，取 10ul 粪便稀释液，接种到含有 200ul 培养液的 96 孔板中进行厌氧培养，体外培养 24 小时。通过吸取培养孔中的培养液，分离培养液中的 16S rRNA，进而通过测血的方法，探索不同培养物对粪便菌群的影响。结果发现：通过分析菌群多样性以及 LEfSe 分析发现，苦参碱能够体外抑制条件致病菌 Hydrogenorobacterium 以及 Alcaligenaceae 的生长，并增加肠道中产丁酸盐的益生菌种类的相对丰度。
结论 苦参碱有可能通过影响肠道菌群中的 Hydrogenorobacterium 以及 Alcaligenaceae 来发挥药理作用。

PO-0558

临床分离非痰液标本中鲍曼不动杆菌整合子的分布与耐药性分析

王童、朱玉、朱雯雯、魏取好
上海市奉贤区中心医院

目的 整合子在细菌耐药性产生和播散中起着重要的作用，本研究旨在了解临床分离自非痰液标本中鲍曼不动杆菌中整合子的分布。

方法 收集 2016 年 1 月至 2019 年 12 月非重复分离自就诊患者非痰液标本的中鲍曼不动杆菌，采用 Phoenix 100 全自动微生物分析仪进行细菌鉴定和药物敏感性试验，PCR 筛查第 1、2 类整合酶基因，整合酶基因阳性菌株通过长片段 PCR 扩增整合子可变区，通过测序确定可变区基因盒种类。
结果 76 株非重复分离自就诊患者非痰液标本的中鲍曼不动杆菌中，有 10 株（13.2%）检测到第 1 类整合酶基因，未检出第 2 类整合酶基因。第 1 类整合酶阳性菌株可变区耐药基因盒有 aacA4(7 株)、catB8（7 株）、aadA1（7 株）、dfrA17（3 株）、aadA5（3 株）。其中 aacA4、aadA1、aadA5 赋予宿主细菌对氨基糖苷类抗菌药物耐药，catB8 赋予宿主细菌对氯霉素类抗菌药物耐药，dfrA17 赋予宿主细菌对甲氧苄啶耐药。与第 1 类整合酶阴性菌株相比，第 1 类整合酶阳性菌株对？？、？？抗菌药物的耐药率较高，差别具有统计学意义（P＜0.05）。【如果耐药率没有差别，则写：第 1 类整合酶阴性和阳性菌株对临床常用抗菌药物的耐药率之间的差别无统计学意义，（P＞0.05）】
结论 第 1 类整合子在非痰液鲍曼不动杆菌中的检出率低于肠杆菌科细菌，携带 1 类整合子的菌株对？？抗菌药物具有较高的耐药率。【整合子中耐药基因盒对鲍曼不动杆菌耐药性贡献有限。】

PO-0559

核苷（核苷酸）类似物抗病毒治疗对 PIVKA-II 在慢性乙肝相关肝细胞癌诊断应用中的影响

杨紫伟、吕萍
中国医科大学附属第一医院

目的 探讨核苷（核苷酸）类似物抗病毒治疗对血清 PIVKA-II 在慢性乙肝相关肝细胞癌诊断应用中的影响。
方法 收集 65 例慢性乙型肝炎、63 例慢性乙肝肝硬化和 81 例慢性乙型肝炎相关肝细胞癌患者，根据是否接受过抗病毒治疗将患者分为治疗组和未治疗组。采用 SPSS22.0 统计软件进行非参数 Mann-Whitney U 检验、卡方检验、受试者工作曲线分析及 logistic 回归分析。
结果 经过抗病毒治疗的肝细胞癌患者 PIVKA-II 中位水平明显低于未治疗患者（27.13ng/mLvs739.87ng/mL,P=0.001）。ROC 曲线分析结果显示，经过抗病毒治疗的患者肝细胞癌最佳诊断阈值为 13.20ng/mL（<40.0ng/ml）。当以 13.20ng/mL 作为诊断肝细胞癌临界值时，可以有效提高肝细胞癌诊断灵敏度，降低漏诊率。
结论 核苷（核苷酸）类似物抗病毒治疗会降低患者血清 PIVKA-II 水平，在应用 PIVKA-II 进行慢性乙肝相关肝细胞癌诊断时，应考虑抗病毒治疗对 PIVKA-II 水平的影响，可降低 PIVKA-II 的诊断阈值。

PO-0560

MiRNAs 作为乳腺癌潜在预后生物标志物构建及评估

张开炯
四川省肿瘤医院（四川省第二人民医院四川省癌症防治中心）

目的 基于 TCGA 数据库筛选乳腺癌预后相关的 miRNAs 生物标记物。
方法 首先，从癌症基因组图谱（TCGA）数据库中获得乳腺癌 miRNAs 表达和临床数据，分析 miRNAs 在乳腺癌组织和正常组织差异表达情况。其次，将所有乳腺癌肿瘤样本随机分为训练集和验证集，对差异表达明显的 miRNAs 采用单因素 Cox 分析和最小绝对收缩和选择算子（LASSO）Cox 回归分析筛选预后相关性，对 LASSO 回归分析有意义的 miRNAs 进行逐步多因素 Cox 回归分析，建立预后风险评估模型，并采用受试者工作特征曲线（ROC）评估模型 1、3、5 年预测能力。再次，将训练组构建的风险模型纳入验证组进行验证，以明确所构建风险预后模型的可靠性。

结果 与正常组织相比，乳腺癌组织中 269 个 miRNAs 存在明显差异表达（FDR<0.05，fold change>2），其中 204 个 miRNAs 表达上调，65 个 miRNAs 表达下调。在训练集中采用单因素 Cox 分析和 LASSO 回归分析，发现 18 个差异表达的 miRNAs 与乳腺癌预后不良相关。对 18 个 miRNAs 采用逐步多因素 Cox 回归分析，筛选出 8 个 miRNAs 组合（hsa-mir-3923、hsa-mir-105-2、hsa-mir-3927、hsa-mir-449c、hsa-mir-106a、hsa-mir-1262、hsa-mir-605 和 hsa-mir-3929）用于乳腺癌不良预后模型构建。在训练集和验证集中，发现该风险模型可明显区分乳腺癌高危组和低危组（p 均<0.01），且该模型具有良好的预后和预测准确性。
结论 筛选的 8 个 miRNAs 组合的评分模型可作为预测乳腺癌不良预后的生物标记物。

PO-0561

耐吡咯类药物白色念珠菌 ERG3、ERG5 与 ERG11 基因突变研究

李倩珺
广州医科大学附属第一医院

目的 研究耐吡咯类药物白色念珠菌的 ERG11、ERG3 与 ERG5 基因的突变与其耐药性关系。
方法 收集 417 株临床镜检有真菌的阴道分泌物标本进行真菌培养，筛选白色念珠菌，进行微量肉汤稀释法得到氟康唑、酮康唑、克霉唑、硝酸咪康唑四种药物对白色念珠菌的敏感性和 MIC 值。根据 CLSI-M27 文件药敏试验标准，筛选出耐药的白色念珠菌。提取 DNA，扩增 ERG11、ERG3 与 ERG5 基因，扩增后的 PCR 产物进行双向测序，将测序结果与 GenBank 中的标准序列（SC5314）和 GenBank 序列号：AF069752 比较分析。
结果 氟康唑对白色念珠菌耐药率为 9.05%。酮康唑的抑菌率总体比克霉唑、硝酸咪康唑强。ERG11 突变检测中发现 18 种错义突变，其中 G465S、M527I 未见报道。ERG3 发现 17 种错义突变。ERG5 发现 12 种错义突变。
结论 在广州医科大学附属第一医院外阴阴道念珠菌病患者中，白色念珠菌仍为主要病原体，光滑念珠菌的比例上升。耐吡咯类药物白色念珠菌 ERG11、ERG3、ERG5 基因出现若干错义突变位点，其中某些位点突变导致的氨基酸变异可能与其耐药性产生有关。

PO-0562

Laparoscopic liver resection for hepatocellular carcinoma complicated with significant portal hypertension: a propensity score-matched survival analysis

Yuan Hong
The First Affiliated Hospital of Kunming Medical University

Background Significant portal hypertension (SPH) is a relative contraindication for patients with resectable hepatocellular carcinoma (HCC). However, increasing evidence indicates that hepatic resection is feasible for patients with HCC and SPH.
Methods HCC patients with cirrhosis who underwent laparoscopic liver resection (LLR) across two centers from April 2013 to April 2018 were included. Surgical and survival outcomes were analyzed to explore potential prognostic factors. Propensity score-matched analysis was performed to minimize bias.
Results A total of 151 patients were divided into two groups based on the presence (SPH, n=68) or absence (non-SPH, n=83) of SPH. Patients in the SPH group were associated with a longer operation time, more blood loss, and later TNM stage (P<0.05) than patients in the non-SPH group. However, there were no significant differences noted in the postoperative 90-day

mortality rate (n=0), overall postoperative complications (P=0.785), Clavien-Dindo classification (P=0.105), conversion to open surgery (P=0.504), or length of hospitalization (P=0.379). The same results were obtained after a propensity score-matched analysis. The 1-, 3-, and 5-year overall survival (OS) and recurrence-free survival rates in the SPH group were 77.9%, 40.6%, 31,8%, 64.3%, 41.0%, and 20.5%, respectively, and those in the non-SPH group were 90.4%, 54.3%, and 38.3% and 87.9%, 52.8%, and 24.2%, respectively (log-rank P>0.05). Alpha-fetoprotein>400 μg/L [hazard ratio (HR): 5.24, 95% confidence interval (CI): 2.89-9.49], ascites (HR: 2.69, 95% CI: 1.53-4.71), American Society of Anesthesiologists (ASA) (III vs. II) (HR: 2.78, 95% CI: 1.44-5.36) and tumor diameter>5 cm (HR: 2.99, 95% CI: 1.40-6.38) independently predicted worse OS.
Conclusions LLR for patients with HCC complicated with SPH appears feasible at the price of increasing operation time and blood loss. Alpha-fetoprotein, ascites, ASA, and tumor diameter may predict the prognosis of HCC complicated with SPH after LLR. Prospective trials with a larger sample size are necessary to confirm these results.

PO-0563

AP1M2 对恶性肿瘤的系统分析：泛癌分析

伊远学、徐建、申友锋、高悦益
重庆精准医疗研究院

目的 为了筛选新的肿瘤标志基因，用于肿瘤的早期筛查，我们通过比对 GTEx、CCLE、TCGA 数据库中多个肿瘤中差异表达基因情况。发现 AP1M2 在乳腺浸润癌中显著差异表达，因此本研究对 AP1M2 基因与患者的生存率、免疫浸润、肿瘤新抗原等的关联性进行泛癌分析。
方法 我们使用 GTEx、CCLE、TCGA 泛癌数据库分析了 AP1M2 基因表达在肿瘤组织及其对照正常组织的分布。使用卡普兰-迈耶生存率图和 COX 回归分析来评估 AP1M2 对肿瘤患者临床预后的影响。然后我们研究了不同类型肿瘤中 AP1M2 表达与免疫浸润水平的相关性。此外，我们还研究了 AP1M2 与肿瘤免疫新抗原、微卫星不稳定性、DNA 修复基因、DNA 甲基转移酶之间的相关性，分析了各种肿瘤中 AP1M2 基因突变的频率。使用 GSEA 富集分析方法对不同类型的肿瘤进行了功能富集分析。
结果 AP1M2 在大多数癌症中高度表达，其表达水平和肿瘤患者的预后之间存在明显的联系。在 AP1M2 对肿瘤患者临床预后和免疫浸润影响的研究中，我们发现 AP1M2 在乳腺浸润癌中的表达与患者总生存率和巨噬细胞和树突细胞、CD4+T 细胞、CD8+T 细胞以及 B 细胞的浸润水平显著相关。同时乳腺浸润癌中 AP1M2 表达与肿瘤免疫新抗原和微卫星不稳定性呈显著相关 。GSEA 分析是为了确定 AP1M2 对肿瘤的影响，结果表明在多数肿瘤中的 ACE2 的表达水平影响了肿瘤相关的途径和免疫相关的途径的激活。
结论 这些发现表明，AP1M2 的表达水平与大多数癌症类型的预后与免疫浸润水平显著相关，包括 CD8+T 细胞、CD4+T 细胞、巨噬细胞、中性粒细胞和树突细胞，特别是乳腺癌患者。这些发现表明，AP1M2 可能会影响乳腺浸润癌患者的肿瘤环境，很有可能作为乳腺浸润癌的早期筛查甚至治疗靶点，有助于提高乳腺浸润癌早期筛查效率和患者的总体生存率。

PO-0564

A Nomogram Based on Clinicopathological Characteristics for Predicting the Risk of Lymph Node Metastasis in Small Size Non-small Cell Lung Cancer

Yuan Hong、Yong Duan
The First Affiliated Hospital of Kunming Medical University

Background Accurate lymph node metastasis (LNM) prediction is critical for therapeutic decision-making and prognostic evaluation, particularly in small-size non-small lung cancer (NSCLC) patients. The purpose of this study was to design and evaluate a nomogram for the dynamic preoperative prediction of LNM in patients with small-size NSCLC.
Method The primary size ≤ 2 cm NSCLC patients were selected from the Surveillance, Epidemiology, and End Results (SEER) database from 2010–2015 and randomly divided into a training cohort and an internal validation cohort according to the ratio of 7:3. External validation was performed using data from Kunming Medical University's First Affiliated Hospital. Seven variables were screened by Lasso-logistic regression analysis on the training cohort as potential predictors. The nomogram was developed based on these predictors and was validated by both the internal and external cohorts. As a result, evaluate the performance of the model through calibration curve, C-index, the area under the receiver operating characteristic curve (AUC), and decision curve analysis (DCA).
Results A total of 8,614 patients were included in the study, of whom 13% (1,112/8,614) were confirmed with positive LNM. Age, pathological grade, laterality, histology, T-status, size and pleural invasion were determined as independent predictors and used to plot a nomogram. The C-index was 0.717 and model's AUC was 0.717 (95% CI: 0.677-0.648). The model was further validated in the internal and external cohorts with AUC 0.680 (95% CI: 0.418-0.859) and 0.732 (95% CI: 0.753-0.727) and provided excellent calibration. We also conducted a DCA, which showed that our nomogram adds more net benefits than the treat-none and treat-all lines in the decision curve.

PO-0565

METTL3 介导的 CYP2B6 基因 m6A 甲基化修饰位点研究

逯素梅[1]、李永清[2]、张丹彤[1]、马万山[1,2]
1. 山东第一医科大学第一附属医院(山东省千佛山医院)
2. 山东大学附属千佛山医院

实验目的 RNA 序列不变的情况下，在 RNA 上进行化学修饰调控 RNA 的分子功能，进而调控生命发生发展的一系列研究被称为表观转录组学。其中 N6-methyladenosine (m6A)修饰是目前认为的真核生物中信使 RNA(mRNAs)、长链非编码 RNA (LncRNA)和微小 RNA (miRNAs)上最普遍的修饰。课题组前期研究发现，高脂饮食诱导下，肝组织 CYP2B6 基因 m6A 甲基化修饰水平显著升高，且受 METTL3 调控。本研究旨在明确 m6A 甲基化转移酶 METTL3 介导下的 CYP2B6 基因 m6A 甲基化修饰位点。
实验方法 培养人正常肝细胞 LO2，借助小干扰 RNA（siRNA）或者慢病毒载体进行甲基化酶 METTL3 的干扰表达或者过表达实验。设计多个不同的 CYP2B6 m6A 甲基化位点特异性引物，提取 RNA 后进行 MeRIP-qPCR 实验。
实验结果 小干扰 RNA 干扰 METTL3 的效果（对照组=1.0, METTL3-/- 组=0.22±0.048, P<0.05）与慢病毒感染过表达 METTL3 的效果(对照组=1.0, METTL3+/+ 组=29.36±5.84, P<0.05）显著。在干扰 METTL3 实验中(METTL3-/-)，位点 66 bp 处对照组 input%=3.494±1.081，METTL3-/- 组 input%=1.490±0.562，m6A 修饰水平下降显著(P<0.05）；位点 1291/1391/1561/1601 bp 的对照

组 input%=6.986±1.384，METTL3-/-组 input%=3.203±0.845，m6A 修饰水平下降显著(P<0.05）；而基因位点 425 bp, 812 bp 处修饰水平无明显差异(P>0.05）。同样，在过表达 METTL3 实验中(METTL3+/+)，位点 66 bp 的对照组 input%=4.389±1.532, METTL3+/+组 input%=8.962±2.064 (P<0.05); 位点 1291/1391/1561/1601 bp 的对照组 input%=11.344±3.673, METTL3+/+ 组 input%=24.486±6.382 (P<0.05），而基因位点 425 bp, 812 bp 处变化不明显(P>0.05）。
实验结论 METTL3 介导的 CYP2B6 基因 m6A 甲基化修饰位点主要发生在 5'-UTR 的 66bp 和 3'-UTR 的 1291/1391/1561/1601 bp 处。

PO-0566

Detecion of peripheral basophils in adult-onset minimal change disease

Qingjun PAN、Huanqin Han、Shuzhen Liao、Hua-feng Liu
Affiliated Hospital of Guangdong Medical University

Nowadays, the pathogenesis of minimal change disease (MCD) is still not well-known, and the current understanding on MCD is mainly based on data derived from children, and very few adults. Here, we comprehensively analysed the correlation between the changes of peripheral basophils and the incidence rate and relapse of adult-onset MCD. The results showed that in patients at the onset of MCD, the ratio and activation of basophils were all higher than those of healthy controls (all P < .05). In vitro test results showed that basophils from healthy controls can be activated by the serum taken from patients with MCD. Among 62 patients at the onset of MCD, with complete remission after treatment and 1 year of follow-up, the relative and absolute basophil counts before treatment were higher in the long-term remission group (n = 33) than that of the relapse group (n = 29). The basophil counts were significantly higher in the infrequent relapse group (n = 13) than that of the frequent relapse group (n = 16; P < .05). These findings suggested that basophil may play a pathogenic role in adult-onset MCD, and the increased number and activation of peripheral basophils could predict recurrence in adult MCD.

PO-0567

Detection of IgG4 Autoantibodies in Systemic Lupus Erythematosus Patients

Qingjun PAN、Lei Shi、Jun Cai、Yiming He、Hua-feng Liu
Affiliated Hospital of Guangdong Medical University

Pathogenic autoantibodies can cause inflammation and tissue injury in systemic lupus erythematosus (SLE). Although IgG4 is considered non-inflammatory owing to the unique structure of its hinge region, the role of IgG4 autoantibodies in SLE remains largely unknown. The titers of serum anti-nuclear-IgG antibodies (ANA-IgG) and anti-nuclear-IgG4 antibodies (ANA-IgG4) in newly diagnosed SLE patients were detected. The effects of IgG4 purified from SLE patients (SLE IgG4) and healthy controls on complement consumption and inflammatory cytokine production were evaluated in vitro. The therapeutic effects of mouse IgG1 (functionally resembles human IgG4) purified from lupus-prone MRL-lpr/lpr mice (lupus IgG1) and control mice on disease progression were examined in MRL-lpr/lpr mice. The results showed that SLE patients with equal titers of total serum ANA-IgG (1:3,200) were divided into group I with lower ANA-IgG4 titers (≤ 1:10) and group II with higher ANA-IgG4 titers (≥ 1:100), and disease activity, inflammatory cytokine production, complement consumption, and renal-function parameters in group I SLE patients were more severe than those in group II. Further, compared with control IgG4, SLE IgG4 inhibited complement consumption by autoantibody-autoantigen immune

complexes, and also inhibited inflammatory cytokines production by SLE PBMCs in vitro. Moreover, compared with control IgG1, lupus IgG1 exhibited a therapeutic effect on lupus by attenuating disease progression in MRL-lpr/lpr mice. These findings, for the first time, suggest that IgG4 autoantibodies can attenuate SLE progression by suppressing complement consumption and inflammatory cytokine production. Hence, this study may provide novel therapeutic strategies against SLE and other autoimmune diseases.

PO-0568

衰老机体内炎性因子的变化及二甲双胍抗衰老机制研究

张丽霞
山西医科大学第二医院

目的 本课题拟研究老年人体内促炎因子肿瘤坏死因子-α（Tumor Necrosis Factor α, TNF-α）以及抗炎因子白介素-10（Interleukin-10, IL-10）与机体衰老之间的潜在关联，并建立老年小鼠模型进一步验证 TNF-α 及 IL-10 与衰老过程中肝损伤之间的病理生理关系，通过给予衰老小鼠补充二甲双胍（Metformin, Met），探究 Met 是否可以通过调控炎性因子的变化对衰老过程中肝损伤发挥一定的保护作用。
方法 实验一：招募 2017 年 1 月至 6 月在山西医科大学第二医院健康查体的人员共 62 名，其中年龄在 20-35 岁的青年人与年龄在 60-75 岁的老年人各 31 名。收集两组人群基本信息包括年龄、性别、身高、体重，测量空腹血糖、血压，酶联免疫吸附实验检测两组人群血清中 TNF-α 以及 IL-10 的含量；实验二：3 组雌性昆明小鼠分别为：对照组（Control 组，月龄=2 月）、老年组（Aging 组，月龄=20 月）、二甲双胍治疗组（Aging+Met 组，16 月龄开始补充二甲双胍，连续给药 16 周），每组各 8 只。检测小鼠体重及肝脏重量计算肝脏系数；HE 染色观察肝细胞病理损伤；β 半乳糖苷酶染色观察肝细胞衰老程度；免疫组织化学法以及 Western blot 测肝脏中 TNF-α、IL-10 的含量；生化定量法检测肝脏谷胱甘肽（glutathione, GSH）及丙二醛（malondialdehyde, MDA）含量。
结果 临床研究发现，与青年组相比，老年人群体质指数、平均动脉压以及空腹血糖含量升高，血清中 TNF-α 水平升高，IL-10 水平降低，差异具有统计学意义（$P<0.05$）；动物实验中发现，与对照组相比，衰老小鼠肝系数显著下降；肝细胞胞浆疏松，局部炎性细胞浸润明显；SA-β-Gal 表达量增高；肝脏中 TNF-α 水平升高而 IL-10 水平下降；GSH 水平降低，MDA 水平升高。与衰老组相比，补充 Met 可抑制肝脏萎缩；肝细胞胞浆丰富，细胞排列趋近整齐；SA-β-Gal 表达量降低；肝组织内 TNF-α 水平降低而 IL-10 水平升高；肝脏中抗氧化物酶 GSH 含量升高，MDA 水平降低。
结论 结合临床研究和动物实验，本课题揭示了老年机体内存在促炎因子 TNF-α 表达的上调以及抗炎因子 IL-10 表达的下调，这种促-抗炎性细胞因子的失衡可能是引起机体炎性老化的关键；外源性给予二甲双胍可通过调控炎性因子的改变，重塑促-抗炎细胞因子的平衡，减轻氧化应激引起的损伤，从而达到干预衰老的目的。

PO-0569

6σ 质量管理规则在内分泌项目的质量策略优化中的应用

翟媛媛、马瑾、贺娇
西安市第十医院西安市精神卫生中心

目的 根据两种不同的总允许误差标准(TEa)确定不同的西格玛值，绘制性能验证图并分析质量目标指数（QCI），改进我院内分泌项目的质量控制策略。
方法 分别以我国卫生部临检中心室间质量评价标准和生物学变异的“最适”标准的总允许误差（TEa）为性能规范目标，以 2020 年半年间我院在新产业生物 MAGLUMI-2000PLUS 和采用迈瑞 CL6000i

化学发光免疫分析仪上测定的 11 个内分泌项目的累积在控室内质控是数据计算不精密度（CV），以 2020 年第一次卫生部临检中心室间质评偏倚数据的加权均值为偏倚（Bias）来源，计算 σ 值，应用标准化西格玛性能验证图选择合适的质量控制规则，并计算各项目的质量目标值指数（QGI），分析项目性能不佳的原因，提出优化方法。
结果 按照 NCCL 的标准，11 个内分泌项目中 3σ 以下的项目占比为 9.09%；按照生物学变异标准，10 个内分泌项目 3σ 以下的项目占比 50%；加权合成 σ 总后，3σ 以下的项目没有变化；按照 NCCL 的标准，针对不同的 σ 值选择不同的质控策略。其中，FT4、TT4、TSH、P、T 需改进精密度，FT3、TT3 需改进精密度和正确度。
结论 精神专科医院可以综合应用合适的 6σ 质量规范，科学的评价内分泌项目的性能指标，优化质控策略，保证检测项目的质量水平。

PO-0570

武汉火神山医院应急检验保障体系的建设与思考

夏欣一
中国人民解放军东部战区总医院

新型冠状病毒流行期间，检验科在诊断、疗效评估、预后判断等环节上发挥了重要作用。通过分析火神山医院应急检验保障体系的建设经验，为突发疫情下新建传染病医院的应急检验保障体系的建设提供思路和参考。1.选址设计：远离人流、工作流密集交叉的独立区域。实验室内部三区两通道模式设计，兼顾人流、物流、标本流及医疗垃圾运送通道。设施区域间的压力梯度，保证空气由洁净区流向污染区；2. 组织体系建设：建立感控小组，明确主任为科室感控工作的第一责任人，建立联络员制度，确保感控工作的上传下达和制度的末端落实；3.实验室管理：建立应急状态下严格执行的检验科质量管理体系、检验危急值报告制度、核酸标本采集转运流程等规范性文件，明确划分清洁区、半污染区、污染区，中间设置缓冲区，工作人员均实行 3 级防护，全程建立常态化感控培训机制；4.工作流程：火神山医院检验科迅速完成仪器设备安装调试、人员培训、信息系统建设。后续检验项目分阶段逐步展开，一期开展血细胞分析、临床生化、免疫学，输血相关检验，二期开展核酸、微生物免疫学、细胞因子、流式细胞分析，三期开展抗体分型、定量及多种病原核酸检测。5.临床保障：检验团队 3 天内展开 9 大项 208 个基础检验项目，9 天内拓展至 35 大项近 500 小项，累计检测各种临床标本 5 万余件。全程“零暴露”“零感染”。讨论与思考：1.应急体系的建设是必要手段：建立一套科学先进的应急体系，系统规范管理突发卫生事件，提升应急工作效率和质量；2.分阶段重点建设是关键：早期工作保障临床急需项目，后续针对临床诊治提出的新需求，积极拓展；3.优化人员配置是核心：遵循“平战结合”的战略原则，平时应加强人员的培训和演练，建立应急梯队；4.生物安全是底线：建立健全相关管理制度，严格规范操作。

PO-0571

IFN 诱导 AML 细胞 SARI 表达及其作用水平和 STAT1 通路的探讨

江贤栋、刘书涵、陈巧倩、郑志远
福建医科大学

目的 1 分析 IFN 对 AML 细胞株 SARI mRNA 和蛋白的表达变化情。 2 探讨 IFN 诱导的 SARI 基因对 AML 细胞生物学活性的影响。3 探讨 IFN 诱导 AML 细胞 SARI 表达是否激活 STAT1 通路。
方法 1 采用 RT-PCR 和 qPCR 筛选 SARI mRNA 中、低表达的 HL60 和 NB4 细胞作为实验细胞株；在不同时间选取不同浓度的 IFN-β/γ 处理 HL60 和 NB4 细胞，通过 qPCR 和 Western blot 检测 SARI mRNA 和蛋白的表达水平。 2 采用 MTS 法、细胞克隆形成实验及 AnnexinV-PE/7-AAD 双染

法检测 HL60 和 NB4 细胞增殖、凋亡等生物学活性指标的改变。3 运用 WB 检测 IFN-β/γ 对 HL60、NB4 细胞 STAT 信号通路蛋白 STAT1、STAT3、STAT5 及其磷酸化蛋白和 SARI 蛋白的影响；采用 WB 检测氟拉达滨和 IFN-β/γ 同时作用 HL60、NB4 细胞后，STAT1、p-STAT1 和 SARI 蛋白的表达变化。
结果 1 在 3 种 AML 细胞株中，SARI mRNA 表达水平为 Kasumi-1＜NB4＜HL60，且低于正常外周血细胞的 SARI mRNA 表达水平。 2 不同剂量的 IFN-γ 和 IFN-β 分别作用 HL60、NB4 细胞，其 SARI mRNA 的表达水平均显著高于对照组（p＜0.05）。 3 IFN-γ 和 IFN-β 分别作用 HL60 和 NB4 细胞 12h、15h，在 12h 时加药组的 SARI 蛋白表达水平显著高于对照组（p＜0.05），相比 15h 的 SARI 蛋白表达水平没有明显变化（p>0.05）。 4 与对照组相比：MTS 比色法显示，加药组细胞增殖速度减缓（P＜0.05）；克隆形成实验，加药组细胞克隆形成率明显减低（P＜0.05）；流式细胞术凋亡检测，加药组细胞总凋亡率增加（P＜0.05）。5 IFN-γ 组和 IFN-β 组的 STAT1、p-STAT1 和 SARI 蛋白的表达水平显著高于对照组（P＜0.05）；氟拉达滨可以降低 STAT1 蛋白的表达；IFN-γ+Flu 组和 IFN-β+Flu 组的 STAT1、p-STAT1 蛋白表达水平显著低于 IFN-γ+DMSO 组和 IFN-β+DMSO 组（P＜0.05）。
结论 1 IFN-γ 和 IFN-β 可以上调 HL60、NB4 细胞的 SARI mRNA 和蛋白表达水平。 2 IFN-β/γ 诱导的 SARI 表达明显抑制 HL60 和 NB4 细胞增殖，诱导细胞凋亡，主要为早期凋亡。3 氟拉达滨可以降低 IFN-β/γ 上调的 HL60、NB4 细胞 STAT1 和 p-STAT1 蛋白的表达，提示 IFN-β/γ 可能是通过激活 STAT1 通路诱导 SARI 表达。

PO-0572

第三方医学实验室快速响应新冠疫情

杨思雨
沈阳金域医学检验所有限公司

目的 本文介绍在新冠疫情期间第三方实验室如何快速响应支持政府筛查工作。
方法 政府要求所有可以承接新冠筛查检测的实验室应具备有效性，准确性，安全性以及时效性。为能达到相关要求，本公司于相关职能部门表达能够提供的检验能力及水平并配备适宜的人员，设备和设施等资源，建立质量关系体系以及管理文件，建立内外部的沟通制度。为实现日检测量最大化，采取多种管理模式，在疫情期间，各部门全员配合，除三大部门（实验室，业务部，物流部）以外，其他部门参与辅助工作，包括枪头的摆放，试剂的拆箱和标本的摆放等工作。实验室常规项目采取外包设置，全员参与到新冠检测当中，将全部人员分为三个班次，分别为早班、中班、晚班进行全天轮转工作。分析结果的人员为本班次检测负责人，负责处理检测过程中出现的问题。检测室设有小组长，负责检测中的各项问题。采用全自动加样系统提升检测效率，调取大区内可调控的检测资源，实现产能最大化。
结果 有效并准确完成政府分配的所有任务。在原有基础上，此轮转机制更是提升了日检测的效率。
结论 在疫情期间，做到了快速响应政府筛查号召，为精准施策、救治关口前移赢得了宝贵时间。

PO-0573

新冠疫情下儿童常见呼吸道病毒的流行病学变化特征

柳鹏程、徐梦华、曹凌峰、苏犁云 、卢丽娟、贾然、董妞妞、徐锦
复旦大学附属儿科医院

目的 新冠疫情期间，国家采取了各种公共卫生干预手段，如居家隔离、关闭公共娱乐场所和学校、戴口罩等，这些措施不仅有效限制了新冠病毒的传播，对其他常见呼吸道病毒的流行也会产生影响。

本研究旨在阐述新冠疫情防控常态化下的人为公共卫生干预手段对儿童常见呼吸道病毒流行特征的影响。
方法 收集 2019 年（疫情前）和 2020 年（疫情期间）于复旦大学附属儿科医院就诊，临床诊断为下呼吸道感染（LRTIs）的住院患儿的呼吸道标本（鼻咽抽吸物/肺泡灌洗液）。使用直接免疫荧光法检测呼吸道合胞病毒（RSV）、腺病毒（ADV）、副流感病毒 1-3 型（PIV1-3）、甲型流感病毒（FluA）、乙型流感病毒（FluB）、偏肺病毒（MPV），使用实时荧光定量 PCR 检测鼻病毒（RV），并比较分析 2020 年和 2019 年的病毒检测结果。
结果 研究共纳入 7107 例患儿，其中 2019 年 4600 例，2020 年 2507 例。相比较于 2019 年，2020 年 RSV、ADV、FluA、FluB、和 MPV 的检出率显著下降，即使在 6 月份中小学复学后，这些病毒的检出率仍未见上升。然而，2020 年 RV 的检出率却增高，特别在复学后显著上升。此外，PIV 的检出率在 2020 年 9 月后出现上升趋势，并且呈现与 2019 年不同的流行趋势。2020 年的混合感染率相比较于 2019 年显著下降。
结论 新冠疫情防控常态化下的人为公共卫生干预措施对儿童常见呼吸道病毒的流行特征产生显著的影响。在大部分呼吸道病毒流行降低的情况下，我们仍需警惕个别病毒像 PIV 和 RV 一样“复现”，并且这种“复现”可能会呈现与以往不同的流行趋势。

PO-0574

新型冠状病毒实验室核酸检测过程生物安全防护措施探讨

周明莉
成都市第三人民医院

目的 探讨和制订适合新型冠状病毒核酸检测实验室核酸检测过程的生物安全防护措施，为临床实验室实施核酸检测提供行之有效的生物安全防护。
方法 参考国家卫生健康委员会颁布的新型冠状病毒感染的肺炎诊疗方案及国家相关法律法规及专家共识等，对新型冠状病毒核酸检测实验室核酸检测过程的生物安全防护进行阐述。
结果 从标本采集，样本运输、接收及保存、核酸检测整个过程，废弃物的处理等环节，根据实际情况制定了合理、切实可行的生物安全防护流程。
结论 通过制定并实施新型冠状病毒核酸检测实验室的核酸检测过程生物安全防护措施，有效地降低感染传播风险，预防控制新型冠状病毒对实验室环境和人员的感染。

PO-0575

苏州某三甲医院污水中产 TMexCD-TOprJ 耐碳青霉烯类革兰阴性杆菌的分布及其特征研究

朱婕、杜鸿
苏州大学附属第二医院

目的 替加环素是治疗碳青霉烯酶耐药革兰阴性杆菌（carbapenem-resistant gram-negative bacteria，CR-GNB）的为数不多的有效药物之一，2020 年有报道发现一种新型的介导替加环素耐药的 RND 型外排泵基因簇 tmexCD-toprJ。目前，tmexCD-toprJ 样基因簇主要在中国养鸡场中传播，并已扩散至人，本研究旨在分析产 TMexCD-TOprJ 的 CR-GNB（TMexCD-TOprJ-producing CR-GNB，TMCR-GNB）在苏州某三甲医院污水中的流行情况。
方法 通过聚合酶链反应（PCR）对 2019 年医院污水中初筛的 CR-GNB 检测 tmexCD-toprJ 基因携带情况；通过微量肉汤稀释法进行药敏实验；通过二代测序技术获得菌株的全基因组数据，通过系统发育分析对 tmexCD-toprJ 进行分型，通过精细注释分析其遗传学特征。

结果 从苏州某三甲医院污水中分离出 5 株 TMCR-GNB：1 株为携带 tmexCD2-toprJ2、blaIMP-4、blaNDM-1 的解鸟氨酸拉乌尔菌，这是 blaIMP-4、blaNDM-1 共存于解鸟氨酸拉乌尔菌的首次报道；其余 4 株为携带 tmexCD3-toprJ3 的假单胞菌属菌株，同时分别携带 blaIMP-1、 blaVIM-2 中一种碳青霉烯酶基因。5 株 TMCR-GNB 均表现出对头孢菌素类、β 内酰胺类、氨基糖苷类等多种类抗生素耐药。碳青霉烯酶基因 blaIMP-4、blaNDM-1 、blaIMP-1、 blaVIM-2 均位于各自所携带的质粒上，基因簇 tmexCD-toprJ 位于解鸟氨酸拉乌尔菌的质粒及假单胞菌属菌株的染色体上，其周围骨架基因排列构成相似，位于转座子 Tn6855 上，推测其携带 tmexCD-toptJ 基因簇在染色体和质粒间移动或造成进一步传播，而假单胞菌属菌株可能成为该外排泵基因簇的储存库。
结论 质粒介导的碳青霉烯酶基因、新型替加环素耐药基因已经传播至医院污水中，这突出了对环境中携带外排泵基因簇 tmexCD-toprJ 的监测的重要性，虽然目前 tmexCD-toprJ 仅在中国检出，但其可能通过全球人口流动、鸟类迁徙造成全球流行。

PO-0576

普通人群 SAR-CoV-2 核酸筛查 PCR 结果分析

朱爱兰、郑登滋、徐丛荣、李秀兰、王清泰、江芳华
福建中医药大学附属第二人民医院

目的 分析普通人群 SAR-CoV-2 核酸筛查 PCR 异常扩增曲线产生的原因，并采取相应的处理措施
方法 统计分析本实验室 2021 年 3 月异常扩增曲线出现的频率和类型。
结果 本实验室 SAR-CoV-2 核酸扩增检测无效率为 0.63%（79/12513），质控内标污染占比为 0.93%（116/12513），扩增曲线受到抑制占比为 1.34%（168/12513），SAR-CoV-2 核酸 ORF1ab 假阳性占比为 0.04%（5/12513），SAR-CoV-2 核酸 N 基因假阳性占比为 0.04%（5/12513）。
结论（1）试剂尽量不要反复冻融；混匀样本，加样准确，尽量避免吸入痰液可以减少内标出现无效扩增及扩增受抑制的情况。（2）实验室要注意通风透气，防止气溶胶聚集太多。每次实验完毕都要及时消毒可以避免假阳性出现。

PO-0577

Contribution of BDNF/TrkB signalling in the rACC to the development of pain-related aversion via activation of ERK in rats with spared nerve injury

Le Zhang 、Chuan Wang
The Second Hospital, Cheeloo College of Medicine, Shandong University

Purpose Neuropathic pain resulting from peripheral nerve injury is a serious clinical problem that is clinically expressed as allodynia and hyperalgesia. In fact, patients with persistent pain frequently suffer from a series of aversive emotions including anxiety, fear and depression, which are more distressing than the pain itself. It is well acknowledged that the rACC is a key structure in the processing of affective pain, but the underlying molecular mechanism of how neuropathic pain-related aversive states arise in the rACC is still unclear. Brain-derived neurotrophic factor (BDNF), a member of the neurotrophin family of proteins, is widely distributed in the pain-related pathway and limbic system of the central nervous system, suggesting that it is likely to play a crucial role in pain-related functions. Although a large number of studies have focused on the generation of persistent pain mediated by BDNF/TrkB signalling, knowledge of the role of this signalling in the rACC in relation to the development of neuropathic pain-related aversion is still largely incomplete. Previously, we have demonstrated that BDNF/TrkB signaling participates in

spontaneous pain-related aversion via NR2B receptors. It was recently reported that the increased number of pERK positive cells in the rACC of inflammatory rats could be completely suppressed by an administration of a TrkB receptor antagonist. Therefore, in this study, we aim to investigate whether this BDNF signalling in the rACC contributes to the formation of pain-related negative emotions via activation of ERK in rats with peripheral nerve injury.
Methods A spare nerve injury (SNI) was done in rats to imitate NP model. Paw withdrawal threshold (PWT) was used for evaluation of hypersensitivity in NP, and conditioned place avoidance (CPA), a behavioural phenotype was conducted to reflect pain-related aversion. qRT-PCR, western blot, ELISA, immunofluorescence and immune-histochemistry were performed to determine the quantity of involved genes in NP.
Results Compared with that in the sham-operated group, the mRNA and protein level for BDNF were markedly increased in the rACC of surgical rats. The SNI rats showed increased CPA score when compared with controls. However, the increased CPA score could be blocked by CTX-B, a highly selective TrkB receptor antagonist, suggesting BDNF participates in the acquisition of CPA via its high affinity receptor TrkB. Subsequently, we found administration of exogenous BDNF into the rACC of intact rats also induced CPA, which further demonstrated that BDNF was the key factor in producing pain-related aversion. Thereafter, blockage of BDNF/TrkB signaling could downregulate the activation of ERK.
Conclusion Our study showed that enhanced BDNF expression in the rACC participates in the aversive state of neuropathic pain, and activated ERK is an indispensable downstream effector of the BDNF/TrkB signalling pathway. This research is clinically significant and suggests that a new strategy targeting BDNF-related signalling in the rACC is likely to be useful for the alleviation of pain-related emotional disturbance due to peripheral nerve injury.

PO-0578

E-钙粘蛋白在三维球形体培养维持间充质干细胞的干性中的作用

张世昌、梁婷婷
江苏省人民医院（南京医科大学第一附属医院）

目的 体外球形体培养能有效维持间充质干细胞（MSCs）的干性，本研究探讨 E-钙粘蛋白在三维球形体培养维持间充质干细胞的干性中的作用。
方法 以旋转生物反应器内培养的三维球形体 MSCs 为研究对象，利用 RT-PCR、western blot、免疫组化染色观察球形体培养 MSCs 中 E-钙粘蛋白表达的变化，采用基因转染和 shRNA 干扰技术改变球形体培养 MSCs 的 E-钙粘蛋白表达，检测球形体培养 MSCs 细胞增殖、克隆形成、多向分化潜能等干性指标的变化。
结果 RT-PCR、免疫组化染色、western blot 结果显示三维球形体培养显著提高 E-钙粘蛋白在 MSCs 中的表达；基因转染上调 E-钙粘蛋白的表达可显著提高 MSCs 形成球形体的数量，shRNA 下调 E-钙粘蛋白的表达可明显减少 MSCs 形成球形体的数量，提示 E-钙粘蛋白在 MSCs 的球形体形成中发挥重要作用；过表达 E-钙粘蛋白表达可显著提高球形体培养 MSCs 的增殖能力、克隆形成率、干性相关基因和多向分化潜能，shRNA 抑制 E-钙粘蛋白表达可显著降低球形体培养 MSCs 的增殖能力、克隆形成率、干性相关基因和多向分化潜能，表明 E-钙粘蛋白的表达有利于球形体培养 MSCs 的干性维持，提示 E-钙粘蛋白在生物反应器内球形体培养 MSCs 的干性维持中发挥关键作用。
结论 生物反应器内球形体培养通过提高 E-钙粘蛋白的表达，促进体外培养 MSCs 的干性维持，有利于建立既能大规模扩增又能维持 MSCs 干性的体外培养方法，为 MSCs 的临床转化奠定基础。

PO-0579

Trichostatin A, a histone deacetylase inhibitor, suppresses proliferation and promotes apoptosis of esophageal squamous cell lines

Junfen Ma
the First Affiliated Hospital of Zhengzhou University

Aim Histone deacetylases (HDACs)-mediated epigenetic modification plays crucial roles in numerous biological processes. The tumorgenesis and development esophageal squamous cell carcinoma (ESCC) are involved in both genetic and epigenetic mechanisms. However, the effects of the HDACs inhibitor on ESCC are not fully investigated. Here, we treated ESCC cells with trichostatin A (TSA) and evaluated its antitumor effects and related mechanism.
Methods The proliferative ability of the ESCC cells treated with different concentrations of TSA (0.1–5.0μM) was assessed by the MTT. The cell cycle phase distribution of ESCC
was measured by flow-cytometry. The cell apoptosis in ESCC cell lines treated with different dose of TSA for 48h was evaluated by apoptosis assay. The protein levels of p21, p27, Bcl-2 and Bax were investigated by western-blot.
Results Our results indicated that TSA can suppress the proliferation of ESCCs, cause G1 phase arrest through inducing the expression of p21 and p27. TSA can also induce cell apoptosis through enhancing the expression of proapoptotic proteins Bax and decreasing the expression of antiapoptotic protein Bcl-2. Furthermore, we found that TSA inhibited the expression of PI3K, and reduced the phosphorylation of Akt and ERK1/2 in both EC9706 and EC1cell lines. The high levels of acetylated histone H4 were detected in TSA-treated ESCC cell lines.
Conclusion These results indicate that TSA supresses ESCC cells growth by inhibiting the activation of the PI3K/Akt and ERK1/2 pathways. TSA can also promote cell apoptosis through epigenetic regulation the expression of apoptosis.

PO-0580

miR-106a 通过靶向 LKB1 调控 HPV 16 阳性宫颈癌细胞的增殖和自噬

陈翰祥
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 探讨 miR-106a 在 HPV 16 阳性宫颈癌恶性转化中的作用及机制。
方法 收集 56 例因子宫良性病变切除子宫患者的 HPV 阴性的正常宫颈组织（对照组）及 78 例 HPV 16 阳性宫颈癌患者的宫颈癌组织（宫颈癌组），采用实时荧光定量 PCR (RT-qPCR)检测 miR-106a 在组织及细胞中的表达。统计分析 miR-106a 在组织两组间的表达差异，并验证 miR-106a 与患者临床病理学参数的关系。采用 ROC 曲线评估 miR-106a 的诊断价值。通过 CCK-8，平板克隆，EdU 实验检测 miR-106a 对宫颈癌细胞增殖的影响。Western blot 检测 miR-106a 作用后宫颈癌细胞自噬相关蛋白的变化，并采用共聚焦显微镜观察自噬体的形成。通过生物信息学软件预测 miR-106a 的靶基因，并使用双荧光素酶实验验证。使用 Western blot 验证 miR-106a 调节的信号通路。构建 HPV16 E6/E7 稳定表达细胞系，探究 HPV 对 miR-106a 的影响。
结果 miR-106a 在 HPV 阳性宫颈癌组织和细胞中高表达，且 miR-106a 主要由 E7 致癌基因激活，表达差异有统计学意义。miR-106a 高表达与 HPV 阳性宫颈癌患者的肿瘤大小、FIGO 分期、淋巴结转移、脉管浸润以及低组织学分级呈显著相关性(P 均<0.05)，且 miR-106a 的表达达可以明显地区分对照组和肿瘤组。miR-106a 通过靶定抑癌基因 LKB1 促进宫颈癌细胞增殖抑制自噬，并激活 AMPK/mTOR 信号通路。

结论 miR-106a 在宫颈癌恶性转化过程中可能发挥了重要作用。miR-106a 有望成为 HPV 感染相关宫颈癌的潜在诊断标志物和治疗靶点。

PO-0581

Puerarin exhibits antiinflammatory properties in gunpowder smog-induced acute lung injury in rats via regulation of the renin-angiotensin system and the NFκB signaling pathway

Fan Zhang [2]、Yu Wang[1]、Peipei Liu[1]、Ping Di[1]、Mianyang Li[1]、chengbin Wang[1]
1. Chinese People's Liberation Army General Hospital
2. 解放军总医院第一医学中心检验科

Puerarin, which is a widely used in Traditional Chinese Medicine, was previously demonstrated to regulate the subsets of CD4+ lymphocytes in gunpowder smog-induced acute lung injury (ALI). However, the underlying mechanism remains largely unknown. Previous studies on autoimmune diseases have revealed that the renin-angiotensin system (RAS) and NF-κB participate in regulating the levels of CD4+ T lymphocytes. The aim of the present study was to further investigate the mechanisms underlying the protective effects of puerarin. Wistar rats were randomly divided into four groups as follows: Normal control, puerarin control, smoke inhalation injury and puerarin treatment plus smoke inhalation injury groups. The levels of angiotensin II (Ang II) in lung tissue and in the circulation, and the levels of interleukin (IL)-6, IL-1β, IL-17A and tumor necrosis factor (TNF)-α in the bronchoalveolar lavage fluid (BALF) were assayed using ELISA kits. The expression of Ang II type 1 receptor (AT1-R), angiotensin-converting enzyme (ACE) and ACE2 were examined by immunohistochemical analysis and western blotting. Phosphorylated (p-) NF-κB p65 and NF-κB inhibitor α (IκB-α) protein expression levels were also determined using western blotting. Puerarin treatment reduced the levels of inflammatory cytokines in the BALF. Furthermore, puerarin treatment significantly decreased the levels of Ang II, AT1-R and ACE, which were increased following smoke inhalation. Conversely, puerarin treatment upregulated the expression of ACE2, which was downregulated following smoke inhalation. Additionally, puerarin decreased the expression of p-NF-κB p65 and increased that of IκB-α. Thus, the antiinflammatory effects of puerarin were partly mediated via the RAS and via regulation of the NFκB signaling pathway in rats with gunpowder smog-induced ALI.

PO-0582

Prevalence and genotypes of human papillomavirus among men in Yunnan province, China

Ya Xu [1]、Yu Zhang[2]、Xin Fan[1]、Guiqian Zhang[1]、Ziqin Dian[1]、Yi Sun[1]
1. the First People's Hospital of Yunnan Province
2. 昆明理工大学

Human papillomavirus (HPV) infection is one of the most common sexually transmitted infections. Persistent infection is associated with the development of cervical cancer. Men could serve as a medium for HPV transmission among women, and little is known about the prevalence and genotypes of HPV infection among men in Yunnan province. This study is designed for investigating these parameters among men in this region. Clinical information was collected from January 2015 to May 2020, and a total of 369 men who sought to get tested for HPV were included in this study. HPV screening was performed using the HPV GenoArray Test Kit and the anatomical site of sample collection is urethra. The mean age was 36.15 ± 9.08 years. Our

results revealed that the prevalence of HPV infection among men was 23.8% in Yunnan Province, and there was no association between age and HPV prevalence in men. There were 72 (81.81%) individuals positive for a single HPV type and 16 (18.19%) positive for multiple types. The highest prevalent oncogenic HPV types were types 52, 51, and 16. The prevalence of HPV in men was relatively high, and the most prevalent types of HPV infection were similar between men and women from this region.

PO-0583

The association between gut microbiome and blood glucose in pig

Haiyue Liu[1,2]、Guolin Hong[1,2]
1. The Department of Laboratory Medicine, the First Affiliated Hospital of Xiamen University, Xiamen, China；Xiamen Key Laboratory of Genetic Testing, Xiamen, China.
2. 厦门市基因检测重点实验室

Background The present study compared the diversity of gut microbiota in Bama pig (pig) with or without high glucose. Diabetes or prediabetes is a disease with elevation of blood glucose and would finally lead to various cardiovascular diseases (CVDs). Importantly, diabetes is prevalence in China in recent years due to unhealthy life style and dietary habits. More importantly, the popularizing and treatment rate are extremely low in China. Previous studies in pig models of metabolic diseases and nutrient abortion had leaded a fulfillment of the translational gap to develop new therapies for better human health. Metabolic disorder is commonly accompanied with abnormal blood glucose or diabetes. Previous study have use pig model to search for the metabolic pathway of small intestine epithelial cells blood glucose level, which provided novel and significant insights into the control of blood sugar during the absorption stage in the intestine. Additionally, some researchers suggested that pig models is good for the study on metabolic syndrome and obese type 2 diabetes. These studies have shown pig to be suitable models for glucose-related disease. It was reported that pig gut microbiota showed enriched function in metabolic pathways, which could be influenced by the age, genetics, diet and environmental factors. And, some metabolic-related dietary components such as cholesterol, affected the intestinal microbiota in a major way to regulate the metabolism. But there is lack of data about the porcine gut microbiome at different blood glucose levels. The cause and effect of gut microbiota and diabetes were depicted in recent years. Exploring and unveil the underlying mechanism in gut microbiota and diabetes would provide some attracting therapeutic targets for the diagnosis and treatment of diabetes or prediabetes. In the present study, we aim to explore the relationship between blood glucose and gut microbiome.
Methods First, the fecal samples of pig were collected. Second, 16S rRNA V4 hyper-variable DNA regions from the pig were amplified using the stool metagenomic DNA and sequenced with MiSeq sequencing platform. Briefly, all animals were anesthetized for blood sampling and single housed for fecal collection. All fecal samples from experimental animals were collected randomly by trained person from the SPF Experimental Animal Center and stored at -20 degree for short time (less than 12 hr) and then stored at -80 degree until DNA extraction.
Results And the male pig have a consist higher alpha diversity than the female ones when statistic with Shannon, Chao1, observed_species, PD_Whole_tree index, with a significantly different in Shannon diversity (T-Test). We further used LefSe to pick the biomarkers between high and normal blood glucose groups of each gender. We found that female pig had more biomarkers than the male pig with increased (20 vs. 12) and decreased (3 vs. 1) taxa in high blood glucose group compared to normal blood glucose group. None of the biomarkers were coexisted in female and male pig. Butyricimonas, Campylobacterales, Catenibacterium, Clostridiaceae, Epsilonproteobacteria, Helicobacter, Heliobacillus, Methanobacteria, Methanobacteriales, Methanobrevibacter, Mobiluncus, Natronincola, Porphyromonas, Veillonella were high abundant in female pig with high blood glucose, while Prevotella, Ruminococcaceae,

Robinsoniella were high abundant in normal blood glucose group. Whereas, in male groups Chloroplast, Cloacibacillus, Cyanobacteria, Gracilibacteraceae, Neisseriaceae, Neisseriales, Peptostreptococcaceae, Porphyromonas, Pseudomonadaceae, Streptophyta Peptoniphilus were abundant in high blood glucose group and Anaerovorax found to be abundant in normal blood glucose group.
Conclusion The gut microbiota were different in pig with or without high glucose.

PO-0584

Syk/JNK/GSDMD 在金黄色葡萄球菌感染过程中的作用机制研究

刘瑞卿[2]、申艳娜[1]、田德润[1]、刘畅[1]、高爱娇[1]、王琳[1]、唐慧欣[1]、刘亚珊[1]
1. 天津医科大学医学检验学院
2. 天津医科大学医学检验学院

目的 金黄色葡萄球菌（金葡菌）是严重危害人类生命健康的一种革兰阳性病原菌。本课题组前期研究发现，Syk 及 JNK 在金葡菌感染过程中发生磷酸化，进而激活 NLRP3 炎症小体，上调 IL-1β 等炎性因子的分泌过程，然而其具体机制尚不明确。且 caspase-1 可触发细胞焦亡过程，引起胞膜成孔，进而交换细胞内外物质。因此本课题拟探讨 Syk、JNK 在胞外菌金葡菌感染过程中对细胞焦亡关键蛋白 GSDMD 及 IL-1β 等炎性因子分泌的调控作用，以便为金葡菌感染提供新的治疗靶点。
方法 1.金葡菌感染 Syk/JNK 抑制剂及 siRNA 预处理的小鼠单核巨噬细胞（J774A.1 cells）及小鼠腹腔巨噬细胞（PECs）24h 后，western blot 检测 NEK7、IL-1β 及焦亡蛋白表达水平的变化。RT-PCR 检测 NEK7、IL-1β 及 GSDMD mRNA 表达水平的变化。Co-IP 检测 NLRP3-NEK7 复合物水平。
2.金葡菌感染 Syk/JNK 抑制剂预处理的 J774A.1 cells 及 PECs 48h 后，ELISA 检测细胞上清液中 IL-1β 及 IL-18 水平变化。
3.金葡菌感染 NEK7-siRNA 预处理的 J774A.1 cells 及 PECs 24h 后，western blot 检测细胞裂解物中 NEK7、IL-1β 表达水平的变化。RT-PCR 检测细胞中 NEK7、IL-1β 及 GSDMD mRNA 表达水平的变化。
4.Western blot 检测 IL-1β 及焦亡蛋白 GSDMD 在金葡菌感染 J774A.1 cells 过程中的时间变化趋势。
结果 1.与未处理组相比，Syk/JNK 抑制剂及 siRNA 处理组中 NEK7 蛋白及 mRNA 表达水平明显回升，伴随 IL-1β 蛋白及 mRNA 水平明显降低及 GSDMD mRNA 水平明显降低；Co-IP 结果表明，Syk/JNK 抑制剂处理组中 NLRP3-NEK7 复合物的形成明显低于未处理组。
2.与未处理组相比，Syk/JNK 抑制剂及 siRNA 处理组中细胞上清液中 IL-1β 及 IL-18 蛋白水平明显减少。
3.与未处理组相比，NEK7-siRNA 处理组中 IL-1β 蛋白及 mRNA 水平明显降低， GSDMD mRNA 水平明显降低。
4.Western blot 结果表明，随着 GSDMD-N 表达逐渐增多，细胞内 IL-1β 蛋白水平先增多后逐渐降低的趋势。
结论 Syk/JNK/NEK7 参与调控金葡菌感染过程中细胞焦亡关键蛋白 GSDMD 的表达及 IL-1β 炎性分子分泌过程。

PO-0585

基于信息化平台的临床实验室质量管理探索

杨悦林、钱净、张鸿伟、黎海生、赵晓丽、胡大春
昆明市第一人民医院

目的 探索基于信息化平台的临床实验室质量管理。
方法 利用计算机编程技术设计不同功能模块，构建信息化平台。采集实验室一定时期内的质量体系运行原始数据，应用该平台统计分析检验前标本可接受性、检验后不正确检验报告、样本实验室内周转时间、室内质量控制效能等多维度质量指标。
结果 2018 年度的质量指标分析表明，实验室的检验前标本可接受性为 99.92%。进一步的多维度质量分析显示，抗凝样本发生凝聚在样本不合格原因中排名第一（占比 53%）；不正确检验报告率为 0.006%。临床血液体液组不正确报告占比高达 33.3%；急诊/住院样本在实验室内的周转时间(中位数，分钟)分别为：生化检验组 198/57、自动化免疫检测组 306/63、三大常规检测组 37/14、凝血组 90/56；实验室不同定量项目室内质控开展率 100%、定量项目 CV%达标率 88.89-100%、偏倚达标率 75-100%、总误差达标率 86.68-100%、六西格玛达标率 62.5-100%。
结论 本研究建立的临床实验室质量管理信息化平台既能实现质量体系中大量复杂数据的快速和真实获取，也能辅助实验室人员对质量问题进行更深层次的挖掘分析。

PO-0586

探讨第三方医学实验室在大规模人群新型冠状病毒核酸筛查中的生物安全防护措施

魏琦、都伟杰、王倩倩、李志强、毛源
合肥金域医学检验实验室有限公司

目的 探讨第三方医学实验室在大规模人群新型冠状病毒核酸筛查期间如何做好实验室日常生物安全防护措施。
方法 第三方医学实验室在检测能力和服务网络等方面有特殊优势，近期安徽省六安市新冠疫情期间，本实验室根据国家、省、市卫建委有关文件要求，积极开展新冠核酸的检测工作。从标本的运输、检验前、检验中、检验后、突发事件等各个环节均涉及生物安全防护措施。例如物流运输整个过程秉持“合法合规、全面防护”，包括承运资质、人员防护、包装防护等；检验前的样本灭活；检验中个人防护用品的穿、戴；检验后样本的处理；空气消毒、物体表面及地面的消毒；实验室新冠标本溢洒事故的处理。
结果 此次六安市大规模人群新型冠状病毒筛查，本实验室严格按照防护措施做好每日生物安全工作，共检测 16 万份样本，未发生医务人员感染事件。
结论 本实验室生物安全防护措施对防止医务人员感染有良好的预防和控制效果，可以为新冠疫情期间各实验室做好生物安全防护提供参考作用。

PO-0587

中国主要 HIV-1 亚型和亚簇在抗病毒治疗期间免疫恢复差异研究

葛章文
贵州省人民医院

研究目的 CRF01_AE 和 CRF07_BC 是在中国流行的主要 HIV-1 亚型。然而，在接受联合抗逆转录病毒治疗（cART）后，我们还不清楚病毒的亚型、亚簇和相应的嗜性类型是否是导致免疫恢复差

异的影响因素。我们对在中国流行的主要 HIV-1 亚型、亚簇进行调查研究，分析在 cART 治疗期间与免疫恢复相关的因素，为精准的 cART 方案的制定提供科学依据。
研究方法 我们对 cART 期间不同亚型、亚簇和嗜性感染者之间 CD4+T 细胞的恢复过程以及达到免疫恢复和早期免疫恢复所需的时间进行了深入分析。广义估计方程用于分析与 CD4+T 细胞恢复时计数变化相关的因素；K-M 用于分析随治疗时间达到免疫恢复或早期免疫恢复的比例；Cox 用于分析影响免疫恢复速度快慢的相关因素。
研究结果 （1）与 CRF07_BC 和 CRF01_AE 5 簇人群相比，CRF01_AE 和 CRF01_AE 4 簇感染者在 cART 期间呈现出更差的免疫恢复：CD4+T 细胞计数更低（P ≤ 0.003），免疫恢复速度更慢（P ≤ 0.022），达到免疫恢复的患者百分比更低（P < 0.001）以及达到免疫恢复的平均时间更长（P < 0.001）。（2）与 CCR5（R5）嗜性病毒相比，CXCR4（X4）嗜性病毒在 CRF01_AE（P < 0.001）、4 簇（P < 0.001）和 5 簇（P ≤ 0.029）中均表现出更差的免疫恢复。此外，在 CRF01_AE、CRF01_AE 4 簇、达到免疫恢复的 CRF01_AE 4 簇和达到早期免疫恢复的 CRF01_AE 4 簇中发现 X4 嗜性的比例明显高于对应的 CRF07_BC（P < 0.001）、CRF01_AE 5 簇（P < 0.001）、达到免疫恢复的 CRF01_AE 5 簇（P < 0.001）和达到早期免疫恢复的 CRF01_AE 5 簇（P < 0.001）。（3）相对于 CRF07_BC 和 CRF01_AE 5 簇病毒，我们在 CRF01_AE（P < 0.001）和 CRF01_AE 4 簇（P≤0.004）病毒人群基因组中发现更高比例的 X4 嗜性倾向的氨基酸编码基因。
研究结论（1）我们的研究表明，在 cART 的中国患者中，CRF01_AE 亚型和 CRF01_AE 4 簇与 CRF07_BC 亚型和 CRF01_AE 5 簇相比免疫恢复更差。（2）CRF01_AE 和 CRF01_AE 4 簇免疫恢复更差的原因是两者中含有更高比例的 X4 嗜性病毒。（3）将来为了提高治疗的效果，我们建议在中国各地区的 cART 方案中应考虑当地 HIV-1 的亚型和亚簇类型。此外，我们研究结果还提示将来 cART 中应谨慎使用 CCR5 抑制剂。

PO-0588

原发免疫性血小板减少症患儿血小板相关抗体及淋巴细胞亚群的变化及临床意义

张加勤、洪国斧
厦门大学附属第一医院

目的 免疫性血小板减少症（ITP）是一种常见的获得性自身免疫性血液系统疾病， ITP 的发生、发展与患者免疫状态密切相关，患者体液免疫和细胞免疫均存在不同程度的异常，尤其是与淋巴细胞各亚群含量及功能的改变密切相关。然而，较少关注患者外淋巴细胞亚群各细胞数量的变化。为此，本研究检测 ITP 患儿及健康对照者白细胞总数及其分类、血小板相关抗体（PA-Ig）和 T 淋巴细胞、NK 细胞、B 细胞数量及其百分比的变化趋势，以探讨其在 ITP 发病中的作用及临床意义。
方法 选取 2014 年 1 月~2016 年 12 月初次就诊于本院的血小板减少症患者，其中 ITP 患者，67 例，男 36 例，女 31 例，年龄 1 月~12 岁，中位年龄 4.35 岁。利用全自动血细胞分析仪分别对 67 例 ITP 患儿和 42 例健康对照者外周血进行血细胞计数及分类；流式细胞术检测两组 PA-Ig、淋巴细胞亚群含量，采用双平台法计算淋巴细胞各亚群的绝对数量。应用 SPSS 19.0 软件包进行统计学分析，淋巴细胞各亚群含量及细胞计数进行正态和方差齐性检验后，数值用`χ± s 表示，两组间比较采用 t 检验，三组间比较采用单因素方差分析（One-Way ANOVA），多组样本两两比较采用最小显著差（the least significant difference，LSD） t 检验，计数资料比较采用 χ2 检验，P< 0.05 为差异有统计学意义。
结果 ITP 患儿外周血血小板平均数量明显低于正常对照组(P<0.05)，白细胞平均数量差异不具统计学意义(P>0.05)，而淋巴细胞平均含量和平均数量与健康对照组相比均显著降低（P<0.05）；ITP 患儿 PA-IgG、PA-IgM、PA-IgA 阳性率分布为为 89.55%（60/67）、46.27%（31/67）和 34.38%（23/67）,各类型抗体阳性率比较不具统计学差异（P>0.05）；ITP 组 PA-Ig 显著高于健康对照组

（P<0.05），且 ITP 组血小板平均数量与 PA-Ig 水平均呈负相关；与健康对照组相比，ITP 组 CD3+ 淋巴细胞、CD4+ 淋巴细胞、CD3-CD（16+56）+ NK 百分比和数量及 CD4+/CD8+ 的比值均显著降低（P < 0.05），CD8+T 淋巴细胞百分比略升高（P<0.05），CD19+B 淋巴细胞百分比和数量则显著升高（P< 0.05）。

结论 细胞免疫及体液免疫异常是 ITP 发生、发展的病理基础，PA-Ig 及淋巴细胞亚群的变化可较好地反映 ITP 的病理进程, 可为 ITP 诊断和疗效观察提供依据。

PO-0589

一例单核细胞增多类白血病反应

王科勇
西安医学院第一附属医院

一、病例资料

患者男，93 岁，因无诱因出现抽搐于 2020 年 8 月 31 日急诊入院，入院查体：营养不良，慢性病容，未见明显异常。既往结核病史 50 年已治愈，前列腺增生 10 年，2 型糖尿病 10 年。辅助检查：维生素 B12 100.62pg/mL；β-羟丁酸 1.49mmol/L；胃蛋白酶原 1237.6mcg/L,胃泌素 179.93pmol/L，初步诊断：1.慢性硬膜下血肿；2.中度贫血；3 维生素 B12 缺乏症；4.低钾血症；5.低钠血症；6.心律失常，心房颤动；7.2 型糖尿病。予以调节胃肠道功能、促进胃肠动力，补液，等对症治疗。入院第二日血常规检查显示白细胞 11.87x10^9/L，单核细胞比例 34.7%，形态学检查可见单核细胞比例明显升高，胞体大，多不规则，胞浆丰富，灰蓝色或灰红色，可见明显颗粒及空泡，染色质纤细网状，部分细胞形似幼单细胞。未行骨髓穿侧检查。经对症治疗好转出院，一月后又以“低血容量休克”入院，基本状况同前，血常规显示白细胞 27.04x10^9/L，单核细胞比例 71.7%。对症治疗后血象恢复正常

二、讨论

单核细胞显著升高一般多见于血液系统恶性肿瘤，但根据该患者具体临床情况分析，并不考虑血液病。由于患者年龄较大，造血功能明显减低，髓系增生减低，导致红细胞计数减少，血红蛋白水平减低，血小板显著减少，引起单核细胞比例相对升高。另外一方面，该患者中期白细胞总数升高，单核细胞比例达到 71.7%，考虑为感染并发症引起，单核细胞是最重要的抗原递呈细胞, 在机体损伤治愈、抗御病原的入侵和对疾病的免疫方面起着重要的作用，患者出现外周血单核细胞计数的增加以及部分幼稚单核细胞与感染并发症的发生有关, 其原因可能为下丘脑-垂体-肾上腺皮质轴和交感神经系统激活, 刺激骨髓池中幼稚的单核细胞释放入外周血，综上所述，该患者可能为单核细胞型类白血病反应。类白血病指在原发病的基础上，机体在某些病理因素刺激下表现出来的一种类似白血病的血象反应，刺激因素去除后即可恢复，与该患者病情基本相符。

PO-0590

Outcomes of Methadone Maintenance Therapy Combined with Rilpivirine/Efavirenz in Treatment-Naive HIV-Infected Patients

Cuixian Yang 、Huiqin Li
Yunnan Infectious Diseases Hospital

Background Injecting drugs is associated with a high risk of HIV infection, alongside the risk of a drug overdose and mental health problems.

Objective To evaluate the effect of methadone maintenance treatment (MMT) combined with rilpivirine (RPV)-based regimens on drug use of HIV individuals.

Methods This study was a prospective, open-label, controlled, drug-drug interaction trial at a single center for 24 weeks. Participants on stable MMT were randomly divided into two groups administered RPV/TDF/3TC (RPV group) and EFV/TDF/3TC (EFV group), respectively. Adjustment doses of methadone were monitored for 12 weeks. HIV-1 RNA was used to evaluate the effects of antiretroviral therapy at week 24. Acute opioid withdrawal-, drug craving questionnaire- and MOS-HIV scales were used to assess study outcomes.
Results 22 and 18 cases of HIV-infected drug users were recruited in the RPV and EFV groups, respectively. Thirty-one cases had completed monitoring and clinical evaluation at week 24. In the RPV and EFV groups, 32% and 56% of the participants had methadone dose adjustment, respectively, indicating a significantly lower rate in the RPV group. The rates of individuals with HIV RNA levels from 50-500 copies/ml were 94% (RPV group) and 90% (EFV group). The drug craving questionnaire scale scores decreased in both groups. After one week of treatments, acute opioid withdrawal scale scores increased in both groups, with no significant difference between them.
Conclusion Concomitant administration of RPV does not significantly affect methadone and could decrease withdrawal symptoms. An RPV-based regimen may be used as first-line treatment in IDUs with HIV-infection.

PO-0591

m6A 甲基化修饰调控去卵巢骨质疏松大鼠 BMSCs 中特定 lincRNA 的表达

曹成建[1,2]、张芳[2]、刘伟平[1]、陈喻[1]、万科幸[1]、王昕[1]、宋耀辉[1]、殷明刚[1,2]
1. 自贡市第一人民医院检验科
2. 自贡市第一人民医院，自贡市医学科学院

目的 RNA m6A 修饰是近年才深入研究的表观遗传学调控机制，课题组前期筛选出去卵巢（OVX）绝经后骨质疏松（PMOP）大鼠模型骨髓间充质干细胞（BMSCs）差异表达的长链非编码 RNA lincRNA7140，本课题拟探讨 m6A 修饰是否参与调控了 lincRNA7140 的表达。
方法 SD 雌性大鼠 20 只随机平均分成假手术对照组（Control）及去卵巢组（OVX）组，采用 OVX 建立 PMOP 大鼠模型，microCT 验证模型是否成功建立。分离原代培养两组大鼠 BMSCs，并用流式及免疫组化验证 BMSCs。生物信息学分析 lincRNA7140 上可能的 m6A 状态及位点。m6A 甲基化定量测定试剂盒分析两组 BMSCs 中整体 RNA m6A 甲基化水平，RNA 甲基化免疫共沉淀结合 qPCR 方法（MeRIP-qPCR）检测两组细胞中 lincRNA7140 m6A 修饰水平。
结果 microCT 显示成功建立 PMOP 大鼠模型，流式细胞术及免疫组化也显示分离培养的为 BMSCs。生物信息学分析推测 lincRNA7140 上存在 4 个可能的 m6A 修饰位点。与 Control 组相比，OVX 组整体 RNA m6A 甲基化水平偏低，而 MeRIP-qPCR 分析显示 OVX 组 lincRNA7140 m6A 水平下调，差异均具有统计学意义（$P<0.05$）。
结论 PMOP 大鼠 BMSCs 中特定 lincRNA（lincRNA7140）的表达受到了 m6A 甲基化的调控，这可能在其骨质疏松状态中发挥关键的调控作用。

PO-0592

一项基于不同科室及不同标本类型中 EB 病毒核酸检测情况的大样本数据分析

孙奎霞、孙立颖
北京大学第一医院

目的 了解不同科室送检样本的 EB 病毒核酸检出情况，分析 EB 病毒核酸在不同标本类型中的检出率，帮助临床医师选择更合适的标本送检。
方法 收集 5494 份我院各科室自 2015 年 1 月~2021 年 3 月送检样本的 EB 病毒核酸检测数据，根据荧光定量 PCR 检测结果，分析来自各科室送检样本的 EB 病毒核酸阳性检出率，以及不同标本类型（血清、血浆、淋巴细胞、支气管肺泡灌洗液、脑脊液、拭子、羊水、乳汁、引流液等其他体液）中 EB 病毒核酸阳性检出率。
结果 5494 份样本中，EB 病毒核酸阳性的检出率为 13.7%（750/5494）。3093 份男性患者的样本中，EB 病毒核酸阳性检出率为 14.9%（460/3093），2401 份女性患者的样本中，EB 病毒核酸阳性检出率为 12.1%（290/2401））。送检样本最多的科室为儿科（29.2%，1602/5494），其次为血液科（20.0%，1098/5494）。EB 病毒核酸阳性检出率最高的为血液科（27.1%，298/1098），其次为皮肤科（21.0%，12/57）。儿童患者标本 EB 病毒核酸阳性检出率为 10.5%（168/1602)，成人患者标本检出率为 15.0% (582/3892)。送检最多的标本类型是血清标本（74.4%，4086/5494），其次为淋巴细胞（15.7%，865/5494）。EB 病毒核酸阳性检出率最高的标本类型为淋巴细胞（48.0%，415/865），其次为肺泡灌洗液（35.3%，88/249）和咽拭子（31.8%，7/22），而送检最多的血清样本 EB 病毒核酸阳性检出率仅为 5.6%（228/4086）。
结论 成人和儿童均应重视 EB 病毒核酸检测，提高重点相关科室的送检率。选择送检样本时应根据疾病情况，尽量送检淋巴细胞、肺泡灌洗液及咽拭子等标本进行检测以提高 EB 病毒核酸检出率。

PO-0593

低氧环境下绒毛膜外滋养细胞的自噬功能受损与子痫前期的关系

龙安雄、田春杰、钟国梁、何秋阳、马顺高
大理白族自治州人民医院

目的 研究子痫前期患者胎盘滋养细胞的自噬水平以及低氧环境下绒毛膜外滋养细胞自噬受损对其细胞功能的影响。
方法 首先收集子痫前期患者及正常孕妇分娩后的胎盘组织，免疫组化检测自噬抑制相关标记物 SQSTM1 的表达；其次利用 2%氧气浓度模拟孕早期母胎界面低氧环境，建立该条件下滋养细胞系 HTR8/SVneo 的单培养及其与子宫微血管内皮细胞的共培养模型，利用 3-MA 作为自噬抑制剂，分为正常对照组和自噬抑制组，免疫组化检测滋养细胞中自噬相关蛋白 LC3Ⅱ的表达，transwell 小室和流式细胞术分别检测滋养细胞的侵袭性以及血管细胞的凋亡。
结果 子痫前期患者胎盘组织中 SQSTM1 的表达显著高于正常孕妇（P＜0.05）；低氧条件下，单培养和共培养的 HTR8/SVneo 细胞中的 LC3Ⅱ的表达显著高于自噬抑制组（P＜0.05）；单培养组中，自噬抑制组中穿过 transwell 小室的 HTR8/SVneo 细胞数量显著小于对照组（P＜0.05），共培养组中，自噬抑制组内皮细胞的凋亡水平显著小于对照组（P＜0.05）。
结论 子痫前期患者胎盘滋养细胞的自噬功能受抑制，低氧条件下滋养细胞自噬功能受损能够引起该细胞的侵袭功能下降及抑制该细胞诱导血管内皮细胞的凋亡，该机制可能参与了子痫前期的发生发展。

PO-0594

A Scoring Model Based on 4 Immune-Related LncRNA Subtypes and Tumor-Infiltrating Immune Cells Predicts the Prognosis and Drug Sensitivity of Breast Cancer

Zhaolei Cui 、Yan Chen
Fujian Cancer Hospital

Background Immune-related long non-coding RNAs (lncRNAs) are involved in the occurrence and development of breast cancer (BC). We sought to develop a prognostic risk model based on an immune-related lncRNA signature combined with tumor-infiltrating immune cells and evaluate its performance in predicting BC prognosis and tumor sensitivity to immunotherapy and chemotherapy.
Methods The gene expression profiles and clinical data of BC patients were downloaded from The Cancer Genome Atlas (TCGA), and immune-related lncRNAs were screened using co-expression network analysis. We utilized clustering analysis to identify potential lncRNA subtypes associated with BC. Their differences in underlying mechanisms involved in carcinogenesis were analyzed by GSEA. BC patients were randomly assigned to a training cohort and a validation cohort, and a least absolute shrinkage and selection operator (LASSO)-derived risk model was constructed using a training cohort and validated in the validation cohort. The RiskScore of each patient was calculated for risk stratification of BC patients. Then, the performance of the risk model was assessed in low- and high-risk patients using survival analysis, and PD-L1 and PD-L2 expressions, as well as tumor sensitivity to the chemotherapy agents paclitaxel and rapamycin, were compared between the two groups. Finally, the correlation between the signature-calculated RiskScore and tumor-infiltrating lymphocytes was evaluated.
Results Ultimately, 815 immune-related lncRNAs associated with BC were identified based on transcriptome and clinical data of 1,109 BC tissues and 113 normal controls. All BC patients were clustered into Cluster 1 (n=996 cases) and Cluster 2 (n=73 cases). Patients in Cluster 1 exhibited enhanced PD-L1 and PD-L2 gene expressions versus those in Cluster 2. GSEA enrichment analysis showed that the JAK-STAT signaling pathway was a principal mechanism responsible for functional differences between the two Clusters of BC. Four immune-related lncRNA subtypes (MAPT-AS1, LINC01871, AC110995.1, and ST7-AS1) were selected and subject to LASSO regression to construct a prognostic model. This effectively predicted longer survival of low-risk patients compared with high-risk individuals. Univariate and multivariate COX regression revealed that the model could serve as an independent prognostic predictor. Besides, high-risk patients had lower PD-L1 and PD-L2 expression levels and lower IC50 values of paclitaxel and rapamycin versus low-risk patients. The RiskScore was associated with distinct tumor-infiltrating immune cell subpopulations in the low- and high-risk groups.
Conclusion This risk model based on 4 immune-related lncRNA subtypes is highly practical and accurate in predicting BC prognosis, which can be used to guide the choice of immunotherapies and chemotherapies in BC.

PO-0595

Identification of Adriamycin Resistance Genes in Breast Cancer based on Microarray Data Analysis

Yingfeng Lin、Zhaolei Cui、Yan Chen
福建省肿瘤医院

Objective Breast cancer is a common malignant tumor with increasing incidence worldwide. This study aimed to investigate the molecular mechanisms of the adriamycin (ADR) resistance in breast cancer.
Methods The GSE76540 dataset downloaded from the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (GEO) database was adopted for analysis. Differentially expressed genes (DEGs) in chemo-sensitive cases and chemo-resistant cases were identified using the GEO2R online tool respectively. Go analysis and KEGG enrichment analysis of DEGs were carried out by using the DAVID online tool. The protein-protein interaction (PPI) network was constructed using the Search Tool for the Retrieval of Interacting Genes (STRING) and visualized with Cytoscape software. The impact of key tumor genes on the survival and prognosis were described.
Results A total of 1481 DEGs were excavated, including 549 up-regulated genes and 932 down-regulated genes. According to the GO analysis, the DEGs were significantly enriched in: extracellular matrix organization, positive regulation of transcription from RNA polymerase II promoter, lung development, positive regulation of gene expression, axon quidance and so on. The results of KEGG pathway enrichment analysis showed that the most enriched DEGs can be detected in: pathways in cancer, PI3K AKT signaling pathway, focal adhesion, ras signaling pathway and so on. In the PPI network analysis, hub genes of CDH1, ESR1, SOX2, AR, GATA3, FOXA1, KRT19, CLDN7, AGR2, ESRP1, RAB25, CLDN4, IGF1R, CLDN3 and IRS1 were detected. Finally, there is a correlation filter out these hub genes in resistance of ADR.
Conclusions Hub genes associated with ADR resistance were identified using bioinformatic techniques. The results of this study may contribute to the development of targeted therapy for breast cancer.

PO-0596

科学城地区新型冠状病毒灭活疫苗接种后中和抗体阳性率评价

王芳、方堃、刘阳、王丹、陈沂、袁丹
四川省科学城医院

目的 分析科学城地区 111 名成年人新型冠状病毒灭活疫苗接种后中和抗体产生的阳性率，为新型冠状病毒疫苗免疫接种管理提供参考。
方法 选取科学城地区于 2021 年 1 月-3 月完成全程接种且自愿中和抗体检测的人员 111 名，采集空腹静脉血，采用磁微粒化学发光免疫分析法进行血清中和抗体定量检测，同时收集接种者的基本信息和疫苗接种情况，将按照第 2 针接种后第 3、7、14、28 天分组和年龄、性别分组，对中和抗体产生的阳性率进行统计分析。
结果 111 名接种人员中和抗体阳性人数为 96 名，阳性率为 86.5%。性别和年龄分组差异无统计学意义（P>0.05）。按接种完成间隔时间分组，其中接种第 3 天中和抗体阳性率为 23.1%（3/13），第 7 天中和抗体阳性率为 100%（14/14），第 14 天中和抗体阳性率为 96.8%（30/31），第 28 天中和抗体阳性率为 92.5%（49/53）。经比较，差异有统计学意义（$\chi 2=51.333$， $P<0.05$）。
结论 新型冠状病毒疫苗接种后产生中和抗体的时间不一，其中第 7 天中和抗体产生的阳性率最高，随后有降低的趋势，应结合实际情况适时检测中和抗体水平，加强免疫，以降低新型冠状病毒肺炎的感染。

PO-0597

ARA55 participates in TGFβ1-induced epithelial-mesenchymal transition in CNE2 nasopharyngeal carcinoma cells

Zhaolei Cui 、Xiaoqin Xin、Yan Chen
Fujian Cancer Hospital

Objective ARA55 (androgen receptor coactivator 55kDa protein) was first identified as a TGFβ1-inducible protein and function as a molecular scaffold in coordinating protein-protein interactions. Herein, we focused on validating the functional role of ARA55 in TGFβ1-induced epithelial-mesenchymal transition (EMT) in human CNE2 nasopharyngeal carcinoma cells.
Methods Expression of ARA55 in the CNE2 cells was stimulated by TGFβ1 (5ng/ml), and a commercial RNA interference plasmid (siRNA-ARA55) was utilized to silence ARA55 expression in response to TGFβ1 induction.
Results Our results manifested that forced expression of ARA55 enhances growth as well as migration and invasion of the CEN2 cells. In contrast, cells depleted of ARA55 resulted in suppressed cell proliferation and metastasis capability, along with a down-regulation of N-cadherin and up-regulation of Claudin-1. Further co-immunoprecipitation analysis exhibited that induced ARA55 yields a direct physical interaction with Smad7 in TGFβ1 signaling.
Conclusions Our data demonstrate that ARA55 exerts a causative role and functions as a critical regulator in TGFβ1-mediated EMT in CNE2 nasopharyngeal carcinoma cells through binding with Smad7.

PO-0598

A novel peptide binding to the C-terminal domain of connective tissue growth factor for the treatment of bleomycin-induced pulmonary fibrosis

Han Xiao
Zhongda Hospital Southest University

Objective Idiopathic pulmonary fibrosis is known to be a chronic symptom of a deadly interstitial lung disease with a poor prognosis and few treatment options. It is commonly believed that collagen is secreted to repair lung damage due to various causes. However, pulmonary fibrosis and collagen deposition occurs if damage is insufficiently repaired and, as a consequence, the accumulation of excessive proliferation of fibroblasts and super-abundant extracellular matrix leads to tissue stiffness. Connective tissue growth factor (CTGF) is a multifunctional, cysteine-rich, heparin-binding protein, with a molecular weight of 38 kDa, and was first described by Bradham et al in 1991. CTGF is induced by TGF-β, which is an important downstream mediator that induces fibrosis by regulating secretions of fibroblasts and maintenance of the extracellular matrix. In the present study, we screened positive phage clones from a random dodecapeptide library with a CTGF/C domain, and determined the coding sequence of small peptides 810A using sequencing. Treatment with 810A in vitro and vivo to investigate whether it can anti-pulmonary fibrosis in mice.
Methods Using phage display technology, we screened a small peptide 810A that can be specific bind characteristics with CTGF. Then we applied to Human bronchial epithelial cells (16HBE cells) to evaluate its function towards cells by MTT testing, cell migration experiment and western blot. 810A in mouse model of bleomycin (BLM)-induced pulmonary fibrosis was evaluated by leukocyte counts in bronchoalveolar lavage fluid (BALF), hydroxyproline contents and pathological examination.

Results Biopanning of phages specifically bound to CTGF/C from peptide library and their immunoreactivity assay

Enriched phage at a concentration of 1.9×106 pfu·mL-1 were obtained after 4 rounds of panning and screening. Sequencing of 10 randomly positive phage clones revealed that a peptide, 810A, was confirmed in 8 sequencings, and two peptides, termed 810B and 810C, were each confirmed in one sequencing. The phage clone 810A demonstrated specific binding characteristics to PKW-CTGF and TrxA-CTGF and the DNA concentration of 810A cloned phages bound to PKW-CTGF and TrxA-CTGF was 8.456 ± 0.546 μg·mL-1, 8.663 ± 0.207 μg·mL-1 respectively, which was significantly higher than 810B and 810C ($P<0.05$). 810A exhibited the highest immunoreactivity compared with 810B and 810C, and also had a dose-dependent relationship between OD450 value and 810A concentration ($Y = -0.033X2 + 0.4297x + 0.0587$ [$R2 = 0.988$]), and the concentration for 50% of maximal effect (EC50) of 810A was 2.547 ± 0.092 μg·mL-1.

810A effectively inhibited CTGF-induced proliferation and migration of 16HBE cells

To investigate the inhibitory effect on cell proliferation induced by CTGF at 0.1 μg·mL-1, 810A was added at the indicated concentrations, and cellular growth was determined using the MTT assay. Under continuous incubation for 24, 48, and 72 h, 810A at a concentration of 10 μg·mL-1 significantly inhibited the proliferation of cells induced by 0.1 μg·mL-1 CTGF. In the cell migration assay, CTGF at 1 μg·mL-1 significantly promoted cell migration, and this phenomenon could be inhibited after the addition of 810A at concentrations > 0.1 μg·mL-1. The 810A peptide at concentrations of 10–1000 μg·mL-1 demonstrated an inhibition rate > 70% in the cell migration assay, similar to that of CTGF-monoclonal antibody, with a half maximal inhibitory concentration (IC50) of 1.612 ± 0.1549 μg·mL-1.

Intervention with 810A attenuated changes in pulmonary index and hydroxyproline content in mice

The anti-fibrotic effects of 810A in BLM-induced pulmonary fibrosis model C57BL/6 mice were further studied. The 810A interventional group demonstrated a certain degree of reduction in lung wet-dry weight ratio and pulmonary index compared with the BLM model group; moreover, the pulmonary index in the intervention group was significantly down-regulated at day 28. On days 14 and 28, 810A intervention clearly reduced the levels of hydroxyproline production compared with the positive control. These results were highly consistent with the pulmonary index data.

Effect of 810A intervention on lung histopathology

The effects of 810A intervention on pulmonary fibrosis was further evaluated using histopathological analysis. Uniform and small alveoli were observed in the negative control group, and severe alveolitis and lung fibrotic injury in the BLM group manifested as interalveolar inflammation, obliteration of the alveolar space, and continuous collagen deposition. After 810A intervention, these histopathological findings were significantly attenuated. Masson’s trichrome staining to detect collagen deposition in the lung tissues confirmed similar results. In the quantitative histological analysis of fibrotic changes, a numerical fibrotic scale was used in a subset of animals. The BLM group demonstrated significantly higher Ashcroft scores of fibrosis at 7, 14, and 28 days compared with the control group ($P < 0.05$). In contrast, the 810A treatment group demonstrated significantly lower Ashcroft scores in fibrosis compared with the untreated groups. Furthermore, after giving 810A i.p. CTGF levels were significantly reduced at 810A interventional group in 28 days.

Conclusions In summary, a CTGF/C-specific binding peptide (i.e., 810A), was screened using phage display techniques, and could effectively inhibit the proliferation, migration, and expression of TGF-β and α-SMA in cells pretreated with CTGF. In in vivo experiments using an animal model of BLM-induced pulmonary fibrosis, the peptide demonstrated similar effects, which effectively reduced the onset and development of pulmonary fibrosis in mice.

PO-0599

生物信息学分析 BATF2 在头颈部肿瘤的表达及其预后价值

林莺莺、崔兆磊
福建省肿瘤医院

目的 通过 TCGA 和 GEPIA 数据库分析 BATF2(basic leucine zipper transcription factor, ATF-like 2)在头颈部鳞状细胞癌(head and neck squamous cell carcinoma，HNSCC)中的表达和预后价值。
方法 利用 TCGA 数据库、GEPIA 数据库分析 BATF2 在不同癌症组织中的表达进行对比；在 TCGA 数据的基础上，通过 R 语言进行 BATF2 与基因的共表达及相关性分析，分析这些基因与 BATF2 可能存在的相互作用通路。通过 UALCAN 数据库分析 BATF2 的表达情况与 HNSCC 生存期的关系，评估预后价值，得到预后风险比（HR）森林图。
结果 BATF2 在 HNSCC 中的表达处于中等水平，WARS、GBP5、GBP1 与 BATF2 相关性最强，呈正相关；BATF2 表达与丝氨酸蛋白酶抑制剂因子 Serpin B3 呈正相关（r=0.13,P=0.0025）。BATF2 的表达在 HNSCC 患者预后评估中不具有统计学意义。
结论 BATF2 在 HNSCC 中呈中低水平表达，对 HNSCC 中所有癌种的生存期评估尚无统计学差异。

PO-0600

脂肪细胞促进肿瘤 PD-L1 表达的作用及干预策略研究

张猜
郑州大学第一附属医院

肥胖增加患癌危险及癌症相关的病死率已是不争事实，但其深层机制尚未阐明，探究肥胖促进肿瘤生长的机制并研发有效药物十分必要。
目的 研究 PMQ 对脂肪细胞促 B16F1 细胞 PD-L1 表达的影响。
方法 （1）采用 Cocktail 法诱导 3T3-L1 前脂肪细胞分化，油红 O 染色检测 3T3-L1 前脂肪细胞分化 6 天后胞内脂质蓄积情况。收集分化第 7 ~ 8 天的培养基上清配制不同比例的分化成熟 3T3-L1 脂肪细胞条件培养基，未分化的前脂肪细胞条件培养基以同样条件干预 B16F1 细胞作为对照。条件培养基干预 B16F1 细胞 48 h 后采用 Western blot 检测 B16F1 细胞 PD-L1 蛋白表达。（2）MTT 和 EdU 法检测 PMQ 干预 B16F1 细胞 48 h 对其细胞活力和增殖的影响，并检测 B16F1 细胞 PD-L1 的 mRNA 和蛋白表达。
结果（1）3T3-L1 脂肪细胞条件培养基（25%，50%）可上调 B16F1 细胞 PD-L1 蛋白表达，3T3-L1 前脂肪细胞条件培养基（25%，50%）无此作用；（2）PMQ（1、3、10 μM）干预 48 h 不影响 B16F1 细胞活力和增殖；（3）PMQ（1、3、10 μM）干预 48 h，浓度依赖性地下调 B16F1 细胞 PD-L1 的 mRNA 和蛋白表达水平。
结论（1）3T3-L1 脂肪细胞条件培养基可上调 B16F1 细胞 PD-L1 蛋白表达；（2）PMQ 不影响 B16F1 细胞活力和增殖，可浓度依赖性地下调 B16F1 细胞 PD-L1 水平。

PO-0601

EGCG 通过阻断 HDAC6-PI3K/AKT/mTOR 信号轴激活小胶质细胞自噬过程和 Aβ 清除

陈妍、洪宏海、张宗桃
广州医科大学附属第三医院

目的 通过体内外实验研究 EGCG 对小胶质细胞 Aβ 清除的调控作用，阐明其分子机制及其对 AD 治疗的潜在价值。
方法 1.通过动物行为学实验观察 EGCG 能否改善 AD 小鼠的认知障碍；
2.利用 ThS 染色和免疫荧光染色方法观察 EGCG 治疗小鼠的 $A\beta_{1-42}$ 沉积和胶质细胞激活情况；
3.利用 MTT 法检测药物处理后细胞的活性情况；
4.利用 Western blot 检测药物处理后细胞中各种蛋白的表达水平。
结果 1. EGCG 改善 AD 小鼠的认知功能障碍；
2. EGCG 促进小胶质细胞增殖，保护小胶质细胞免受 $A\beta_{1-42}$ 诱导的毒性损害；
3. EGCG 促进小胶质细胞摄取细胞外 $A\beta_{1-42}$，且没有引起炎症反应；
4. EGCG 通过抑制 PI3K/AKT/mTOR 通路来诱导小胶质细胞自噬作用进而降解细胞内 $A\beta_{1-42}$；
5. EGCG 通过下调组蛋白去乙酰化酶 6（HDAC6），来促进 $A\beta_{1-42}$ 的摄取和自噬、促进小胶质细胞 $A\beta_{1-42}$ 的清除；
6. EGCG 通过调控小胶质细胞 $A\beta_{1-42}$ 清除作用来保护神经元细胞免受 $A\beta_{1-42}$ 毒性损害。
结论 EGCG 通过对 HDAC6 的调控，一方面上调 RAGE 受体的表达，增加小胶质细胞对胞外 Aβ 的吞噬，另一方面抑制 PI3K/AKT/mTOR 信号通路，促进小胶质自噬及随后的 Aβ 胞内降解，最终保护小胶质细胞及周围的神经元细胞免受 Aβ 毒性的损害。

PO-0602

贵州省黔西南地区儿童地中海贫血发病情况及基因分布分析

杜林、吴海婴、王曼丽
兴义市人民医院

目的 调查黔西南地区儿童地中海贫血发病情况，并分析其基因分布。
方法 选择黔西南州区内儿童为研究对象，共纳入 48930 名儿童。对研究对象进行地中海贫血初筛，根据筛查结果，对可疑地中海贫血患儿进行基因诊断，并进行基因分型。
结果 48930 名儿童初筛共 1002 例为可疑地中海贫血，其中男性和女性 α 地中海贫血检出率有显著差异(P <0.05)、β 地中海贫血检出率无显著差异(P >0.05)。465 例初筛为可疑 α 地中海贫血，经基因诊断确诊 149 例，筛检阳性比例为 32%；537 例初筛为可疑 β 地中海贫血，经基因诊断确诊 162 例,筛检阳性比例为 30.2%。α 地中海贫血中，东南亚--SEA 基因型构成比最高(48.9%)，其次为-α3,7 基因型(26.5%)和 CS 基因型（16.4%）；β 地中海贫血中，17N 基因型最高(57.3%)，其次为 41-42N 基因型(27.6%)和 654M 基因型（9.9%）。α 地中海贫血基因检出--SEA 等位基因数频率最高，检出频率 61.2%；β 地中海贫血 17N 等位基因数最高，检出频率 58.6%。
结论 黔西南地区儿童地中海贫血发病率较高，基因分布情况复杂，且与贵州其他少数民族聚居区发病基因型存在较大差距，应加强常规筛查及基因学诊断，找到地贫基因频率分布的民族依赖性、性别依赖性或地区依赖性证据。

PO-0603

艰难梭菌抗原和毒素因子检测质控品的研制和临床应用

王庆忠、刘学杰、张敏敏、夏启航
上海市临床检验中心

目的 研制生物安全合格，稳定性强，通用性好的艰难梭菌（*Clostridium difficile*）谷氨酸脱氢酶抗原及毒素检测质控品，用于临床医疗机构实验室室间质量评价。
方法 采用本中心实验室保存的艰难梭菌 ATCC9689 标准菌株作为出发菌株，厌氧培养。收集培养得到的菌体，制备菌悬液，后经超声处理。检测所得破壁悬液的蛋白浓度和细菌培养活性。系列稀释得到最终工作浓度的质控品。采用美国 Alere 艰难梭菌谷氨酸脱氢酶抗原及毒素检测试剂盒评估研制质控品的稳定性和均匀性。所得质控品经本中心室间质量评价网，分发到临床医疗机构实验室，经所在实验室采用各自的检测系统检测回报结果，评价其临床应用价值。
结果 出发菌株经厌氧培养得到合适的菌悬液。经超声处理，破壁悬液蛋白浓度达到 0.56mg/ml。经 4 万倍稀释，试剂盒测定为抗原和毒素阳性，厌氧和好养菌检测，均未检测到细菌生长。制备的质控品在 37℃条件下可稳定 2 周，在-4℃条件下，可稳定 12 月。经质控网络实验室回报数据，2019 年 9 家实验室，2020 年 18 家实验室和 2021 年 23 家实验室，5 批次质控数据，临床检测所采用的酶联免疫层析法和酶联免疫荧光法均质评合格。
结论 本中心自制的艰难梭菌谷氨酸脱氢酶抗原及毒素检测质控品具有 生物安全合格，稳定性强，通用性好的特点。

PO-0604

KCTD12 loss promotes RhoA/RhoB/Rac1-dependent cervical cancer cell metastasis

Liping Li[1]、mei xue[1]、miao juan chen[2]
1. Department of Clinical Laboratory, The Third Affiliated Hospital of Nanchang University, Jiangxi, Nanchang
2. 广州市妇女儿童医疗中心

The metastasis of early stage cervical tumor remains the primary cause of recurrence of cervical cancer. However, its mechanisms is still unclear. To find the key molecular markers for the recurrence and treatment of cervical cancer is the key to reduce the postoperative recurrence rate and mortality.

Our previous studies found that blocking KCTD12 (potassium channel tetramerization domain containing 12) promotes the metastasis of cervical cancer cells. In addition, the negative correlations between the expression of KCTD12 and clinical staging was identified in cervical cancer tissues. Differential proteomics analysis was applied to probe the regulatory mechanism of KCTD12 on the metastasis of cervical cancer cells. The results indicated ARHGEF2, RhoA, RhoB and Rac1 play roles in promoting metastasis of silencing KCTD12 cells. To probe the regulatory effect and molecular mechanism of KCTD12 on the metastasis of cervical cancer cells, real-time fluorescence quantitative PCR, luciferase reporter gene system, co-immunoprecipitation, immunofluorescence localization and other experimental techniques were studied systematically by using in vivo and in vitro cell function experiments.

It was found that blocking KCTD12 enhanced the density and length of filopodia in cervical cancer cells, as a result of promoting the metastasis in cervical cancer cells. And higher expression KCTD12 inhibited the density and length of filopodia and metastasis and in cervical cancer cells. The mechanism study further found that KCTD12 protein regulates the filopodia and metastasis of cervical cancer cells through the activation of RhoA, RhoB and Rac1, which depends on the expression of ARHGEF2. Further research also confirmed silencing KCTD12

stimulates the HDAC6 expression and acetylation of tubulin, which results in ARHGEF2 released from tubulin and functions as activator for RhoA, RhoB and Rac1.

KCTD12 downregulation promotes HDAC6 protein expression, facilitates tubulin deacetylation and depolymerization, which leads to ARHGEF2 releasing from tubulin, which in turn activates RhoA/RhoB/Rac1-GTP and promotes cellular metastasis. KCTD12 therefore constitute an inhibition target in the treatment of cervical cancer.

PO-0605

新冠疫情下实验室认可对完善检验科质量管理体系的价值分析

孙昭辉、公衍文
山东大学第二医院

目的 实验室认可是实现医院检验科质量管理标准化的有效路径，也是完善检验质量体系的重要手段，探讨新冠疫情下 ISO15189 实验室认可在医院检验科质量管理体系完善中的作用。
方法 实验室认可是实验室质量管理的有效手段，在实验室质量管理过程中，依据实验室认可规则和要求，通过采取 PDCA 的方法，按照认可文件中质量体系要求，进一步规范室内质量控制等记录表格、完善仪器设备和检验项目的标准化操作规程（SOP）、程序文件以及质量手册等。根据监督评审中发现的问题，追本溯源，加以整改完善。加强督导检查和培训考核。并对 P、D、C、A 的每一个环节逐项检查，有检查，有追踪，有落实，最终达到质量管理体系逐渐完善的目标。
结果 通过采取上述措施，利用 PDCA 管理手段，在人、机、料、法、环、测等 6 个环节得到明显改善。（1）人员方面：通过持续强化培训考核，实验室人员能够按照分工，岗位职责明确，人员的责任心得到明显提升，室内质量控制失控纠正及时率明显提升，错误报告率明显降低。（2）仪器设备的使用、维护保养方面：能够按照仪器手册，进行系统验证，保证检测系统的良好状态。（3）试剂和耗材：对在用试剂进行准确度、精密度、干扰实验等各项性能验证，保证结果的可靠性。在新冠疫情防控要求下，实验室采取更加严格规范的操作程序，从标本采集开始，直到检验报告的审核签发，每一个环节都采取上述措施进行日常监督和专项督导，使得质量体系文件在各个环节得到有效执行，并加以完善，显著提高了检验质量。
结论 质量体系建设与完善是实验室认可的目标，是提升检验工作质量的主要手段。

PO-0606

重组慢病毒颗粒构建 LONP1 低表达稳转胰腺癌细胞株模型

王海、李丽
东南大学附属中大医院

目的 采用重组慢病毒构建 LONP1 蛋白低表达稳转胰腺癌 PANC1 和 BxPC3 细胞株模型。
方法 在 12 孔培养板中接种靶细胞，待细胞融合率 40%左右时加入吉玛基因公司构建的重组慢病毒颗粒感染靶细胞 PANC1 和 BxPC3，用 1ug/mL 嘌呤霉素进行抗性细胞筛选。在不同时间段用倒置荧光显微镜观察荧光效率，并用 Western Blot 和 PCR 方法检测 LONP1 基因表达水平以验证获得的慢病毒稳转细胞株。
结果 与对照组比较，胰腺癌 PANC1 和 BxPC3 慢病毒稳转细胞株低表达 LONP1 mRNA 和蛋白质水平。
结论 用重组慢病毒颗粒能成功构建 LONP1 低表达胰腺癌 PANC1 和 BxPC3 细胞株模型。为进一步研究 LONP1 基因在胰腺癌中的调控作用奠定基础。

PO-0607

系统性红斑狼疮早期肾损害不同诊断指标临床比较及意义

杨志鹏
山东大学第二医院

目的 探讨不同血清指标单独及联合检测在狼疮肾炎诊断中的临床意义。
方法 纳入 2020 年 1 月---—2020 年 11 月于 风湿免疫科确诊的新发狼疮肾炎住院患者 50 例为观察组，同期系统性红斑狼疮（肾脏未累及）住院患者 50 例为病例对照组，同期健康体检者 50 例为正常对照组。3 组均采用免疫比浊法检测血清补体 C1q、补体 C3、补体 C4、免疫球蛋白 IgG，采用 ELISA 法检测血清抗 C1q 抗体、抗核小体抗体水平，采用受试者工作特征曲线（ROC 曲线）分析评价各检测指标单独及联合检测在狼疮肾炎诊断中的应用价值，差异性分析采用 t 检验，以 P<0.05 为差异有统计学意义。
结果 观察组血清补体 C1q（118.00±30.50mg/L）、补体 C3（0.775±0.182g/L）及补体 C4（0.070±0.013g/L）水平明显低于病例对照组和健康对照组，阳性率（分别为 80.0%、70.0%、84.0%）则明显升高（P<0.05）；观察组血清免疫球蛋白 IgG（22.11±4.87g/L）、抗 C1q 抗体（89.30±20.34Au/ml）及抗核小体抗体（76.85±18.34Ru/ml）水平和阳性率（分别为 76.0%、88.0%、90.0%）均明显高于病例对照组和健康对照组（P<0.05），血清补体 C1q、补体 C3、补体 C4、免疫球蛋白 IgG、抗 C1q 抗体、抗核小体抗体单独检测诊断狼疮肾炎的曲线下面积（AUC）分别为 0.819、0.705、0.742、0.702、0.851、0.894；血清补体 C1q、补体 C4、免疫球蛋白 IgG、抗 C1q 抗体、抗核小体抗体联合检测诊断狼疮肾炎的 AUC 为 0.997。
结论 各血清指标单独检测均有较好的敏感性，具有一定的诊断效能，联合应用多项血清指标具有更高的诊断价值，对 LN 的诊断及治疗有重要临床意义。

PO-0608

高敏肌钙蛋白 I 与核素运动心肌显像相互关系研究

杨冰花、蔺亚晖、周洲
中国医学科学院阜外医院

目的 核素心肌灌注显像（MPI) 能准确诊断心肌缺血及心肌缺血的部位、程度和范围。高敏肌钙蛋白可用于评估运动所致的心肌受损。因此在运动负荷试验的前提下分别进行核素心肌灌注显像（MPI）和高敏肌钙蛋白 I（hs-cTnI)检查，分析不同运动负荷等级下 MPI 结果与 hs-cTnI 浓度值的相关关系。
方法 选择 2019 年 1-12 月有 MPI 检查和 hs-cTnI 浓度结果的患者 532 例，排除需要进一步做心肌显像确诊和结果不确定的患者后剩余 522 例。MPI 检测方法选用踏车运动，按起始负荷量 25W 随后每级增加 25W 将运动级别分为 1，2，3，4，5，6 级。hs-cTnI 检测选用雅培平台。将 MPI 结果与 hs-cTnI 浓度检测结果进行统计学分析。
结果 心肌显像正常患者 hs-cTnI 浓度均值 3ng/l，心肌显像异常患者 hs-cTnI 浓度均值 5ng/l，表明心肌显像异常 hs-cTnI 浓度值越高；运动级别 2,3,4,5,6 分别对应的 hs-cTnI 浓度均值为 3.8ng/l,2.8ng/l,2.7ng/l,2.9ng/l,2.1ng/l,得出运动级别越低，hs-cTnI 浓度值越高；心肌显像异常但心电图正常时，hs-cTnI 浓度均值为 4ng/l,心电图阳性 hs-cTnI 浓度均值为 6ng/l，表明心肌显影异常且心电图阳性时 hs-cTnI 浓度值越高。
结论 在踏车运动负荷试验后，心肌显像异常比心肌显像正常时 hs-cTnI 浓度值高；运动级别越低相对应的 hs-cTnI 浓度值越高；心肌显影异常且心电图阳性时与 hs-cTnI 浓度成正相关。

PO-0609

TBHQ attenuates ferroptosis against 5-fluorouracil induced intestinal mucositis via Nrf2/HO-1 pathway

Li Li
The First Affiliated Hospital of Chengdu Medical

Purpose Intestinal mucositis is a common side effect caused by chemotherapy and radiotherapy. Nevertheless, there are limited drugs that can ameliorates intestinal mucositis efficiently. Tert-butylhydroquinone (TBHQ) is a wildly used food preservative with known immunomodulatory activity. However, whether TBHQ has an effect on intestinal mucositis is still unknown.
Methods We investigated the role and mechanism of TBHQ on 5-fluorouracil (5-FU) induced intestinal epithelial cell injury and intestinal mucositis in mice. We established a model of intestinal epithelial cells (HIECs) injury and a mice model of intestinal mucositis.
Results TBHQ significantly ameliorated 5-FU-induced intestinal epithelial cell damage in vitro and intestinal mucositis in vivo. Moreover, ferroptosis was proved to be involved in 5-FU-induced intestinal mucositis and TBHQ markedly hampered the activation of ferroptosis. Mechanistically, TBHQ effectively activated Nrf2/HO-1 pathway in vitro and in vivo, and selective knock down of Nrf2 significantly abolished the anti-ferroptotic functions of TBHQ in 5-FU treated HIECs.
Conclusion TBHQ attenuates ferroptosis against 5-FU induced intestinal mucositis, identifying TBHQ as a novel potential protective agent for intestinal mucositis.

PO-0610

FGA Knock-out via CRISPR-Cas9 in a Mouse Model Promotes Hepatocellular Carcinoma Metastasis

Xiaoli Zhou[1]、Renwei Jing[2]
1. Department of Laboratory Medicine, Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China.
2. Department of Cell Biology and Key Laboratory of Immune Microenvironment and Disease (Ministry of Education), Tianjin Medical University, Qixiangtai Road, Heping District, Tianjin, 300070, China

PurposeIt is critical to find out new targets for hepatocellular carcinoma therapy. FGA gene has been identified to be related to lung metastasis in non-small-cell lung cancer(NSCLC). However, the function of FGA gene in HCC is still unknown. CRISPR-Cas9-based genetic editing is a powerful tool for generating loss-of-function mutations.
Methods We constructed the murine HCC cell line Hepa1-6 stablely expressing Cas9. Then the FGA-KO cell line was generated with the clustered regularly interspaced short palindromic repeat (CRISPR)-Cas9 system. Single-guide (sg) RNA targeting the FGA gene was designed, and introduced into the Hepa1-6 cell line with Cas9 expression (Hepa1-6-Cas9) by lentivirus infection.
Results Analysis based on the data-mining of ONCOMINE revealed that FGA gene was down-regulated in the HCC compared with the normal liver, indicating its tumor suppressive role. FGA gene, which is frequently mutated in various cancer types in TCGA, was found significantly associated with a poor overall survival and predicted a poor relapse-free survival. Moreover, the knock-out of FGA gene promoted the metastasis of HCC.
Conclusions Using both in vitro and in vivo approaches, we described the profound role of FGA gene. This study verified the potential role of FGA in liver cancer and provided novel candidate target on treatment and therapy of HCC metastasis.

PO-0611

过酸或过碱尿液调整 pH 复测干化学的必要性探讨

丁荣
东南大学附属中大医院

目的 尿干化学蛋白模块易受尿液 pH 值影响，验证调整尿液 pH 值是否能排除过酸或过碱尿液对干化学检测结果的影响。
方法 选取我院住院患者尿液 pH≤5.5 且沉渣结果管型阳性标本 5 例；pH≥8.0 且干化学尿蛋白阳性标本 5 例，分别用磺基水杨酸法、贝克曼库尔特 AU5800 全自动生化分析仪进行尿蛋白检测，在 pH 计辅助下，用 NaOH 或冰乙酸分别调整 pH 至 6.0~6.5，再次进行干化学、磺基水杨酸法、生化分析仪法进行检测，比较调整 pH 前后结果差异，分析是否有必要对过酸或过碱尿液调整 pH 值进行干化学复测。
结果 五例 pH≤5.5 且尿沉渣结果管型阳性标本调整 pH 值前生化分析仪结果四例阳性，其中磺基水杨酸法三例阳性；调整 pH 值后干化学、生化分析仪、磺基水杨酸法结果均四例阳性。五例 pH≥8.0 且干化学蛋白阳性标本调整 pH 值前生化分析仪法四例阳性，其中磺基水杨酸法三例阳性；调整 pH 后生化分析仪法、磺基水杨酸法、干化学法均四例阳性，且其中两例干化学尿蛋白阳性程度明显减低，更符合生化分析仪定量结果。
同时发现 pH≥8.0 三例尿路感染标本中两例白细胞酯酶结果在调整 pH 值后阳性程度有所减低。
磺基水杨酸法不不符合的两例尿液标 pH 计测定结果分别为 4.13、9.48，过低或过高的 pH 值对磺基水杨酸检测造成干扰。
结论 pH≤5.5 且尿沉渣结果管型阳性的标本，四例干化学结果为假阴性，一例磺基水杨酸法为假阴性，调整 pH 值后均可纠正。pH≥8.0 且干化学尿蛋白阳性的标本，一例为干化学结果假阳性，一例磺基水杨酸法为假阴性，调整 pH 值后均可纠正，且干化学尿蛋白结果更符合生化分析仪定量结果。调整 pH 值后干化学尿蛋白、白细胞酯酶结果更符合尿沉渣结果，且操作简便，因此可作为尿干化学结果的纠正手段。

PO-0612

F7 mutation spectrum and molecular characteristics in Chinese factor VII deficiency patients

can Lou、guanqun Xu、yu Liu、jing Dai、qiulan Ding、xuefeng Wang、wenman Wu
ruijin hospital

Introduction Hereditary factor VII (FVII) deficiency is an autosomtic recessive bleeding disorder caused by mutations on F7 gene with a prevalence of 1/500 000.
Aim Current study investigated the genetic variations and the clinical phenotypes associated with FVII deficiency in 56 unrelated Chinese patients to describe the mutation spectrum of F7 gene.
Methods The nine exons, exon-intron boundaries and the 5′ untranslated region of F7 gene was directly sequenced by PCR and the mutation was confirmed by reverse PCR. To investigate the pathogenicity of some identified and novel mutations, we characterised the missense mutations in CHO-K1 cells transiently transfected with expression vectors harboring the wild-type FVII cDNA (FVIIwt) or possessing the p.Ser342Gly, p.Cys238Phe, p.Gly420Asp, p.Gly432Ser, p.Ala252Val and p.Val336Met mutations.
Results Totally 29 different mutations, including 20 missense mutations and 6 splicing mutations, had been identified on the F7 gene. The nucleotide transition c.1224T>G (p.His408Gln) in exon 8 constitutes a hotspot of mutation, with 19 patients harboring the genetic variance. 8 novel mutations, Ser342Gly, Cys238Phe, Gly420Asp, Gly432Ser, Ala252Val, Val336Met, IVS1a+4C>T and c.146delA, were revealed. Compared with the FVIIwt, we found that the secretion of mutants except p.Val336Met were significantly reduced and that of p.Gly432Ser was slightly decreased.

The mutations of p.Cys238Phe, p.Ala252Val and p.Gly420Asp could be classified as type I mutations based on their recombinant expression data of antigen and activity.
Conclusion The severity of bleeding diathesis was not correlated with FVII:C levels detected in patients, and the deficiency of FVII did not prevent patients developing venous thrombosis. Few patients were homologous or compound heterozygous for major gene rearrangements including nonsense mutation, large insertion or deletions, indicating that complete deficiency of FVII was not compatible with life.

PO-0613

External Quality Assessment (EQA) program for autoantibodies assays: a 5-years experience in Chongqing

Qiongwen Hu、Pu Liao
Chongqing General Hospital, University of Chinese Academy of Sciences,

Objective Autoantibodies assays play a very important role in the diagnosis and treatment of autoimmune diseases. In recent years, more and more clinical laboratories have carried out autoantibody assays. Participation to External Quality Assessment (EQA) programs is an essential requirement for laboratories. In this study, we aimed to report an overview of the EQA results of autoantibodies detection in Chongqing between 2017 and 2021.
Methods These EQA programs was implemented twice a year from october 2017 through may 2021, including anti-CCP and antinuclear antibodies (anti-dsDNA, anti-ENA, ANA). The proficiency testing （PT） database was reviewed and analyzed to assess the testing performance of the participating laboratories and the impact of the program over time.
Results The number of laboratories participated in the EQA program of anti-CCP increased from 14 in 2017 to 33 in 2021. The number of laboratories participated in the EQA program of antinuclear antibodies increased from 16 in 2017 to 30 in 2021. Most participating laboratories had a PT score of 80% or above and they were recognized as qualified. The laboratory methodology of ANA, anti-ENA and anti-dsDNA was relatively simple between these participations. Indirect immunofluorescent assay (IIFA) was the main test method of ANA. Immunoblotting (IBT) was the main test method of anti-ENA. IBT and IIFA were main test methods of anti-dsDNA. However, there were various detection methods of anti-CCP. The number of laboratories using enzyme-linked immunosorbent assay (ELISA) and chemiluminescence immunoassay (CLIA) have significant difference between 2017 and 2021. The number of laboratories using ELISA in may 2021 was less than that in october 2017 (P=0.026). The number of laboratories using CLIA in may 2021 was more than that in october 2017 (P=0.043). The HEp-2 cell patterns of ANA included Nuclear Speckled, Nuclear Centromere, Nuclear Homogeneous, Nuclear Nucleolar and Cytoplasmic Speckled during these EQA programs. The proportion of correct laboratories is between 76.5% and 100.0%.
Conclusion In conclusion, we reported the development of EQA program for autoantibodies assays in Chongqing between 2017 and 2021. The number of autoantibodies testing laboratories is increasing year by year. The laboratory methodology is constantly improving. Most of the participant laboratories had satisfactory performance for the results in these EQA schemes.

PO-0614

一例 DNMT3A 基因杂合缺失导致的 Tatton-Brown-Rahman 综合征的遗传学分析

余秀蓉、王志红
联勤保障部队第九〇〇医院

目的 对一个临床表现为说话和语言发育延迟、智力障碍、运动发育延迟、脑发育不全、全面性发育迟缓、身材高大的先证者及其家系进行遗传学分析。
方法 收集先证者表型，分别采集先证者及其父母（表型正常）的外周血，通过 Trio-WES+Trio-CNVseq 寻找可疑的致病变异，然后对发现的可疑致病变异进行致病性分析。
结果 Trio-WES 结果显示先证者 DNMT3A 基因 EXON:2-23 杂合缺失，其父母亲均为野生型。Trio-CNVseq 结果显示先证者染色体核型 46,XY，染色体微缺失/微重复检测结果 seq[GRCH37]del(2)(p24.1p23.3)(chr2:23608318-25907862)位置存在约 2.30Mb 的可能致病性的杂合缺失，该区域包含 DNMT3A 基因，其父母亲均为野生型。DNMT3A 基因变异导致的 Tatton-Brown-Rahman 综合征临床表现为身材高大、巨头畸形、圆脸、睑裂狭小、视神经发育不全、智力障碍、癫痫发作、全身性低张力、脐疝、房间隔缺损、脊柱侧弯、小脑扁桃体下疝畸形 I 型、脑软化、小睑裂等。经查阅 HGMD、OMIM 和 Clinvar 数据库，先证者的杂合缺失为未报道过的新发（denovo）变异。根据 ACMG 遗传变异分类标准与指南，该变异符合 PVS1+PS2+PM2，可以判断为致病性变异。此外，先证者突变符合 Tatton-Brown-Rahman 综合征常染色体显性遗传（AD）疾病发病机制，先证者及其家系成员符合表型及基因型的共分离。
结论 根据生物学致病性分析、遗传模式以及临床表型基因型比对，提示先证者 DNMT3A 基因变异的危害性与其表型存在相关性，即先证者 DNMT3A 基因杂合缺失导致 Tatton-Brown-Rahman 综合征可能性大。DNMT3A 基因新发致病性变异的检出为该家系的遗传咨询和分子诊断提供了可靠依据，丰富了该基因的突变谱。

PO-0615

免疫固定电泳在异体干细胞移植后寡克隆条带检测中的应用

林炜炜[2]、徐燕萍[1]、李敏[1]、沈莉菁[3]
1. 上海交通大学医学院附属仁济医院 检验科
2. 上海交通大学医学院附属仁济医院 检验科
3. 上海交通大学医学院附属仁济医院 血液科

目的 明确免疫固定电泳在异体干细胞移植后中寡克隆条带检测意义。
方法 取我院在 2020 年 3 月后行异体干细胞移植的 8 例多发性骨髓瘤（MM）患者，利用免疫固定电泳技术对移植前及移植后不同时间点进行免疫球蛋白克隆检测。在免疫固定电泳结果中出现的与初诊 M 蛋白不同，且彼此分开、比较狭窄而不连续的 3 个或 3 个以上的区带定位寡克隆条带。
结果 8 例多发性骨髓瘤患者包括 3 例 IgG kappa 型，2 例 IgG lambda 型和 2 例 IgA kappa 型，1 例未分泌型。8 例患者均接受了异体骨髓干细胞移植治疗。移植后，有 4 例患者血清出现了明显的克隆转换和寡克隆免疫球蛋白，移植后出现的寡克隆条带均为 IgG 型。最早出现在移植后 2 个月（见附图），最晚在移植后 5 个月出现，其余病例在继续随访中。4 例移植后寡克隆条带均在 M 蛋白减弱期间出现，并随 M 蛋白的消失，寡克隆条带逐渐增强。
结论 免疫固定电泳是随访异体干细胞移植患者免疫重建的有效方法。

PO-0616

扩张型心肌病候选基因多态性的最新研究进展

施小晴
郑州大学第一附属医院

扩张型心肌病（DCM）的发病率和病死率很高，是引起心力衰竭（心衰）和心脏移植的主要原因。ＤＣＭ 的发病机制有很多种，其中遗传因素起关键作用，许多单核苷酸多态性（ＳＮＰ）位点已被发现与 ＤＣＭ 相关。本篇综述概括了近几年 ＤＣＭ 的遗传研究进展，并总结了截止到目前发现的与 ＤＣＭ 易感性相关的 ＳＮＰ，旨在为ＤＣＭ 的预防和控制提供参考。

PO-0617

ODF1 基因多态性与断头精子发生的关系

张朵
中国人民解放军联勤保障部队第 900 医院

目的 探讨 ODF1 基因变异与人类断头精子发生的关系。
方法 收集断头精子（acephalic spermatozoa syndrome, ASS）患者精液和血液标本，提取精子中的 RNA，通过 RT-PCR 的方法扩增 ODF1 cDNA，Sanger 测序对扩增产物进行检测。提取血细胞 DNA，针对 ODF1 cDNA 中发现的变异位点设计扩增 ODF1 DNA 相应位点的引物，PCR 扩增后，Sanger 测序对 DNA 扩增产物进行检测。生物信息学分析 ODF1 基因变异位点可能对蛋白质高级结构产生的影响。100 名已生育男性的血液 DNA 作为对照。
结果 10 例 ASS 患者中，3 例携带 ODF1 基因一处 27bp 纯合缺失（c.760T_787Gdel，p.Asn219_Cys227del），3 例患者为该位点杂合子携带者，10 例 ASS 患者的变异频率为 0.450。其中纯合子占 30%。100 例对照中，该位点的变异频率为 0.321，其中纯合子仅占 1.9%。生物信息学分析发现该缺失为一基因多态性（rs568456031），在千人数据库中的变异频率为 0.313。在人类疾病数据库中，未对该多态性做注释。
结论 ODF1 基因多态性（rs568456031）可能对 ASS 患者发病起某种程度辅助作用，是 ASS 发病的修饰基因。

PO-0618

消化道粘液腺癌卵巢转移伴睾酮增高 1 例

王宁、王承缙、张月香
天津市中心妇产科医院

本文中患者女，47 岁，主因“查体发现盆腔肿物”入院，彩超提示：子宫上方略偏右侧至子宫上方可见一 109×109×81mm 肿块，内大部分为中强回声团块。入院后查肿瘤标记物：CA199：35U/ml，睾酮：433.0ng/dl，择日行开腹探查术，术中见：宫底部及后壁可见浆膜下子宫肌瘤，直径分别 1cm，右卵巢囊实性肿物 12×11×10cm 大小，表面光滑，直肠前壁及右骶韧带处可见病灶，质硬，直径均 2+cm 大小，膀胱腹膜折返病灶直径 1.5cm。考虑右侧卵巢肿物，切除右附件送冰冻结果为（右侧附件肿物）腺癌，部分呈肠型上皮，不除外转移性。术中快速免疫组化结果显示：CK7（部分+），CK20（部分+），Pax-8（-），CDX-2（小灶弱+）。病理回报右侧卵巢肿物：粘液腺癌（肠型），组织学形态及免疫表型均支持为消化道来源，其中直肠前壁病灶癌组织达两侧边缘（肌层及浆膜侧），卵巢肿瘤间质内可见较多散在或小团黄素化间质细胞，符合功能性间质。术后复查患者睾酮下降至 32.3ng/dl。卵巢转移瘤最常起源于胃肠道，尤其是胃和结肠，且卵巢粘液

性肿瘤常常伴有功能性间质，导致雌激素升高表现，但消化道粘液腺癌卵巢转移伴睾酮增高报导较少。本患者术前由于功能间质分泌导致睾酮升高，术后睾酮较前明显下降，为存在功能间质的消化道粘液腺癌卵巢转移患者的早期诊断和术后治疗效果评估提供了新思路。

PO-0619

3 个多囊肾病家系的胚胎植入前遗传学诊断

张在卉、王志红
联勤保障部队第九〇〇医院

目的 探讨携带多囊肾病（polycystic kidney disease，PKD）致病基因突变的家系中，胚胎植入前遗传学诊断（preimplantation genetic diagnosis，PGD）技术在帮助实现孕育正常后代、阻断 PKD 致病基因垂直传递中的可行性及效果。
方法 选择 3 个已明确分子诊断并要求 PGD 助孕的 3 个 PKD 家系，ADPKD 家系 1： PKD2 基因 IVS10+2T>C 杂合突变；ADPKD 家系 2： PKD2 基因 c.602delG 杂合突变；ARPKD 家系 3：PKHD1 基因 c. [889T>A];[11314C>T]复合杂合突变），采用囊胚滋养外胚层细胞活检、单细胞全基因组扩增（whole genome amplification，WGA）及 NGS（Next-generation sequencing）平台，运用联合诊断单基因病和染色体病非整倍体高通量测序与连锁分析（mutated allele revealed by sequencing with aneuploidy and linkage analyses，MARSALA）策略进行胚胎植入前遗传学诊断，挑选健康胚胎进行移植，在孕中期行羊水穿刺产前诊断，新生儿出生后进行跟踪随访。
结果 3 个家系 4 个 PGD 周期共检测 15 枚囊胚，每个家系均获可移植胚胎，其中包括正常基因型的整倍体胚胎 6 枚，表型正常的 ARPKD 携带者基因型的整倍体胚胎 2 枚。家系 1 先后移植 3 枚胚胎但未受孕，家系 2,3 移植正常胚胎后成功受孕，羊水产前诊断结果与 PGD 结果一致，且已生育健康后代，生后随访一切正常。
结论 对于明确致病基因突变的 PKD 家庭，基于 MARSALA 策略的 PGD 技术能够阻断致病基因的垂直传播，帮助生育健康胎儿。

PO-0620

端粒保护蛋白在肿瘤发生和治疗中的作用机制

高川力
川北医学院

端粒保护蛋白组成了蛋白复合物 shelterin，shelterin 是由六个端粒保护蛋白所构成的，其功能复杂多种多样。但该蛋白复合物有一重要的功能就是能够维持染色体末端稳定性。当端粒保护蛋白对端粒保护不足时则会引起 DNA 双链断裂等情况，从而产生 DNA 损伤等，使端粒暴露在有害环境下，这可能导致端粒和基因组完整性受损，进而引发肿瘤。在现代生活中，由于生活压力增大，生存环境不良，食品安全得不到保障等因素，人们所患癌症的几率越来越高，所患癌症的种类越来越多样。目前对于肿瘤的治疗主要有放射疗法和化学疗法两种，肿瘤放射治疗是利用放射线治疗肿瘤的一种局部治疗方法，而化学疗法则是利用化学药物清除癌细胞的一种治疗方式。这两种方式对癌细胞的作用都可能导致癌细胞突变或者死亡。癌细胞中 DNA 损伤修复反应（DDR）的结果是放射治疗和化学治疗后癌症发展和癌症结局的重要决定因素。DNA 损伤修复反应（DDR）与癌症发展的易感性有关，它可能导致对治疗的敏感度上升，从而可以用来改善癌症；它也可能突变后产生耐药性，使我们治疗癌症的难度加大。鉴于端粒保护蛋白与 DDR 之间的关系，端粒保护蛋白可能会成为治疗癌症新的靶点，通过端粒保护蛋白来增强对放射疗法和化学疗法的肿瘤敏感性，以此提高癌症治疗效果。

PO-0621

环状 RNA hsa_circ_0008591 在乳腺癌中的表达及功能研究

董相君、孔雪、王传新
山东大学第二医院

目的 乳腺癌是全球最常见的恶性肿瘤，严重危害女性健康。环状 RNA（circular RNA, circRNA）是一种具有连续闭合环状结构的非编码 RNA，不易被核酸外切酶降解，在生物体内更加稳定，这使其具有成为生物标志物的潜能。然而，circRNAs 在乳腺癌进展中的作用尚未完全阐明。本研究旨在探讨新型 circRNA hsa_circ_0008591 在乳腺癌中的表达水平及其生物学功能。
方法 选取 6 对乳腺癌组织与对应癌旁正常组织进行高通量 circRNA 芯片检测，根据 fold change>2 或＜0.5、p 值＜0.05 且转录本长度在 500-1500nt 的标准，对组织中差异表达的 circRNA 进行初步筛选。使用 GO 和 KEGG 分析，进一步选取与细胞周期、细胞增殖等生物学作用相关的 circRNAs，采用实时荧光定量 PCR（quantitative real-time PCR， qRT-PCR）对 circRNAs 在细胞系及血清样本中的表达水平进行验证，最终选定候选分子。通过 sanger 测序确定其环化位点，利用 RNA 酶、放线菌素 D 实验验证其环状特性及稳定性。使用质粒转染的方式，在乳腺癌细胞 MDA-MB-231 中过表达 hsa_circ_0008591。通过 RTCA 实时细胞检测技术评估 hsa_circ_0008591 对乳腺癌细胞增殖能力的影响。采用 TargetScan、miRDB、miRTarbase、Tarbase 四种数据库预测其下游靶基因并利用 cytoscape 软件构建其 ceRNA 互作网络。
结果 根据 circRNA 芯片结果和初步筛选标准，发现 2656 个在乳腺癌组织中差异表达的 circRNAs。GO 和 KEGG 分析结果显示，共有 19 个 circRNAs 与细胞周期和增殖作用相关，其中有 6 个上调和 13 个下调。qRT-PCR 结果表明，乳腺癌细胞株 hsa_circ_0008591 的表达水平明显低于正常乳腺上皮细胞，其在乳腺癌患者血清样本的表达也明显低于健康对照者，这与芯片数据一致，作为最终研究对象。qRT-PCR 显示转染了过表达质粒后，乳腺癌细胞系 MDA-MB-231 中 hsa_circ_0008591 的表达水平明显升高。RTCA 结果证实，过表达 hsa_circ_0008591 后，乳腺癌细胞的增殖能力明显减弱。TargetScan、miRDB、miRTarbase、Tarbase 数据库及互作网络提示其可能通过 ceRNA 机制调控下游靶基因从而抑制乳腺癌的增殖作用。
结论 研究表明 hsa_circ_0008591 在乳腺癌中低表达并可抑制乳腺癌的增殖，可作为乳腺癌患者潜在诊断的分子标志物及治疗靶点。

PO-0622

The Relation of Coagulation Test with Varying Levels of Thyroid Stimulat-ing Hormone

Guangzhen Fu 、Liang Ming
The First Affiliated Hospital of Zhengzhou University

Aim To investigate the changes in coagulation test results in subjects with varying serum levels of thyroid stimulating hormone.
Methods We performed a one-year retrospective analysis to retrieve combined results of activated partial thromboplastin time (APTT), prothrombin time (PT), fibrinogen (Fib), D-dimer, free thyroxine (fT4), tri-iodothyronine (fT3), and thyroid stimulating hormone (TSH) from inpatients who were referred by general practitioners for routine blood testing. Cumulative results were retrieved for 2794 such inpatients.
Results Patients with a TSH level <0.34 μIU/mL had higher PT values (10.43±1.02 vs 10.27±0.91) and Fib values (3.00±0.92 vs 2.7±0.56) compared with patients with 0.34 μIU/mL < TSH < 5.6 μIU/mL. Conversely, the PT values (10.01±0.95 vs 10.27±0.91) were lower and APTT (33.70±4.17 vs 32.56±4.12) values higher in patients with TSH > 5.6 μIU/mL compared to patients with 0.34 μIU/mL < TSH < 5.6 μIU/mL.

Conclusions There are changes in coagulation test results in subjects with varying levels of thyroid stimulating hormone.

PO-0623

Infectious endophthalmitis caused by Abiotrophia defectiva after penetrating injury in Child：A case report and case review

Jin Deng、mei kang、quanfeng liao、weili zhang、siying wu、ya liu
west china hospital of sichuan university

Background There have been few reports of endophthalmitis caused by Abiotrophia defectiva. We report a case of infective endophthalmitis caused by Abiotrophia defectiva in a 7-year-old Tibetan girl with a pencil injury. We aim to understand that Abiotrophia defective can also cause eye infections, and this pathogen should be covered during empirical antibiotic treatment.
Case presentation: A 7-year-old girl was stabbed with a pencil on her left eye. She developed vision loss, redness, and eye pain. The vitreous humor was taken from the left eye during vitrectomy and lens extraction and sent for examination and culture. Abiotrophia defectiva bacteria were isolated in the specimen.
Conclusions In addition to being known to cause infective endocarditis, Abiotrophia defectiva can also cause potentially infectious endophthalmitis. In addition, clinicians should send samples to infected patients in time, look for evidence of disease, make accurate pathogen diagnosis, and change the treatment plan in time based on the results of drug sensitivity tests.

PO-0624

胰腺癌来源的外泌体表型质谱分析

李雁儒
山东大学第二医院

肿瘤细胞来源的外泌体蕴含丰富的蛋白和特异性核酸等物质，在磷脂双分子层膜的保护作用下稳定存在于多种体液，实时反映机体荷瘤状态，被认为是液体活检最佳对象。

我们通过超速离心法对 8 对健康和胰腺癌患者血清进行外泌体富集，通过透射电镜和纳米颗粒跟踪分析对富集的外泌体进行表征，Western blot 验证其表面蛋白的存在。然后进行液相色谱串联质谱分析，筛选差异表达的蛋白分子，Western blot 及流式细胞术验证蛋白表达差异及亚细胞定位。最后通过大样本检测，构建联合诊断模型进行疾病诊断。

通过数据库、Western blot 及流式细胞术等多轮验证，最终筛选出 2 个定位于外泌体膜表面的蛋白分子，分别是 MUC5AC、LRG1。最终构建可用于癌症诊断的联合诊断模型。

PO-0625

6s 管理在临床实验室分析前质量管理中的应用

陈姝樾
重庆市人民医院

分析前质量管理具有影响质量因素的多环节性、复杂性、质量缺陷的隐蔽性、以及质量保证工作中非检验人员完全可控性、工作责任难确实性等特点。为保证检验质量更好的起到支持和辅助疾病的临床诊疗作用，临床实验室必须进行严格而全面质量管理，须贯穿于检验分析前、分析中、分

析后持续改进的过程。本文结合实验室管理经验，将 6s 管理法应用于临床实验室管理，从分析前流程的各个要素入手阐述对临床实验室分析前质量管理心得。
目的 探索 6s 管理法在临床实验室管理中的应用；
方法 将 6s 管理法中对各种生产要素（如人员、机器、材料、方法等）以整理（Sort）、整顿（Straighten）、清扫（Shine）、清洁（Standardize）、素养（Sustain）、安（Safety）为核心的管理模式应用于临床实验室分析前质量管理过程中，探索应用 6s 管理优化实验环境和流程前后对实验室分析前阶段质量管理的影响；
结论 在引入 6S 管理后优化了工作环境，提高了工作效率，提升了员工的综合素养，多维度降低了标本不合格率，使服务水平跃上了新台阶。

PO-0626

产 KPC-2 肺炎克雷伯菌 ST11 在重症监护室病人胃肠道的分布调查及遗传相关性分析

曹小利[1]、李阳[2]
1. 南京大学医学院附属鼓楼医院
2. 南京鼓楼医院

目的 分析产 KPC-2 肺炎克雷伯菌 ST11 在我院重症监护室住院病人胃肠道的定植情况，并分析 blaKPC-2 阳性肺炎克雷伯菌 ST11 菌株之间的遗传相关性。
方法 采集我院重症监护室 ICU 病人的肛拭子，使用含有 0.5%美罗培南的麦康凯平板筛选碳青霉烯不敏感肺炎克雷伯菌，K-B 法测定其对临床常用抗菌药物的敏感性；采用 PCR 法和 DNA 测序技术检测 blaKPC-2 基因；多位点序列分型技术分析利用 blaKPC-2 阳性肺炎克雷伯菌菌株的序列分型（ST），筛选出 ST11 菌株。脉冲场凝聚电泳(PFGE)技术分析产 blaKPC-2 肺炎克雷伯菌 ST11 菌株之间的遗传相关性。
结果 总共 收集肛拭子 125 个，阳性培养细菌中，30 株为碳青霉烯耐药肺炎克雷伯菌。27 株为肺炎克雷伯菌 ST11，26 株细菌携带 blaKPC-2 基因,25 株细菌为产 KPC-2 肺炎克雷伯菌 ST11。PFGE 结果显示 19（76%）株产 KPC-2 肺炎克雷伯菌 ST11 菌株之间有很大的遗传相关性。
结论 产 blaKPC-2 肺炎克雷伯菌 ST11 在我院重症监护室病人胃肠道中定植广泛，可能是其感染的主要病原菌，需加强感染控制措施。

PO-0627

碳青霉烯耐药大肠埃希菌的基因组学特点分析，重在关注 NDM 和 KPC-2 的共存

曹小利
南京大学医学院附属鼓楼医院

目的 分析碳青霉烯耐药大肠埃希菌（CREC）的基因组流行病学特征，调查共携带 blaNDM 和 blaKPC 的大肠埃希菌在我院的流行情况，并分析该类细菌的播散特点。
方法 对 2015 年从江苏南京 6 家医院收集的 11 株 CREC 菌株，进行全基因组测序组装后，分析耐药基因、毒力因子、多位点序列型（MLST）、血清型和 FimH 型的分布并构建系统发育树。对于从我院 2013-2017 年期间收集的 CREC 菌,使用 PCR 和 DNA 测序法筛选共携带 blaNDM 和 blaKPC 的菌株,使用脉冲场凝聚电泳技术（PFGE）进行遗传相关性分析；使用接合实验分析基因的可转移性。

结果 所有的 CREC 都携带了至少一种碳青霉烯酶编码基因，其中，9 株 CREC 细菌携带 blaNDM-5，3 株携带 blaKPC-2，2 株携带 blaNDM-1，3 株同时携带 blaNDM-5 和 blaKPC-2。11 株 CREC 株中，有 10 株携带 blaCTX-M 基因。MLST 分析发现 7 种不同的序列分型（ST），2 株细菌为 ST410，其余的 6 种 ST 型依次为 ST3489、ST156、ST683、ST297、ST167 和 ST361；其次，11 株细菌中鉴定出 6 种不同的血清型和 8 种 Fim 型；11 株细菌的质粒图谱虽然呈多样性，但每株细菌都含有质粒复制子 IncX3。系统发育分析表明，11 个 CREC 分离株之间有很大的遗传多样性；脉冲场凝胶电泳显示 6 株共携带 blaNDM 和 blaKPC 的分离株之间都存在较大的遗传多样性。结合实验表明 blaNDM 是可转移的，但与 blaKPC 基因不在同一质粒。
结论 blaNDM 是 CREC 中主要的碳青霉烯酶基因，blaNDM-5 是主要的 blaNDM 基因，可能通过 IncX3 质粒水平传播。MLST、Fim 分型、血清分型和进化树发育表明了 CREC 的遗传多样性。

PO-0628

Impact of environmental cleaning on the colonization and infection rates of multidrug-resistant Acinetobacter baumannii in patients within the intensive care unit in a tertiary hospital

xiaoli cao[1]、Yang Li[2]
1. Nanjing Drum Tower Hosiptal
2. 南京鼓楼医院

Objective To continuously evaluate the effect of environmental cleaning on the colonization and infection rates of multidrug-resistant Acinetobacter baumannii (MDR-AB) in the patients within an intensive care unit (ICU).
Methods Environmental cleaning on the high-touch clinical surfaces (HTCS) within a comprehensive ICU was evaluated through monitoring fluorescent marks when the overall compliance with hand hygiene during 2013-2014 was monitored. Meanwhile, samples from the HTCS and inpatients were collected and sent for bacterial culture and identification. The drug susceptibility testing was further implemented to monitor the prevalence of MDR-AB. The genetic relatedness of MDR-AB collected either from the HTCS or inpatients was analyzed by pulsed field gel electrophoresis (PFGE) when an outbreak was doubted.
Results The overall compliance with hand hygiene remained relatively stable during 2013-2014. Under this circumstance, the clearance rate of fluorescence marks on the environmental surfaces within ICUs significantly increased from 21.9% to 85.7%, and accordingly the colonization and infection rates of MDR-AB decreased from 16.5‰ to 6.6‰ and from 7.4‰ to 2.8‰, respectively, from the beginning to the end of 2013. However, during 2014, because of frequent change and movement of cleaning workers, the clearance rate of fluorescence marks decreased below 50%, and the overall colonization and infection rates of MDR-AB correspondingly increased from 9.1‰ to 11.1‰ and from 1.5‰ to 3.9‰, respectively. PFGE displayed a high genetic relatedness between the MDR-AB strains analyzed, indicating a dissemination of MDR-AB during the surveillance period.
Conclusion For the easily disseminated MDR-AB within ICUs, the clearance rateof fluorescence labeling on HTCS is negatively correlated with the hospital infection rate of MDR-AB. Such an invisible fluorescence labelling is an effective and convenient method to continuously monitor cleanness of medical environment within hospitals.

PO-0629

铁死亡相关基因对 EMT 的作用及其氧化机制的研究

孙露露
德州市人民医院

目的 转化生长因子-β1 (TGF-β1)诱导的上皮-间充质转化(EMT)被认为参与肺纤维化的发病机制。新出现的证据表明，铁死亡和肺纤维化发生之间存在共同的原因。
方法 通过检测 a-平滑肌动蛋白(a-SMA)、e -钙粘蛋白(E-cadherin)、溶质载体家族 7 成员 11 (SLC7A11)和谷胱甘肽过氧化物酶 4 (GPX4)的含量以及测定活性氧(ROS)、丙二醛(MDA)和谷胱甘肽(GSH)来探知 EMT 与铁死亡的相互作用及其机制。并分别用显微镜和透射电镜(TEM)观察细胞形态和线粒体的超微结构。
结果 Erastin 可诱导 A549 细胞发生铁死亡，使 A549 细胞中 E-cadherin、a-SMA、SLC7A11 表达水平降低，伴 ROS 和 MDA 水平升高以及谷胱甘肽的减少。TGF-β1 促进线粒体超微结构的变化和铁死亡相似，同时 A549 细胞在 EMT 过程中，间充质细胞形态发生改变，GSH 含量降低，SLC7A11，ROS 和 MDA 表达增加。Fer-1 恢复了 erastin 诱导的铁死亡，而对 TGF-β1 引起的形态学变化无影响。此外，Fer-1 还能减少 ROS 和 MDA，早期 SLC7A11 表达增加，随后 GSH 表达增加。然而，Fer-1 对上述指标的影响随时间的不同而不同。TGF-β1 诱导的 A549 细胞中 EMT 和 Erastin 诱导的铁死亡中 GPX4 表达无显著性差异。
结论 Erastin 促进肺上皮细胞去上皮化，但抑制肌成纤维细胞的分化过程；Fer-1 能部分抑制 TGF-β1 诱导的 EMT，但能逆转 Erastin 诱导的铁死亡。TGF-β1 能延缓铁死亡，但不能预防铁死亡。脂质过氧化，谷胱甘肽消耗和 SLC7A11 抑制是 A549 细胞 EMT 和铁死亡的常见原因，但在特异性上有所不同。GPX4 在 A549 细胞中参与 EMT 和铁死亡的确切作用有待进一步研究。

PO-0630

中部地区 2020 年 300 例腺样体肥大患儿的血清过敏原分析

马翔、柯欢、曾叶、刘翔、向赟
华中科技大学同济医学院附属武汉儿童医院

目的 探讨中部地区 2020 年腺样体肥大患儿的血清过敏原分布情况及其检测的临床意义。
方法 应用江苏浩欧博过敏原体外诊断试剂检测门诊及住院 300 例腺样体肥大患者和随机筛选的 300 例非腺样体肥大儿童的血清中常见的吸入性和食物性过敏原特异性 IgE 水平，比较两组病例的过敏原特异性 IgE 水平差异性。
结果 腺样体肥大组，126 例(42.0%)存在 1 级以上过敏原，27 例(9.0%)存在 2 级及以上过敏原，非腺样体肥大对照组，57 例(18.0%)存在 1 级以上过敏原，14 例(4.7%)存在 2 级及以上过敏原。腺样体肥大组血清过敏原特异性 IgE 阳性率由高低的顺序为屋尘螨占 17.0%，粉尘螨占 14.0%，虾占 12.5%，牛奶占 11.3%，鸡蛋占 7.5%，屋尘占 6.1%，螃蟹占 5.1%，交链孢霉占 3.2%，猫上皮占 2.9%，狗上皮占 1.8%，蟑螂占 1.1%。
结论 腺样体肥大患儿的过敏原特异性 IgE 水平阳性率明显高于对照组。吸入性尘螨和食物性鸡蛋白是腺样体肥大患儿最常见的过敏原，腺样体肥大发病率可能与过敏反应之间有密切关系。

PO-0631

临床实验室人事管理系统的开发和应用

承宝贵、郭非凡、姚恒、吕康琪、李敏、熊丹、张秀明
深圳市罗湖医院集团

目的 在经济快速发展的现代，互联网的出现给社会以及人民大众带来了巨大的好处。其中之一就是通过运用网络，使得各种管理越来越方便。由于经济的发展，人才流动不再受地域限制，并且流动量较大。因此对于一些“以人为本”的企业、政府、实验室等来说，人才非常的重要。需要在现有的人事管理系统基础上，结合计算机以及相关的专业知识，开发一套适用于实验室的人事管理系统。
方法 通过研究国内外的开发背景，对实验室中人事管理的应用进行概述，阐述其应用特点、优势以及开发前景。
结果和结论 根据 ISO15189 中的人员准则条款对员工进行管理。在人事管理系统中可以很清晰的查看到员工的教育经历、工作经历、培训记录、任职等情况。人事管理系统的功能是将实验室内部员工的全部信息进行系统性的集中管理，并对信息进行编号管理，通过电脑能够对信息进行查询、保护信息的安全， 为实验室在人事管理工作上提供便利。与其他人事管理系统相比，实验室人事管理系统有操作方便、保密性强、存储量大等优点。本系统是从实验室人事管理实际需求进行开发的，适用于不同的实验室。

PO-0632

临床实验室流程式电子记录系统的开发和应用

郭非凡、承宝贵、姚恒、吕康琪、李敏、熊丹、张秀明
深圳市罗湖医院集团

目的 为了使临床实验室适应于不断发展变革的大环境，满足实验室实验、管理等需求，讨论研究智能化管理在临床实验室管理中的应用模式，结合临床实验室的目的需求，提出了“标准化智慧实验室管理平台”系统。该系统通过利用互联网技术与实验室相关管理相结合，从而实现了实验室管理的信息化与高效化。基于“标准化智慧实验室管理平台”的理念，设计了多种模式板块，其中电子记录系统在传统纸质记录的基础上运用互联网技术实现信息快速高效查找，进一步提高了管理效率。此次就“标准化智慧实验室管理平台”中的电子记录系统的开发与应用进行讨论。
方法 通过研究电子记录系统的开发背景，对电子记录系统的概述以及应用进行研究，阐述临床实验室流程式电子记录系统的应用特点及其发展前景。
结果与结论 电子记录系统依据 ISO15189《医学实验室质量和能力认可准则》“管理记录”和“技术记录”的每个条款要求将所有表格电子化。依据互联网对实验室中的人员数据的存档、查询、统计等以及对实验室中仪器数据的查询、监控、统计等以电子形式存在的信息，从而起到更为及时清晰准确的监察与提醒作用。电子记录系统不仅可以实现对指南文档等的 记录，也实现了对于日常工作中的直观电子化记录。相较于纸质记录，电子记录可操作性强、保存期限长，并且还可以实现查询功能、数据统计功能与提醒监督功能。电子记录系统不仅可以作为“标准化智慧实验室”的特色模块，其本身也可以作为一种独立的系统板块。

PO-0633

浅谈检验医师如何发挥在临床诊疗中的积极作用

沈国银
上海市第一人民医院嘉定分院

随着医学技术的飞速发展，医学检验已经发展成为包含临床血液学检验、临床体液学检验、临床生化检验、临床微生物学检验、临床免疫学检验、分子生物学检验等多门亚专业学科组成的独立的一级临床学科---检验医学。实验室检查在疾病的临床诊断、疗效观察，预后评估等方面发挥着越来越重要的作用。现代医学的发展离不开检验医学，但在临床诊疗的过程中，由于医生和检验人员专业信息结构的不对等，当临床医生对于某个患者的检验结果有异议时，检验人员却无法给出合理的解释。长此以往两者之间将产生不信任和隔阂。2003 年国际标准化组织发布的 ISO15189：2003《医学实验室---质量和能力的专用要求》、《医疗机构临床实验室管理办法》中第 20 条规定都提出：医疗机构临床实验室除对患者的标本进行各种检测外，还应当提供临床检验结果的解释和咨询服务。这时就需要检验医师积极参与到临床诊疗中，作为桥梁作用，将有限的检验数据转化为有价值的临床诊断信息。2003 年中国医师协会检验医师分会在北京成立，标志着检验医师队伍正式诞生。

本文从以下几个方面探讨在新医科背景下检验医师如何发挥在临床诊疗中的积极作用，从而提高检验医师在医疗过程中的职业满足感和价值感。

1. 培养检验医师人才，提高检验医师人文文化素质和临床思维。
2. 检验医师参与整个检验过程，包括分析前，分析中，分析后三个阶段。
3. 检验医师作为临床和检验沟通的桥梁，与临床的沟通方式可以多样化。

3.1 检验医师在审核报告的过程中发现异常报告或怀疑的结果直接电话与临床沟通。

3.2 解释性报告、诊断报告的签发是检验医师直接参与临床决策的一种方式，检验医师对异常结果能根据疾病的发生发展与检验指标的关系，给出书面解释分析以及进一步检查的建议。

3.3 检验医师参与临床查房和 MDT，提高检验在临床诊断治疗中的参与度。

3.4 由医教科牵头组织，定期开展与临床交流的沟通会议。

3.5 举办检验医学学术讲座，向临床介绍推广检验新技术新方法。

3.6 通过院内 OA 系统、微信公众号等现代化自媒体，设检验专栏，包括国内外检验动态、检验案例分析等。

3.7 加强与临床医生的科研合作，利用实验室检测技术上的优势，申请并参与临床科研课题。

4. 检验科开设检验咨询门诊，有助于减轻临床医生的负担，提升检验医学科的影响力。

综上，我国检验医师的培养尚处于起步阶段，国家卫健委和教育部应从政策层面给予扶持，提高检验医师认同度，医院清晰界定检验医师和技师的岗位职责。检验与临床平等对话，临床接纳检验医师参与临床诊疗，才能更好地为患者服务，共同促进医学的进步发展。

PO-0634

Analysis of blood specimen rejection in the preanalytical phase to improve specimen quality

Keping Chen
Zhongda Hospital, School of Medicine, Southeast University

Background The preanalytical phase is liable for the most errors in the clinical laboratory. This study analyzed the causes and frequencies of specimen rejection in preanalytical phase and aimed to improve the specimen quality and patients' safety.

Methods The records of rejected blood specimens from the clinical laboratory of Zhongda Hospital between January 2014 and December 2018 were collected, and the causes, frequencies,

and sources of rejected specimens were further analyzed. The delayed time was also investigated to estimate the impact of different errors on the turnaround time.
Results Insufficient specimen was the major error causing rejection, accounting for 49% of the total 27,110 rejected specimens. This error often happened in the otorhinolaryngology head and neck surgery department. The second common error was clotted specimens, followed by hemolyzed specimens. The Neonatal Intensive Care Unit (NICU) had the highest frequency of specimen rejection. The medical examination department had the longest delayed time. Compared with other errors, the average delayed time caused by collecting specimens in wrong containers ranked first, and there was a significant difference in the quartile distribution of delayed time for each error type ($p \leq 0.001$).
Conclusions The identification and management of specimen errors in preanalytical phase were crucial activities to improve the specimen quality and patents' safety. To continuously improve specimen quality, the education to the nurses and other medical staff were needed to short the turnaround time.

PO-0635

Epidemiological and clinical characteristics of respiratory viruses in 4403 pediatric patients from multiple hospitals in Guangdong, China

Yajie Zhang
Department of Laboratory Medicine, Nanfang Hospital, Southern Medical University, Guangzhou

Background Acute respiratory infections (ARI) cause considerable morbidity and mortality worldwide, especially in children. Unfortunately, there are limited multi-center data on common viral respiratory infections in south China.
Methods A total of 4403 nasal swabs were collected from children in 10 cities in Guangdong, China in 2019. Seven respiratory viruses, influenza A virus (IFA), influenza B virus (IFB), respiratory syncytial virus (RSV), adenoviruses (ADV) and parainfluenza virus types 1–3 (PIV1, PIV2 and PIV3), were detected by direct immunofluorescence antibody assay. The personal information and clinical characteristics were recorded and analyzed.
Results The results showed that at least one virus was detected in 1099 (24.96%) samples. The detection rates of RSV, IFA, ADV, PIV3, PIV1 and PIV2 were 7.13% (314/4403), 5.31% (234/4403), 4.02% (177/4403), 3.04% (134/4403), 1.70% (75/4403) and 1.16% (51/4403), respectively. The detection rate of RSV was highest in 0–6-month-old children at 18.18% (106/583), while the detection rate of IFA was highest in 12–18-year-old children at 20.48% (17/83). The total detection rates in winter and spring were 35.67% (219/614) and 34.56% (403/1166), higher than those in summer, 17.41% (284/1631), and autumn, 19.46% (193/992).
Conclusions RSV and IFA were the main respiratory viruses in children. With increasing age the detection rate of RSV decreased in children, but the trends for the detection rates of IFA and IFB were the opposite. This study provided the viral etiology and epidemiology of pediatric patients with ARI in Guangdong, China.

PO-0636

m6A 甲基化修饰促进结直肠癌奥沙利铂耐药的分子机制及在耐药预测中的应用价值研究

齐秋晨
山东大学第二医院

目的 探讨 m6A 甲基化修饰促进结直肠癌奥沙利铂耐药的分子机制及在耐药预测中的应用价值。
方法 采用 Dot blot、Western blot 法分析结直肠癌奥沙利铂耐药及其亲代细胞中 m6A 水平差异和甲基转移酶及去甲基化酶的表达变化；体内外功能实验分析 m6A 修饰对结直肠癌奥沙利铂耐药的影响；利用耐药细胞 HCT116/OXA 及其亲代细胞 HCT116 进行 MeRIP-seq 和 RNA-seq 联合分析，利用生物信息学技术筛选耐药细胞中 m6A 修饰及转录水平均特异性上调的基因，并应用耐药及其亲代细胞，通过 qRT-PCR 和 MeRIP-qPCR 等验证，筛选 m6A 调控奥沙利铂耐药的潜在靶基因。
结果 建立的奥沙利铂耐药的结直肠癌细胞中 RNA 的 m6A 修饰水平显著上调，并且伴有甲基转移酶 METTL3 表达的异常升高。体内外功能实验表明，过表达野生型 METTL3 后 m6A 水平增加，并且显著降低了结直肠癌细胞对奥沙利铂的敏感性。MeRIP-seq 测序结果显示耐药细胞中 89 个 m6A 特异性上调的基因，联合 RNA-seq 测序分析，获得 24 个耐药细胞中 m6A 修饰及转录水平同时上调的候选基因，GO 富集分析显示候选基因大多与 EMT 相关。
结论 m6A 甲基化修饰上调能够促进结直肠癌奥沙利铂耐药，其可能通过增加 EMT 相关基因的 m6A 修饰水平，促进 EMT 从而促进奥沙利铂耐药。

PO-0637

检验科投诉原因分析及防范措施探讨

赵晓丽、钱净、阳春丽、马永鑫、徐跃轩、黎海生、张鸿伟
昆明市第一人民医院

目的 分析检验科投诉产生的原因及预防措施，并对防范措施有效性进行评价。
方法 将检验科近 4 年接受的 43 例投诉，分两个阶段来分析，第一阶段：2016 年 1 月～12 月，总结归类分析投诉的原因，制定预防措施，第二阶段：2017 年 1 月～2019 年 12 月，对不同阶段投诉发生率、投诉构成比变化进行比较，并评定各种预防措施的有效性、可行性。
结果 1. 2016 年 1 月～12 月我科共接到有效投诉 20 例，总结归类分析投诉的原因，其中前五位投诉内容为：报告发放不及时 4 例，采血时等候时间长 4 例，检验结果不准确 3 例，手工计费失误 3 例，危急值漏报 2 例。2. 采取预防措施后，2017-2019 年每年投诉量均较 2016 年明显减低，分别为：2017 年 7 例，2018 年 8 例，2019 年 8 例。3. 2017-2019 年的年投诉量较 2016 年降低 60%以上，至 2019 年 “ 报告发放不及时”、“ 采血时等候时间过长”、“手工计费失误”等投诉发生率为 0。
结论 分析投诉的产生原因，制定行之有效地预防措施并实施，可进一步规范检验流程，提高检验质量和服务质量，完善质量管理体系。

PO-0638

基于患者风险管理的自动审核规则设置

李云飞、马建锋
江苏省人民医院（南京医科大学第一附属医院）

目的 设计实验室检测结果自动审核规则，在避免错误结果被误审发出报告的前题下，提高自动审核率，减轻员工工作强度。

方法 排查临床检测过程中，检测结果发生错误的原因，评估错误产生的可能性，可能导致的严重程度，通过认真讨论研究，征询临床专家建议，规定在室内质控合格，样本采集、运输、接收等满足质量要求条件下，符合以下条件时，仍强制执行人工审核程序：1 有项目结果达到规定限值样本；2 重症监护病房患者样本；3 脑脊液样本；4 与前回结果比较，同一项目两次结果有一次超过正常参考区间，且变化大于规定的百分偏差和/或绝对偏差；5 反映临床诊治密切相关联项目变化幅度，其中一项结果超过正常参考上限 1 倍，其它项仍有在正常区间内；6 有逻辑关系项目，结果不符合逻辑关系；7 婴幼儿（3 岁以下）和老年人（85 岁以上）。要求员工进行纠正或强烈关注，据此设定自动审核规则，再次评价规则设定后的剩余风险，保证临床诊治风险在可控范围内。
结果 该规则能有效地降低导致临床诊疗错误报告发出的风险，剩余风险在可控范围内。
结论 实验室可以通过设置自动审核规则，建立安全高效智能审核系统，并通过人工审核规避不可控风险，提高工作效率，保障临床诊安全。

PO-0639

circNEIL3 functions as a ceRNA by mediating pyroptosis via PIF1 upregulation in lung adenocarcinoma radiotherapy

Ting Zhang
The First Affiliated Hospital of Chengdu Medical College

Background Lung cancer remains the leading cause of cancer-related mortality worldwide, constituting 18% globally and 19% of all cancer-related deaths in China. It is estimated that 85% of human lung cancers are non-small cell lung cancer, with lung adenocarcinoma (LUAD) being the predominant subtype, accounting for 50% of cases. Radiotherapy is widely used in the treatment of clinical tumors, related to lung cancer, prostate cancer, kidney cancer, and many others. However, ionizing radiation can cause a range of opportunistic infections and systemic inflammation, with life-threatening tumor recurrence and metastasis still prevalent in patients. Although radiotherapy has been widely used in the treatment of lung adenocarcinoma (LUAD), the curative effects are relatively poor and further improvements are required. Circular RNAs (circRNAs) represent a category of non-coding RNAs that are abundant, stable, and specific in organisms, and thus may have great potential in cancer treatment. However, little is known about the role of circRNAs during radiotherapy in LUAD.
Methods We established and explored the expression profiles of 1875 dysregulated circRNAs in non-irradiated and irradiated A549 cells by RNAseq and verified 10 circRNAs by RT-qPCR. Then, gain-of-function and loss-of-function experiments of circNEIL3 in LUAD were performed. The competing endogenous RNA network and its heatmap were used to identify the downstream targets of circNEIL3. Luciferase reporter assay and AGO2 immunoprecipitation were conducted to evaluate the interaction between circNEIL3, miR-1184, and PIF1. Functional experiments were performed using LDH, IL-1β, and IL-18 release assays, flow cytometry, western blotting, and RT-qPCR.
Results We identified circNEIL3 as a significantly downregulated circRNA in both A549 and H1299 LUAD cells treated with 0, 2, or 4 Gy of radiation, respectively. circNEIL3 knockdown promoted radiation-induced cell pyroptosis, whereas circNEIL3 overexpression had the opposite effects. Importantly, the effects of circNEIL3 overexpression on inhibiting pyroptosis were reversed by PIF1 knockdown. Mechanistically, circNEIL3 can mediate pyroptosis by directly binding to miR-1184 as a sponge and release inhibition of miR-1184 on PIF1. In addition, our experiments further demonstrated that circNEIL3 mediates radiation-induced cell pyroptosis by regulating the DNA damage repair pathway, and finally impacts LUAD survival.
Conclusion We demonstrated that circNEIL3 exerted its function as a ceRNA by directly binding to miR-1184, and then abrogated the endogenous inhibitory effect of miR-1184 on the target gene PIF1. Low-expression PIF1 could weaken DNA damage repair and drive cell pyroptosis, ultimately affecting survival in lung cancer treatment with radiation. These results suggest that the circNEIL3/miR-1184/PIF1 axis mediates cell pyroptosis by regulating the DNA damage repair

pathway. Therefore, circNEIL3-related pyroptosis induction may serve as a potential therapeutic target to enhance radiotherapy of lung cancer.

PO-0640

胶质母细胞瘤进展相关 lncRNA 预后风险评估模型的构建

李小萌
山东大学第二医院

目的 通过 TCGA 数据库构建胶质母细胞瘤进展相关的 lncRNA 预后风险评估模型。
方法 从 TCGA 数据库下载胶质母细胞瘤和低级别胶质瘤样本的表达数据及临床信息，通过 R 语言分析筛选胶质母细胞瘤和低级别胶质瘤中差异表达的 lncRNA 分子，使用单因素 cox 回归分析筛选出于预后相关的分子，通过多因素 cox 回归进一步筛选出分子建立风险评估模型，使用 K-M 生存分析和 ROC 曲线对模型的预测效能进行验证，使用基因本体(GO) 、京都基因与基因组百科全书(KEGG)预测模型的功能。
结果 以| log2 fold change |＞2 且 FDR＜0.01 为标准筛选出 259 个进展相关差异表达的 lncRNA 分子，经过单因素 cox 回归分析，得到 19 个预后相关分子，通过多因素 cox 回归分析最终获得了 4 个进展及预后相关分子构建了预后风险评估模型，风险评分 =0.1202×HOXC-AS2+0.1195×SMIM25+0.1501×AGAP2-AS1+0.1577×OSMR-AS1。K-M 分析表明高风险组的患者生存明显短于低风险患者且有统计学意义。在测试集、验证集和 TCGA 总集中 3 年 AUC 值分别为 0.952、0.804 和 0.905，5 年 AUC 值分别为 0.929、0.844 和 0.882。KEGG 和 GO 分析结果显示，模型中 lncRNA 分子可能参与了免疫分子相关的肿瘤代谢通路。
结论 由 HOXC-AS2、SMIM25、AGAP2-AS1、OSMR-AS1 分子构成的进展相关 lncRNA 预后风险评估模型能够预测患者预后，有望成为临床预后评估的新靶点。

PO-0641

Survival analysis of immune-related lncRNA in glioblastoma

xiaomeng li
The Second Hospital of Shandong University

Background A variety of regulatory approaches including immune modulation have been explored as approaches to either eradicate antitumor response or induce suppressive mechanism in the glioblastoma microenvironment. Thus, the study of immune-related long noncoding RNA (lncRNA) signature is of great value in the diagnosis, treatment and prognosis of glioblastoma.
Methods Glioblastoma samples with lncRNA sequencing and corresponding clinical data were acquired from the Cancer Genome Atlas (TCGA) database. Immune-lncRNAs co-expression networks were built to identify immune-related lncRNAs via Pearson correlation. Based on the median risk score acquired in the training set, we divided the samples into high- and low-risk groups and demonstrate the survival prediction ability of the immune-related lncRNA signature. Both principal component analysis (PCA) and gene set enrichment analysis (GSEA) were used for immune state analysis.
Results A cohort of 151 glioblastoma samples and 730 immune-related genes were acquired in this study. A five immune-related lncRNA signature (AC046143.1, AC021054.1, AC080112.1, MIR222HG, and PRKCQ-AS1) was identified. Compared with patients in the high-risk group, patients in the low-risk group showed a longer overall survival (OS) in the training, validation and entire TCGA set (P=1.931e-05, P=1.706e-02 and P=3.397e-06, respectively). Additionally, the survival prediction ability of this lncRNA signature was independent of known clinical factors and

molecular features. The area under ROC curve (AUC) and stratified analyses were further performed to verify its optimal survival predictive potency. Of note, the high- and low-risk groups exhibited significantly distinct immune state according to the PCA and GSEA analyses.
Conclusions Our study propose that a five immune-related lncRNA signature can be utilized as a latent indicator of prognosis and potential therapeutic approach for glioblastoma.

PO-0642

SUN5 介导精子头尾连接的分子机制：基于 Sun5 基因敲除小鼠的研究

张芸飞[1]、杨林飞[1]、黄利华[1]、刘刚[2]、张新星[1]、邢晓为[1]、聂新民[1]
1. 中南大学湘雅三医院
2. 中南大学基础医学院

目的 无头精子症是一种罕见的遗传和生殖疾病。研究表明，大约 33~47%的无头精子症发病由 *SUN5* 突变导致，但其分子机制尚不清楚。本研究通过 *Sun5* 基因敲除小鼠模型，探究 Sun5 介导精子头尾连接的分子机制，对了解无头精子症的发病机制和临床治疗具有重要意义。
方法 1. 建立 *Sun5*$^{-/-}$小鼠模型，通过 HE 染色和透射电镜对 *Sun5*$^{-/-}$小鼠的表型进入深入分析。
2. 通过免疫共沉淀(co-IP)和免疫荧光探究 Sun5 与 Nesprin3 之间的相互作用。
3. 通过免疫荧光和透射电镜观察 *Sun5* 基因敲除对 Nesprin3 和中心体在精子形成中定位的影响。
4. 通过 iTRAQ 检测 *Sun5* 基因敲除对睾丸蛋白表达谱的影响，并对差异蛋白进行生物信息学分析。
结果 1. *Sun5*$^{-/-}$小鼠 Sun5 蛋白表达缺失。HE 染色显示 *Sun5*$^{-/-}$小鼠睾丸沿管腔排列的精子头明显减少；附睾管腔中可见大量的精子尾部，少见精子头。*Sun5*$^{-/-}$小鼠附睾的精子头尾连接断裂。进一步超微结果显示小鼠精子的头尾连接装置在精子形成的 9-10 期远离细胞核，在 13-14 期出现了完全的断裂。
2. Co-IP 结果显示，SUN5 和 Nesprin3 能够相互作用；进一步免疫荧光实验结果显示 Sun5 和 Nesprin3 共定位于精子的头尾连接处，表明 Sun5 和 Nesprin3 相互作用形成 LINC 复合物介导精子头尾连接。
3. 免疫荧光实验结果显示 *Sun5* 缺陷使 Nesprin3 在精子形成过程中在核后极植入窝处的定位发生改变；超微结构显示 *Sun5*$^{-/-}$小鼠中心体与细胞核的距离增大。表明 Sun5 缺陷引起 Nesprin3 定位改变，导致中心体及尾部结构不能锚定于植入窝，引起精子头尾连接断裂。
4. 通过 iTRAQ 技术筛选了 103 个差异蛋白，其中 47 个上调蛋白，56 个下调蛋白。生物信息学结果表明，这些差异蛋白参与细胞蛋白复合物组装、精子运动等多个生物学过程。
结论 1. *Sun5* 基因敲除导致小鼠精子头尾连接断裂，出现无头精子症的表型，说明 *SUN5* 基因是无头精子症的致病基因之一。
2. Sun5 与 Nesprin3 形成特异性的 LINC 复合物定位于精子头尾连接处，介导精子的头尾连接。
3. Sun5 对 Nesprin3 和中心体的定位是必须的。Sun5 缺陷导致 Nesprin3 在精子发育过程中不能锚定植入窝，从而导致中心体失去了和细胞核的联系，引起精子头尾断裂，这可能是 Sun5 缺失导致精子头尾断裂的重要机制之一。
4. *Sun5* 基因敲除改变了小鼠睾丸蛋白的表达谱。这些与精子发生过程相关的下调蛋白可能也参与了精子的头尾连接的组装，可能是引起精子头尾连接断裂的另一重要原因。

PO-0643

非高密度脂蛋白胆固醇（Non-HDL-C）临床应用价值探索

蒙立业、张禾、干伟、贺勇
四川大学华西医院实验医学科

目的 探索非高密度脂蛋白胆固醇（Non-HDL-C）在动脉粥样硬化患者中的诊断价值，并建立数据模型，验证 Non-HDL-C 在不同模型中预测动脉粥样硬化的价值。
方法 收集 2021 年 1 月至 2021 年 4 月四川大学华西医院临床诊断为动脉粥样硬化患者的血脂检测结果，同时收集同期健康体检人群血脂实验室检测结果。非高密度脂蛋白胆固醇计算方法为：Non-CHOL-C=总胆固醇（CHOL） -高密度脂蛋白胆固醇（HDL-C）。通过 ROC 分析 Non-HDL-C 在诊断动脉粥样硬化中的 cutoff 值，以及通过 logistic 回归分析 Non-HDL-C 在不同模型中预测动脉粥样硬化的价值。
结果 ROC 分析结果显示 Non-HDL-C 在诊断动脉粥样硬化 AUC 为 0.73（95%CI:0.72~0.74），P 值小于 0.01，cutoff 值为 2.68 mmol/L；TG 在诊断动脉粥样硬化 AUC 为 0.71（95%CI:0.70~0.72），P 值小于 0.01，cutoff 值为 1.54 mmol/L；CHOL 在诊断动脉粥样硬化 AUC 为 0.79（95%CI:0.78~0.80），P 值小于 0.01，cutoff 值为 3.86 mmol/L；HDL-C 在诊断动脉粥样硬化 AUC 为 0.77（95%CI:0.76~0.78），P 值小于 0.01，cutoff 值为 1.08 mmol/L；LDL-C 在诊断动脉粥样硬化心脏病 AUC 为 0.80（95%CI:0.79~0.81），P 值小于 0.01，cutoff 值为 2.19mmol/L。Non-HDL-C 在预测动脉粥样硬化时，相比较于正常人群，其比值比（OR）为 2.53（95%CI：2.38~2.70）；Non-HDL-C 联合 LDL-C 模型预测动脉粥样硬化的 ROC 曲线下面积 0.87（95%CI：0.86~0.88）。Non-HDL-C 联合 CHOL 模型预测动脉粥样硬化的 ROC 曲线下面积 0.82（95%CI：0.81~0.83）。Non-HDL-C 联合 LDL-C、CHOL 模型预测动脉粥样硬化的 ROC 曲线下面积 0.88（95%CI：0.87~0.89）。
结论 Non-HDL-C 在预测动脉粥样硬化心脏病中存在一定的应用价值，联合动脉粥样硬化心脏病血脂指标能提高其诊断价值。

PO-0644

溶血对脑脊液生化检测项目的干扰研究

刘静、杨伟明、王小中、吕娇凤
南昌大学第二附属医院

目的 探讨脑脊液（CSF）标本溶血对 CSF 常用生化检测项目总蛋白（TP）、微量蛋白（mALB）、乳酸脱氢酶（LDH）、天门冬氨酸氨基转移酶（AST）、肌酸激酶（CK）和葡萄糖（Glu）的干扰情况。
方法 选择 TP、mALB、LDH、AST、CK 和 Glu 浓度分别接近正常参考区间上限的 CSF 标本各 1 例，外观清亮，经 Sysmex 全自动血细胞分析仪检测 CSF 标本中血红蛋白（Hb）含量为 0g/L，此为基础样品。同时收集同一病人的血常规标本制备溶血干扰原液。按照 WS/T 416-2013《干扰实验指南》，首先制备干扰物高实验浓度样品（H）与低实验浓度样品（L），再将 H 和 L 样品按照梯度比例混合得到实验样品系列。用 Beckman AU5400 全自动生化分析仪按照升序、降序、升序进行 3 次检测，记录结果计算干扰效果并进行回归分析。
结果 溶血对 TP、LDH、AST 和 CK 等项目的检测有明显的正向干扰效果，溶血程度越高干扰越明显，呈线性相关；对 mALB、Glu 的干扰效果不明显（最大干扰物浓度为 8.75g/L），溶血程度与干扰效果之间无相关性。
结论 溶血脑脊液标本不适合于 TP、LDH、AST 和 CK 等项目的检测；当溶血脑脊液标本中 Hb 浓度≤8.75g/L 时，可用于 mALB 和 Glu 的检测。

PO-0645

COVID-19-another influential event impacts on laboratory medicine management

yuntao luo、jinghua wang、minmin zhang、qingzhong wang、rong chen、xueliang wang、hualiang wang
Shanghai center for clinical laboratory

Back ground Before public health emergencies became a major challenge worldwide, the scope of laboratory management was only related to developing, maintaining, improving and sustaining the quality of accurate laboratory results for improved clinical outcomes. Indeed, quality management is an especially important aspect and has achieved great milestones during the development of clinical laboratories.
Current status However, since the coronavirus disease 2019 (COVID-19) pandemic continues to be a threat worldwide, previous management mode inside the separate laboratory could not cater to the demand of the COVID-19 public health emergency. Among emerging new issues, the prominent challenges during the period of COVID-19 pandemic are rapid-launched laboratory developed tests (LDTs) for urgent clinical application, rapid expansion of testing capabilities, laboratory medicine resources and personnel shortages. These related issues are now impacting on clinical laboratory and need to be effectively addressed.
Conclusion Different from traditional views of laboratory medicine management that focus on separate laboratories, present clinical laboratory management must be multidimensional mode which should consider consolidation of the efficient network of regional clinical laboratories and reasonable planning of laboratories resources from the view of overall strategy. Based on relevant research and our experience, in this review, we retrospect the history trajectory of laboratory medicine management and also, we provide existing and other feasible recommended management strategies for laboratory medicine in the future.

PO-0646

Hypermethylation-mediated silencing of CCBE1 drives change of mitochondrial activity to promote HCC progression via TGF-β signaling pathway

Guangang Tian、Qian Gong
Clinical Laboratory, Zhongshan Hospital Qingpu Branch, Fudan University

Purpose Hepatocellular carcinoma (HCC) is a complex and heterogeneous tumor driven by multi steps and tumor microenvironment do an important role in the development and progression of cancer. Extracellular matrix (ECM) proteins, as part of tumor microenvironments, play crucial roles in tumor development and metastases. CCBE1, as a 44-KD extracellular matrix glycoprotein, modulates lymphangiogenesis through promoting the formation of mature VEGF-C from pro-VEGF-C. Whereas, none study was performed to clarify the role of CCBE1 in HCC. Here, we aim to uncover the underlying functions of CCBE1 and its mechanism involved in the initiation and development of HCC.
Methods Real-time PCR, western blotting and immunohistochemistry were used to test CCBE1 expression. Cell proliferation was determined by CCK8, colony-forming and subcutaneous injection assays. Transwell assay and in vivo metastasis assays were performed to test the ability of cell motion. Bisulfite sequencing was adopted to explore the methylation level of CCBE1. Mitochondrial tracker, JC-10 and seahorse XF24 extracellular flux analyzer were implemented to determine the mitochondrial activity, including mitochondrial morphology, mitochondrial membrane potential and oxygen consumption rate (OCR), et.

Results In this study, we first reported that CCBE1 expression was significantly down-regulated in tumor compared non-tumor tissues by data mining, as well as verified in HCC tissues. Additionally, poor prognosis emerged in the CCBE1 low expression patients. Following, the mechanism of CCBE1 down regulation resulted from higher methylation level of CCBE1 promoter by bisulfite sequencing PCR (BSP) in HCC cells lines and tissues, which could be confirmed by DCA treatment in HCC cells. Furthermore, in vitro and in vivo assays found that CCBE1 overexpression or treatment with recombined CCBE1 protein dramatically suppressed HCC cell proliferation, migration and invasion. Interestingly, the GSEA analysis showed that CCBE1 was related with parkinson's disease, a mitochondrial dysfunction disease. Hence, mitochondrial activity was selected to study. And the results showed that CCBE1 dysregulation destroyed mitochondrial dynamic equilibrium and mitochondrial membrane potential. Meanwhile, we found that CCBE1 overexpression could decrease OCR of HCC cells, while no effect was done on Extracellular acidification rate (ECAR), which further indicates that CCBE1 may affect mitochondrial activity. Further research found that CCBE1 overexpression could decrease the Phosphorylation level of Drp1 via inhibiting the TGF-β signaling pathway. Moreover, it could reverse the phosphorylation of Drp1 treatment with TGF-β.
Conclusions In this study, we describe CCBE1 as a key mediator in the development of HCC. Under hypermethylation level of CpG island in promoter, HCC cells acquire growth and metastasis advantage by impaired mitochondrial activity via TGF-β signaling pathway in the CCBE1 deficient microenvironment. Significantly, our researches provide new evidence for epigenetic control of tumor microenvironment, and suggest matricellular protein CCBE1 may serve as a novel prognostic marker and act as a HCC suppressor.

PO-0647

护理人员培训模式对检验标本不合格率的影响分析

朱宇、高佳、李佳、王宗丹、郑翠玲、崔巍
国家癌症中心/国家肿瘤临床医学研究中心/中国医学科学院北京协和医学院肿瘤医院检验科

目的 探讨护理人员培训模式在检验分析前质量控制中的作用。
方法 分别于不同时间段采用护士长集中培训和病区针对性培训两种模式对护理人员进行标本采集注意事项培训，分析培训前、后 3 个月患者检验标本不合格率及类型变化。
结果 护士长集中培训前、后 3 个月的标本总不合格率分别为 0.251%（646/257641）和 0.238%（572/240569），呈下降趋势但无统计学差异（X^2=0.858，P=0.354）。病区针对性培训前、后 3 个月的标本总不合格率分别为 0.225%（708/314756）和 0.169%(511/302776)，总不合格率显著下降（X^2=24.710，P<0.001）；其中，乳糜血（0.032% vs.0.004%，X^2=64.595，P<0.001）、溶血（0.052% vs.0.019%，X^2=46.618，P<0.001）和采集量错误（0.038% vs.0.028%，X^2=4.112，P=0.043）标本不合格率显著减少。
结论 病区针对性培训在降低检验标本不合格率中的作用优于护士长集中培训。检验科应根据培训目的及效果不断优化培训模式，促进检验质量不断提升。

PO-0648

i2000SR 全自动免疫分析仪检测高敏肌钙蛋白 I 的性能评价

刘春燕、葛若卿、刘爽、李晓苗、张新
新疆生产建设兵团医院

建立及评价 i2000SR 全自动免疫分析仪(简称 i2000SR)检测高敏肌钙蛋白 I(hs-cTnI)的功能灵敏度(FS)、精密度、空白限(LoB)、检出限(LoD)、定量检测限(LoQ)和线性范围。

方法 参照美国临床实验室标准化协会(CLSI)EP17-A 文件和相关文献，将 hs-cTnI 空白样本和系列浓度样本在 i2000SR 上进行检测，采用统计学方法确定血清 hs-cTnI 的 FS、精密度、LoB、LoD、LoQ 及线性范围。
结果 i2000SR 检测 hs-cTnI 的功能灵敏度为 1.93pg/ml。高值样品(15100.0pg/ml)批内变异系数(CV)和批间 CV 分别为 1.52%和 3.54%；中值样品(190.0pg/ml)批内 CV 和批间 CV 分别为 2.90%和 3.83%；低值样品(20.0pg/ml)批内 CV 和批间 CV 分别为 7.60%和 0.82%。按 CLSI EP17-A 文件建立的 LoB、LoD、LoQ 分别为 0.45pg/ml、1.45pg/ml 和 1.90pg/ml。在检测范围内，i2000SR 预期值和实测值的线性方程为 Y=0.937X+1428.727，R2=0.997。
结论 i2000SR 检测 hs-cTnI 的高值不精密度低于厂家说明书提供的值，中值和低值的不精密度高于说明书的值；本研究所得 LoB、LoD、LoQ、FS 与厂家说明书提供的基本一致；为临床的诊断治疗提供准确、可靠的检验结果。

PO-0649

中性粒细胞与淋巴细胞比值和血小板与淋巴细胞比值对 HIV/AIDS 相关弥漫大 B 细胞淋巴瘤患者预后的作用

张米、杨翠先、董兴齐、张玮
云南省传染病医院

目的 现有的 HIV+弥漫大 B 细胞淋巴瘤(DLBCL)预后标志物不能准确预测患者的预后。本研究旨在分析中性粒细胞与淋巴细胞比值(NLR)和血小板与淋巴细胞比值(PLR)对 EB 病毒阳性 HIV/AIDS-DLBCL 患者预后的影响。
方法 本研究纳入了 2014-2017 年 45 例新诊断的 HIV/ AIDS-DLBCL 患者，其中 EB 病毒阳性患者 30 例，EB 病毒阴性患者 15 例。对临床资料进行回顾性分析。
结果 45 例 HIV/AIDS-DLBCL 患者中，EB 病毒阳性组和阴性组间的 1-、3-、5 年总生存率两两比较差异有统计学意义(P<0.05);NLR 组与 PLR 组总生存期比较差异有统计学意义(P<0.05)， PLR 组与 EB 病毒阳性组总生存期比较差异有统计学意义(P<0.05)。Cox 回归分析发现 NLR 和 PLR 是 HIV/ AIDS 相关性 DLBCL 的独立预后指标。
结论 中性粒细胞与淋巴细胞比值(NLR)和血小板与淋巴细胞比值(PLR)在 EB 病毒阳性的 HIV/AIDS 相关 DLBCL 患者中具有预测预后的价值，可作为疾病监测和疗效评价的重要依据。

PO-0650

动态监测 EB 病毒持续感染在 HIV/AIDS 相关弥漫大 B 细胞淋巴瘤患者中的临床意义

杨翠先、张玮、董兴齐
云南省传染病医院

目的 分析 EB 病毒 DNA 水平变化对 HIV/AIDS 相关弥漫大 B 细胞淋巴瘤患者临床预后的影响。
方法 本研究采用双向研究方法，以云南省传染病医院 2014 年 1 月-2019 年 6 月收治的艾滋病相关 DLBCL 患者为研究对象。应用 SPSS23.0 中 t 检验、Kaplan-Meier、Cox 回归模型分析，应用 Graphpad Prism 8.0 中的 Survival 方法绘制生存曲线。
结果 根据纳入和排除标准，本研究共入组 45 例 AIDS-DLBCL 患者，其中初诊时 EBV（-）组 15 例，EBV（+）组 30 例，且均已经完成至少 3 次 CHOP21/R-CHOP21 治疗。入组患者中 80.0%患者为男性，主要为汉族患者（80.0%），平均年龄 48.96±11.45 岁，其中 EBV（+）组平均年龄 49.30±11.61 岁。45 例 AIDS-DLBCL 患者的 1 年、3 年和 5 年总生存率分别为 71.1%、59.4%和

42.1%。其中 1 年总生存率与 5 年总生存率相比，其差异有统计学意义（P=0.029）。在 1 年生存率中，EBV（+）组生存率（60.0%）明显低于 EBV（-）组（93.3%）（P=0.020），而两组的 3 年生存率和 5 年生存率差异均无统计学意义。[罗兰 1] 总生存期的分析中，EBV（+）组总生存期显著短于 EBV（-）组（P=0.022），其中位生存时间分别为 14 个月和 27 个月；EBV（+）组中的治疗后转阴的患者有 14 例，治疗后持续阳性/反复阳性的患者有 16 例，而治疗后转阴的患者的总生存期显著长于治疗后持续阳性/反复阳性的患者（P<0.001），其中位生存时间分别为 7 个月和 22 个月）。

结论 EB 病毒感染与 HIV/AIDS 相关弥漫大 B 细胞淋巴瘤患者的临床预后相关，且是影响患者临床预后的相关危险因素，在临床诊疗过程中应加强 EB 病毒感染的监测。

PO-0651

县级医院临床实验室检验质量专项检查的结果分析

于登程
夏津县人民医院

目的 本次实验分析县级医院临床实验室检验质量专项检查的结果。

方法 本次实验组建了 5 个专家组，对我省 50 家县级医院临床实验室检验质量进行了专项检查，具体从量体系、室内质控、室间质评、性能验证与比对试验、现场考核五项条目进行，并统计县级医院临床实验室检验质量专项检查得分；并通过主观考察方式总结县级医院临床实验室检验质量存在的问题。

结果 县级医院临床实验室检验质量专项检查优秀医院 30 家，合格医院 18 家，不合格医院 2 家；县级医院临床实验室检验质量存在的问题主要有部分实验室的质量体系概念模糊、部分实验人员质量控制意识薄弱且技能欠缺、大部分实验室参加的专业科目较少、大部分实验室并没有实现规划化管理、部分专业科目检验存在问题、部分医院实验室条件较差。

结论 县级医院临床实验室检验质量总体较为良好，但是存在个别医院专项检查不合格，并且还存在较多问题有待解决。

PO-0652

HCV 基因分型和肝纤维化血清学指标的研究

邓洪荣[1]、陈冉[2]
1. 昆明医科大学
2. 昆明医科大学第二附属医院

目的 研究丙型肝炎病毒（Hepatitis C Virus，HCV）感染者不同基因型的临床特征，观察天冬氨酸氨基转移酶/血小板比值(APRI 评分)、4 因子的纤维化指数(FIB-4 指数)联合诊断肝纤维化的潜在诊断价值，为临床诊疗奠定基础。

方法 收集昆明医科大学第二附属医院 98 例 HCV 感染者的临床资料以及血清学指标，根据基因分型将研究对象分为 GT1b 组、GT2a 组、GT3a 组、GT3b 组、GT6a 组，使用统计分析软件对其性别、年龄、病毒载量、ALT、AST、APRI 评分、FIB-4 指数进行差异性分析。以 B 超或肝组织病理学诊断肝硬化、肝癌为金标准，绘制 APRI 评分、FIB-4 指数以及联合诊断的受试者工作特征曲线（Receiver operating characteristic curve,ROC）曲线，评价 APRI 评分、FIB-4 指数对肝纤维化的诊断效能。

结果 98 例患者，GT3b 型占比最高（46.8%）；HCV 感染者多分布在 40-59 岁，不同基因型的 HCV 感染者年龄差异有统计学差异（P<0.001）。不同基因型的丙肝相关肝硬化患者的 APRI 评分有统计学意义（P=0.031）。其中，GT 6a 的 APRI 评分显著高于 GT 1b、GT 3a，差异有统计学

意义（P=0.031）。APRI 评分、FIB-4 指数以及其联合诊断肝纤维化的 ROC 曲线下面积（Area Under Curve,AUC）分别为 0.66、0.77、0.79（P<0.05），APRI 评分和 FIB-4 指数单独诊断肝纤维化时的诊断界值分别为 0.99、1.97；其所对应的灵敏度分别为 82.6%、97.8%；而两者联合诊断时灵敏度和特异度分别为 87.0%，69.2%。

结论 HCV 感染者基因分型以 3b 型为主，男性较女性多，感染者呈中老年人群分布。HCV GT6a 的 APRI 评分较 GT1b、GT3a 高，可能与 GT 6a 高度遗传异质性和耐药相关替代突变率高有关。在使用 APRI 评分诊断肝纤维化时，GT6a 型的诊断界值是否有必要较 GT1b、GT3a 型高仍需进一步研究探讨。此外，FIB-4 指数可能对丙肝相关肝硬化有潜在重要的筛查价值，APRI 评分和 FIB-4 指数两者联合诊断较单独诊断肝硬化的价值高。通过对 HCV 基因型分布以及相关血清学指标的研究，有望为慢性丙肝防控给予帮助。

PO-0653

跨膜型 TNF-α 通过正向信号和反向信号促进活化诱导的细胞死亡

张萌[1]、王晶[2]、李卓娅[2]
1. 郑州大学第一附属医院
2. 华中科技大学同济医学院

目的 已知分泌性肿瘤坏死因子 α (sTNF-α)介导活化诱导细胞死亡(AICD)。然而，tmTNF-α 在 AICD 中的作用仍不清楚。

方法 我们利用 PHA 诱导 Jurkat 细胞死亡建立 AICD 模型，转染 AS 或 siRNA 沉默相应基因，利用 Annexin-V-FITC/PI 标记和流式细胞术检测凋亡，利用 real time PCR 和 western blot 分别检测 mRNA 和蛋白水平。

结果 我们发现，在 Jurkat 和原代人 T 细胞 AICD 过程中，tmTNF-α 的表达显著增加，并伴随着凋亡增强。抑制或增强活化 T 细胞中 tmTNF-α 的表达分别抑制或促进 AICD。用外源性 tmTNF-α 处理活化的 T 细胞可显著增加 AICD，提示 tmTNF-α 作为效应分子介导 AICD。由于 tmTNF-α 具有受体功能，我们使用一种抗 TNF-α 的多克隆抗体来触发 tmTNF-α 的反向信号转导，可上调 FasL、TRAIL 和 tmTNF-α 的表达来增强 AICD，并通过上调 DR4、TNFR 1 和 TNFR2 而增强活化 T 细胞对 AICD 的敏感性。敲除 TNFR1 或 TNFR2 的表达几乎完全阻断了 tmTNF-α 反向对 sTNF-α 或 tmTNF-α 增强 AICD 的敏感性。

结论 我们的结果表明，tmTNF-α 作为一个死亡配体介导 AICD，作为一个受体增强活化 T 细胞对 AICD 的敏感性。靶向活化的 T 细胞的 tmTNF-α 可能有助于治疗自身免疫性疾病。

PO-0654

男男性接触者不当的直肠冲洗器具使用可能是导致 HIV 感染风险高的机制之一

楚振兴、徐俊杰
中国医科大学附属第一医院

背景 在全球范围内 HIV 影响着男男性接触者(MSM)的健康。直肠冲洗 (Rectal douching，RD)是 MSM 为了直肠的清洁，在肛交前后被广泛采用，报道提示 RD 与感染 HIV 的风险增加相关。 然而 RD 如何增加 HIV 感染风险的机制并不十分清楚，并且在我国 MSM 中的 RD 行为研究数据有限。该研究旨在评估 RD 行为与 MSM 的感染 HIV 的内在关系。

方法 2017 年 8 月至 2018 年 12 月，在沈阳对成年 MSM 进行了一项横断面研究。通过面对面访谈问卷的形式收集了研究对象的人口统计学、性行为和最近一次肛交的 RD 的数据。采用多因素 logistic 回归分析并确定 HIV 感染有关的影响因素。
结果 研究期间总共有 515 名符合条件的 MSM 参与了调查（中位年龄：31 岁）。在最近一次肛交中，28.3%(146/515) 进行了无安全套被插入性肛交(CRAI)，超过一半(61.6%,317/515)在肛交前或之后发生了 RD。在进行 RD 的 MSM 中，96.8%(307/317）在肛交前进行了 RD，而 62.5%（198/317）在肛交后进行 RD。使用的辅助冲洗设备主要是淋浴管 (85.3%, 262/307)，仅 8.1%(25/307)在性行为前使用商业化 RD 辅助器。RD 的主要原因是(95.5%)为了个人卫生，14.1%因他们性行为时没有使用安全套并认为 RD 可以将直肠内 HIV 病毒冲洗掉，预防 HIV 感染。HIV-1 和梅毒的患病率分别为 11.7%(60/515)和 13.2%(68/515)。HIV 感染与 RD 呈正相关(adjusted odds ratio(AOR),2.8;95% CI,1.4–5.4)，性交前进行 RD(AOR,2.2;95%CI,1.2–4.2)，RD 和 CRAI 之间的交互作用(AOR,3.5;95% CI,2.0–6.2)，使用淋浴管(VS.商品化冲洗器)辅助 RD(AOR,3.3;95% CI,1.0–11.3)等因素也与 HIV 感染存在统计学关联，其他危险因素包括肛交后进行 RD，无套肛交，使用亚硝酸盐吸入剂和梅毒感染。
结论 本次调查发现 RD 在沈阳 MSM 中使用率高。非商业性 RD 工具不当使用（如淋浴管，具有锋利的边缘），RD 与 CRAI 的交互作用与 HIV 感染相关。建议针对性交前/后使用淋浴软管进行 RD 和 CRAI 的 MSM 进行相关健康教育。这可能有助于 MSM 了解 RD 与 HIV 感染之间的关系，以减少 HIV 在 MSM 人群中的传播。毕竟横断面研究对因果关系的论证存在方法学限制，未来需要前瞻性队列研究的开展来进行因果验证。

PO-0655

用于 SARS-CoV-2 污染环境洗消的新型光敏式病毒消杀技术及其应用

苏宁、蒋元素、种慧敏、李文满、孙献歌、尚美云、李博文、魏昆、邓少丽、鲁卫平、黄庆
中国人民解放军陆军特色医学中心

目的 快速、高效切断病原体传播途径是遏制疫情蔓延的有效手段。早在新型冠状病毒肺炎(COVID-19)疫情初期，已根据以往冠状病毒对理化因子的抗力经验制定了相应的消毒措施与方案，但是不合理的消毒剂使用方式存在巨大的安全隐患。因此，现行消毒措施显然无法满足目前疫情常态化对消毒安全性的需求。光化学法具有反应条件温和、高效、无害化等显著特点，已被证实是抗病毒药物的有效替代品。本课题组基于新型冠状病毒(SARS-CoV-2)及其模式生物，系统地评价了几种临床常用光敏剂的生物安全性，成功筛选到一种安全性极高的新型光敏剂，并建立了适用于新型冠状病毒污染环境的新型光敏式病毒消杀技术。
方法 根据细胞活性、凋亡和周期结果，基于生物安全性最高的新型光敏剂，经田口实验优化，确定光敏剂浓度、光照时间与光照功率的最佳组合参数，最终结果由生物安全 3 级实验室进行验证。
结果 成功筛选到一种生物安全性高于亚甲蓝、新亚甲蓝及甲苯胺蓝的新型光敏剂，构建了适用于新型冠状病毒污染环境的新型光敏式病毒消杀技术，并成功研制光敏式病毒灭活仪科研样机及其配套设备。相关技术及设备对 SARS-CoV-2 及其模式生物消杀效率达 99.99%以上；同时，SARS-CoV-2 核酸检测实验室现场测试结果显示，物表及空气中的细菌消杀率达到 99.9%以上，消杀率符合《医疗机构消毒技术规范》相关规定。
结论 本课题组所研发的新型光敏式病毒消杀技术和科研样机生物安全性高，对以 SARS-CoV-2 为代表的 RNA 包膜类病毒具有特异性杀灭作用，可对污染区和潜在污染区，特别是工作人员作业、穿脱防护用具等情况下代替常规洗消技术，避免传统消毒技术对人体造成的刺激、伤害及潜在安全隐患，实现真正意义“人机共存”。

PO-0656

云南高血压患者 NPR-C 配体 ANP 水平研究

赵晓丽、钱净、朱丹、杨如风、田敏、黎海生
昆明市第一人民医院

目的 观察云南原发性高血压患者外周血中 ANP 水平的变化，探讨其与原发性高血压发病机制之间的关系。
方法 收集 2019 年 6 月至 9 月在我院心内科诊断的原发性高血压患者 44 例，设为病例组，收集我院体检中心的健康体检患者 44 例，作为健康对照组。采用 ELISA 方法检测研究对象外周血中 ANP 水平。
结果 原发性高血压患者外周血中 ANP 水平显著低于正常人（p<0.05）；以高血压病发生与否为因变量，以血清 ANP 为自变量进行 logistic 回归分析，结果显示 ANP 与高血压偏回归系数为 0.071，P 值为 0.002（P<0.05），具有统计学意义；采用 person 相关性分析分别对 ANP 与 SBP/DBP 进行分析，结果显示 ANP 与 SBP 的相关系数为-0.374，P 值为 0.000（P＜0.05）；ANP 与 DBP 的相关系数为-0.331，P 值为 0.002（P＜0.05），都具有统计学意义，但是相对于 DBP,ANP 与 SBP 的相关性更显著。
结论 外周血中 ANP 浓度降低与血压升高密切相关；NPR-C 配体 ANP 参与了原发性高血压的发病；ANP 影响着 SBP/DBP 的水平变化，尤其对 SBP 的影响更为显著。

PO-0657

TROP2 靶向的 ICG@PLGA 纳米粒子的构建及对三阴乳腺癌协同诊断与治疗研究

张雷、金岳心子、徐娟、孙子微、林明鑫、魏嘉、陈文秀
江苏省人民医院（南京医科大学第一附属医院）

目的 制备可靶向三阴乳腺癌(TNBC)，同时具有检测与治疗功能的靶向纳米粒子，并验证其功能。
方法 以羧基端 PLGA 为原料，复乳溶剂挥发法制备内部包裹 ICG 的纳米粒子，通过酰胺反应在纳米粒子表面连接可靶向人滋养层细胞表面抗原 2（TROP2）的单克隆抗体。紫外-可见 (UV-Vis) 分光光度计检测 ICG 的释放，激光共聚焦显微镜观察靶向纳米粒子体外结合人乳腺癌细胞 MDA-MB-231 的能力，小动物活体成像观察靶向纳米粒子在裸鼠原位肿瘤模型中的运行分布规律。红外光照射后，检测靶向纳米粒子对肿瘤细胞的杀伤及抑制肿瘤生长的能力。
结果 所制备的靶向纳米粒子为规则圆形，粒径在 200nm 左右，体外可与乳腺癌细胞结合或被吞噬进入肿瘤细胞内，红外线照射后会产热至培养液温度升高，杀伤肿瘤细胞。肿瘤模型鼠体内，靶向纳米子可靶向至肿瘤组织，通过活体成像可对肿瘤进行诊断，并可通过红外照射产热，杀伤肿瘤细胞，抑制肿瘤组织生长。
结论 本项目构建的 ICG@PLGA 纳米复合体，可通过 TNBC 细胞过表达的 TROP2 抗原靶向至肿瘤组织，同时通过纳米粒子中 ICG 的光热效应和成像功能，实现集诊断、靶向性治疗、热疗于一体的精准诊断与治疗。

PO-0658

Nomograms incorporating marital status can predict overall survival among patients with colorectal cancer

Hua Wang
Department of Laboratory Medicine, Renji Hospital, School of Medicine, Shanghai Jiaotong University

Background Marital status is an independent prognostic factor for many cancers, although there are no studies that have described using nomograms that incorporated marital status to predict survival after surgery for colorectal cancer (CRC). This study aimed to determine whether nomograms that included marital status could predict overall survival (OS) among patients with CRC.
Methods Data were extracted from the Surveillance, Epidemiology, and End Results database for 8,375 patients who were diagnosed with CRC between 2010 and 2014. Univariate Cox regression analyses were performed to select variables for inclusion in the nomograms. Significant variables from the univariate analyses were entered into multivariate Cox proportional hazards models. Predictive values were evaluated on the basis of the areas under receiver operating characteristic curves (AUCs) and Harrell's concordance index (c-index).
Results Married patients with CRC had significantly better 5-year OS than unmarried patients ($P < 0.001$). The AUCs for predicting 5-year OS using the multivariate Cox regression models were 0.749 for all patients, 0.707 for single patients, 0.719 for married patients, and 0.718 for divorced patients. Nomograms were developed to predict 5-year OS according to marital status, and the c-index values for predicting 5-year OS were 0.695 among all patients (95% confidence interval [CI]: 0.679–0.711), 0.729 among single patients (95% CI: 0.697–0.759), 0.716 among married patients (95% CI: 0.696–0.735), and 0.728 among divorced patients (95% CI: 0.687–0.769).

PO-0659

Ct 通过激活经典和非经典炎症小体通路诱发 GSDMD 介导的细胞焦亡

唐玲丽、方奕元、冯晓晶、蒋萍
中南大学湘雅二医院

目的 研究 GSDMD 介导的细胞焦亡在沙眼衣原体（Chlamydia trachomatis, Ct）繁殖发育周期中的作用及机制，为进一步深入探究防治沙眼衣原体的感染提供新思路。
方法（1）利用 L2 血清型 Ct 感染 HeLa 细胞，在感染过程中不同时间点（0h、12h、24h、36h、48h），于光学显微镜和电镜下观察细胞形态的改变；检测培养上清中 LDH 和 IL-1β，IL-18 的水平；Western blot 检测细胞裂解液焦亡效应蛋白 GSDMD、GSDME 的表达及活化情况。（2）加入 GSDMD-NT 打孔活性抑制剂 NSA 干预，以间接免疫荧光染色法观察子代 EB 的释放和再感染情况。（3）NLRP3 抑制剂 MCC950 和 Caspase-4 抑制剂 Z-LEVD-FMK 分别对 Hela 细胞进行预处理，在 Ct 感染 36h 时分别收集细胞裂解和培养液，Western Bolt 和自动生化仪分别检测细胞焦亡经典和非经典通路指标 NLRP3、Caspase-1、Caspase-4、GSDMD 的表达及 LDH 水平的变化。
结果（1）Ct 感染 HeLa 细胞 24h 后，观察到细胞呈肿胀膨大、气泡状突起的细胞焦亡样改变；LDH 和 IL-1β、IL-18 水平较阴性对照组显著升高（$P<0.001$）；GSDMD 全长表达逐渐降低，其活化片段开始表达，并且随着时间逐渐增强，未检测出 GSDME 活化。（2）GSDMD 打孔活性抑制剂 NSA 干预后，上清液中子代 Ct 感染率较正常感染组降低。（3）抑制剂 MCC950 和 Z-LEVD-FMK 分别干预后，GSDMD 活化片段呈剂量依赖性逐渐减弱，LDH 水平降低（$P<0.001$）。
结论 Ct 可能通过激活经典和非经典炎症小体通路诱发 GSDMD 介导的细胞焦亡促进沙眼衣原体的感染播散。

PO-0660

伴有红细胞和血小板异常的家族性高胆固醇血症临床特征及基因研究

李佳明[1]、王学锋[1]、彭真萍[2]、丁秋兰[2]
1. 上海交通大学医学院附属瑞金医院输血科
2. 上海交通大学医学院附属瑞金医院检验科

目的 研究一个伴有红细胞和血小板异常的家族性高固醇血症家系的临床及分子生物学特征。
方法 回顾性分析 1 例家族性高胆固醇血症患者及家系成员的临床资料；应用高效液相色谱法检测血清中豆固醇和谷固醇含量；二代基因测序技术检测先证者和家系成员基因变异情况，并复习国内外相关文献进行探讨。
结果 先证者自幼贫血合并多部位黄色瘤，35 岁因反复胸闷行冠脉造影示冠状动脉三支严重病变，腹部超声示：脾肿大，低密度脂蛋白、豆固醇和谷固醇均升高，血常规示：贫血合并血小板低下，血涂片可见口型、靶型红细胞，大血小板散在可见。进一步行二代基因测序及基因预测模型提示：患者存在 LDLRAP1 基因纯合突变。该突变形成的蛋白截断体丢失多个稳定蛋白结构区域，不具备正常功能。 LDLRAP1:NM_015627.2:exon4:c.C415T:p.Q139X，为该家系的致病基因变异。父母近亲结婚，均为杂合突变。携带 LDLRAP1 基因变异的 3 例家系成员其低密度脂蛋白轻度增高。同时，患者也存在 ABCG8 基因变异，ABCG8:NM_022437.3:exon13:c.T1895C:p.V632A,ABCG8:NM_022437.3:exon8:c.C1199A:p.T400K。父母为纯合突变。其中 3 例携带 ABCG8 基因变异的家系成员豆固醇和谷固醇轻度增高，2 例家系成员出现高密度脂蛋白增高。患者经降脂治疗后，贫血及血小板减少均有所改善。
结论 植物固醇血症与家族性高胆固醇血症临床症状相似，极容易混淆，尤其患者合并贫血及血小板减少。基因检测作为家族性高胆固醇血症诊断及鉴别诊断的金标准，可提高诊断准确率。本例患者同时出现 LDLRAP1 及 ABCG8 基因变异，其临床表现及治疗方案的选择更加复杂，应结合低密度脂蛋白及植物固醇浓度测定，综合考虑，以免耽误最佳治疗时机。

PO-0661

METTL3 介导的 m6A 修饰对电离辐射诱导的非小细胞肺癌 EMT 和侵袭转移中的作用机制及临床价值研究

齐秋晨
山东大学第二医院

目的 探讨 METTL3 对电离辐射诱导的非小细胞肺癌（NSCLC）EMT 和侵袭转移中的作用及机制，并探讨其作为放疗预后标志物的临床价值。
方法 采用划痕实验和 Transwell 小室迁移和 Matrigel 侵袭实验检测电离辐射对 NSCLC 细胞迁移侵袭能力的影响；采用免疫荧光法、qRT-PCR、Western blot、Dot blot 检测电离辐射对 NSCLC 细胞 EMT、 METTL3 表达及 m6A 修饰水平的影响；构建构建 METTL3 过表达和 RNAi 慢病毒载体，分析辐照后各组肺癌细胞模型 EMT 标志物表达的变化；利用 MeRIP-seq 及生物信息学分析技术挖掘出辐射过程中 METTL3 介导的 m6A 修饰调节的候选基因，对其进行功能鉴定，并进一步研究其 mRNA 甲基化调控的机制。
结果 X 射线辐照后 NSCLC 细胞 RNA m6A 修饰上调，且 m6A 转移酶 METTL3 表达异常增加；下调 METTL3 可以阻止 IR 诱导的 m6A 甲基化，且电离辐射诱导的 A549 细胞 EMT 及迁移侵袭能力明显减弱。MeRIP-seq 及 MeRIP-qPCR 验证 TGFβ2 是辐射过程中 METTL3 介导的 m6A 修饰调控的靶基因，机制研究表明电离辐射通过 METTL3 诱导 TGFβ2 的 m6A 修饰增加，通过 m6A-IGFBP2 依赖机制抑制 TGFβ2 的降解，激活下游 Smad3 通路，促进 NSCLC 细胞的 EMT 及侵袭

转移。临床价值评估发现 NSCLC 患者 METTL3 高表达与放疗后生存期呈负相关，有望成为潜在的放疗预后标志物。
结论 METTL3 是电离辐射诱导 NSCLC 细胞 EMT 和侵袭转移的关键蛋白，为放疗后 NSCLC 转移的防治提供新的研究靶点。

PO-0662

Re-evalute the Prognostic Value of Absolute Lymphocyte Count in Children with Immune Thrombocytopenia

ximei yang
Jiangxi children's Hospital

Objective Different from the report that absolute lymphocyte count (ALC) can predict the prognosis of children with Immune Thrombocytopenia (ITP), the aim of this study was to prove that the difference of ALC between acute and chronic/persistent ITP children was caused by age.
Methods We collected the datas of 1060 children diagnosed as ITP from january 2015 to december 2019 from hospital information system of Children's Hospital of jiangxi province, China. Of them, 242 children who were initial diagnosed as ITP and treated with immunoglobulin and hormone were selected as the study objects. Of 242 children, 141 were diagnosed as acute ITP, 101 were diagnosed as chronic/persistent ITP. According to age and gender, 58 healthy children were matched to the acute ITP group as the normal group 1 and 37 healthy children matched to chronic/persistent ITP group as the normal group 2. All subjects were divided into four groups according to their age, which were ≤12 months group, ≤24 months group, ≤72 months group and > 72 months group. Then the ALC of acute and chronic/persistent ITP children in different age groups were analyzed and compared, as well as the comparison between acute and chronic/persistent ITP children and normal control group.
Results Before age stratification, there were significant differences in ALC between acute ITP group and chronic/persistent group (P= 0.000). However, we found that the median age of acute ITP group (18months) was younger than that of chronic/persistent group(46months). After age stratification, 44.7% (63 / 141) and 12.80% (18 / 141) of children with acute ITP were in ≤12 months group and ≤24 months group, while 47.5% (48 / 101) and 29.7% (30 / 101) of children with chronic ITP were in ≤72 months group and > 72 months group, respectively. The median ALC of acute ITP in ≤12 months, ≤24 months, ≤72 months and >72 months were 6.28*109/L, 5.91*109/L, 3.77*109/L and 1.87*109/L, respectively. The median ALC of chronic/persistent ITP were 4.54*109/L, 4.03*109/L,3.15*109/L and 1.95*109/L, respectively. No matter acute ITP (P=0.000)or chronic/persistent ITP(P=0.000), there were significant differences in the median ALC among the four age groups. But there were no significant difference in the same age group between acute group and chronic/persistent ITP(≤12 months group: P=0.052, ≤24 months group: P=0.518, ≤72 months group: P=0.209, > 72 months group: P=0.622). In addition, we found that when the age was > 72 months, the median ALC of both acute and chronic ITP patients was significantly different from that of the normal control, but there was no difference when the age < 72 months.
Conclusion ALC has no value in predicting the prognosis of ITP in children, the difference bwteen the acute ITP and chronic/persistent ITP may be due to the difference of age.

PO-0663

采用间接法建立乌鲁木齐地区三碘甲状腺原氨酸、甲状腺素、促甲状腺激素的参考区间

宋雪、黄睿、王昌敏
新疆维吾尔自治区人民医院

目的 采用间接法建立乌鲁木齐地区甲状腺功能三碘甲状腺原氨酸（T_3）、甲状腺素（T_4）、促甲状腺激素（TSH）指标的人群参考区间，并与厂家提供的参考区间进行比较，以验证间接法建立人群甲状腺功能指标参考区间的可靠性。
方法 选择 2021 年 1 月至 5 月在新疆维吾尔自治区人民医院体检中心进行体检的健康人群的 T_3、T_4 和 TSH 数据。使用 SPSS 17.0 统计软件，通过 Kolmogorov-Smirnov（K-S）检验分析其数据的正态性，性别间比较采用 Mann-Whitney *U* 检验。非正态数据使用 Minitab 软件进行 Box-Cox 转换成近似正态分布的曲线。采用 Turkey 法剔除异常离群值后建立参考区间，以 $P_{2.5}$ 和 $P_{97.5}$ 作为项目的参考区间上、下限。并与现有厂商的参考区间比较计算相对偏差 d（difference）和参考变化值（reference change value，RCV）。相对偏差低于 RCV（d＜RCV）认为自建参考区间与厂商给定的参考区间之间差异无统计学意义，高于 RCV（d＞RCV）则认为两者间差异有统计学意义。
结果 经 K-S 正态性检验，T_3、T_4 和 TSH 三个项目的数据均不服从正态性分布。本研究初步纳入 6335 人，经 Box-Cox 转换以及用 Turkey 法剔除离群值后，T_3 组最终纳入 6244 人，T_4 组最终纳入 6230 人，TSH 组最终纳入 6140 人。性别间比较，T_3 和 TSH 在性别间参考区间的建立上具有统计学意义（P＜0.001）。采用间接法建立乌鲁木齐地区参考区间，其中，T_3：男性 0.82~1.86 ng/mL，女性：0.80~1.86 ng/mL；T_4：5.57~10.47μg/dL；TSH：男性：0.801~5.660 uIU/mL，女性：0.918~6.746 uIU/mL。参考区间与厂商相对偏差及参考变化值 RCV 的比较**结果** T_3：男性相对偏差：（$d_{上}$=2.5%，$d_{下}$=7%），女性相对偏差：（$d_{上}$=0%，$d_{下}$=7%），RCV：30.97%；T_4：相对偏差：（$d_{上}$=9.2%，$d_{下}$=25.74%），RCV：9.15%；TSH：男性相对偏差：（$d_{上}$=196%，$d_{下}$=34.76%），女性相对偏差：（$d_{上}$=240%，$d_{下}$=65%），RCV：12.05%。由此可知，T_4 和 TSH 的参考区间与厂商的参考区间存在明显差异，T_3 的参考区间与厂商的参考区间无差异。
结论 相比于直接应用厂商的参考区间，采用间接法建立的参考区间的方法较为可靠，具备经济、简便且更贴近受检人群的特点。

PO-0664

儿童 20556 例食物过敏原与 19453 例吸入过敏原定量检测及流行特征分析

郑力胜[1]、李会强[2]、沈永明[1]
1. 天津市儿童医院
2. 天津医科大学医学检验学院

目的 探讨儿童特异性过敏原的检测结果分布和其规律，为儿童过敏性疾病的预防和诊疗提供科学的参考依据。
方法 应用酶联免疫捕获法，定量检测过敏原特异性 IgE，，对 2019 年 1 月至 2020 年 3 月就诊于天津市儿童医院患儿的 20556 例食物过敏原组合与 19453 例吸入过敏原组合的数据进行统计分析。通过大量数据，分析基于儿童特点，不同性别、年龄等因素的过敏原流行特征。
结果 食物过敏原组合阳性率 64.05%（13167/20556），吸入过敏原组合阳性率 50.47%（9818/19453），食物性过敏原阳性率前三位依次是鸡蛋（49.71%，10219/20556）、牛奶（29.43%，6050/20556）、小麦面粉（18.92%，3889/20556），吸入性过敏原阳性率前三位依次是屋尘（31%，6031/19453）、交链孢霉（21.62%，4206/19453）、粉尘螨（12.59%，

2450/19453），食物过敏原组合中不同性别阳性率为男（63.08%，7845/12436）,女（65.54%，5322/8120），吸入过敏原组合中不同性别阳性率为男（51.92%，6145/11835）,女（48.21%，3673/7618），食物过敏原组合中不同年龄组阳性率为<1 岁（42.54%，1401/3293），1-3 岁（78.14%，5731/7333）,4-6 岁（68.37%，4078/5965），＞6 岁（49.39%，1958/3964）。吸入过敏原组合中不同年龄组阳性率为<1 岁（19.72%，489/2480），1-3 岁（49.55%，3459/6981）,4-6 岁（58.03%，3468/5976），＞6 岁（59.81%，2402/4016）。

结论 不同性别、年龄组中过敏原阳性率有显著性差异，有必要视流行病学特征，指定合理规避高风险过敏原，对过敏性疾病的预防、诊断和治疗有着重要的临床义。

PO-0665

PGRN 在 GGN-ADC 增殖中的作用及机制研究

皇改改、周宇、陈蓉、赵富锋、闫兰芳、郑川、马铭
成都市双流区第一人民医院

研究背景 随着多层螺旋 CT 的广泛普及、人民健康意识的增强以及新型冠状病毒肺炎（corona virus disease 2019,COVID-19）疫情形势的严峻,使肺部局灶性磨玻璃结节（ground glass nodule，GGN）的检出率明显升高。研究发现，肺多发 GGN 手术切除的病灶多数为肺腺癌（adenocarcinoma，ADC）或者癌前病变（占 98.9%）。GGN-ADC 是肺癌的一种早期表现形式，其生物学行为属于惰性，早期手术治疗后的 5 年生存率基本可达 100%，但目前 GGN-ADC 的相关机制仍不清楚。近年来，越来越多的证据证明感染在 GGN-ADC 中发挥着重要的作用，颗粒蛋白前体(progranulin, PGRN)是一种抗感染调控因子, 由 GRN 基因编码、593 个氨基酸组成的外分泌蛋白。PGRN 普遍存在，于肺、脂肪等多种组织和细胞中都有表达, 在抗炎、癌症等多种疾病中扮演着重要的角色，因此我们猜想 PGRN 可能可通过抗炎从而抑制 GGN-ADC 的发生发展。

研究方法 取正常和 GGN-ADC 肺组织（N=3）,采用免疫组化及 Western blot 检测正常组和 GGN-ADC 组中 PGRN、TNF-α 和 Ki-67 的表达；采用 I 型胶原酶连续消化法分离 GGN-ADC 组的肺癌细胞，Western blot 检测肺癌细胞中 PGRN 的表达情况；转染腺病毒 Ad-PGRN 过表达 PGRN，克隆形成实验检测增殖能力，qPCR 和 Western blot 检测 TNF-α 和 Ki-67 的水平。

研究结果 与正常肺组织相比，GGN-ADC 肺组织和细胞中 PGRN 的水平均明显降低，TNF-α 和 Ki-67 的表达显著增加；过表达 PGRN 抑制 GGN-ADC 的增殖，TNF-α 和 Ki-67 的基因和蛋白水平均降低。

研究结论 PGRN 可抑制炎症，对 GGN-ADC 的增殖发挥负向调控作用。

PO-0666

检验科人员职业倦怠状况及其影响因素分析

邓冯莉[1,2,3]、刘子杰[1,2,3]
1. 昆明医科大学第一附属医院医学检验科
2. 云南省检验医学重点实验室
3. 云南省实验诊断研究所

背景 检验人员职业倦怠所造成的检验质量的下降，不仅关系到患者对医院的满意度还影响诊疗质量，因此检验人员职业倦怠研究具有重要意义。

目的 调查检验人员职业倦怠状况及影响因素，为针对性职业倦怠管理及实验室管理提供科学依据。

方法 采用网络问卷调查的形式对国内三甲医院的 300 名在职在岗的检验人员进行调查，获得人口学等基本情况、职业倦怠情况、职业倦怠影响因素等资料；运用描述性统计分析、t 检验及方差分析等统计方法，探索检验人员职业倦怠情况及与各影响因素之间的关系。

结果 共获得有效问卷 280 份。49%的检验人员伴有职业倦怠，其中轻度、中度占 41%。其在“情绪耗竭感、行为不当、成就感低、及倦怠总分在性别、工作年限、是否正式编制、婚否以及是否有子女等人口学因素亚组中存在显著差异（p＜0.05）。女性检验人员职业倦怠受个人因素影响的程度略高于男性，未婚人员的职业倦怠高于已婚人员，合同制人员的职业倦怠高于编制内人员。有子女人员职业 倦怠高于无子女职业倦怠。

结论 检验人员职业倦怠较严重，且在性别，婚姻状况、是否有编制及有无子女为主要差异。人员的素质是保证检验质量的关键因素，在今后的工作中应重视检验人员职业倦怠监控，及时给与针对性的辅导和干预。

PO-0667

BNP 在亚临床甲状腺功能减退和甲状腺功能减退患者中的特征分析

高章伟、蔺亚辉
中国医学科学院阜外医院

目的 脑钠肽（BNP）由心室心肌细胞分泌，用以调节血压和血容量的稳态，充血性心力衰竭时血浆 BNP 水平升高。本研究的目的是通过分析亚临床甲状腺功能减退、甲状腺功能减退患者中 BNP 水平差异，评估患者甲状腺功能减低状态对血浆 BNP 水平的影响。

方法 回顾性分析 2018 年 1 月至 2019 年 1 月期间于我院内分泌科住院的患者的病历共 447 人作为研究对象，将患者分为确诊为亚临床甲状腺功能减退（61 例）、甲状腺功能减退（344 例）和甲状腺功能正常对照（42 例）三组，比较三组患者的一般临床资料，分析三组患者生化指标特征差异及其与各组分的相关性。

结果 亚临床甲状腺功能减退组血浆 BNP 水平显著高于甲状腺功能减退组以及对照组。三组患者 BNP 浓度分别为：亚临床甲状腺功能减退组 793.85±1230.68 pg/ml，甲状腺功能减退组 228.72±571.46 pg/ml，健康对照组 344.32±753.10 pg/ml，三组间 BNP 浓度有显著性差异（P<0.05）；多重线性回归分析提示亚临床甲状腺功能减退组 BNP 水平与 FT4 值具有独立相关性（r^2=0.2750，p<0.001）。

结论 血浆 BNP 的水平受甲状腺的功能状态影响，BNP 水平在亚临床甲状腺功能减退组升高，提示亚临床甲状腺功能减退发生心力衰竭的风险更高。

PO-0668

重庆市某三甲综合医院 2020 年细菌耐药性分析

唐朋、王晶晶、全念、邱宗文、张立群
陆军军医大学第二附属医院检验科

目的 了解陆军军医大学第二附属医院 2020 年常见病原菌的分布和耐药情况，指导临床合理使用抗生素，辅助抗感染治疗。

方法 搜集本院 2020 年 1 月-12 月住院和门诊患者送检的临床样本中分离的菌株，参考美国临床和实验室标准协会（CLSI）2019 年抗菌药物敏感性试验执行标准（M100-29th）对药敏结果进行判断，并采用 WHONET5.6 软件对分离菌株的来源和耐药性进行分析。

结果 2020 年共检出非重复菌株 4125 株（真菌除外）。其中革兰氏阳性菌 1340 株，占 32.5%；革兰氏阴性菌 2785 株，占 67.5%。全院分离病原菌排列前 5 位分别是大肠埃希菌、肺炎克雷伯菌、铜绿假单胞菌、金黄色葡萄球菌和鲍曼不动杆菌，病原菌来源主要以痰液、尿液、无菌体液为主。耐药数据分析显示：耐甲氧西林金黄色葡萄球菌（MRSA）和耐甲氧西林凝固酶阴性葡萄球菌（MRCNS）检出率分别为 25.7%和 71.2%；未检出万古霉素耐药的肠球菌，利奈唑胺耐药的屎肠

球菌检出率为 1.5%；碳青霉烯耐药的鲍曼不动杆菌（CRABA）和碳青霉烯耐药的铜绿假单胞菌（CRPAE）检出率分别为 85.3%和 12.9%；碳青霉烯耐药的肠杆菌目细菌（CRE）总检出率为 12.3%，其中碳青霉烯耐药的大肠埃希菌（CRECO）、肺炎克雷伯菌（CRKPN）和阴沟肠杆菌（CRECL）检出率分别为 1.6%、28.1%和 13.8%。

结论 细菌耐药形势严峻，尤其以碳青霉烯耐药的鲍曼不动杆菌、肺炎克雷伯菌、铜绿假单胞菌和阴沟肠杆菌为主，必须进一步加强多重耐药菌监测和院感控制，防止耐药菌在院内广泛传播，同时需要进一步规范抗菌药物合理使用。

PO-0669

表面增强拉曼散射技术无标记检测乳腺癌细胞来源外泌体

王新慧
山东大学第二医院

外泌体含有不同的双分子特征，反映了释放细胞的成分，成为液体活检的重要物质。为了区分不同的细胞来源的外泌体，表面增强拉曼光谱（SERS）已被应用于检测癌细胞来源的（MCF-7）外泌体和正常细胞来源的（MCF-10A）外泌体。从细胞培养基的上清液中分离外泌体。结果表明，外泌体在 800~1 800 cm-1 区域具有自己独特的特征拉曼光谱。与 MCF-10A 来源的外泌体的光谱相比，MCF-7 来源的外泌体核酸的相对拉曼峰强度明显更高，脂质的相对拉曼峰强度有所降低或拉曼峰消失。 结果表明，SERS 技术可以高灵敏度地检测来自不同细胞的外泌体的细微分子变化，并区分乳腺癌细胞来源的外泌体和正常细胞来源的外泌体。 SERS 技术可以为癌症的早期诊断提供一种快速、无标记、无损的检测方法

PO-0670

Westgard 西格玛规则在急诊生化分析项目质控管理中的应用

张鸿伟、敖帅、张社强、钱净
昆明市第一人民医院

目的 通过对我科急诊生化分析项目进行 Westgard 西格玛性能评价，选择个性化的质控规则，确定合适的分析批长度，并根据质量目标指数（QGI）提出改进方向，指导质量持续改进。

方法 收集我科急诊生化检测系统 21 个分析项目所涉及两个批号的 22 个月的质控数据所得到的累积不精密度 CV、与对等组的偏倚 BIAS 以及我科设定的允许总误差 TEa，将数据输入我科的 Unity Real Time 质控管理平台，系统会根据 Westgard sigma 规则自动计算出 σ 值、推荐的质控规则、假失控率和误差检出率等性能特征；并根据最新推出的分析批长度 Westgard Sigma 规则流程图，评估、确定各分析项目的合适的分析批长度；而对于 σ＜6 的分析项目，通过计算其 QGI，查找方法性能不佳的原因进行持续改进。

结果 1. 21 个生化分析项目的实际 CV、实际 BIAS 和实际总误差 TE 均小于质量目标,其中：有 4 个项目 σ≥6,采用单规则, 3 个项目 5≤σ<6,采用单规则, 4 个项目 4 ≤σ< 5,采用四规则, 8 个项目 3≤σ< 4,采用多规则，实现了个性化质控规则的选择；2. 21 个生化分析项目的分析批长度不尽相同，其中分析批长度为 1000 的有 4 个项目，分析批长度为 450 的 3 个项目，分析批长度为 200 的有 4 个项目，分析批长度为 45 的有 8 个项目；3.对于 σ＜6 的 17 个分析项目中，QGI<0.8 有 16 个项目,提示优先改进精密度；1 个项目 QGI>1.2,提示优先改进正确度。

结论 可以通过对定量检测项目进行 Westgard 西格玛性能评价，根据性能特征来选择个性化的质控规则，根据分析批长度 Westgard Sigma 规则流程图评估、确定合适的分析批长度，并根据质量目标指数 QGI 进行质量持续改进，确保病人检测结果的质量。

PO-0671

microRNA-4731-5p suppresses breast cancer cell glycolysis and reverse epithelial-mesenchymal transition through regulation of PAICS-induced phosphorylation of FAK

lei lang[1]、jing tao[2]、chaomei yang[1]、wei li[1]
1. Chongqing Emergency Medical Center
2. 重庆医科大学附属儿童医院

Background microRNAs (miRNAs) are differentially expressed in breast tumor and serve as tumor promoters or suppressors. In this study, we aim to find out the function of miR-4731-5p in breast cancer progression.
Methods A total of 50 breast cancer patients were enrolled for sample collection followed by determination of expression of miR-4731-5p, PAICS and FAK. Besides, the miR-4731-5p and PAICS expression in breast cancer cells was also detected with its role in glycometabolism, migration, invasion, epithelial-mesenchymal transition (EMT) of breast cancer cells analyzed through gain- and loss-of function assays. The targeting relation between miR-4731-5p and PAICS was confirmed by dual-luciferase assay. Xenograft tumor in nude mice was constructed to observe the tumorigenesis and metastasis ability of breast cancer cells.
Results Decreased miR-4731-5p expression and increased PAICS expression was observed in breast cancer tissues and cells. PAICS was confirmed as the potential target of miR-4731-5p. miR-4731-5p was demonstrated to inhibited glycolysis, EMT, migration and invasion in breast cancer cells through inhibition of PAICS-dependent phosphorylation of FAK. In vivo assay also confirmed the regulatory role of miR-4731-5p/PAICS/FAK axis in in vivo tumorigenesis in breast cancer.
Conclusion Our results indicated that miR-4731-5p inhibits breast cancer cell glycolysis and EMT through inhibition of PAICS-dependent phosphorylation of FAK, suggesting that miR-4731-5p and its targets may serve as therapeutic targets in breast cancer treatment.

PO-0672

白藜芦醇预处理脐带 MSCs 源性 exosomes 调控 Wnt/β-catenin 信号抑制肺癌转移

尹磊
苏州大学附属儿童医院

目的 干细胞经不同因素（如缺氧、炎症、细胞因子、药物）刺激会呈现不同的表型和功能，其分泌的外泌体（exosomes，Ex）组分和功能也会随之改变。因此，可干预干细胞的表型，调控其分泌的 Ex 的组分，进而增强 Ex 的疗效。我们前期发现白藜芦醇（resveratrol，Res）处理人脐带间质干细胞（human umbilical cord-derived mesenchymal stem cells，hucMSCs），可促进其增殖、分化，分泌更高水平的 PDGF-DD，增强其对顺铂诱导的肾毒性的保护作用。在此，我们探究能否通过 Res 调控 hucMSCs 的表型影响其分泌的 Ex 的组分和功能。
方法 Res 处理 hucMSCs，CCK8、成骨成脂诱导实验检测检测其增殖和分化，Luminex、ELISA 、WB、IF、qRT-PCR 技术检测 hucMSCs 蛋白和 mRNA 改变； 超速离心法收集 Res 预处理 hucMSCs 的 Ex（Res-Ex），透射电镜、NanoSight LM10 系统、CD63、CD81 检测对其进行表征和鉴定；小鼠肺癌转移瘤实验和细胞实验对 Res-Ex 的功能和组分进行研究。
结果 Res 处理可增加 hucMSCs 的细胞活性，促进其成骨成骨成脂分化，抑制炎症因子分泌和 Wnt/β-catenin 信号， 增强 Wnt/β-catenin 信号抑制因子 DKK3 的表达。Res 处理不影响 hucMSCs

Ex 分泌、粒径分布及表面分子（CD63、CD81）表达，促进 Ex 转运 DKK3。Res-Ex 作用肺癌细胞或肺癌模型，可拮抗 Wnt/β-catenin 信号，抑制肺癌转移。
结论 Res 调控 hucMSCs 促进其 Ex 转运 DKK3 失活 Wnt/β-catenin 信号，抑制肺癌转移。

PO-0673

竞争 ELISA 法检测 COVID-19 患者血清靶向 RBD 中和抗体水平及影响因素分析

陈晓玲、郑友限、陈秋婷、陈明春、刘建忠
泉州市疾病预防控制中心

目的 基于竞争 ELISA 法检测靶向新型冠状病毒受体结合域 （RBD）的中和抗体，探讨新型冠状病毒肺炎（COVID-19）患者血清中和抗体水平及其影响因素。
方法 收集 2020 年 2 月 24 日前国家传染病信息报告系统中泉州地区 37 例 COVID-19 患者的 65 份血清，同时选取 39 例已完成新型冠状病毒疫苗接种者血清和 44 例疫情爆发前完成采集的健康体检者血清作为对照；采用竞争 ELISA 法检测靶向 RBD 中和抗体；组间比较采用非参数 Kruskal-Wallis 检验，并用广义线性混合模型进行影响因素分析。
结果 COVID-19 患者及疫苗接种者靶向 RBD 中和抗体水平均显著高于健康体检者（Z=78.498、61.242，P 均=0.000）；COVID-19 患者靶向 RBD 中和抗体水平男性高于女性，未复阳组高于复阳组，重型低于轻型、普通型，差异有统计学意义（t=2.235、-9.104；-2.210、-2.526，P 均＜0.05）；核酸检测 CT 值越大（即病毒载量越低），或治疗前 LC 越低、CRP 越高，则患者靶向 RBD 中和抗体水平越高（t=6.156、-6.695、-4.219，P 均＜0.05）；是否复阳与核酸检测阳性持续时间交互作用的影响有统计学意义（t=8.218，P＜0.05）；距离发病时间可显著影响靶向 RBD 的中和抗体水平（β=0.065,t=505.326,P＜0.05），发病 5-10 天可检测到靶向 RBD 中和抗体并增长，15-25 天达峰值进入平台期。
结论 COVID-19 患者在感染后产生新型冠状病毒中和抗体水平随时间改变，且与性别、病毒载量、治疗前 LC 与 CRP 水平及病情转归相关。

PO-0674

新型冠状病毒持续存在状态下医学实验室的安全管理

谢滨姣、祖爽、谢盼盼、张俊涛
黑龙江金域医学检验实验室有限公司

目的 近两年来全球疫情形式严峻，国内多地反复发现确诊病例，颇有类似流感病毒一样长期传播存在的趋势。由于新冠病毒有 1-14 天的潜伏期，第三方检验实验室的委托客户很可能不具备检测新型冠状病毒的条件，或者患者处于潜伏期，病毒拷贝数较低无法检测识别出来。因此第三方检测实验室存在接收的每一例样本均有可能是携带新型冠状病毒的，实验室随时可能面临病原微生物暴露的院感风险。如何能够在隐形安全风险下安全运营，成为目前实验室安全管理的重要课题。
方法 由实验室安全主任召集安全委员会进行风险评估研讨会，针对本课题进行讨论。
讨论内容共分以下几个方面：1.标本收取的安全管理；2.标本检测的安全管理；3.实验室消毒的相关要求。
结果 1.标本收取的安全管理：应将所有设有发热门诊的客户建立清单，发放给物流和实验室员工，要求发热门诊客户所有患者必须送检新冠病毒核酸检测，对于发热门诊的标本专人收取，采用三级个人防护，配备负压运输车，并匹配相应的消毒剂供收取标本后进行防护设施、标本箱、运输车消杀使用；未设有发热门诊的客户应保持对新冠病毒发病早起的临床症状及检测项目结果趋势的敏感

度，如有疑似病例，建议在送检普通项目的同时加做新冠病毒核酸检测，同时将可疑情况反馈给委托实验室，匹配发热门诊标本的接收配置，以保障标本收取人员的安全。
2.标本检测的安全管理：应建立实验室专项课题组，收集文献、教材等相关资料，分析各个检测项目标本是否能够进行灭活，并积极开展灭活与非灭活标本的比对实验；对于无法进行灭活的标本，应在离心、检测等步骤中尽可能的避免气溶胶的产生，尽可能在生物安全柜内操作标本。
3.实验室管理的相关要求：在实验室整体管控上，应不断完善文件体系，针对不同风险点均设立应急预案；同时加强人员培训，通过应急演练加强人员应对突发情况的应变能力。应做好每日现场环境、仪器设备、废弃标本等的消毒方案及应急处理；所有安全相关设备的定期维护保养、校准核查，判定设备处于异常状态的标准文件及应急预案；建立实验室环境洁净度监控的工作频次、流程制度，并按期执行，以保证实验室的安全运营。
结论 疫情持续存在的前提下，实验室的生物安全工作成为运营管理的首要任务，实验室管理层应不断完善文件体系及工作流程，防范于未然。

PO-0675

Oxidized ATM enhances triple negative breast cancer cell invasion via the p-EGFR/MEK/ERK signaling pathway during hypoxia

lei lang[3]、tenghua yu[1]、jing tao[2]、weijie fu[3]、shenshen zhi[3]、wei li[3]
1. 江西省肿瘤医院
2. 重庆医科大学附属儿童医院
3. 重庆市急救医疗中心

BACKGROUND Ataxia-telangiectasia mutated protein kinase (ATM) is activated upon DNA damage and plays an anti-tumorigenic role by repairing DNA double-strand breaks (DSBs). However, recent reports have shown a DNA damage-independent activity of ATM (called oxidized ATM) under hypoxia promoting tumor cell growth and invasion in several cancers, including breast cancer. However, the role of oxidized ATM in triple negative breast cancer (TNBC) progression remains unclear.
METHODS Immunohistochemistry and western blotting were applied to detect the levels of oxidized ATM in different breast tissues and cell lines. Transwell assay was used to detect the cell invasion abilities in different treatments. We validated the molecular mechanism of our results through immunohistochemistry and Western blot analysis in vitro and in vivo.
RESULTS In the absence of DNA damage, enhanced oxidized ATM protein exists not only in breast cancer tissues, but also in TNBC cell lines. ATM knockdown or inhibition of p-ATM reduce the expression of p-EGFR protein level and weaken the invasiveness of TNBC cell lines under hypoxia. And exogenous EGF or Honokiol (an activator of ERK) can rescue the invasiveness of breast cancer cells under hypoxia. Mechanically, we reveal that oxidized ATM enhances cell invasion via the p-EGFR/MEK/ERK signaling pathway in vitro and in vivo.
CONCLUSIONS Our research provides novel insight into the role of oxidized ATM in promoting tumor metastasis via p-EGFR/MEK/ERK signaling pathway and its possible role as a therapeutic target in TNBC.

PO-0676

Role of ErbB3 overexpression in tumor metastasis of ErbB2-positive breast cancer and its preliminary molecular mechanisms

Ruxue Jia[1,2]、Zhuolin Li[1,2]、Yating Wu[1,2]、Qun Ren[1,2]、Tingting Lin[1,2]、Huimin Niu[1,2]、Xiaoming Huang[1,2]、Shenghang Zhang[1,2]、Shuiliang Wang[1,2]
1. Affiliated Dongfang Hospital of School of Medicine, Xiamen University
2. 联勤保障部队第九〇〇医院检验科

Objective ErbB2 positive breast cancer is a type of breast cancer with higher malignancy. However, our understanding of the molecular mechanism of breast cancer metastasis is still very limited. Here, we mainly investigate the role of ErbB3 overexpression in the metastasis of ErbB2 positive breast cancer and other malignant biological phenotypes.
Methods ErbB3 overexpressing ErbB2 positive breast cancer cell lines were constructed by lentivirus transduction; MTS and cell cloning assay were used to detect the effect of ErbB3 overexpression on the proliferation of ErbB2 positive breast cancer; The effect of ErbB3 overexpression on metastasis and invasive growth of ErbB2 positive breast cancer was detected by Transwell and Transwell invasion assay; Western blot analyses were performed to determine the expression and activation of proteins; qRT-PCR was carried out to analyze the mRNAs and miRNAs expression levels; Clinical samples of ErbB2 positive breast cancer were analyzed by immunohistochemical assay.
Results ErbB3 overexpression not only significantly promoted the growth and proliferation of ErbB2 positive breast cancer, but also significantly enhanced its invasion and migration. The preliminary mechanism investigation showed that ErbB3 overexpression could not only significantly induce the up-regulation of transcription factors such as ZEB1 in ErbB2-positive breast cancer cells to promote the EMT phenotype, but also significantly promote the up-regulation of MMP2 and MMP9 expressions with activation of downstream Akt and MAPK signalling pathways at the same time. In addition, RT-qPCR analysis also confirmed that ErbB3 overexpression down-regulated the expression of miR-203 and miR-542-3p, both of which may target ZEB1 and other EMT-regulating transcription factors. Analysis of clinical samples preliminarily suggested that ErbB3 overexpression may be associated with clinical metastasis in patients with ErbB2-positive breast cancer.
Conclusion Our data strongly suggest that ErbB3 overexpression can significantly enhance ErbB2 positive breast cancer metastasis and other related malignant biological phenotypes through the formation of ErbB2 / ErbB3 heterodimer.

PO-0677

9 号染色体嵌合重复伴超雄综合征的细胞遗传学分析一例

耿丹、杜荷香、潘璠、霍志连、李清鲜
太原金域临床检验所有限公司

染色体疾病是由于生物个体在生殖遗传中出现染色体数目或结构异常，而引起的流产、死胎、先天畸形、发育迟缓、不孕不育等一系列临床症状的疾病，是造成出生缺陷的重要因素之一，因此借助染色体核型分析及高通量测序技术等协助诊断尤为重要。

目的 通过对一例呼吸窘迫综合征、左侧肾上腺囊肿的早产儿进行染色体核型分析及遗传病全外显子组基因测序，明确发病原因，并探究临床病因与染色体变异的相关性，同时评估传统核型分析与高通量测序技术的应用价值。

方法 首先对患儿进行外周血染色体 G 显带核型分析，其次利用高通量测序技术（二代测序）进行全外显子组测序检测，明确致病基因。

结果 患儿传统染色体核型分析结果为 47,XYY[36]/48,XYY,+mar[34]/46,XY[20]，考虑此核型中存在嵌合超雄综合征核型及常染色体不平衡变异。高通量测序结果提示该患儿 Y 染色体拷贝数为 2，9 号染色体 p21.1p13.1 区域存在约 6.2Mb 片段重复，且 11 号染色体发生大片纯合现象。
结论 该患儿的临床病因与基因拷贝数变异相关，综合传统核型分析结果及全外显子组基因测序结果，考虑传统核型中的标记染色体为 9 号染色体重复片段，11 号染色体发生大片纯合现象可能为 11 号染色体发生部分单亲二倍体，这可能导致该区域隐性遗传病的发病风险增加，也可能是整条 11 号染色体发生单亲二倍体，同时存在超雄综合征核型。9 号染色体嵌合重复、11 号染色体发生单亲二倍体是导致该患儿发育异常、呼吸窘迫、左侧肾上腺囊肿、夭折等临床症状的主要因素。传统核型分析可检测患儿染色体的具体形态，但不能精准识别标记染色体，具有一定的局限性。而高通量测序技术可精准地检测覆盖范围内的绝大多数（约 98%）点突变及大多数（90%）的致病性拷贝数变异。两种检测技术相结合，可精准检测致病基因以协助诊断，在出生缺陷领域颇有临床意义。

PO-0678

长沙县妇幼保健院孕妇缺铁性贫血及铁缺乏的现状分析

杨牡丹[1]、周珂[2]
1. 长沙县妇幼保健院
2. 湖南师范大学医学院

目的 研究长沙县妇幼医院缺铁性贫血及铁缺乏的现状。
方法 选取 2020 年 1 月-2020 年 12 月在长沙县妇幼医院门诊进行产检的孕妇 14018 例为研究对象，通过孕妇年龄、孕周、血常规、血清铁蛋白含量、铁剂补充类型等指标，统计分析孕妇铁缺乏、贫血、缺铁性贫血患病率及铁剂补充情况。
结果（1）产检孕妇妊娠期贫血的患病率为 31.3%（4382/14018），其中缺铁性贫血占 57.8%（2534/4382），缺铁性贫血及铁缺乏的患病率分别为 18.1%（2534/14018）和 49.8%（6986/14018）。（2）孕妇铁缺乏、贫血及缺铁性贫血的患病率随孕周增长均呈上升趋势，三个不同孕期组比较差异均有统计学意义（$P < 0.05$）；三个不同年龄组比较差异均无统计学意义（$P>0.05$）。（3）随孕周的增长，孕妇血清铁蛋白及血红蛋白浓度均呈下降趋势，差异有统计学意义（$P < 0.05$）。（4）全部孕妇中补充了铁剂有 9426 例，占 67%，其中最常用的为琥珀酸亚铁片和多糖铁复合物胶囊。
结论 本地区的孕妇铁缺乏、贫血及缺铁性贫血的患病率仍处于较高水平；尤其是随孕周增长，孕妇对铁的需求量也持续增加，铁缺乏、贫血及缺铁性贫血患病率均上升，血清铁蛋白及血红蛋白浓度均下降；科学补铁对改善孕期保健质量、防治妊娠期缺铁性贫血意义重大。

PO-0679

血清异常凝血酶原与甲胎蛋白对肝癌诊断价值的比较——荟萃分析

阳迎
中国人民解放军陆军军医大学第二附属医院

背景与目的 肝癌（HCC）是常见的恶性肿瘤之一，其早期诊断对患者行早期根治切除术及相应放化疗、延长患者生存期、提高患者生活质量有极大帮助，其早期诊断方法包括超声、CT、血清学检查等，血清学标志物包括应用最为广泛的甲胎蛋白（AFP）、异常凝血酶原（DCP）、甲胎蛋白异质体比例(AFP-L3%)等等，本文旨在比较 DCP 与 AFP 对肝癌的诊断价值，明确其在临床诊断中的应用价值。

方法 在中国知网、万方数据库、中国生物医学数据库、PubMed、Medline 及 Cochrane Library 数据库中系统的检索有关 AFP 及 DCP 对肝癌诊断价值的文章，通过制定的纳入排除标准进行筛选，通过 QUADAS-2 对纳入的文献进行质量评价，最终通过 Meta Disc 进行数据合并。
结果 最终我们共纳入了 19 篇文章，AFP 及 DCP 对肝癌诊断价值中汇总的灵敏度、特异度、阳性似然比、阴性似然比分别为（0.63，0.85，4.64，0.42）、（0.68，0.89，6.40，0.34），AFP 受试者工作特征曲线下面积（AUC）为 0.81，DCP 的 AUC 为 0.89。
结论 在肝癌诊断中，异常凝血酶原与甲胎蛋白相比具有较高的灵敏度及特异度。

PO-0680

53244 例山西省女性人乳头瘤病毒感染率及型别分布情况分析

吴佳丽、畅锴
太原金域临床检验所有限公司

人乳头瘤病毒（huamn papillomavirus，HPV）属 DNA 病毒，具有多种不同的型别，是人类乳头状瘤、疣等疾病的致病原因。根据导致疾病的不同分为高危型和低危型。高危人乳头瘤病毒(high risk-huamn papillomavirus，HR-HPV)持续感染与宫颈癌、阴茎癌、外阴癌、阴道癌和肛门癌、复发性呼吸道乳头状瘤病和某些头颈部恶性肿瘤相关，尤其与宫颈癌的发生关系密切。
目的 通过分析山西省地区女性 HPV23 分型感染情况及亚型分布特点，了解山西地区 HPV 感染分布情况，从而为宫颈癌的预防提供重要依据。
方法 收集山西地区 53244 例女性标本，通过聚合酶链式反应（PCR）体外扩增技术和 DNA 反向点杂交法相结合的 HPV 基因分型检测技术方法，检测 53244 例山西省女性标本 HPV 感染率及型别分布情况分析。
结果 53244 例女性送检标本中共检出 HPV 阳性标本为 14494 例，阳性率为 27.22%，其中 HR-HPV 检出 14494 例（78.90%）、LR-HPV 检出 3872 例（21.10%），其感染的的主要基因分型占比总标本的比例分别为 HPV16 型（4.15%）、HPV52 型（4.24%），HPV53 型 （2.54%）、HPV58 型（2.65%）、HPV51 型（2.04%）、HPV42 型（2.16%）、HPV81 型（2.22%）；不同年龄组别感染 HPV 分型不同，其中≤30 岁、31~40 岁和>50 岁年龄组以 HPV52 型为主，感染率依次分别为 4.69%、3.69%和 5.35%；41~50 岁年龄组以 HPV16 型为主，感染率为 3.84%。山西各地区间 HPV 感染率及型别分布情况分析，差异具有统计学意义(P <0.05) 。
结论 山西省女性人群感染的分型类型主要为 HPV16、52、53、58、51、42、和 81 型最为常见，为指导山西地区女性进行预防 HPV 感染筛查提供理论依据，对宫颈癌的早期诊断、疫苗接种和研发也有非常重要的意义。

PO-0681

岳阳市 6700 例人群血清中 25-羟基维生素 D 含量的检测结果分析

陈静、蒋华科、龚燕飞
岳阳市第一人民医院

目的 探讨岳阳市不同年龄阶段人群血清中维生素 D 的含量，分析原因并寻找有效防治措施。
方法 高效液相色谱串联质谱法检测血清标本中 25-羟基维生素 D 的含量并对检测结果进行统计分析。
结果 岳阳市地区 6700 例开展了维生素 D 检测项目的人体中，血清 25-羟基维生素 D 平均水平为 21.75+9.35ng/mL，结果显示严重缺乏 356 人（5.31%）、缺乏 2940 人（43.88%）、不足 2388 人（35.64%）、正常 1016（15.16%）、过量 0 人，其中男 2203 人（24.75+9.41ng/mL），女 4497 人（20.63+9.10ng/mL）。14 岁及其以下年龄人群的平均维生素 D 含量为

(26.04±10.36)ng/mL，14 岁以上年龄的人群体内平均维生素 D 含量为 (20.25±8.50)ng/mL。综上所述，男性含量稍高于女性，14 岁及其以下年龄的人群含量稍高于 14 岁以上人群，但是整体处于含量不足的状态。

结论 岳阳市地区的人群随着年龄的增长，体内血清中 25-羟基维生素 D 含量正常水平比率逐渐降低，建议在日常生活中，应多外出活动，并且注意对维生素 D 进行合理补充，从而维持体内维生素 D 的正常含量。

PO-0682

记录上墙对实验室人员质量意识提升的探究

杨国青、王慧
贵州金域医学检验中心有限公司

目的 为了更好的促进实验室质量建设、提升人员质量意识，有效降低因人员疏漏造成的记录缺失，确保记录能够连贯完整，保障实验室质量体系的健康运行。

方法 回顾性分析 2015-2020 年贵州金域医学检验中心实验室各种质量体系检查（包括 ISO15189、内审、集团巡检、日常检查、飞行检查、监管检查）开具的不符合项，分析记录上墙实施前后上墙记录开具的不符合项的变化情况，以及实施记录上墙后未上墙记录开具的不符合项的变化趋势和实施记录上墙后每年开具的不符合项数量变化情况的相关性。

结果 ①记录上墙后上墙的记录不符合项较之前下降 23%，两年后上墙记录不符合项数量降为 0；②实施记录上墙后，未上墙记录的不符合项数量逐年减少，下降幅度≥6%；③实施记录上墙后，每年开具的不符合项数量逐年降低，下降幅度≥10%，降低趋势高于未上墙记录的不符合项。

结论 记录上墙后，促使工作人员每日自我检查记录是否填写完整，同时其他人员也可以一目了然的看到其记录是否漏填，起到间接监督作用。随着人员自我检查习惯的形成，其他未上墙的记录的及时填写也得到了持续的改善，因记录问题被开具的不符合项的直接下降，形成了良性的自我激励和奖励机制，反促其自觉的去审视自查自纠存在的质量问题，不符合项数量不断下降，质量体系持续完善。说明记录上墙的实施，对实验室人员的质量意识提升起到了明显的促进作用并在其过程中形成了质量体系自查自纠持续改善的长效机制。

PO-0683

Monocyte to Lymphocyte Ratio and Red Cell Width Distribution to Lymphocyte Ratio were Useful Markers in Assessment of Disease Prognosis and Diagnosis Value in Primary Biliary Cirrhosis Patients

Yanting Jiang、Xi Li、Wei Zhou、Sihui Li、Min Jin、Jian Wang
First Affiliated Hospital of Guangxi Medical University

Objective Although there have been extensive investigations on monocyte to lymphocyte ratio (MLR) and red cell width distribution to lymphocyte ratio (RLR), their roles in Primary Biliary Cirrhosis(PBC) remain unclear. The purpose of the present study was to evaluate MLR and RLR levels in adult PBC patients and explore their clinical significance.

Methods A retrospective study involving 71 patients with PBC and 170 patients with Autoimmune hepatitis (AIH) were collected, and 170 healthy subjects were included as healthy control group (HC group). All clinical characteristics of the PBC patients were extracted from their medical records. MLR and RLR levels among PBC patients, AIH patients and HC group were compared,

and receiver operating curve (ROC) was used to evaluate the diagnostic value of each index in the diagnosis of PBC.
Results MLR and RLR in PBC group was higher than that in AIH group and in HC group (each P<0.05). The area under ROC curve (AUC) of MLR and RLR in diagnosis of PBC were 0.821 and 0.797 respectively (each P < 0.05). The combination of MLR and RLR increases the diagnostic performance of PBC (AUC=0.868, P<0.05). Spearman correlation analysis showed that RLR was negatively correlated with C3 (r=−0.384, p<0.01) and C4 (r=−0.321, p=0.03), and positively correlated with Mayo score (r=0.618, p<0.01). There was a positively correlation between MLR and Mayo score (r=0.354, p<0.01). In PBC patients with Child-pugh classification, MLR and RLR levels in B+C group were significantly higher than that in A group (each P <0.05).
Conclusion Elevated levels of MLR and RLR may prove to be a useful marker for estimating the prognosis of PBC disease, and the combined detection of MLR and RLR has certain clinical diagnostic value in patients with PBC.

PO-0684

Comparison of two different systems for testosterone measurement

Wei Zhang
Jiangsu Province Hospital (The First Affiliated Hospital with Nanjing Medical University)

Objective To evaluate the concordance of two different detection systems of CLIA in the testosteronelevels measurement.
Methods Serum specimens from 155 patients were collected at Jiangsu Province Hospital June 2018. Testosterone levels were assayed using two different chemiluminescence immunoassays on platforms manufactured by Roche and Beckman. Liquid chromatography with tandem mass spectrometry (LC-MS/MS) were used to reanalyze the top ten serum sample which had the maximum difference between Beckman and Roche. Passing-Bablok regression equations, Spearman correlation coefficient (r) and Bland-Altman plots were used to estimate the relationship and bias among the testosterone results obtained with the different analyses. The χ2 test was performed to analyze the results from the different methods.
Results The regression equation (y = 0.538 + 1.020 x) highlighted the presence of proportional systematic difference, there was significant deviation from linearity (P < 0.01). The Spearman correlation coefficient (r= 0.971, P < 0.001) indicated that the results of Beckman and Roche had good correlation. The Bland-Altman plot analysis showed a significant systematic difference in the two methods, Beckman measurements were in average 22.4% (95% CI, 7.88 to 36.83) higher compared to Roche ones. The overall coincidence rate was 91.84% between the Beckman and Roche methods.
Conclusions Two detection systems do not have the consistency of the testosterone assays, it is recommended to use LC-MS/MS to confirm the testosterone level.

PO-0685

男性激素五项参考区间的建立及其临床价值

王希部
深圳市罗湖区人民医院

目的 建立深圳罗湖区实验室男性激素五项的适合参考区间，探究其在男性不育症的临床价值，为临床诊疗提供帮助。
方法 采集 2020 年 5 月-10 月在深圳罗湖区人民医院体检表观健康的男性成人 399 例静脉全血，然后离心取血清。被检者年龄在 17-56 岁之间，将其分为≤30 岁，30-40 岁，＞40 岁三组，采用美国

雅培发光仪检测雌二醇（E2）、促卵泡成熟激素（FSH）、促黄体生成素（LH）、泌乳素（PRL）、睾酮（TESTO）的水平，并同时取精液进行精液常规分析，标准按 WHO 底五版要求进行。另外选取同期不育患者 30 例作为对照。

结果 促卵泡成熟激素（FSH）、促黄体生成素（LH）、泌乳素（PRL）三个年龄组别间水平分布具有差异，部分年龄组之间有统计学差异（P<0.05）。睾酮（TESTO）、雌二醇（E2）不同年龄组之间未见明显差异（P>0.05）。除 PRL 外，精液正常男性与少弱精症不育男性激素水平不同，具有统计学差异（P<0.05）。建立了成年男性激素五项的本地区参考区间。

结论 不同种族、地区人群，男性激素水平并不完全一致。应建立本地区实验室的参考区间，能更好的指导临床在不育症患者中的诊断和治疗。

PO-0686

Does Maternal Hypothyroidism during Pregnancy have Association with Autism Spectrum Disorder in the Offspring? A systematic review and Meta-analysis

Haolong Li
Department of Clinical Laboratory, Peking Union Medical College Hospital, Peking Union Medical College and Chinese Academy of Medical Sciences, Beijing, China

Objective Hypothyroidism is a common disorder appeared in pregnant women, which has been proved to cause autism spectrum disorder (ASD) in their offspring by several studies. The aim of this study is to systematically evaluate the association of maternal hypothyroidism during pregnancy and ASD in offspring by using available data.

Methods Four electronic databases were searched up to October 20,2019 respectively, including PubMed, EMBASE, Web of Science and Scopus. Two investigators independently extracted data by using a standard form that covered essential information on the eligible studies: first author, publication year, country, study period, study design，patient groups, sample size，maternal thyroid status, diagnostic standards of ASD and maternal hypothyroidism, effect size with 95% CI (preferentially adjusted effect size), and potential confounders considered. We used the STATA 15 to combined and analyzed the data from included studies to calculate the relationship between maternal hypothyroidism and ASD. Hazard ratio and relative risk were assumed equal to OR when we computed the pooled effect size.

Results Seven observational studies were included. Maternal hypothyroidism during pregnancy was associated with the ASD in offspring in our main meta-analysis (OR=1.29, 95%CI: 1.07-1.56). In subgroup analysis, there was a strong association between maternal hypothyroidism during pregnancy and ASD in the offspring in Asian population (OR=4.46, 95% CI: 1.67–11.90), whereas the association in western population did not significantly change (OR=1.27, 95% CI: 1.15–1.40). The results of sensitivity analysis were robust and no publication bias was detected.

Conclusion In conclusion, maternal hypothyroidism during pregnancy could increase the risk of ASD in the offspring. More studies are needed to further confirm whether pregnant women received the treatment could decrease the risk of ASD in the offspring.

PO-0687

miR-142a-3p enhances FlaA N/C protection against radiation-mediated intestinal injury by modulating IRAK1/NF-kB signaling pathway

Teng Liu
The First Affiliated Hospital of Chengdu Medical College

Purpose Investigate the role of FlaA N / C protein - mediated pyroptosis inhibition related miRNA in radiation protection.
Methods Mice and HIEC cells were received 10 Gy irradiation after FlaA N / C pretreatment or IRAK-1/4 Inhibitor I treatment or PDTC treatment . CCK-8 assay was used to evaluate cell viability, LDH relase was used to analyze cytotoxicity, caspase-1 activity assay, IL-1β level, flow cytometry were used to analyze pyroptosis in cells, HE staining was used to evaluate the damage of intestinal tissue, CO-IP was used to detect the activation of inflammation, immunohistochemistry, western blot analysis and immunofluorescence were used to analyze activation of pyroptosis -related proteins the activation of NF-kB signaling pathways, real time PCR was used to detect expression of IRAK1 and miR-142a-3p, Mouse & Rat miRNA OneArray was used to determine the change of relevant miRNA after FlaA N / C pretreatment, Luciferase reporter assay and FISH were used to detect the interaction between miR-142a-3p and IRAK1.
Results FlaA N/C reduces radiation-induced pyroptosis in vivo and vitro, miR-142a-3p expression increased after FlaA N / C pretreatment. Up regulating the expression of miR-142a-3p inhibits radiation-induced pyroptosis in HIEC, down regulating the expression of miR-142a-3p leads to radiation-induced pyroptosis in HIEC after FlaA N/C pretreatment. IRAK1 is a direct target of miR-142a-3p and plays an important role in radiation-induced pyroptosis in HIEC. Inhibiting IRAK1 can reduce radiation-mediated pyroptosis in mice intestinal. MiR-142a-3p down regulation IRAK1 suppressed the NF-kB pathway. Inhibiting NF-kB signaling pathway can reduce radiation-mediated pyroptosis in mice intestinal.
Conclusion Flagellin A N/C regulates miR-142a-3p to inhibit radiation-induced pyroptosis via IRAK1/NF-kB signal pathway in intestine cells.

PO-0688

瘦素、血栓素 B2 以及白细胞计数对 2 型糖尿病合并冠心病的预测价值研究

李海霞、魏静、李萍、贾彩霞、严辰媛、马菲菲、魏书瑶、冯珊珊、哈小琴
中国人民解放军联勤保障部队第九四〇医院

目的 通过分析 2 型糖尿病合并冠心病（T2DM 合并 CHD）患者脂联素（ADP）、瘦素（LEP）、内皮素 1（ET-1）、前列腺素 I2（PGI2）、血栓素 B2（TXB2）等血管内皮细胞损伤标志物以及白细胞计数和淋巴细胞计数的变化，为 T2DM 合并 CHD 的诊断预测提供参考依据。
方法 选择兰州市某三甲医院 2020 年 7 月-11 月期间确诊的 T2DM 合并 CHD 和 2 型糖尿病（T2DM）患者各 50 例，收集两组患者的基本资料，酶联免疫吸附法（ELISA）检测两组患者的血管内皮损伤指标。Logistic 回归分析 T2DM 合并 CHD 的影响因素，ROC 曲线分析各影响因素对 T2DM 合并 CHD 的预测价值，以 P<0.05 为差异具有统计学意义。
结果 年龄（OR=1.120，95%CI：1.026~1.223，P=0.011）、LEP（OR=1.706，95%CI：1.146~2.542，P=0.009）、TXB2（OR=1.024，95%CI：1.002~1.047，P=0.031）和白细胞计数（OR=2.514，95%CI：1.131~5.590，P=0.024）是 T2DM 患者合并 CHD 的危险因素，ADP（OR=0.403，95%CI：0.197~0.825，P=0.013）、eGFR（OR=0.929，95%CI：0.869~0.994，

P=0.034）和淋巴细胞计数（OR=0.089，95%CI：0.013~5.596，P=0.013）是 T2DM 患者合并 CHD 的保护因素。年龄、LEP、TXB2 以及白细胞计数的 AUC 曲线下面积较大分别为：0.818（95%CI：0.736~0.899，P<0.001）、0.688（95%CI：0.580~0.796，P=0.001）、0.753（95%CI：0.658~0.847，P<0.001）、0.689（95%CI：0.585~0.793，P=0.001）。

结论 年龄、LEP 和白细胞计数是 T2DM 合并 CHD 的危险因素，ADP、eGFR 和淋巴细胞计数是 T2DM 合并 CHD 的保护因素。年龄、LEP、TXB2 以及白细胞计数的 AUC 曲线下面积较大，可能对 T2DM 合并 CHD 具有一定的预测价值。

PO-0689

TM、TAT、PIC 和 t-PAIC 对 2 型糖尿病血栓的诊断价值研究

李萍、严辰媛、贾彩霞、孙志鹏、马菲菲、冯珊珊、魏书瑶、何斯、李香影、刚乔建、李海霞、魏静、哈小琴
中国人民解放军联勤保障部队第九四〇医院

目的 探讨 TM、TAT、PIC 和 t-PAIC 对 2 型糖尿病和 2 型糖尿病合并血栓性疾病的诊断价值。

方法 选取兰州市某三甲医院的 2 型糖尿病患者（T2DM 组），2 型糖尿病合并血栓患者（T2DM+T 组）以及其他非相关疾病者（Control 组）作为研究对象。用全自动分析仪检测研究对象的血糖，血脂以及凝血指标，用化学发光免疫法检测血栓四项水平。用 ROC 曲线分析各指标对研究疾病的诊断预测价值。

结果 三组间在 FPG、GSP、TG、TC、HDL、LDL、HCY、SOD、APTT、PT、FIB、FDP 和 D-Dimer 上的差异均具有统计学意义（P＜0.05）；T2DM+T 组和 T2DM 组血栓四项水平均高于 Control 组（P＜0.05）。ROC 曲线分析显示对 T2DM 具有诊断价值的指标有 FPG、GSP、TG、FIB、FDP、D-Dimer、TM、TAT 和 PIC，血栓四项联合诊断的价值仅次于 FPG 和 GSP，特异度达 89.8%；对 T2DM+T 具有诊断价值的指标有 FPG、GSP、TG、LDL、HCY、PT、FIB、FDP、D-Dimer、TM、TAT、PIC 和 t-PAIC，且血栓四项联合诊断的价值较高，AUC=0.902，敏感度和特异度均为 837%。

结论 TM、TAT、PIC 和 t-PAIC 对 2 型糖尿病合并血栓患者的诊断价值高于对 2 型糖尿病患者的诊断价值，有望在临床推广此项检测，提高对 2 型糖尿病合并血栓疾病的早期预防和诊疗效能。

PO-0690

19646 例门诊妇女阴道微生态特征分析

韩阳
西安医学院第一附属医院

目的 分析妇科门诊不同症状患者的阴道微生态特征，对临床诊疗提供指导。

方法 回顾性分析 2019 年 01 月至 12 月西安医学院第一附属医院妇科门诊因不同症状就诊患者的阴道微生态（菌群密集度、多样性、优势菌、病原菌、Nugent 评分、菌群功能及炎症反应指标）检测结果。

结果 19646 例患者年龄范围为 16-87 岁，平均年龄（32.94±9.67）岁。其中，阴道微生态正常者 1043 例（5.31%）,阴道微生态异常者 18603 例（94.69%）。在阴道微生态异常的患者中，不能通过镜检明确病原菌者 12926 例（94.69%）；通过镜检发现明确病原菌者 5677 例（28,90%），其中包括单纯性阴道炎 5308 例（5308/18603，28.53%），混合性阴道炎 369 例（369/18603，1.98%）。单纯性阴道炎中以外阴阴道假丝酵母菌病（Vulvovaginal Candidiasis, VVC）为主（3015/5308，56.80%），其次为细菌性阴道炎（Bacterial Vaginosis, BV）（2025/5308，38.15%）。混合性阴道炎中含两种者以 BV+VVC 为主（319/369，86.45%），其次为 TV+BV（43/369, 11.65%），TV+VVC 仅占 1.36%；含三种者为 BV+VVC+TV （2/369，0.54%）。

结论 阴道微生态异常在妇科门诊患者发生率高，未明确感染的阴道微生态失调患者构成比最高，有明确病原菌诊断的部分患者存在混合感染；阴道微生态评价能够指导临床医师全面评价阴道微生态状况。

PO-0691

散射比浊法测定尿游离轻链、尿微量白蛋白及尿 α1-微量球蛋白在肾损伤疾病中的应用

刘红、刘颖、李巧霞、黄国虹、王昌敏
新疆维吾尔自治区人民医院

目的 探讨散射比浊法测定尿游离轻链、尿微量白蛋白及尿 α1-微量球蛋白在肾损伤疾病中的应用。
方法 选择我院住院的慢性肾脏病患者 100 例为病例组，男 60 例，女 40 例，年龄 25～72 岁。健康体检者 50 例为对照组，男 21 例，女 29 例，年龄 23～75 岁，均无急、慢性肾脏病、糖尿病、高血压、血液病及其他严重疾病，近期未服用肾毒性药物。所有入选本组受试者经知情同意后，均留取新鲜晨尿 10 ml，3000 r/min 离心 5 min，取上清液进行检测。采用双光径免疫浊度分析系统(贝克曼公司生产的 IMMAGE 特种蛋白分析仪)及其随机配套试剂。两组采用速率散射比浊法检测尿 κ 与 λ 轻链、尿 mALB 及尿 α1-MG 的浓度水平，并对两组检测结果进行比较，以受试者工作特征（ROC）曲线及曲线下面积（AUC）评价各项指标在肾脏疾病中的敏感性。
结果 两组性别、年龄等一般资料差异无统计学意义（P>0.05）。病例组尿 κ 和 λ 轻链，尿 mALb，尿 α1-MG 的阳性率明显高于对照组，通过 ROC 曲线、诊断试验结果显示：尿 κ 与 λ 轻链、尿 mALb 和 α1-MG 的尿液浓度 AUC 及 95%CI 分别为 0.766(0.708~0.818)、0.546(0.465~0.625)、0.855(0.810~0.898)、0.806(0.765~0.859)，联合 4 种尿液指标分析得到的最优化的 AUC 及 95%CI 为 0.906(0.870~0.955)，差异具有显著性（P＜0.001）。
结论 尿游离轻链 κ 与 λ 联合尿 mALB 和 α1-MG 的检测可以作为肾脏疾病的诊断指标，为肾脏病的临床诊断，疗效的观察和预后的判断，预防早期发生及其发展趋势以及治疗提供科学依据，对临床研究具有重要的价值。

PO-0692

Health economic evaluation of noninvasive prenatal testing and serum screening for Down syndrome

Gefei Xiao
Zhuhai Center for Maternal and Child Healthcare

Background Down syndrome (DS), also known as trisomy 21 (T21), is the most common genetic disorder associated with intellectual disability. There are two methods commonly used for prenatal testing of DS: serum screening (SS) for biomarkers in maternal serum and noninvasive prenatal testing (NIPT) for aneuploidy by cell-free DNA (cfDNA) in maternal plasma. However, cost-effectiveness analyses of these two methods are mostly based on data derived from simulations with various models, with theoretical values calculated. In this study, we statistically analyzed clinical DS screening data and pregnancy outcomes during the follow-up of pregnant women in Zhuhai City, China. The economics of the two mainstream prenatal DS screening methods was evaluated from a public health perspective.
Methods A retrospective analysis was performed on the data of 17,363 pregnant women who received SS and NIPT during gestation in Zhuhai from 2018 to 2019, and a cost-effectiveness analysis was performed with four screening strategies. In strategy I, all pregnant women received SS, and those with T21 risk ≥1/270 had invasive prenatal diagnosis (IPD). In strategy II, all

pregnant women received SS, those with T21 risk ≥ 1/270 had IPD, and those with 1/270 > T21 risk ≥ 1/1,000 had NIPT; then, women at high risk based on NIPT also had IPD. In strategy III, all pregnant women received SS, and those with T21 risk ≥1,000 had NIPT; then, women at high risk based on NIPT results had IPD. In strategy IV, all pregnant women received NIPT and those at high risk based on NIPT results had IPD. Finally, to assess the cost and effectiveness of DS screening, the total costs were calculated as the sum of screening and diagnosis as well as the direct and indirect economic burden during the average life cycle of DS patients.
Results A total of 22 of the 17,363 (1/789) pregnant women had DS, of which only one woman was over 35 years of age. SS detected 1,024 cases at high risk of T21 (≥1/270), 8 cases were true positive, with a positive predictive value of 0.78% and a detection rate of 36.4%. NIPT detected 27 cases at high risk of T21 (Z ≥ 3) and 22 cases of DS, with a positive predictive value of 81.5% and a detection rate of 100%. Strategy I had the largest total cost of 65.54 million CNY, strategy II and III had similar total costs of 40 million CNY, and strategy IV had the lowest total cost of 14.91 million CNY. By comparison, the screening strategy with NIPT alone had the highest health economic value for DS.
Conclusions SS was greatly affected by nuchal translucency and the accuracy of gestational age measured by ultrasonography. Unstandardized ultrasonography was an important reason for the low DS detection rate with SS. The influence of interfering factors on NIPT was much lower than in SS. NIPT can be used as an alternative to SS and as a primary screening strategy of prenatal DS screening for secondary prevention and control of birth defects. NIPT greatly decreased the frequency of IPD and the miscarriages associated with IPD, saved the limited medical and health resources, and greatly increased DS detection rate. Therefore, NIPT has great social and economic benefits.

PO-0693

PD-L1 expression on CTCs in breast cancer patients and its clinical value

Xueling Liu[1,2]、Qing Li[2]、Zhen Cai[1]、Jinghui Hou[2]
1. Nanfang Hospital, Southern Medical University
2. 中山大学孙逸仙纪念医院

Objective To investigate the expression and clinical value of PD-L1 on circulating tumor cells (CTCs) in peripheral blood of breast cancer patients.
Methods 100 patients with newly diagnosed breast cancer were selected to study the expression of PD-L1 on CTCs in peripheral blood,and analyze the relationship between the number and EMT typing of $CTCs^{PD\text{-}L1(+)}$ in peripheral blood,the mean expression level of PD-L1 on CTCs and the clinicopathological characteristics of the patients.50 breast cancer patients in treatment were selected to compare the changes in the total number of CTCs,the number of $CTCs^{PD\text{-}L1(+)}$,mean expression level of PD-L1 on CTCs and serum tumor markers (CEA, CA125, CA153 and CYFRA21-1) levels before and after a fresh round of treatment.
Results The mean expression level of PD-L1 on mixed-type CTCs（0.88）was significantly higher than that on epithelial-type CTCs（0.57）and mesenchymal-type CTCs（0.40),and the mean expression level of PD-L1 on CTCs in breast cancer patients with mixed-type CTCs as major type was dramatically higher than other types of patients as well.The typing of $CTCs^{PD\text{-}L1(+)}$ was associated with the age,HER-2 status,Ki-67 status,molecular classification,tumor size, lymph node metastasis,TNM staging,CA153,CYFRA21-1 and LDH of breast cancer patients($P<0.05$).No correlation was found between the mean expression level of PD-L1 on CTCs,the total number of $CTCs^{PD\text{-}L1(+)}$ and the clinicopathological characteristics of breast cancer patients ($P>0.05$). However,significant linear correlations were observed between epithelial-type $CTCs^{PD\text{-}L1(+)}$and serum ALP levels($r=-0.213$,$P=0.034$), mesenchymal-type $CTCs^{PD\text{-}L1(+)}$ and quantity of metastatic foci($r=0.197$,$P= 0.049$), mixed-type $CTCs^{PD\text{-}L1(+)}$ and Ki-67 status ($r=-0.213$, $P=0.034$).There were statistically significant differences ($P<0.05$) in the total number of CTCs,the

number of CTCs$^{PD\text{-}L1(+)}$ and the mean expression level of PD-L1 on CTCs of breast cancer patients before and after treatment, while the differences in changes of the serum tumor markers (CEA, CA125, CA153 and CYFRA21-1)levels were not statistically significant (P>0.05).
Conclusion PD-L1 expression on CTCs might play an important role in promoting the process of epithelial-mesenchymal transition of CTCs.The EMT typing of CTCs$^{PD\text{-}L1(+)}$ was related to some clinicopathological characteristics of breast cancer patients, and the progression of breast cancer could be estimated based on this.The expression of PD-L1 on CTCs in peripheral blood of breast cancer patients was more sensitive than serum tumor markers in the assessment of efficacy.Therefore,PD-L1 on CTCs could be used as an important indicator for the choice of treatment options,efficacy assessment and progression monitoring of breast cancer.

PO-0694

M2 样肿瘤相关巨噬细胞通过增加胶质瘤 IL-6 的表达促进血管拟态的形成

张琳
山东大学齐鲁医院

背景 胶质瘤是一种高度血管化的恶性脑肿瘤，因此，靶向内皮细胞的抗血管生成药物备受瞩目。然而，近期数据发现，这种看似非常具有潜力的抗血管疗法，临床应用后却出现了疗效短暂和疗效欠佳的问题。血管拟态概念的提出，使人们意识到在肿瘤组织中除了由内皮细胞构成的血管外，还有由肿瘤细胞构成的功能类似于正常血管的血供形式，即血管拟态（VM）。然而，到目前为止，VM 在胶质瘤中的形成机制尚未十分明确。作为肿瘤微环境免疫浸润的重要组成部分，巨噬细胞已被证明在肿瘤生长和血管生成中起重要作用。然而，巨噬细胞是否会在胶质瘤 VM 形成过程中发挥着关键作用，目前尚不清楚。
目的 探索血管拟态和 CD163+巨噬细胞在胶质瘤组织中的表达情况，分析 M2 样巨噬细胞是否会影响胶质瘤血管拟态的形成，并探讨其相关的作用机制。
方法 本研究回顾性纳入行胶质瘤切除术的患者 87 例。采用免疫组化的方法检测血管拟态和 CD163+巨噬细胞在胶质瘤中的表达情况，并分析两者之间的相关性。采用成管实验检测血管拟态的形成。利用 qRT-PCR 和 Western Blot 检测血管拟态相关指标的表达。利用 qRT-PCR 和 ELISA 检测 IL-6 的表达。采用成管实验、qRT-PCR、ELISA 以及 Western Blot 检测相关的信号机制。
结果 在本课题中，我们发现，VM 数目和 CD163+细胞浸润密度均与肿瘤级别呈正相关，与患者生存期呈负相关。体外实验结果显示，M2 样巨噬细胞可以促进胶质瘤 VM 的形成。同时，M2 巨噬细胞可以显著促进胶质瘤细胞 IL-6 的分泌。此外，IL-6 中和抗体可阻断 M2 样巨噬细胞介导的 VM 形成。使用 PKC 抑制剂可以抑制 M2 诱导的 IL-6 上调，进一步抑制胶质瘤 VM 形成。
结论 总之，我们的研究结果表明，M2 样巨噬细胞通过激活 PKC 信号通路促进胶质瘤细胞 IL-6 的分泌，进而促进胶质瘤 VM 的形成。

PO-0695

昆明某院肾移植受者 HLA-A、B、DRB1 抗原分布频率分析

蒲丹
昆明市第一人民医院

目的 分析昆明某院肾移植受者 HLA-A、B 和 DRB1 抗原分布频率，为肾移植 HLA 组织配型提供可靠的科学数据。
方法 收集 2016 年 4 月至 2021 年 5 月昆明市第一人民医院 1934 例肾移植受者 HLA 抗原检测数据，分析 HLA-A、B 和 DRB1 抗原种类和分布频率。

结果 HLA-A 抗原出现 19 种，其中 A11、A2 和 A24(9)抗原分布频率较高，分别为 29.87%、23.62%和 17.34%。HLA-B 抗原出现 38 种，其中 B46、B62(15)和 B60(40)抗原分布频率较高，分别为 11.19%、10.88%和 8.96%。HLA-DRB1 抗原出现 16 种，其中 DR12(5)、DR4 和 DR15(2)分布频率较高，分别为 20.47%、13.84%和 10.76%。
结论 肾移植受者 HLA-A、B 和 DRB1 抗原中，A11、B46 和 DR12(5)分别为分布频率最高的抗原，符合南方汉族人群 HLA 基因多态性分布。

PO-0696

2015-2020 年产妇围产期血培养感染病原体细菌分布和耐药性分析：一项多中心回顾性研究

邹琴[1]、邹华[1]、申燕[1]、余浪[1]、周玮[1]、盛成林[2]、廖昂[3]、李春莉[1]
1. 重庆市妇幼保健院
2. 万州妇幼保健院
3. 永川妇幼保健院

Bloodstream infections (BSIs) cause morbidity and mortality in postpartum patients, resulting in poor prognosis for both mother and neonate. This study retrospectively analyzed the pathogen distribution and drug sensitivity among postpartum patients with BSIs to identify appropriate antibacterial agents for perioperative therapy. All bacteremia cases between January 2015 and December 2020 from three Health Centers for Women and Children in Chongqing, China, were retrospectively reviewed. The present data showed that E. coli dominated BSIs during the past 6 years at our study centers. Additionally, an increasing trend in anaerobic bacteria detection in BSIs was observed.The increasing resistance rate of E. coli against fourth-generation cephalosporins needs additional attention.

PO-0697

粪肠球菌利奈唑胺低水平耐药生物膜形成及细胞壁厚度相关性研究

高睿
重庆市人民医院

目的 观察低水平耐药粪肠球菌生物膜形成及细胞壁厚度，探索其耐药机制是否与生物膜形成及细胞壁厚度改变相关。
方法 5 株利奈唑胺低水平耐药粪肠球菌（MIC：4-16 mg/L）体外诱导至高水平耐药，采用结晶紫染色方法对耐药菌诱导前后生物膜形成能力进行半定量分析；采用透射电子显微镜观测耐药粪肠球菌的细胞壁厚度。
结果 结晶紫染色生物膜半定量试验结果显示 MIC 为 16 mg/L 的耐药粪肠球菌生物膜形成能力为弱阳性，而 MIC 为 8 mg/L 的耐药菌以及标准野生株 ATCC 29212 生物膜形成为阴性。低水平耐药菌诱导利奈唑胺 MIC 大于 256 mg/L 后生物膜形成能力依旧为阴性和弱阳性。透射电镜观察结果显示利奈唑胺低水平耐药菌与敏感菌 ATCC 29212 细胞壁厚度无明显差异，耐药菌在含有菌体 1/2 MIC 利奈唑胺培养下，细菌细胞壁厚度与无抗生素培养细菌细胞壁厚度存在显著性差异，具有统计学意义。
结论 生物膜形成可能并不是造成粪肠球菌对利奈唑胺产生耐药的原因，利奈唑胺作用下细胞壁增厚仅适量的减少细菌对利奈唑胺的敏感性，但并非造成利奈唑胺耐药的主导因素。

PO-0698

Extracellular Vesicles Derived From Talaromyces marneffei Yeasts Mediate Inflammatory Response in Macrophage Cells by Bioactive Protein Components

Biao Yang
Zhujiang Hospital, Southern Medical University

Extracellular vesicles (EVs) loaded with proteins, nucleic acids, membrane lipids, and other virulence factors could participate in pathogenic processes in some fungi such as Cryptococcus neoformans and Candida albicans. However, the specific characteristics of EVs derived from Talaromyces marneffei (TM) still have not been figured out yet. In the present study, it has been observed that TM-derived EVs were a heterogeneous group of nanosized membrane vesicles (30–300 nm) under nanoparticle tracking analysis and transmission electron microscopy. The DiI-labeled EVs could be taken up by RAW 264.7 macrophage cells. Incubation of EVs with macrophages would result in increased expression levels of reactive oxygen species, nitric oxide, and some inflammatory factors including interleukin-1b, interleukin-6, interleukin-10, and tumor necrosis factor.Furthermore, the expression of co-stimulatory molecules (CD80, CD86, and MHC-II) was also increased in macrophages stimulated with EVs. The level of inflammatory factors secreted by macrophages showed a significant decrease when EVs were hydrolyzed by protease, while that of DNA and RNA hydrolase treatment remained unchanged. Subsequently, some virulence factors in EVs including heat shock protein,mannoprotein 1, and peroxidase were determined by liquid chromatography–tandem mass spectrometry. Taken together, our results indicated that the TM-derived EVs could mediate inflammatory response and its protein would play a key role in regulating the function of RAW 264.7 macrophage cells.

PO-0699

青海省海南州某地区藏族健康人群中 25-羟维生素 D 调查研究

韩启福
青海省人民医院

目的 了解青海省海南州某地区藏族健康人群中 25-羟维生素 D[25-hy droxyvitamin D,25-(OH)D]水平。
方法 收集 2017 年 3 月至 2017 年 4 月在青海省海南州某地区长期居住的藏族健康人群血清标本 429 例。根据年龄、性别进行分组。采用化学发光免疫分析法测定 25 羟维生素 D。
结果 调查的 429 名藏族人群中，425 人存在维生素 D 缺乏，占 99.06%；3 人存在维生素 D 不足，占 0.69％；维生素 D 充足者仅 1 人，占 0.23％。研究对象年龄与维生素 D 水平呈弱负相关（R＝0.275；P＝0.076）。
结论 青海省海南州某地区藏族人群中血清维生素 D 平均水平低下，普遍存在维生素 D 缺乏或不足，应加强健康教育，提高社区居民对维生素 D 不足现况的认识。

PO-0700

女性生殖道支原体感染和耐药性临床分析

童梦佳
重庆金域医学检验所有限公司

支原体是一种无细胞壁的原核生物，呈多态性，一般有球形、双球形和丝状三种基本形态，可通过除菌滤器，是能在无生命的培养基中生长繁殖的最小原核细胞型微生物。大小是在细胞与病毒之间，在电子显微镜下支原体细胞膜的超微结构分三层，内、外层为蛋白质和糖类，中间层为脂类，其中胆固醇含量最多，故支原体的代谢活动很有限。而支原体科分为两个属，即支原体属解脲支原体（UU）是非淋球菌性泌尿生殖器炎症的主要病原体，在妇科方面其中解脲支原体（M.urealyticum）和人型支原体（ Mycoplasma hominis）是人类泌尿生殖道常见且公认有致病作用的支原体，已成为性传播疾病最常见的病原体之一。除了尿道炎之外，尚可导致男性附睾炎，前列腺炎，女性白带增多，子宫内膜炎，腹痛，宫颈炎，盆腔炎，更可导致不孕和流产，以及新生儿眼炎和肺炎等，受到人们广泛的关注。因此，了解女性生殖道支原体感染的临床分析情况具有重要的临床意义。由于广谱抗生素的滥用，使耐药菌日益剧增，给临床诊断和治疗带来了较大的困难，并且多数女性感染者症状轻微或无症状常被忽视，目前该病的患病率呈上升趋势。因此，了解女性生殖道支原体感染的临床和耐药性分析情况具有重要的临床意义。

PO-0701

青海省临床实验室临检专业急诊标本 TAT 调查分析

韩启福
青海省人民医院

目的 调查青海省临床实验室临检专业急诊标本检验前和实验室内周转时间现状，分析急诊标本检验前和实验室内周转时间的影响因素，为实验室质量改进提供依据。
方法 通过网络平台向参加 2019 年青海省临床检验中心开展室间质量评价计划的 138 家临床实验室发放调查表，各临床实验室按要求统计 2019 年 3 月份数据，在线填报临床检验专业质量指标调查表，用 WPS 软件对回报数据的三大常规和凝血专业 TAT 相关信息进行统计分析，统计 TAT 在不同时间段内的实验室比率（数量）及超出阈外值的实验室比率（数量）。
结果 本次向全省临床实验室共发放调查表 138 份，实验室填报率 100%(138/138)，填写不完整或填写数据无效的实验室共 16 家。调查结果显示我省实验室三大常规急诊标本检验前 TAT（P90）、中位数在 60min 内的实验室分别约占 90.9%(110/121)和 97.58%(121/124)；三大常规急诊标本实验室内 TAT（P90）、中位数在 30min 内的实验室分别约占 35.54%(43/121)和 52.42%(65/124)，超出阈外值(≥30min)的实验室分别约占 64.46%(78/121)和 47.58%(59/124)。实验室凝血专业急诊标本检验前 TAT（P90）、中位数在 60min 内的实验室分别约占 89.19%(99/111) 和 97.34%(110/113)；凝血专业急诊标本实验室内 TAT（P90）、中位数在 60min 内的实验室分别约占 81.08%(90/111)和 88.35%(99/112)，超出阈外值(≥60min)的实验室分别约占 18.92%(21/111)和 11.61%(13/112)。
结论 青海省临床实验室三大常规和凝血专业急诊标本实验室内周转时间（TAT）超出阈外值的实验室较多，部分实验室需要优化标本周转环节，缩短标本 TAT，应根据自己实验室的情况，建立自己的目标 TAT。

PO-0702

新生儿遗传代谢病筛查的分析前质量控制

高娜娜、王青、彭德志、王佳佳
济南金域医学检验中心有限公司

新生儿遗传代谢病筛查是出生缺陷三级防控的重要组成部分,严格的分析前质量控制对于保证筛查结果的准确性、避免假性实验结果有重要意义，分析前质量控制主要包括标本采集、递送、验收和储存等环节。本文通过评估分析前各环节，找出新生儿遗传代谢病筛查项目分析前过程中易出错点，同时规范分析前操作流程，提高新生儿遗传代谢病筛查准确率，推动妇幼卫生的三级预防措施。

PO-0703

Ferroptosis is critical in diabetic atherosclerosis through HMOX1 regulated lipid peroxidation pathway

Fan Ai[2]、Zhijun Meng[1]、Hongping Liang[1]
1. Clinical laboratory, Shanxi provincial people's hospital
2. Clinical laboratory, Shanxi provincial people's hospital

Introduction The patients with diabete dramatically accelerate atherosclerosis. Although improved diabetes treatment strategy has prevented the pathogenesis, diabetic atherosclerosis is still the main causes of morbidity and mortality. It is urgent to clarify its in-depth mechanism and to identify new therapeutic targets for preventing diabetic atherosclerosis.
Hypothesis We assessed the hypothesis that ferroptosis and HMOX1 may be implicated in diabetes atherosclerosis through comprehensive in-depth bioinformatics analysis.
Methods and Results Analysis of gene expression profiles (GSE30169 and GSE6584) provided a total of 91 differentially expression genes (DEGs) including 68 up-regulated and 23 down-regulated genes (A). Ferroptosis, a pathway of programmed cell death dependent on iron, and HMOX1, a kind of heme oxygenase, were identified as key factors in diabetes atherosclerosis (B). To explore the potential mechanism, we measured the iron content and the reactive oxygen species (ROS) generation and conducted a lipid peroxidation assay. Compared with animals on normal diet (ND), ferroptosis and HMOX1 expressiones in $ApoE^{-/-}$ mice on high fat diet (HFD) were significantly increased (C, n = 8). Ferroptosis inhibitor ferrostatin-1 (Fer-1) effectively attenuated the diabetic atherosclerosis area in HFD animals (D, n = 10, $P < 0.01$ vs HFD). In addition, Fer-1 restored the ferroptosis related proteins (GPX4 and SLC7A11) with high glucose high lipid (HGHL) treatment in mouse arterial endothelial cells (MAECs) (E, n=6). Furthermore, HMOX1 deficiency rebalanced Fe^{2+} overload, decreased iron content, reduced ROS, and alleviated the lipid peroxidation, which led to the reduction of ferroptosis in diabetic endothelial cells (F).
Conclusions The present study demonstrates that ferroptosis is critical in diabetic AS progression and that HMOX1 is an implicated factor responsible for ferroptosis in diabetic AS development, suggesting that HMOX1 may serve as a potential detection or drug development target.

PO-0704

髋关节置换术后血液嗜冷杆菌致感染 1 例

何文燕、郭洪
重庆金域医学检验所有限公司

髋关节置换发展至今已有 60 余年，目前该技术已经相当成熟；但髋关节置换术后易出现假体松动，甚至炎症反应严重时需要进行手术治疗。进行相应治疗前，均需进行诊断明确松动部位，如内衬、髋臼、股骨柄。同时也要找到病因，如是否为细菌感染导致的松动，通过实验室检查来进行鉴别诊断明确病因。根据病人实际情况来选择适宜的治疗方案。出现假体松动一定要重视，积极进行诊治，不要让病情日益发展，耽误合适治疗时机。本司微生物室于 2021 年 4 月 21 日从左髋关节置换术后假体松动后采集到的组织标本内分离培养到血液嗜冷杆菌，该菌为临床罕见菌，并通过组织病理检查和 DNA-病原微生物宏基因组检测，确认是否为该菌的感染。

PO-0705

Sysmex XN-1000 血液分析仪在临床体液检测中的性能评估

杨亚平
陆军军医大学第一附属医院（西南医院）

目的 通过临床体液标本细胞计数评估 Sysmex XN-1000 血液分析仪的体液检测功能。
方法 Sysmex XN-1000 在体液模式下检测脑脊液标本（n=86）、胸水标本（n=53）和腹水标本（n=67），根据美国临床实验室标准化委员会(NCCLS)有关指南文件 Ep9-A 对 Sysmex XN-1000 血液分析仪进行空白计数，精密度，线性范围等参数进行性能评价，再与显微镜手工计数结果进行比对。
结果 Sysmex XN-1000 检测非血性脑脊液，胸水和腹水标本白细胞计数和红细胞计数的空白计数极低；精密度较高(CV%〈10.0%)；线性良好(相关系数 r〉0.990)；以上参数符合仪器检测要求；与手工计数法结果进行秩和检验，差异无统计学意义(P〉0.05)。
结论 Sysmex XN-1000 全自动血细胞分析仪体液检测模块的主要评估指标均能够满足临床实验室需求，可以直接用于非血性脑脊液、胸水和腹水等体液标本的检测，对于血性体液标本可以结合手工计数法进行判读。

PO-0706

胃肠间质瘤基因突变特点及其与临床病理特征关系

王梦莹
攀枝花市中心医院

目的 分析胃肠间质瘤患者基因突变特点及其与临床病理特征之间的关系。
方法 收集西南地区某医院确诊的胃肠道间质瘤患者基因检测结果与临床病理资料，并分析两者间的关系。
结果 1.270 例患者中男 133 例，女 137 例。中位发病年龄为 58 岁。发病部位为胃的 144 例，小肠 94 例，直肠 9 例，结肠 4 例，其他部位 19 例。肿瘤最大径以≥5cm，＜10cm 为主，核分裂象以＜5 个/50HPF 为主。
2.270 例患者中 220 例检测到 c-kit 突变，其中 c-kit11 外显子突变 190 例，9 号外显子突变 26 例，13 号外显子突变 9 例， 17 号外显子突变 6 例。9 号外显子突变均为 A502-Y503 重复突变，主要发病部位为小肠。11 号外显子突变类型多样，主要为缺失突变和点突变，突变绝大部分发生于

550-580 位点，其中以 557-560 位点最突出。而 13 号和 17 号外显子均为点突变。7 例检测到 PDGFRA 突变，其中 3 例为 12 号外显子突变，4 例为 18 号外显子突变。
3.女性患者肿瘤最大径小于 5cm 比例高于男性患者。野生型患者核分裂象＜5/50HPF 的比例明显大于发生 c-kit 和 PDGFRA 突变的患者。野生型患者 CD117 阳性率低于突变型。野生型患者 SMA 阳性率高于突变型，PDGFRA 突变患者大于 50 岁的频率高于其他突变的频率。c-kit9 突变发生在小肠上的的频率大于其他突变。c-kit11 突变中点突变和混合突变发生在胃上的概率小于其他类型突变。
结论 胃肠间质瘤最好发部位为胃，c-kit 的 11 外显子突变是 GIST 最常见的基因突变类型。绝大多数 GIST 病例 CD117 与 DOG-1 为阳性。c-kit11 突变类型与发病部位有关。PDGFRA 突变患者可能较 c-kit 突变患者预后差，c-kit9 突变的患者原发部位多在小肠上，野生型患者预后较突变型患者好，联合基因检测和免疫组化结果可以更好地诊断 GIST。

PO-0707

重庆市渝中区人群 SLCO1B1 和 ApoE 基因多态性分析及与血型的相关性探索

王丽英[1]、王梦艳[2]
1. 重庆市人民医院
2. 重庆医科大学

目的 分析重庆市渝中区人群中 SLCO1B1 和 ApoE 基因频率分布特点，验证基因型与血脂之间的关系，并探索基因多态性与血型之间的相关性。
方法 回顾性分析 2020 年 5 月-2021 年 1 月于重庆市人民医院渝中院区就诊的 760 例人群 SLCO1B1 和 ApoE 基因型别数据，并统计研究对象的 TG、TC、LDL-C 以及 HDL-C 等血脂数据，计算不同基因型分布概率，分析基因多态性与血脂水平的相关性。进而抽样测定 226 例研究对象的血型，探索 ApoE 和 SLCO1B1 基因型别分布与血型型别之间的关联性。
结果 SLCO1B1 各基因型所占比例为：*1a/*1a 型 5.00%，*1a/*1b 型 30.53%，*1b/*1b 型 39.21%，*1a/*15 型 4.34%，*1b/*15 型 19.21%，*15/*15 型 1.71%；ApoE 各基因型频率为：E2/E2 型 0.92%、E2/E3 型 14.47%、E2/E4 型 1.58%、E3/E3 型 65.93%、E3/E4 型 15.92%、E4/E4 型 1.18%。统计学分析显示：SLC01B1 基因多态性与 HDL-C 浓度水平呈负相关，相关系数为 0.072，而与 TG、TC、LDL-C 浓度水平均不具有相关性；ApoE 基因多态性与 HDL-C 呈负相关，相关系数为 0.088，与 LDL-C 呈正相关，相关系数为 0.105，但 ApoE 基因与 TG、TC 二者无相关性。SLCO1B1 和 ApoE 基因多态性分布与血型型别之间无相关性（P>0.05）。
结论 SLC01B1 和 ApoE 基因频率分布存在明显不均，二者基因多态性与血脂水平有相关性。SLC01B1 和 ApoE 基因型与血型分布无相关性。

PO-0708

降钙素原在骨髓移植后细菌血流感染患者感染菌群的特点及预后的相关性

王春燕
北京大学人民医院

目的 本研究回顾性分析了 197 例骨髓移植术（HSCT）后血培养阳性的细菌血流感染患者，探讨了 PCT、CRP、D-Dimer 和 WBC 等指标水平在全身细菌感染的表现及预后的相关性。

方法 选取 2016 年 10 月至 2020 年 5 月，北京大学人民医院血液科 197 例接受异体骨髓移植手术（HSCT）后血培养阳性的细菌血流感染患者参与研究。收集其临床资料，检测炎症及生化指标。根据患者是否粒细胞缺乏、感染细菌类型、感染部位及感染预后分别将患者分为两组。比较两组的各项指标的不同，分析其临床意义。

结果 粒细胞缺乏组的 PCT[1.64(0.25,10.12) ng/ml]明显高于非粒细胞缺乏组[0.76(0.28-2.72) ng/ml]，（p<0.05）；粒细胞缺乏组 D-Dimer[455(272,868) ng/ml]明显低于非粒细胞缺乏组[918.5(446,3716) ng/ml]，（p<0.05）。骨髓移植术后细菌血流感染患者革兰氏阳性菌感染组 PCT[0.31(0.19,1.32) ng/ml], 革兰氏阴性菌感染组[1.96(0.38,7.92) ng/ml]，真菌感染组[0.87(0.15,1.69) ng/ml]，（p<0.05）。骨髓移植术后细菌血流感染患者革兰氏阳性菌感染组 WBC[1.35(0,5.30) 10^9/L], 革兰氏阴性菌感染组[0.02(0,0.68)10^9/L]，真菌感染组[0.06(0,4.77)10^9/L]，（p<0.05）。具体感染部位主要集中在肺部(26 例)，肛周（25 例）及消化系统（19 例），不同感染部位之间 PCT 差异不明显；Kaplan-Meier 生存曲线分析提示患者预后，PCT 值越低，患者的生存率越高。

结论 骨髓移植术后细菌血流感染患者中，血清 PCT、D-Dimer、WBC 及生化指标的变化对患者感染细菌类型感染部位及疾病预后有辅助判断价值。

PO-0709

影响尿液检验分析前质量的因素及应对措施

张异、丁少君、陈博文
杭州迪安医学检验中心有限公司

目的 从检验项目的要求、患者准备、样本采集、标本运送四个环节来总结影响尿液检验前质量的因素并提出应对措施。

方法 对 2020 年 7 月 1 日至 2020 年 12 月 31 日，共计 8414 份尿液样本进行回顾性的分析。

结果 不合格的尿液样品标本共占总样本数量的 5.35%，主要为标本受到污染（31.1%）、尿液样本量不足（26.2%）、标记不明确的尿样（11.1%）。

结论 在实验中要加强检验人员、医护人员与患者之间的沟通，改善实验室规章制度及监督制度，不断提高自身专业领域知识和解决学术问题；保证尿液检验分析前质量的标准要依靠整个医疗过程中每一个人的努力,确保把尿液标本不合格率作为临床质量考核的标准，要不断深入研究与探索检验质量和各种影响因素之间的关系，这样才能提高尿液检验的质量和效率。

PO-0710

NR4A2 促进幽门螺杆菌诱导的炎癌恶性转化

冯一民
山东大学第二医院

目的 探讨 NR4A2 在幽门螺杆菌感染所致的慢性炎症到癌症恶性转化中的作用，为寻求新的胃癌防治生物靶标提供理论依据。

方法 1. NR4A2 在幽门螺杆菌感染胃部组织标本中的表达分析: 通过 Real-time PCR 及免疫组化检测幽门螺杆菌感染阳性的癌旁正常组织、浅表性胃炎、萎缩性胃炎伴肠化生及胃癌组织病例标本中 NR4A2 的表达水平。2. 体外分析幽门螺杆菌及其毒力因子 CagA 调控 NR4A2 对胃癌细胞增殖的影响: 通过 Real-time PCR 及 western blot 检测幽门螺杆菌感染及 CagA 转染对 NR4A2 的表达影响；利用细胞克隆形成实验及 MTT 实验验证幽门螺杆菌及 CagA 对细胞增殖的影响；通过细胞转染 NR4A2 siRNA 及过表达质粒证实 NR4A2 参与幽门螺杆菌诱导的细胞增殖。3. 动物实验分析 NR4A2 在幽门螺杆菌感染所致炎癌恶性转化中的作用：利用幽门螺杆菌标准菌株 SS1 进行蒙古沙

鼠灌胃造模，筛选稳转细胞系进行裸鼠皮下种植成瘤实验，检测幽门螺杆菌对细胞增殖及炎癌恶性转化的影响，并揭示 NR4A2 在此过程中的作用。
结果 1. 组织标本检测中，NR4A2 的表达升高不仅发生在胃部肿瘤组织中，也发生在胃炎标本中，NR4A2 的异常表达是一个早期事件。2. 幽门螺杆菌感染胃癌上皮细胞可以诱发 NR4A2 表达的上调，NR4A2 促进幽门螺杆菌感染引发的细胞增殖。3. 动物实验表明幽门螺杆菌可以引起胃炎直至胃癌的发生，而 NR4A2 促进此过程的发生。
结论 NR4A2 的活化存在于幽门螺杆菌感染所致的炎症早期，先于肿瘤的发生而存在，提示 NR4A2 作为胃癌早期检测与诊治的潜在靶点，在胃癌的预防、预后及治疗中具有广泛的应用前景。

PO-0711

m6A 去甲基化酶 ALKBH5 在胃癌中的表达与预后的相关性研究

冯一民
山东大学第二医院

目的 探索 m6A 去甲基化酶 ALKBH5 在胃癌组织中的表达，及其与胃癌病理分级、临床分期和预后的相关性。
方法（1）采用 TCGA 数据库中 183 例胃癌病例数据，分析 ALKBH5 在胃癌中的表达情况，分析 ALKBH5 表达与病理分级，临床分期和疾病预后的关系；
（2）采用 RT-PCR 和免疫组化方法检测 80 对胃癌/正常胃粘膜组织中 ALKBH5 表达情况，分析 ALKBH5 表达与病理分级、临床分期和疾病预后的关系；
结果（1）RT-PCR 和免疫组化结果显示，ALKBH5 在胃癌组织中的表达量低于正常胃部组织，$p<0.005$；
（2）根据病理分级，恶性程度越高的病例，ALKBH5 蛋白表达越低。胃癌 TNM 分期病程越晚期，ALKBH5 蛋白表达越低
（3）分析 TCGA 数据，结果显示：低表达组生存期较高表达组短，$p<0.01$。
结论 ALKBH5 在胃癌中低表达，且其表达水平与临床分期、病理分级及预后等负相关。ALKBH5 表达减少可能与胃癌的发生发展相关。

PO-0712

2 种不同方法消除脂血对生化项目检测干扰的对比分析

范雯雯
潍坊医学院附属医院

目的 探讨稀释法和高速离心法消除脂血对生化项目检测干扰是否具有可比性；为日常检验工作中脂血标本检测提供有效的方法。
方法 随机抽取 50 例脂血标本，经常规离心后用日立 7600 全自动生化仪检测丙氨酸氨基转移酶（ALT）、天门冬氨酸氨基转移酶（AST）、γ-谷氨酰基转移酶（GGT）、前白蛋白（PA）、C 反应蛋白（CRP）、β2 微球蛋白（BMG）。分别经高速离心后和生理盐水 1:9 稀释后再次检测以上项目。比较高速离心前后、生理盐水稀释前后结果的差异。
结果 ALT、AST、GGT 三项经高速离心处理后检测结果差异有统计学意义。PA、CRP、BMG 三项经生理盐水稀释处理后检测结果差异有统计学意义。
结论 对酶类项目可采取高速离心法消除脂血对检测结果的影响；免疫比浊法项目可以用生理盐水稀释法减少脂血的影响。

PO-0713

Identification of costimulatory molecules based signatures for predicting prognosis risk and immune infiltration in patients with Clear cell renal cell carcinoma based on TCGA

Chengjiang Wu
The Second Affiliated Hospital of Soochow University

Objective To explore the prognostic value of costimulatory molecules genes in the Clear cell renal cell carcinoma (ccRCC) patients and its effect on immune cell infiltration.
Methods Gene expression and clinical characteristics of patients with ccRCC were acquired from TCGA. A total of 60 costimulatory molecule genes were also obtained from TCGA-ccRCC including 13 genes of B7/ CD28 costimulatory molecules family and 47 genes of TNF family. The least absolute shrinkage and selection operator (LASSO) Cox regression model was utilized to construct a multigene signature in the TCGA cohort. Data processing and drawing were based on R and Perl programming languages. Real-time PCR and immunohistochemistry were used to verify the expression of differentially expressed genes.
Results The initial dataset in the study was consisted of 539 ccRCC samples and 72 normal samples. The expression of 55 costimulatory molecule genes in ccRCC and normal tissues were obviously differential which met the condition of FDR<0.05. LASSO Cox regression analysis results indicated that 13 risk genes were optimally used to construct prognostic model of ccRCC. Patients in the high-risk group showed significantly reduced OS compared with patients in the low-risk group. Receiver operating characteristic (ROC) curve analysis confirmed the predictive value of prognosis model of ccRCC (AUC>0.7). There are substantial differences in immune cell infiltration between high- and low-risk groups. Functional analysis revealed that immune-related pathways were enriched, and immune status were different between two risk groups. The genes and proteins expression from Real-time PCR and immunohistochemistry were consistent with DEGs from TCGA.
Conclusions By stratifying patients with all independent risk factors, the prognostic score model developed in this study may improve the accuracy for prognosis prediction to patients with ccRCC. The difference in the distribution of immune cells between two risk groups confirmed that costimulatory molecules could be used as targets and prognostic markers for immunotherapy.

PO-0714

Circular RNA circ_0001073 suppresses the progression of non-small cell lung cancer via miR- 582-3p/RGMB axis

Xuefen Jing、Cuifeng Wang
The First Affiliated Hospital of Baotou Medical College, Inner Mongolia University of Science and Technology

Background Reportedly, circular RNAS(circRNAs) exert a crucial regulatory role in cancer. circ_0001073 is derived from exons 3-5 of the ACVR2a gene, which inhibits cancer progression. However, the role and mechanism of circ_0001073 in non-small cell lung cancer(NSCLC)is unclear.
Methods Microarray analysis was employed to filter differentially expressed circRNAs in NSCLC tissues.Circ_0001073, microRNA-582-3p(miR-582-3p)and repulsive guidance molecule b(RGMB)mRNA expression was examined by qRT-PCR analysis. Cell multiplication was measured by the CCK-8 experiment. The Scratch-healing experiment and Transwell experiment were adopted to evaluate cell migration and invasion, respectively. Flow cytometry was applied to analyze the apoptosis. Western blot was employed to assess RGMB protein expression.

Additionally, dual-luciferase reporter gene experiments and RIP experiments were applied to probe the binding sites betweer miR-582-3p and circ_0001073 or RGMB, respectivel.
Results Circ_0001073 was remarkably under-expressed in NSCLC tissues and cells .Circ_0001073 overexpression impeded the multiplication, migration and invasion of NSCLC cells in vitro and enhanced the apoptosis. circ_0001073 directly bound to miR-582-3p and acted as a miRNA sponge to regulate RGMB expression. Besides, miR-582-3p overexpression or knockdown of RGMB remarkably reversed the malignant phenotypes of NSCIC cells induced by up-regulation of circ_0001073.
Conclusion circ_0001073 up-regulates RGMB expression through adsorbing miR-582-3p to inhibit NSCLC progression, suggesting its potential as an innovative therapeutic target in NSCLC.

PO-0715

军队援鄂医疗队组建新冠专科医院检验科的实践与启示

谢志雄
联勤保障部队第 909 医院

针对新型冠状病毒肺炎疫情，军队援鄂医疗队承担了湖北省妇幼保健院光谷院区新冠专科医院的诊疗任务。40 名检验人员进驻后迅速进行检验科建设并开展临床检验，为新冠专科医院临床科室的诊疗工作提供了有力的保障。文章从检验科实验室改造、仪器试剂采购、培训和工作方式、质量管理、感控防护等方面，总结新冠专科医院检验科组建和开展工作的经验，提出高效的卫勤组织指挥体系、军民深度融合卫勤保障机制、严密组织和科学管理模式对新冠专科医院检验科建设的重要性，为提升军队机动卫勤力量检验科在执行多种军事或非军事行动中的综合能力提供经验借鉴。

PO-0716

不合格标本拒收后的风险管理

张艳
新疆生产建设兵团医院

目的 探讨及评估本院由于不合格标本拒收后导致危急值延迟报告的风险。
方法 应用失效模式与效应分析（FMEA）方法评估 2017 年 12 月至 2018 年 09 月，新疆生产建设兵团医院分析前不合格检验标本拒收导致的 41 例危急值延迟报告的风险。利用头脑风暴及经验制定改进措施，通过两个月的实施后，进行实施前后的数据对比（实施后数据为 2018 年 12 月至 2019 年 09 月）并进行效果确认。
结果 本院分析前过程中潜在的失效模式共 23 项，其中不可接受风险有 11 项，需采取措施降低风险有 3 项。其他为可接受风险。标本采集不合格拒收后导致危急值延迟报告的有 41 例标本，均为失效模式中不可接受的风险。改进措施实施后共 33 例危急值延迟报告数据，较实施前下降 19.5%。
结论 因此，通过风险管理可减少因不合格标本拒收导致的危急值延迟报告，为临床提供即时、准确和可靠的检验数据。

PO-0717

后疫情时代下重庆市医学检验实验室应对突发公共卫生事件生物安全现状调查

徐兰兰、万雅芳
重庆市人民医院

目的 了解 SARS-CoV-2 后疫情时代下重庆市医学检验实验室应对突发公共卫生事件生物安全现状。
方法 同时对重庆市 341 家医学检验实验室发放调查问卷，调查内容包括实验室生物安全设施设备配置、实验室生物安全体系文件运行，实验室风险评估及应急体系运行，实验室开展病原微生物核酸检测情况、实验室个人防护用品配置、实验室应对突发公共卫生事件能力等，在规定时间内所有实验室均有效回报。
结果 341 家医学检验实验室包括：二级医疗机构占比 66.0%，三级医疗机构占比 24.6%，独立医学检验中心占比 9.4%；所有实验室均为生物安全二级实验室（BSL-2）；所有实验室均具有生物安全二级实验室要求的基本仪器设备配置，13.7%实验室未按照国家相关要求进行安装和年度维护检验；21.4%实验室具有负压条件的核心工作区；60.3%实验室具有完整的体系文件且全员培训知晓；80.0%实验室定期进行风险评估，并对识别的风险执行有效的预防和改进措施；89.6%实验室制定了各种突发事件应急预案，并进行全员培训演练； 60.1%实验室已开展新型冠状病毒核酸检测；64.0%实验室储备的防护物资可满足突发公共卫生事件应急状态下 2 周以上工作需要；目前 44.8%实验室的设施设备条件和 28.3%实验室人员储备不能满足应对突发公共卫生事件需要。
结论 新冠背景下重庆市医学检验实验室在实验室基础设施和检测能力建设、生物安全管理能力等方面已有了很大提升，为贯彻《中华人民共和国生物安全法》，完善风险防控体系和提高应急能力，各实验室还需加强设施设备投入和人员储备，以应对各种突发公共卫生事件需要。

PO-0718

岳阳地区儿童急性呼吸道感染病毒的检测情况分析

李童、杨昊
岳阳市妇幼保健院

目的 分析急性呼吸道感染住院患儿中常见呼吸道病毒流行病学特征。
方法 回顾性分析 2020 年 11 月-2021 年 1 月岳阳市妇幼保健院住院的 ARTI 患儿 528 例作为研究对象。采用直接免疫荧光法检测患儿鼻咽分泌物中呼吸道合胞病毒 (respiratory syncytial virus, RSV)、副流感病毒 (parainfluenza virus，PIV)1、2、3 型、腺病毒 (adenovirus，ADV)、流感病毒 (influenzavirus，Flu)A 型和 B 型这 7 种常见呼吸道病毒的抗原。
结果 528 例住院患儿中，病毒检出阳性 154 份，总检出率为 29.17%；其中 PIV-1 检出 8 份 (5.19%)，PIV-3 检出 52 份 (33.77%)，RSV 检出 88 份 (57.14%)，ADV 检出 5 份 (3.25%)，还有 1 例混合感染标本 RSV+ PIV-1 (0.65%)。154 例阳性样本中，男 94 例，女 60 例，男女比例：1.57:1。男性患儿病毒检出阳性率 (30.52%) 与女性患儿 (27.28%) 相比差异无统计学意义 ($P > 0.05$)。肺炎 (47.22%) 和支气管肺炎 (33.44%) 等下呼吸道感染的疾病表现最常见，且 RSV 在下呼吸道感染患者中的阳性检出率均最高。总病毒阳性检出率在不同临床诊断 ARTI 中差异有统计学意义($P < 0.05$)。
结论 本研究表明在该地区 ARTI 患儿主要感染病毒种类为 RSV，其次是 PIV-3。且常见呼吸道病毒检出率在下呼吸道感染患儿中明显高于上呼吸道感染患儿。患儿感染呼吸道病毒后常见的临床表现主要为肺炎，其次是支气管肺炎。

PO-0719

中国西部汉族人群的 WDFY4 多态性与肺结核易感性的相关性研究

黄杰、黄利君、刘莉萍、张静、何秋蓉
四川大学华西第四医院

目的 验证在中国西部汉族人群中单核苷酸多态性（Single Nucleotide Polymorphisms，SNPs）位点 rs148252819 和 rs147766980 与结核易感性的相关性。
方法 本研究共招募了中国西部地区 899 例活动性结核病患者和 1535 例健康对照。采用改进后的多重 SNP 分型试剂盒对 2434 个样本的 WDFY4 的 rs148252819 及 rs147766980 位点进行分型。使用 PLINK version 1.09 进行 SNP 多态性分析。
结果 在 WDFY4 基因上的 rs148252819 位点中，以 G 等位基因为参照等位基因，携带 A 等位基因可能降低结核病的患病风险（OR=0.3388，95%CI=0.1295-0.8865，P=0.021）；相较于 GG 基因型，AA 基因型和携带 A 等位基因的基因型的发病风险降低（显性模型：OR=0.3369，95%CI=0.1285-0.8832, P=0.027）。而 rs147766980 中，以 G 等位基因为参照等位基因，携带 A 等位基因可能增加结核病的患病风险（OR= 1.418，95%CI=1.016-1.98，P=0.039）；相较于 GG 基因型，AA 基因型和携带 A 等位基因的基因型均可能增加结核病的发病风险（显性模型：OR=1.449，95%CI=1.029-2.041, P=0.034）。
结论 WDFY4 中的 rs148252819 及 rs147766980 位点在中国西部人群中均与结核病易感性的相关，提示我们这个 SNP 可能是潜在的预测结核发病风险的标志物。

PO-0720

临床检验危急值分析及持续改进效果评估

肖春梅、柴华、李富荣、朴文花
宁夏回族自治区人民医院

目的 对本院检验科 2019 年及 2020 年危急值数据进行回顾性统计分析，评估危急值持续改进效果，分析当前危急值的临床适宜性，探讨医学检验危急值持续改进的管理方法。
方法 收集我院 2019 年及 2020 年所有危急值报告数据，利用瑞美实验室管理系统（LIS）对危急值项目发生率、科室分布率、报告频率较高的危急值项目的科室分布率及血液内科、重症医学科危急值调整前后的报告频率进行统计。
结果 2020 年危急值报告发生率为 1.46%，与 2019 年（1.56%）相近。危急值报告最多的项目依次为 MYO（18.7%）、TNT-HS（18.1%）、NT-proBNP（10.72%）；2020 年危急值在临床科室报告频率较高的前五位科室依次为：重症医学科（20.6%）、急诊科（18.4%）、心血管内科（11.5%）、呼吸内科（7.78%）、肾内科（7.6%）；20 年 MYO 在重症医学科报告频率（27.1%）最高；TNT-HS 在心血管内科报告频率（28.6%）最高；NT-ProBNP 在重症医学科报告频率（20.4%）最高，其次为心血管内科（19.3%）；血液内科 PLT、NEU#、WBC 危急值报告频率调整前依次为 50.2%、33.4%、23.4%；调整后依次为 23.7%、NEU#15.6%、12.5%；调整后较调整前大幅下降；重症医学科 MYO、TNT-HS、NT-ProBNP 危急值报告频率调整前依次为：32.2%、25.8%、30.1%；调整后依次为 27.1%、20.4%、20.4%；调整后较调整前明显降低。
结论 血液内科和重症医学科危急值持续改进效果明显，MYO、TNT-HS、NT-proBNP 危急值项目上报率高，可能与危急值界限的设置及疾病种类有关，需要调整和优化。建议三级甲等医院按照科室、病种、年龄对危急值实施精细化设置和管理。

PO-0721

艾滋病病毒抗体筛查试验假阳性的原因分析

来金欣、李正康、邓倩昀、张玉、甘慧泉、顾兵
[广东省人民医院(广东省医学科学院) 检验科

目的 分析艾滋病病毒抗体筛查试验假阳性的原因。
方法 回顾性分析 2017 年 1 月至 2020 年 1 月到我院进行人艾滋病病毒（HIV）抗体检测的患者临床资料。
结果 总共 170 260 例进行 HIV 抗体检测的标本纳入分析，74 例临界值标本复测后结果为阴性。在最初筛查有反应的 404 例样本中，真阳性和假阳性的比率分别为 26.24％（106/404）和 69.80％（282/404），女性的假阳性率 89.93％（125/139）显著高于男性（59.25％，157/265）（χ2=40.71，P <0.001）。男性与女性的特异性均超过 99%，但男性的阳性预测值（37.94％，95％CI：36.98％～38.90％）高于女性（7.41％，95％CI：7.04％～7.78％）。当 COIs≥70 时，有 97.26％（71/73）的病例确证感染了 HIV。通过对基础疾病和年龄进行分层分析发现，假阳性率随着年龄的增长而增加，在 60 岁以上（39.01％，110/282）或心血管疾病（31.56％，110/282）的患者中发现假阳性率最高。一例患者被证实是异嗜性抗体的干扰导致假阳性结果。
结论 女性、高龄、异嗜性抗体是 HIV 筛查试验假阳性反应的潜在干扰因素,重视这些潜在的干扰因素可以更好的为临床医生与患者正确解释结果提供依据。

PO-0722

基于生物信息学的非小细胞肺癌诊断及预后关键基因研究

翟秀明[1]、周丹丹[2]
1. 重庆医科大学附属第三医院（捷尔医院）
2. 重庆市中医院

目的 探讨非小细胞肺癌的潜在关键基因及其在诊断与预后方面的价值。
方法 从 GEO 数据库下载数据集 GSE18842、GSE19188、GSE30219 和 GSE40791，应用 R 软件 limma 包进行标准化及差异表达基因的筛选。应用 DAVID 数据库对差异表达基因进行 GO（Gene Ontology）分析和 KEGG（Kyoto Encyclopedia of Genes and Genomes）通路分析。运用 STRING 和 Cytoscape 软件构建差异表达基因的蛋白质-蛋白质相互作用网络，应用 MCODE 及 cytohubba 插件筛选出与非小细胞肺癌相关的最显著模块及枢纽基因。在 GEPIA 和 Kaplan Meier plotter 数据库中验证枢纽基因的表达及预后情况。
结果 通过对四个数据集分析，共获得 258 个差异表达基因，包括 91 个上调基因和 167 个下调基因。GO 分析和 KEGG 通路富集分析表明，差异表达基因在细胞周期、细胞分裂、有丝分裂核分裂、蛋白激酶结合、肝素结合等方面显著富集。通过蛋白互作网络鉴定出 10 个与非小细胞肺癌相关的枢纽基因，包括 RRM2、CDK1、UBE2C、MAD2L1、BUB1B、CCNA2、KIF20A、BUB1、KIF11、CCNB2。GEPIA 数据库证明 RRM2、UBE2C、MAD2L1、KIF20A、CDK1、CCNB2 的表达在非小细胞肺癌患者中显著增高(P<0.05)，而 KIF11、CCNA2、BUB1B 和 BUB1 仅在肺鳞癌中具有统计学意义（P < 0.05），在肺腺癌中无统计学意义（P > 0.05）。Kaplan Meier plotter 数据库表明，仅 RRM2 和 KIF11 与非小细胞肺癌患者的生存预后相关(P<0.05)。
结论 RRM2 可能在非小细胞肺癌的发生过程中起重要作用，有望成为非小细胞肺癌的个体化诊断、预后评估的潜在生物标志物。

PO-0723

新型冠状病毒 2019-nCov 核酸检测实验室核酸污染监测及解决办法

李文静、刘萍、穆红
天津市第一中心医院

聚合酶链反应（ Polymerase Chain Reaction， PCR）是敏感性极高的核酸扩增反应，能将极少量的 DNA 扩增数百万倍。实验过程中的任何一个环节可能发生的极其微量的污染，都足以导致假阳性的结果的产生。

目的 结合本实验室的环境污染监测实际，对核酸实验室环境污染的监测、发现和清除提出一些处理策略。

方法 采用新型冠状病毒 2019-nCov 核酸检测试剂盒（荧光 PCR 法-达安基因）进行核酸污染监测，包括 2019-nCov ORF 基因、N 基因以及内标基因，核酸提取采用达安基因核酸提取试剂盒（磁珠法）。环境污染监测采用物表监测和空气监测，物表监测（每周一次）采用采样管拭子蘸取灭菌重蒸水后，分别各采样点位进行涂抹采样，尽可能大的范围内往返涂抹，之后将拭子置于病毒采样管中按照病人标本流程进行标准操作；实验室空气监测（每日），在实验室每个位点放置敞盖的灭菌蒸馏水，静置过夜，第二天跟着病人标本同时进行扩增。

结果 对实验室进行了 4 次物表监测和 30 次空气监测，ORF 基因、N 基因结果均为阴性，内标基因在第 3 次物表以及第 18 次空气检测出现阳性，阳性为点位为生物安全柜台面及生物安全内部空气，ct 值分别为 39.46 和 38.44，为弱阳性结果。立即对整个提取室进行过氧化氢空气消毒，消毒过程生物安全柜面板抬到最高，30%过氧化氢喷 30min，密闭 1 小时后开窗通风 24 小时，实验室再次使用之前进行物表及空气监测，结果均为阴性。

结论 核酸实验室有必要进行定期的核酸污染监测，过氧化氢对消灭核酸污染效果显著。

PO-0724

血液检测指标与贝伐珠单抗联合化疗治疗卵巢癌预后的相关性探讨

王旭
天津医科大学肿瘤医院

目的 本研究以联合应用贝伐珠单抗与化疗的卵巢癌(OC)患者为研究对象，根据对患者的病理特征、肿瘤标志物、血清生化、血常规、出凝血等血液学参数进行分析，探索影响卵巢癌(OC)患者预后的危险因素，寻找联合贝伐珠单抗和化疗的最大获益人群，便于临床制定诊疗方案。

方法 回顾性收集 2019 年 6 月至 2020 年 12 月于天津市肿瘤医院接受贝伐珠单抗联合化疗的 90 例卵巢癌（OC）患者的临床资料、复发情况并进行电话随访。收集首次入院时和用贝伐珠单抗前患者的肿瘤标志物、血清生化、血常规、出凝血等血液学参数，应用单因素 Cox 回归分析分别与生存和进展情况进行生存分析，并将影响因素进行多因素 Cox 回归分析确定预后的独立危险因素。

结果 1.以中位数为截断值进行单因素 Cox 分析，首次入院时 ALB<40g/L、CA125>450U/L、HE4>218U/L 和 Fbg>3.12g/L 与总生存时间相关；2.连续变量单因素 Cox 分析，首次入院时 LDH、FDP 和 D-二聚体与无进展生存时间相关，中性粒与淋巴细胞比值>4.5 是无进展生存时间的影响因素；3. 以中位数为截断值进行单因素 Cox 分析，用贝伐珠单抗前 ALB<44g/L、HCT<36.5%和 HGB<120g/L 与总生存时间相关；4.通过多因素 Cox 分析，首次入院时只有 HE4>218U/L 是总生存时间的独立危险因素；LDH 是无进展生存时间的独立危险因素；用贝伐珠单抗前 ALB<44g/L 是总生存时间的独立危险因素。

结论 首次入院时 HE4 和用贝伐珠单抗前 ALB 水平与总生存时间相关，首次入院时 LDH 为无进展生存时间的独立危险因素，这三个血液检测指标有望成为预测联合贝伐珠单抗和化疗的卵巢癌患者预后的生物学标志物。

PO-0725

高血清核黄素与结直肠癌风险

马妍慧
上海交通大学医学院附属新华医院

目的 本研究是一项回顾性研究。
方法 我们分析了 2019 年 1 月至 2020 年 3 月，上海交通大学医学院新华医院结直肠外科 83 名 CRC 患者和 307 名对照者血清核黄素水平与 CRC 风险之间的关系。年龄、性别、体重指数、腺瘤息肉切除和疾病状况作为混杂因素进行了调整，以平滑样条图、亚组分析和多变量逻辑回归分析以估计核黄素和 CRC 风险之间的相对风险。
结果 充分调整混杂因素后，血清核黄素是 CRC 患者的危险比（OR=1.08[1.01,1.15]，P=0.0310）。与正常水平核黄素相比，高水平的核黄素（OR = 2.17 [1.02, 4.61], P = 0.0434）与 CRC 发生显著相关。
结论 高水平的血清核黄素是结直肠癌的危险因素， CRC 患者核黄素水平高的意外发现值得进一步调查。

PO-0726

CD74 regulates cellularity and maturation of medullary thymic epithelial cells partially by activating the canonical NF-κB signaling pathway

Hongxia Wang
Laboratory Medicine Center, Nanfang Hospital, Southern Medical University

Thymic epithelial cells (TECs) are indispensable for T cell development, T cell receptor (TCR) repertoire selection, and specific lineage differentiation. Medullary thymic epithelial cells (mTECs), which account for the majority of TECs in adults, are critical for thymocyte selection and self-tolerance. CD74 is a nonpolymorphic transmembrane glycoprotein of major histocompatibility complex class II (MHCII) that is expressed in TECs. However, the exact role of CD74 in regulating the development of TECs is poorly defined. In this research, we found that loss of CD74 resulted in a significant diminution in the medulla, a selective reduction in the cell number of mature mTECs expressing CD80 molecules, which eventually led to impaired thymic CD4+ T cell development. Moreover, RNA-sequence analysis showed that CD74 deficiency obviously downregulated the canonical NF-κB signaling pathway in mTECs. Our results suggest that CD74 positively controls mTEC cellularity and maturation partially by activating the canonical NF-κB signaling pathway.

PO-0727

External Quality Assessment for Severe Acute Respiratory Syndrome Coronavirus 2 RNA Detection in Chongqing, China

Yuanyuan Guo
Department of Laboratory Medicine ,Chongqing General Hospital, University of Chinese Academy of Sciences, Clinical Laboratory Centre of Chongqing City.

Background Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) poses a huge threat to public health. Therefore, clinical laboratories must have the ability to detect SARS-CoV-2 RNA. With the enhanced detection in Chongqing, many laboratories rapidly implemented assays for the molecular detection of SARS-CoV-2 based on real-time reverse transcription polymerase chain reaction(rRT-PCR) assays. This study aimed to improve the detection capabilities of clinical laboratories by evaluating their performance for SARS-CoV-2 RNA detection through the external quality assessment (EQA) programs of 2020 in Chongqing to contribute to the prevention of this epidemic.
Methods The EQA panels consist of eight positive samples with concentrations within 2.7–5.0 log10 copies/mL quantified by digital PCR and two negative samples with other human coronaviruses clinicallyvalidated by four commercial assays. All 21 samples from four rounds were distributed to the participating laboratories through cold-chain transportation.Depending on the results from each sample, laboratories were asked to use one or two assays to detect SARS-CoV-2 RNA. Test results and raw data were also required. All data were evaluated, and the testing performance of commercial assays was compared. For the rounds, all laboratories used commercial assays.
Results Four rounds of EQA programs were performed, and the percent agreements of participants were 97.5% (39/40), 97.5% (39/40), 98.9%(88/89), 100.0% (131/131). Only three false negative results and one false positive result were obtained. Statistical significance in the Ct values of ORF region and N region of SARS-CoV-2-RNA was found by using one-step, one-step concentration, and magnetic bead methods ($P<0.05$). The Ct values of ORF region of SARS-CoV-2-RNA in P5 and P6 were significantly different in the different batches of reagent A ($P<0.05$). The ORF region of SARS-CoV-2-RNA was not detected in a batch of reagentB.
Conclusions The majority of laboratories in Chongqing have reliable diagnostic ability for SARS-CoV-2 detection. Our data emphasized the importance of EQA for monitoring the performance of clinical laboratories. However, clinical laboratories must first effectively evaluate the performance of reagents prior to their usage.

PO-0728

中国东部啮齿动物携带巴尔通体物种的分析

秦祥荣
山东大学第二医院

巴尔通体（Bartonella）是一种通过媒介传播的革兰氏阴性兼性细胞内寄生细菌。在全球范围内，巴尔通体物种分布与啮齿动物及跳蚤寄生虫有关。目前中国的啮齿动物携带巴尔通体物种的率以及基因多样性尚不清楚。我们调查了来自中国东部的啮齿动物中巴尔通体物种的携带率和以及遗传多样性。我们从 2015 年至 2016 年在山东省胶南县捕获了啮齿动物，并通过 PCR 扩增柠檬酸合酶（gltA）基因和 RNA 聚合酶 β 亚基（rpoB）基因检测了啮齿动物脾脏中的巴尔通体。我们发现，有 8.38%（16/191）的啮齿类动物为 Bartonella 阳性， gltA 和 rpoB 基因均为阳性。将啮齿类动物的巴尔通体序列进行系统发育分析分为五个进化枝，分别与 Tribocorum，B。rattimassiliensis，grahamii，B。fuyuanensis 和 B. Queenslandensis 密切相关。这项研究表明，在中国东部的啮齿

动物中，巴尔通体的生物分布广泛，基因型多种多样，在中国应监测这些巴尔通体对公共健康带来的威胁。

PO-0729

分泌蛋白 REG4 促进结肠癌细胞增殖的机制研究

倪东升
重庆市人民医院

结肠癌是消化道最常见的恶性肿瘤之一，结肠癌在我国的发病率呈逐年上升的趋势，发病年龄也有年轻化趋势。现有的粪便潜血试验、血液癌胚抗原等标志物检测等传统早期诊断方法对结肠癌灵敏度低，导致部分患者在首次确诊时已发生转移，降低了患者的生存期。因此，寻找结肠癌新的诊断标志物具有重要临床意义。近年来发现，再生基因（regenerating gene，Reg）家族与消化系肿瘤密切相关，且为分泌蛋白，其有望成为消化系肿瘤诊断和治疗的新分子，但其在肿瘤发生发展中参与的分子机制、调控机制以及受体及受体后途径还不确切，尚需进一步的研究。其中，Reg4 主要在胃、小肠、结肠及胰腺等消化系统中表达,正常组织表达水平相对较低。运用生物信息学分析，我们证实家族成员 Reg4 在结肠癌中表达量增高约 5.5 倍；利用无标记细胞分析仪和克隆形成实验证实，Reg4 具有促进结肠癌细胞增殖和非锚定生长的作用；免疫印迹实验显示在结肠癌细胞系 HTC116 中敲低 Reg4 抑制 STAT3 Y705 磷酸化，在结肠癌细胞系 HTC116 和 HT29 中过表达 Reg4 促进 STAT3 Y705 磷酸化，荧光定量 PCR 证实在结肠癌细胞系 HTC116 中过表达 Reg4 促进 STAT3 信号通路下游靶基因 SOCS3 和 c-FOS 转录；免疫印迹实验、无标记细胞分析显示和克隆形成实验分别证实在结肠癌细胞系 HTC116 中使用 STAT3 抑制剂 Stcttic 可回复过表达 Reg4 促进的 STAT3 Y705 磷酸化、肿瘤细胞增殖和非锚定生长。总之，我们的研究结果表分泌蛋白 Reg4 是决定结肠癌细胞增殖和生长的重要基因，有望成为结肠癌诊断的新标志物。

PO-0730

乳腺癌治疗过程中激素受体状态的改变

公娉
山东大学第二医院

研究目的 在中国，乳腺癌的发病率逐年上升，乳腺癌是女性常见的恶性肿瘤之一，也是女性常见的死亡原因。手术治疗是其主要的治疗方式，化疗、放疗、内分泌治疗、靶向治疗等个体化综合治疗策略的不断成熟使得乳腺癌获得了理想的疗效和预后，但仍有一部分患者出现复发和转移。乳腺癌激素受体状态的测定是内分泌治疗选择的基础，所以，乳腺癌原发肿瘤的激素受体状态已经成为常规的分子病理学检查。但是，乳腺癌患者的激素受体状态缺乏大数据的统计。乳腺癌患者激素受体状态在治疗前后是否出现改变，经过治疗之后的复发转移癌巢的激素受体状态与原发肿瘤是否存在差异尚知之甚少。本研究旨在大数据统计分析山东省乳腺癌患者激素受体状态，研究乳腺癌患者雌激素受体（estrogen receptor, ER）、孕激素受体（Progesterone receptor, PR）等生物标志物在乳腺癌原发肿瘤、新辅助化疗、复发转移过程中的变化，探讨生物学特性改变的临床意义以及对预后的影响。
研究方法 回顾性分析 2005 年-2016 年于山东大学齐鲁医院收治的乳腺癌患者 5305 例，其中有完整的病理信息的患者 4786 例。回顾性分析其临床病理资料，其中术前接受穿刺的患者 71 例，接受新辅助化疗的患者 301 例，原发肿瘤及转移部位均进行病理学检查的患者 39 例。应用内分泌治疗的患者 1839 例，用免疫组织化学的方法进行同时检测患者手术前后、新辅助化疗前后、复发转移灶以及原发灶的 ER、PR、HER-2、Ki-67 等生物标志物的变化以及其生存情况，做出生存曲线。计量资料比较采用 t 检验，计数资料比较采用卡方检验（Chi-square test，X2 检验），等级资料的

比较采用 wilcon 秩和检验。Kaplan-Meier 法计算生存率及绘制生存曲线。以 p＜0.05 视为异有统计学意义。
研究结论 中国的乳腺癌患者激素受体状态阳性占大多数，激素受体阳性患者预后较好。

PO-0731

Growth inhibition and induction of apoptosis of triple-negative breast cancer cell by valproic acid via down-regulation of EGFR

Shuiliang Wang[1,2]、Yunfeng Fu[1,2,3]、Zhuolin Li[1,2]、Yating Wu[1,2]、Ruxue Jia[1,2]、Shenghang Zhang[1,2]
1. 中国人民解放军联勤保障部队第 900 医院检验科
2. 厦门大学附属东方医院福建省适配体技术重点实验室
3. 中国人民解放军联勤保障部队第 900 医院基础医学实验室

Objective To explore the possible anti-tumor effect of valproic acid (VPA) against triple-negative breast cancer (TNBC) and its underlying molecular mechanism.
Methods MTS assay was carried out to evaluate the effect of VPA (0, 0.25, 0.5, 1, 2 or 4 mmol/L) on survival of TNBC cell MDA-MB-231. Crystal violet staining was used to detect the effect of VPA (0, 0.125, 0.25 or 0.5 mmol/L) on clone formation of MDA-MB-231. Induction of apoptosis of MDA-MB-231 treated with VPA (0.5 mmol/L) for either 24h or 48h was analyzed by detecting of cleavage of poly ADP-ribose polymerase (PARP) with Western blot as well as apoptotic-ELISA, and real-time quantitative reverse transcriptase PCR (qRT-PCR) was used to analyze the mRNA expression level of EGFR in MDA-MB-231. The effect of VPA (0.25, 0.5 or 1 mmol/L) on expression of EGFR and its downstream Akt signaling pathway in MDA-MB-231 was also detected by Western blot analysis. MiRNAs specific qRT-PCR was also carried out to analyze the effect of 0.5 mmol/L of VPA for either 24h or 48 h on expression of both miR-133a and miR-133b in MDA-MB-231. One-way ANOVA and dunnet-t test were used for statistical analysis. Results As compared with control (0 mmol/L of VPA), treatment with different doses of VPA (0.25, 0.5, 1, 2 or 4 mmol/L) significantly decreased the survival rate of MDA-MB-231 cultured in vitro in a dose-dependent manner (100％±0.46％ vs 86.97％±0.21％, 77.66％±0.17％, 66.81％±0.59％, 46.68％±0.45％, 15.89％±0.25％; P<0.0001). Meanwhile, treatment with different doses of VPA (0.125, 0.25 or 0.5 mmol/L) also significantly decreased the mean clone numbers of MDA-MB-231 (769.33±22.03 vs 599.33±39.00, 492.00±52.00, 263.33±14.74; P<0.05 ） as compared with control (0 mmol/L of VPA). While treatment with 0.5 mmol/L of VPA for 24h does not show any effect on apoptosis of MDA-MB-231 (apoptosis rate being 0.13±0.00 vs 0.14±0.00; P>0.05), long term treatment with 0.5 mmol/L of VPA (48h) did significantly induce apoptosis as compared with control (apoptosis rate being 0.13±0.00 vs 0.80±0.00; P<0.05). Although treatment with 0.5 mmol/L of VPA for 24h or 48h didn’t alter the mRNA expression of EGFR in MDA-MB-231, our Western blot analysis indicated that the protein expression of EGFR was significantly down-regulated, and the downstream Akt signaling pathway was inhibited accordingly in MDA-MB-231 treated with VPA (0.25, 0.5 or 1 mmol/L) for 24h. In addition, the expression of miR-133b targeting EGFR mRNA was significantly up-regulated in MDA-MB-231 treated with 0.5 mmol/L of VPA either for 24h or 48h as indicated by qRT-PCR analysis (1± 0 vs 6.21±0.89, 4.58±0.62; P<0.001) as compared with control (0 mmol/L of VPA).
Conclusions VPA exhibits favorable effect on inhibition of growth and induction of apoptosis of TNBC cell MDA-MB-231 in vitro. Our preliminary mechanism study suggested that treatment with VPA could down-regulate the expression of EGFR via up-regulation of EGFR mRNA-targeted miR-133b, which in turn inhibits the downstream Akt signaling pathway and induces growth inhibition and apoptosis of MDA-MB-231. VPA as a potential candidate of therapeutic drug for patient with TNBC is worthy of further investigation.

PO-0732

未接受核苷类似物治疗的慢性乙型肝炎患者潜在耐药相关变异流行特征

钱福初、邹伟华、金芳、李栋立、沈宇娟
湖州市中心医院

目的 乙型肝炎病毒（HBV）逆转录酶（RT）区域潜在的耐药（DR）相关变异可能与抗病毒药物的有效性和疾病进展有关。本研究调查未接受核苷类似物（NAs）治疗的中国慢性乙型肝炎患者潜在DR 相关变异的患病率和临床特征。
材料与方法 选择湖州市中心医院的 206 例未经治疗的慢性乙型肝炎患者作为研究对象。提取血清DNA，用巢式聚合酶链反应（nest-PCR）扩增 HBV-RT 区。通过直接测序分析了 42 个潜在的 DR 相关变异体。
结果 慢性乙型肝炎患者中，乙型肝炎病毒基因型 121 例（58.7%），丙型肝炎病毒基因型 85 例（41.3%）。在 42.7%（88/206）的患者中检测到潜在的 DR 相关变异。原发性和继发性 DR 变异检出率为 7.28%（15/206），包括 rtL80I/V、rtI169T、rtV173L、rtL180M、rtA181T/V、rtM204I/V 和 rtN236T。rt53、rt82、rt221、rt233、rt237 和 rt256 处的变异对基因型 B 具有特异性，而 rt38、rt84、rt126、rt139、rt153、rt191、rt214、rt238 和 rt242 处的变异对基因型 C 具有特异性。A-B 结构域间变异频率（3.96%）显著高于功能结构域（1.17%）和非 A-B 结构域（1.11%）。多因素 logistic 回归分析显示，在未经治疗的慢性乙型肝炎患者中，较低的 HBV-DNA 载量（$<10^6$ IU/ml）是与潜在 DR 相关变异相关的独立因素（$P<0.05$）。
结论 在未经治疗的中国慢性乙型肝炎患者中，潜在的 DR 相关变异是常见和复杂的。此外，这些变异可能导致血清 HBVDNA 降低。然而，潜在的 DR 相关变异对抗病毒治疗和肝病进展的影响还需要进一步研究。

PO-0733

血清 25-羟基维生素 D 水平与老年性高血压及其脑卒中的相关性研究

袁勇、孔凡斌、高辉
昆明市延安医院

目的 探讨血清 25-羟基维生素 D（25-(OH)D）的水平与原发性高血压发生发展的相关性。
方法 选择 2020 年 12 月-2021 年 5 月在昆明市延安医院老年病科住院的年龄≥60 岁高血压患者作为研究对象，共 152 例，按其是否合并有脑卒中，将病例分为单纯高血压组和高血压合并脑卒中组，选取同期健康体检者 66 例作为对照组，收集临床资料，同时用全自动生化分析仪检测 25-(OH)D 及其生化指标，采用统计学软件 SPSS 23.0 分析所收集资料和数据与高血压的关系。
结果 高血压 2 级和高血压 3 级患者血清 25-(OH)D 水平（15.68±5.74ng/mL、13.99±8.34ng/mL）显著低于正常对照组（21.75±6.40ng/mL），随着高血压分级的增加，血清 25-(OH)D 水平水平逐级降低；高血压合并脑卒中组血清 25-(OH)D 水平（16.20±7.99ng/mL）显著低于高血压组（16.61±7.23ng/mL）（p＜0.05）。高血压 2 级和高血压 3 级的 25-(OH)D、TC、HDL-C、LDL-C 的浓度水平均低于对照组，且高血压 3 级组的 HDL-C、血清 25-(OH)D 均低于高血压 2 级组，TC、LDL-C 均高于高血压 2 级组；高血压组及高血压合并脑卒中组 25-(OH)D、HDL-C、LDL-C、TC 的浓度水平均低于对照组，且高血压合并脑卒中组低于高血压组（P＜0.05）。线性回归分析结果显示，HDL-C、hs-CRP 是影响 25-(OH)D 的独立危险因素（p＜0.05）。
结论 低水平的 25-(OH)D 与老年高血压的发生、发展有相关性，且随高血压分级程度越高，25-(OH)D 水平越低。25-(OH)D 降低可能是高血压发生发展和导致心脑血管合并症的风险因子。

PO-0734

残余胆固醇和非高密度脂蛋白胆固醇与急性缺血性脑卒相关性的研究

袁婷、韦四喜、冯占辉、杨文秀、夏英、黄海
贵州医科大学附属医院

目的 将急性缺血性脑卒中（AIS）分为大动脉粥样硬化型（LAA）、小动脉闭塞型（SAO）和心源性栓塞型（CE）三个亚组，通过分析残余胆固醇（RC）和非高密度脂蛋白胆固醇（Non-HDL-C）在 AIS 及三个亚组患者中的变化，探讨 AIS 诊断与 RC 和 Non-HDL-C 等指标的相关性。
方法 收集 2019 年 1 月至 12 月在贵州医科大学附属医院确诊的急性缺血性脑卒中 151 例患者作为疾病组，同期体检健康人群 191 例作为对照组，首先分析两组血糖（Glu）、血脂相关指标和同型半胱氨酸（Hcy）等的水平差异及相关性；进一步亚组分析 LAA、SAO 和 CE 相关指标的水平差异。
结果 AIS 组 Glu、甘油三酯（TG）、RC 和 Hcy 水平高于对照组，高密度脂蛋白胆固醇（HDL-C）水平低于对照组，且男性患者 Non-HDL-C 水平高于对照组（P＜0.05）；Logistic 回归分析提示 RC 和 Non-HDL-C 水平升高是男性 AIS 发生的危险因素，而女性 AIS 发生的危险因素是 RC 水平升高；ROC 曲线和约登指数提示 RC 和 Non-HDL-C 水平预测男性 AIS 发生的临界值分别是 0.295 mmol/L 和 3.560 mmol/L，联合检测 ROC 曲线下面积（AUC）是 0.752；RC 水平预测女性 AIS 发生的临界值是 0.255 mmol/L。男性 LAA 组和 SAO 组 Glu、TG、TC、LDL-C、RC 和 Non-HDL-C 水平高于 CE 组，HDL-C 水平低于 CE 组，且 LAA 组 Hcy 水平也高于 CE 组（P＞0.05）。女性 LAA 组和 SAO 组 Glu、TG、TC、LDL-C 和 Non-HDL-C 水平高于 CE 组，HDL-C 和 Hcy 水平低于 CE 组，且 LAA 组 RC 水平也高于 CE 组，除 TG 差异有统计学意义外（P＜0.05），其余差异均无统计学意义（P＞0.05）。
结论 RC 和 Non-HDL-C 与 AIS 发生有关，且在 AIS 的发生中具有一定预测价值。

PO-0735

骨髓中破骨细胞数目增多与 KLF7 及 IL-6 蛋白表达水平的相关性研究

李伟
石河子大学医学院第一附属医院

目的 本研究在收集正常体重及肥胖受试个体一般资料、血清样本及骨髓标本的基础上，分析骨髓中 KLF7 及相关炎症因子表达水平与成骨细胞及破骨细胞数目的相关性，为骨髓相关疾病的临床治疗寻找分子靶标并提供新的理论依据。
方法 (1) 2019 年 9 月-2020 年 10 月，在石河子大学医学院第一附属医院收集正常体重个体(n = 24)及肥胖个体(n = 24)一般资料、血清样本及骨髓标本，检测血清中血糖、血脂及 IL-6、TNF-α 及 MCP-1 的含量。(2) 运用免疫组化染色比较正常及肥胖个体骨髓中成骨细胞与破骨细胞的占比分布。(3)运用免疫组化检测骨髓中 KLF7、IL-6、TNF-α 及 MCP-1 的表达水平。(4) 应用 SPSS 20.0 软件进行统计学数据分析。正态分布数据使用 t-检验分析、非正态分布数据使用非参数秩和检验分析。P<0.05 认为差异有统计学意义。
结果 1、肥胖受试个体血清中总 FFA 含量与 IL-6、TNF-α 及 MCP-1 水平显著高于正常体重个体。
2、肥胖受试个体骨髓中破骨细胞显著增多(P<0.05)。
3、肥胖受试个体骨髓中 KLF7、IL-6、TNF-α 及 MCP-1 水平显著高于正常体重个体。
4、骨髓中 KLF7 及 IL-6 表达水平与破骨细胞数量显著正相关。
结论 肥胖后，骨髓中破骨细胞数目增多可能与 KLF7 及 IL-6 蛋白表达水平增加相关。

PO-0736

Identification of A LncRNA Signature as Potential Prognostic Biomarker in Gastric Cancer

Shuang Shi、Chuan'xin Wang
The Second Hospital of Shandong University

Purpose Gastric cancer, with the high rate of metastasis and the low overall 5-year survival rate, is one of the most common malignancies and the major causes of cancer-related deaths worldwide. LncRNA shows potential in diagnosis and prognosis of cancers, so we study novel prognostic lncRNA candidates involved in gastric cancer.
Material and Methods Firstly, we analyze the dataset obtained from TCGA, and identify deregulated RNAs in gastric cancer. Then multiply Cox proportional model and Robust likelihood-based survival model were used to constructed a prognostic signature. CeRNA network and function enrichment analysis were used to investigate the potential mechanism and function of target lncRNAs. And the further experiment validate the function of LINC01929.
Results The results showed that 847 lncRNAs deregulated and 78 lncRANs associated with the overall survival in gastric cancer. 10 up-regulated lncRNAs were chose to construct a prognostic signature. CeRNA network and function enrichment showed several famous cancer-ralated pathway and GO terms were identified in our study. And LINC01929 up-regulated in 43 pairs of clinical gastric cancer tissues, and knockdown LINC01929 can suppress cell proliferation, invasion and migration of gastric cancer cells in vitro.
Conclusion Collectively, our findings indicated that the 10-lncRNA signature could be a prognostic indicator, and serve as a part of ceRNA network to regulate the cancer-related pathways in gastric cancer.

PO-0737

埃希菌属与 IFN-γ 相互作用调控 T2DM 发生的机制研究

吕美君、李莉莎
成都中医药大学附属医院

目的 通过分析 T2DM 患者差异性肠道菌群与细胞因子表达水平的相关性，探讨肠道菌群和细胞炎症因子相互作用网络诱发 T2DM 的作用机制。
方法 本研究进行了一项病例对照实验。招募初发 T2DM 患者和健康人各 30 例作为研究对象，并采集其空腹血浆和无菌粪便样本，检测空腹血糖、HbAlc、空腹胰岛素、TC、TG、HDL 和 LDL 等生化指标；采用流式细胞技术检测两组细胞因子表达水平的差异，并通过 16 SrRNA 三代全长测序技术分析两组肠道菌群的差异性；评估差异肠道菌群及细胞因子的相关性，揭示其可能的作用机制。
结果 与健康对照组相比，T2DM 患者空腹血糖(p<0.001)、HbA1c(p<0.001)、空腹胰岛素(p=0.03)等血糖指标均升高，BMI(p<0.001)、TG(p=0.035)和 LDL(p=0.026)等脂质指标也显著升高，且 TG 与血糖呈正相关关系；血清细胞因子 IL-2(p=0.0000006)、IL-6(p=0.000193)、TNF-α(p=0.016)、IFN-γ(p=0.000036) 和 IL-17(p=0.004) 表达水平显著上调；肠道中 Megamonas funiformis(p=0.0016)、Escherichia (p=0.049)丰度显著升高，而 Bacteroides stercoris (p=0.0068)，Bacteroides uniformis(p = 0.033)和 Phascolarctobacterium faecium(p = 0.033)丰富降低。通过 pearson 相关性分析发现，差异表达的 Escherichia 与 IFN-γ(r=0.73)具有显著的正相关关系。
结论 肠道细菌 Escherichia 与细胞因子 IFN-γ 间的相互作用网络可能具有驱动内脏脂肪组织巨噬细胞的激活而触发炎症的作用，由此抑制脂肪细胞中胰岛素信号传导，诱发胰岛素抵抗。

PO-0738

BubR1 基因表达对肝癌细胞对紫杉醇的敏感性的影响

刘斌
南华大学附属第二医院

目的 探讨 BubR1 基因在紫杉醇治疗肿瘤中的作用。
方法 构建针对 BUBR1 基因的特异性短发夹 RNA 载体，导入人肝癌细胞株 HepG-2，转染 48 h 后，运用实时荧光定量 PCR、Western 印迹法评价 RNA 干扰效果；BubR1 表达下调的肝癌细胞及对照组细胞用不同浓度(1、3、10、30、100、300、1000 和 3000 nmol/L)的紫杉醇处理，MTT 法检测细胞增殖情况。
结果 shRNA- BubR1 可有效抑制 BubR1 的 mRNA、蛋白水平以及内源性表达。MTT 结果显示，BubR1 表达下调的细胞在不同浓度紫杉醇作用下的增殖抑制率与对照组相比明显增加 ($P<0.05$)，并呈现剂量依赖性。
结论 下调 BubR1 的表达能增强肝癌细胞对紫杉醇的敏感性

PO-0739

儿童肺炎支原体流行及耐药情况调查研究

张辉
泰安市中心医院

目的 了解本地区儿童肺炎支原体的流行特征及耐药情况，探索相关耐药机制。
方法 对 3371 份儿童咽拭子标本进行 MP 快速分离培养及药敏实验，根据培养结果分析肺炎支原体流行特征，通过药物敏感实验测定肺炎支原体分离株对大环内酯类药物的耐药情况;选择耐药组及敏感组各 50 个样本进行核酸提取，使用巢式 PCR 扩增 23S 核蛋白体 RNA(23SrRNA)V 区基因,扩增产物进行全自动 DNA 测序,对测得序列进行耐药位点分析。
结果 3371 份临床送检咽拭子标本中分离 MP 1315 株,阳性率为 39.01%。不同年份儿童肺炎支原体阳性率存在差异，冬春季节阳性率明显高于夏秋季节，患儿<1 岁组阳性率为 15.56%，明显低于 3-5 岁组和 6-12 岁组，不同性别阳性率差异无统计学意义；大环内酯类药物敏感试验表明敏感株占 20.76%，其中罗红霉素，依托红霉素和克拉霉素敏感性大于 70%，乙酰螺旋霉素和交沙霉素敏感性较低； 耐药组 42 株样本的 23SrRNA V 区基因发生点突变,突变率 84%，其中 38 株突变位点在 23SrRNA V 区中心环的 2063 位,4 株突变位点在 2064 位，敏感组未发现 23SrRNA V 区基因发生 2063 位和 2064 位点突变。
结论 儿童肺炎支原体感染阳性率较高，且受不同年份季节气候、及不同年龄组社会活动特点等多种因素影响，肺炎支原体对大环内酯类抗生素耐药率高,不同药物耐药情况存在差异，耐药性的分子基础是 23SrRNA V 区基因的点突变,其中 2063 位点突变占主导地位，基因突变监测是肺炎支原体耐药监测的有效补充。各地应积极进行肺炎支原体流行特点、耐药情况监测，建立相应的防控及治疗措施。

PO-0740

没药倍半萜抗前列腺癌作用机制研究

王小玲
山东大学第二医院

本研究对从没药(myrrh)中分离得到的两个吉玛烷型倍半萜类化合物 1(10)E- 2-methoxy-8,12-epoxygermacra-1(10),7,11-trien-6-one (1)和 1(10)E-2-methoxy-5- acetoxy-furanogermacra-1(10)-en-6-one (2)进行了抗前列腺癌活性研究。结果显示，两个化合物在较高浓度时(80 μmol/L)对大肠癌 HT29 细胞增殖有显著的抑制作用，在浓度为 40 μmol/L 时对前列腺癌激素依赖性细胞 LNCaP、激素非依赖性细胞 PC3、PC3M、DU145 均具有明显的抑制活性。Western Blot 实验显示，化合物 1 和 2 均能在雄激素存在的情况下显著降低雄激素受体(AR)的表达、并减少 AR 向细胞核定位；荧光素酶活性分析表明，两个化合物能抑制 AR 启动子的表达活性；细胞免疫荧光结果也证实 ST 化合物对 AR 表达的抑制作用。进一步实验表明，这两个化合物能非常显著的抑制 PSA 启动子和 hk2-ARE 元件报告基因的表达活性，使 PSA 蛋白水平显著降低，表明化合物能显著抑制 AR 的转录激活功能。通过免疫共沉淀检测化合物对 AR 与 AR 辅助激活因子 SRC-1 和 ARA70 蛋白间相互作用的影响，结果显示，倍半萜化合物明显降低这种蛋白间的相互作用。

总之，本研究结果表明，从没药中得到的两个倍半萜单体化合物可以抑制前列腺癌细胞的增殖，其作用机制可能通过阻滞细胞周期、抑制 AR 的表达、抑制 AR 与辅助激活因子的相互作用，从而降低 AR 的功能，抑制细胞增殖。本项研究结果为没药抗肿瘤活性的研究提供了依据，也为前列腺癌的药物治疗提供了更为广阔的思路。

PO-0741

六西格玛理论在全血细胞计数质量控制中的应用

刘双、王悦、丛琳、周汉王、于梅
解放军总医院海南医院

目的 运用六西格玛理论（6σ）分析和评价我室全血细胞计数项目室内质量控制规则，了解我室血细胞分析仪检测系统的室内质量控制水平，选用适宜的室内质量控制规则，并指导其性能质量改进。
方法 统计 2019 年及 2020 年共 4 次国家卫生健康委临床检验中心全血细胞计数 8 个项目的室间质量评价结果，计算偏倚（|Bias%|）；收集 2020 年 4 月-2021 年 1 月本实验室近 10 个月所有的在控室内质控数据，计算高、中、低三个水平的合成变异系数（CV%）表示不精密度值；按照中华人民共和国卫生行业标准 WS/T406-2012 临床血液学检验常规项目分析质量要求的允许总误差（TEA%）作为质量规范。按公式计算各检测项目的 σ 值，并计算目标指数（QGI），选择是否优先改进其性能。
结果 本实验室使用高、中、低三个水平的质控品，高水平质控品（WBC、RBC、PLT、HCT、MCV、MCH、MCHC）、中水平质控品（WBC、RBC、PLT、MCHC）与低水平质控品（WBC、RBC、MCV）的 σ 值均大于 6，表现为世界一流水平，选用 13S 规则。中水平质控品（HGB、HCT、MCV、MCH）与低水平质控品（PLT、MCH）表现为良好(4≤σ<5)，选用 13S22sR4S41s 规则。低水平质控（HGB、HCT、MCHC）表现为优秀(5≤σ<6)，选用 13S22sR4S 规则。
结论 六西格玛应用于全血细胞计数检验项目，可有效评价其检测性能，并有助于提高全血细胞计数检验项目的质量水平。

PO-0742

A study on the optimal condition of rapamycin inhibiting the development of AS

Fei Yu 、Hongyun Jing、Ling Ding、Jiashan Li、Xiuru Guan*
The first Affiliated Hospital of Harbin Medical University

Background and purpose Rupture of atherosclerotic plaques and secondary thrombosis are the main causes of acute clinical cardiovascular events. It is important to inhibit the development of atherosclerosis.Rapamycin (RAPA), an mTOR inhibitor and autophagy inducer, which can stabilize atherosclerotic plaques. However, The optimal conditions for the inhibition of AS by rapamycin have not been determined. Here, the optimum concentrations and time of rapamycin exposure to induce autophagy in macrophages was investigated.
Methods Foam cell models were established through incubation of THP-1-derived macrophages with ox-LDL. Then we determined cell viability by using CCk-8 test. And we detected the process of foam cell formation by oil red O staining, and the protein expression levels of p62 and LC3 were detected by Western blot. Furthermore, the inflammatory factor IL-18 was determined by ELISA.
Results Rapamycin treatment at low dose and short time could inhibit the foaming of macrophages,inducing autophagy by decreasing p62 protein levels and enhancing LC3Ⅱ/Ⅰ expression. RAPA also weakened IL-18 content in the medium. The most obvious effects of rapamycin were treated with 100nmol/L for 24 hours in the study. However, the stress of excess rapamycin or Longer time may exacerbate the foaming of macrophages and cause autophagy blocking.
Conclusions Overall, for the first time our results show that rapamycin is a double-edged sword. Lower concentration and time could induce complete autophagy, but longer time and higher doses otherwise. It is expected that we should take full advantage of its merits for clinical treatment of AS.

PO-0743

褪黑素促进顺铂诱导的卵巢癌细胞凋亡及其机制研究

赵金金[1]、张海光[2]、莫清江[1]、鲁广建[1]、焦路阳[1]
1. 新乡医学院第一附属医院检验科
2. 新乡医学院第一附属医院妇产科

背景 卵巢癌严重威胁女性生命健康，顺铂作为治疗卵巢癌的常用药物发挥重要作用，然而卵巢癌细胞对顺铂的耐药通常导致治疗的失败。寻找新的方法增强卵巢癌对化疗药物的敏感性将极大提高卵巢癌的治疗效果。
目的 研究褪黑素是否能够提高卵巢对顺铂的敏感性并探讨其机制。
方法 以 PBS 作用于卵巢癌细胞（OVCAR3）作为对照组，以顺铂、褪黑素、顺铂+褪黑素作为实验组 1， 2， 3 ；分别作用 24， 48 ，72 小时后 MTT 检测细胞增殖情况，流式细胞术检测细胞凋亡情况；Western blot 检测凋亡相关蛋白及信号通路蛋白的表达。
结果 MTT 结果显示，顺铂和褪黑素作用 24，48， 72 小时均能抑制 OVCAR3 细胞增殖，同对照组相比具有统计学意义，顺铂和褪黑素组相比差异无统计学差异，顺铂+褪黑素组对卵巢癌细胞增殖的抑制更加明显，同对照组、顺铂组、褪黑素组相比差异均具有统计学意义；流式细胞术结果显示，顺铂和褪黑素作用于卵巢癌细胞 24， 48， 72 小时后都使细胞凋亡的比例增加，作用时间越长凋亡比例越高，顺铂和褪黑素作用效果同 PBS 组相比具有统计学意义，顺铂+褪黑素组不同时间点卵巢癌细胞的凋亡比例同其余三组相比均升高，差异具有统计学意义；western blot 检测凋亡相关蛋白显示，顺铂、褪黑素均能使促凋亡蛋白 BAX 表达升高，凋亡抑制蛋白 BCL-2 的表达降低，

顺铂+褪黑素组对 BAX 和 BCL-2 的影响更显著；检测信号通路蛋白发现，褪黑素组 p-ERK 的表达高于 PBS 组及顺铂组，差异具有统计学意义。
结论 褪黑素能够通过 ERK 通路调控凋亡相关蛋白 BAX 与 BCL-2 的比值增强卵巢癌细胞 OVCAR3 对顺铂的敏感性。

PO-0744

云南汉族人群 Tim-1 基因启动子区多态性与支气管哮喘的关联研究

彭传梅[1]、王杨[1]、董玉琳[1]、鲁祥辉[1]、狄勇[2]
1. 昆明市延安医院
2. 昆明医科大学

目的 探讨 Tim-1 基因启动子区多态性及其 mRNA 水平与云南汉族人群支气管哮喘易感性的关联。
方法 采用聚合酶链反应-限制性片段长度多态性（PCR-RFLP）方法，对 180 名云南汉族支气管哮喘病人和 180 名健康体检者 Tim-1 基因启动子区多态性位点-416G > C 和-1454G > A 的基因多态性进行检测，并对不同基因型进行测序验证，同时分别采用 qRT-PCR 法和散射比浊测定法检测疾病组和健康组 Tim-1 mRNA 的表达水平和血浆总免疫球蛋白 E（IgE） 的水平。
结果 Tim-1 启动子区多态性位点-146G > C 和-1454G > A 的基因型及等位基因频率差异在支气管哮喘组和健康体检组两组之间具有统计学意义（P<0.05）； 支气管哮喘组和健康体检组中 Tim-1 mRNA 的表达差异有统计学意义（ P<0.001）；支气管哮喘组和健康体检组中血浆 IgE 的水平差异有统计学意义（ P<0.001）；支气管哮喘组-146G > C 位点携带 CC 基因型的病人 Tim-1mRNA 水平高于携带 GG 型和 GC 型的病人，-1454G > A 位点携带 AA 基因型的病人 Tim-1mRNA 水平高于携带 GG 型和 GA 型的病人；携带-416CC 和-416GC 的支气管哮喘病人，其 IgE 水平明显高于携带-416GG 的病人，携带-1454GG 基因型的病人，其 IgE 水平明显高于携带-1454AA 基因型的病人。
结论 云南汉族人群 Tim-1 启动子区多态性位点-416G > C 和-1454G > A 的基因多态性与支气管哮喘遗传易感性相关；相比于健康体检者，支气管哮喘患者的 Tim-1mRNA 和 IgE 的表达明显升高；支气管哮喘组 Tim-1 两位点不同基因型与其 mRNA 水平和血浆 IgE 的表达高低密切相关。

PO-0745

PAICS is involved in the occurrence and development of gastric cancer, and participates in DNA damage response

Nan Huang、Fenyong Sun
Shanghai Tenth People`s Hospital of Tongji University

Objective PAICS, a key enzyme in the de novo purine synthesis, has been reported to be associated with the occurrence and development of many tumors, but not in gastric cancer. Purine nucleotides are important materials for DNA synthesis. Whether the enzymes related to purine synthesis pathway are involved in DNA damage response has not been clarified. This study aims to explore the biological function of PAICS in gastric cancer and whether it participates in DNA damage response process.
Methods Firstly, the expression and prognosis value of PAICS in gastric cancer was analysed using public data from the TCGA database with bioinformatics technology; then, the proliferation and apoptosis of gastric cancer cells after interfering PAICS was detected with CCK8, colony formation and flow cytometry in vitro. The tumorigenicity of gastric cancer cells after interfering PAICS was detected with subcutaneous tumorigenesis experiment in vivo. Finally, after the

interference of PAICS, the expression of γH2AX, a DNA damage repair marker, was measured along with immunofluorescence and comet assay, in order to verify whether PAICS was involved in DNA damage repair process.
Results Bioinformatics analysis showed the significantly high expression of PAICS in GC, and the relation with prognosis. CCK8, colony formation assay as well as apoptosis assay showed that the interference of PAICS inhibited GC cell proliferation and induced apoptosis. Tumor formation assay in nude mice verified that the interference of PAICS decreased the tumorigenicity of GC cells. Comet assay, γH2AX expression and immunofluorescence experiments demonstrated the occurrence of DNA damage after interfering PAICS. Co-immunoprecipitation demonstrated that PAICS interacted with histone deacetylase 1/2 (HDAC1/2), thus participating in DNA damage repair by influencing histone acetylations. In vivo and in vitro drug sensitivity experiments indicated that the sensitivity of GC cells to chemotherapy drugs could be enhanced via interfering PAICS.
Conclusion PAICS plays an oncogenic role in gastric cancer, which facilitates the occurrence and development of GC and is related to the prognosis of GC patients. Meanwhile, PAICS maintains genome stability through interaction with HDAC1/2. The interference of PAICS enhances the sensitivity of GC cells in response to chemotherapy drug, cisplatin.

PO-0746

新型冠状病毒疫苗接种的环境管理策略

宗玉龙、刘城、王瑾、赵书平
泰安市中心医院

目的 检测新型冠状病毒疫苗接种处的核酸，为环境管理提供依据。
方法 使用荧光定量 PCR 方法，对新冠疫苗接种处的环境样本以及全院重点部位环境样本进行核酸检测。
结果 通过对全院 56 处环境样本进行核酸检测，有 10 处核酸阳性，均为疫苗接种室样本。
结论 应加强新冠疫苗接种处的环境管理，避免因疫苗接种导致的其它部位核酸阳性。

PO-0747

Dual functions of p62 in the process of macrophage-derived foam cells formation and progress

Hongyun Jing、Wei Yang、Fei Yu、Ling Ding、Xiuru Guan*
The First Affiliated Hospital of Harbin Medical University

Background and aims Autophagy is one of the important defense mechanisms for cells to maintain inner environment stability. Recently, autophagy got more attention in atherosclerotic lesions because it played important roles in lipid metabolism. Our previous study showed that during macrophage-derived foam cells formation and progress the autophagy marker p62, a chaperone for selective autophagy of cargo, accumulated. However, details regarding to the autophagy and p62 effect on atherosclerosis has remained unknown. In this study, we monitored the p62 expression level, lipid droplet accumulation and light chain 3 I/II level suffering from three kinds of concentrations (overexpression, basic and knockdown) in p62 to investigate the role of p62 on the plaque stability under different states of autophagy induced by different concentration of oxidized low-density lipoprotein.
Results Under basic state of autophagy, p62-silencing resulted in autophagy dysfunction and the increase of the secretion of increased interleukin-1β; Overexpression of p62 induces autophagy and inhibits the secretion of IL-1β. When autophagy disordered, p62-silencing will ease the

autophagy disorder and reduce the secretion of IL-1β；Overexpression of p62 will aggravate autophagy disorder, which further aggravates the secretion of IL-1β leading to cell death and promoting AS. These results suggested that autophagy at different stages during the development of foam cells, via p62, has two distinct effects on plaque stability. Therefore, p62 will be an attractive target for the treatment of atherosclerosis.

PO-0748

Study on Inhibition of Chlamydia Trachomatis Activity by Single Drug of Huanglian Daochi Powder in Vitro

Bin Liu
Second affiliated hospital of south China universit

Objective To study the inhibitory effect of single drug of huanglian daochi powder on the activity of chlamydia trachomatis in vitro.
Method Huanglian daochi powder was prepared by water extraction method. Then, in vitro cytotoxicity test, MIC value determination, MBC value determination and combined drug sensitivity test were carried out on the standard Chlamydia trachomatis strain E. To study the inhibitory effect of single drug of huanglian daochi powder on the activity of chlamydia trachomatis in vitro.
Results Among the 14 traditional Chinese medicines, most of them had similar TD0 on McCoy cells, with the range of 6.12-12.50mg/ mL. Some traditional Chinese medicines, such as talc, were affected by the material texture, and TD0 value was higher. The MIC and MBC values of Rhubarb and Rhizoma Coptis were measured in the 14 tested Huanglian Daochi powder, suggesting that Rhubarb and Rhizoma Coptis had a strong inhibitory effect on Ct activity, and Rhubarb had a stronger inhibitory effect on Ct activity than Rhizoma Coptis. After iodine staining, it was observed under the microscope that with the increase of the concentration of the liquid, the volume of inclusion bodies decreased and the number of inclusion bodies gradually decreased until they disappeared. The diameters of inhibition ring of 14 traditional Chinese medicines to gonococcal drug resistant strains were Bamboo＞leaf Rush＞Rhizoma coptidis＞Rhubarb＞Gypsum＞Rehmanniae rehmanniae＞Polygonum quanum＞Radix Pallis＞Polygonum japonica＞Talc＞Licorice＞Gardenia＞Lotus seed heart＞Polygonum sinensis in order. Among 14 drugs, rhizoma coptidis combined with 13 others, the combined drug sensitivity test of the detected Rhubarb and Rhizoma coptidis with in vitro anti-CT activity was conducted according to the above method, and the FIC value was 1, indicating that the two drugs had no synergistic or antagonistic effect.
Conclusion Huanglian daochi powder had inhibitory effect on Chlamydia trachomatis activity in vitro, Licorice, Rhubarb, Gardenia, Polygonum japonica and so on had high inhibitory effect.

PO-0749

浙江地区汉族脑梗死患者氯吡格雷药物基因 CYP2C19 的基因多态性研究

林学飞
杭州迪安医学检验有限公司

目的 了解浙江地区汉族脑梗死患者吡格雷药物基因多态性分布情况。
方法 选取 2019 年 1 月至 2020 年 8 月应用氯吡格雷治疗的浙江地区汉族脑梗死患者 282 例为对象，其中男 200 例、女 82 例。收集外周静脉血,提取基因组 DNA,进行扩增及 CYP2C19 基因序列结果判断。分析其在浙江地区汉族脑梗死患者中的分布特点，以利于指导用药和疾病防治。

结果 共纳入脑梗死患者 282 例，基因扩增结果显示 CYP2C19 基因型分布为*1/*1 型 33.33%，*1/*2 型 40.42%、*1/*3 型 7.45%、*1/*17 型 3.19%，*2/*2 型 12.06%、*2/*3 型 3.19%、*3/*3 型 0.35%。超快代谢型、快代谢型、中间代谢型和慢代谢型患者所占比例分别为 3.19%（9 例)、33.33%(94 例)、47.87%(135 例)和 15.60%（10 例）。CYP2C19 基因代谢表型与珠中江地区、广东河源地区、厦门地区、遵义地区相比较，差异无统计学意义（P>0.05)；与豫北地区、云南楚雄地区相比较，差异有统计学意义（P<0.05)。
结论 浙江地区汉族脑梗死患者 CYP2C19 基因以*1/*2 型、*1/*1 型为主；基因代谢表型以中间代谢型和快代谢型为主。

PO-0750

Factors influencing the reference interval of thyroid-stimulating hormone in healthy adults: A systematic review and meta- analysis

Dongyang Xing、Delong Liu、Ri Li、Jiancheng Xu
Jilin University First Hospital

Background Many studies have reported that the thyroid- stimulating hormone (TSH) reference interval is susceptible to external factors, such as age, sex, race, region and iodine intake. However, no meta- analysis has comprehensively explored the effect of these factors on the TSH reference interval.
Methods Articles published from January 1960 to January 2020 were searched in PubMed, Embase, Cochrane, Scopus, Medline English databases and CNKI, WanFang and CQVIP Chinese databases. In total, 19 studies were ultimately included. All data were analysed using Review Manager 5.3, STATA 16.0 software, GraphPad Prism 8.0 and Microsoft Excel 2010 to draw the TSH concentration curve.
Results The TSH reference interval was significantly influenced by sex and age. The mean of TSH concentration in females was 0.27 mIU/L higher than that in males. Reference interval of TSH is divided into 20– 59 years old and >60 years old age groups in males, and 20– 39 years old and >40 years old age groups in females. Regardless of sex, TSH concentrations all increase with age. In iodine- deficient areas, TSH reference intervals were generally lower than those in iodine- sufficient or iodine- excessive
areas. The TSH reference interval in Asia and North American countries was generally higher than that in most European countries. In the subgroup analyses of sample size, region and assay methods and manufacturers, the between- group differences were significant.
Conclusion The TSH reference interval was significantly influenced by sex, age, iodine intake, sample size, region, and assay methods and manufacturers, but other factors should not be ignored. Therefore, it is necessary for each laboratory to validate an appropriate TSH reference interval based on local conditions.

PO-0751

高良姜素对人头颈部鳞癌细胞的生长抑制作用及其机理

朱丽萍
上海交通大学医学院附属第九人民医院

目的 探讨高良姜素在体内和体外实验中对人头颈部鳞癌细胞的抗肿瘤作用及其机制
方法 通过 MTT 法检测人头颈部鳞癌细胞 WSU-HN4、WSU-HN6 和 WSU-HN13 经不同浓度高良姜素处理后细胞增殖能力的变化；通过流式细胞术分析高良姜素对人头颈部鳞癌细胞周期和细胞凋

亡的影响；通过 Western Blot 方法检测高良姜素对人头颈部鳞癌细胞中 p21、cyclin D1、Bax 和 Bcl-2 等细胞周期、细胞凋亡相关蛋白的表达或磷酸化水平的影响；建立人头颈部鳞癌的裸鼠荷瘤模型，给荷瘤小鼠腹腔注射高良姜素，观察记录肿瘤的体积和体重，并监测小鼠的体重、生化指标和小鼠的生存情况，初步评价高良姜素的抗肿瘤作用和生物安全性。
结果 体外实验中高良姜素以时间和剂量依赖性方式抑制人头颈部鳞癌细胞的增殖，并通过影响 cyclinD1、CDK4、CDK6 和 p21 等细胞周期相关蛋白的表达诱导细胞周期阻滞在 G0/G1 期，通过上调促凋亡蛋白 Bax 和下调抗凋亡蛋白 Bcl-2、Bcl-xl 的表达诱导细胞凋亡。在体内实验中高良姜素能够抑制裸鼠荷瘤模型中肿瘤的生长，并能明显增加肿瘤组织中凋亡细胞的比例，下调 cyclinD1 蛋白的表达。
结论 本研究从细胞和动物实验入手，首次证实高良姜素对人头颈部鳞癌细胞的生长抑制作用，体外和体内实验结果表明，高良姜素通过诱导细胞凋亡和 G0/G1 期细胞周期阻滞的方式明显抑制人头颈部鳞癌细胞的增殖和生长。因此，高良姜素可作为一种新的人头颈部鳞癌辅助治疗药物，并具有广阔的临床应用前景。

PO-0752

基于数据库分析 TM4SF1 在卵巢癌中的表达和临床意义

李荣[1,2]、王芳[1]
1. 南京医科大学第一附属医院（江苏省人民医院检验医学部）
2. 南京医科大学附属妇产医院（南京市妇幼保健院）

目的 探究 TM4SF1 在卵巢癌中的表达情况及临床意义。
方法 收集 Oncomine、GEPIA 数据库中关于 TM4SF1 的数据信息，并对数据库中的资料进行二次分析；运用 Coexpedia、STRING 数据库分析 MECOM 在卵巢癌中共表达及互作蛋白情况；利用 Kaplan-Meier Plotter 分析卵巢癌患者中 TM4SF1 mRNA 的表达水平与患者预后的关系。
结果 Oncomine 数据库在不同类型肿瘤中有关 TM4SF1 基因的研究共 547 项，差异有统计学意义的有 138 项，其中在卵巢癌中有 10 项研究，均显示 TM4SF1 高表达；这一结果在 GEPIA 数据库中也得到证实；共表达分析发现了 504 个与其共表达的基因；蛋白互作分析发现 TM4SF1 蛋白可能与 RHBG、MYO10、C1D、CD63、CD37、TSPAN31、CD53、TSPAN1、DDR1、TSPAN4 蛋白有相互作用；TM4SF1mRNA 高表达组卵巢癌患者总体生存率低于低表达组（$P<0.05$）。
结论 TM4SF1 基因在卵巢癌中高表达，且其翻译的蛋白通过和多种蛋白相互作用发挥其生物学效应，其 mRNA 表达水平与卵巢癌患者生存预后相关，有望为卵巢分子靶向治疗提供新的思路。

PO-0753

Analysis of heart injury laboratory parameters in 273 COVID-19 patients

Huan Han[1]、linlin xie[2]、rui liu[1]、jie yang[1]、fang liu[3]、yong feng[2]、chengliang zhu[1]
1. Department of Clinical Laboratory, Renmin Hospital of Wuhan University
2. 武汉大学基础医学院
3. 武汉大学生命科学学院

Background Since December, 2019, an outbreak of pneumonia caused by a novel coronavirus (SARS-CoV-2) has raised intense attention in Wuhan, Hubei province, China. This disease, named COVID-19 by World Health Organization (WHO), spreads rapidly around the country and worldwide. SARS-CoV-2 infection caused mildly to seriously and fatally respiratory, enteric, cardiovascular, and neurological diseases.

Method We enrolled 273 COVID-19 patients who were admitted to Renmin Hospital(Wuhan, China). All patients were classified into moderate, severe and critical groups according to their symptoms. We detected and analyzed the main laboratory indicators related to heart injury, CK-MB, MYO, ultra-TnI and NT-proBNP, in COVID-19 patients and investigated the correlation between heart injury and severity of the disease.
Results The positive rate of CK-MB had no difference between the mild, severe and critical groups. While the positive rate of MYO, ultra-TnI and NT-proBNP is higher in severe cases and critical cases as compared to mild cases, the differences among the groups were statistically significant ($P<0.05$). After a pairwise comparison by Bonferroni correction, it was observed that the levels of NT-proBNP and MYO were significant increased in severe cases and critical cases compared to mild cases ($P<0.0167$), but no difference between severe cases and critical cases ($P>0.0167$). The increase of ultra-TnI only showed significantly difference between the mild cases and severe cases ($P<0.0167$), while there was no difference between mild cases and critical cases, severe cases and critical cases ($P>0.0167$).
Conclusion It was found that higher concentration in venous blood of CK-MB, MYO, ultra-TnI and NT-proBNP were associated with the severity and case-fatality rate of COVID-19. Careful monitoring of the myocardiac enzyme profiles is of great importance in reducing the complications and mortality in COVID-19 patients.

PO-0754

江苏地区产 OXA-232 肺炎克雷伯菌的流行病学特征

付宏煜、杜鸿
苏州大学附属第二医院

目的 产 OXA-48 样碳青霉烯酶肠杆菌科在不同生态系统中的快速传播给临床带来巨大挑战。近年来 OXA-232 样肠杆菌科在中国开始出现，以肺炎克雷伯菌最为常见。我国不同地区产 OXA-232 肺炎克雷伯菌 (OXA-232-producing K. pneumoniae，OXA-232Kp) 的分子流行病学特征与遗传环境所知甚少。描述临床 OXA-232Kp 的流行病学特征。
方法 收集 2018 年 9 月至 2019 年 9 月江苏 5 家医院临床分离的非重复碳青霉烯耐药肺炎克雷伯菌 (Carbapenem- resistant Klebsiella pneumoniae, CRKP)，采用微量肉汤稀释法和 Phoenix-M50 自动微生物系统进行药敏分析；PCR 结合测序检测 blaOXA-232 基因；脉冲场凝胶电泳（PFGE）分析菌株同源性；质粒测序分析携带 blaOXA-232 基因的质粒周围环境。
结果 1. 共收集 78 株 CRKP 菌株，其中 3 株菌株携带 blaOXA-232 基因，2 株 OXA-232Kp 菌株来自痰液 (66.7%)，1 株来自泌尿道 (33.3%)。
2. 所有 3 株 OXA-232Kp 对头孢菌素类、氨曲南、复方新诺明、喹诺酮类药物均耐药，2 名患者出院前经抗生素哌拉西林-他唑巴坦、阿米卡星、头孢他啶、庆大霉素等治疗后恢复。
3. MLST 分析均属于 ST15 型，基于 Gel J 分析≥85%的基因连锁率，分离菌株属于同一克隆。
4. 3 株菌株质粒均不能发生转移，提示该质粒为非接合质粒。该质粒与曾在中国东部报道的携带 blaOXA-232 的质粒 质粒周围环境相同。
结论 本文首次调查 OXA-232Kp ST15 在江苏地区的流行病学特征。携带 blaOXA-232 基因的质粒具有高度的同源性，表明该 6141 bp 的 ColE 型质粒对 blaOXA-232 基因在中国的流行具有重要作用。

PO-0755

Clinical Value of Serum Calcium in Elderly Patients with Sepsis

Huan Li
Renmin Hospital of Wuhan University

Purpose To explore the clinical value of serum calcium (Ca) in elderly patients with sepsis.
Materials and Methods The clinical data and laboratory data of elderly patients with sepsis (n = 165) and elderly population for physical examination (n = 67) in Renmin Hospital of Wuhan University from January 2020 to November 2020 were collected. We analyzed serum Ca levels in sepsis and septic shock firstly, and then continued to investigate them in the survival group and the death group. Meanwhile, we also assessed the correlation between serum Ca and PCT. Finally, ROC curves of serum Ca in sepsis were carried out to differentiate septic shock and judge the prognosis.
Results The serum Ca levels of the elderly patients with sepsis were lower than that of the control group (median 1.98 vs 2.31 mmol/L, $P < 0.001$), and the more severe the sepsis, the lower the serum Ca levels. Sepsis patients with decreased serum Ca had higher shock rate and mortality. There was a negative correlation between serum Ca and PCT ($r = -0.2957$, $P < 0.001$). And ROC curve analysis demonstrated that the areas under the curve (AUC) of serum Ca for differentiating sepsis from septic shock and the prognosis of elderly patients with sepsis were 0.770 and 0.802, respectively.
Conclusion Serum Ca has a certain value for the early recognition of elderly patients with sepsis and the judgment of the severity of the disease, as well as a potential evaluation value for differentiating sepsis from septic shock and prognosis.

PO-0756

Distinct Interactions of EBP1 Isoforms with FBXW7 Elicits Different Functions in Cancer

Yuli Wang [1]、Pengju Zhang[2]、Jianhua Mao[3]、Guangwei Wei[2]
1. The Second Hospital of Shandong University
2. 山东大学
3. Life Sciences Division, Lawrence Berkeley National Laboratory

Background The ErbB3-binding protein EBP1 is a member of the proliferation-associated 2G4 protein family and is ubiquitously expressed in all human tissues and is involved in the regulation of cell growth and differentiation. EBP1 encodes two different protein isoforms, the long form P48 and short form P42, due to alternative splicing of pre-mRNA, which are believed to have different cellular activities. The predominant P48 isoform can promote cell proliferation or survival including cancer cells and localizes to both cytoplasm and nucleus. Moreover, correlation of high expression level of P48 with poor clinical outcomes in patients suggests that P48 is closely related with cancer progression. In contrast, the P42 isoform, which lacks the N-terminal 54 amino acids, is considered to be a potent tumor suppressor because of its growth-inhibitory function. Although it is reported that P48 has an oncogenic activity and P42 plays a suppressive role in various cancer cells, the underlying mechanism regarding the distinctive functions of the 2 isoforms of EBP1 in cancer remains largely unclear.
FBXW7 (F-box and WD40 domain protein 7) functions as a substrate recognition subunit of the SCF (SKP1/CUL1/F-box protein) E3 ubiquitin ligase complex to regulate a network of proteins with central roles in cell division, growth, and differentiation. FBXW7 contains two important functional domains: the F-box domain, which interacts directly with SKP1 to recruit ubiquitin-conjugating enzymes, and the WD40 domain, which binds to a consensus phosphor-binding motif

called the CDC4 phosphodegron (CPD) in its substrates. FBXW7 has been characterized as a general tumor suppressor. FBXW7 mutation or deletion is often observed in multiple human cancers including colorectal cancer, and loss of FBXW7 function results in tumorigenesis. Accumulating data indicate that FBXW7 exerts its antitumor function mainly through targeting multiple oncoproteins for ubiquitination and proteasomal degradation, such as cyclin E, Notch, mTOR, Aurora A, and c-Myc. However, a detailed understanding of the full set of FBXW7 substrates and the mechanisms that link FBXW7 deficiency to tumorigenesis is still lacking.
In this study, we used proteomics approach to globally screen FBXW7-regulated proteins in colorectal cancer cells, and we first identified that EBP1 P48 expression was dramatically upregulated in FBXW7-deficient cells. However, the underlying mechanism of FBXW7 mediates EBP1 isoforms is still unclear.
Methods The aim of the present study was to detect whether EBP1 isoforms interact with the SCF-type ubiquitin ligase FBXW7 to exert different roles in tumorigenesis. The binding between FBXW7 and EBP1 isoforms, and the ubiquitin of EBP1 isoforms were detected by Co-immunoprecipitation. MTT, colony formation, transwell and matrigel assays were used to detect cell phenotypes which mediated by FBXW7 deficiency. Besides, nude mice were used to verify whether P48 mediates FBXW7 loss-induced metastasis in vivo. EBP1 isoforms regulated substrate degradation of FBXW7 were detected by qRT-PCR and western blot.
Results EBP1 isoforms interact with the SCF-type ubiquitin ligase FBXW7 in distinct ways to exert opposing roles in tumorigenesis. P48 bound to the WD domain of FBXW7 as an oncogenic substrate of FBXW7. P48 binding sequestered FBXW7α to the cytosol, modulating its role in protein degradation and attenuating its tumor suppressor function. In contrast, P42 bound to both the F-box domain of FBXW7 as well as FBXW7 substrates. This adapter function of P42 stabilized the interaction of FBXW7 with its substrates and promoted FBXW7-mediated degradation of oncogenic targets, enhancing its overall tumor-suppressing function.
Conclusion our study uncovers a physical and functional relationship among FBXW7 and EBP1 isoforms (P48 and P42). Two EBP1 isoforms distinctively modulate the role of FBXW7 by different and independent mechanisms. The knowledge of the role of FBXW7 and EBP1 isoforms in the molecular mechanisms governing tumorigenesis sheds new lights on improving current anticancer therapies.

PO-0757

环状 RNA 在原发性肝细胞癌中的研究进展

蔡馨
武汉大学人民医院

原发性肝细胞癌（HCC）是世界上常见的恶性肿瘤之一，研究调控 HCC 的侵袭迁移机制对于肝癌的临床诊断和治疗具有重要意义。环状 RNA（circRNA）作为非编码 RNA 家族的重要成员，因其环状结构高度稳定，在肝细胞中起微小 RNA（miRNA）海绵作用，以竞争内源性 RNA 机制调控 miRNA 或促进靶基因表达，在 HCC 进展中起重要作用。探讨 circRNA 在 HCC 发病中的作用机制，将有助于筛选 HCC 诊断标志物和研发治疗的有效靶点。

PO-0758

the role of ADAM17 in platelet production in pediatric ITP

Qi Wang、Xi Jia、Jia Wei
Children’s Hospital of Soochow University

Objectives To explore the role of ADAM17 in platelet production in pediatric ITP

Methods Patients Twenty preliminary diagnostic ITP children without any treatment hospitalised at the Department of Haematology of the Children's Hospital of Soochow University, from March 2019 to July 2020, were enrolled in this study. Twenty one healthy non-hematological and non-surgical children served as the control group. The study was approved by the Medical Ethics Committee of the Children's Hospital of Soochow University.

Next-generation RNA-Seq

Megakaryocytes from ITP or healthy donor children were purified by a single-step gradient solution (1.5%/3% bovine serum albumin) for RNA-Seq. In brief, RNA was prepared for sequencing according to Ribo-Zero™ rRNA removal Kit (illumina) for poly-A RNA. Sequencing was carried out using a 2x150bp paired-end (PE) configuration; image analysis and base calling were conducted by the HiSeq Control Software (HCS) + OLB + GAPipeline-1.6 (Illumina) on the HiSeq instrument. The sequences were processed and analyzed by GENEWIZ.

Giemsa staining of bone marrow smears

The bone marrow smears were fixed with icy methanol for 30 seconds, and then covered with 1×Giemsa working solution for 15 minutes at room temperature. Megakaryocytes were captured under 1000× magnification using an Olympus BX 40 microscope. For each slice, at least 5 random megakaryocytes were selected for examination. Fetal liver cell culture and megakaryocyte purification

The embryos of ADAM17Zn△/+ mice were isolated at the day 14.5 of pregnancy, a single-cell suspension through a 100 μm filter. Cells were cultured in Dulbecco's modified Eagle medium at 37oC and 5% CO2 for four days. On the fourth day, mouse fetal liver cells were allowed to sediment in a single-step gradient solution (1.5%/3% bovine serum albumin) to purify mature megakaryocytes.

Assays of proplatelet formation

Purified megakaryocytes were seeded at a density of 5 × 105 cells per well in 24-well plates. Quantification of PPF-MKs (proplatelet forming megakaryocytes) was determined by the number of megakaryocytes with more than two pseudopods per well examined under bright field microscopy.

Flow cytometry

For ploidy analysis, 75% cold ethanol pre-fixed megakaryocytes were treated with

0.02 mg/ml RNase A and then double-stained with 0.01 mg/ml propidium iodide and FITC-conjugated rat anti-mouse CD41 antibody for 30 minutes at room temperature.CD41 positive cells were selected to assess ploidy. To quantify ADAM17, platelets were labeled with FITC-conjugated mouse anti-human CD41 antibody and PE-conjugated mouse anti-human ADAM17 antibody. A FACS (BD FACS Canto II) flow cytometer was used for the flow cytometric analysis. CD41 positive platelets were selected to assess the expression of ADAM17. A cocktail of CD3-FITC/CD16+56-PE/CD45-Percp-Cy5.5/CD4-PC7/CD19-APC/CD8-APC-Cy7 monoclonal antibody.

Results Autoantibody-negative children with ITP had significantly lower CD4+ T cells (Ctrl 36.2±1.0; ITP 24.8±1.6) ($P<0.001$) and higher CD8+ T cells (Ctrl 23.7±0.6; ITP 33.6±2.0) ($P<0.001$)compared to control children. The bone marrow megakaryocytes from ITP children showed impaired proplatelet formation, which had more vacuoles instead of new-born platelets, but the size or maturation of nucleus was normal. The RNA-seq of bone marrow megakaryocytes from children with ITP shows decreased expression of ADAM17, Notch and cytoskeleton related genes (ARHGEF, MYO9B), while increased expression of ARHGAP, MYOM1, MYLK. The expression of platelet ADAM17 from ITP children (ITP 44.5±18.1) was also significantly decreased compared to the control group (Ctrl 248.1±18.3) ($P<0.0001$). Fetus of ADAM17 $^{Zn△/Zn△}$ mice exhibited severe thrombocytopenia with bleeding spots in head, neck and abdomen. The induced megakaryocytes from ADAM17 $^{Zn△/Zn△}$fetal liver suspension cells had normal ploidy distribution compared with ADAM17$^{+/+}$ megakaryocytes. The numbers of protruding barbell-like proplatelets in ADAM17 $^{Zn△/Zn△}$ megakaryocytes were significantly decreased. We found the expression of p-MLC was significantly higher in ADAM17 $^{Zn△/Zn△}$ megakaryocytes compared to ADAM17$^{+/+}$ megakaryocytes.

Discussion In this study, we found that the expression of ADAM17 was down-regulated in megakaryocytes/platelets from children with ITP. ADAM17 Zn△/ Zn△ megakaryocytes exhibit poor proplatelet formation and higher expression of p-MLC, a downstream of RhoA signaling pathway. ADAM17 is important in proplatelet formation for thrombopoiesis and lower expression of ADAM17 is possible an innate pathogenesis of pediatric ITP.
Autoantibodies against GPIb/GPIIb in ITP contribute to platelet consumption through over-activation of macrophagocytes and poor platelet production by interfering with megakaryopoiesis. Besides the production of autoantibody, dysregulation of immunity is also involved in ITP pathogenesis. Reduced regulatory T cells cause decreased immunosuppressive effect on B cells (plasma cells) and severe accumulation of CD8+ cytotoxic T cells in ITP which leads to direct platelet lysis. ITP children with negative autoantibody selected in our study, 16 out of 20 had lower CD4+ T cells and higher CD8+ T cells, ADAM17 can cleave L-selectin expressed on CD4+/CD8+ T controlled by myeloid-derived suppressor cells (MDSC) and regulate T cell proliferation or function through LAG-3, but the possible way of altered T cells in regulating the expression of megakaryocyte/platelet ADAM17 is not clear. Study of Bortezomib induced thrombocytopenia during relapsed multiple myeloma therapy shows accumulation of RhoA in megakaryocytes, which enhanced phosphorylation of myosin light chain inhibits proplatelet formation. Cytoskeleton arrangement is vital in proplatelet formation, RhoGTPase is a key switch. At the early stage of megakaryopoiesis, RhoA prevents actomyosin accumulation to facilitate megakaryocyte polyploidization, whereas it is downregulated gradually at the late stage of megakaryopoiesis, We also found increased expression of p-MLC in ADAM17 Zn△/ Zn△megakaryocytes, giving the clues of aberrant cytoskeleton arrangement in megakaryocytes without ADAM17. TNF-α, one substrate of ADAM17, can regulate RhoA by different mechanisms in tubular epithelial cells, further study of TNF-α and RhoA may help to understand the mechanism of ADAM17 in regulating megakaryocyte cytoskeleton arrangement.

PO-0759

四种国产尿液干化学分析仪一致性研究评价

诸佩超
上海市临床检验中心

目的 比较 UA-5800、URIT-1600、U120 Ultra、弘益尿干化学分析仪与 AX-4030 的一致性。
方法 UA-5800、URIT-1600、U120 Ultra、弘益分别与 AX-4030 比较，比较酸碱度（pH 值）、比重（SG）的均值差异百分率，比较尿胆原（URO），胆红素（BIL）、酮体（KET）、潜血（BLD）、蛋白质（PRO）、亚硝酸盐（NIT）、白细胞（LEU）、葡萄糖（GLU）的阳性率和符合率。
结果 UA-5800、URIT-1600、U120 Ultra、弘益与靶机 AX-4030 的 pH 均值差异百分率<10%，SG 均值差异百分率<1%；AX-4030 与 U120Ultra 的 BLD(P<0.01)、PRO（P<0.05）阳性率差异有统计学意义，其它阳性率比较结果无显著差异；非 pH、SG，UA-5800 与 AX-4030 一般符合率 92.2%-99.2%，Kappa 值 0.64-0.92，URIT-1600 与 AX-4030 一般符合率 96.6%-99.1%，Kappa 值 0.75-0.98，U120 Ultra 与 AX-4030 一般符合率 90.4%-97.7%，Kappa 值 0.67-0.88，弘益与 AX-4030 一般符合率 98.5%-100%，Kappa 值 0.94-1。
结论 UA-5800、URIT-1600、U120 Ultra、弘益部分项目由于敏感度不同存在差异，但其所达到的效果基本一致，能够满足基本的临床需要。尿液干化学分析属于一种初筛手段，国产尿机检测速度快，其中 URIT-1600 测试速度 480 个/小时，弘益测试速度 500 个/小时，能满足大样本医院的测试需求；同时这四种国产性能比较高，能满足市场需求。

PO-0760

利用六西格玛方法优化生化免疫自动审核系统

孟国艳
昆明市第一人民医院

目的 探索利用六西格玛精益管理方法改进并优化已实施的生化免疫自动审核系统的效率。
方法 六西格玛是一套系统的、集成的业务改进方法体系，通过 DMAIC 流程，在已经实施的生化免疫自动审核系统中相关项目的通过率等有关数据作为现状调查数据，查找原因并确定主要原因，优化自动审核的流程，消除自动审核过程中的缺陷和无价值作业。比较利用六西格玛精益管理方法改进优化前后自动审核系统的通过率、真阳性率、真阴性率和假阳性率的变化，并制定下一步改进计划。
结果 生化免疫项目自动审核通过率由 63.61%提升至 83.22%，检测项目的样本周转时间（TAT）由 2.3 小时缩短至 1.5 小时。
结论 使用六西格玛精益管理的方法可以有效推进自动审核系统效率提升，保证自动审核系统高效运行，该方法亦可用于实验室其他项目自动审核系统的改进。

PO-0761

亚抑菌浓度苯唑西林诱导金黄色葡萄球菌临床株 Lpl 脂蛋白表达的作用

蒋苳芳
贵州航天医院

目的 探讨亚抑菌浓度 β-内酰胺类抗菌药物对金黄色葡萄球菌临床株脂蛋白 Lpl 的诱导作用。
方法 遴选我国主要流行克隆群 CC239(ST239)中的菌株作为实验对象，在检测菌株抗生素敏感性的基础上，采用亚抑菌浓度苯唑西林（OXA）进行处理，SDS-PAGE 分析菌体蛋白；制备重组 Lpl-His 蛋白及其多克隆血清，采用 Western blot 对诱导蛋白进行鉴定。
结果 遴选的 6 株 ST239 型临床分离的 MRSA 菌，抗菌药物敏感性检测显示 t030 和 t037 菌株对利福平和复方新诺明的敏感性呈相反趋势，但都能在亚抑菌浓度 OXA 诱导下产生一约 30 kDa 的蛋白质，经制备脂蛋白 Lpl 抗体，Western blot 鉴定该受 OXA 诱导表达的蛋白质为金葡菌 Lpl，其诱导作用具有剂量依赖效应。
结论 亚抑菌浓度苯唑西林可诱导金葡菌 MRSA 临床分离株产生脂蛋白 Lpl，该诱导蛋白在金葡菌致病性中的作用值得深入研究。

PO-0762

Analysis of PLXNA1, NRP1 and NRP2 variants in a cohort of patients with isolated hypogonadotropic hypogonadism

Wenting Dai[1]、meichao Men[2]、Dan-na Chen[3]、Jia-da Li[4]、Xinying Wang[4]、Wang Zeng[4]、Fang Jiang[4]、Ruizhi Zheng[5]
1. Zhuzhou Central Hospital
2. 湘雅医院
3. 长沙医学院
4. 中南大学生命科学院
5. 河南省人民医院

Backgroud Isolated hypogonadotropic hypogonadism (IHH) is a clinical syndrome described by failure of gonadal function secondary to defects on the synthesis, secretion or action of the gonadotropin-releasing hormone (GnRH). The secreted glycoprotein SEMA3A binds its receptors NRP1 or NRP2 to located correct GnRH neuron migration, with an additional role of the NRP co-receptor PLXNA1. Therefore, variants in NRP1, NRP2 and PLXNA1 have been related to defective GnRH neuron development in mice and inherited GnRH deficiency in humans.
Method Whole-exome sequencing and pedigree analysis were performed to examine the genotypic and phenotypic spectra of these genes in a large cohort of IHH probands from China.
Results We identified ten heterozygous missense variants in PLXNA1, five heterozygous missense variants in NRP1, and two heterozygous missense variants in NRP2. NRP1 variants were found only in KS individuals and were strongly linked to hearing loss (25%, 2/8). 85.00% (17/20) of patients also harbored variants in other IHH-associated genes.
Conclusion Our study greatly enriched the genotypic and phenotypic spectra of PLXNA1, NRP1 and NRP2 in IHH. Our results may conducive to the genetic counseling, diagnosis, and treatment of IHH with mutations in PLXNA1, NRP1and NRP2 gene. Furthermore, Our results indicated that NRP1 were strongly linked to hearing loss (2/8 individuals). Moreover, whether the SEMA3A-NRP1 pathway interact with PROK2-PROKR2 pathway in the development of GnRH neurons is worth further study.

PO-0763

The AST/ALT Ratio (De Ritis) represents an unfavorable prognosis in patients with SFTS in early-stage based on exploration of clinical characteristic: An observation cohort study

Lianzi wang、yuanhong Xu
Department of Clinical Laboratory, the First Affiliated Hospital of Anhui Medical University, No. 218 Jixi Road, Hefei, Anhui, 230032, China

Background Severe fever with thrombocytopenia syndrome (SFTS), a wide distribution infectious disease caused by SFTSV with a high mortality which became a threat to public health, in this research, we aimed to investigate the epidemiological and clinical characteristics of patients infected with SFTS, further looking for prognostic risk factors for SFTS.
Methods In this retrospective and cross-sectional study, we enrolled patients from the First Affiliated Hospital of Anhui Medical University confirmed SFTS from September 1, 2019 to December 12, 2020. Cases were analyzed for epidemiological, demographic, clinical, and laboratory data. Logistic regression models were used to assess the association between predictors and outcome variables. A generalized additive mixed model (GAMM) was conducted to

analyze the change trend of AST/ALT in SFTS patients received ribavirin. P values ≤ 0.05 were considered statistically significant.
Results Clinical and laboratory results of 107 hospitalized patients with SFTSV infection were retrospectively described. Mean age at the onset of the disease was 60.38±11.29 years old and the ratio between male and female was 1:1.2. Fever and thrombocytopenia were the most typically feature of SFTS, furthermore, many patients accompanied by neurological complications, gastrointestinal symptom, muscle symptoms and other nonspecific characteristic, and the data of laboratory results showed an abnormal in markers of blood routine, coagulation function and biochemical.
107 patients were grouped into two group according to the status of patients in the end,
survivors had a higher level of PLT counts, TP and eGFR, meanwhile, level of APTT, TT, D-D, FDP, ALT, AST, AST/ALT-ratio, Creatinine, CK, LDH and PCT was higher in non-survivors, results from univariate cox regression revealed that elevated level of FDP, TT, AST/ALT-ratio and PCT as well as decreased level of eGFR and patients with central nervous system symptoms were significant predictors for prognostic of SFTS, results from multivariate logistic regression analysis in three adjusted models showed AST/ALT-ratio was an independent risk factor for prognosis of SFTS patients, Kaplan–Meier survival analysis showed that SFTS patients with AST/ALT-ratio >2.683 was associated with a shorter futime therefore indicated an unfavorable prognosis in all three adjusted models. Treatment of ribavirin may increase platelet counts meanwhile decrease AST/ALT-ratio of SFTS patients.
Conclusion SFTS is an emerging infectious disease, could lead to a multiple organ injury, AST/ALT-ratio was an independent risk factor for prognosis of SFTS patients,
further investigation should be done in order to better understand this disease and guide the clinical treatment.

PO-0764

AKT 抑制剂 Perifosine 对非酒精性脂肪性肝病（NAFLD）进展的促进作用

荆振唐
山东大学第二医院

目的 明确 AKT 抑制剂 Perifosine 是否促进 NAFLD 进展。
方法 通过高脂饲料喂养建立小鼠（C57BL/6、BALB/c）非酒精性脂肪性肝病模型，在给予高脂饲料喂养第 5 周后，将小鼠随机分组并对小鼠进行 DMSO 或 Perifosine 每日腹腔注射。通过各种生化、病理及分子生物学技术研究手段，研究 Perifosine 在体内外通过对 AKT 的抑制影响 FLIP，进而对 NAFLD 进展产生影响。
结果 通过高脂饲料的喂养，成功建立 C57BL/6 和 BALB/c 脂肪肝模型，Perifosine 组小鼠整体体重水平高于 DMSO 组。同时采血检测显示，Perifosine 组小鼠血脂、转氨酶水平高于 DMSO 组，肝脏 HE 染色、油红 O 染色显示 Perifosine 组病理学损伤程度较重。进一步研究表明，Perifosine 通过抑制 AKT，使 AKT 磷酸化水平降低，从而下调 FLIP 的表达，FLIP 是脂肪性肝炎及其代谢异常的关键抑制剂，从而导致实验小鼠 NAFLD 的进展加快，促进发展。
结论 Perifosine 通过抑制 AKT 活化，下调 FLIP 表达，增加小鼠脂肪性肝炎及其代谢异常的发生率，使得 NAFLD 进展加快。提示 AKT 抑制剂类药物的使用可能会加速 NAFLD 的进展。

PO-0765

HBV 编码的 miRNA 通过激活机体先天免疫来抑制 HBV 复制

赵晓晴
山东大学第二医院

我们之前的研究发现乙型肝炎病毒 (HBV) 可以编码一种 microRNA (HBV-miR-3)，它可以通过靶向 HBV 转录本来抑制 HBV 的复制。然而，HBV-miR-3 是否通过影响宿主先天免疫来调节 HBV 的复制尚不清楚。在这里，我们探究了 HBV-miR-3 在 HBV 感染后先天免疫反应中的重要功能。我们发现在 HBV 感染的 HepG2-NTCP 细胞中 HBV-miR-3 的表达以剂量和时间依赖性方式逐渐增加。HBV-miR-3 通过激活 JAK/STAT 信号通路下调肝细胞中的 SOCS5 的表达来增强干扰素诱导的抗病毒作用。此外，HBV-miR-3 可以通过外泌体转运作用于巨噬细胞从而促进了其向 M1 的转化。另外，含有 HBV-miR-3 的外泌体通过抑制 SOCS5 介导的 EGFR 泛素化来促进 IL-6 的分泌。简而言之，这些结果表明 HBV-miR-3 可以激活先天免疫反应，通过多种途径抑制 HBV 复制，从而抑制 HBV 诱导的急性肝细胞损伤并影响持续性 HBV 感染的进展。

PO-0766

溶酶体功能在自噬介导卵巢癌顺铂耐药的机制研究

马丽伟
郑州大学第一附属医院

目的 探讨溶酶体参与了自噬介导卵巢癌顺铂耐药性机制研究。
方法 MTT 法检测细胞生存率; 免疫荧光检测自噬相关蛋白 p62 和 LC3 变化，再通 LysoTracker 染色观察溶酶体变化; cathepsin D 试剂盒检测酶活性改变; 流式细胞术检测细胞凋亡; Western blot 检测凋亡相关蛋白表达。
结果 对于不同浓度的顺铂，SKOV3 /DDP 细胞比 SKOV3 细胞的生存率高; 6 mg /L 的顺铂作用下，与 SKOV3 细胞相比，在 6 h、12 h 和 24 h，SKOV3 /DDP 细胞 LC3 的表达增高，p62 逐渐下降，LysoTrakcer 着色增强， cathepsin D 活性增高; 与自噬抑制剂 3-MA 相比，CQ 更加明显地增加顺铂诱导 SKOV3 /DDP 细胞的凋亡率($P < 0.05$) ，LysoTracker 着色明显减弱， cathepsin D 活性降低，细胞色素 C、cleaved caspase-3 和 Bax 表达增加，Bcl-2 表达降低($P < 0.05$) 。
结论 卵巢癌耐药细胞自噬水平增加、利用氯喹等抑制细胞溶酶体从而抑制细胞自噬能够增加化疗药物的敏感性，因此，我们推测溶酶体或许是介导肿瘤化疗药物耐受的重要决定因素，这可能主要是通过溶酶体内 ATP 维护溶酶体功能和稳态，维持自噬的流量，从而介导癌症细胞对化疗药物的耐药。本研究以人卵巢癌细胞 SKOV3 细胞和 SKOV3/DDP 细胞为研究对象，基于 ATP 影响溶酶体功能调控自噬通量，探讨溶酶体参与卵巢癌顺铂耐药性的作用机制，为肿瘤化疗药物耐受的治疗提供新的策略。

PO-0767

胎肾组织微环境对 hiPSCs 定向分化的诱导作用研究

李开霖、孙超、刘晓立、赵升田
山东大学第二医院

终末期肾病是指各种慢性肾脏疾病的终末阶段，具有高发病率和高致死率的特点，是世界范围内危害人类健康的公共卫生问题。目前临床上针对终末期肾病较为理想的治疗方式是肾移植，移植后，生存期较长，患者可以保证基本生活质量。但是肾移植面临的最大问题是肾源缺乏，大多数终

末期肾病患者只能通过透析来维持生命，在等待中经受痛苦甚至死亡。利用再生医学技术构建结构成熟、功能良好、可移植的新肾脏，既可以解决肾源短缺问题，也可以作为慢性肾病的模型探究其发病机制，因此，肾脏再生研究具有重要的研究意义和临床价值。

根据对哺乳动物肾脏器官发生的现有认识，现在有许多关于通过定向分化人类诱导多能干细胞（hiPSCs）生成人肾脏类器官的报道。肾脏类器官在人类肾脏发育、疾病模拟和肾脏再生等方面都有广阔的应用前景。然而，这种类器官模型的实用性最终将取决于它们的发育准确性。通过文献检索和本团队的前期研究，我们发现肾脏类器官研究存在两个急需解决的关键问题：一、传统方法使用生长因子和化合物诱导 hiPSCs 定向分化存在诱导效率低、肾单位成片段状的问题，大量非肾细胞的存在导致肾脏类器官的结构和功能成熟度较低；二、大量诱变剂的使用导致体内研究存在生物安全性问题。为解决上述问题，我们研究团队根据胚胎肾脏早期的发育特征，设计了一种新颖的生物诱导方法，利用胎肾发育微环境诱导 hiPSCs 定向分化。采取的研究方案如下：将大鼠胚胎肾制成单细胞悬液，与 hiPSCs 共培养至 3D 结构，结果显示胎肾组织微环境对 hiPSCs 定向分化的诱导作用显著，诱导效率和结构成熟度相比传统方法更高，该过程的关键分子机制本课题组正在研究中。本课题的研究成果为解决当前肾脏类器官研究面临的瓶颈问题提供了新思路。与传统的化学方法相比较，该技术更符合肾脏发育的一般规律，也具有更高的生物安全性。

PO-0768

云南地区 816 例新生儿细胞遗传学检测结果分析

冷玉春
昆明金域医学检验所有限公司

目的 对云南地区 816 例新生儿的细胞遗传学结果进行分析，为倡导本地区产前筛查和产前诊断的重要性提供科学依据。
方法 对 2019 年至 2020 年送至我公司的 816 例新生儿的外周血样本分别抽取 0.1ml、0.2ml、0.3ml、0.4ml 梯度接种至外周血淋巴细胞培养基进行培养，制备 G 显带标本，进行核型分析，按照《ISCN》（2016）描述核型。
结果 816 例新生儿中检出染色体异常 162 例，涉及异常核型 42 种（不包括染色体多态性），染色体异常检出率 19.85%（162/816），其中常染色体异常 153 例，性染色体异常 9 例。常染色体异常中 21-三体 133 例，占染色体异常结果的 82.10%（133/162），包括标准型 121 例、易位型 7 例以及嵌合型 5 例。检出 18-三体 5 例，占染色体异常结果的 3.09%（5/162）。
结论 云南地区新生儿染色体异常检出率较高，其中大多数为三体患儿，建议进一步加强本地区一、二级预防措施的实施，减少缺陷患儿的出生。

PO-0769

偏离度分析模型在体外诊断试剂成本管控中的应用

田丽、夏洪韬、赵明才、胡娟、杨国庆
遂宁市中心医院

目的 分析试剂成本率偏离原因，为优化资源使用效率和科学决策提供参考。
方法 以四川省某三甲公立医院开展的 112 个检验项目为研究对象，利用回顾性分析建立标准值，运用偏离度分析模型对数据进行研究。
结果 （1）2018-2020 年试剂成本和试剂成本率逐年上升，与检验总人次和检验收入变化趋势不一致；（2）试剂成本率标准值 33.26%，试剂单位成本标准值 4.89 元/人份，利用效率标准值 77.50%；（3）2020 年试剂成本率偏离度 4.87%；（4）利用效率、试剂单位成本、检验人次对该

院 2020 年试剂成本率偏离度的影响分别为 4.14%、0.46%和 0.27%；（5）试剂成本率正偏离的检验项目有 90 个，负偏离有 22 个；（6）前十项检验项目导致试剂成本率偏离 2.60%。
结论 （1）树立精细化管理意识，应用科学监督工具，实时评估分析试剂成本管控情况，找出运营存在问题，有针对性地采取措施，以达到试剂成本的合理管控；（2）建立标准值和偏离度分析模型能有效填补监管漏洞，实时、真实地呈现各个因素间和各检验项目间的关系和影响，有利于厘清责任科室和具体因素，提高医院科学管理水平；（3）医院应自上而下重视试剂成本的精细化管理。医院决策层应重点关注影响大的检验项目，从医院整体层面分析评估和制定措施；科室管理层应动态监测试剂单位成本或利用效率偏离度高的检验项目，及时挖掘深层次原因，采取适宜管控措施，避免潜在风险。

PO-0770

Improving equivalence in fibrinogen evaluation between the prothrombin time-derived fibrinogen assay and Clauss method using a pooled plasma calibrator

Sheng Wang、Xiaoyong Duan、Yan Zhang、Liuchun Wu、Xingtai Liu
Sinopharm Gezhouba Central Hospital

Aims Both the Clauss and Prothrombin Time-derived fibrinogen (PT-Fib) methods have widely been used in fibrinogen (Fib) evaluation. We aimed to improve the interchangeability between these two methods.
Methods Thirty fresh plasmas of low, normal, and high Fib concentration were mixed to prepare the pooled human plasma. The Fib concentration was assessed by the Clauss method. The PT-Fib values were further recalibrated by the assigned plasma pools and the precision, linearity and reference intervals were verified according to the guidelines of American Society for Clinical and Laboratory Standards (CLSI) EP15-A and EP6-A documents. Finally, the recalibrated PT-Fib method was compared with Clauss method by the simultaneous Fib test of total 5268 coagulation samples.
Results The results indicated that the recalibrated PT-Fib method can detect the Fib concentration with clinically acceptable third-order linearity in the range of 1.27-8.00 g/L. Only one result out of 39 healthy people tested using the recalibrated PT-Fib method did not fall within the reference range defined by the manufacturer. We also found more than 99% of results between these two methods were interchangeable in the range of 1.51 to 8.00 g/L. The disagreement between these two methods was found only in patients with certain underlying conditions.
Conclusions After recalibrattion, the consistency between the PT-Fib and Clauss methods was enhanced and the interchangeability was improved. The application of the recalibrated PT-Fib method provided accurate and reliable results with the manufacture provided reagents and improved detection speed and cost-effectiveness.

PO-0771

运用 6sigma 管理方法缩短门诊凝血实验室内周转时间的研究

郑欣、胡骏、张雪清、张俊、姚冬婷、胡晓波
上海中医药大学附属龙华医院

目的 探讨运用 6sigma 管理方法缩短门诊凝血实验室内周转时间 (TAT) 的效果。
方法 通过界定、测量、分析、改进、控制五大步骤，对门诊凝血实验室内 TAT 较长的主要原因进行调查分析，找出其中的关键因素，并针对性地制定改进方案和控制计划。

结果 经过七个月的持续质量改进后，门诊凝血实验室内 TAT 显著缩短，中位数 M 由 127.5 min 缩短到 66 min,达标率由 47.0 %提高到 93.9 %，百万机会缺陷数 (DPMO) 由 530 035 ppm 降低到 61 002 ppm。分别采用 Mood 中位数检验和双比率检验对改进前后的数据进行统计，结果显示改进前后 TAT 和 TAT 达标率的差异均具有统计学意义 (P＜0.05)。
结论 本研究采用 6sigma 管理方法，通过基线数据分析和头脑风暴，找出了影响门诊凝血实验室内 TAT 的关键未落实原因，并针对性地进行改进，最终取得了明显成效。将 6sigma 管理理念引入检验科的质量管理体系，有利于深挖潜在的、隐藏的问题，进而解决问题，持续改进，不断促进检验的发展与进步，在实验室管理方面具有推广价值。

PO-0772

衍生化及非衍生化串联质谱法在遗传代谢疾病筛查诊断中的应用及比较

张瑞、周磊、杨柳、刘家云
空军军医大学西京医院

目的 考查并比较了衍生化和非衍生化串联质谱（MS/MS）法在测定 11 种氨基酸和 22 种酰基肉碱中的应用及意义，为其有效防治遗传代谢病的精准诊疗提供更为科学依据。
方法 利用衍生化 MS/MS 法和非衍生化 MS/MS 法分别分析比较了 1060 例出生 3 天至 1 岁儿童的干血滤纸片。采足后跟血于空白采血滤纸上，完全渗透。衍生化法：用已知浓度的同位素内标萃取液萃取干血滤纸片中的 33 种待测物质, 经过 20 分钟衍生化反应后, 用串联质谱仪分析血片中 33 种待测物质的质谱谱图并计算其浓度；非衍生化法：用已知浓度的同位素内标萃取液萃取干血滤纸片中的 33 种待测物质, 加热震荡 45 分钟后, 用串联质谱仪分析血片中 33 种待测物质的质谱谱图并计算其浓度。
结果 非衍生化串联质谱法的批内 CV 为 2.06-7.39%，批间 CV 为 3.64-10.97%；衍生化串联质谱法的批内 CV 为 4.14-10.95%，批间 CV 为 6.14-12.91%。经统计学分析男、女之间氨基酸和酰基肉碱含量无显著性差异(P>0.5)。
结论 衍生化法与非衍生化串联质谱法进行血滤纸片氨基酸和酰基肉碱分析, 均有较高的回收率, 能够达到较高的精确性和准确性,其中非衍生化法简便易行，样本处理步骤少时间短，但是衍生化法灵敏度更高检出限更低，两种方法均能灵敏，特异地测定血中氨基酸和酰基肉碱浓度，满足临床对遗传代谢疾病筛查及诊断的需要。

PO-0773

信息管理系统改进在凝血功能常规检验分析前阶段中的应用及效果评价

马跃飞、欧启水
福建医科大学附属第一医院

目的 评价信息管理系统改进在凝血功能常规检验分析前阶段中的应用效果。
方法 完善信息管理系统,改进相关功能。对比信息管理系统改进前（2012 年 10 月至 2014 年 6 月）和改进后（2014 年 7 月至 2016 年 3 月）相同时间段内凝血功能常规检验的分析前错误数量和比例、TAT 的变化。观察"不规范报告数"、"临床投诉量"和"满意率"等指标是否优化以评价信息管理系统改进后的效果。

结果 改进了信息管理系统的监控和提醒功能,包括实现对标本全过程各节点的实时监控功能、增加患者采集信息的条目、增加采集和送检提醒功能和信息反馈功能、报警功能等。信息管理系统改进后分析前错误数量和比例下降（采集量不符合要求 0.61%vs 0.20%,标本凝固 0.41%vs 0.26%,溶血或脂血 0.067%vs 0.038%,TAT 超时 0.23%vs 0.098%,患者基本资料不全 0.16%vs 0.038%）。标本运送反应时间（TAT1）、送检时间（TAT2）、实验室报告时间（TAT3）的中位数值和 TAT1+TAT2、TAT3 的离群值占比均下降。标本在检验科之外的流转时间减少了 10.5 min。评价指标上,由分析前错误导致的"不规范报告数"由 7 份减少到 3 份,"临床投诉量"由 5 次降为 2 次,临床对凝血功能常规检验流程和结果的总体满意率由 89.7%上升为 96.0%。
结论 改进信息管理系统能有效监控凝血功能常规检验分析前影响因素,减少实验室不易觉察的分析前错误,是保证检验质量的重要举措。

PO-0774

M2 巨噬细胞与非小细胞肺癌不良预后的相关性

王云杰
西安医学院第一附属医院

巨噬细胞是肿瘤微环境中重要的免疫细胞，在肿瘤的发生与进展中扮演着重要的角色。在肿瘤微环境中，肿瘤细胞将巨噬细胞等募集至周围，微环境发生改变，巨噬细胞的表型随之而改变，可极化为促肿瘤的 M2 型，以及抑制肿瘤的 M1 型。M2 型巨噬细胞能够促进肿瘤微环境血管的生成，帮助肿瘤细胞逃避机体免疫监视，促进其生长。肺癌目前仍是全世界癌症的主要死亡原因，而非小细胞肺癌（non-small cell lung cancer，NSCLC）占原发性肺癌的 85%以上，其中 70%NSCLC 为鳞癌(squamous cell carcinoma) 或者腺癌(adenocarcinoma)。在中国，肺癌是发病率和死亡率最高的恶性肿瘤，且晚期肺癌患者 5 年生存率仍低于 15%众多研究表明，巨噬细胞与肿瘤的预后具有具有一定的相关性。此篇文章，将对巨噬细胞在非小细胞肺癌中的分布以及巨噬细胞表型与人类非小细胞肺癌预后的关系进行讨论。

PO-0775

WTAP facilitates progression of endometrial cancer via CAV-1/NF-κB axis

Qin Li
Yantai Yuhuangding Hospital

The N6-methyladenosine (m6A) modification is one of the most prevalent methylations in eukaryotic mRNA and it is essential for the development of many important biological processes as multiple types of tumors. One of the most important enzymes catalyzing generation of m6A on mRNA is Wilms' tumor 1-associating protein (WTAP), however, the potential role of WTAP in endometrial cancer (EC) still remains unknown. Here, we investigated WTAP expression level in cancer tissue and paracancerous tissue from EC patient. Subsequently, WTAP was knocked down by siRNA in endometrial cancer cell line of Ishikawa and HEC-1A respectively. Cell proliferation, migration and invasion were studied. The expression of Caveolin-1 (CAV-1) was detected by qPCR. The enrichments of m6A and METTL3 on CAV-1 were detected using RIP-qPCR. The activity of NF-κB was studied using Western Blot. We observed that WTAP was dramatically up-regulated in cancer tissue, and enhanced cell proliferation, migration and invasion and decreased apoptotic in EC in vivo and in vitro, which indicated higher tumor malignancy and worse survival outcome. After WTAP was knocked down in EC cells, CAV-1 was significantly upregulated, and the enrichments of m6A and METTL3 at 3'UTR region of CAV-1 were decreased. Moreover, the activity of NF-κB signaling pathway was inhibited by its regulator CAV-

1. Taken together, we concluded that WTAP could methylate 3'UTR of CAV-1 and downregulate CAV-1 expression to activate NF-κB signaling pathway in EC, which promoted endometrial cancer progression.

PO-0776

Exosomal miR-451a in serum correlates with clinical stage in pancreatic cancer patients

Jia Chen、Weiqin Chen、Zhen Li、Xiaobo Hu
Department of Laboratory Medicine, Longhua Hospital, Shanghai University of Traditional Chinese Medicine

Objectives The aim of this study was to explore the diagnostic efficiency of serum exosomal miR-451a as a novel biomarker for pancreatic cancer (PC).
Methods Serum samples were collected prior to treatment. Firstly, we analyzed miRNA profiles in serum exosomes from 8 PC patients and 8 healthy volunteers. We then validated the usefulness of selected miRNAs as biomarkers using the other 138 PC patients and 49 healthy controls.
Results miR-451a is significantly upregulated in serum-derived exosomes from PC patients compared to expression in those from healthy individuals. Serum exosomal miR-451a had better diagnostic power than CA19-9 in identifying PC patients. In addition, exosomal miR-451a showed a significant association with clinical stage in PC and had better diagnostic performance on late-stage patients. And it was a frequent event that miR-451a was upregulated in pancreatic cancer tissues.
Conclusions Serum exosomal miR-451a might serve as a new diagnostic marker for PC diagnosis and malignancy assessment.

PO-0777

糖尿病小鼠模型中 FGF15 对肝糖代谢的影响

陈茜
山东大学第二医院

背景 成纤维细胞生长因子 15（FGF15）是由远端回肠表达和分泌的细胞因子，它可以通过内分泌方式调节肝糖代谢。减肥手术后，BAs 和 FGF15 均升高。
实验方法 通过高脂饮食和链脲佐菌素诱导肥胖的糖尿病大鼠模型，并分为 SHAM 组和 SG 组。 在手术后第 12 周评估 SG 的减肥和抗糖尿病作用。 然后，我们在手术后第 12 周检测了血清和门静脉中的 TBA 以及 FXR 激动型胆汁酸亚型的水平。然后我们通过 PAS 染色试剂盒和糖原测定试剂盒对肝糖原含量进行了染色和检测，并通过 RT-PCR 检查了肝糖异生的关键酶的表达水平。最后，检测回肠 FXR，FGF15 和肝 FGFR4 的组织表达及其与葡萄糖代谢有关的信号通路。
研究结果 SG 手术组大鼠肝脏中糖原含量和 PAS 阳性细胞百分比明显高于 SHAM 组。 此外，SG 组 G6Pase 和 PEPCK 的 mRNA 水平显著下降。 另外，SG 组的血清和门静脉的 TBA 水平显着高于 SHAM 组。 根据 RT-PCT 和免疫组织化学结果，SG 组回肠 FGF15 和肝 FGFR4 的 mRNA 和蛋白表达水平均显着升高。此外，与 SHAM 组相比，SG 手术大鼠的 FXR mRNA 水平也显着升高。免疫印迹结果表明，在 SG 操作的大鼠中 ERK1 / 2 的磷酸化增加，而 GS 的磷酸化被抑制。另外，SG 组 CREB 的磷酸化程度下降和 PGC-1α 的表达下降说明 CREB-PGC-1α 途径的抑制。
结论 SG 术后升高的胆汁酸通过激活受体 FXR 诱导回肠远端 FGF15 表达。而且，活化的 FGF15 对肝糖原合成和糖异生的作用有助于进一步 SG 的抗糖尿病作用。

PO-0778

82 例常德市新型冠状病毒肺炎患者的实验室指标分析

仇玄、张瑶、林立中、王丽志、和珂莉、吴建华
常德市第一人民医院

目的 回顾性分析新型冠状病毒肺炎患者首次入院的临床特征和相关实验室检测结果。
方法 收集 2020 年 1 月 24 日到 3 月 9 日期间常德地区 82 例 COVID-19 患者首次入院时一般临床资料、患者入院后首次实验室检查结果。将入组患者分为非重症组和重症组，比较两组之间实验室检查的差异，寻找新冠肺炎重症患者的危险因素。
结果 82 例 COVID-19 患者中非重症患者 60 例、重症患者 22 例。首诊症状主要为发热（52 例）、咳嗽（48 例）、咳痰（12 例）等。与非重症组相比，重症组血常规中的淋巴细胞计数显著降低，中性粒细胞与淋巴细胞比值、超敏 C 反应蛋白（CRP）、血沉（ESR）显著增加，差异均有统计学意义（P<0.05）；重症组白蛋白显著减少，天冬氨酸转氨酶、肌酸激酶同工酶、D-二聚体显著增加，差异均有统计学意义（P<0.05）。NLR 为分析新型冠状病毒肺炎重症的显著影响因素，即 NLR 每增加 1 个单位，患重症新型冠状病毒肺炎概率增加 1.212（1.003, 1.465）倍。NLR、ESR、降钙素原（PCT）为联合预测重症新冠肺炎的最优模型，其 AUC 为 0.767，灵敏度为 66.7%，特异度为 87.3%。
结论 COVID-19 患者首次入院部分实验室指标出现特征性改变，且重症患者实验室指标改变也具有特异性，NLR、ESR、PCT 可作为联合预测重症新冠肺炎的模型。本结果为新冠肺炎重症患者的早期识别和治疗方案的制定提供实验室参考依据。

PO-0779

持续性高危型 HPV 感染女性的男性配偶中 HPV 的感染率及其与女性感染的基因型一致性分析

王丽娜
山东大学第二医院

目的 HPV 感染是最常见的性传播感染之一。持续性高危型 HPV（hrHPV）感染是导致宫颈癌发病的主要原因之一，然而 hrHPV 感染阳性女性的性伴侣 HPV 患病率和基因型分布了解甚少。本项研究旨在研究 hrHPV 阳性女性的男性性伴侣的 HPV 患病率和基因型分布，评估 hrHPV 感染和伴侣之间的类型特异性和一致性。
方法 2019 年 1 月至 2020 年 6 月在山东大学第二医院进行子宫颈癌筛查妇女性，选择 208 例 hrHPV 阳性且持续一年以上的女性与其稳定的男性伴侣同时入组。 所有受试者均通过 cobas 4800 HPV DNA 检测对 HPV 基因分型试验进行了测试，女性患者同时进行薄层液基细胞学检查。
结果 208 例 hrHPV 阳性女性中，HPV16/18 感染阳性患者 46 例，其余 162 例为其他 12 种 hrHPV 阳性。其 208 例男性配偶中，138 例 hrHPV 阳性，HPV16/18 感染阳性者 26 例，其余 102 例为其他 12 种 hrHPV 阳性；且 HPV16/18 感染女性与配偶 HPV 感染一致性为 26/46（56.5%），其他 12 种 hrHPV 感染女性与配偶 HPV 感染一致性为 70/162（43.2%）。
结论 我们证明了 HPV 男性感染的高流行以及感染分型与性伴侣之间的相关性。

PO-0780

Progranulin 在 FSGS 中的作用及机制研究

李荃新
山东大学第二医院

目的 局灶性节段性肾小球硬化（FSGS）病理生理机制尚不明晰，但肾小球足细胞损伤是促进其发生发展的重要始动因素。最新研究表明，Progranulin 参与肾脏疾病的发生。表观遗传调节因子 Progranulin 是 DNA 甲基化和组蛋白泛素化的调控因子，在胚胎的发育及肿瘤的发生中扮演重要角色，但在肾脏疾病中的作用知之甚少。我们前期工作证实，Progranulin 在 FSGS 足细胞中表达显著降低并加重足细胞损伤，过表达 Progranulin 明显减少足细胞凋亡并抑制 Notch1 的表达。本课题探究 Progranulin 在 FSGS 中的作用及调控机制。
方法 本课题运用 cre-loxp 技术构建足细胞 Progranulin 敲除小鼠等手段深入研究 Progranulin 在 FSGS 足细胞损伤中的作用及探讨自噬信号通路在足细胞中的分子调控机制；并进一步以腺相关病毒为载体过表达 Progranulin 作为 FSGS 治疗手段的初步探究。
结果 Progranulin 在 FSGS 肾脏组织中表达降低，敲除 Progranulin 可以进一步加重阿霉素诱导的肾脏损伤，过表达 Progranulin 可以减轻在 FSGS 足细胞损伤，Progranulin 可以通过调控足细胞的自噬水平调控足细胞损伤。
结论 在 FSGS 中，Progranulin 的缺失通过调控足细胞自噬加重足细胞损伤，Progranulin 可能作为 FSGS 治疗的潜在靶点。

PO-0781

Polybrominated diphenyl ethers and decabromodiphenyl ethane in paired hair/serum and nail/serum from corresponding chemical manufacturing workers and their correlations to thyroid hormones, liver and kidney injury markers

Dong Yu
Shandong Academy of Occupational Health and Occupational Medicine,Shandong First Medical University & Shandong Academy of Medical Sciences

We detected the polybrominated diphenyl ethers (PBDEs) or decabromodiphenyl ethane (DBDPE) in paired hair-serum and nail-serum samples collected from the corresponding chemical manufacturing workers. The levels of decabrominated diphenyl ether (BDE-209) or DBDPE in the serum, hair and nail samples were all signif- icantly higher than those reported in other studies, and the “work place” (pretreatment or posttreatment work- shop) was the primary influencing factor that affected the levels of specific BFRs in vivo. For BDE-209 workers, the BDE-209 in both the hair and nail samples were significantly and positively related to the BDE-209 in the serum, indicating that both hair and nails can be used as noninvasive biomatrices to reflect internal exposure to BDE-209. In DBDPE workers, hair rather than nails was more suitable for use as a noninvasive biomatrix to infer the DBDPE exposure level. A series of serum biomarkers reflecting thyroid hormones and liver and kidney injuries were tested to calculate the correlations between hair or nail BFR levels and the levels of the biomatrices. The BDE- 209 in the hair samples was significantly and positively correlated with the total protein (TP), and the nail BDE-209 level was significantly and positively related to the total bilirubin (TBIL), indirect bilirubin (IDBIL)

PO-0782

铜绿假单胞菌 crpP 基因和携带 crpP 的整合性接合元件研究

朱志宸[1]、杨慧盈[2]、杜鸿[1]、周冬生[2]
1. 苏州大学附属第二医院
2. 北京微生物学与流行病研究所

目的 crpP 是一种新型的氟喹诺酮类药物耐药基因，主要位于铜绿假单胞菌携带的整合性接合元件（integrative and conjugative element，ICE）上。crpP 基因和携带 crpP 的 ICE 的多样性和流行性仍待阐明。本研究旨在为 crpP 基因和携带 crpP 的 ICE 提供深入的生物信息学和流行病学见解，为后续相关研究提供理论依据。
方法 使用二代或三代测序技术获得菌株全基因组序列，通过生物信息学分析鉴定 crpP 基因及携带 crpP 的 ICE 并统计它们的流行率及分布状况；通过系统发育分析制定 crpP 基因亚型和携带 crpP 的 ICE 的分型/命名方案；通过克隆和药物敏感性实验评估 CrpP 酶对喹诺酮类药物敏感性的影响；通过精细注释和比较基因组学分析确定携带 crpP 的 ICE 的遗传学特征。
结果 1. 37 种 crpP 基因亚型可被划分至 6 个初级分组（crpP-1 至 crpP-6），crpP-1 分组的基因主要分布在铜绿假单胞菌中。
2. 6 种 CrpP-1 分组的 CrpP 酶被证实能介导菌株对氟喹诺酮类药物敏感性下降。
3.携带 crpP 的 ICE 因具有高度保守的 45 bp 序列左端和右端附着位点，并显示出相似的骨架基因排列构成，而定义为一个新的 Tn6786 家族。这些 ICE 可被划分成 4 组（A 组至 D 组），且详细的遗传解剖分析显示 22 个代表性的携带 crpP 的 Tn6786 类 ICE 在核苷酸序列和模块结构上都表现出高度的多样性。
4.crpP 基因在我国临床分离的铜绿假单胞菌中的阳性率为 53.5%（107/200），且都位于染色体携带的涵盖了上述四个分组的 Tn6786 类 ICE 中。
结论 crpP 基因在我国临床分离的铜绿假单胞菌中普遍存在，且都位于染色体携带的 Tn6786 类 ICE 中。这类 ICE 正处于进化的活跃阶段，并很有可能成为除了 crpP 外其余细菌有益基因传播的重要载体。

PO-0783

Identification of key genes and pathways in discoid lupus skin via bioinformatics analysis

Qian Dong、Kang Chen、Jinye Xie、Weijia Wang
中山市人民医院

Discoid lupus erythematosus (DLE) is the AQ4 most common skin manifestation of lupus; however, the molecular mechanisms underlying DLE remain unknown. Therefore, we aimed to identify key differentially expressed genes (DEGs) in discoid lupus skin and investigate their potential pathways.To identify candidate genes involved in the occurrence and development of the disease, we downloaded the microarray datasets GSE52471 and GSE72535 from the Gene Expression Database (GEO). DEGs between discoid lupus skin and normal controls were selected using the GEO2R tool and Venn diagram software. The Database for Annotation, Visualization, and Integrated Discovery (DAVID), Enrichr, and Cytoscape ClueGo were used to analyze the Kyoto Encyclopedia of Gene and Genome pathways and gene ontology. Protein-protein interactions (PPIs) of these DEGs were further assessed using the Search Tool for the Retrieval Interacting Genes version 10.0.Seventy three DEGs were co-expressed in both datasets. DEGs were predominantly upregulated in receptor signaling pathways of the immune response. In the PPI network, 69 upregulated genes were selected. Furthermore, 4 genes (CXCL10, ISG15, IFIH1, and IRF7) were found to be significantly upregulated in the RIG-I-like receptor signaling pathway, from analysis of Enrichr and Cytoscape ClueGo.The results of this

study may provide new insights into the potential molecular mechanisms of DLE. However, further experimentation is required to confirm these findings.

PO-0784

妊娠期妇女血脂水平参考区间的建立与探讨

舒静[1]、罗晓婷[2]
1. 西南医科大学附属医院
2. 西南医科大学

目的 通过回顾性分析建立妊娠期妇女特异性血脂水平参考区间，为临床妊娠期妇女血脂水平判断提供参考和依据。
方法 收集 2019 年 1 月至 2020 年 1 月在西南医科大学附属医院建档的 1193 例健康妊娠期女性血脂检测指标。按孕周将正常孕妇分为早期妊娠 P1 组（<14 周）、中期妊娠 P2 组（14~27 周）、晚期妊娠 P3 组（>27 周）。分析不同孕期孕妇血脂代谢水平，采用非参数法分别建立血脂参考区间，并对其进行验证，评估其临床适用性。
结果 (1)除 HDL-C 外，TG、TC、LDL-C、ApoA1、ApoB 从 P1 到 P3 组呈现逐渐上升的趋势；HDL-C 从 P1 组开始上升，P2 组达峰值，P3 组较 P2 组有所下降；ApoA1 在 P3 组达峰值，但较 P2 组上升程度并不显著。（2）P1 组 TG、TC、HDL-C、LDL-C、ApoA1、ApoB 分别是 2.89~5.65mmol/L、0.31~2.41mmol/L、1.13~2.48mmol/L、1.06~3.22mmol/L、1.32~2.29g/L、0.44~1.32g/L；P2 组分别是 3.41~7.37mmol/L、0.69~3.73mmol/L、1.28~2.82mmol/L、1.34~4.25mmol/L、1.56~2.59g/L、0.61~1.75g/L；P3 组分别是 4.02~7.87mmol/L、1.23~4.50mmol/L、1.28~2.69mmol/L、1.77~4.67mmol/L、1.58~2.61g/L、0.80~1.91g/L。（3）除早期妊娠 LDL-C 外，其他妊娠期血脂各项指标 RIs 与目前使用的 RIs 结果判断差异均具有统计学意义（P<0.05）。
结论 通过回顾性分析建立的孕妇血脂参考区间符合妊娠期妇女血脂水平的生理变化，为临床动态监测妊娠期妇女的血脂水平变化，评估孕妇健康状况，以及妊娠期相关疾病的预防、诊断和疗效监测等提供了科学的依据。

PO-0785

Matrix Metalloproteinase 3 as a Valuable Marker for Patients with COVID-19

Shengjie Shi、Xiaobing Xie
First Hospital of Hunan University of Chinese Medicine

Background The situation of the coronavirus disease 2019(COVID-19) continues to evolve, our study explored the significance of serum levels of Matrix Metalloproteinase 3 (MMP3) as a marker for patients with COVID-19.
Methods Sixty-two COVID-19 patients in the First Hospital of Hunan University of Chinese Medicine and Loudi Center for Diseases Prevention and Control, from January to March 2020, were sampled as the novel coronavirus pneumonia infected group. One hundred and thirty-one cases from the First Hospital of Hunan University of Chinese Medicine, including 67 healthy individuals and 64 non- COVID-19 inpatients, served as the non-infected group. Approximately every 5 d, sera from 20 cases were collected and analyzed thrice, using an automatic biochemical analyzer, to detect serum MMP3 concentrations. The correlation was analyzed between MMP3 and other pro-inflammatory cytokines. Following normality tests, differences in serum MMP3 levels between the infected and non-infected group were analyzed via SPSS (version 25.0) software, using the Wilcoxon rank-sum test.

Results The MMP3 concentration was 44.44（23.46~72.12）ng/ml in the infected group and 32.42 (28.16~41.21）ng/ml in the non-infected group. The difference between the two groups was statistically significant (Z=-2.799, P=0.005<0.05). A positive correlation was found between MMP3 and IL-1β(r=0.681, P=0.000<0.05), and IL-6(r=0.529, P=0.002<0.05).Serum MMP3 concentration, measured over three separate time points, were 55.98 (30.80~75.97) ng/ml, 34.84 (0.00~51.84) ng/ml, and 5.71 (0.00~40.46) ng/ml, respectively.
Conclusion Detection of serum MMP3 levels may play an important role in the development of therapeutic approaches for COVID-19 and may indicate the severity of the disease.

PO-0786

表皮葡萄球菌 psm-mec 过表达菌株的构建

杨永长
电子科技大学附属医院·四川省人民医院

目的 构建表皮葡萄球菌 psm-mec 过表达菌株，探讨 psm-mec 的功能。
方法 PCR 扩增含启动子的 psm-mec 基因片段 p221，利用穿梭质粒 pLI50 构建 psm-mec 过表达质粒 p221, 采用电转化技术将重组质粒导入金黄色葡萄球菌 RN4220 进行修饰。提取质粒后电转化表皮葡萄球菌 ATCC1222，筛选阳性克隆。菌落 PCR，real time RT-PCR 和 DNA 序列分析进行验证。半定量生物被膜分析法检测 p221 菌株生物被膜。
结果 PCR 扩增出含启动子的 psm-mec 序列的 p221 片段，酶切鉴定结果显示 psm-mec 过表达质粒 p221 构建正确，菌落 PCR，real time RT-PCR 和 DNA 序列分析结果表明表皮葡萄球菌 psm-mec 过表达菌株 p221 构建成功。与 ATCC12228 相比，psm-mec 过表达菌株 p221 生物被膜形成量明显增加，提示 psm-mec 影响表皮葡萄球菌生物被膜形成。
结论 成功构建了表皮葡萄球菌 psm-mec 过表达菌株，psm-mec 增加表皮葡萄球菌生物被膜形成。

PO-0787

白细胞假性减少一例

钱香
江苏省人民医院（南京医科大学第一附属医院）

目的 老年女性帕金森病患者，住院期间其中一次血常规结果为：WBC 0.11×109/L，WNR 散点图上也显示 WBC 数量减少。依据复片规则推片镜检后发现：WBC 总数应在正常范围内。查看仪器原始数据我们发现：WBC 计数在 WNR 通道为 0.11×109/L，在 WDF 通道为 9.70×109/L。本文旨在探讨导致 WBC 计数在 WNR 通道假性减少的原因。
方法 将患者血浆置换成生理盐水后再测；在体外模拟全血在 WBC 通道的状态，即在患者全血中按比例加入溶血剂；在本例患者血浆和血细胞层中分别加入 WNR 溶血剂。
结果 血浆置换后，WBC 计数在 WNR 通道为 9.41×109/L，在 WDF 通道为 8.93×109/L，说明影响来自于血浆。在体外模拟全血在 WBC 通道的状态，即按比例加入溶血剂，结果显示：本例患者 WNR 管出现凝块，而对照管未出现凝块，说明是因为强酸性溶血剂使得血浆发生了凝固。又在本例患者血浆中加入 WNR 溶血剂，也形成凝块，而血细胞层则无，进一步证实干扰来源于血浆。将凝块进行涂片，可见纤维状凝固物内包裹 WBC。
结论 该患者当天下午重新抽血再测时已经无此现象；查阅患者的病例资料，发现其前一日输注了大剂量的白蛋白，当日早上五点半采血时无输液。分析为输注的白蛋白，在 WNR 强酸环境下发生了凝固，网络了 WBC，导致其假性减低，影响 WNR 通道结果，而不影响 WDF 通道结果。

PO-0788

急性胰腺炎患者的血清 HCY 水平与其发生 SIRS 的相关性研究

王宏波[1]、王宇鹏[1]、石婷[1]、彭剑桥[1]、谭超超[1]、叶湘漓[2]
1. 湖南省人民医院
2. 湖南师范大学医学院

目的 寻找急性胰腺炎（AP）患者血清 HCY 水平与其发生 SIRS 之间的关系，探讨高 HCY 血症是否是 AP 患者发生 SIRS 的独立风险因子。
方法 收集 AP 患者入院后 48 h 内的 HCY 数据，依据其血清水平分为<15 μmoL/L 组、15~20 μmoL/L 组和>20 μmoL/L 组，比较在不同血清 HCY 水平下 AP 患者 SIRS 的发生率和平均持续时间的差异；接着收集 HCY、APACHE Ⅱ评分、CTSI、C 反应蛋白和白细胞计数等数据进行 ROC 曲线分析，探讨 HCY 能否作为 SIRS 的预测因子；再将发生 SIRS 的 AP 患者的血清 HCY 水平分别与 APACHE Ⅱ评分和 CTSI 进行分析，探讨高 HCY 血症是否影响发生 SIRS 的 AP 患者的预后；最后对各变量进行单因素和多因素 Logistic 回归分析，探讨高 HCY 血症是否是 AP 患者发生 SIRS 的独立风险因子。
结果 与<15 μmoL/L 组相比，15~20 μmoL/L 组和>20 μ moL/L 组的 SIRS 发生率和平均持续时间均显著增加，且差异有统计学意义（p <0.001）；ROC 曲线分析显示，高 HCY 水平对于 AP 患者发生 SIRS 有一定的预测作用（AUC=0.643）；Pearson 相关分析显示，发生 SIRS 的 AP 患者，其 HCY 水平与 CTSI 之间存在明显的相关性（r=0.313，p <0.001）；同时，发生 SIRS 的 AP 患者的 APACHE Ⅱ评分越高，其 HCY 水平也越高（p <0.001）；单变量和多变量 Logistic 回归分析表明，高 HCY 血症是 AP 患者发生 SIRS 的独立风险因子（HR：1.010；95% CI：0.997-1.018；p =0.039）。
结论 血清 HCY 水平与 AP 患者发生 SIRS 密切相关，高 HCY 血症可能是 AP 患者发生 SIRS 的独立风险因子。

PO-0789

应用 ROC 曲线确定孕妇 IgG-抗 A、抗 B 抗体效价在 ABO 新生儿溶血病的最佳临界值

张强[1]、张敏[2]
1. 东南大学附属中大医院
2. 东南大学

目的 应用 ROC 曲线评价孕妇抗体（IgG 抗-A、抗-B）效价在预测 ABO 新生儿溶血病中的诊断价值，分别确定其最佳诊断临界值。
方法 选择本院 440 例母胎血型不合的 O 型孕妇，应用微柱凝胶法检测 IgG-抗 A 抗体 259 人次（病例组 22 例，对照组 234 例），IgG-抗 B 抗体 254 人次（病例组 16 例，对照组 238 例），进行非匹配病例对照研究和绘制 ROC 曲线，利用 Youden 指数确定最佳临界值，检测新生儿溶血指标（溶血三项）。
结果 IgG 抗 A、抗 B 抗体效价在病例组均显著高于对照组（p<0.05），ABO-HDN 发病率在 IgG-抗 A 检测组和 IgG-抗 B 检测组分别为 8.60%、6.30%。孕妇 IgG-抗 A、抗 B 抗体的 ROC 曲线下面积分别为 0.947、0.959，均具有显著统计学意义（p<0.05），最佳临界值均为 1:256。
结论 ABO 新生儿溶血病时孕妇 IgG-抗 A、抗 B 抗体效价显著升高，产前筛查 O 型孕妇的抗体（IgG-抗 A、抗 B）效价对于 ABO 新生儿溶血病的发生具有极佳的早期预测价值。ROC 曲线简单有效，可直观确定诊断试验的最佳临界值。

PO-0790

NLRP3 炎症小体对脑血管周细胞生长和功能的影响

权文强、李冬
上海市同济医院(同济大学附属同济医院)

目的 探究 NLRP3 炎症小体对脑血管周细胞生长和功能的影响及作用机制。收集 9 月龄正常（NLRP3+/+）及敲除（NLRP3-/-）的转基因小鼠大脑，左侧大脑经 PFA 固定后切片，免疫荧光染色分析大脑血管总长、血管周细胞数量变化；右侧大脑组织匀浆后分离血管，采用 Western blot 法检测血管匀浆中周细胞标志物 PDGFRβ 和 CD13 的蛋白水平；利用不同浓度 NLRP3 抑制剂 MCC950 处理脑周细胞株 HBPC/ci37,MTT 法检测周细胞增殖情况，Western blot 检测 PCNA、Ki67、PDGFRβ、CD13 等蛋白变化；利用不同浓度重组的 IL-1β 蛋白刺激 HBPC/ci37 细胞，Western blot 检测 AKT、ERK、NFκB 等增殖相关信号通路激活情况。
结果 免疫荧光染色显示 NLRP3-/-转基因小鼠的脑血管总长与 NLRP3+/+小鼠相比明显缩短（P<0.01），血管周细胞明显减少（P<0.05）；血管匀浆的 Western blot 结果显示周细胞标志物 PDGFRβ 和 CD13 的蛋白水平明显下降（P<0.01）。体外实验结果显示不同浓度的 MCC950 均能够抑制周细胞 HBPC/ci37 增殖，且抑制作用呈浓度依赖性（P<0.01）；MCC950 同时也抑制了周细胞 HBPC/ci37 的 p-AKT（P<0.01），p-ERK（P<0.05）蛋白水平，作用呈浓度依赖性；而加入 IL-1β 蛋白刺激周细胞 HBPC/ci37 可激活 p-AKT 蛋白表达水平（P<0.01），PDGFRβ、CD13 的表达水平升高（P<0.01）；加入 AKT 抑制剂后 p-GSK3β 水平明显下降（P<0.001），同时 PDGFRβ、CD13 的表达水平明显下降（P<0.05）。
结论 NLRP3 炎症小体参与脑血管周细胞的生长和增殖，其通过激活 AKT 信号通路来维持大脑中周细胞的正常功能水平。

PO-0791

武汉地区孕妇地中海贫血基因突变类型与频率分析

里进[1]、杨媛媛[2]、叶光明[1]、李一荣[1]
1. 武汉大学中南医院
2. 湖北中医药大学

目的 对湖北武汉孕妇地中海贫血携带率、基因突变类型、基因频率情况等进行分析，了解本地区地中海贫血基因分布和基因突变类型，为预防、控制武汉重型及中间型地中海贫血患儿的出生和地中海贫血孕妇临床治疗提供数据支撑。
方法 通过收集从 2018 年 1 月至 2021 年 3 月对 2452 例婚前、孕前、产前、体检及新生儿等在武汉中南医院进行基因筛查的人员进行调查（除重复基因筛查人员和不合格筛查人员外），记录地中海贫血携带率，基因突变类型和基因突变频率。
结果 在 2452 例地中海贫血基因分析中，地贫基因携带者 301 例，携带率为 12.28%。α－地中海贫血 158 例，携带率为 6.44%，其中 α－地贫孕妇人 78；β－地中海贫血 141 例，携带率为 5.75%，其中 β－地贫孕妇 47 人；复合型地贫 2 例（α3.7 杂合和 IVS-2-654 杂合）其中孕妇一人，携带率为 0.082%。缺失型 α－地贫（SEA 杂合，α3.7 杂合，α4.2 杂合，α4.2 纯合 SEA 和 α3.7 双重缺失）孕妇分别为 21 例，46 例，6 例，1 例，1 例；突变型 α－地贫（CS142 杂合，QS125 杂合）孕妇分别为 1 例，2 例；突变型 β－地贫（-28 杂合，-29 杂合，Cap 杂合，CD17 杂合，CD26 杂合，CD41-42 杂合，CD71-72 杂合，IVS-2-654 杂合）孕妇分别为 1 例，1 例，2 例，8 例，1 例，14 例，2 例，18 例。
结论 从本研究结果推断武汉地区地贫分布特点：α－地中海贫血前三位主要为 SEA 杂合基因型（占比为 41.77%），α3.7 杂合基因型（占比 39.24%），α4.2 杂合基因型（占比 7.59%）；β－

地中海贫血前三位主要为 IVS-2-654 杂合基因型（占比 41.84%），CD41-42 杂合（占比 26.95%），CD17 杂合（占比 22.7%）。

PO-0792

Development and implementation of a LIS-based validation system for autoverification toward zero defects in the automated reporting of laboratory test results

Di Jin[1]、Qing Wang[1]、Dezhi Peng[1]、Jiajia Wang[1]、Bijuan Li[2]、Yating Cheng[2,3]、Nanxun Mo[2,3]、Xiaoyan Deng[2]、Ran Tao[2,3]
1. Jinan Kingmed Center for Clinical Laboratory
2. 广州医科大学
3. 广州金域医学检验中心有限公司

Background Validation of the autoverification function is one of the critical steps to confirm its effectiveness before use. It is crucial to verify whether the programmed algorithm follows the expected logic and produces the expected results. This process has always relied on the assessment of human-machine consistency and is mostly a manually recorded and time-consuming activity with inherent subjectivity and arbitrariness that cannot guarantee a comprehensive, timely and continuous effectiveness evaluation of the autoverification function. To overcome these inherent limitations, we independently developed and implemented a laboratory information system (LIS)-based validation system for autoverification.
Methods We developed a correctness verification and integrity validation method (hereinafter referred to as the "new method") in the form of a human-machine dialog. The system records personnel review steps and determines whether the human-machine review results are consistent. Laboratory personnel then analyze the reasons for any inconsistency according to system prompts, add to or modify rules, reverify, and finally improve the accuracy of autoverification.
Results The validation system was successfully established and implemented. For a dataset consisting of 833 rules for 30 assays, 782 rules (93.87%) were successfully verified in the correctness verification phase, and 51 rules were deleted due to execution errors. In the integrity validation phase, 24 projects were easily verified, while the other 6 projects still required the additional rules or changes to the rule settings. Taking the Hepatitis B virus (HBV) test as an example, from the setting of 65 rules to the automated releasing of 3000 reports, the validation time was reduced from 452 hours (manual verification) to 275 hours (new method) , a reduction in validation time of 177 hours. Furthermore, 94.6% (168/182) of laboratory users believed the new method greatly reduced the workload, effectively controlled the report risk and felt satisfied. Since 2019, over 3.5 million reports have been automatically reviewed and issued without a single clinical complaint.
Conclusion To the best of our knowledge, this is the first report to realize autoverification validation as a human-machine interaction. The new method effectively controls the risks of autoverification, shortens time consumption, and improves the efficiency of laboratory verification.

PO-0793

Systematic Approach of Reference Genes for Pan-Cancer in Platelets Based on RNA-Sequence Data

guishu yang、huaichao luo
Sichuan Cancer Hospital & Institute, Sichuan Cancer Center, School of Medicine, University of Electronic Science and Technology of China

Background In recent years, there are many studies have shown that some messenger RNA (mRNA) in platelets were potential biomarkers for the diagnosis of early-stage pan-cancer, and RT-qPCR allows presence of these mRNA transcripts to be quantified. Therefore, studies about more accurate normalization of transcript level were required, which were performed by using the most stable reference genes.
Methods The candidate reference genes were screened out from the dataset of the platelets' transcriptome of the pan-cancer and the stability of the gene expression was verified in systematic approaches. Here screening of reference genes in platelet for pan-cancer has been done and evaluation of the stability gene expression was performed in systematic approaches. Bioinformatics and functional analysis were performed from RNA-seq of tumor-educated platelets dataset followed by gene expression analysis and validation of candidate genes.
Results 285 candidate genes were obtained from the dataset GSE68086, and seven reference genes (YWHAZ, GNAS, GAPDH, OAZ1, PTMA, B2M and ACTB) were generated from 95 candidate genes after optimizing the mean > 1 and coefficient of variation (CV) < 1 from the 285 of our pre-evaluation reference genes and 73 known reference genes. Finally, three highly stable expression candidates: GAPDH, B2M and ACTB were selected and validated in 50 subjects.
Conclusions We identified seven reference genes, three of which: GAPDH, B2M and ACTB were found to be highly stable reference genes which are sorted orderly through the different algorithm. Finally, GAPDH is recommended as the most suitable reference gene for platelet transcript analysis.

PO-0794

长沙地区 HbA1c 参考区间的建立

向哲邑、叶思霈
湖南省人民医院

目的 通过统计分析建立适用于长沙地区临床实验室糖化血红蛋白的一致性参考区间，并验证其适用性。
方法 选取 2020 年 7 月到 2021 年 1 月期间若干例体检的健康志愿者，统一于每天的 8：00-10：00 采集体检人员的静脉血液，进行 HbA1c 检测。按参考人群的纳入及排除标准（即无慢性疾病、未接受药物或饮食治疗等）选择 200 例参考人群，分为男、女两组，每组按年龄分别分为≤45 岁（青年组），45～60 岁（中年组），≥60 岁（老年组）。其中青年组 78 例，中年组 54 例，老年组 69 例，记录其相关的基本资料，收集其 HbA1c 的数值，对其进行统计学分析，建立适用于长沙地区健康人群 HbA1c 的一致性参考区间。
结果 长沙地区健康成人 HbA1c 总体水平 95%的参考区间为 5.1%~6.3%，女性 HbA1c 水平 95%的参考区间为 5.1%~6.3%，男性 HbA1c 水平 95%的参考区间为 5.2%~6.4%。由于对男、女总体水平的分析发现性别间 HbA1c 水平的差异无统计学意义，故参考区间并未分性别建立。由于各年龄组 HbA1c 水平的分布均服从正态分布，且中年组和老年组之间的两两比较差异性不显著，故合并成中老年组，得出 HbA1c 水平的参考区间为：青年组 5.13%~6.13%，中老年 5.29%~6.58%。

结论 综上所述，长沙地区健康成人 HbA1c 总体水平为 5.1%~6.3%，性别间 HbA1c 水平的差异无统计学意义。按年龄组建立本地区 HbA1c 水平的参考区间为：青年组 5.13%~6.13%，中老年 5.29%~6.58%。HbA1c 水平随着年龄的增长有明显上升的趋势。

PO-0795

建立儿童及青少年骨源性碱性磷酸的参考区间

陈灿星[1]、胡志峰[1,2]、姚少濠[1,2]、张玲[1,2]、刘勇[1,2]、褚冬霞[1]、宗智慧[1]、陶然[1,2]
1. 广州金域医学检验中心有限公司
2. 广州医科大学金域检验学院

目的 通过回顾 23959 名健康体检者（年龄区间 0-18 岁）的骨源性碱性磷酸酶（Bone Alkaline Phosphatase）定量检测结果，建立不同年龄段，不同性别的骨源性碱性磷酸酶的参考区间。
方法 回顾分析 2020 年 7 月至 2020 年 12 月送检本中心实验室的健康体检人群（儿童和青少年），用贝克曼库尔特 ACCESS2 免疫分析仪定量检测骨源性碱性磷酸酶的结果，按年龄、性别分组，采用双侧限值 P2.5～P97.5，建立儿童及青少年（0-18 岁）正常的参考区间，并观察骨源性碱性磷酸酶在儿童及青少年的分布特征。
结果 1 岁以下骨源性碱性磷酸酶参考区间为（44.28-121.91）μg/L，1-3 岁参考区间为（38.29-120.07）μg/L，4-6 岁参考区间为（42.27-117.35）μg/L，7-9 岁参考区间为（38.07-118.69）μg/L，且 9 岁以下，男孩和女孩间骨源性碱性磷酸酶的结果差异无统计学意义（P＞0.05）。10-18 岁男性参考区间为（20.58-126.88）μg/L，10-18 岁女性参考区间为（11.68-121.58）μg/L，且男女间骨源性碱性磷酸酶的结果差异有统计学意义（P＜0.05）。
结论 实验室应根据本地区检测人群、实验室仪器和检测试剂建立骨源性碱性磷酸酶定量分析的参考区间。儿童及青少年，骨源性碱性磷酸酶浓度明显比成人高，且 1 岁以下及青春期间浓度最高。建立儿童及青少年骨源性碱性磷酸的不同年龄和性别的参考区间，有助于辅助筛查维生素 D 缺乏性、佝偻病等疾病。

PO-0796

药食同源小分子化合物对成骨细胞分化和骨形成的调控作用

印崇[1,2,3,4]、卫萍[5]、于阳[6]、梁欢[3]、田野[3]、邓旭东[3]、骞爱荣[3]、郭晓兰[1,4]
1. 川北医学院附属医院检验科
2. 川北医学院附属医院院士专家工作站&表观遗传与 RNA 药物研究室
3. 西北工业大学生命学院
4. 川北医学院检验系&转化医学研究中心
5. 广西农业科学院
6. 天津医科大学药学院

目的 小分子化合物研究一直是现代医学领域的热点，而中药和食物中的小分子活性化合物成分研究在近年来引起了愈来愈多的关注。新近研究发现，一些小分子化合物可以通过调控成骨细胞中关键调控因子的功能，对成骨细胞的功能起调控作用，该方向目前在骨骼系统疾病研究领域受到了广泛的关注。作者前期文献调查发现，食品用火麻中的多肽类成分对于脊椎动物的钙沉积和 wnt 信号通路有显著的促进作用，因此推测火麻多肽可能是一种潜在的药食同源小分子化合物，为了深入研究火麻多肽的功能，开展了如下研究。
方法 通过碱提法提取了食用火麻蛋白，并使用胰蛋白酶对火麻蛋白进行酶解消化，经超滤、透析后合成火麻多肽。验证火麻蛋白和火麻多肽的细胞学和动物学毒性后，在安全浓度下用火麻蛋白和火麻多肽处理前成骨细胞 MC3T3-E1 和人骨髓间充质干细胞，并用火麻多肽对去卵巢骨质疏松小鼠进行灌胃，检测处理后细胞的成骨分化水平，以及小鼠的骨形成水平。

结果 结果表明，火麻蛋白和火麻多肽不具备任何细胞学和动物学毒性，细胞学实验结果表明，火麻蛋白和火麻多肽处理，可以显著提高前成骨细胞 MC3T3-E1 和人骨髓间充质干细胞的碱性磷酸酶活性和成骨标志基因表达水平，此外对于 Bmp2 和 wnt 信号通路的下游基因表达均有显著的促进效果；体内实验表明，火麻多肽可以对去卵巢骨质疏松小鼠的骨质疏松起显著的治疗作用。
结论 本研究证明了火麻蛋白和火麻多肽对于成骨细胞分化和骨形成的促进作用，说明了火麻中有效成分可以起到促进骨形成，抑制骨质疏松的效果。研究结果对于推进火麻这一特色作物的药食同源和转化医学研究有积极的促进作用。

PO-0797

LncRNA LOC100912373 modulates PDK1 expression by sponging miR-17-5p to promote the proliferation of fibroblast-like synoviocytes in rheumatoid arthritis

Chang Fan、xiaoya cui、sen chen、shaopeng huang、kaiquan huang、hui jiang
The First Affiliated Hospital of Anhui University of Chinese Medicine

Rheumatoid arthritis (RA) is a common autoimmune disease and characterized by chronic inflammation, abnormal synovial cell proliferation, and joint swelling and tenderness, and it causes patients substantial pain. To date, the pathogenesis of RA remains unclear, and specific treatment is still lacking in the clinic. Evidence from previous research indicated that the long noncoding RNA (lncRNA) LOC100912373 is a key lncRNA and involved in RA. However, our understanding of the specific mechanism of lncRNA LOC100912373 in RA development and progression is still in its infancy. In this study, fibroblast-like synoviocytes (FLSs) were cultured by enzyme-dispersed and substrate-attached explant methods. The MTT method, flow cytometry and transmission electron microscopy were used to determine the effect of lncRNA LOC100912373 on FLSs. The expression of key genes such as lncRNA LOC100912373, miR-17-5p, PDK1 and AKT in FLSs was detected by RT-qPCR, immunofluorescence and Western blot. The localization of lncRNA LOC100912373 was determined by fluorescence in situ hybridization. The specific targeting relationship between lncRNA LOC100912373 and miR-17-5p/PDK1 was verified by RNA immunoprecipitation and luciferase reporter gene analysis. The results showed that lncRNA LOC100912373 localized in the cytoplasm and was highly expressed in the synovial tissues and FLSs of AA rats. LncRNA LOC100912373 overexpression promoted the proliferation of FLSs. In addition, lncRNA LOC100912373 could bind to miR-17-5p, and the expression of lncRNA LOC100912373 was negatively correlated with miR-17-5p and positively correlated with PDK1/AKT. In conclusion, lncRNA LOC100912373 may upregulate the expression of PDK1 by sponging miR-17-5p, accelerating the phosphorylation of AKT and inducing the proliferation of FLSs, thus promoting the occurrence and development of RA.

PO-0798

Transcriptome-wide high-throughput m6A sequencing of differential m6A methylation patterns in the human rheumatoid arthritis fibroblast-like synoviocytes cell line MH7A

Hui Jiang [1]、kefeng cao[2]、chang fan[1]、xiaoya cui[1]、yanzhen ma[1]、kaiquan huang[1]
1. 安徽中医药大学第一附属医院(安徽省中医院)
2. 太和县中医院

Introduction N6-methyladenosine (m6A) is the most frequent internal modification in eukaryotic mRNAs and is closely related to the occurrence and development of many diseases, especially tumors. However, the relationship between m6A methylation and rheumatoid arthritis (RA) is still a mystery.
Methods Two high-throughput sequencing methods, namely, m6A modified RNA immunoprecipitation sequence (m6A-seq) and RNA sequence (RNA-seq) were performed to identify the differentially expressed m6A methylation in human rheumatoid arthritis fibroblast-like synoviocytes cell line MH7A after stimulation with TNF-α. Gene Ontology (GO) analysis and Kyoto Encyclopedia of Genes and Genomes (KEGG) analyses were used to obtain enriched GO terms and significant KEGG pathways. Then, four candidate genes, Wilmstumor 1-associating protein (WTAP), receptor-interacting serine/threonine protein kinase 2 (RIPK2), Janus kinase 3 (JAK3) and tumor necrosis factor receptor SF10A (TNFRSF10A) were selected to further validate the m6A methylation, mRNA and protein expression levels in MH7A cells and synovial tissues of adjuvant arthritis (AA) rats by RT-qPCR and western blot.
Results Using m6A-seq, we identified a total of 206 genes with differentially expressed m6A methylation, of which 118 were significantly upregulated and 88 genes were significantly downregulated. Likewise, 1207 differentially mRNA expressed mRNAs were obtained by RNA-seq, of which 793 were upregulated and 414 downregulated. Further joint analysis showed that the m6A methylation and mRNA expression levels of 88 genes changed significantly, of which 30 genes displayed increased m6A methylation and decreased mRNA expression, 57 genes displayed decreased m6A methylation and increased mRNA expression increased, and 1 gene displayed increased m6A methylation and increased mRNA expression. GO and KEGG analyses indicated that these unique genes were mainly enriched in inflammation-related pathways, cell proliferation and apoptosis. In addition, the validations of WTAP, RIPK2, JAK3 and TNFRSF10A were in accordance with the m6A and RNA sequencing results.
Conclusion This study established the transcriptional map of m6A in MH7A cells and revealed the potential relationship between RNA methylation modification and RA related genes. The results suggested that m6A modification was associated with the occurrence and course of RA to some extent.

PO-0799

A novel pooling strategy with sample concentration for screening of SARS-CoV-2

Xueliang Wang 、Zhongqiang Huang、Jian Song、Ran Zhao、Yanqun Xiao、Hualiang Wang
Shanghai Centre for Clinical Laboratory

Purpose The COVID-19 pandemic caused by SARS-CoV-2 has resulted in significant shortages of RT-PCR testing supplies. Sample pooling has the potential to improve available RT-PCR testing capacity. However, compromised sensitivity caused by the sample dilution in the traditional sample pooling (TSP) can lead to higher rates of false-negative results in low-viral-load

specimens. We aim to overcome the challenge by a novel strategy, namely sample pooling concentration (SPC).
Methods Three or eight individual nasopharyngeal samples previously tested for SARS-CoV-2 were pooled into a single sample. Automated RNA extraction were processed individually and in pools (TSP strategy and the SPC strategy) and subsequently tested by RT-PCR.
Results Our results show that the sample dilution from traditional pooling (TSP strategy) led to a mild, but expected, loss in Ct value. This drop in sensitivity was responsible for all of the false-negative results in samples with low viral loads. However, use of the SPC strategy yielded 100% accuracy with no loss of sensitivity.
Conclusion We conclude that the SPC method as a resource-efficient strategy may facilitate early detection and elimination of COVID-19 community transmission.

PO-0800

Recent Progress of Nanozymes in the Detection of Pathogenic Microorganisms

Fengfeng Zhao
Department of Clinical Laboratory of Zhongda Hospital, Southeast University

Infectious diseases are among the world's principal health problems. It is crucial to develop rapid, accurate and cost-effective methods for the detection of pathogenic microorganisms. Natural enzymes are generally proteins but also include catalytic RNA produced by living cells. Recently, considerable progress has been achieved in the field of inorganic enzyme mimics (nanozymes). Compared with natural enzymes, nanozymes have higher stability and lower cost. More interestingly, their properties can be designed for various demands. Herein, we introduce the latest research progress on the detection of pathogenic microorganisms by using various nanozymes. We also discuss the current challenges of nanozymes in biosensing and provide some strategies to overcome these barriers.

PO-0801

Interleukin-8 as a Biomarker for Disease Prognosis of Coronavirus Disease-2019 Patients

Lili Li[2]、Jie Li[3]、meiling gao[1]、huimin fan[1]、Yanan Wang[4]、Xin Xu[1]、Chunfeng Chen[4]、 Junxiao Liu[4]、Jocelyn Kim[5]、Roghiyh Aliyari[5]、jicai zhang[3]、yujie jin[3]、xiaorong Li[4]、feng ma[4]、minxin shi[6]、genhong cheng[5]、heng yang[4]
1. Center for Systems Medicine, Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China
2. Center for Systems Medicine, Institute of Basic Medical Sciences, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China
3. Department of Laboratory Medicine, TaiHe Hospital, Hubei University of Medicine, Shiyan, China
4. Department of Scientific Research, Suzhou Func Biotech Inc, Suzhou, China
5. Department of Microbiology, Immunology & Molecular Genetics, University of California, Los Angeles, Los Angeles, CA, United States
6. Department of Surgery, Affiliated Tumor Hospital of Nantong University, Nantong, China

The widespread prevalence of coronavirus disease-2019 (COVID-19) which is caused by severe respiratory syndrome coronavirus 2 (SARS-CoV-2) infection, has resulted in a severe global public health emergency. However, there are no sensitive biomarkers to predict the disease prognosis of COVID-19 patients. Here, we have identified interleukin-8 (IL-8) as a biomarker candidate to predict different disease severity and prognosis of COVID-19 patients. While serum IL-6 become obviously elevated in severe COVID-19 patients, serum IL-8 was easily

detectible in COVID-19 patients with mild syndromes. Furthermore, IL-8 levels correlated better than IL-6 levels with the overall clinical disease scores at different stages of the same COVID-19 patients. Thus, our studies suggest that IL-6 and IL-8 can be respectively used as biomarkers for severe COVID-19 patients and for COVID-19 disease prognosis.

PO-0802

CD4+，CD8+T 淋巴细胞计数和重症新型冠状病毒肺炎相关性的 meta 分析

张海鹏[1]、吴婕[2]
1. 天津医科大学第二医院
2. 天津医科大学总医院

Purpose We investigate the relationship between CD4+T counts, CD8+T counts, CD4/CD8 ratio and the severity of COVID-19 patients.
Methods We searched PubMed, EMBASE and Web of Sciences without date (until Jun 2, 2020) or language restrictions.
Results 13 studies included a total number of 1647 patients were considered. Both CD4+T and CD8+T counts significantly reduced in severe COVID-19 group compared with non-severe group [CD4+T (MD: -0.22×10^9/L, 95%CI: -0.27 to -0.17×10^9/L, I^2=89%); CD8+T (MD: -0.14×10^9/L, 95%CI: -0.18 to -0.11×10^9/L, I^2=88%)]. And there was no significant difference in CD4/CD8 ratio (MD: 0.17, 95%CI: -0.12 to 0.46, I^2=91%).The details are presented in Fig 1.
Conclusions Both CD4+T and CD8+T counts may serve as biomarkers for predicting severity of COVID-19.

PO-0803

硫化氢代谢异常影响胚胎转运

宁楠楠
山东大学齐鲁医院

目的 异位妊娠严重影响育龄期女性健康，其中输卵管妊娠所占比例较高。硫化氢是一种气体信号分子，该信号系统参与体内的多种生理和病理过程。胱硫醚-γ-裂解酶和胱硫醚-β-合成酶是硫化氢代谢的两种关键酶。
方法和结果 通过免疫印迹和免疫荧光，发现胱硫醚-γ-裂解酶和胱硫醚-β-合酶存在于人输卵管上皮细胞，硫化氢信号传导抑制输卵管的自发收缩。借助 GYY4137、NaHS 和胱硫醚-β-合成酶敲基因小鼠，发现硫化氢信号传导的异常导致小鼠胚胎滞留在输卵管并且发育滞后。
结论 研究结果揭示了输卵管胚胎运输的新调节机制，为异位妊娠预防和治疗研究提供帮助。

PO-0804

Diagnostic Value of Hemoglobin and Prognostic Nutritional Index for Colorectal Cancer in Familial Adenomatous Polyposis Patients

Xueliang Ding、Shaobo Tian、Yanan Chu、Jia Hu、Guobin Wang、Lin Wang、Zheng Wang
Wuhan Union hospital

Colorectal cancer (CRC) is a major cause of mortality in familial adenomatous polyposis (FAP) patients. We aimed to analyze the value of hemoglobin (Hb) and prognostic nutritional index (PNI) for CRC diagnosis in FAP patients. A total of 43 patients were considered with FAP from January 2005 to June 2020 in Wuhan Union Hospital, 19 of them were confirmed as CRC patients. The differences of Hb and PNI levels between FAP patients with CRC and without CRC were detected by Non-parametric test or Student's t-test. Logistic regression analysis was performed to analyze the factors affecting Hb and PNI levels. The diagnostic efficacy of Hb and PNI for CRC in FAP patients was evaluated by receiver operating characteristic (ROC) curve analysis. We found that Hb and PNI levels were lower in FAP patients with CRC compared with patients without CRC. In CRC patients, lower Hb levels were associated with advanced lymph node metastasis and stage; lower PNI levels were related to larger tumor size. CRC was the main factor leading to the low levels of Hb (OR=0.179, 95%CI: 0.047-0.674) and PNI (OR=0.231, 95%CI: 0.057-0.932) in FAP patients. The area under the ROC of Hb and PNI for CRC diagnosis in FAP patients were 0.703 (95%CI: 0.545-0.861) and 0.765 (95%CI: 0.622-0.909), respectively. The value of Hb and PNI are closely associated with CRC, and can be used for CRC diagnosis in FAP patients.

PO-0805

双氢青蒿素下调食管癌细胞 hTERT 的分子机制

李青容
川北医学院

目的 探讨双氢青蒿素（DHA）下调人食管癌细胞端粒酶逆转录酶（hTERT）的分子机制。
方法 采用 CCK8 和平板克隆形成实验检测 DHA 对食管癌细胞株 Eca109、KYSE150 及 TE1 细胞增殖的影响；采用 Transwell 实验和划痕实验检测 DHA 对食管癌细胞迁移的影响；采用荧光显微镜和流式细胞术检测 DHA 处理后的食管癌细胞内活性氧（ROS）的含量；采用 qPCR 和蛋白免疫印迹检测相关 mRNA 和蛋白的表达水平。通过裸鼠皮下注射 Eca109 细胞建立食管癌裸鼠移植瘤，监测给药后肿瘤体积的变化，WB 和 IHC 检测处理组 hTERT 蛋白表达变化。
结果 DHA 能在体外显著抑制食管癌细胞株 Eca109、KYSE150 和 TE1 细胞增殖和迁移，并能显著下调 hTERTmRNA 和蛋白表达，且呈时间和剂量依赖性。进一步的分子机制研究显示， DHA 显著上调食管癌细胞内活性氧（ROS）产生，并下调 hTERT 启动子结合的转录因子 SP1 表达。采用抗氧化剂（NAC）抑制 DHA 诱导的食管癌 ROS 产生后，SP1 和 hTERT 下调程度降低。此外，在上述细胞株中过表达 SP1 后，hTERT 蛋白表达水平显著增强，且食管癌 Eca109、KYSE150 和 TE1 细胞的增殖和迁移能力显著增加。在裸鼠体内，DHA 可显著抑制食管癌裸鼠移植瘤的生长，肿瘤体积显著小于对照组，差异有统计学意义（$P<0.05$）；且与对照组相比处理组 hTERT 蛋白表达显著降低。
结论 DHA 通过 ROS/SP1/hTERT 信号轴抑制食管癌细胞增殖和转移，有望成为一种新的抗食管癌药物。

PO-0806

滤泡调节性 T 细胞与滤泡辅助性 T 细胞在 ANCA 相关性小血管炎中的临床意义研究

龙彦[1]、冯景泓[1]、马寅婷[1]、孙媛媛[1]、徐丽娟[2]、宋英[1]、刘忱[1]
1. 北京大学人民医院
2. 北京大学医学部免疫学研究室

目的 探讨滤泡调节性 T 细胞与滤泡辅助性 T 细胞在 ANCA 相关性小血管炎患者血清自身抗体产生中的潜在作用；
方法 本研究共入选 26 例活动期 ANCA 相关性小血管炎（AAV）患者和 22 例年龄及性别匹配的对照组患者，利用流式细胞术对循环 TFR 及其亚群、TFH 及其亚群进行全面系统地分析，采用 ELISA 法检测血清 IL-4、IL-10、IL-12、IL-17A、IL-21 及 TGF-β 等细胞因子，同时收集患者血清 MPO-ANCAs、PR3-ANCAs 及血肌酐等临床资料。
结果 本研究结果显示活动期 AAV 患者循环 TFR 水平和 TFR/ TFH 比值明显降低，且循环 TFR 中转录因子 Helios，FoxP3 及 Ki-67 表达水平显著降低，同时 TFR 功能分子 TIGIT 明显降低而拮抗分子 CD226 表达显著升高，提示 AAV 患者循环 TFR 的功能和增殖能力可能受损。而 TFH 表面功能分子 ICOS 及 PD-1、转录因子 Ki-67 表达水平明显上调，结果提示活动期 AAV 患者中 TFH 的功能增强。此外，AAV 患者中循环记忆 B 细胞和浆细胞水平显著升高，并与 TFR 水平和 TFR/TFH 比值呈明显负相关。另外，TFR、TFR/TFH 比值与血清 MPO-ANCA 水平呈负相关而 TFH 与血清 MPO-ANCA 水平呈正相关。TFR 和 TFR/TFH 比值与肾功能损伤指标血清 SCr，BUN 呈显著负相关，血清 IL-4 和 IL-21 升高与 TFR 和 TFR/TFH 比值减低密切相关。
结论 本研究结果提示 AAV 患者 TFR 降低及 TFR/TFH 失衡与自身抗体水平升高有关，并可能与肾功能损伤密切相关，而血清 IL-4 和 IL-21 升高可能是导致 TFR 变化及其与 TFH 失衡的潜在原因。

PO-0807

医院临床实验室 HIV 感染的筛查、确认及报告

王娟[1]、华文浩[2]、刘芳遥[3]、崔丽艳[4]
1. 北京肿瘤医院
2. 北京大学人民医院
3. 北京市海淀区疾病预防控制中心
4. 北京大学第三医院

艾滋病又称获得性免疫缺陷综合征（Acquired Immune Deficiency Syndrome，AIDS），是由机体感染人类免疫缺陷病毒（human immune deficiency virus，HIV）而引发的全身疾病，疾病后期可继发各种机会性感染、恶性肿瘤和中枢神经系统病变最终导致死亡。感染 HIV 者包括 HIV 感染者和艾滋病患者均为传染源。艾滋病在我国的传播呈现快速增长的趋势，已成为严重威胁我国人民健康的公共社会问题。近几年来中国疾病预防与控制中心对于 HIV 感染筛查策略有所变化，中美间筛查策略也有细微差别。本文简要介绍了 HIV 感染者筛查的血清学生物标志物及中美筛查和确认策略，并对医疗机构 HIV 筛查报告发放模式提出建设性的意见。

PO-0808

Circulating serum exosomal long non-coding RNAs FOXD2-AS1, NRIR, and XLOC_009459 as diagnostic biomarkers for colorectal cancer

Miao Yu [2]、Li Xie[1]、Xingguo Song[1]、YaJing Zhao[1]
1. Department of Clinical Laboratory, Shandong Cancer Hospital and Institute, Shandong First Medical University and Shandong Academy of Medical Sciences
2. Shandong Provincial Third Hospital, Cheeloo College of Medicine, Shandong University

Exosomes derived from cancer cells encapsulate various kinds of tumor-specific molecules, thus can interact with adjacent or distant cells to mediate information exchange. Long non-coding RNAs (lncRNAs) in exosomes have the potential as diagnostic and prognostic biomarkers in different types of cancers. The current study was aimed to identify circulating exosomal lncRNAs for the diagnosis of colorectal cancer (CRC).
Methods Exosomes were isolated from the serum by ultracentrifugation and verified by transmission electron microscope (TEM), qNano and immunoblotting. Exosomal lncRNAs FOXD2-AS1, NRIR, and XLOC_009459 were selected by lncRNA microarray and validated by qPCR in 203 CRC patients and 201 healthy donors. The receiver operating characteristic curve (ROC) was used to assess the diagnostic efficiency of serum exosomal lncRNAs.
Results Exosomal FOXD2-AS1, NRIR, and XLOC_009459 (TCONS_00020073) levels were significantly upregulated in 203 CRC patients and 80 early-stage CRC patients compared to 201 healthy donors, possessing the area under the curve (AUC) of 0.728, 0.660 and 0.682 for CRC, as well as 0.743, 0.660 and 0.689 with 73.1% for early-stage CRC, respectively. Notably, their combination demonstrated the markedly elevated AUC of 0.736 for CRC and 0.758 for early-stage CRC, indicating their potential as diagnostic biomarkers for CRC.
Conclusions Our data suggested that exosomal lncRNAs FOXD2-AS1, NRIR and XLOC_009459 act as the promising biomarkers for the diagnostics of CRC and early-stage CRC.

PO-0809

The significant of blood index and biochemistry index in patients with rheumatoid arthritis

Wei Zhou、Xi Li、Yanting Jiang、Sihui Li、Min Jin、Jingzhe Sui、Jian Wang
First Affiliated Hospital of Guangxi Medical University

Background The aim of this study is to demonstrate the clinical significance of the platelet-to-lymphocyte ratio (PLR) and the ratio of aspartate aminotransferase (AST) to alanine aminotransferase (ALT) in patients with rheumatoid arthritis (RA).
Methods A total of 215 patients with RA, 115 patients with osteoarthritis (OA), and 303 healthy controls (HCs) were included in this study. Data on the AST and ALT levels were collected from liver function test reports, and data on the number of platelets and lymphocytes were obtained from a routine blood analysis. Moreover, all the laboratory parameters of patients with RA, patients with OA, and HCs were retrospectively analyzed.
Results The results obtained in this study showed that patients with RA had the highest PLR and AST/ALT ratio, whereas HCs had the lowest ratios ($p < 0.05$). Receiver operating characteristic (ROC) analysis showed that PLR+AST/ALT can produce highly sensitive and moderate specificity, distinguishing patients with RA from HCs, with a sensitivity of 91.1%, specificity of 75.3%, and area under the ROC curve (AUC) of 0.907. Spearman's analysis showed the PLR is negatively correlated with the erythrocyte sedimentation rate and C-reactive protein levels ($p < 0.005$).

Conclusions Combined detection of PLR and AST/ALT is better than each indicator individually and can improve the diagnostic efficiency of RA.

PO-0810

乳腺癌来源外泌体微小 RNAs 和长链非编码 RNAs 的研究进展

叶婷、万雪、刘靳波
西南医科大学附属医院

外泌体是一种直径为 30-150nm 的微囊泡，其内部包含蛋白质、脂质、代谢产物、微小 RNAs（miRNAs）和长链非编码 RNAs（LncRNAs）等活性物质，它通过介导细胞间信息交流、调节肿瘤微环境促进肿瘤发生发展。miRNAs 和 LncRNAs 是非编码 RNAs 中重要的组成部分，通过外泌体介导在乳腺癌的发生发展中起重要作用。本文主要总结乳腺癌细胞来源外泌体 miRNAs 和 LncRNAs 在乳腺癌进展、微环境和耐药等方面的作用，乳腺癌微环境来源外泌体 miRNAs 和 LncRNAs 对乳腺癌发生发展的影响，以及外泌体 miRNAs 和 LncRNAs 作为乳腺癌的生物标志物的临床潜力。

PO-0811

PD-1 等免疫负调控分子在早期宫颈鳞癌患者手术治疗前后外周血中的表达情况分析

林雨虹
福州市第一医院

目的 探讨 PD-1 及相关细胞因子在宫颈鳞癌(Cervical squamous cell carcinomas, CSCC)外周血中表达的特点及临床意义。
方法 选择 2018 年 1 月到 2020 年 12 月福州市第一医院手术治疗的 50 例 CSCC 患者作为研究对象，通过 ELISA 法和流式细胞术检测外周血中 PD-1、PD-L1、叉头样转录因子 p3（Foxp3）和调节性 T 淋巴细胞(Regulatory T lymphocytes, Tregs)的表达水平，并术后随访 6 个月。
结果 CSCC 组外周血中 PD-1 蛋白(ELISA)是正常对照组的约 59.5 倍(72.64/1.22)，PD-L1 约 10 倍(2.99/0.30)，Foxp3 约 17 倍(38.92/2.23)，且在患者手术后随访中观察到下降趋势；同时 CD4+占淋巴细胞比例是正常对照的约 1.7 倍(0.59/0.34)，Tregs 约 1.7 倍(0.12/0.07)，以及 PD-1+的 Tregs 约 1.8 倍(0.75/0.41)。
结论 PD-1、PD-L1、Foxp3 以及 Tregs 是促进 CSCC 发展的重要因素，可作为预判 CSCC 临床手术疗效的潜在的生物靶标。

PO-0812

妊娠晚期血脂与妊娠期并发症及妊娠结局的关系

李偌铱、李新月
空军特色医学中心

目的 近年来随着我国居民生活方式的改变，人群血脂异常总体患病率明显升高，且肥胖及高龄产妇逐渐增多，妊娠期血脂水平会进一步升高，可造成病理性高脂状态。妊娠晚期脂质代谢异常可能导致患者产后发生脂代谢异常的风险增加，且新生儿发生早产、巨大儿、胎儿生长受限及将来患心血管疾病的概率增加，且妊娠期间脂质代谢异常与子痫前期、妊娠期糖尿病、肝内胆汁淤积及自发

性早产发病明显相关，严重影响母儿预后。本文旨在探索妊娠晚期血脂水平与妊娠期并发症及围产期结局的关系，并综合分析孕晚期血脂水平对妊娠结局的影响。
方法 回顾性选取我院 2018 年 3 月至 2019 年 2 月定期产前检查并分娩的孕晚期孕妇，分为血脂正常组和血脂异常组，并收集所有孕妇产检资料及妊娠结局资料，比较不同孕期并发症孕妇的血脂水平，并比较血脂正常组和异常组不良妊娠结局的发生情况。
结果 血脂异常组孕妇年龄、孕前 BMI 及孕晚期 BMI 均明显高于血脂正常组，差异有统计学意义(P<0.05)；血脂异常组 GDM（妊娠期糖尿病）、HDCP（妊娠期高血压）发病率均高于血脂正常组，但无统计学差异(P>0.05)；孕晚期高 TC 及 LDL-C 降低是妊娠期糖尿病的危险因素(P<0.05)；孕晚期血脂指标与 HDCP 发生风险没有相关性(P>0.05)；妊娠期高血压疾病组 TG 明显高于正常妊娠组，差异有统计学意义(P<0.05)；但血脂正常组与血脂异常组的围产期结局包括剖宫产、早产、巨大儿、胎膜早破、胎儿窘迫及产后出血，均没有发现统计学差异(P>0.05)。
结论 妊娠期脂代谢异常与妊娠期并发症关系密切，因此监测孕期血脂水平并及时控制，有利于改善母婴妊娠结局。

PO-0813

Analysis of association between thyroid-associated hormones and cardiovascular risk factors in older people by mining real-world data

Chaochao Ma、Xinqi Cheng、Ling Qiu
Department of Clinical Laboratory, Peking Union Medical College Hospital, Peking Union Medical College & Chinese Academy of Medical Science

Background The association between thyroid-related hormones and cardiovascular disease risk factors(CRFs) in older people is unclear. The study aims to analyze the association between thyroid-related hormones and CRFs and their clustering in the elderly.
Methods 3213 older people were included in our study. Thyroid-related hormones and other medical information were downloaded from electronic health records. Binary logistic regression models were established to calculate the odds ratios (ORs) for single CRFs according to the thyroid associated hormones quartile. Disordered multiclass logistic regression was performed to analyze the association between clustering of CRFs and level of thyroid hormones.
Results The influence of TSH of higher level within the reference interval on dyslipidemia was statistically significant. (Q4: OR=1.396, 95% CI :1.104-1.765, P=0.005). The higher level of FT3 level within the reference interval had a association with dyslipidemia (Q4:OR=0.587,95% CI :0.467-0.738,P<0.001) and overweight (Q3:OR=1.433, 95% CI:1.131-1.81; Q4:OR=1.388, 95% CI:1.087-1.771). High level of FT4 within the reference interval is statistically related to diabetes(Q4:OR=1.685, 95%CI 1.050-2.704) and overweight (Q4:OR=0.697, 95% CI:0.554-0.875). Compared with Q1 level, Q2 (OR=0.772, 95% CI: 0.609-0.978, P=0.032), Q3 (OR=0.767,95% CI:0.600-0.979, P=0.033) and Q4 (OR=0.645,95% CI:0.498-0.836, P=0.0001) levels of TT4 had a statistically significant impact on overweight. Individuals with high level of TSH and TT3 within RI were more likely to have clustered CRFs (³3 risk factors) than those with low level, while TT4 was the opposite.
Conclusion The association between thyroid associated hormones and CRFs in elderly were analyzed and it provided reference for thyroid hormone management in patients.

PO-0814

血吸虫病 Sj26GST-mRNA 疫苗的免疫原性研究

廖琳
郴州市第一人民医院

目的 体外合成血吸虫病 Sj26GST-mRNA 候选疫苗并评价其免疫原性。
方法 利用信息学软件分析 Sj26GST 基因序列的密码子偏好性、GC 含量和 mRNA 二级结构，优化 Sj26GST 编码区序列，并将 β 球蛋白 3'和 5'UTR 序列插入优化序列的两端；将上述序列连接到 pcDNA3.1（+）上，体外转录，琼脂糖凝胶电泳鉴定序列的准确性；利用脂质体（Lip2000）将 Sj26GST-mRNA 转染到 HeLa 细胞中，Western blot 鉴定其在真核细胞内的表达；Sj26GST-mRNA 与鱼精蛋白 1:1 混合于 Balb/c 小鼠左后腿股四头肌肌肉注射免疫 3 次（每间隔两周免疫一次），分别在 2、4、6、8 周小鼠尾部收集免疫后的血清，ELISA 法检测各组小鼠血清中 Sj26GST 特异性 IgG 水平；无菌分离各组小鼠脾淋巴细胞，ELISA 法检测脾淋巴细胞上清中 TNF-α、INF-γ、IL-4、IL-6 的含量其增值水平；流式细胞术分析了 Sj26GST-mRNA 免疫 Balb/c 小鼠脾细胞内 T 淋巴细胞表型。
结果 生物信息学软件分析显示优化后的 Sj26GST 基因序列具有更高的稳定性，体外转录后琼脂糖凝胶电泳显示 PCR 扩增到与预期大小（5000bp）一致的特异性条带；Western blot 检测 Sj26GST-mRNA 成功在 HeLa 细胞中表达；Sj26GST-mRNA 免疫 Balb/c 小鼠后第 2 周即产生 Sj26GST 蛋白特异性抗体，第 8 周达到最大；末次免疫 14 d 后，Sj26GST-mRNA 免疫的 Balb/c 小鼠脾淋巴细胞增殖指数明显高于对照组；Sj26GST-mRNA 免疫的 Balb/c 小鼠脾淋巴细胞上清中 TNF-α、IFN-γ、IL-6 含量显著增加，IL-4 的含量没有统计学差异。
结论 成功构建稳定表达的 Sj26GST-mRNA 候选疫苗可诱导高水平的特异性 Sj26GST 蛋白抗体和 Th1 型细胞免疫应答。

PO-0815

关于中国计量学院研制的新型冠状病毒核酸标准物质 GBW(E)091089 和 GBW(E)091090 适用性讨论

吴俊华
杭州迪安医学检验中心有限公司

目的 验证中国计量学院新型冠状病毒核酸标准物质 GBW(E)091089、GBW(E)091090 的 1ab(ORF1ab)基因片段是否在中山大学达安基因股份有限公司、圣湘生物科技股份有限公司、上海复星长征医学科学有限公司、上海伯杰医疗科技有限公司研制的新型冠状病毒核酸检测试剂盒（RT-PCR 法）1ab(ORF1ab)基因检测片段范围内。
方法 将中国计量学院新型冠状病毒核酸标准物质 GBW(E)091089 稀释，按照各试剂盒要求反应体系加入反应液，重复 20 孔，上扩增仪进行扩增，分析 1ab(ORF1ab)基因检出情况。
结果 上海伯杰医疗科技有限公司研制的新型冠状病毒核酸检测试剂盒（RT-PCR 法）能够检测出 1ab(ORF1ab)基因，中山大学达安基因股份有限公司、圣湘生物科技股份有限公司、上海复星长征医学科学有限公司研制的新型冠状病毒核酸检测试剂盒（RT-PCR 法）不能检出 1ab(ORF1ab)基因。
结论 中国计量大学新型冠状病毒核酸标准物质 GBW(E)091089、GBW(E)091090 的 1ab(ORF1ab)基因片段在上海伯杰医疗科技有限公司研制的新型冠状病毒核酸检测试剂盒（RT-PCR 法）1ab(ORF1ab)基因检测片段范围内，不在中山大学达安基因股份有限公司、圣湘生物科技股份有限公司、上海复星长征医学科学有限公司研制的新型冠状病毒核酸检测试剂盒（RT-PCR 法）1ab(ORF1ab)基因检测片段范围内。若要对达安、圣湘、复星新型冠状病毒核酸检测试剂盒（RT-

PCR 法）1ab(ORF1ab)基因检测结果进行验证或评价则需选择开放阅读框 1ab(ORF1ab)基因全基因片段的标准物质。

PO-0816

锌指蛋白 ZNF692 在乳腺癌细胞中高表达可促进乳腺癌的发生发展

张文武、肖斌、李林海
广州医科大学附属第六医院 清远市人民医院检验医学部

目的 探究 ZNF692 在乳腺癌细胞中的表达水平及其对乳腺癌细胞增殖、侵袭和迁移的影响以及对其分子机制初步探索。
方法 利用 TCGA 数据库挖掘 ZNF692 在乳腺癌组织及癌旁组织中的差异表达，分析 ZNF692 的表达与分子分型、TNM 分级和临床分期等临床病理特征的相关性；通过慢病毒系统构建稳定表达 ZNF692 的乳腺癌细胞株；通过 CCK8 实验和克隆形成实验分析过表达 ZNF692 对乳腺癌细胞增殖及集落形成能力的影响；通过伤口愈合实验、Transwell 细胞迁移、侵袭实验阐明过表达 ZNF692 对乳腺癌细胞体外迁移和侵袭的影响；采用免疫荧光实验明确 ZNF692 的亚细胞定位；利用 RNA-seq 联合 CUT&TAG 实验对 ZNF692 的下游靶基因进行筛选并通过 RT-qPCR 验证。
结果 ZNF692 在乳腺癌组织中表达显著上调（$P<0.001$）；对于不同的乳腺癌分子分型，ZNF692 在 TNBC 型、HER2+型、Luminal A 型、Luminal B 型均表达升高；过表达 ZNF692 促进乳腺癌细胞增殖、侵袭和迁移；ZNF692 定位于细胞核；ZNF692 能够影响 JAK1、SOCS3 等基因的表达。
结论 ZNF692 在乳腺癌细胞中高表达，可能通过 JAK-STAT 通路促进乳腺癌发生发展，有望作为乳腺癌诊断、治疗的潜在分子靶标。

PO-0817

陕西省 1 万例女性叶酸代谢能力分析

梁建萍、文少佳、张强、朱亚荣
西安金域医学检验所有限公司

目的 分析陕西省女性叶酸代谢能力水平，为指导女性个体化合理补充叶酸以及预防新生儿出生缺陷等疾病提供指导意义。研究将女性孕期缺乏叶酸的风险，分为四个等级，即“未见风险”“低度风险”“中度风险”“高度风险”，从而根据风险程度合理用药。
方法 本研究收集了 1 万例女性外周血标本并提取基因组 DNA，之后采用实时荧光定量 PCR 的方法进行叶酸代谢基因检测，分别对亚甲基四氢叶酸还原酶（MTHFR）基因的 C677T、A1298C 位点以及甲硫氨酸合成酶还原酶（MTRR）基因 A66G 位点进行基因检测，最后根据基因型结果并结合现有文献的数据所总结的公式评估叶酸代谢能力水平从而判断其风险等级。
结果 所检测的陕西省 1 万例女性样本中，对于 MTHFR 基因 C677T、A1298C 位点而言 A1298C 位点突变频率小于 C677T 位点的突变频率。同时综合 MTRR 基因 A66G 位点基因型， 统计得出“未见风险”“低度风险”“中度风险”“高度风险”四个风险等级的人群占比分别为 22%、39%、27%、12%。“高度风险”人群明显少于其他三个风险等级人群。
结论 陕西省女性 MTHFR 基因和 MTRR 基因基因型存在差异，叶酸代谢能力不同，存在不同程度的叶酸缺乏。叶酸代谢基因因此需要进行叶酸代谢基因检测，根据分型结果给予个体化补服合适剂量的叶酸，以预防出生缺陷。

PO-0818

Long non-coding RNA LINC00641 promotes the growth and invasiveness of hepatocellular carcinoma by sponging miR-501-3p

hai tao xie
Department of Clinical Laboratory, The First Affiliated Hospital, University of South China

Long non-coding RNA LINC00641 has been reported to regulate tumor progression in several cancers. However, the expression and function of LINC00641 in hepatocellular carcinoma (HCC) is still unclear. In this study, we measured the expression of LINC00641 in 79 pairs of HCC and adjacent normal liver tissues. The clinical significance of LINC00641 in HCC was explored. We also investigated the function of LINC00641 in HCC proliferation and invasion. We observed that LINC00641 expression was significantly increased in HCC relative to normal tissues ($P < 0.0001$). High expression of LINC00641 was significantly associated with vascular invasion, advanced TNM stage, and reduced overall survival in HCC patients. Knockdown of LINC00641 inhibited the proliferation, colony formation, and invasion of HCC cells. In contrast, overexpression of LINC00641 promoted HCC cell growth and invasiveness. In vivo studies confirmed that knockdown of LINC00641 restrained tumorigenesis of HCC cells. Mechanistic studies revealed that LINC00641 inhibited the expression of miR-501-3p, which has been previously reported to act as a tumor suppressor in HCC. Furthermore, luciferase reporter assays validated that LINC00641 harbored a target site for miR-501-3p. Rescue experiments demonstrated that LINC00641-induced proliferation and invasion of HCC cells was reversed by co-expression of miR-501-3p. Taken together, LINC00641 contributes to aggressive phenotype of HCC cells by sponging miR-501-3p and represents a promising therapeutic target for this disease.

PO-0819

长链非编码 RNA OIP5-AS1 在鼻咽癌细胞株 5-8F 和 CNE-1 中的生物学功能研究

谢海涛
南华大学附属第一医院

目的 探讨长链非编码 RNA OIP5-AS1 对鼻咽癌细胞株 5-8F 和 CNE-1 生物学功能的影响。
方法 构建 OIP5-AS1 慢病毒干扰载体，转染鼻咽癌细胞株 5-8F 和 CNE-1，运用流式细胞术、CCK8 实验、划痕试验等检测沉默 OIP5-AS1 对鼻咽癌细胞生物学功能的影响。
结果 敲除 OIP5-AS1 基因后，细胞 G1 期百分比增高、细胞增殖速度变慢和划痕中心区细胞数减少。
结论 长链非编码 RNA OIP5-AS1 能促进鼻咽癌细胞 5-8F 和 CNE-1 的增殖、侵袭和转移能力。

PO-0820

Assessment of patient-based real-time quality control algorithm performance on different types of analytical error

Xincen Duan[1]、Beili Wang[1]、Jing Zhu[1]、Wenqi Shao[1]、Hao Wang[1]、Junfei Shen[1]、Wenhao Wu[1]、Wenhai Jiang[1]、Kwok Leung Yiu[2]、Baishen Pan[1]、Wei Guo[1]
1. Department of Laboratory Medicine, Zhongshan Hospital, Fudan University
2. Roche Diagnostics

Background Patient-based real-time quality control (PBRTQC) has gained attention because of its potential to detect analytical errors in situations wherein internal quality control is less effective. Multiple PBRTQC algorithms have been proposed. However, there is a lack of comprehensive comparison of the performance of PBRTQC algorithms on different types of analytical errors. Thus, a comparative study was conducted.
Methods The performance of six different PBRTQC algorithms was evaluated on three types of analytical errors using 906,552 test results for outpatient serum sodium, chloride, alanine aminotransferase, and creatinine at the Department of Laboratory Medicine at Zhongshan Hospital, Fudan University in 2019. The performance results were compared and assessed.
Results The moving average, moving median, exponentially weighted moving average, and moving quartiles performed similarly for effectively detecting constant errors (CE) and proportional errors (PE) but not random errors (RE). The moving sum of positive patients and moving standard deviation could detect RE for serum sodium and chlorides but performed poorly on detecting the CE and PE.
Conclusions This study demonstrated the importance of assessing the potential source of error of a particular analyte and the corresponding type of analytical error before choosing a quality control algorithm for implementation.

PO-0821

POCT 项目的院内质量管理体会

孙瑞营、续薇
吉林大学第一医院

目的 为了面对当前 POCT 操作人员结构复杂、设备类型多样、质量保证与信息化建设急待提高的现状，提出 POCT 质量要求及院内管理方案。
方法 查阅近年来 ISO/TS、CLSI、GB/T、POCT 中国专家共识、CAP、JCI 医院评审标准、三级综合医院评审标准实施细则等文件的要求，综述对 POCT 质量管理的要求；总结近三年来我院临床 检验（质控）中心共五次对全院 57 个科室送检的 5418 份标本进行 POCT（血糖、血气、HCG）项目比对的数据，提出 POCT 管理质量管理中对人员资质、设备管理、室内质量控制、设备比对、项目比对的要求。
结果 ①建立院内 POCT 统一的组织管理模式；②发布院内 POCT 质量管理体系文件 24 份并有效实施；③院内培训 POCT 操作人员 2874 人，考核合格后给予院内授权 2844 人，占院内护士总人数的 90%；④POCT 科室开展室内质控占 100%；⑤开展全院 POCT 检验的项目比对，比对结果符合率>80%为合格；血糖项目参加比对仪器共 908 台次，一次性符合率 100%为 241 台次（26.54%），一次性符合率 80%为 142 台次（15.64%），校准后一次性符合率 100%为 136 台次（14.98%），校准后一次性符合率 80%为 124 台次（13.66%）；血气分析项目参加比对仪器共 83 台次，均合格；HCG 项目参加比对仪器共 1 台，均合格；⑥全部科室应用 POCT 信息化操作软件，基本实现院内 POCT 管理。

结论 对照国内外 POCT 质量管理要求，分享院内 POCT 管理做法，相信能够加强院内 POCT 质量管理的同质化与一致性，保证 POCT 检验在临床诊疗中发挥作用。

PO-0822

大数据回顾性分析策略优化临床常规生化报告 TAT

朱晶、邵文琦、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 探讨通过大数据回顾性分析策略优化常规生化报告 TAT。
方法 回顾性分析 2020 年 4 月至 12 月常规生化门诊标本每个工作日各时间段平均、最大和最小测试数，以及同时段全自动生化分析仪平均、最大和最小负荷量，优化门诊标本和病房标本上样方式和仪器负荷分配方式。统计优化前后的常规生化门诊和病房报告 TAT 各时间点：门诊标本和病房标本的接收时间、上前处理仪器时间、上全自动生化分析仪时间、出结果时间和报告确认时间。计算 TAT 各时间段的中位数时间，90%百分位数时间和极值时间。
结果 TAT 大数据回顾性分析策略能更科学有效地根据实时标本量和测试数指导工作人员进行门诊和病房标本间的上样和仪器负荷分配。经本研究策略优化后的门诊常规生化标本从上前处理仪器至上全自动生化分析仪的中位数时间从 23.6 分钟降至 18.3 分钟（下降 22.5%）；从上全自动生化分析仪至出结果的中位数时间从 38.7 分钟降至 26.9 分钟（下降 30.5%）。同期病房标本 TAT 并无明显变化。
结论 通过以 TAT 大数据回顾分析为策略，指导门诊和病房标本上样和仪器负荷分配方式，可有效提升工作效率，降低标本接收至出结果的时间。在不影响病房标本 TAT 的前提下，提高门诊标本检测速度，缩短门诊标本 TAT。

PO-0823

活动性肺结核患者多功能 T 细胞的免疫应答

秦爽、陈瑞麒、蒋雨洁、朱恒悦、陈栎江、陈彦凡、沈默、林向阳
温州医科大学附属第一医院

目的 结核病仍然是全世界传染病致死的主要原因。本项研究中，我们旨在评估肺结核患者外周血 T 细胞的免疫状态，并进一步探索多功能 T 细胞的作用。
方法 本研究招募了 30 例活动性肺结核（APTB）患者，30 例潜伏性结核感染（LTBI）患者，25 例治愈性肺结核（CPTB）患者和 25 例健康对照（HCs）。 通过流式细胞仪检测外周血 T 细胞的表型和功能。用结核分枝杆菌（Mtb）特异性抗原 ESAT-6-CFP10 短期刺激各组患者的外周血单个核细胞（PBMCs）和 APTB 患者的胸水细胞（PFCs）后，检测 Mtb 特异性 $CD4^+$ T 细胞和 Mtb 特异性 $CD8^+$ T 细胞的频率、分化程度和细胞因子的表达，并进一步检测其多功能 T 细胞的频率和迁移能力。
结果 与 HCs 和 LTBI 患者相比，APTB 患者的 $CD4^+$ T 和 $CD8^+$ T 细胞较少，但 $CD8^+$ T 细胞上颗粒酶 A，颗粒酶 B 和穿孔素的表达增加。 与 LTBI 和 CPTB 患者相比，APTB 患者的结核分枝杆菌特异性 $CD8^+$ T 细胞表现为具有更高分化程度的 $CD45RA^-CCR7^-$ 细胞，并且其具有更高频率的多功能 $CD4^+$ T 和 $CD8^+$ T 细胞。 重要的是，APTB 患者胸水中多功能 $CD4^+$ T 细胞的频率高于外周血，并且其外周血中表达迁移受体 CXCR3 的多功能 $CD4^+$ T 细胞的比例降低，而其 CXCR3 对应的配体，即趋化因子 MIG，IP-10 和 I-TAC，在血浆和胸水中的浓度显著升高，且胸水中的浓度显著高于外周血由此形成浓度梯度。
结论 APTB 患者的 T 淋巴细胞减少可能导致 $CD8^+$ T 细胞的代偿性激活，其外周血中的多功能 $CD4^+$ T 细胞可以在 CXCR3 和相关的趋化因子的作用下迁移到肺部感染部位。 多功能 $CD4^+$ T 细

胞和多功能 $CD8^+$ T 细胞频率升高可作为活动性肺结核的标志，并在监测疾病治疗疗效中具有重要意义。

PO-0824

The study on the impact of COVID-19 on common respiratory viruses infections in Southwest China

Yanjun Si、minjin wang、tangyuheng liu、huiyu zhong、xingbo song、binwu ying
West China Hospital，Sichuan University

Objectives This study aims to investigate the impact of COVID-19 on common respiratory viruses infections. Knowing the epidemiological patterns of common respiratory viruses may be valuable to improve the diagnostic and therapeutic efficacy of patients during the coronavirus disease-19 pandemic.
Method we analyzed common 12 respiratory tract pathogens in clinical specimens collected from 1206 patients in in Southwest China with fever and respiratory symptoms during Nov 16, 2019 through January 15, 2020 (pre-pandemic period), and from 2343 patients during January 16, 2020 through Mar 16, 2020. All data were analyzed to unravel the epidemiological patterns.
Results The detection rates of the human rhinovirus (15.01% VS 8.02%), influenza A H3N2 (9.78% VS 2.90%) and bocavirus (4.81% VS 1.75%) were appreciably reduced but the influenza B virus (0.33% VS 3.88%), mycoplasma pneumoniae (, 1.16% VS 2.52%) and human metapneumovirus (2.99% VS 3.37%) were appreciably increased among the patients during the COVID-19 pandemic. Moreover, the co-infection was observed in 212 specimens. Notably, bocavirus was the most common virus tending to occur in co-infection with other respiratory pathogens in this study.
Conclusion Interventions for mitigating spread of SARS-CoV-2 likely also reduced transmission of other pathogens. However, the increased positive rates of influenza B virus, mycoplasma pneumoniae and human metapneumovirus also suggested an risk of infection during the pandemic period. The findings highlight the importance of understanding the transmission patterns of the common respiratory virus in COVID-19 regions, which can provide information support for the development of appropriate treatment plans and health policies, while eliminating unnecessary fear and tension.

PO-0825

长链非编码 RNA RP11-490M8.1 抑制脂多糖诱导的人脐静脉内皮细胞炎症

刘雪辉[1]、伍绍国[1]、胡炎伟[2]
1. 广州市第十二人民医院广州市职业病医院
2. 广州市妇女儿童医疗中心

目的 探讨 LncRNA RP11-490M8.1 在内皮细胞中对炎症因子调控作用的初步研究。
方法 我们收集三对 AS 斑块组织和动脉内膜正常组织进行基因芯片分析，挖掘表达显著异常的基因；用脂多糖处理内皮细胞、构建慢病毒载体过表达 LncRNA RP11-490M8.1，以实时荧光定量 PCR（qRT-PCR）检测 LncRNA RP11-490M8.1 和细胞炎症因子如 TNF-α、IL-6，NF-κB 的 RNA 水平，以免疫印迹（western blot）检测细胞炎症因子（IL-6,TNF-α，NF-κB）的蛋白表达水平；将内皮细胞接种于 6 孔细胞培养板中，分为 4 组进行干预：①慢病毒空载体对照组（对照组）；②慢病毒空

载体加 LPS（LV-MOCK +LPS）；③慢病毒过表达组（LV- LncRNA RP11-490M8.1）；④ LncRNA RP11-490M8.1 过表达加 LPS（LV-LncRNA RP11-490M8.1 +LPS）。
结果 基因芯片分析发现 LncRNA RP11-490M8.1 在 AS 斑块中表达下调，qRT-PCR 和 western blot 结果显示 LPS 上调炎症因子（IL-6,TNF-α，NF-κB）的表达；慢病毒过表达 LncRNA RP11-490M8.1 后炎症因子表达下调，表明 LncRNA RP11-490M8.1 负向调控炎症因子的表达；分组干预实验结果显示 LncRNA RP11-490M8.1 能减弱 LPS 对炎症因子的诱导作用。
结论 在内皮细胞中 LncRNA RP11-490M8.1 抑制 LPS 诱导的炎症因子（IL-6,TNF-α，NF-κB）表达，LncRNA RP11-490M8.1 很可能是阿托伐他汀钙发挥抗炎作用的靶向分子，为动脉粥样硬化的发展提供新的方向。

PO-0826

Bioinformatics analysis of differentially expressed genes in bladder cancer

Tingting Long、Shanying Deng、Yuemei Chen、Chunying Zhang、Hong Jiang
West China Hospital of Sichuan University

Objective To identify the key candidate genes in bladder cancer using bioinformatics analysis.
Methods The gene expression profiles of GSE40355, GSE37815 and GSE13507 were downloaded from the Gene Expression Omnibus (GEO) database. The differentially expressed genes (DEGs) between bladder cancer and normal samples were extracted with GEO2R online tool. The gene ontology (GO) functional and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses of DEGs were performed by DAVID. A protein-protein interaction (PPI) network was constructed using STRING and visualized in Cytoscape software. MCODE was used for module analysis of the PPI network. For the analysis of overall survival among the key identified genes, Kaplan-Meier method was implemented. At last, GEPIA and UALCAN were applied to determine the expression of the core genes in bladder cancer.
Results The 215 DEGs were identified including 31 upregulated and 184 downregulated genes, and enriched in cellular component (CC), biological processes (BP) as while as molecular function (MF). As for the KEGG-pathway, the DEGs were mainly associated with staphylococcus aureus infection, systemic lupus erythematosus, complement and coagulation cascades. The PPI network contained 170 nodes and 532 edges, and AURKB, CCNB2, DCN, PLEK, C1QB, CXCL12 and CSF1R were screened as hub genes. Beside the three most significant sub-modules of DEGs were extracted. Two of the 7 genes, including DCN and CXCL12 were associated with the overall survival of patients with bladder cancer. Both GEPIA and UALCAN databases indicated that expression of DCN and CXCL12 were down-regulated in bladder cancer model.
Conclusion The identified DEGs, especially the core genes may provide potential targets for the diagnosis and treatment of bladder cancer.

PO-0827

Bioinspired Soft Robot with Incorporated Microelectrodes

Ting Wang
the First Affiliated Hospital of Nanjing Medical University,

Bioinspired soft robotic systems that mimic living organisms using engineered muscle tissue and biomaterials are revolutionizing the current biorobotics paradigm, especially in biomedical research. Recreating artificial life-like actuation dynamics is crucial for a soft-robotic system.

However, the precise control and tuning of actuation behavior still represents one of the main challenges of modern soft robotic systems.

This method describes a low-cost, highly scalable, and easy-to-use procedure to fabricate an electrically controllable soft robot with life-like movements that is activated and controlled by the contraction of cardiac muscle tissue on a micropatterned sting ray-like hydrogel scaffold.

The use of soft photolithography methods makes it possible to successfully integrate multiple components in the soft robotic system, including micropatterned hydrogel-based scaffolds with carbon nanotubes (CNTs) embedded gelatin methacryloyl (CNT-GelMA), poly(ethylene glycol)diacrylate (PEGDA), flexible gold (Au) microelectrodes, and cardiac muscle tissue. In particular, the hydrogels alignment and micropattern are designed to mimic the muscle and cartilage structure of the sting ray. The electrically conductive CNT-GelMA hydrogel acts as a cell scaffold that improves the maturation and contraction behavior of cardiomyocytes, while the mechanically robust PEGDA hydrogel provides structural cartilage-like support to the whole soft robot. To overcome the hard and brittle nature of metal-based microelectrodes, we designed a serpentine pattern that has high flexibility and can avoid hampering the beating dynamics of cardiomyocytes. The incorporated flexible Au microelectrodes provide electrical stimulation across the soft robot, making it easier to control the contraction behavior of cardiac tissue.

PO-0828

2013-2020 年寄生虫室间质评结果回顾性分析及总结

邓山鹰
四川大学华西医院

目的 通过对寄生虫形态学的室间质评结果进行回顾分析及总结，进一步提高临床检验人员发现和识别寄生虫的能力。

方法 回顾分析 2013~2020 年我室参加寄生虫形态学检验室间质评的 200 份样本回报结果，其中 80 份来自美国病理家协会，120 份来自卫生部临检中心，统计回报结果正确率，分析寄生虫（卵）辨认错误的原因，并总结少见及相似寄生虫的形态特征和鉴别要点。

结果 200 份样本中 195 份识别结果正确，正确率为 97.5%；80 份美国病理家协会样本中 77 份识别正确，3 份识别错误，12 份未评分，正确率为 96.3%；120 份卫生部临检中心样本中 118 份识别正确，2 份识别错误，正确率为 98.3%。美国病理家协会与卫生部临检中心样本共涉及 30 种寄生虫 47 种不同生活史形态。相似寄生虫卵鉴别包括：阔节裂头绦虫卵、肺吸虫卵、肝片形吸虫卵和姜片虫卵，脱蛋白质膜受精蛔虫卵与退变钩虫卵，钩虫卵与东方毛圆线虫卵，马来微丝蚴与班氏微丝蚴；少见寄生虫卵鉴别包括：微小膜壳绦虫卵与缩小膜壳绦虫卵；大便中食物残渣与寄生虫卵的鉴别及各种包囊的鉴别。

结论 通过阶段性收集整理寄生虫室间质评资料进行回顾分析，并定期进行混合虫卵样本的镜下复习、寄生虫图谱复习以及少见与相似寄生虫（卵）的形态复习，可提高寄生虫检验质量，提升检验人员的能力。

PO-0829

GRK3 在口腔鳞癌细胞增殖、迁移及侵袭中的作用

张晗、罗清琼、朱丽萍、陈福祥
上海交通大学医学院附属第九人民医院

目的 探讨沉默 G 蛋白偶联受体激酶 3（GRK3）对口腔鳞癌（OSCC）细胞增殖、迁移和侵袭的影响及其可能机制。

方法 利用 Oncomine 数据库分析 GRK3 在正常口腔组织及 OSCC 组织中的表达水平。用 RNA 干扰技术下调 OSCC 细胞 WSU-HN6 和 CAL27 的 GRK3 表达水平，用 qPCR 法验证干扰效率。用 CCK-8 法和流式细胞术分别检测 OSCC 细胞的增殖能力和凋亡水平，用 Transwell 小室法检测 OSCC 细胞的迁移和侵袭能力，用 qPCR 法检测细胞周期、上皮-间质转化（EMT）和基质金属蛋白酶（MMPs）相关分子的表达水平。
结果 GRK3 在 OSCC 组织中的表达水平显著高于正常口腔组织（P<0.001）。转染 si-GRK3 后，OSCC 细胞的 GRK3 表达水平均下调 70%以上。沉默 GRK3 可显著抑制 OSCC 细胞的增殖、迁移和侵袭能力（均 P<0.001），对细胞凋亡无显著影响（P＞0.05）。下调 GRK3 后，OSCC 细胞的细胞周期蛋白 D1（Cyclin D1）、Cyclin D3、周期蛋白依赖性激酶 2(CDK2)和 CDK4 表达降低（均 P<0.05）；EMT 相关分子波形蛋白（Vimentin）、Zeb1 和 Slug 表达降低，E-钙黏蛋白（E-Cadherin）表达升高（均 P<0.05）；MMP3 和 MMP9 表达降低（均 P<0.05），MMP2 和 MMP7 无明显变化（均 P＞0.05）。
结论 GRK3 可通过调节细胞周期相关分子促进 OSCC 细胞的增殖能力，并通过调控 EMT 和 MMPs 促进其迁移和侵袭能力。

PO-0830

无创性 IgA 肾病病理分级诊断模型建立

刘记宏、刘子杰
昆明医科大学第一附属医院

目的 分析 IgA 肾病 Lee 病理分级与高血压病程及临床常规实验室指标之间的相关关系，通过不同病理分级研究对象的实验室指标组间差异，建立无创性病理分级诊断模型。
方法 采集昆明医科大学第一附属医院肾内科经肾穿刺活检确诊的 112 例原发性 IgA 肾病患者，收集患者的病历资料及实验室常规监测指标，通过回顾性分析，采用单因素和多因素回归分析逐步筛选变量，最终通过有序 Logistic 回归构建 IgA 肾病的无创性病理分级诊断模型。
结果 高血压病程与 IgA 肾病 Lee 病理分级之间显著相关(r=0．246，p=0．009)；同时，血肌酐（OR=1.31，p=0.000）、尿酸（OR=1.58，p=0.045）、尿总蛋白（OR=1.26，p=0.039）、无抽烟史（OR=0.27，p =0.025）、血红蛋白（OR=0.97，p =0.028）与 IgA 肾病 Lee 氏分级有相关性。通过患者的血红蛋白、白蛋白、血肌酐、尿酸、血清 C3、尿总蛋白数据，建立了 IgA 肾病 Lee 病理分级诊断模型，该模型准确性高达 74%（c2 =62.248，p=0.000），可为临床诊疗提供有力依据。
结论 我们最终通过有序 logistic 回归建立了无创性 IgA 肾病 Lee 病理分级诊断模型。

PO-0831

The functional characteristics and clinical value of peripheral NK and NKT cells in patients with chronic hepatitis B cirrhosis

Xin Wei[1]、Weifeng Yao[2]、He Chen[1]、Zhongxin Wang[1]
1. The First Affiliated Hospital of Anhui Medical University
2. 浙江省立同德医院

Objective To explore the functional characteristics of peripheral NK and NKT cells in patients with chronic hepatitis B cirrhosis (HBV-LC) and their correlation with the disease.
Methods Collected 25 compensated HBV-LC patients (HBV-CLC), 25 decompensated HBV-LC patients (HBV-DLC) and 25 health individuals (HC) at the same period. Detected changes in the frequency and absolute number of peripheral NK and NKT cells. Expression of activation markers,

activating- and inhibitory receptors, and cytotoxic molecules on peripheral NK and NKT cells were detected, and analyzed the correlation between NK/NKT and HBV-LC.
Results Compared with HC, the frequency and absolute number of peripheral NK and NKT cells in HBV-LC patients were significantly reduced (P<0.05), but HBV-DLC patients had significantly higher expression of activation markers (P<0.05); although there was no significant difference in the expression of activating- and inhibitory receptors (P>0.05), peripheral NKT cells in HBV-LC patients significantly expressed cytotoxic molecules, while the cytotoxic ability of peripheral NK cells in HBV-DLC patients was significantly impaired (P>0.05). Besides, NK/NKT also has a certain diagnostic value for HBV-DLC.
Conclusion The functional characteristics of peripheral NK and NKT cells in HBV-LC patients, especially in HBV-DLC patients, has undergone significant changes, which have certain diagnostic value for HBV-DLC. These findings may provide a new perspective and theoretical basis for the immune prevention and treatment of HBV-LC patients.

PO-0832

改良胶体金试剂盒检测广州地区人群弓形虫感染现状

杨兆收[1,2]、官煜彬[2]、杨小蓉[2]、陈少莲[2]
1. 广东药科大学
2. 广东药科大学附属第一医院

目的 前期我们改造了检测弓形虫感染的胶体金试剂盒，检测人体内抗弓形虫抗原的 IgG 和 IgM 抗体，诊断弓形虫感染与否。其特异性和灵敏性明显提高。本研究旨在此试剂盒检测广州地区人群的感染现状。
方法 收集 2020 年 05 月-2020 年 07 月广东药科大学附属第一医院住院病人和体检健康人的新鲜分离的血清。其中住院病人血清 637 个，体检健康人血清 202 个。根据公司提供的操作说明书，定性检测血清中的人抗弓形虫 IgG 抗体和 IgM 抗体。检测结果用阴性或阳性表示。通过卡方检验分析住院病人和健康人的弓形虫感染差异性，以及不同性别、年龄段、不同病种人群之间的感染差异性。
结果 胶体金检测结果显示，广州地区人群弓形虫感染阳性率为 6.55%。IgG 单阳性率 4.65%，IgM 单阳性率 2.03%，双阳性率 0.24%。其中年轻组的 IgM 阳性率高于老年组（Old 0.93%，Young 2.73%，P=0.072）。住院病人 IgG 阳性率大于健康人（Inpatients 5.45%，Health 2.48%，P=0.079）。此外男性感染阳性率高于女性（Female 5.13%，Male 7.91%，P=0.106）。特别是肿瘤患者中男性阳性率显著大于女性（Female 1.49%，Male 9.00%，P=0.045）。
结论 胶体金试剂盒可以快速检测患者体内抗弓形虫抗体，可及时为诊断弓形虫感染及治疗提供依据。广州地区的男女弓形虫感染率差异明显。肿瘤患者的男女感染率差异尤为显著。性别差异对开辟预防和治疗弓形虫感染的方法提供科学依据。

PO-0833

Research and development of blood transfusion management system based on Bayesian network

Keyu He、Qiang Zhang、Min Zhang
Zhongda Hospital, Southeast University

Aim This study processed the historical blood use data through Bayesian network machine learning, and develops an artificial intelligence blood transfusion management system to optimize patient blood management and blood resource allocation.

Method The database included clinical cases that used red blood cells transfusion to treat anemia in February, May, August, and November 2019, and excluded cases of surgical operations, active bleeding (trauma, gastrointestinal bleeding, etc.), hematological tumors and patients under 10 years old. Set the patient's gender, age, blood type, hemoglobin concentration, application, blood transfusion, and physician as the weight parameters; also set the blood transfusion department's inbound volume, outbound volume, applied volume, resource tension, and difference between application and actual delivery as weight parameters, and establish the original model. Taking 80% of the cases in the database (340 cases) as the training sample, the patient-related information is set as a Bayesian network model with 9 nodes and 17 directed edges. Based on the Bayesian network, the structure learning and parameter learning of the database are carried out, and the red blood cell transfusion management system is finally constructed.
Result The Weka model found that the classification accuracy of the Bayesian network model was 92.9%, and the other 20% of the cases in the database (85 cases) were used as test samples, and the test set prediction accuracy was 92.9%, indicating that the external consistency of the model was good, and the red blood cell transfusion management system was successfully constructed. This study also found that when blood resources become scarcer, some departments/physicians are more inclined to aggressive blood transfusion strategies, to achieve priority to blood resources.
Conclusion This research has successfully constructed a clinical red blood cell transfusion management system, which can help the blood transfusion department identify unqualified red blood cell applications and assist in evaluating physicians/departments. The degree of blood resource tension is an important parameter for unqualified applications.

PO-0834

区域性即时检测管理体系建立的初探

杨翌翔、韦薇、侯彦强
上海市松江区中心医院

目的 区域医学检验中心的出现实现了区域内大部分检验结果的同质化，但保留在基层单位的即时检测项目难以保证检验质量，试图建立区域性即时检测管理体系以提升即时检测项目的管理水平，进而促进区域内即时检测质量的提升。
方法 在区域卫生主管部门的主导下，组织区域医学检验中心，卫健委检验专业质量控制管理小组，和区域内其他医疗卫生机构的相关负责人，成立卫健委区域即时检测管理办公室。分析区域内即时检测管理工作的现状，针对监督管理不到位、人员资质不统一、培训考核不完善以及比对工作不规范四大方面因素，卫健委区域即时检测管理办公室建立起区域性即时检测管理体系，依托区域医学检验中心的多方面优势，采取相关措施，集中力量解决问题。
结果 通过建立区域性即时检测管理体系，实现了卫健委检验专业质量控制管理小组对各医疗机构即时检测工作的有效监管，区域医学检验中心对人员资质、培训考核和比对工作的统一实施，使得区域性即时检测管理工作能够落到实处。
结论 在充分发挥区域医学检验中心专业技术、人才和硬件等方面优势的基础上，初步建立覆盖辖区内医疗机构的区域性即时检测管理体系，能够解决区域内即时检测管理工作中的弱点和难点，提高整个区域即时检测管理体系的管理效率，还能促进各机构医疗质量管理水平的进一步提升。

PO-0835

Amphiphilic peptide-operated nanovalves for targeted drug delivery and control release on mesoporous silica nanoparticles

Fengfeng Zhao
Department of Clinical Laboratory of Zhongda Hospital, Southeast University

Objective A simple but smart pH-responsive end-capped mesoporous silica nanoparticle (MSN)-based drug delivery system (DDS) was demonstrated.
Methods The nanovalve systems were constructed by the self-assembly behavior of peptide-based amphiphile (P45) in the presence of Doxorubicin hydrochloride (Dox). A series of characterizations confirmed that the DDSs had been successfully fabricated.
Results Dox molecules are entrapped by nanovalves in the pores of MSNs, and an in vitro release experiment demonstrated that the P45/Dox@MSNs exhibited “zero premature release” in the physical environment. However, a rapid accelerated release was triggered by an acidic atmosphere in cellular cytosol. Moreover, detailed investigations confirmed that the enhanced cellular uptake of P45/Dox@MSNs due to the RGD motif of the nanovalves, exhibiting an obvious toxicity to cancer cells.
Conclusion Therefore, the multifunctional DDSs constructed here can serve as a promising platform to realize targeted drug delivery and controlled drug release by using diversified bioactive native amphiphilic peptide.

PO-0836

12 例凝血因子 X 缺陷症患者的出血倾向和凝血功能状态的相关分析

汪建茹[2]、白欢[1]、唐宁-通讯作者[1]
1. 华中科技大学同济医学院附属同济医院检验科
2. 湖北医药学院附属襄阳市第一人民医院检验科

目的 分析 12 例凝血因子 X 缺陷症患者出血倾向和凝血功能状态，以提高对该病的认识。
方法 对纳入研究的 12 例患者进行止凝血筛查，检测 APTT 和 PT，利用凝固法检测患者血浆 FX:C，同时对 FX 基因采用 DNA 直接测序法进行基因诊断，并分析 12 例患者出血倾向。
结果 12 例凝血因子 X 缺陷症患者中 10 例为遗传性、2 例为获得性：10 例遗传性凝血因子 X 缺陷症患者中 4 例患者无出血倾向，APTT 和 PT 基本正常，FX:C 为 40%-50%，F X 基因突变都为 c.746A>C 杂合突变；另 5 例患者表现为月经过多、外伤性出血难止等轻微出血倾向，APTT 和 PT 轻度或明显延长，FX:C 为 30%-50%，FX 基因突变分别为 c.871C>T、c.871C>T、c.1252G>A、c.452G>A、c.1252G>A，都为杂合突变；另 1 例患者表现为血便、血尿、下肢淤青等较严重出血倾向，APTT 和 PT 显著延长，FX:C 为<1.0%，FX 基因突变为 c.746A>C 纯合突变，为国际首次报道。2 例获得性凝血因子 X 缺陷症患者中 1 例表现为月经过多，外伤性出血不易止等轻微出血倾向，APTT 和 PT 轻微或明显延长，FX:C 9%；另一例表现为下肢血肿的中度出血倾向，考虑由浆细胞病诱发所致，其 APTT 和 PT 均显著延长，FX:C 为 3%。
结论 除凝血因子 X 重度缺乏者外，凝血因子 X 缺陷症患者通常临床出血症状较轻或无临床出血表现。

PO-0837

预警新兴的医院内感染致病菌：洋葱伯克霍尔德菌复合群

刘玥[1,2]、崔琳[3]、胡屹[2,4]、武洁[5]、许学斌[1]
1. 上海市疾病预防控制中心
2. 复旦大学公共卫生学院
3. 上海市临床检验中心
4. 复旦大学公共卫生安全教育部重点实验室
5. 上海市第一妇幼保健院医院

洋葱伯克霍尔德氏菌复合群(Burkholderia cepacia complex, Bcc)是一组革兰阴性非发酵菌，具有种群生物多样性，其特殊能量新陈代谢路径可作为植物病防治的生物调节剂；Bcc 亦可导致人体不同部位的感染，最常定植于囊性纤维化和慢性肉芽肿患者肺部，也可通过导管等开放性通道感染人体其他器官，易感者有特定人种和年龄组；各类非无菌药剂、医用消毒剂的内源性污染和医疗设备表面污染是导致健康看护机构感染暴发的主要源头；阻断传播链中危害控制的关键点在于增补制药企业基于 Bcc 高敏感性检测方法的标准化法典制定、各类医疗机构潜在院内感染及针对潜在医院感染风险加强 Bcc 基线监测。

PO-0838

基于 TCGA 数据库筛选微小 RNA（miRNA）用于原发性乳腺癌诊断的生物信息

何谦、尹阳
西安交通大学第二附属医院

目的 基于肿瘤基因图谱（the cancer genome atlas，TCGA）数据库筛选微小 RNA（miRNA）用于原发性乳腺癌的早期诊断。
方法 从 TCGA 上下载原发性乳腺癌 miRNA 表达数据，应用多种工具将癌症组与正常组比较获得差异表达 miRNA。分析差异 miRNA 作用的靶基因与乳腺癌高频突变基因之间的关系，得到备选 miRNA，将备选 miRNA 与乳腺癌前 20 名差异表达的 miRNA 求交集，得到目标 miRNA，将目标 miRNA 做 ROC 曲线分析。
结果 TCGA 数据包含原发性乳腺癌组织 1075 例，正常对照乳腺组织 95 例，共有 1870 条 miRNA 的表达数据。其中乳腺癌组织中表达升高至 3 倍以上的 miRNA 90 个，下调至 1/3 的 miRNA 39 个，共得到差异表达显著 miRNA129 个， 利用 miRwalk 软件预测到相对应 18413 个靶基因。我们在 c-Bioportal 数据库中筛选出原发性乳腺癌突变发生率大于 5%的基因 12 个。18413 个靶基因中包含这 12 个高频基因，此 12 个基因为差异 miRNA 的靶基因同时也是高频基因，故将此 12 个基因对应 63 个 miRNA 作为备选 miRNA。将备选 miRNA 与乳腺癌前 20 名差异表达的 miRNA 求交集得到目标 miRNA 6 个：hsa-mir-4732，hsa-mir-486，hsa-mir-592，hsa-mir-449，hsa-mir-187，hsa-mir-196a，将这 6 个 miRNA 进行 ROC 曲线分析，预测其作为肿瘤标志物的诊断能力。
结论 基于 TCGA 数据库的生物信息学方法可简便而可靠地筛选目标 miRNA 进行后续研究，有较高的参考价值。

PO-0839

双氢青蒿素通过 TGFβ-Smads 信号通路抑制三阴性乳腺癌细胞增殖和转移

何谦
西安交通大学第二附属医院

目的 拟证实青蒿素通过抑制 TGF-β 信号通路从而调节核基质蛋白 CIZ1 表达，抑制乳腺癌增殖和转移的作用。
方法 体外培养人乳腺癌 MDA-MB-231 细胞，采用 CCK-8 法检测青蒿素及其衍生物双氢青蒿素 DHA 对细胞增殖的抑制作用；划痕实验检测药物对乳腺癌细胞迁移能力的影响；RT-qPCR 和 Western blot 分别检测其对 CIZ1、Snail 及 TGF-β1 的 mRNA 及蛋白表达水平的影响;通过划痕实验、Transwell 体外侵袭实验和 Western blot 技术进一步探究外源施加 TGF-β1 或 TGF-β1 通路抑制剂 SD-208，激活/抑制 TGFβ1-smads 通路对药物抗转移作用及其分子机制的影响。
结果 1. 青蒿素及 DHA 对人乳腺癌 MDA-MB-231 细胞系的增殖有显著抑制作用，呈浓度-时间依赖性 。2. DHA 以浓度依赖性明显抑制乳腺癌细胞系的迁移能力，抑制 CIZ1、Snail、TGF-β1 的 mRNA 及蛋白表达水平。3. TGFβ1 处理可增强乳腺癌细胞的转移能力，TGFβ1 处理增强 MDA-MB-231 细胞 CIZ1、snail 蛋白表达及 smad2/3 蛋白磷酸化水平；DHA 可以逆转 TGFβ1 诱导的以上效应，且随着药物浓度提高，DHA 对以上效应的抑制能力进一步增强；施加 TGF-β1 通路抑制剂 SD-208，DHA 的抗肿瘤转移活性也能得到增强。DHA、SD-208、DHA+SD-208 的联合处理组均能显著抑制了 CIZ1、snail 和磷酸化 smad2/3 蛋白表达。
结论 DHA 通过抑制 TGFβ1/Smads 通路和 CIZ1 蛋白显著抑制乳腺癌 MDA-MB-231 细胞增殖和迁移，并可有效逆转 TGF-β1 诱导的乳腺癌细胞转移增强效应，并发挥抗乳腺癌转移作用。本研究初步证实了 TGF-β1/Smad 信号通路与 CIZ1 蛋白及其级联调控关系可能成为调控乳腺癌进展和转移过程的新作用机制。

PO-0840

COVID-19 流行后武汉市 3100 例儿童呼吸道病原体感染情况分析

马俊娥、崔湘铧、刘芮、韩欢、祝成亮
武汉大学人民医院

目的 分析 COVID-19 流行后儿童呼吸道病原体的感染情况，并且与 COVID-19 流行前的感染情况做对比，观察在采取一系列防控措施后，病原体感染率是否存在变化。
方法 收集 COVID-19 流行前后武汉大学人民医院儿科住院患儿的咽拭子和血清，采用直接免疫荧光法检测腺病毒（ADV）、流感病毒 A、B(IFA、IFB)、副流感病毒 1、2、3（PIV1、PIV2、PIV3）及呼吸道合胞病毒（RSV）7 种呼吸道常见病毒抗原，采用间接免疫荧光法检测 2 种呼吸道非典型病原体 IgM 抗体，即肺炎支原体(MP)和肺炎衣原体(CP)。检验结果进行统计学分析。
结果 COVID-19 流行后，3100 例呼吸道感染患儿中，共有 1112 例患儿检出病原体，检出率为 35.87%，九种呼吸道病原体中 MP 的检出率最高（28.19%）,其次为 PIV1 （4.00%）、RSV（3.35%）、PIV3 （1.94%）、CP（0.77%）、ADV（0.32%）、PIV2（0.03%），未检出 IFA、IFB；存在病原体混合感染，混合感染率为 2.71%；男女患儿 PIV1、PIV3 以及 MP 的感染具有统计学差异（P<0.05），其中女性患儿 PIV1 和 MP 感染率较高，男性患儿 PIV3 感染率较高，其他病原体感染并无统计学差异；PIV1、PIV3、RSV 和 MP 的感染率在各年龄组间具有统计学差异（P<0.05），各病原体感染分别集中在 0～6 岁、0～3 岁、0～3 岁、1～6 岁；此外，与 COVID-

19 流行前的 7818 例患儿相比，COVID-19 流行后患儿总体的病原体感染阳性率明显下降，差异具有统计学意义（P<0.05）。

结论 MP 是本院儿科患儿呼吸道感染的主要病原体，女性患儿较男性患儿感染率高，1～6 岁感染率最高，针对 COVID-19 的一系列防护措施可有效减少儿童呼吸道病原体的感染。

PO-0841

A machine learning approach to personalized dose adjustment of lamotrigine using noninvasive clinical parameters

Xiuqing Zhu[1]、wencan Huang[2]、haoyang Lu[1]、zhanzhang Wang[1]、xiaojia Ni[1]、Jinqing Hu[1]、Shuhua Deng[1]、Yaqian Tan[1]、Lu Li[1]、Ming Zhang[1]、Chang Qiu[1]、Yayan Luo[1]、Hongzhen Chen[1]、Shanqing Huang[1]、Tao Xiao[1]、Dewei Shang[1]、Yuguan Wen[1]

1. Department of Pharmacy, The Affiliated Brain Hospital of Guangzhou Medical University (Guangzhou Huiai Hospital)

2. 广州市民政局精神病医院

The pharmacokinetic variability of lamotrigine (LTG) plays a significant role in its dosing requirements. Our goal here was to use noninvasive clinical parameters to predict the dose-adjusted concentrations (C/D ratio) of LTG based on machine learning (ML) algorithms. A total of 1141 therapeutic drug monitoring measurements were used, 80% of which were randomly selected as the "derivation cohort" to develop the prediction algorithm, and the remaining 20% constituted the "validation cohort" to test the finally selected model. Fifteen ML models were optimized and evaluated by tenfold cross-validation on the "derivation cohort," and were filtered by the mean absolute error (MAE). On the whole, the nonlinear models outperformed the linear models. The extra-trees' regression algorithm delivered good performance, and was chosen to establish the predictive model. The important features were then analyzed and parameters of the model adjusted to develop the best prediction model, which accurately described the C/D ratio of LTG, especially in the intermediate-to-high range (≥ 22.1 μg $mL^{-1}g^{-1}$day), as illustrated by a minimal bias (mean relative error (%) = + 3%), good precision (MAE = 8.7 μg $mL^{-1}g^{-1}$day), and a high percentage of predictions within ±20% of the empirical values (60.47%). This is the first study, to the best of our knowledge, to use ML algorithms to predict the C/D ratio of LTG. The results here can help clinicians adjust doses of LTG administered to patients to minimize adverse reactions.

PO-0842

新型冠状病毒肺炎患者血浆 CRP，PCT，IL-6 水平检测的临床诊断价值

马俊娥[1]、崔湘铧[1]、刘芮[1]、韩欢[1]、邬开朗[2]、刘芳[2]、祝成亮[1]

1. 武汉大学人民医院

2. 武汉大学病毒学国家重点实验室

目的 评估单独及联合检测新型冠状病毒肺炎(Coronavirus Disease-2019，COVID-19)患者血浆 c 反应蛋白（C reactive protein,CRP）、降钙素原（procalcitonin,PCT）、和白介素-6(Interleukin-6,IL-6)水平的临床诊断价值。

方法 选取 2020 年 1 月 1 日至 2020 年 2 月 2 日期间武汉大学人民医院 COVID-19 确诊患者 96 例，其中普通型 41 例，重型 45 例和危重型 10 例，另选 40 例健康者作为对照组，收集 96 位患者的 CRP，PCT 和 IL-6 以及 40 位健康者的 CRP，PCT 检测结果并绘制 ROC 曲线；

结果 与对照组相比，COVID-19 组患者的 CRP 和 PCT 水平显著增高,（CRP 分别为 0.4，60.35mg/L，PCT 分别为 0.053，0.087ng/ml ）；在 COVID-19 患者中，普通型患者的 CRP，PCT 水平明显低于重型、危重型患者，(CRP 分别为 36.8，84.9，94.1 mg/L，PCT 分别为 0.060，0.118，0.224 ng/ml)；普通型患者的 IL-6 水平低于危重型，（分别为 8.42，73.65pg/ml）；差异均具有统计学意义 (P<0.05)；ROC 曲线显示 PCT 和 CRP 诊断 COVID-19 价值较高，评估重型和危重型 COVID-19 患者，CRP 的价值最高，且三个指标联合检测可以提高评估效能；评估危重型 COVID-19 患者，IL-6 有较高的预测价值。
结论 血浆 CRP，PCT 和 IL-6 水平可能是诊断 COVID-19 的潜在生物标志物，并且其血浆水平可以评估 COVID-19 的严重程度，三指标联合检测可以提高评估效能，对 COVID-19 的临床诊断和治疗具有重要的参考价值。

PO-0843

Analysis of adjunctive serological detection to nucleic acid test for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection diagnosis

Rui Liu
Renmin Hospital of Wuhan University

Background The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) caused coronavirus disease 2019 (COVID-19) epidemic in China, December 2019. The clinical features and treatment of COVID-19 patients remain largely elusive. However, accurate detection is required for SARS-CoV-2 infection diagnosis. We aimed to evaluate the antibodies-based test and nucleic acid-based test for SARS-CoV-2-infected patients.
Methods We retrospectively studied 133 patients diagnosed with SARS-CoV-2 and admitted to Renmin Hospital of Wuhan University, China, from January 23 to March 1, 2020. Demographic data, clinical records, laboratory tests, and outcomes were collected. Data were accessed by SARS-CoV-2 IgM-IgG antibody test and real-time reverse transcriptase PCR (RT-PCR) detection for SARS-CoV-2 nucleic acid in COVID-19 patients.
Results Of 133 COVID-19 patients, there were 44 moderate cases, 52 severe cases, and 37 critical cases with no differences in gender and age among three subgroups. In RT-PCR detection, the positive rate was 65.9%, 71.2%, and 67.6% in moderate, severe, and critical cases, respectively. Whereas the positive rate of IgM/IgG antibody detection in patients was 79.5%/93.2%, 82.7%/100%, and 73.0%/97.3% in moderate, severe, and critical cases, respectively. Moreover, the IgM and IgG antibodies concentrations were also examined with no differences among three subgroups.
Conclusion The IgM-IgG antibody test exhibited a useful adjunct to RT-PCR detection, and improved the accuracy in COVID-19 diagnosis regardless of the severity of illness, which provides an effective complement to the false-negative results from a nucleic acid test for SARS-CoV-2 infection diagnosis after onsets.

PO-0844

Clinical characteristics of COVID-19 patients with hepatitis B virus infection — a retrospective study

Rui Liu
Renmin Hospital of Wuhan University

Background & Aims The outbreak of coronavirus disease 2019 (COVID-19) has been declared a pandemic. Although COVID-19 is caused by infection in the respiratory tract, extrapulmonary manifestations including dysregulation of the immune system
and hepatic injury have been observed. Given the high prevalence of hepatitis B virus
(HBV) infection in China, we sought to study the impact of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and HBV coinfection in patients.
Methods Blood samples of 50 SARS-CoV-2 and HBV coinfected patients, 56 SARSCoV-2 mono-infected patients, 57 HBeAg-negative chronic HBV patient controls and 57 healthy controls admitted to Renmin Hospital of Wuhan University were collected
in this study. Complete blood count and serum biochemistry panels including markers indicative of liver functions were performed. Cytokines including IFN-γ, TNF-α, IL-2, IL-4, IL-6 and IL-10 were evaluated. T cell, B cell and NK cell counts were measured using flow cytometry.
Results SARS-CoV-2 and HBV coinfection did not significantly affect the outcome of the COVID-19. However, at the onset of COVID-19, SARS-CoV-2 and HBV coinfected patients showed more severe monocytopenia and thrombocytopenia as well as more
disturbed hepatic function in albumin production and lipid metabolism. Most of the disarrangement could be reversed after recovery from COVID-19.
Conclusions While chronic HBV infection did not predispose COVID-19 patients to more severe outcomes, our data suggest SARS-CoV-2 and HBV coinfection poses a higher extent of dysregulation of host functions at the onset of COVID-19. Thus,
caution needs to be taken with the management of SARS-CoV-2 and HBV coinfected patients.

PO-0845

Analysis of Nucleic Acid and Antibody Detection Results for SARS-CoV-2 Infection

Juanjuan Chen
Renmin Hospital of Wuhan University

Background RT-PCR of virus nucleic acid test (NAT) has become the standard method to diagnose SARS-CoV-2 infection. However, there are still many limitations, especially the problem of the high false negative rate. Therefore, the aim of this study was to investigate the positive rate of SARS-CoV-2 NAT and evaluate the diagnostic performance of SARS-CoV-2 IgM and IgG antibody detection in novel coronavirus infection.
Methods A total of 10,309 suspected or high-risk cases of infection with SARS-CoV-2 in Wuhan Hubei, China, were tested for virus NAT by RT-PCR. Among those cases, 762 COVID-19 patients and 143 patients with non-COVID-19 who were tested for SARS-CoV-2 IgM and IgG during the NAT period were screened. The difference between the two test methods was analyzed using the chi-square test.
Results The positive rate of 10309 cases was about 36% (95%CI: 95%CI: 33.39%–-39.67%). SARS-CoV-2 was present in various types of specimens, and alveolar lavage fluid had the highest positive rate ([52.38% (95%CI: 31.02–-73.74)).)].The clinical sensitivity of serum SARS-CoV-2 IgM and IgG was 77.17% (588/762) and 94.88% (723/762), respectively, and the clinical specificity was 93.71% (134/143) and 90.21% (129/143). The AUC of SARS-CoV-2 IgG and combination of IgG with IgM were equally larger than IgM (0.973 (95%CI: 0.964-0.983) vs 0.930

(95%CI: 0.910–-0.949)). IgG antibody had the highest specificity ([100.0% (95%CI: 100.00%–-100.00%))%)]and sensitivity ([94.0% (95%CI: 92.45%-95.55%))%)]when detected alone or in combination with IgM antibody. The total coincidence rate of SARS-CoV-2 antibodies detection and SARS-CoV-2 NAT for the diagnosis of SARS-CoV-2 infection was 92.04% (833/905). Among the 34 SARS-CoV-2 NAT-negative patients with clinical symptoms and CT imaging features, 29 (85.29%) patients were positive for SARS-CoV-2 IgM, and 31 (91.76%) were positive for IgG.
Conclusions SARS-CoV-2 NAT should be considered for many types of specimens, and the combined test of SARS-CoV-2 IgM and IgG can make up for the problem of missed NAT in COVID-19 patients.

PO-0846

Incidence, clinical risk and prognostic factors for liver metastasis in patients with cervical cancer: A Population-Based Retrospective Study

Hang Liu[2]、Xiangsen Ye[3]、Di Li[1]、Qian Yao[1]、Yan Li[1]
1. Department of Clinical Laboratory, Renmin Hospital of Wuhan University
2. Department of Clinical Laboratory, Renmin Hospital of Wuhan University
3. Department of Clinical Laboratory, The Central Hospital of Wuhan, Tongji Medical College

Background Cervical cancer is one of the most frequent malignancies in women, particularly metastasis resulting in a poor prognosis. However, the clinical characteristics of cervical cancer patients with advanced liver metastasis have not been well investigated. We aimed to evaluate the incidence, clinical risk and prognostic factors for hepatic metastasis in cervical cancer patients.
Materials and Methods The clinical features of patients diagnosed with cervical cancer were collected from the Surveillance, Epidemiology and End Result (SEER) public cancer database between 2010 and 2015. Multivariate logistic and Cox regression models were performed to identify potential risk and prognostic factors for liver metastasis in patients with cervical cancer.
Results A total of 431 patients (2.32%) developed liver metastasis in our analysis. The following characteristics were significantly associated with the development of liver metastasis: black ethnicity, uninsured status, higher tumor stage, poorer differentiated grade, non-squamous histology, non-surgery of primary site, patients with any additional lung, bone, and brain metastasis. Multivariate Cox regression showed that patients with additional lung metastasis, without radiotherapy, and without chemotherapy were negatively correlated with overall survival. Concurrent chemotherapy and radiotherapy was a favorable prognostic factor to improve overall survival, and chemotherapy showed to increase cause-specific survival. Additional lung metastasis was an independent characteristic for both risk and prognostic factors for hepatic metastasis in patients with cervical cancer.
Conclusion Our results found several potential clinical features that may be used to assess the risk and prognosis of liver metastasis in patients with cervical cancer. These associated factors may provide clinical indications for the early identification and treatment of cervical cancer patients with hepatic metastasis.

PO-0847

FAM122A 通过下调 GATA1 转录活性抑制红细胞分化

陈婧
上海交通大学医学院附属第九人民医院

目的 FAM122A 是进化上高度保守但功能未知的蛋白。我们发现 FAM122A 在 $CD71^{+}$的早期阶段红细胞中高表达，提示 FAM122A 可能在红系分化中具有潜在作用。
方法 1. 检测 FAM122A 在红系分化过程中的表达：采用 hemin 诱导的 K562 细胞以及 EPO 诱导的 $CD34^{+}$细胞体外诱导模型。
2. 探讨 FAM122A 是否参与红系分化。将 $CD34^{+}$细胞进行 FAM122A 基因的敲低或过表达，发现 FAM122A 不影响红系早期 BFU-E、CFU-E 的生成，但明显抑制终末红系分化。
3. 研究 FAM122A 抑制红系分化的作用机制。利用质谱以及 RNA-seq 分析，发现红系特异转录因子 GATA1 是潜在的介导 FAM122A 调控红系分化的关键分子。FAM122A 不影响 GATA1 的表达，两者存在直接相互作用。EMSA 实验发现 FAM122A 阻碍 GATA1 与其 DNA 靶序列的结合，ChIP 实验及双荧光素酶报告系统证实 FAM122A 抑制 GATA1 与其靶基因启动子区 DNA 的结合，抑制 GATA1 转录活性。
4. GEO 数据分析，发现 FAM122A 在 β-地中海贫血病人细胞中异常高表达，提示 FAM122A 可能参与红系分化异常相关疾病的发生。
结果 本项研究发现 FAM122A 在红系终末分化阶段表达下调，且过表达 FAM122A 显著抑制红细胞的终末分化。FAM122A 与 GATA1 相互作用，抑制 GATA1 与其靶基因的结合及其转录活性，抑制红细胞分化。GEO 数据分析，发现 FAM122A 在 β-地中海贫血病人中显著高表达。
结论 本课题的研究揭示了 FAM122A 参与调控红系分化的新功能，这不仅对于全面认识红系分化信号调控网络具有重要的理论和实践指导意义，而且为体外有效扩增红细胞提供新的思路。

PO-0848

川东北地区 MM 患者骨髓瘤细胞免疫表型特征及其临床意义

祝静、龙思琪、蒋瑶、刘文
川北医学院附属医院

目的 明确我国川东北地区多发性骨髓（MM）患者骨髓瘤细胞免疫表型的特征及其临床意义。
方法 流式细胞术检测川北医学院附属医院 2018 年 1 月至 2020 年 1 月期间血液科住院的 MM 患者骨髓瘤细胞的免疫表型，分析 CD38、CD138、CD19、CD56、CD20、CD117、CD27、CD28、CD33、cKappa、cLambda 在不同临床分期之间表达率的差异以及其与病情评估指标 LDH、白蛋白、β2-MG、血红蛋白的关系。
结果 川东北地区 MM 患者骨髓瘤细胞 CD 分子的阳性表达率从高到低依次为 CD38（100%）、CD138（100%）、CD56（77.9%）、CD19（55.8%）、cLambda（55.8%）、CD28（54.8%）、CD117（48.1%）、CD27（44.2%）、cKappa（44.2%）、CD33（26.9%）、CD20（21.2%）。ISS 不同分期 CD27 的阳性表达率比较，差异有统计学意义（$P<0.05$）；CD56+组 LDH、白蛋白低于 D56-组，CD117+组白蛋白水平高于 CD117-组，CD27+组 β2-MG 低于 CD27-组，CD28+组的血红蛋白高于 CD28-组（$P<0.05$）；CD19+组与 CD19-组相比、CD20+组与 CD20-组相比以及 CD33+组与 CD33-组相比，血清 LDH、β2-MG、白蛋白及血红蛋白均无显著差异（$P>0.05$）。
结论 川东北地区 MM 患者 CD27 的阳性率越低，ISS 分期越晚，可能病情更重；CD27+组、CD56+组、CD117+组以及 CD28+组的疾病活动度、肿瘤负荷、肿瘤消耗及瘤细胞可能对骨髓的浸润及抑制程度均分别的低于相应的阴性组。

PO-0849

Luteolin transforms the polarity of bone marrow-derived macrophages to regulate the cytokine storm

Shuxia Wang、Xiaoming Yao
Affiliated Hospital of Integrated Traditional Chinese and Western Medicine, Nanjing University of Chinese Medicine; Jiangsu Province Academy of Traditional Chinese Medicine

Background and objective Macrophages are indispensable regulators of inflammatory responses. Macrophage polarisation and their secreted inflammatory factors have an association with the outcome of inflammation. Luteolin, a flavonoid abundant in plants, has anti-inflammatory activity, but whether luteolin can manipulate M1/M2 polarization of bone marrow-derived macrophages (BMDMs) to suppress inflammation is still unclear. This study aimed to observe the effects of luteolin on the polarity of BMDMs derived from C57BL/6 mice and the expression of inflammatory factors, to explore the mechanism by which luteolin regulates the BMDM polarity.

Methods M1-polarized BMDMs were induced by lipopolysaccharide (LPS) + interferon (IFN)-g and M2-polarization were stimulated with interleukin (IL)-4. BMDM morphology and phagocytosis were observed by laser confocal microscopy; levels of BMDM differentiation and cluster of differentiation (CD)11c or CD206 on the membrane surface were assessed by flow cytometry (FCM); mRNA and protein levels of M1/M2-type inflammatory factors were performed by qPCR and ELISA, respectively; and the expression of p-STAT1 and p-STAT6 protein pathways was detected by Western-blotting.

Results The isolated mouse bone marrow cells were successfully differentiated into BMDMs, LPS+IFN-g induced BMDM M1-phenotype polarization, and IL-4 induced M2-phenotype polarisation. After M1-polarised BMDMs were treated with luteolin, the phagocytosis of M1-polarized BMDMs was reduced, and the M1-type pro-inflammatory factors including IL-6, tumour necrosis factor (TNF)-a, inducible nitric oxide synthase (iNOS), and CD86 were downregulated while the M2-type anti-inflammatory factors including IL-10, IL-13, found in inflammatory zone (FIZZ)1, Arginase (Arg)1 and CD206 were upregulated. Additionally, the expression of M1-type surface marker CD11c decreased. Nevertheless, the M2-type marker CD206 increased; and the levels of inflammatory signalling proteins phosphorylated signal transducer and activator of transcription (p-STAT)1 and p-STAT6 were attenuated and enhanced, respectively.

Fig. 1 The differentiation proportion of BMDM.

Fig. 2 Effect of luteolin on the phagocytic activity in polarised BMDMs. The BMDMs that have phagocytosed Gram-positive bacilli (a) or Candida albicans (b) are stained with Wright-Giemsa Stain to visualize in the field.

Fig. 3 Effect of luteolin on the expression of BMDM surface markers CD11c and CD206.

Fig. 4 Effects of luteolin on the protein levels of p-STAT1/6 in polarized BMDMs.

Conclusions Our study suggests that luteolin may transform the BMDM polarity from a pro-inflammatory M1-phenotype to an anti-inflammatory M2-phenotype through p-STAT1/6. Simultaneously, inflammatory factors are analogously altered from pro-inflammatory to anti-inflammatory type. In light of these findings, our research provides a novel insight into the role of naturally occurring luteolin holds promise as an anti-inflammatory and immunomodulatory agent.

PO-0850

The value of serum amyloid A levels for predicting disase severity in COVID-19 patients: A systematic review and meta-analysis

Wenjie Huang、Lihong Wu、Yangyang Liu、Lin Sun、Fangrong Gan、Jianlin Chen、Yifan Sun
Affiliated Liutie Central Hospital of Guangxi Medical University

Backgroud An abundance of clinical reports focused on the serum amyloid A (SAA) have been report on severe coronavirus disease 19 (COVID-19), but a systematic analysis synthesizing these findings has not been performed.
Methods A comprehensive literature search was conducted in PubMed, Embase databases and Web of Science from their outbreak to February 1, 2021. Two investigators independently reviewed suitable studies. Pooled standardized mean difference (SMD), 95% confidence intervals (CI), and correlation coefficient (r) were computed using random-effect model.
Results We included 19 of 317 titles identified by our search, involving a total of 1806 mild cases and 1529 severe cases. Compared with the mild group, the severe group had markedly higher SAA levels (SMD=1.155, 95% CI 0.89, 1.42). Subgroup analysis manifested that SAA level difference between severe group and mild group were associated with age, sample size and detection method. Sensitivity analyses showed the credibility and robustness of our results. In addition, In six studies in 1144 severe COVID-19 patients and critical COVID-19 patients, SAA was significantly higher in critical patients (SMD=0.476, 95% CI 0.13, 0.82).
Conclusion High circulating SAA levels were markedly associated with COVID-19 severity, especially for participants subject age less than 60 when compared to mild COIVD-19 patients, and the concentrations of SAA were also significantly higher in critical COVID-19 when compared to severe COVID-19 patients. Further studies, in larger cohorts, are needed to confirm whether the SAA is a useful tool in discriminating between COVID-19 patients with stable disease, those with acute exacerbations, and subjects without disease.

PO-0851

Human decidual stromal cells in early pregnancy induce functional re-programming of monocyte-derived dendritic cells via crosstalk between G-CSF and IL-1β

Huayang Wang
Qilu Hospital of Shandong Universtiy

Objective To explore the effect of early pregnancy decidual stromal cells (DSCs) on monocyte-derived DCs and the relevant mechanisms.
Methods DSCs in early pregnancy were isolated and co-cultured with monocyte-derived dendritic cells in vitro. The functions and phenotypes of dendritic cells were analyzed. The secretion profile of DSCs were analyzed and the role of DSC-derived G-CSF on modification of dendritic cells was further investigated by neutralizing antibody. Last, the G-CSF secretion from DSCs in healthy pregnancy and spontaneous abortion (SA) patients was analyzed.
Results DSC-conditioned DCs showed altered phenotypes, secretion profiles and Th2 priming potential. G-CSF concentration was significantly up-regulated in the co-culture supernatant between DSCs and DCs. Supplementation of G-CSF neutralizing antibody partly reversed the reprogramming of DCs mediated by DSCs. Furthermore, G-CSF production was promoted by IL-1β, which was mainly produced by DCs and significantly up-regulated after their cultivation with DSCs. Interestingly, the effects of DSC on IL-1β production of DCs occurred in their immature stage but not their mature stage. Lastly, no significant difference of G-CSF was found in DSCs

from healthy early pregnancy women and spontaneous abortions (SA) patients. However, DSCs from SA patients secreted less G-CSF in response to exogenous rhIL-1β or DC cultivation.
Conclusion Our study bolster the understanding of the decidual immunomodulatory microenvironment during early pregnancy, and brings new insight into the potential clinical value of G-CSF in pregnancy disorders.

PO-0852

RDW 在医院获得性肺炎实验室诊断中的价值评估

王书侠[1]、姚孝明[2]、王志国[2]
1. 南京中医药大学附属中西医结合医院 江苏省中医药研究院
2. 南京中医药大学附属中西医结合医院

背景和目的 医院获得性肺炎（HAP）是住院患者最常见的并发症，常见的病原体主要为细菌、真菌等。红细胞分布宽度（RDW）是血球分析仪快速、自动计算出的一种红细胞指数。RDW 越高，表明红细胞的离散程度越大。RDW 过去一直用于贫血的诊断或鉴别诊断，近来有研究发现，其与自身免疫性疾病、心血管病、消化系统疾病、感染性疾病等均有密切关系。本文探讨 RDW 在 HAP 实验室诊断及其感染菌群中的价值评估。
方法 回顾性分析住院患者的痰培养结果及其相应的血常规衍生参数 RDW，痰培养结果分为痰培养阳性组（HAP）和痰培养阴性组（疑似 HAP），随机抽取同期健康体检者作为对照组；并采用受试者工作特征曲线（ROC）及曲线下面积（AUC）分析 RDW 对 HAP 及感染菌群的诊断价值。
结果 相对于对照组[12.85（12.27~13.3）]和痰培养阴性组[13.15（12.57~14.2）]，住院患者痰培养阳性组的 RDW 水平[15.4（14.2~14.6）]显著升高，RDW 的异常（升高）率（58.9 %）也显著升高；痰培养阳性组的菌群以革兰氏阴性杆菌为主（68.49 %），其次为革兰氏阳性球菌（16.43 %）和真菌（15.07 %）；阴性杆菌组的 RDW 水平[15.9（14.35~17.4）]相对于阳性球菌组[14.8（14.17~15.3）]和真菌组[14.9（14.05~16.17）]有显著性差异。ROC 曲线分析显示，RDW 诊断 HAP 感染的 AUC 为 0.81；区分革兰氏阴性菌与革兰氏阳性菌及真菌的 AUC 分别为 0.75 和 0.72。
结论 RDW 不仅可作为怀疑 HAP 感染和非感染的初步评估，还可以作为 HAP 感染菌群尤其革兰氏阴性菌感染的初判，以辅助抗生素的治疗。怀疑 HAP 患者同时观察 RDW 的水平，必要时动态监测 RDW 的变化，可以给我们在 HAP 的实验室诊断上得到不少启示。RDW 将是一项很有前景的炎性生物标志物。

PO-0853

医学检验领域能力验证数据防串通措施的探讨

郭晓俊、蒋玲丽、王青
上海市临床检验中心

目的 为保证能力验证结果评价科学、客观、公正和有效,对能力验证计划防止数据串通的措施进行了探讨。
方法 从样品设计、发样方式、检测周期和统计设计 4 个方面介绍了防止数据串通的措施, 以 2018 年-2020 年上海市临床检验中心实施的血凝检测和内分泌检测能力验证计划为例，对实施前后的数据比较来分析，探讨能力验证防止数据串通措施的具体实施方法。
结果 在样品的设计时分别取不同浓度水平样品，分割水平设计（采用合理的样品近似浓度水平，但样品不同），同时增加编制序号的数量，使参加者无法从编号上辨别样品的区别；采用盲样随机化处理发放样品；检测周期的设计应缩短结果上报周期，将样品邮寄时间及大概到达时间提前告知参加者，让参加者提前准备实验条件，以最快的速度、最短的时间完成检测并上报结果；在统计方

法的设计时通过采用标准化四分位间距的统计方法计算分割水平样本，同时能统计系统误差和随机误差。
结论 设计分割水平样品、盲样随机化处理发放样品、缩短能力验证结果上报周期和采用标准化四分位间距的统计方法等几种措施可以有效地防止能力验证数据的串通，从而保证医学实验室能够出具更加准确地检测报告以服务于临床，最终保障患者的治疗和健康。

PO-0854

Psychological Effects of COVID-19 on Mental Health of Parents of Children with Hematopathy

Xu Chen[1]、Yuanyuan Gao[2]
1. First Affiliated Hospital of Soochow University
2. 苏州大学附属儿童医院

Background We explored whether parents of children with hematopathy had more psychosocial problems than parents of healthy children during the COVID-19 outbreak.
Methods An online survey was used in this study, a total of 1116 parents participated, mental health variables were assessed via the Simplified Coping Style Questionnaire (SCSQ) and the Symptom Check List-revised (SCL-90-R).
Results Compared with parents of healthy children (n=731), parents of children with hematopathy (n=385) have a higher possibility (70.9% vs. 33.2%, P<0.01) of negative coping style. Parents of children with hematopathy are more concerned to the media reports related to the epidemic (46.9% vs. 10.4%). In SCL-90-R somatization, obsessive-compulsive, and anxiety scale, parents of children with hematopathy have higher scores than parents of healthy children (12.50±1.69 vs.12.23±1.37, p<0.01; 13.42±6.69 vs. 10.47±2.25, p<0.01; 15.21±5.53 vs. 10.52±2.34, p<0.01, respectively). History of visiting Wuhan, and history of epidemics occurring in the community are the independent risk factors of two groups' parental obsessive-compulsive and anxiety symptoms (P<0.01).
Conclusions Parents of children with hematopathy have obvious serious symptoms of obsessive-compulsive and anxiety during the outbreak of COVID-19. Providing psychological interventions to parents of children with hematopathy needs to be realized.

PO-0855

自发性狼疮肾炎模型小鼠肾小球系膜细胞分离、原代培养及鉴定

陈鹤鸣、林婷、宋艳芳、林青
福建中医药大学附属人民医院

目的 原代培养及鉴定自发性狼疮肾炎模型小鼠肾小球系膜细胞，探索分离、培养的最佳条件。
方法 对照组 ICR 小鼠和模型组 MRL/lpr 小鼠各 9 只，在 12、14 和 18 周龄时检测小鼠的自身抗体以及尿蛋白；通过肾脏组织病理切片，观察小鼠狼疮肾炎发病情况。采用细胞筛网分离出肾小球，结合优生选择法原代培养肾小球系膜细胞。通过细胞形态学、免疫细胞化学技术鉴定 MRL/lpr 小鼠肾小球系膜细胞。
结果 模型组小鼠，ANA 和抗 ds-DNA 抗体明显增高（P<0.05），尿蛋白在 14 和 18 周龄明显增高（P<0.05），肾脏组织染色显示，MRL/lpr 小鼠从 12 周开始即表现出狼疮肾炎相关的病理改变。种植 25d 后，MRL/lpr 小鼠肾小球系膜细胞逐渐铺满培养瓶底，相差显微镜下呈星形、梭形。免疫细胞化学显示抗 α 平滑肌肌动蛋白（α-SMA）阳性、抗足细胞裂孔膜蛋白（nephrin）阴性，排除其他肾小球固有细胞。

结论 改良后的自发性狼疮肾炎小鼠肾小球系膜细胞的原代培养操作简单，在保证动物模型发病的同时，获得稳定、活性强、纯度高的细胞。

PO-0856

医院水环境中碳青霉烯类耐药细菌多样性及耐药基因研究

史庆丰
复旦大学附属中山医院

目的 调查医院内不同水环境中碳青霉烯类耐药细菌的分布及其耐药基因污染现状。
方法 使用 mSuper CARBA 显色平板（含美罗培南 4μg/mL）对医院门诊区域、普通病房、行政楼和重症监护室的洗手池、拖把清洗和废液倾倒处水槽孔进行采样，培养 48 小时后使用 MALDI-TOF 质谱仪对细菌进行鉴定。同时使用数字 PCR 微滴法对样本进行碳青霉烯耐药基因 blaKPC、blaNDM、blaOXA-23、blaOXA-48 鉴定。
结果 共采集 71 个水环境样本，49 个（69.01%）样本培养出碳青霉烯类耐药细菌，以嗜麦芽窄食单胞菌的检出率最高（43.66%），其次为鲍曼不动杆菌（15.49%）；39 份水环境样本可鉴定出至少 1 种耐药基因，其中 blaNDM 检出率显著高于其它三个耐药基因（$\chi 2=48.086$，$P=0.001$），9 份细菌培养阴性样本可鉴定出 blaKPC 或 blaNDM 耐药基因。
结论 医院水环境中广泛定植碳青霉烯类耐药细菌，ICU 和普遍病房水环境 blaNDM 耐药基因污染严重，可能成为医院感染多重耐药菌来源，今后应加强对此类环境的消毒管理。

PO-0857

医学实验室质量体系内部审核技巧和方法分享

陈振朋、张维
西安金域医学检验所有限公司

目的 内部审核，也称为第一方审核，用于内部目的，由组织自己或以组织的名义进行，可作为组织自我合格声明的基础。掌握合适有效的内部审核技巧，是内审成功与否的关键。
方法 医学实验室质量体系内部审核是审核实验室质量体系是否符合所依据的标准以及是否有效的运行。内审员的选择及内审技巧和方法的掌握是内审成败的关键所在。
结果 1. 审核员的要求和基本能力：审核员要求对所要审核的体系和内容有较为清晰的认识和理解，同时审核员不能审核自己科室体系；
2. 审核员所需具备的基本素质和能力：有道德、思想开明、善于交谈、善于观察、自立、有丰富的质量管理经验、掌握一定的内审技巧。
3. 审核技巧：首先在面谈时，需要选择正确的面谈对象，提问应单刀直入，直截了当的明确问题，掌握正确的提问技巧，如 5W1H 法：WHAT、WHEN、WHERE、WHO、WHY、HOW 。提问时应注意开放式提问与封闭式提问相结合，以开放式提问为主。在听受审者谈话时，审核者应真诚、耐心、专心聆听，并多给予反馈和鼓励。审核员在现场要带着问题去观察，寻找客观事实。查阅文件和记录时，应细心核对，确认是否按体系去做，受控的记录和文件可以作为客观证据。要善于联想和追溯，质量体系各要素之间是有逻辑上的关联性。
4. 审核中需注意：控制审核进度；控制审核氛围和现场纪律；抽样有代表性；从表面显现寻找问题实质；与被审方负责人确认不符合事实。
5. 审核方法自下而上和自上而下审核；正向和逆向审核；按部门或按要素审核。
结论 在质量体系审核中，选择合适的审核员，并掌握相应的审核技巧和方法，关系到本次审核的质量和成败。

PO-0858

一例发生于年轻患者的母细胞性浆细胞样树突状细胞肿瘤实验室检查及临床病理特点总结并文献复习

黄林林[1]、唐梅[1]、周宇[1]、许玉玲[2]、敬敏[1]、左梅琳[1]、杨友谊[1]、陈虹[1]、罗军[2]
1. 四川金域医学检验中心
2. 广西医科大学第一附属医院

目的 探讨发生于年轻患者的母细胞性浆细胞样树突状细胞肿瘤（BPDCN）实验室多平台检查诊断、临床病理特点总结及文献复习。
方法 回顾研究广西医科大学第一附属医院血液内科的一例 21 岁患者，腹股沟皮下包块，大小约 2cm，手术切除送实验室检查，并做骨髓细胞及流式细胞分析，通过细胞形态、免疫表型、流式细胞及分子等多平台检测进行综合诊断、临床病理特点总结并复习文献。
结果 中等大小母细胞样肿瘤细胞弥漫浸润，核分裂易见，免疫表型 CD2、CD7、CD123、CD4、CD56 均为强阳性,Ki-67 高表达，CD3、CD20、CD34、MPO、S-100、MUM-1、CD10 均为阴性，CD99、TDT 部分阳性，骨髓流式细胞可见一群异常幼稚细胞，CD123 强阳性，CD33、CD7、CD2、CD4、CD56 和 CD304 阳性，TDT 弱阳性，考虑不典型 BPDCN。骨髓细胞呈急性白血病骨髓象，但细胞形态不典型，需鉴别 AML-M5 及 BPDCN。白血病融合基因检测：阴性。染色体核型：46，XY。血液肿瘤全外显子 NGS 检测：IKZF1、JAK1、VAV1 基因突变阳性。综合诊断为：符合母细胞性浆细胞样树突状细胞肿瘤。该患者先后用 VDCLP、Hyper-CVAD 方案化疗 4 个疗程，过程顺利，随访 10 个月，现在患者一般情况良好，等待移植治疗。
结论 母细胞性浆细胞样树突状细胞肿瘤是一种非常罕见的临床进展呈高度侵袭性的淋巴造血系统肿瘤，临床表现复杂，容易误诊，常见皮肤损害、骨髓受累，少数以淋巴结肿大、脾大、发热起病，中老年发病，年轻患者罕见，典型标志 CD4、CD123、CD56、CD304、CD303、TCL1 阳性表达。BPDCN 必须结合组织形态、免疫表型、骨髓细胞、分子检测等多平台检查综合诊断，其预后极差，复发率高，中位生存期不足 2 年，缺乏标准的治疗方案,目前多采用化疗联合造血干细胞移植综合治疗，年轻患者预后好于老年人。

PO-0859

血清淀粉样蛋白 A 在眼科疾病应用的研究进展

刘晓娜
济南市明水眼科医院

血清淀粉样蛋白 A（SAA）是一种非特异性急性时相反应蛋白，其作为炎症标志物的临床价值近年来得到广泛关注。SAA 水平变化对于感染性疾病的早期诊断、危险评估、疗效观察及预后评价都具有重要临床价值。SAA 能与血浆中的高密度脂蛋白结合，是载脂蛋白家族中的异质类蛋白质，作为淀粉样沉积的前体物质，是在研究淀粉样变性的过程中被发现的。在健康人体血液中微量存在，当机体发生炎症反应时，SAA 由单核巨噬细胞产生的 IL－1、IL－6 和 TNF－α 等炎症相关因子刺激肝细胞分泌，在病毒或细菌感染 3～6h 内明显升高，且半衰期短，仅 50 分钟。在机体急性炎症时期其血浆浓度可升高 1000 多倍，并在疾病的恢复期快速下降并恢复至正常水平，因此成为目前反映炎症感染最为敏感的实验室标志。SAA 在全身炎症性疾病中的临床应用较广泛，但在局部炎症性疾病中的临床应用报道比较少见。本文就 SAA 在眼科的临床应用进行综述。

PO-0860

Serum vitamin D and vitamin-D-binding protein levels in children with chronic hepatitis B

Caizhi Huang[1]、Jie Zhang[1]、Lin Zhang[1]、Cuihua Yu[2]、Yi Mo[1]、Liya Mo[1]
1. Hunan Children's Hospital
2. 长沙市第一医院

AIM To explore vitamin D and VDBP serum levels in children with CHB and the association of vitamin D and VDBP with HBV replication and hepatic fibrosis.
METHODS We enrolled 204 children with CHB admitted to Hunan Children' Hospital in summer and autumn between 2018 and 2019 and 170 healthy controls. CHB patients included: 164 hepatitis B e antigen (HBeAg) positive and 40 HBeAg negative; 193 hepatitis B surface antigen (HBsAg) positive and 11 HBsAg negative; 164 with detectable HBV deoxyribonucleic acid (DNA) and 40 with undetectable HBV DNA; 131 with HBV genotype B and 23 with HBV genotype C; and 27 without hepatic fibrosis and 97 with hepatic fibrosis. Serum levels of 25(OH)D, VDBP, liver function markers, and other clinical parameters were collected to analyze their association with vitamin D and VDBP. Mann-Whitney U test, Kruskal-Wallis H test, or t test was used to analyze serum 25(OH)D and VDBP levels in different groups. Spearman rank correlation test was utilized to analyze the correlation of 25(OH)D and VDBP with other markers. Statistically significant factors determined by univariate analysis were further analyzed by binary multivariate logistic regression analysis. $P < 0.05$ was considered statistically significant.
RESULTS Children with CHB had lower serum 25(OH)D (56.64 ± 17.89 nmoL/L) and VDBP [122.40 (70.74-262.84 μg/L)] levels than healthy controls had ($P < 0.001$). Serum 25(OH)D and VDBP levels were significantly different among the different grades of hepatic fibrosis ($P < 0.05$). VDBP levels in children with HBV genotype C, HBsAg, HBeAg, and detectable HBV DNA were significantly lower than those in children with HBV genotype B, no HBsAg, no HBeAg, and undetectable HBV DNA ($P < 0.05$). Serum 25(OH)D level was negatively correlated with age and serum total bilirubin level ($r = -0.396$ and -0.280, respectively, $P < 0.001$). Serum VDBP level was negatively correlated with HBV DNA (log10 IU/mL) ($r = -0.272$, $P < 0.001$). Serum 25(OH)D level was not correlated with VDBP level ($P > 0.05$). Univariate ($P < 0.05$) and multivariate logistic regression analysis showed that low level of 25(OH)D (odds ratio = 0.951, 95% confidence interval: 0.918-0.985) and high level of HBV DNA (odds ratio = 1.445, 95% confidence interval: 1.163-1.794) were independently correlated with hepatic fibrosis ($P < 0.01$).
CONCLUSION Serum levels of 25(OH)D and VDBP are decreased in children with CHB. Serum VDBP level is negatively correlated with HBV replication. Low level of 25(OH)D is independently associated with hepatic fibrosis in children with CHB. There is no significant association between serum levels of 25(OH)D and VDBP.

PO-0861

Study of decreased serum levels of retinol binding protein 4 in majordepressive disorder

Qian Yao、Li Yan
Renmin Hospital of Wuhan University

Background Studies in western populations find that obesity and depression are positively correlated. Adipokines secreted by adipose tissue may serve as the crosstalk link between peripheral tissue and central nervous system,which mediates the relationship between obesity and depression.

Objective This study aimed to investigate serum retinol-binding protein 4 (RBP4) concentration inpatients with major depressive depression (MDD) and clarify its possible association with depression.
Methods Major depressive disorder patients (n = 237), healthy controls (n = 48) were collected from June 2017 to October 2019.The measurement of RBP4 levels was performed by Advia 2400 automatic biochemistry analyzer. Depressive symptoms of patients were assessed using the 24-item Hamilton Depression Scale (HAMD24).
Results (1) Serum RBP4 levels of MDD patients were significantly lower than that of the control group [(34.25 ± 8.82)mg/L vs(37.56 ± 8.83)mg/L](P < 0.05)which was independent from obesity;(2)The level of RBP4 [(31.13 ± 9.16) mg/L] in suicide attempt (SA) group was significantly lower than that in the control group andnon-suicide attempt (non-SA) group [(35.55 ± 8.37)mg/L](P < 0.05); (3) There was no significant correlation between serum RBP4 concentration and HAMD-24score (P > 0.05); serum RBP4 concentrations were positively associated with age,age of onset and duration of disease (r=0.325,0.298,0.135; P < 0.001, P < 0.001, P = 0.038) in depressive patients. (4) The level of serum RBP4 was positively correlated with TC,TG,and LDL-C(r=0.350,0.207,0.268;P < 0.001,P=0.001,P < 0.001),but not with other blood lipid indexes. ROC curve of RBP4 for MDD revealed an area under the curve of 0.603 and a sensitivity of 81.3%,specificity of 80%.
Conclusion The level of RBP4 in patients with MDD was lower than that in the normal control group, which might be related to the prognosis of patients with depression.

PO-0862

Autoimmune Epilepsy in Western China: Disease Characteristics and Prevalence

Shuo Guo[1]、Minjin Wang[2]、Yanbing Zhou[1]、Zirui Meng[1]、Yu Zhang[2]、Mingxue Zheng[2]、Xingbo Song[2]、Binwu Ying[2]
1. West China Hospital, Sichuan University
2. 四川大学华西医院

OBJECTIVE In western China, autoimmune epilepsy is an uncommon but important disease, and its true incidence is unknown. Delineating the characteristics and actual prevalence of autoimmune origin epilepsy in western China is critical to help patients receive immunotherapy, which is more effective than traditional antiepileptic therapy.
The aim of this study was to illustrate the characteristics and prevalence of autoantibodies in patients in western China with epilepsy of unknown etiology.
METHODS From January 2017 to June 2019, 639 patients with unexplained epilepsy were assessed retrospectively. Neuronal autoantibodies were assessed in 471 individuals with an APE2 score higher than 4, including 12 common neural-specific autoantibodies, antibodies against four common pathogens associated with central nervous system infections, or neurophagocytosis, and two thyroid-related autoantibodies.
RESULTS According to the APE2 score, suspected autoimmune epilepsy accounted for 44.37% of the cases of epilepsy with unknown etiology (209/471 patients). Sixty-nine patients were positive for neural-specific autoantibodies in CSF or serum that indicated that 33.02% (69/209 patients) exhibited suspected autoimmune epilepsy. 14.65% (69/471 patients) of the patients exhibited epilepsy of unknown etiology. Among the patients, 32 (46.38%) expressed NMDAR-Ab, 14 (20.29%) expressed GABABR-Ab, 10 (14.49%) expressed LGI1-Ab, 7 (10.14%) expressed GFAP-Ab, 3 (4.34%) expressed Yo-Ab, 2 (2.90%) expressed CASP2-Ab, and 1 (1.45%) expressed Hu-Ab. Compared to patients with non-autoimmune epilepsy, the positive rates of thyroid-related antibody expression and the neurophagocytosis pathogen levels of HSV-IgG and T. gondii-IgG were significantly different in patients with autoimmune epilepsy.

CONCLUSION This study elucidated the disease characteristics and prevalence of autoimmune epilepsy in western China, allowing for better identification and diagnosis of autoimmune epilepsy in the future.

PO-0863

Bacillus subtilis spores expressing Clonorchis Sinensis paramyosin (CsPmy) can positively regulate the intestinal microbiota of Ctenopharyngodon idellus.

Hengchang Sun[1]、Mei Shang[1]、Jiao Gong[1]、Wenying Zhou[1]、yan Huang[2]、Xinbing Yu[2]、Bo Hu[1]
1. The Third Affiliated Hospital, Sun Yat-sen University, Guangzhou, China
2. 中山大学中山医学院

Background Clonorchis sinensis is a pandemic zoonosis in China. For *Ctenopharyngodon idellus* (grass carp), *Bacillus subtilis* spores expressing paramyosin of *Clonorchis sinensis* has been proved to be a potent oral vaccine against *Clonorchis sinensis* cercaria infection. However，how the *Bacillus subtilis* spores affect the intestinal microbiota in grass carp deserves further study.
Method Bacillus subtilis spores were prepared in our previous study and were mixed with the pellet feed of grass carp. Grass carp, weigh 120-150 g, were divided into Bs-CotC-CsPmy，Bs-CotC and NC group in aquariums and were fed with *Bacillus subtilis* spores expressing with or without CsPmy for 8 weeks, respectively. Pellets Feed without spores were used as control. Then, fishes were sampled and the intestine tissues were used for whole-genome DNA extraction. The genomic DNA was extracted using OMEGA D3350 Bacterial DNA Kit (Omega, USA). The V3-V4 regions of 16S ribosomal DNA of bacteria were amplified, purified, and pooled in equimolar and paired-end sequenced (2 × 250 bp) on an Illumina MiSeq platform. The microbial community and diversity were evaluated. And changes in the microbiota were also analyzed.
Results Microbial community richness and diversity were significantly elevated in the Bs-CoC-CsPmy spore treated group. And 45 unique OTUs were found in the Bs-CoC-CsPmy group. The number of sequences related to Pseudomonas in the Bs-CoC-CsPmy group decreased compared with that in the NC group. Candidate probiotics including *Lactobacillus*, *Streptococcus*, and *Micrococcus* were also detected and analyzed. Higher- abundance Lactobacillus and Streptococcus genus were found in the Bs-CoC-CsPmy group. Additionally, bacteria associated with digestion were also investigated. The abundance of *Rikenellaceae*, *Ruminococcaceae*, and *Lachnospiraceae* (at the family level) varied in different groups, but they were dramatically increased in the BH group compared with other groups. Moreover, the abundances of *Odoribacter, Desulfovibrio*, and *Alistipes* were higher in the Bs-CoC-CsPmy group than those in the NC group.
Conclusion Oral administration of *Bacillus subtilis* spores expressing *Clonorchis sinensis* paramyosin reduced the abundance of potentially pathogenic bacteria (e.g., *Flavobacterium*) and enhance the abundance of probiotics (e.g. *Streptococcus*, *Lactobacillus*) or bacteria associated with digestion in grass carp.

PO-0864

First Case of Infective Endocarditis Caused by Methylobacterium radiotolerans

Ruifei Chen[1,2]、Xinkun Qi[1,2]、Bing Ma[2]、Poshi Xu[1,2]、Youhua Yuan[2]
1. Department of Clinical Laboratory of Central China Fuwai Hospital
2. 河南省人民医院

Methylobacterium radiotolerans is mainly present in the environment and has rarely been isolated from clinical samples. Here, we report for the first time a clinical case of severe infective endocarditis (IE) caused by M. radiotolerans. Several methods, including 16S rRNA amplification and sequencing, and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) were used to identify the bacterial sample isolated from the patient's cardiac vegetation. Drug sensitivity test was conducted by disk diffusion on blood Mueller-Hinton agar. This isolate was identified as M. radiotolerans. Drug susceptibility tests revealed that this isolate was susceptible to aminoglycosides and ciprofloxacin and was resistant to aztreonam. This is the first report of M. radiotolerans detection in the heart. This finding broadens the spectrum of pathogens that cause IE and serves as an encouragement to clinical personnel to pay attention to the diagnosis and treatment of severe IE caused by this rare pathogen.

PO-0865

嗜酸性粒细胞性肠炎一例

孙改河
郑州大学第一附属医院

一般资料
主诉: 女性患者，44 岁，因"腹痛 15 天，发现白细胞升高，CA125 升高 2 天"。实验室检查：大便常规：外观粘液样稀便，潜血阳性，镜检可见白细胞++++/Hp，涂片瑞氏染色为大量嗜酸性粒细胞。目前诊断：1.嗜酸性粒细胞性胃肠炎；2.低蛋白血症。
患者 2016 年 7 月 7 日加用激素治疗，口服醋酸泼尼松片治疗，密切观察患者病情变化。腹泻次数逐渐减少，自 10 余次减少至 1 次，临床症状逐步改善，于 2016 年 7 月 19 日出院，7 月 26 来院复查血液分析结果显示正常。
讨论 1. 嗜酸性粒细胞性胃肠炎(eosinophilic gastroenteritis,EG)是一组原因不明，以原发性胃肠道组织中嗜酸性粒细胞异常浸润为特征，伴有外周血嗜酸性粒细胞升高以及胃肠道症状表现的少见胃肠道疾病。病变可累及从食管到直肠的全胃肠道壁各层。1937 年 kaijser 最早描述了本病，可能与食物、药物等引起的 I 型变态反应有关，发病率约为 1-20/10 万。临床表现无特异性，容易误诊误治。按照病变部位分为局限性和弥漫性，按照浸润程度分为黏膜型、肌层型、浆膜层。诊断主要根据患者临床表现、血象、放射学和内镜病理检查结果进行诊断。
2. 实验室要注重细节，大便常规镜检发现有不明细胞成分时，可以涂片进行瑞氏染色。常见的细胞，不同寻常的比例，同样有玄机，值得深究和探讨。
3. 嗜酸性粒细胞比例增高伴 CA125 增高，不一定就是肿瘤、寄生虫，还需要考虑过敏性疾病，需要多结合病史分析。
4. 实验室检查结果要综合分析，长期腹部不适伴血液嗜酸性粒细胞增高应排除 EG。

PO-0866

Immune-associated molecule CTNNB1 for predicting the survival and tumor immunotherapy in hepatocellular carcinoma

Mei Shang、Minqi Luo、Wenying Zhou、Huimin Dong、Hengchang Sun、Sheng Liu、Jiao Gong、Bo Hu
The third Affiliated Hospital of Sun Yat-sen University

Objective Emerging study has inferred that immune checkpoint genes and the gene CTNNB1 encoding β-catenin act as the vital role in the pathogenesis and growth of liver cancer. Nevertheless, the differentially expression and its value to evaluate the prognosis of immune checkpoint genes in hepatocellular carcinoma (HCC) with or without different CTNNB1 status are still in blank.
Methods We comprehensively collected and analyzed gene expression data from HCC tissues and normal tissues in The Cancer Genome Atlas (TCGA) database. Differentially expressed genes analysis was applied to investigate the potential immune checkpoint genes that affecting the process of HCC, including the patient survival. Moreover, correlation analysis, gene-gene co-expression and survival analysis helped identify key immune checkpoint biomarkers associated with CTNNB1 mutations.
Results It was shown that five immune checkpoint genes (CD274, PDCD1, CTLA4, LAG3, and HAVCR2) were lowly expression in HCC tumors, and some of them might be highly related to the pathogenesis of HCC. The comparisons of CTNNB1 wild-type and mutant patients revealed that elevated expressions of PDCD1, CD274, CTLA4, and HAVCR2 were found in CTNNB1 wild-type group. Infiltration and survival analysis confirmed that CTNNB1-wildtype expression level was raised significantly than CTNNB1-mutation in CD8+ T cell, CD4+T cell, macrophage, neutrophil cell and dendritic cell (besides B cell). Also, HCC patients in CTNNB1 mutation group with high expression of CD274 ($p<0.001$), PDCD1 ($p=0.012$) had a better survival.
Conclusions Totally, our research screened potential differentially expression of immune checkpoint genes in different stages of HCC, and provided comprehensive and new immune checkpoint genes connected with CTNNB1 mutations, availing a theoretical insight for immunotherapy, especially the individualized management.

PO-0867

基层社区医疗机构检验科质量体系建立初探

张崇唯[1]、唐小兵[2]、应斌武[1]
1. 四川大学华西医院
2. 成都市成华区第七人民医院

目的 提升基层社区医院及卫生服务中心检验部门质量，保障结果准确度，建立检验科整体质量保障体系，剖析 5 年“医联体”模式下社区检验科的经验与收获。
方法 通过“华西-成华社区联盟”架构下，华西医院实验医学科派出专人及对应专家对基层社区 3 家社区公立医院及 8 家社区卫生服务中心检验科人员进行培训，并督导其工作人员建立质量管理文件体系，对常用检测仪器配置、调试，分享社区医院检验科存在诸多问题的解决思路，并针对社区医疗机构检验科在人员、仪器、管理上存在的困难探讨出可行的改进措施。
结果 检验人员专业素质通过“医联体”模式管理整体得到显著提升，中级检验职称从“0”到现在的 6 人，学术论文也从“0”到 5 篇，其中核心期刊 1 篇。日常检测中的准确率明显提高，各社区对检验科仪器的校准率达 90%，设备的在用状态监控及维护率达到 95%，检验效能得到显著提升。90%社区检验科建立了质量管理制度流程，使其检验全过程均有制度监管，且有两家社区医院顺利通过国家评审从无等级医院升级为“二乙综合医院”。 “联盟检验”模式从 11 家社区医院受益发展到全区域

20 家社区检验能力和报告质量得到显著提升，大部分检验项目达到同质化标准，促进作用十分明显。

结论 社区医院直接影响我国广大基层医疗水平和在传染病防控中的首诊作用。检验科以“请进来走出去”方式，结合技、管、扶的创新“医联体”模式，改进影响检验质量体系的各种因素。把从单纯依靠三级医院“输血”转变为社区检验科自身能“造血”，探索出一条适合广大社区医院检验科高质量可持续发展的途径。

PO-0868

MARCO 基因多态性与肝细胞癌发生风险的关联研究

苏真珍、蔡蓓
四川大学华西医院

目的 胶原样结构巨噬细胞受体（macrophage receptor with collagenous structure，MARCO）组成性表达于巨噬细胞表面。既往已有研究证实巨噬细胞在肝细胞癌（hepatocellular carcinoma，HCC）中具有重要的肿瘤抑制作用，而 MARCO 的低表达与 HCC 发生发展密切相关。鉴于 MARCO 表达受抑可能与其基因突变相关，本研究拟探讨 MARCO 基因多态性与 HCC 发生风险之间的关系。

方法 本研究共纳入 420 例 HCC 患者及 519 例良性肝脏疾病患者。以基质辅助激光解吸电离飞行时间质谱法对 MARCO 基因中的两个单核苷酸多态性（single nucleotide polymorphisms，SNP）位点（rs17009726 and rs6761637）进行分型检测。

结果 HCC 及对照组间各 SNP 基因型及等位基因型的分布差异无统计学意义。但 rs17009726 AG 基因型更多见于 HCC 组[HCC 者中为 106（25.2%），良性肝病对照组中为 105（20.2%），显性模型中，p=0.074，校正比值比（AOR）为 1.383，其 95%置信区间（CI）为 0.969~1.974]。与此同时，rs6761637 TC 基因型也更常见于 HCC 患者[HCC 者中为 105（25.0%），良性肝病对照者中为 105（20.2%），显性模型中，p=0.081，AOR=1.374，95% CI=0.962~1.961]。

结论 我们的初步研究结果提示携带特异性 MARCO 基因型的个体可能更易发生 HCC，但需要继续扩大研究样本量以证实相关研究结论。

PO-0869

The promoting effects of n-butanol extracted fraction of Tetrastigma hemsleyanum (TH-b) on the maturation and function of human dendritic cells

yuchong zhu、Jun-quan Liu
Hangzhou Golden Domain Medical Laboratory Co., Ltd., Hangzhou 310053, China

Objective Different extracts of Tetrastigma hemsleyanum (T. hemsleyanum) were compared in our study to find the active ingredient and its optimal concentration, which might be beneficial to the maturation and function of human dendritic cells (DCs).

Methods Isolated mononuclear cells from the peripheral blood of healthy donors were induced via GM-CSF, IL-4, and IFN-γ and LPS to be maturation DCs.DCs were incubated with different fractions of T. hemsleyanum extracts in concentration gradient. Phagocytosis and killing of Candida spores test was employed to evaluate different functional fractions for immune responses. The expression of co-stimulatory molecules CD80, CD86 and MHC II (HLA-DR) and IL-12 secretion were tested by flow cytometry and ELISA respectively to estimate the maturation states and immunoregulation ability. In the following study, DCs induced with various extracts in

different dosages were co-cultured with PBMCs in order to observe potential immunoreaction for proliferation of lymphocytes.
Results The expression of CD195 on DCs cultured for 8 days was significantly increased compare to the base line (85.3% vs. 2.4%, P<0.05). TH-b was found to increase DCs' phagocytosis function, and 0.62μg/ml was the optimal concentration. The expression of CD80, CD83, CD86, and HLA-DR on the surface of DCs increased after induction by TH-b. After 48 hours cultured with TH-b, IL-12 secreted by DCs increased significantly. And when treated with 0.62μg/ml TH-b, DCs secreted the highest level of IL-12(526.3pg/ml), which was significantly higher than that of the control group (260.1pg/ml) (P<0.05). The cell proliferation rates were significantly higher when the ratios of DCs after TH-b induction to lymphocytes were 1:1 and 1:10 than that of control group(P<0.05).
Conclusion N-butanol extracted fraction of T. hemsleyanum (abbreviated as TH-b) showed promoting effects on the maturation and phagocytosis function of human dendritic cells, and could enhance the expression of co-stimulatory molecules CD80, CD86 and IL-12 secretion at a low concentration. The optimal dosage for clinical application might be 0.62μg/ml.

PO-0870

降钙素原、C 反应蛋白及血清淀粉样蛋白 A 联合检测在感染性疾病中的诊断价值

戚佩谊
南方医科大学珠江医院

感染性疾病是一类高发性疾病，多数感染性疾病患者早期症状缺乏特异性，对其准确、有效的诊断一直是临床医生面临的重大问题。虽然其检测方法很多，如白细胞计数、C-反应蛋白(C-reactive protein，CRP) 、红细胞沉降率及体温等，但这些方法的特异性和灵敏度都不够高，不利于临床的诊断。因此对感染性疾病行早期诊断存在尤为重大的意义，在感染性疾病诊断中常采用血清降钙素原(Procalcitonin， PCT) 、C 反应蛋白(C－reactive protein， CRP) 、血清淀粉样蛋白 A(Serum amyloid A， SAA) 等检测方法。PCT 属于常见炎性因子。大量研究调查发现 PCT 检测在细菌感染早期诊断中临床应用价值较高。CRP、 SAA 是常用的感染疾病诊断炎症反应标志物，但临床上就其应用价值存在较大争议，吴金霞、罗菊梅［13］的研究表明 PCT 联合 CRP 在诊断脓毒血症的过程中，其准确性、特异性以及敏感性分别为 97.11%、75.00%、 98.00%，显著高于单独检测 PCT 或者 CRP 的诊断方式。这与王碧玉［14］、柴 林，肖敏，杨贤义等［15］研究学者的研究成果一致。管建［16］的研究结果显示，细菌感染组患儿的 PCT、CRP 水平高于病毒感染组及健康组，病毒感染组及健康组 PCT、CRP 水平差异无统计学意义。同时，细菌感染组 PCT、CRP 单独检测阳性率均高于其他两组，提示 PCT、CR 是诊断细菌性感染的敏感指标，但对于诊断病毒性感染缺乏特异性，另外细菌感染组及病毒感染组患儿 SAA 水平及阳性率差异无统计学意义，但均高于健康新生儿组，提示 SAA 在诊断新生儿感染性发热方面具有重要意义，弥补了 PCT、CRP 的不足。
综上所述，PCT、CRP、SAA 三者联合检测对感染性疾病的诊断价值更高，值得推广应用。

PO-0871

脱发人群肠道菌群变化特点

强永杰
南方医科大学珠江医院

目的 研究通过分析脱发人群与正常人群肠道菌优势菌群变化与菌属组成结构变化，为未来脱发治疗方法提供一定的思路。
方法 实验组通过采集 10 例脱发人群（30-40 岁）大便样本，进行细菌、真菌涂片染色，细菌真菌培养（稀释后培养）鉴定，找到优势菌群；通过二代测序方法分析肠道菌群组成种类对照 10 例，为健康未脱发人群（30-40 岁）。提取粪便样本总 DNA;根据细菌 16SrDNA V3~V5 区设计引物进行扩增,利用 Illumina Miseq 平台进行高通量测序;测序结果经过 Reads 拼接,OTUs(operational taxonomic units)聚类,物种注释,α 多样分析,主成分分析,最终得到样品物种信息。
结果 涂片：实验组大便涂片革兰氏染色球/杆菌比例明显高于对照组；细菌、真菌培养：实验组双歧杆菌、消化链球菌、乳杆菌、产气荚膜梭菌、肠杆菌检出比例低于对照组；二代测序：实验组其中拟杆菌门(Bacteroidetes)占比 46.94%，厚壁菌门(Firmicutes)占比 30.58%，对照组实验组其中拟杆菌门占比 60.96%，厚壁菌门占比 41.51%包含幽门螺杆菌的螺杆菌属检出比例升高，实验组平均占比比对照组高 0.03%。
结论 表明实验组（脱发组）和对照组（未脱发组）菌群结构存在显著差异。这些结果表明,脱发人群与未脱发人群在肠道菌群多样性方面没有明显差异,但在菌群结构上存在较大差异;同时脱发人群肠道菌群致病菌数量多于健康人群,而拟杆菌类有益菌低于健康人群。由于有研究表明，脱发与生物素合成相关，未来可进一步细菌对生物素合成情况进行研究。

PO-0872

西南地区 398 例克氏综合征患者临床特征分析

王念、周汶静、林立、周易、宋兴勃、巫丽娟、钟慧钰、叶远馨
四川大学华西医院

目的 分析西南地区克氏综合征患者临床特征，探讨染色体核型、临床症状、血清性激素水平在克氏综合征患者诊断中的临床应用价值及诊断意义。
方法 回顾性分析我院 398 例克氏综合征患者的主要临床症状、外周血染色体核型以及其中 206 例具有血清性激素结果的纯合型（47，XXY）克氏综合征患者和随机收集的同期的 180 例染色体核型正常的男性对照的血清性激素水平，进行比较分析。
结果 398 例 KS 患者中，其年龄范围主要集中在 11-30 岁，以 21-30 岁年龄段所占比例最高，占比 61.05%。同时，该类患者的临床来源以泌尿外科为主共 306 例占比 76.89%。对 334 例具有明确的临床症状信息的 KS 患者进行分组分析，其中以睾丸发育不良综合征（TDS）所占比例较高为 55.99%。在 398 例克氏综合征患者的染色体核型分析中纯合型 （47，XXY）381 例，占比 95.75%，嵌合型（47，XXY/46,XY）3 例/（47，XXY/46,XX）2 例共占比 1.25%和变异型 12 例，占比 3.0%。在 206 例非嵌合型克氏综合征患者血清素卵泡生成素（FSH）、黄体生成素（LH）、PRL（泌乳素）及睾酮（T）水平分析中，KS 组血清 LH 和 FSH 均明显高于正常对照组（P<0.05），血清 PRL 在两组间无显著性差异（P>0.05），而血清 T 水平明显低于对照组（P<0.05）。
结论 西南地区克氏综合征患者以 TDS 为主要临床表现，以 FSH 、LH 及 T 激素的改变最为明显。综合分析临床主要症状、染色体核型、血清性激素水平有助于提高克氏患者的临床诊断效率。

PO-0873

流式细胞仪在对血液系统肿瘤免疫表型分析中最低检测限的稀释性验证

金咏梅、赵玮晨、蒋能刚、廖红艳、粟军
四川大学华西医院

目的 对流式细胞仪在诊断血液系统肿瘤方面的最低检测限进行稀释性验证。
方法 选取 4 例不同血液系统肿瘤患者骨髓，包括髓系肿瘤、B 淋巴系肿瘤、T 淋巴系肿瘤及浆细胞系肿瘤，对标本中白血病细胞用正常人骨髓白细胞进行稀释，浓度包括 1%、0.1%、0.01%，按不同疾病个体化抗体组合方案，加入相应抗体对目的细胞进行标记，上机实验观察结果。以 CD45/SSC 双参数散点图设门进行分析，各浓度梯度标本收集到 20 个及以上白血病细胞时视为阳性，同一样本重复 10 次，有 9 次及以上为阳性时判断为最低检测限达到或低于该浓度。
结果 BD FACSCantoⅡ流式细胞仪在诊断血液系统肿瘤方面的最低检测限为 0.01%。
结论 BD FACSCantoⅡ流式细胞仪在诊断血液系统肿瘤方面的最低检测限为 0.01%，能够很好地满足临床的需求。

PO-0874

评估血清 Hcy 及 Betaine 水平在妊娠合并糖尿病病人中的诊断价值

王雅茹、张诗田、刘蕊、屈恩帅、牛文彦
天津医科大学朱宪彝纪念医院

目的 目前有关血清 homocysteine（Hcy）、叶酸、vitamin B12（VitB12）水平与血糖浓度以及妊娠期糖尿病（GDM）风险的研究结果尚不确定。 Hcy 水平在 GDM 中的研究相对较少，且结果之间不一致，甜菜碱（betaine）和 vitamin B12 之间的关系也没有得到很好的研究，特别是在怀孕期间。而 betaine 和甜菜碱-同型半胱氨酸甲基转移酶（BHMT）在 Hcy 转化成蛋氨酸途径中起着重要作用。本实验旨在分析 Hcy、betaine 在妊娠合并糖尿病病人中的表达水平，以及与叶酸、VitB12、生化指标等数据之间的相关性，评估 Hcy 作为风险因子在妊娠合并糖尿病病人中的诊断价值，并进一步探究 BHMT 和 betaine 水平对 Hcy 水平的影响，为临床预防和治疗妊娠合并糖尿病病人提供理论依据。
方法 入院就诊的怀孕妇女，按照 ADA 诊断标准，将人群分为对照组和妊娠合并糖尿病组（包含 2 型糖尿病伴妊娠和 GDM 人群）。ELISA 法检测血清 Hcy、VitB12、叶酸以及 BHMT 水平。甜菜碱含量检测试剂盒检测 betaine 水平。全自动生化分析仪及糖化血红蛋白分析仪检测血脂及 HbA1c 水平。血糖分析仪检测空腹静脉血糖（FPG）水平。SPSS 分析 Hcy、betaine 与多指标之间的相关性，ROC 曲线评估 Hcy、betaine 对妊娠合并糖尿病的诊断价值。
结果 血清 Hcy 水平在妊娠合并糖尿病患者中明显增高，而 betaine、VitB12 水平明显减低，叶酸和 BHMT 水平无统计学意义。Hcy 与 betaine 呈负相关，与 FPG、HbA1c 呈正相关。Betaine 与 VitB12 呈正相关。Hcy 在妊娠合并糖尿病患者中的诊断价值为 0.7145，而 betaine 对其诊断无意义，两者联合检测也未增加其诊断价值。妊娠合并糖尿病患者中，GDM 患者占 67%，Hcy 水平低于 T2DM 伴妊娠患者，但两者之间无统计学意义，betaine 水平在两组中同样无统计学意义，Hcy 水平在这两组中的诊断价值分别为 0.7261、 0.7087。
结论 Hcy 可作为风险因子，对妊娠合并糖尿病患者有一定的诊断价值，同时提示妊娠期间，除了补充叶酸、VitB12 外，betaine 的补充也是非常有必要的。

PO-0875

基于甘特图提高科研课题进度及科研人员管理能力*

雷明德
重庆市东南医院

目的 探索建立基于甘特图管理模式的科研人才培养评估体系并应用于人才评价。
方法 根据近三年的参与科研申请并通过的立项课题，多角度对比上述科研共同参与人员 A、人员 D 两人的科研学习参与度及课题贡献量，对比分析科室层面及医院层面对科研课题的各项参数。
结果 人员 A 在课题排名与工作量均无变化，故课题贡献量无变化。人员 D 在课题排名与工作量均在不同程度的发生变化，根据科研量化考核数据分析，人员 D 在 2018 年科研量化比为 2%，2019 年科研量化比为 8.5%，具有统计学差异（u=2.06,P<0.05）。科研课题的性质也由多科室合作发展到区域内多中心合作模式，到 2020 年科研发展为跨区域多中心合作。课题级别分别为区卫健委项目、区卫健委与区科技局联合项目、区科技局项目。
结论 基于甘特图管理模式,提高科研人员积极性及工作能力，为科研管理者及实验室管理者提供参考依据,为医院科研发展提供保障。

PO-0876

血清低密度脂蛋白胆固醇直接测定法与不同公式法间对比

陈波
广州医科大学附属第二医院

目的 探讨低密度脂蛋白胆固醇(LDL-C)直接测定法与多种公式计算法、及其校正公式计算法和自推导公式结果的可比性。
方法 随机抽取 2014 年 6 月至 2014 年 12 月本院患 1654 例，其中男 899 例，女 755 例,年龄范围 58.57±17.86 岁，早晨空腹采静脉血，离心取血清进行总胆固醇（TC）、三酰甘油(TG)、高密度脂蛋白胆固醇(HDL-C)、载脂蛋白 B（ApoB）和 LDL-C 项目测试。并与计算 F 公式、P 公式、D 公式、F’公式、P’公式、D’公式和 C 公式（自推导公式）LDL-C =0.88TC-0.79HDL-C-0.20TG （r=0.985，P<0.01）的相关性，按 TG 浓度分成 3 组分别为 0.33～1.70 mmol／L、1.70～4.52mmol／L 和 4.52～11.65mmol/L 进行公式法与直接测定法结果比较。
结果 根据直接 LDL-C 浓度范围将其分为 10 组进行观察数据基本为正态分布，其浓度主要集中在 1.20～4.80mmol/L 之间，3.00～3.60mmol/L 为构成比最高。将 TG 浓度范围从直方图显示出数据基本为偏态分布，浓度主要集中在 0.90～3.60mmol/L 之间，1.80～2.70mmol/L 为构成比最高，TG 浓度<4.52mmol/L 时，其累计百分数达 98.67%。直接测定法和公式法血清 LDL-C 含量的相关性最高为 C 公式，其次为 D 公式，最低为 P 公式。均数比较 F’公式与直接测定法最近，其次为 F 公式，最远为 P’公式。离散度最小 P 公式，其次为 D’公式，最大为 P’公式。符合率（|差值|<=10%）从大到小分别为 C 公式>F’公式>D’公式>D 公式>F 公式>P 公式>P’公式。TG 在 0.33～1.70 mmol／L 组符合率从高到低分别为 C 公式>D’公式>F’公式 > F 公式>D 公式>P 公式> P’公式,最高是 C 公式（95.89%），最低是 P’公式（47.75%）。TG 在 1.70～4.52mmol／L 组符合率从高到低分别为 C 公式> D 公式> P’公式 > F’公式>F 公式> D’公式>P 公式,最高是 C 公式（93.85%），最低是 P’公式（27.95%）。TG 在 4.52～11.65mmol/L 组符合率从高到低分别为 D 公式>C 公式>F 公式=F’公式= P’公式>D’公式> P 公式,最高是 D 公式（54.55%），最低是 P’公式（4.55%）。
结论 实验结果表明，7 种公式法中 C 公式法具有与直接法良好相关性和一致性（r=0.985，符合率=94.68%），其次 D 公式（r=0.981，符合率=82.10%)与 F’公式（r=0.970，符合率=85.01%)均较好。在 TG 在 0.33～4.52 mmol／L 范围内 C 公式、D 公式、F’公式、F 公式和 D’公式均有较好符合率，在 TG>4.52 mmol／L 范围 7 种公式法符合率均不理想。TG 浓度<4.52mmol/L 时的累计百分数可达 98.67%，也考虑到经济的因素，LDL-C 直接法费用比 TC、TG、 和 HDL-C 贵，而公式计算则

不需要附加费用，因此通常可以采用公式法测定 LDL-C。当 TG 浓度>4.52mmol/L 或监测 LDL-C 时，应采用直接法为佳，这样取得更经济、实惠、相对准确的 LDL-C 结果。

PO-0877

一例多种羧化酶缺乏症的质谱及基因突变分析

谢汛杰
南方医科大学珠江医院

目的 对一例以肺炎、皮疹及严重代谢性酸中毒为先发症状的多种羧化酶缺乏症进行临床观察、质谱及基因分析。
方法 通过临床观察分析症状，同时分别用、串联质谱、气相色谱及高通量测序检测患儿血氨基酸和酰基肉碱谱、尿有机酸谱以及患儿及其父母 BT 及 HLCS 基因突变情况。
结果 患儿临床表现主要为皮肤溃疡、蜕皮，精神反应差，重症肺炎等，串联质谱分析提示支链氨基酸、丙酰肉碱、甲基丙二酰肉碱和 3-羟基异戊酰肉碱明显升高，气相色谱分析提示 3-羟基丙酸、3-甲基巴豆酰甘氨酸、甲基枸橼酸、3-羟基异戊酸明显升高，基因突变分析提示为复合杂合突变，其中 HLCS_ex9 c.1522C>T 源于父亲，HLCS_ex10 c.1711G>A 源于母亲。
结论 本研究的对象是一例症状及质谱结果均符合的多种羧化酶缺乏症，基因分析为复合杂合突变，生物素治疗有明显效果，预后良好，但需要定期监测 3-羟基异戊酰肉碱水平。早期做串联质谱筛查能有效减少遗传代谢病的致残风险。

PO-0878

Emergence of Ceftazidime-Avibactam Resistance Due to A Novel blaKPC-2 Mutation during Treatment of Carbapenem-Resistant Klebsiella pneumoniae Infections

Quanfeng Liao
Department of Laboratory Medicine, West China Hospital of Sichuan University

Objective Klebsiella pneumoniae carbapenemase (KPC)-producing K.pneumoniae have represented a serious health problem in worldwide. The resistance to ceftazidime-avibactam (CAZ-AVI) began to emerge since its approval in 2015. We aim to explore the resistance mechanism of CAZ-AVI.
Methods Phenotypic test and whole-genome sequencing (WGS) analysis were performed in carbapenemase-resistant Klebsiella pneumoniae (CRKP) of HX0917 and HX1016 isolates, collected from the same patient following treatment with CAZ-AVI.
Results We report a case of emergence of CAZ-AVI resistance in ST 11 KPC-2-producing K. pneumoniae (HX1016) during 14 days of exposure with CZA-AVI. Molecular analysis highlighted the A533C mutation in the blaKPC-2 gene, resulting a D178A substitution in protein sequence, which restored the hydrolysis ability of imipenem and meropenem, but not for ertapenem, and the result of phenotypic test was negative. However, the CRKP (HX0917) isolate produced serine-carbapenemase by phenotypic detection and lost its capacity of hydrolyzing carbapenems.
Conclusion The emergence of CAZ-AVI resistance should arouse our attention, the susceptibility testing should be followed by a combination of phenotypic and molecular methods, to make sure that no potential carbapenemase-producing bacteria are missed.

PO-0879

广州郊区某农村井水铊等重金属的健康风险评估

潘心红、李美霞
广州市疾病预防控制中心

目的 通过对广州郊区某农村井水中铊等重金属进行监测，对重金属致癌和非致癌的健康风险进行评估，为饮用井水与水源的安全管理提供了科学依据。
方法 于 2020 年 10 月采集广州郊区农村的 14 口水井的 34 宗井水，对照水源分别为山泉水、末梢水、沟塘水共 12 宗，用电感耦合等离子体质谱仪法（ICP-MS）进行检测，采用国家标准（GB5749 －2006）国家标准和美国环保署 （US EPA） 推荐的健康风险评价模型，对其进行健康风险评估。
结果 农村井水中 Tl 的含量严重超标，超标率高达 70%以上，Pb、Fe、 Mn、PH 值和浑浊度含量也不同程度超标，Tl 超标的平均浓度顺位为井水>末梢水>沟塘水>山泉水；井水中致癌风险 As > Cd，分别为 2.57×10-6 和 3.01×10-8；Tl、Pb、Fe、Mn 等非致癌性健康风险在 65.1×10-8 ～ 0.79×10-8，均低于国际放射防护委员会（ICRP）的推荐值 （5.0×10-5）。
结论 调查表明：广州郊区某农村的井水 Tl 严重超标，Pb、Fe、Mn、PH 值和浑浊度等项目的含量也超标，非致癌物的个人健康风险值依次为 Pb > Mn > Tl > Fe，虽然对暴露人群的健康危险影响较小，但井水中重金属 Tl 污染特别严重，因此广州郊区某农村井水不能饮用，希望有关部门需要定期加强监测与风险评估，防止重大公共卫生事件的发生。

PO-0880

2015-2019 年腹腔积液标本的病原菌分布及耐药性分析

郭媛媛
云南省第二人民医院

目的 分析腹腔积液的病原菌构成和药敏情况，为临床合理用药提供依据。
方法 回顾性分析云南大学附属医院 2015 年 1 月-2019 年 12 月收集的腹腔积液标本分离的病原菌培养及体外药敏试验。
结果 1254 份腹腔积液标本共分离出非重复病原菌 687 株，总检出率为 54.78%，687 株病原菌中主要是革兰阴性菌（60.84%），主要是大肠埃希菌和肺炎克雷伯菌，其次是革兰阳性菌（28.97%），主要是屎肠球菌和表皮葡萄球菌；真菌占 10.19%。革兰阴性菌检出率由 2016 年的 79.82%下降至 2019 年的 53.21%，下降约 1.5 倍，革兰阳性菌检出率由 2016 年的 20.18%上升至 2019 年的 46.79%，上升约 2.5 倍。腹腔感染的主要科室来源是普通外科占 61.3%，其次是 ICU 占 23.8%。产 ESBLs 大肠埃希菌和肺炎克雷伯菌的检出率分别为 64.09%、43.48%，产 ESBLs 的肺炎克雷伯菌对哌拉西林＞90%，对头孢菌素类均＞60%，对喹诺酮类及加酶抑制剂复合制剂耐药率在 40%左右，对阿米卡星耐药率为 10%。产 ESBLs 的大肠埃希菌对青霉素类、第一代和第三代头孢菌素均＞90%，对喹诺酮类耐药率均＞60%，对加酶抑制剂复合制剂耐药率＜20%。产 ESBLs 的肺炎克雷伯菌对碳青霉烯类抗生素敏感性为 100%，不产 ESBLs 的肺炎克雷伯菌对碳青霉烯类抗生素的耐药率接近 20%。
结论 云南大学附属医院腹腔积液分离病原菌中革兰阴性菌检出率逐渐下降，而革兰阳性菌检出率呈上升趋势，产 ESBLs 的检出率较其他医院偏高，对常见抗菌药物耐药率偏高，由于产 RSBLs 会同时存在产碳青霉烯酶，容易被产碳青霉烯酶的机制覆盖，因此产 ESBLs 会出现假阴性，建议临床医生应严格按照药敏试验结果合理使用抗菌药物，同时加强医护人员的无菌意识，加强感染的预防与控制。

PO-0881

High prevalence and fitness of IncFrepB carrying qnrS1 in hypervirulent Klebsiella pneumoniae isolates

Yang Liu 、si chen、wan lagen
First Affiliated Hospital of Nanchang University

Objective The objective of this study was to reveal theprevalence and fitness of plasmids carrying qnrS1 in hypervirulent Klebsiella pneumoniae (hvKP) isolates.
Method Weidentified bacterial virus genes, cps genotypes, and resistance genes by polymerase chain reaction. Plasmid typing wasdetermined byPCR-based replicon typing.Pulsed-field gel electrophoresis andmultilocus sequence typing were conducted to analyze the genetic relatedness.The transferability of qnrS1-carrying plasmidswas analyzed by conjugation experiments and Southern blotting. The fitness of the qnrS1-plasmid carriagewas assessedin vitro competition assays.
Result A total of 299 hvKP isolates carrying qnrS1 resistance gene collected from a Chinese teaching hospitals from 2018 to 2020 were investigated for theprevalence and fitness of plasmids carrying qnrS1. The most frequently capsular serotypes were K64 (85.3%, 245/299). Multilocus sequence typing analysisrevealed K64 capsular serotypes were all ST11, and non-K64 were mainly ST23 type (7/44, 15.9%), andnext by ST11 type (3/44,6.8%).IncFrepB-type replicon was found in90.0% (n =272) of299 isolates with plasmid typing, whereas IncN-type replicon was detected in12.0% (n =36), IncFIB-type replicon in4.3% (n =13) and IncFIIAs-type replicon in1.7% (n =5) of the isolates. Outcomes of the conjugation experiments showed that the qnrS1 gene was carried to the receiver cell on FrepB plasmids.The analysis of the transconjugants showed decreased susceptibility to quinolones and revealed a cotransfer of blaTEM-1 or blaSHV-1 with the qnrS1 alleles. The capsule serotype of 9 donors indicated that non-K64 strains (n=6) formed easier conjugates thanthe K64 strains (n=3) ($p<0.05$). S1 nuclease-PFGE and Southern blotting showedtheqnrS1 genewas located on different size plasmids. However, thefitness of plasmids were differed as only plasmidsof~70 kb cotransfer of blaTEM-1 with the qnrS1 alleles could be stablysub-cultured. The transconjugants with stable plasmid (J53::pK3-qnrS and J53::pK6-qnrS) showedcompetition index valuesof 0.59 and0.61, respectively.
Conclusion IncFrepB-type replicon was found to be the most prevalent type of plasmid carring qnrS1 in hvKP in our hospital. IncFrepB showed diversity, mainly reflected in the size of the plasmid and the carrying status of ESBL-related genes. These plasmid has showed different fitness costs in transconjugants. FrepB plasmidsof ~70 kb carrying TEM-1 genes could be stably disseminated. Therefore,these plasmids mayrepresent the mainqnrS1 genes of thehvKPepidemic in Jiangxi, China,and requiresheightened attention.

PO-0882

改良微量血清杀菌活性测定法与经典血清杀菌活性测定法的比较

徐灵、董成林、吴成志、邵燕、李仁杰、崔邦铨
上海中冶医院

目的 比较改良微量血清杀菌活性（SBA）测定法与经典血清杀菌活性测定法的检测结果。
方法 选择接受头孢唑肟钠静脉滴注治疗的患者 35 例，采集用药后 30 min 的血液标本，同时采用改良微量血清杀菌活性测定法（改良法）与经典血清杀菌活性测定法（经典法）检测血清对标准质控菌株铜绿假单胞菌（ATCC 27853）的 SBA 效价，比较 2 组检测结果。

结果 接受头孢唑肟钠静脉滴注治疗的 35 例患者中，改良法测得的 SBA 效价为 1:4 ~ 1:64（中位数为 1:16），经典法测得的 SBA 效价为 1:4 ~ 1:32（中位数为 1:16），2 组检测结果差异无统计学意义（P >0.05）。
结论 改良 SBA 法与经典 SBA 法检测结果相一致，可替代经典法应用于临床和研究，且其操作更简便，易于推广应用。

PO-0883

基于 VITEK MS 快速检测产碳青霉烯酶肺炎克雷伯菌的方法研究

胡珍、林豪芸、吴文苑
深圳市人民医院

目的 本研究通过对基于 VITEK MS 快速检测产碳青霉烯酶肺炎克雷伯菌（*Carbapenemase-producing Klebsiella pneumoniae*，CPKP）的方法研究，建立用于临床微生物实验室的基于 VITEK MS 快速检测 CPKP 方法。
方法 首先，应用产碳青霉烯酶标准阳性质控菌优化美罗培南水解试验的实验条件和 VITEK MS 仪器参数，建立基于 VITEK MS 快速检测 CPKP 方法。其次，收集 2020 年 3 月至 2021 年 2 月深圳市人民医院检验科微生物实验室临床分离的非重复碳青霉烯耐药肺炎克雷伯菌（*Carbapenem-resistant Klebsiella pneumoniae*，CRKP），按 1:1 比例收集同期的非重复碳青霉烯敏感肺炎克雷伯菌（*Carbapenem-susceptibal Klebsiella pneumoniae*，CSKP），采用聚合酶链式反应（polymerase chain reaction，PCR）检测 CRKP 和 CSKP 的碳青霉烯酶耐药基因，检出 CPKP 和非产碳青霉烯酶肺炎克雷伯菌；用基于 VITEK MS 快速检测 CPKP 的方法分别检测 CRKP 和 CSKP，检出 CPKP 和非产碳青霉烯酶肺炎克雷伯菌。以 PCR 结果评估基于 VITEK MS 快速检测 CPKP 方法的灵敏度和特异度。最后，收集 2016 年 1 月至 2017 年 12 月深圳市人民医院检验科微生物实验室临床分离的经全基因组测序确定的非重复 CPKP，以此菌株为对象，评估基于 VITEK MS 快速检测 CPKP 方法检测 CPKP 的检出率。
结果 本研究通过对美罗培南水解试验中的实验条件和 VITEK MS 仪器参数的激光强度等进行优化，建立了基于 VITEK MS 快速检测 CPKP 方法。共收集非重复 CRKP15 株和 CSKP15 株。PCR 检测 15 株 CRKP 均为 CPKP、15 株 CSKP 均非产碳青霉烯酶肺炎克雷伯菌。应用本研究建立的基于 VITEK MS 快速检测 CPKP 方法，分别检测 15 株 CRKP 均判断为 CPKP，15 株 CSKP 均判定为非产碳青霉烯酶肺炎克雷伯菌。以 PCR 结果，本研究所建立的基于 VITEK MS 快速检测 CPKP 方法的灵敏度和特异度均为 100%。经全基因组测序确定的非重复 CPKP 共 80 株，基于 VITEK MS 快速检测 CPKP 方法检测 78 株为 CPKP，2 株为非产碳青霉烯酶肺炎克雷伯菌。基于 VITEK MS 快速检测 CPKP 方法检测 CPKP 的检出率为 97.5%。
结论 本研究建立的基于 VITEK MS 快速检测 CPKP 方法对 CPKP 检出的灵敏度和特异度高，具有良好的临床应用前景。

PO-0884

脓毒症背景下嗜麦芽窄食单胞菌及其他常见致病菌对适应性免疫的影响研究

阴晟、王敏、麦伟华
中南大学湘雅二医院

研究嗜麦芽窄食单胞菌（StenotroPhomonas maltoPhilia，SMA）血流感染中患者免疫血象表征。通过与其他致病菌的免疫细胞分布模式对比，揭示 SMA 与不同致病菌流感染下免疫情况是否具有差异及分析该现象的内在机制，并证实 SMA 感染对于免疫系统的抑制效应。

方法 回顾性统计分析 2018—2021 年中南大学湘雅二医院单中心临床确诊 SMA 血流感染患者及其他病原菌的免疫细胞及炎症因子，并通过数据结果得出临床细胞免疫调节规律和临床诊断意义。
结果 淋巴细胞百分比和中性粒细胞百分比的中位数能较合理的反映数据的平均水平，PCT 的总体分布受极值影响更大。SMA 与肺炎克雷伯菌在淋巴细胞百分比（P=0.001）和中性粒细胞百分比（P=0.006）临床血流感染总体分布上有统计学意义；与白色念珠菌在中性粒细胞百分比（P=0.022）上有统计学意义。
结论 SMA 血流感染能抑制淋巴细胞的增殖，从而导致适应性免疫应答反应下降。临床需要进一步关注 SMA 的合并感染及及慢性感染，降低因耐药耐药及继发性免疫抑制相关脓毒症的病死率。

PO-0885

鹑鸡肠球菌对万古霉素耐药性监测及耐药基因研究

谢晖
南京大学医学院附属鼓楼医院

目的 调查临床分离鹑鸡肠球菌对万古霉素的耐药情况及耐药机制。
方法 采用 VITEK 2 系统 GP67 卡对 2019 年 1-12 月南京鼓楼医院临床分离 15 株鹑鸡肠球菌进行药敏试验，采用 E-test 法复核菌株对万古霉素最低抑菌浓度（MIC）；采用 PCR 及测序技术分析万古霉素耐药决定基因 vanA、vanB、vanC1 及 vanC2/3；采用 Illumina HiSeq 2000 测序技术对菌株基因组 DNA 进行 Paired-end（PE）测序，利用生物信息学对菌株全基因组序列分析及耐药基因、毒力基因分析。
结果 15 株鹑鸡肠球菌对万古霉素的 MIC 值集中在 4 mg/L 和 6 mg/L，所占比例分别为 40%和 33.3%，检出 1 株（6%）万古霉素高水平耐药株 EG17906（MIC 为 256 mg/L），该菌株对除万古霉素和替考拉宁耐药外，对其余常用抗生素均敏感；15 株菌株均检出 vanC2/3 基因， EG17906 菌株同时检出 vanA 基因；EG17906 菌株经全基因组测序分析 ，基因组大小为 3 765 197 bp ，GC 含量为 40.4% ，总基因数为 3 754，基因组含有 3 592 个编码序列，60 个 tRNA 编码基因以及 10 个完整的 rRNA 基因编码操纵子。耐药基因预测分析该菌株携带 VanC1XY、VanHAX、erm(A)、erm(A) 、 tet(O) 、 cat(pC221) 。 全 基 因 序 列 提 交 至 NCBI 数 据 库 ， GeneBank 号 为 JABMDB000000000。
结论 鹑鸡肠球菌携带 vanC2/3 对万古霉素呈低水平耐药，而同时携带 vanA 基因可造成菌株高水平耐药，需引起重视。

PO-0886

多重耐药鲍曼不动杆菌耐药特征及同源性分析研究

王佳
昆明市延安医院

目的 收集昆明市两家三甲医院多重耐药鲍曼不动杆菌耐药数据，描述相关耐药基因携带情况，并通过分子流行病学调查明确菌株间亲缘关系，从而提供可靠和及时的流行病学资料，指导临床制定合理有效的用药策略。
方法 收集 2018 年 1 月至 2020 年 12 月两家三甲医院临床分离的非重复鲍曼不动杆菌菌株共 92 株，采用 MIC 法和 K-B 法检测鲍曼不动杆菌对临床常用抗菌药物的敏感性，应用 PCR 扩增 7 种 β-内酰胺酶耐药基因（SHV、TEM、IMP、VIM、ADC、OXA-23、OXA-58），同时采用多位点序列分型方法对 92 株多重耐药鲍曼不动杆菌进行分子分型，分析菌株同源性关系。
结果 92 株 MDRAB 对所检测抗生素耐药程度均较高，对青霉素类、单环 β-内酰胺类、头孢菌素类和碳青霉烯类抗菌药物的耐药率高达 100%；在 β-内酰胺酶抑制剂中，耐药率均达到为 90%以上；

对妥布霉素、复方新诺明、阿米卡星、庆大霉素、左氧氟沙星的耐药率两家医院差别较为明显，医院甲对上述药物耐药率高达 80%以上，而医院乙耐药率仅为 65%左右；米诺环素尤为显著，医院甲耐药率达 62%，医院乙耐药率仅为 7.1%；医院甲 MDRAB 对替加环素未出现耐药，医院乙耐药率达到 14.3%。92 株 MDRAB 中，两家医院检出率较高的耐药基因是：OXA-23、TEM、ADC 基因；其中医院甲 47 株分别携带 OXA-23、TEM 基因，占 94%；医院乙却有 41 株携带 OXA-23 基因，占比高达 97.6%；未检出 SHV、IMP、VIM、OXA-58 基因。92 株中 55 株同时携带 TEM+ADC+OXA-23 基因，68 株携带 TEM+OXA-23 基因，携带 TEM+ADC 基因 56 株，携带 ADC+OXA-23 基因 75 株。将 92 株 MDRAB 测序结果提交到 Pubmlst 数据库进行比对，结果共分为 12 个序列型，其中医院甲主要以 ST208 型（58%）为优势型别，其次为 ST1145 型，占 24%；医院乙主要以 ST368 型（30.9%）为主）。

结论 临床分离鲍曼不动杆菌耐药现象严重，对各种类型抗生素普遍耐药，少数菌株对头孢哌酮/舒巴坦和米诺环素具有敏感性，全部菌株对替加环素敏感性较好，提示临床可以使用替加环素作为 MDRAB 感染的治疗。目前，鲍曼不动杆菌耐药日益严重可能由于携带多种耐药基因所导致，携带多种耐药基因是本地区鲍曼不动杆菌多重耐药的重要机制之一。通过我们对两家医院耐药基因检测发现，两家医院耐药基因携带情况不尽相同，这可能与两家医院临床抗生素使用情况和医院管控政策相关。两家医院分别存在不同型别的耐药菌株克隆传播，医院间尚未存在克隆菌株的流行播散。

PO-0887

Co-occurrence of rapid gene gain and loss in an interhospital outbreak of carbapenem-resistant hypervirulent ST11-K64 Klebsiella pneumoniae

Xiaotuan Zhang、Zhuo-ran Liu、luo-gen Liu
The Second Affiliated Hospital, University of South China

We report an outbreak of carbapenemase-producing, hypervirulent Klebsiella pneumoniae in two hospitals that undergo frequent patient transfers. Analysis of 11 complete assembled genomes showed that the bacteria were ST11-K64 strains. Moreover, 12 single nucleotide polymorphisms (SNPs) identified the strains as having originated from the same cluster, and were also indicative of interhospital transmission of infection. Five plasmids were assembled in each of the strains. One plasmid carried several virulence genes, including the capsular polysaccharide regulators rmpA and rmpA2. Two others carried antimicrobial-resistance genes, including one for carbapenem resistance, blaKPC-2. Comparative genomic analysis indicated the occurrence of frequent and rapid gain and loss of genomic content along transmissions and the co-existence of progeny strains in the same ward. A 10-kbp fragment harboring antimicrobial resistance-conferring genes flanked by insert sequences was missing in a plasmid from strain KP20194c in patient 3, and this strain also likely subsequently infected patient 4. However, strains containing the 10-kbp fragment were also isolated from the ward environment at approximately the same time, and harbored different chromosome indels. Tn1721 and multiple additional insert sequence-mediated transpositions were also seen. These results indicated that there is a rapid reshaping and diversification of the genomic pool of K. pneumoniae facilitated by mobile genetic elements, even a short time after outbreak onset. ST11-K64 CR-hvKP strains have the potential to become new significant superbugs and a threat to public health.

PO-0888

Mst2 促进单增李斯特菌感染过程中 JNK/NLRP3 信号通路的活化

高爱娇、申艳娜、刘瑞卿、王琳、唐慧欣、刘亚珊
天津医科大学

目的 单核细胞增生李斯特菌（简称单增李斯特菌）是一种人畜共患的革兰阳性胞内寄生菌，感染后可引起脑膜炎、败血症等致死性疾病，死亡率高达 30%。有研究报道 NLRP3 炎症小体参与宿主防御以抵抗病原体感染，然而单增李斯特菌感染过程中 NLRP3 炎症小体激活的具体潜在机制尚未完全阐明。近年来，研究表明 Mst1/2 在固有免疫中发挥着重要作用。在结核分枝杆菌感染过程中 Mst2 促进趋化因子 CXCL1/2 的表达进而调控免疫反应。在乳腺癌细胞以及高脂、高糖或脂多糖刺激的神经细胞中 Mst1 均可通过介导 JNK 的活化促进细胞凋亡。而 Mst2 是否参与单增李斯特菌感染诱导的炎症反应尚未见报道。因此，我们探究 Mst2 在单增李斯特菌感染过程中活化 NLRP3 信号通路的作用机制。
方法 Western blot 方法检测单增李斯特菌感染的小鼠原代腹腔巨噬细胞中 Mst2 的蛋白水平。比较 Mst2 siRNA 预处理前后的小鼠原代腹腔巨噬细胞经单增李斯特菌感染后，细胞裂解物中 p-JNK、Nek7 蛋白水平、NLRP3 及其下游分子 p20(活化的 caspase-1)、mIL-1β 表达水平。免疫共沉淀方法检测 Mst2 抑制剂预处理前后的小鼠原代腹腔巨噬细胞经单增李斯特菌感染后，胞内 Nek7 与 NLRP3 的结合水平。
结果 在单增李斯特菌感染过程中，Mst2 蛋白水平在感染 60 min 明显升高。与未处理组相比，Mst2 siRNA 处理组 p-JNK 在 2 h 明显降低，Nek7、NLRP3、p20、mIL-1β 蛋白水平在 4 h 明显降低。Mst2 抑制剂处理组 Nek7 与 NLRP3 结合水平在 2 h 显著降低。
结论 单增李斯特菌感染过程中，Mst2 通过促进 Nek7 与 NLRP3 的结合激活 JNK/NLRP3 信号通路。

PO-0889

临床厌氧菌感染的分布特征以药敏分析

张桂华
中国医科大学附属第一医院鞍山医院

目的 分析厌氧菌标本来源、科室、年龄分布特征及药敏试验结果，为临床经验性治疗和合理使用抗菌药物提供依据。
方法 收集 2018 年 5 月—2020 年 1 月医院住院患者所有合格标本中分离到的 45 株厌氧菌，经厌氧菌检测试剂盒鉴定和药敏试验结果分析。
结果 检测出的厌氧菌主要是厌氧消化链球菌 14 株、脆弱拟杆菌 9 株、艰难梭菌 7 株和产气荚膜梭菌 3 株等，还有些厌氧菌受限于检测能力的不足无法确定。对厌氧消化链球菌、脆弱拟杆菌和艰难梭菌的药敏结果分析，它们对阿莫西林/克拉维酸、替卡西林/克拉维酸敏感率都为 100%，此外，甲硝唑对厌氧消化链球菌、脆弱拟杆菌和艰难梭菌均保持很高的敏感性。
结论 厌氧菌引起的临床感染常见，然而厌氧菌感染死亡率高，，临床医生可根据菌株的分布特征及药敏结果对厌氧菌感染进行积极有效的治疗。

PO-0890

2020 年四川省细菌耐药监测网老年人细菌耐药数据分析

张欣、喻华、黄湘宁
电子科技大学附属医院•四川省人民医院

目的 对四川省细菌耐药监测网成员单位 2020 年度老年人细菌分布及耐药情况进行统计分析，为本省临床合理应用抗菌药物提供依据。
方法 各成员单位临床分离菌，采用标准纸片扩散法或自动化仪器检测法，按照统一技术方案测定监测药物对细菌的敏感性，依据 CLSI 指南 2019 年折点标准，用 WHONET 5.6 软件进行数据分析老年（≥65 岁）患者病原菌数据。
结果 共有 103 家医院参加了 2020 年度细菌耐药监测工作，其中数据基本合格纳入分析的共 94 家。按患者首次分离菌株进行统计分析，共收集细菌 89214 株，其中革兰阴性菌 69768 株(78.2%)，革兰阳性菌 19446 株(21.8%)。耐甲氧西林金黄色葡萄球菌(MRSA)和耐甲氧西林凝固酶阴性葡萄球菌(MRCNS)的检出率分别为 30.3%和 81.0%，MRSA 检出率低于全国检出水平，未发现万古霉素及替考拉宁耐药菌株，凝固酶阴性葡萄球菌对利奈唑胺的耐药率为 0.1%。万古霉素耐药粪肠球菌和屎肠球菌分别占 0.4%和 0.8%，自 2014 年起呈明显下降趋势，利奈唑胺耐药粪肠球菌和屎肠球菌分别占 2.1%和 0.5%。按非颅内感染的折点判断，青霉素耐药的肺炎链球菌比例为 0.6%，对头孢噻肟耐药率为 5.8%，略低于全国水平。化脓性链球菌主要对大环内酯类、克林霉素耐药，耐药率均超过 55.0%。革兰阴性菌中分离率前 4 位细菌分别为大肠埃希菌、肺炎克雷伯菌、铜绿假单胞菌和鲍曼不动杆菌，分别为 20749 株(29.7%)、14694 株(21.1%)、9471 株(13.6%)和 6638 株(9.5%)。肠杆菌目细菌对碳青霉烯类抗菌药物总耐药率虽低于 10.0%，但耐药率自 2011 年起有逐渐上升趋势。大肠埃希菌对头孢噻肟和头孢曲松的耐药率均在 54%以上，与全国水平持平，对碳青霉烯类耐药率在 1.5%左右。肺炎克雷伯菌对亚胺培南和美罗培南耐药率分别为 6.1%和 6.5%，呈持续上升趋势。碳青霉烯类耐药铜绿假单胞菌的检出率为 10.9%，显著低于全国平均水平，铜绿假单胞菌对亚胺培南、美罗培南、头孢他啶、头孢哌酮/舒巴坦、阿米卡星和环丙沙星的耐药率分别为 10.5%、8.7%、13.0%、8.4%、1.5%和 14.0%。鲍曼不动杆菌对包括碳青霉烯类在内的大多数监测药物耐药率超过 40%，对亚胺培南和美罗培南的耐药率略低于之前水平。流感嗜血杆菌对氨苄西林耐药率持续升高，耐药率达 70.7%。
结论 我省老年患者细菌耐药仍呈增长趋势，多重耐药和广泛耐药菌株检出率仍保持较高水平甚至呈增长趋势，对临床治疗造成严重威胁，应充分利用本地细菌耐药监测结果进行感控管理，促进抗菌药物合理应用。

PO-0891

Clinical characteristics, resistance mechanisms, and molecular epidemiology of chlorhexidine-resistant Pseudomonas aeruginosa isolated from a teaching hospital in China

Xiangkuo Zheng[3]、Xiaoya Zhang[4]、Beibei Zhou[1]、Shixing Liu[1]、Liqiong Chen[1]、Ying Zhang[2]、Wenli Liao[1]、Weiliang Zeng[2]、Qing Wu[1]、Chunquan Xu[1]、Tieli Zhou[1]

1. Department of Clinical Laboratory, the First Affiliated Hospital of Wenzhou Medical University, Wenzhou, Zhejiang Province, China
2. School of Laboratory Medicine and Life Science, Wenzhou Medical University, Wenzhou, Zhejiang Province, China
3. Department of Clinical Laboratory, the First Affiliated Hospital of Wenzhou Medical University, Wenzhou, Zhejiang Province, China
4. Department of Andrology, Linyi People's Hospital, Linyi, Shandong Province, China

Background Chlorhexidine is applied widely to prevent the spread of bacteria in the hospital environment, however, it can also cause the resistance of bacteria to chlorhexidine. The aim of our present study was to investigate clinical characteristics, resistance mechanisms and epidemiological characteristics of chlorhexidine resistance in *Pseudomonas aeruginosa* clinical isolates.

Methods A collection of 294 *P. aeruginosa* clinical isolates were collected from the First Affiliated Hospital of Wenzhou Medical University from 2018. Sensitivity to antibiotics was determined using the agar dilution method. Relevant clinical data collection considered to be potentially relevant to chlorhexidine-resistance were from the patient medical records. Resistance mechanisms of *P. aeruginosa* to chlorhexidine were analysed by PCR, efflux pump inhibition test and real-time quantitative PCR (qRT-PCR). P. aeruginosa were typed by pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST).

Results A total of 32 chlorhexidine-resistant *P. aeruginosa* isolates were identified. Our results indicated that minimum inhibitory concentrations (MICs) of chlorhexidine to chlorhexidine-resistant strains were ≥64 μg/ml. Relevant clinical data collection showed that chlorhexidine resistance is related to some of the following factors: duration of hospitalization, length of staying in intensive care unit (ICU), duration of mechanical ventilation, chlorhexidine usage and the occurrence of nosocomial pneumonia. Expression of mexA, mexC, mexE, mexX, and oprD genes was upregulated about 6.5-12.8 fold in chlorhexidine-resistant strains than those susceptible strains, suggesting that genes hyperexpression were probably the main mechanism of resistance to chlorhexidine. MLST and PFGE analysis demonstrated that 32 chlorhexidine-resistant strains belong to different sequence types (STs) and electrophoresis pulse types.

Conclusion Overexpression of efflux pump genes was the principal resistance mechanism of chlorhexidine-resistant *P. aeruginosa*. In addition, molecular epidemiological analysis showed that the homology of chlorhexidine-resistant strains was low and there was no obvious clonal transmission.

PO-0892

沙眼衣原体 T3SS 效应蛋白 CT622 的原核表达、纯化、多克隆抗体制备及对 HeLa 细胞增殖的影响

彭彬峰[1]、陈诗诗[2]、舒明艺[3]、陈恩[1]、雷文波[1,3]、刘双全[1]
1. 南华大学附属第一医院检验医学中心
2. 衡阳市中医医院肿瘤内科
3. 南华大学衡阳医学院原生物学研究所，湖南省特殊病原体防控重点实验室

目的 原核表达、纯化沙眼衣原体（Chlamydia trachomatis，Ct）CT622 蛋白，将纯化后的 CT622 蛋白免疫新西兰兔，制备 CT622 多克隆抗体，并初步探讨 CT622 蛋白对 HeLa 细胞增殖的影响，为进一步阐明 CT622 蛋白在沙眼衣原体致病中的作用提供实验依据。
方法 以 Ct D 型基因组为模板，CT622 特异性引物 PCR 扩增 ct622 基因，构建原核表达重组载体 pGEX-6p-1/CT_622。将重组载体经 0.8 mM 的 IPTG 大量诱导表达，采用 Glutathione Sepharose 4B beads 纯化 GST-CT622 融合蛋白，融合蛋白经 PreScission Protease 酶切除 GST 标签离心后取上清获得纯化的 CT622 蛋白。生物信息学分析 CT622 蛋白免疫原性，将纯化的 CT622 蛋白进行去内毒素处理后，与弗氏完全佐剂超声乳化，皮下免疫新西兰兔。将 CT622 蛋白与琼脂糖介质偶联制备成抗原亲和纯化层析柱进行抗体纯化。BCA 测定抗体浓度，SDS-page 鉴定纯化后的 CT622 蛋白多克隆抗体纯度，ELISA 检测抗体效价。用不同浓度的 CT622 蛋白处理 HeLa 细胞 24 h 后，CCK-8 细胞活性检测试剂盒检测细胞存活率（Cell viability%）。
结果 成功表达并纯化了 CT622 蛋白，生信分析表明该蛋白免疫原性良好，经纯化后 CT622 抗体浓度为 0.75 mg/mL，纯度在 85%以上，其效价在 1：512, 000 左右。CCK-8 结果表明，不同浓度 CT622 蛋白处理 HeLa 细胞后，其细胞存活率高于 PBS 对照组，并在 CT622 浓度为 10 μg/mL 时细胞存活率最高。
结论 成功表达并纯化了沙眼衣原体 CT622 蛋白，制备了高效价兔源性抗 CT622 抗体，CT622 蛋白可促进 HeLa 细胞增殖。

PO-0893

神经外科重症患者 CRE 感染发生危险因素及 NLR、PCT、MCP-1 对感染的鉴别诊断价值

张林
郴州市第一人民医院

目的 探讨神经外科重症患者 CRE 感染发生危险因素及中性粒细胞/淋巴细胞比值（NLR）、降钙素原（PCT）、单核细胞趋化蛋白-1（MCP-1）对感染的鉴别诊断价值。
方法 选取 2017 年 2 月～2019 年 3 月我院神经外科重症感染患者 122 例作为研究对象，包括 61 例耐碳青霉烯肠杆菌科细菌（CRE）感染、61 例碳青霉烯敏感肠杆菌科细菌（CSE）感染，比较两组临床资料、NLR、PCT、MCP-1，Logistic 分析 CRE 感染发生危险因素，Pearson 分析 NLR、PCT、MCP-1 与急性生理与慢性健康评分（APACHEⅡ评分）相关性，ROC 分析 NLR、PCT、MCP-1 对神经外科重症患者 CRE 感染的鉴别诊断价值，KM 曲线分析 NLR、PCT、MCP-1 高水平组、低水平组生存率。
结果 两组抗生素药物应用、抗生素药物使用时间、碳青霉烯类使用、APACHEⅡ评分、NLR、PCT、MCP-1 水平相比，差异有统计学意义（P＜0.05）；抗生素药物应用≥2 联、抗生素药物使用时间＞10 d、碳青霉烯类使用、APACHEⅡ评分≥20 分、NLR、PCT、MCP-1 高水平表达均为神经外科重症患者 CRE 感染危险因素（P＜0.05）；神经外科重症 CRE 感染患者 NLR、PCT、

MCP-1 与 APACHEⅡ评分呈正相关关系（P＜0.05）；联合诊断 CRE 感染 AUC 值大于单一诊断（P＜0.05）；CRE 感染患者 NLR、PCT、MCP-1 高水平组病死率高于低水平组（P＜0.05）。
结论 神经外科重症患者 CRE 感染受多种因素影响，其中 NLR、PCT、MCP-1 与病情程度密切相关，有助于 CRE 感染的鉴别诊断，临床可据此采取针对性干预措施，预防 CRE 感染的发生。

PO-0894

质谱分析仪用于耐甲氧西林金黄色葡萄球菌分子分型的研究

张婷婷
宜宾市第一人民医院

目的 评价基质辅助激光解析电离飞行时间质谱技术(MALDI-TOF MS)对耐甲氧西林金黄色葡萄球菌(MRSA)分子分型的应用价值。
方法 收集 2009.1 到 2012.3 来自全国 6 个城市共 270 株 MRSA 菌株，经多位点序列分析（MLST）表型主要为 St239、St5、St59、St45 4 个基因型，使用 ClinProTools 软件建立模型，并用剩余菌株验证得出模型的敏感性和特异性；随机选取试验组 35 株 St239，对照组 43 株包括 20 株 St5、15 株 St59、8 株 St45 构建模型 St239; 随机选取试验组 8 株 St45，对照组 35 株包括 11 株 St5、8 株 St59、16 株 St239 构建模型 St45。
结果 154 株 St239、72 株 St5、30 株 St59、14 株 St45 经检测显示，模型 St239、St45、St5 的交叉效度和可接受度均为 100%，仅模型 St59 的交叉效度为 90.45%，其可接受度也为 100%；模型 St45 能正确区分出 St45 的敏感性和特异性均为 100%，模型 St239 能正确区分出 St239 的敏感性是 95.8%以及特异性是 93.2%，模型 St59 能正确区分出 St59 的敏感性是 86.7%以及特异性是 91.7%，模型 St5 能正确区分出 St5 的敏感性是 50%以及特异性是 95.8%。
结论 MALDI-TOF MS 分型与多位点序列分析（MLST）具有较好的一致性，且具有操作简便、快速、低成本、重复性好、稳定性高的优点。

PO-0895

Activation of mTOR in Th1/Th2 cells in Kelbsiella pneumoniae-caused liver abscess patients

Jie Zhang
Sichuan Academy of Medical Sciences & Sichuan Provincial People’s Hospital

Liver abscesses are space-occupying lesions, which has become a public health problem and the mechanism is still unclear. Klebsiella pneumoniae is a well-known human nosocomial pathogen. Hypervirulent variant of Klebsiella pneumonia (hvKP) isolates can cause serious, life-threatening community-acquired infections in healthy hosts, including liver abscess. Cytokines produced by T helper (Th) cells are of critical importance for the outcome of many infectious diseases. Cytokines produced by T helper (Th) cells are importance for defending infection. In this report, we demonstrated that the balance of Th1/Th2 response was shifted in peripheral blood from Klebsiella pneumoniae-caused liver absecess patients. We again observed that Klebsiella pneumoniae could directly cause increased IFN-γ and IL-4 production in PBMC from healthy people. We demonstrated further that Klebsiella pneumoniae-caused liver absecess partially induces mTOR activation in Th1 and Th2 cells in vivo and in vitro. Collectively, these results suggest that the possibility of targeting mTOR as a strategy to modulate Th1 and Th2 response of host defense to prevent Klebsiella pneumoniae-caused liver absecess.

PO-0896

38 例侵袭性赛多孢霉属感染的临床特征及药敏结果分析

郑燕青[1,2]、鹿秀海[3]、蔡洁[4]、马晓波[1,2]、徐和平[1,2]、洪国斐[1,2]
1. 厦门大学附属第一医院检验科
2. 厦门市基因检测重点实验室
3. 山东眼科医院检验科
4. 厦门大学附属眼科中心检验科

目的 分析了解侵袭性赛多孢霉属感染的临床表现和药敏结果，为赛多孢霉属感染的诊断与治疗提供参考。
方法 收集 2017 年 1 月至 2020 年 12 月收治的 38 例侵袭性赛多孢霉属感染患者的临床资料和分离的病原菌株，对赛多孢霉属感染相关病例的临床表现与治疗效果和药敏结果进行回顾性分析。
结果 38 例侵袭性赛多孢霉属患者中检出尖端赛多孢霉 17 株，波氏赛多孢霉 22 株，桔黄赛多孢霉 1 株。眼外伤、溺水和免疫力降低是赛多孢霉属感染的常见的诱因，临床最常见的赛多孢霉属侵袭性感染主要有角膜炎、肺部感染、糖尿病足、外伤伤口感染，体外药敏结果显示赛多孢霉属对伏立康唑的药敏范围为 0.12-0.5ug/ml，其他抗真菌药物普遍耐药。
结论 侵袭性赛多孢霉属感染主要以外伤为主，预后与患者的自身免疫状态、及时的诊断，和正确使用伏立康唑治疗明显相关。

PO-0897

PTX3 基因多态性与中国非 HIV 相关隐球菌病具有相关性

张为利、廖全凤、刘雅、吴思颖、邓劲、肖玉玲、马莹、谢轶、康梅
四川大学华西医院

Objectives We aimed to conduct an association analysis between the SNPs of pattern recognition receptors (PRR) genes and the susceptibility to cryptococcosis in HIV-uninfected Chinese patients.
Methods Using the SNaPshot SNP typing technique, eight SNPs of PRR genes were typed on 97 HIV-uninfected cryptococcosis patients and 120 healthy controls who admitted to West China Hospital, Sichuan University, China, from 1 March 2018 to 30 December 2018.
Results It was found that that PTX3 rs2305619 polymorphism was associated with cryptococcosis in HIV-uninfected patients. Compared with the GG genotype, AA genotype increased the risk of cryptococcosis in HIV-uninfected patients ($p = .015$, OR, 2.579; 95% CI, 1.202-5.535). In the immunocompetent patients, the AA genotype had a higher risk ($p = .002$, OR, 4.399; 95% CI, 1.745-11.088). Further verification found that the plasma PTX3 level of the AA genotype was significantly higher than the GA or GG genotype (60.28 ± 16.12 vs 7.32 ± 0.79, $p < .001$).

PO-0898

宏基因测序在血流感染临床诊疗中的应用价值分析

胡雪姣、邓倩昀、顾兵
广东省人民医院

目的 探讨病原宏基因组检测（mNGS）对于疑似血流感染患者的早期临床诊疗的价值，以规范和优化 mNGS 的临床使用场景。

方法 纳入 2017-2020 年广东省人民医院疑似血流感染且同时行血培养和 mNGS 检测的患者 290 例，收集其外周血样本，进行常规病原检测和 mNGS 检测以确定病原体。收集患者的所有临床诊疗信息。比较 mNGS 和血培养对血流感染的诊断效能，研究 mNGS 对于疑似血流感染患者的诊断病原或排除感染的临床价值，以及 mNGS 是否能指导调整临床抗生素方案。
结果 290 患者包括 118 例血流感染和 172 例非血流感染患者。118 例血流感染患者中，通过血培养仅检测到 46 例（38.98％），mNGS 检测 105 例（88.98％）；血培养和 mNGS 的灵敏度分别是 38.98%、88.98%，特异度分别是 95.93%、63.37%。mNGS 对血流感染具有 89.34%的阴性预测价值。血培养和 mNGS 的 Kappa 值为 0.142（＜0.2）。约 33%的 mNGS 检测对临床抗生素使用具有有效影响，超过 70%的 mNGS 检测结果对临床诊断或治疗的决策有一定的积极影响。
结论 对于血流感染，mNGS 的敏感性较培养高，但特异性亟待提升。mNGS 对于培养困难的病原体，尤其对立克次体、病毒等感染、混合感染的诊断上优势明显。mNGS 与传统微生物检测互补不替代，mNGS 与血培养联合使用有利于对患者的病因诊断和抗菌治疗，但仍需大样本的前瞻性研究证实。

PO-0899

去铁铵干预下鲍曼不动杆菌耐药性状变化转录组差异分析

高玉红、郑瑞、朱磊、李艺坤
云南省第一人民医院

目的 研究铁离子螯合剂去铁铵作用下，鲍曼不动杆菌转录组基因表达与抗菌药物耐药性变化的关系。
方法 以一株脑脊液中分离得到的耐碳青霉烯鲍曼不动杆菌 PG15 作为模式菌株，肉汤稀释法测定去铁胺对 PG15 的最低抑菌浓度为 32mmol/L，加入去铁胺后测定抗菌药物的最低抑菌浓度变化，并对添加去铁胺前后的鲍曼不动杆菌 PG15（三个重复）进行转录组测序，分析基因表达差异。
结果 添加去铁铵后数种抗菌药物的最低抑菌浓度均降低一倍：亚胺培南、头孢吡肟、左氧氟沙星、四环素、哌拉西林/他唑巴坦对 PG15 的最低抑菌浓度分别由 16μg/mL、32μg/mL、16μg/mL、16μg/mL、128/4μg/mL 降为 8μg/mL、16μg/mL、8μg/mL、8μg/mL、64/2μg/mL。转录组数据显示：添加 32mmol/L 去铁铵后，测试菌株有 1206 个基因表达上调，302 个基因下调，非显著性差异表达基因 1557 个。差异表达基因上调大于 3 倍的 32 个基因中，鲍曼不动杆菌铁载体-鲍曼不动杆菌素的生物合成相关基因占了 18 个；铁结合及转运蛋白基因 4 个；AdeABC 外排泵基因 2 个；其它基因 8 个。上调幅度大于 3 倍的基因主要涉及鲍曼不动杆菌素生物合成基因，分析该现象可能是由于铁螯合剂去铁铵介入后，菌株应对低铁胁迫环境所采取的一种主动适应方式，菌株试图通过提高不动杆菌素的合成量来保证菌体对环境铁元素的摄取优势。其它上调基因还包括 I 型菌毛装配相关基因 csuABCDE（与生物被膜的形成密切相关）有小幅度上调。下调基因有 302 个：其中下调超过 6 倍的基因有 41 个，很多基因功能未明，其余基因多与代谢相关，包括膜双组分运输系统，嘌呤代谢，氨基酸代谢、苯酸盐代谢、丙酮酸代谢基因均下调表达，其它下调的重要基因还包括多药转运体，海藻糖 6-磷酸酶（生物膜形成相关蛋白），6-磷酸葡萄糖酸脱氢酶。
结论 去铁铵增强了鲍曼不动杆菌对部分抗菌药物的敏感性，这与鲍曼不动杆菌在低铁环境下铁载体生物合成基因及外排泵基因表达上调有关。

PO-0900

高毒力高侵袭的甲氧西林敏感金黄色葡萄球菌临床分离株的分析

孙艳
东南大学附属中大医院

目的 金黄色葡萄球菌是院内感染和社区感染常见的致病菌，以往的研究大多关注耐甲氧西林金黄色葡萄球菌（MRSA)，而关于甲氧西林敏感金黄色葡萄球菌（MSSA)的研究较少。从某医院的 ICU 菌血症患者身上分离到一株 MSSA，该患者病情重、治疗药效差，探索该株 MSSA 的致病机制。
方法 对此患者的导管血、上肢血、下肢血、痰标本来源的 MSSA 菌株和金葡菌标准菌株 ATCC29213 进行多位点序列分型，予裸鼠皮下注射浓度为 1*10^8 的 MSSA 和金葡菌标株菌液 100uL，监测裸鼠是否形成皮下脓肿。
结果 此患者多个样本来源的 MSSA 菌株均为 ST188 型，金葡菌标株为 ST5 型，注射 MSSA 菌株裸鼠的皮下脓肿生成速度较注射金葡菌标株的快，皮下脓肿面积更大，皮下组织的血平板涂片见细菌生长，经鉴定为金葡菌。
结论 ST188 型 MSSA 的毒力较 ST5 型金葡菌标株大，侵袭性较金葡菌标株强。

PO-0901

耐碳青霉烯高毒力肺炎克雷伯菌临床及分子流行病学特征

张露丹[1]、曹慧军[1]、周丹[2]、刘宝[1]、费樱[1,2]
1. 贵州医科大学附属医院
2. 贵州医科大学

目的 研究耐碳青霉烯高毒力肺炎克雷伯菌(carbapenem-resistant hypervirulent Klebsiella pneumoniae, CR-hvKP)菌株感染的临床特征、耐药情况、多重耐药的机制和高毒力机制，为临床及时识别该菌提供临床和实验室依据，从而采取行之有效的抗感染治疗措施。
方法 收集 2020 年 1 月 1 日—2020 年 12 月 31 日贵州某三甲医院临床分离拉丝试验阳性且任一碳青霉烯类药物耐药的肺炎克雷伯菌，初步鉴定为 CR-hvKP 菌株。收集感染患者的临床资料和药敏试验结果进行分析，同时采用 PCR 扩增上述菌株的常见碳青霉烯酶基因和毒力基因，并对其进行荚膜血清型和多位点序列分型，采用 ERIC-PCR 进行同源性分析。
结果 本研究中自 10 位发生多部位感染的患者分离 CR-hvKP 共 38 株，均为多重耐药菌，对三、四代头孢菌素、氟喹诺酮类、氨基糖苷类抗生素均 100%耐药，对替加环素、多黏菌素 B 耐药率为 23.7%，未检出对头孢他啶/阿维巴坦耐药菌株。10 位患者有基础疾病、经历过手术或侵入性操作、β-内酰胺类抗生素暴露史、住院天数长、预后不良的临床特征。38 株 CR-hvKP 菌株均检出 blaKPC 基因，而未检出其他常见碳青霉烯酶基因 blaNDM、blaVIM、blaIMP、blaOXA-48；均检出毒力基因 mrkD、rmpA、entB、ybtS、fimH、aerobactin，毒力基因 KfuBC 检出率为 86.85%，未检出 allS、wcaG 两种毒力基因。38 株 CR-hvKP 荚膜血清型均为 K64，多位点序列分型均为 ST11，ERIC-PCR 同源性分析示具有完全相同的 DNA 图谱，提示具有同源性。
结论 本研究中 CR-hvKP 感染的临床特征与 CRKP 感染相似，均是 ST11 型产 KPC 酶的 CRKP 菌株；CR-hvKP 耐药形势严峻，已经检出同时对多黏菌素和替加环素耐药的泛耐药 CR-hvKP 菌株；本研究中检出的 CR-hvkP 菌株，多位点序列分型均为 ST11，荚膜血清型均为 K64，ERIC-PCR 具有完全相同的 DNA 图谱，提示存在爆发流行可能。

PO-0902

Molecular types, virulence and drug resistance features of bacterial strains in simultaneous outbreaks of paratyphoid A and B fever

Xuewei Tong
Hospital of Xinjiang Production and Construction Corps

OBJECTIVE This study investigated the molecular types, virulence, and drug resistance features of the bacterial strains in simultaneous outbreaks of paratyphoid A and B fever, which could provide evidence for preventing the simultaneous transmission of different types of paratyphoid fever.
METHODS The data of the confirmed and suspected paratyphoid fever patients were analyzed in this retrospective study. All the patients were students from a high school in China. The strains were isolated for serological typing and drug sensitivity test. Multiplex polymerase chain reactions (M-PCR), pulsed-field gel electrophoresis (PFGE), and multilocus sequence typing (MLST) were used for molecular typing. Additionally, the virulence genes and drug resistance genes were evaluated.
RESULTS In total, 31 confirmed patients and 35 suspected patients were included in this study. Thirty-two strains of Salmonella Paratyphi were isolated from the 31 confirmed patients; the serotypes were A and B in 19 and 13 patients, respectively, while the intermediate rate of strains against ciprofloxacin was 100%. The molecular types of 11 representative strains by M-PCR were in agreement with the serotypes, while PFGE and MLST suggested the transmissions of Salmonella Paratyphi clones of two origins. The representative strains carried the virulence gene of SPI1-5 and regulatory gene, while Salmonella Paratyphi A also carried the CDT gene. The detection rate of ciprofloxacin-resistant genes was 89.39% in the representative strains.
CONCLUSIONS The simultaneous transmission of Salmonella Paratyphi A and B is characterized by high pathogenicity and poor sensitivity to ciprofloxacin, which should be investigated further in the laboratory and clinical practice.

PO-0903

评估黏菌素肉汤纸片洗脱法和全自动药敏系统检测肠杆菌目和铜绿假单胞菌对黏菌素耐药性的价值

黄嘉仪
复旦大学附属中山医院
上海交通大学医学院附属瑞金医院
上海交通大学医学院检验系

目的 黏菌素是临床用以治疗多重耐药革兰阴性杆菌感染的最后一线抗菌药物。但是，目前开展黏菌素药敏试验对临床实验室来说存在一定困难。为此，实验室标准协会(Clinical and Laboratory Standards Institute, CLSI)开发了一种更容易在临床实验室内开展的新方法，即黏菌素肉汤纸片洗脱法（Colistin Broth Disk Elution, CBDE）。本研究的目的是评估 CBDE 法和 BD PhoenixTM 药敏分析系统对肠杆菌目和铜绿假单胞菌的黏菌素药敏检测性能。
方法 收集 2018-2021 年从临床分离的 179 株细菌包括肠杆菌目细菌和铜绿假单胞菌，同时使用 CBDE、BD PhoenixTM 药敏分析系统和微量肉汤稀释法（reference Broth MicroDilution, rBMD）测定菌株最低抑菌浓度（Minimum Inhibitory Concentration, MIC）值。以 rBMD 作为参考方法，分析这两种方法的性能评价指标。
结果 CBDE 法和 BD PhoenixTM 药敏分析系统的分类一致性（Categories Agreement, CA）分别为 99.44%和 92.73%、基本一致性（Essential Agreement, EA）分别为 97.77%和 92.18%、非常

重大错误（Very Major Error, VME）分别为 0 和 21.67%、重大错误（Major Error, ME）分别为 0.84%和 0、灵敏性分别为 100%和 78.33%，以及特异性分别为 100%和 99.16%。
结论 CBDE 法用于肠杆菌目及铜绿假单胞菌黏菌素药敏检测结果稳定可靠。该方法性能指标在本实验室均达到了行业标准 WS/T639—2018《抗菌药物敏感性试验的技术要求》和 CLSI 规定的标准。而 BD PhoenixTM 药敏分析系统易出现假敏感（VME）情况，超出可接受标准。使用该系统作为黏菌素药敏试验的检测性能存在缺陷。本研究通过使用临床菌株进行性能验证，证明了 CBDE 法以其经济、易操作且准确性高的优点，可以作为 rBMD 的替代方法在本实验室内作为黏菌素药敏试验的常规项目开展使用。

PO-0904

山西省耐甲氧西林金黄色葡萄球菌表型分析及基因研究

侯亚彬[1]、王海如[1]、任洁[1]、张宇[1]、郝崇华[2]
1. 山西医科大学附属人民医院
2. 山西省人民医院

目的 分析耐甲氧西林金黄色葡萄球菌（MRSA）的表型和基因型，研究 MRSA 的多重耐药机制，探寻抗菌药物作用新型靶点，为预防和治疗 MRSA 感染及临床有效合理使用抗菌药物提供帮助。
方法 收集 2019 年 6 月-2020 年 12 月山西省 13 家三甲医院临床分离的连续和非重复的 MRSA 菌株 236 株，采用 K-B 纸片扩散法和药敏分析系统对菌株进行耐药表型确证和药物敏感试验，采用多重聚合酶链反应检测 mecA 基因、毒力基因和耐药基因岛（SCCmec）进行分析。
结果 共收集到 236 株 MRSA 菌株。药敏试验显示，未分离到对万古霉素、利奈唑啉和替考拉宁耐药的 MRSA，但所有菌株均对青霉素、苯唑西林、氨苄西林和头孢唑啉耐药。236 株 MRSA 均携带 mecA 基因。最常见的肠毒素基因是 see（77.5%），其次是 sed（53.9%）和 sec（5.3%）。脱落毒素基因（etb）和中毒性休克综合征毒素（tst）阳性率分别为 49.1%和 8.1%。在 MRSA 分离株中，SCCmecⅡ型、Ⅲ型和Ⅳ型分别占 53.4%、38.2%和 8.4%。
结论 本研究揭示了山西省 MRSA 分离株的耐药性、毒力基因谱和 SCCmec 类型。耐药表型检测显示本地区 MRSA 呈现多重耐药、高度耐药的特点，基因分析表明耐药程度严重，耐药模式复杂。

PO-0905

Chlamydia trachomatis T3SS effector CT622 induces proinflammatory cytokines via TLR2/TLR4-mediated MAPKs/NF-κB pathway in THP-1 cells

Wenbo Lei[1,2]、Binfeng Peng[2]、Mingyi Shu[1]、En Chen[2]、Shuangquan Liu[2]、Zhongyu Li[1]
1. 南华大学衡阳医学院原生物学研究所
2. 南华大学附属第一医院检验医学中心

Chlamydia trachomatis, an obligate intracellular pathogen, which infections leading cause of sexually transmitted diseases and blinding blindness. The pathogenic mechanism of C. trachomatis may be associated with the induction of host inflammatory response. However, yet little is known about the molecular mechanisms for C. trachomatis leading to inductions of proinflammatory cytokines. As a T3SS effector protein, CT622 plays a crucial role in the process of growth and development of C. trachomatis. To date, relatively little is understood about whether CT622 can induce host inflammatory response. In the present study, we investigated the roles and mechanisms of CT622 protein in regulating the inflammatory response in THP-1 cells. Stimulation with CT622 can promotes the expression levels of interleukin-6 (IL-6) and interleukin-8 (IL-8). Our results further indicated that MAPKs and NF-κB signaling pathways are involved in

CT622 induced proinflammatory cytokines. Moreover, the levels of IL-6 and IL-8 were declined after treatment of the cells with MAPKs and NF-κB inhibitors. Similarly, we further investigated the role of TLRs signaling pathways in CT622 induction of proinflammatory cytokines and activation of MAPKs/ NF-κB， our results show that the expression levels of IL-6 and IL-8 were reduced, the phosphorylation of ERK, p38, JNK, and IκBα were attenuated after silencing the Toll-like receptor 4 (TLR4) expression by using siRNA. We also found that after disturbing the expression of TLR2, CT622 induced IL-8 production and activated ERK were also be abrogated, whereas the expression level of IL-6 and the phosphorylation of p38, JNK, and IκBα were not affected. Taken together, these observations illustrated that CT622 contributes to the inflammatory response via TLR2/TLR4-mediated MAPKs/NF-κB pathway in THP-1 cells, which should further promote our understanding of Chlamydial pathogenic mechanisms.

PO-0906

Application of Fibrous Materials in the Diagnosis of Tuberculous Meningitis

Yan Zhang
Department of Clinical Laboratory, the Affiliated Drum Tower Hospital of Nanjing University Medical School, Nanjing 210008, China

Tuberculous meningitis (TBM) is a non-suppurative inflammatory disease of meninges and meninges caused by Mycobacterium tuberculosis (MTB), with high mortality. Traditional methods for laboratory detection of MTB are less sensitive and time-consuming. Some fibrous materials like silica fiber in GeneXpert MTB/RIF kit and paper fiber in acid-fast staining were used for clinical diagnosis of TBM. These detection methods were compared and analyzed. The results showed that the sensitivities of the 3 detection methods were 28.81%, 16.95% and 37.29%, respectively, and the specificity were all 100%, based on clinical diagnosis. The diagnostic efficiency of GeneXpert MTB/RIF technique was significantly better than that of culture method (2=6.174, P=0.013). Although there was no statistically significant difference when compared with acid-fast staining (2=0.957, P=0.328), the GeneXpert MTB/RIF technique has the advantage of accurately distinguishing MTB from non-MTB. The above results indicate that GeneXpert MTB/RIF technique has advantage of high sensitivity, high specificity, accuracy and simple operation. The detection time is short to 2 h, which is greatly shortened compared with 4-8 weeks for Rochelle solid culture method. The fibrous materials have high application value for the diagnosis of TBM.

PO-0907

In vitro bacteriostasis of Coptis chinensis on Staphylococcus aureus and its mechanism

Lingqing Xu、jinyan Li、qianjun He、weihong Wen、 yingxian Tang、zhongwen zhang
The Sixth Affiliated Hospital of Guangzhou Medical University

objective This study aimed to investigate the inhibitory effect of Coptis chinensis on Staphylococcus aureus (S. aureus) in vitro and its mechanism.
Methods 1.A total of 80 strains of S. aureus, half of which were methicillin-resistant S. aureus (MRSA) and the other half of which were methicillin-susceptible S. aureus (MSSA), were collected.
2.Drug sensitivity test was carried out using a VITEK 2 Compact automatic microbial analyzer.
3.The minimal inhibitory concentration (MIC) of Coptis chinensis against the 80 strains of S. aureus was determined using the doubling dilution method; 4.S. aureus was treated with Coptis

chinensis, the optic density value was measured every two hours, the growth curve was drawn, and the exosmosis levels of deoxyribonucleic acid (DNA), ribonucleic acid (RNA), and other macromolecular substances were detected.
Results 1.Of the 80 strains of S. aureus, 34 strains (42.5%) were isolated from secretion samples, 11 strains (13.75%) from pus/puncture fluid samples, 17 strains (21.25%) from sputum/throat swab samples, and 18 strains (22.5%) from blood samples.
2. The MIC of Coptis chinensis against the 80 strains of S. aureus ranged from 16 mg/ml to 128 mg/ml, but the difference in the in vitro inhibitory effect against MRSA and MSSA was not statistically significant.
3.There was no significant difference in the in vitro antibacterial effect of Coptis chinensis on S. aureus from the different samples.
4.After treatment with Coptis chinensis, the growth of S. aureus was significantly inhibited, and the exosmosis levels of DNA, RNA, and other macromolecular substances increased significantly
Conclusion Coptis chinensis has a good inhibitory effect on clinically separated S. aureus, and it could play an important role in managing S. aureus infection, especially in the treatment of MRSA.

PO-0908

Predicting Risk Factors and Outcomes of malignant patients with Gram-negative bacteremia using real-world data

SUJIAO NI、Ruiling ZU、Kaijiong Zhang、pingyao Xu
Sichuan cancer hospital

Background Gram-negative bacteremia(GNB) is a frequently complicated cause of cancer patients morbidity and mortality. The incidence, risk factors and outcomes for GNB remained poorly characterised.
Methods This study retrospectively analyzed the risk factors and outcomes of GNB in malignant patients. The univariable and multivariable logistic regression were used to identify baseline risk factors for GNB and mortality. Then we developed a nomogram to predict 30-day mortality in patients with GNB .
Results The final cohort comprised 1004 malignant patients with Bloodstream infection(BSI)，65.7%(N=660) accquired GNB. In univariate analysis, GNB patients showed association with Gynecologic cancer, Hepatobiliary cancer, Hematologic cancer, Genitourinary cancer , Upper gastrointestinal cancer , Head and neck cancer , Lung and bronchus cancer ,admission to ICU before infection, chronic obstructive pulmonary disease， pulmonary infection, urinary tract infection, soft tissue infection, biliary tract infection, and antibiotic expose were independent factor for GNB infection. Laboratory indicators shows that procalcitonin(PCT) is higher in GNB patients and LYMPH is lower.Multivariate analysis showed Gynecologic cancer, Hepatobiliary cancer, Hematologic cancer, Genitourinary cancer,urinary tract infection, biliary tract infection,surgery and PCT were independent risk factors for GNB. In univariate analysis, Non-survivor groups showed association with: male patients, cardiacdysfunction, renal dysfunction, shock, admission to ICU before infection, stay in ICU after infection, pulmonary infection, surgery, chemotherapy, catheterization, nasogastic tube, mechanical ventilation, fungal drug expose, lower platelet counts (PLT), higher CRP and PCT . Multivariate analysis shows that shock,admission to ICU before infection, pulmonary infection, nasogastic tube,and lower PLT were independent risk factors for death from GNB . We developed a nomogram to predict 30-day mortality in patients with GNB, The C-index of this predictive model was 0.804，which suggested a good prediction capability of this model to predict 30-day mortality in cancer patients with GNB.
Conclusion This large analysis of malignant patients with GNB provided significant risk factors in the infection and mortality. And based on the large cohort, a nomogram was constructed which could reduce the risk of mortality.

PO-0909

肺炎克雷伯菌整合子携带情况及与耐药性和毒力基因的相关性研究

宋国滨[1,2]、王刚[2]、黄颖[2]、徐元宏[2]
1. 同济大学附属东方医院检验科
2. 安徽医科大学第一附属医院检验科

目的 分析肺炎克雷伯菌中整合子携带情况，并对其与耐药性和毒力基因的相关性进行分析，为进一步研究整合子在耐药性与毒力基因中的作用提供数据依据。
方法 运用纸片扩散法和 vitec compact2 仪器进行药敏试验，聚合酶链式反应（PCR）技术检测三种整合酶基因、七种常见毒力基因，并运用 SPSS 软件分析整合子与耐药性和毒力基因携带的相关性，P＜0.05 为具有统计学意义。
结果 我院共收集 133 株肺炎克雷伯菌，其中 I 型整合子检出 58 株，未检出 II 型、 III 型整合子，耐药性检测分析显示菌株对氨苄西林天然耐药以及对米诺还素、多粘菌素 B、替加环素的耐药率分别为 8.27%、2.26%、0%外，对 β 内酰胺类、喹诺酮类、氨基糖苷类、磺胺类抗生素耐药率普遍大于 30%，整合子阳性的菌株耐药率比整合子阴性菌株高，其差异具有统计学意义，但整合子阳性菌株毒力基因携带率低于整合子阴性菌株，其差异具有统计学意义。
结论 我院整合子类型主要以 I 型为主，携带 I 型整合子菌株比整合子阴性菌株普遍耐药，但其毒力基因正好相反，其具体机制应进一步研究，加强抗生素的合理应用，防控多重耐药菌的快速传播。

PO-0910

COVID-19 患者尸检组织单细胞转录组图谱的建立与分析

夏欣一
中国人民解放军东部战区总医院

目的 随着 COVID-19 继续在全球传播，迫切需要更好地了解 COVID-19 的病理特征。已有的大规模尸检发现 SARS-CoV-2 感染会导致多器官和组织损伤，主要是肺部、消化道和免疫系统，进一步了解患者不同器官中各种重要免疫细胞的比例和分子变化为理解 COVID-19 的病理机制具有重要意义。
方法 收集 2 名死于 COVID-19 患者的 2 份骨髓、2 份 PBMC、2 份肺组织和 1 份结肠组织以及外周血 PBMC 作为患者组。正常组单细胞测序结果来源于公共数据库。单细胞转录组测序分析所有两组各类型组织的差异表达基因、细胞类型聚类和鉴定。根据典型标记对细胞类型进行注释，对组织特异性簇进行评分，最终结果用 UMAP 进行可视化处理，用来评估患者组和正常组之间的细胞类型组成是否有显著差异。
结果 共获得 150966 个单细胞转录组数据。其中，21773 个骨髓单个细胞（患者组 17396 个，对照组 4377 个），41571 个 PBMC（患者组 21244 个，对照组 20327 个），47397 个肺单个细胞（患者组 4241 个，对照组 43156 个）,和 40225 个结肠细胞（患者组 1050 个，对照组 39175 个）。首先，绘制了新冠肺炎患者组和对照组不同组织的单细胞图谱。发现在感染后，各组织多种细胞类型的比例发生变化，最明显的是中心粒细胞、T 细胞、AT2、AT1 细胞等。其次，SARS-CoV-2 感染后细胞间的信号转导存在显著差异，且存在组织特异性，主要涉及抗病毒反应，免疫激活，细胞因子和炎症反应等。最后，来自不同组织的中性粒细胞、单核细胞、T 细胞和巨噬细胞在应对病毒感染时具有不同的转录因子调控模式，可有助于提示 COVID-19 的治疗靶点。
结论 本研究通过 2 例 COVID-19 患者死亡病例建立骨髓、血液、肺实质和结肠的单细胞转录组数据图谱，解析不同器官之间的重要免疫细胞细胞比例和较深入的分子层面变化，有助于理解

SARS-CoV-2 是如何影响不同器官而引起系统性免疫反应。为理解病毒感染后不同组织后细胞比例和细胞通讯的改变、感染后不同组织淋巴细胞减少等关键科学问题提供依据。

PO-0911

基于 CRISPR 和侧流层析的 HPV 多重检测和分型的新方法研究

贺云萱、夏欣一
中国人民解放军东部战区总医院

目的 目前 HPV 检测技术众多，但尚存在实验周期长、操作复杂、灵敏度低、特异性差以及大多仅能进行单一型别的分析等局限。为了解决此问题，本研究开创了新型简便、快速检测且同时多重检测 HPV 型别的新技术。
方法 首先利用有特殊标记的特异性引物标记检测靶标 PCR 产物的两端，通过侧流层析试纸进行直接检测；再采用 MY09/11 通用引物对待检测靶标序列进行扩增，通过特异性 crRNA 引导 Cas12a 切割并激活切割单链报告子，以侧流层析试纸显示检测结果；接着使用 Cas/sgRNA 复合物切割多种靶向 DNA，通过 PCR 扩增后，以琼脂糖凝胶电泳图显示结果；最后，通过盲检 30 例临床样本，并将结果与 23 型检测试剂盒的结果对比。
结果 本研究构建了三种不同的检测方法，首先通过 10 种高危型 HPV 质粒分别验证了三种方法的稳定性、特异性和灵敏性，均表现良好，灵敏度最高可达 10-4ng/μl。其次，盲检结果为：基于侧流层析技术的双标记扩增 HPV 分子检测系统检测出 30 例临床样本中阳性符合率为 100%。基于 CRISPR 的侧流层析技术检测 HPV 系统检测阳性符合率为 96.7%。基于 CRISPR 的多重检测技术检测不同的 30 例临床样本中，阳性符合率 92%，综上，这三种方法检测效果均表现良好。
结论 本研究开发了三种新方法，相较于传统的 HPV 检测方法，均表现出操作简单、灵敏度高、准确度高等优点，表明这些方法具有为临床宫颈癌预防、筛查工作提供参考的价值。

PO-0912

EDTA-K2 Improves the Detection Sensitivity of SARS-CoV-2 IgM and IgG Antibodies by Chelating Colloidal Gold in the Immunochromatographic Assay

Xiumei Hu
Nanfang Hospital, Southern Medical University

Objective The coronavirus disease (COVID-19) pandemic, caused by severe acute respira_x0002_tory syndrome coronavirus 2 (SARS-CoV-2), is now rapidly spreading globally. Serological tests are an important method to assist in the diagnosis of COVID-19, used for epidemiolo_x0002_gical investigations. In this study, we aimed to investigate the impact of different types of vacuum collection tubes on the detection of SARS-CoV-2 IgM and IgG antibodies, using the colloidal gold immunochromatographic assay (GICA). Patients and **Methods** A total of 112 patients with COVID-19 and 200 healthy control subjects with no infection were enrolled in this study. Their serum and plasma were collected into four different types of vacuum blood collection tubes. SARS-CoV-2 IgM and IgG specific antibodies in the plasma and serum were then detected by GICA and chemilumines_x0002_cence assay (CA), respectively. In addition, the particle sizes of different colloidal gold solutions in the presence of different anticoagulants and coagulants were evaluated by both laser diffraction (Malvern) and confocal laser microscope, respectively.
Results Our results revealed that anticoagulated plasma with EDTA-K2 improved the positive detection rate of SARS-CoV-2 IgM antibodies. Furthermore, our results shown that the detection results by GICA and CA were highly consistent, especially, the results of EDTA-K2

antic_x0002_oagulated plasma detected by GICA was more consistent with CA results. We confirmed that EDTA-K2 could improve the detection sensitivity of SARS-CoV-2 IgG antibodies by chelating excessive colloidal gold compared with sodium citrate or lithium heparin, these methodologies did not appear to cause false positives. Colloidal gold particles could be chelated and aggregated by EDTA-K2, but not by sodium citrate, lithium heparin and coagulants.
Conclusion GICA is widely used to detect antibodies for the advantages of convenient, fast, low cost, suitable for screening large sample and require minimal equipment. In this study, we found that EDTA-K2 amplified the positive antibody signal by chelating colloidal gold and improved the detection sensitivity of SARS-CoV-2 IgM and IgG antibodies when using the GICA. Therefore, we suggested that EDTA-K2 anticoagulated plasma was more suitable for the detection of SARS-CoV-2 antibodies.

PO-0913

奴卡菌的菌种分型及耐药性分析

杨佩红、周柯、张鹏亮、周磊、刘家云
空军军医大学西京医院

目的 了解奴卡菌的菌种分型及对常用抗菌药物的耐药性，为临床合理用药提供依据。
方法 收集经 VITEK MALDI-TOF MS 技术鉴定，并进行 16S rRNA 基因测序确认非重复的 24 株奴卡菌，采用微量肉汤稀释法检测 12 种抗菌药物的最低抑菌浓度。
结果 24 株奴卡菌来源于本院 2015 年 1 月～2020 年 11 月非重复的临床标本，其中痰液 14 份（58.33%）、肺泡灌洗液 4 份（16.67%）、抽出物 3 份（12.5%）、脓液 2 份（8.33%）、分泌物 1 份（4.17%）；24 位感染患者中，肺部感染占 79.17%（19/24）,其余可见皮肤、足部、脑部等部位感染。所有奴卡菌测序分型结果为：盖尔森基兴奴卡菌 9 株，脓肿奴卡菌 4 株，北京奴卡菌、鼻疽奴卡菌、豚鼠耳炎奴卡菌、新奴卡菌、天美奴卡菌各 2 株，巴西奴卡菌 1 株。选择早期未形成明显干燥且菌龄＜48h 的疑似奴卡菌落进行直接质谱鉴定，VITEK MALDI-TOF MS 技术与基因测序结果的一致性为 91.67%(22/24)。 24 株奴卡菌对利奈唑胺、阿米卡星的敏感性最高，未发现耐药菌株；对磺胺甲基异恶唑的耐药率为 4.17%（1/24）；对亚胺培南、阿莫西林/棒酸、头孢曲松、妥布霉素、米诺环素、多西环素、莫西沙星的耐药率在 12.50～33.33%之间；对克拉霉素、环丙沙星的耐药率较高，分别为 62.50%、75.00%。
结论 临床分离的奴卡菌以盖尔森基兴奴卡菌为多数；奴卡菌对克拉霉素、环丙沙星耐药率较高，利奈唑胺、阿米卡星、磺胺甲基异恶唑对其有良好的抗菌活性。

PO-0914

高毒力肺炎克雷伯菌的毒力基因、耐药机制及分子流行病学研究

李洪甫、胡同平
内蒙古科技大学包头医学院第一附属医院

目的 本研究的目的是分析内蒙古包头地区某三级教学医院 KPN-PLA 患者的临床、微生物学和分子流行病学特征，并与血、尿标本来源 KPN 的荚膜血清型、毒力因子及耐药情况进行对比。
方法 对 2016 年 1 月-2019 年 12 月内蒙古包头地区某三级教学医院收治的 78 株 KPN-PLA 病例 KPN 分离株进行系统研究和全面阐述，并与随机选取的同时期血、尿标本来源 KPN 分离株各 78 株进行对比。采用拉丝试验、聚合酶链反应(PCR)、药敏试验和多位点序列分型等方法对 KPN 的毒力因子、耐药情况和 ST 分型进行鉴定。
结果 78 例 KPN-PLA 病例中，大多数是老年男性，并且有 53.8%的患者伴有糖尿病。脓肿多为右侧单发(44.9%)。常用抗菌药物耐药率较低(<10%)，但仍有 1 株为碳青霉烯耐药菌株。尿标本 KPN

分离株比 KPN-PLA 穿刺液标本和血标本 KPN 菌株具有更高的耐药性。HmKP、aero（+）、K1 和 K2 血清型分别占 80.8%、89.7%、56.4%和 26.9%。除 iroNB(3.8%)外，毒力因子(rmpA、irp2、entB、iucD、aero、wacg、iutA、kfu、ybtA、iroN、fimH、mrkD)的检出率较高(69.2%-100.0%)。KPN-PLA 穿刺液标本 KPN 分离株比血、尿标本 KPN 分离株毒力因子阳性率更高。此外，还发现 ST23 是包头地区 KPN-PLA 的优势序列类型(32.1%)。

结论 KPN-PLA 标本 KPN 分离株具有比血、尿标本来源更强的毒力，并已出现碳青霉烯耐药的 HvKP 菌株，应引起临床高度重视，采取有效措施控制其传播。

PO-0915

云南省艾滋病患者分离新生隐球菌的药物敏感性试验与临床分析

高丽、樊红丽、杨丹丹、谢祺、张桂仙、李正伦
云南省传染病医院

目的 了解云南省艾滋病患者分离新生隐球菌的分布、耐药性及临床治疗效果。

方法 对 2010 年 1 月至 2020 年 12 月临床总共分离的 424 株新生隐球菌，用 VITEK2 Compact 全自动微生物分析仪鉴定菌种，用 ATB FUNGUS 3 板条检测 5 种抗真菌药物的敏感性，并对临床资料进行分析。

结果 424 株新生隐球菌以脑脊液检出比例最高，占 62.50%（265/424）；血液次之，占 30.90%（131/424）；排名第三的是痰液，占 2.83%（12/424）。424 株新生隐球菌对唑类抗真菌药物（除氟康唑外）MIC 均≤2μg/ml，多烯类的两性霉素 B MIC≤4μg/ml，氟康唑及 5-氟胞嘧啶的 MIC≤64μg/ml。对两性霉素 B、氟康唑、5-氟胞嘧啶的敏感性分别为 95.28%（404/424）、80.66%（342/424）、75.71%（321/424）。5 种抗真菌药物的流行病学折点分别为：5-氟胞嘧啶和氟康唑——16μg/ml；两性霉素 B、伊曲康唑和伏立康唑——0.5μg/ml。

结论 新生隐球菌随着抗真菌治疗的实施，有非野生菌株从临床分离，除两性霉素 B 敏感性较高外，其他两种药物均存在不同程度的非敏感株，治疗首选两性霉素 B 和 5-氟胞嘧啶联合治疗。隐球菌作为临床重要的致病真菌，实验室及临床均应给予高度重视。

PO-0916

Clinical and Microbiological Characterization of Invasive Pulmonary Aspergillosis Caused by Aspergillus lentulus in China

Shuying Yu 、Yingchun Xu
Peking Union Medical College, Chinese Academy of Medical Sciences

Invasive Aspergillosis (IA) due to Aspergillus lentulus is associated with high mortality. In this study, we investigated the clinical and microbiological characteristics of 6 fatal cases of proven or probable IA caused by A. lentulus in China. Underlying immunosuppression, prior antifungal exposure and intensive care unit (ICU) hospitalization were important risk factors for invasive A. lentulus infection. Phenotypic differences were observed for A. lentulus isolates including slower growth, reduced sporulation and inability to grow at 48°C, compared with Aspergillus fumigatus complex. ITS sequencing was unable to distinguish A. lentulus from A. fumigatus, but sequencing of the benA, CaM and rod A loci enabled reliable distinction of these closely-related species. Phylogenetic analysis further confirmed that the ITS region had little variation within the Aspergillus section Fumigati whilst the benA gene offered the highest intraspecific discrimination. Microsatellite typing results revealed that only loci on chromosomes 1, 3, 5 and 6b generated detectable amplicons for identification. All A. lentulus isolates showed in vitro resistance to

multiple antifungal drugs including amphotericin B (MIC range 4 to 8 μg/ml), itraconazole (MIC 2 μg/ml), voriconazole (MIC of 4~16 μg/ml) and posaconazole (MIC of 0.5~1 μg/ml). However, MECs for the echinocandin drugs, ranged from 0.03~0.25, ≤0.008~0.015 and ≤0.015~0.03 μg/ml for caspofungin, micafungin and anidulafungin, respectively. A. lentulus is an emerging fungal pathogen in China, causing fatal disease and clinicians as well as laboratories should be alert to their increasing presence.

PO-0917

Genetic Characterization of Carbapenem-resistant Escherichia coli from China, 2015 - 2017

Fengtian Li[2]、Kun Ye[1]、Xin Li[1]、Liyan Ye[1]、Ling Guo[1]、Lifeng Wang[1]、Jiyong Yang[1]
1. Laboratory Medicine Department, First Medical Center of Chinese PLA General Hospital
2. 中国人民解放军总医院第一医学中心

The molecular characteristics of carbapenem-resistant Escherichia coli (CREco) remain unclear.
Methods We conducted a multi-center bacterial resistance monitoring project from 2015 to 2017. The minimum inhibitory concentrations of CREco were determined by broth microdilution method. The genome sequencing of CREco isolates was performed, and single-nucleotide polymorphism (SNP) was analyzed.
Results A total of 144 CREco isolates collected from 10 cities in China were involved in this study. ST167 (n=43) is the most popular type, followed by ST410 (n=14), ST131 (n=9). There were 102 (70.83%) CREco isolates that produced various NDMs, including NDM-1 (n=16), NDM-4 (n=1), NDM-5 (n=79), NDM-6 (n=2) and NDM-9 (n=4). In addition, 15 isolates produced KPC-2, three isolates were IMP-4 positive, and three isolates produced OXA-48. Genetic relatedness and phylogenetic analysis showed that isolates with the same ST had a high degree of homology. Some STs (including ST167, ST410, ST131, ST46, ST405 and ST617) exhibited a trend of outbreak.
Conclusions The majority of CREco belonged to ST167, followed by ST410 and ST131, and most of them carried various NDM-coding genes. The spread of high-risk clones of CREco has occurred in different regions of China.

PO-0918

肠杆菌目细菌快速碳青霉烯酶表型检测方法评价

徐绣宇
重庆医科大学附属第一医院

目的 利用 A 类碳青霉烯酶和 B 类碳青霉烯酶活性分别可以被苯硼酸和乙二胺四乙酸抑制的原理，评价实验室自建快速碳青霉烯酶表型检测方法区分肠杆菌目细菌碳青霉烯酶种类的特异性和灵敏度，评估其用于筛查和鉴定肠杆菌目细菌碳青霉烯酶的临床价值。
方法 连续收集临床分离的碳青霉烯耐药肠杆菌目细菌共 257 株，使用 Vitek MS 全自动细菌鉴定系统进行细菌鉴定，采用微量肉汤稀释法对厄他培南、亚胺培南和美罗培南三种碳青霉烯类抗生素的最低抑菌浓度进行验证。同时采用 PCR 扩增及测序检测碳青霉烯酶基因。其中 117 株碳青霉烯酶基因阳性菌株作为实验组，进行快速碳青霉烯酶表型检测，比较其结果和分子生物学结果的一致性。
结果 117 株碳青霉烯酶基因阳性的菌株的快速碳青霉烯酶表型检测实验结果中，41 株菌生长可被苯硼酸抑制，提示产 A 类碳青霉烯酶。66 株菌生长可被乙二胺四乙酸，提示产 B 类碳青霉烯酶。10 株菌生长仅在苯硼酸和乙二胺四乙酸共同存在时被抑制，提示共同产 A 类碳青霉烯酶和 B 类碳青霉烯酶。PCR 及测序证实 117 株产碳青霉烯酶菌株中，41 株携带 blaKPC-2，44 株携带

blaNDM-1，13 株携带 blaNDM-5，5 株携带 blaIMP-4，1 株携带 blaIMP-8，10 株同时携带 blaKPC-2 和 blaNDM-1，3 株同时携带 blaIMP-8 和 blaNDM-1。
结论 肠杆菌目细菌快速碳青霉烯酶表型检测能准确区分肠杆菌目细菌碳青霉烯酶类型，快速且操作简便，6 小时内可得到检测结果，且能检测出同时产 A 类碳青霉烯酶和 B 类碳青霉烯酶的菌株，适用于临床微生物实验室常规使用。

PO-0919

An efficient SERS platform for Staphylococcus aureus and Listeria monocytogenes ultrasensitive detection via lectin-modified magnetic SERS substrate and streptavidin/aptamer-functionalized SERS tags

Siyun Cheng
徐州医科大学

Objective in order to establish a rapid, accurate and highly sensitive new analytical technique technology for simultaneous detection of *S. aureus* and *L. mono.*
Methods a high-performance SERS-label biosensor for bacteria sensitive detection was construct by using a dual-recognition strategy (Scheme 1). Lectin from Triticum vulgaris (wheat germ agglutinin, WGA) was modified on the surface of Fe_3O_4@Au nanoparticles as magnetic separation for broad-spectrum recognition and efficient bacterial enrichment. Streptavidin (SA)-AuNP integrated with biotin-modified aptamers (bio-aptamers) were fabricated as pathogen-specific SERS probe. In brief, the Fe_3O_4@Au-WGA MNPs were added into sample solution which contain one or more species of bacteria, and incubated for 15 min; during this process, Fe_3O_4@Au-WGA anchored onto the surface of bacteria via strong hydrogen bonding and hydrophobic interactions between WGA molecules and the bacterial cell wall. Then, the Fe_3O_4@Au-WGA-bacteria complexes were magnetically separated and incubated with specific aptamer-modified SERS tags for 45 min to form Fe_3O_4@Au-bacteria-SERS tags sandwich configurations. By magnetic separation, the obtained sandwich complexes were rinsed once with PBST solution to remove excess SERS tags, and their characteristic Raman signals (DTNB for *S. aureus* and MBA for *L. mono*) were measured by a Raman instrument. The generated signal intensity of sandwich complexes was proportional to the concentration of the bacteria in the samples, which provide the foundation for quantitative analysis.
Results Compares with the previous SERS label-based bacteria detection methods, the major innovations of our proposed strategy could manifest in three aspects. First, monodispersed magnetic nanosphere (~200 nm) with roughness Au shell was employed as multifunction platform which not only provide strong magnetic enrichment capacity but also offer excellent SERS property to further enhance the characteristic signal of SERS tags. Second, phytagglutinin WGA was modified onto the Fe_3O_4@Au carrier to provide broad-spectrum recognition ability and high affinity for *S. aureus* and *L. mono* in complex environment. Third, streptavidin was introduced into SERS tags to improve the stability of AuNPs and the coupling efficiency of aptamer. Fe_3O_4@Au-WGA allowed effective separation of 8 species of Gram-positive and Gram-negative pathogen (including *S. epidermidis, P. aeruginosa, S. aureus, L. mono, E. coli, A. baumannii, S. sonnei, and S. typhi*) from PBS solution with efficiency from about 41% to 94%. We select *S. aureus* and *L. mono* as the model bacterias for SERS detection. Under optimal conditions, a strong linear relationship was found between the Raman signal intensity at 1331 cm^{-1} and the logarithmic concentration of *S. aureus*, and between Raman signal intensity at 1588 cm^{-1} and the logarithmic concentration of *L. mono*, respectively, from 10^7 cells/mL to 10 cells/mL, with correlation coefficient (R^2) = 0.993 for *S. aureus*, and R^2 = 0.978 for *L. mono*. The limits of detection (LODs) of the proposed platform for *S. aureus* and *L. mono* was calculated to be 3 and 5 cells/mL, respectively, based on signal-to-noise ratio (SNR) of 3 criterion. Compared with the most of

SERS label-based biosensors for bacteria detection, the method reported in this work exhibited better performance including higher sensitivity, faster testing speed, and more detection channels. The applicability of our platform in practical applications is verified by the detection of low-concentration *S. aureus* and *L. mono* in human urine and orange juice.
Conclusion in this paper, we develop an ultra-sensitive and selective SERS platform based on the efficient and broad-spectrum capture ability of lectin-modified Fe_3O_4@Au MNPs and specific binding ability of streptavidin/aptamer-functionalized SERS tags. As an ultrasensitive and highly selective biosensor for simultaneous detection of *S. aureus* and *L. mono*, the proposed assay has great potential in the application multiple bacteria.

PO-0920

艰难梭菌相关性腹泻模型的构建及肠道菌群结构特征研究

杨芳、刘文恩
中南大学湘雅医院

目的 （1）采用 C57BL/6 小鼠构建 CDAD 动物模型，并通过临床和病理指标对模型进行评估，为研究艰难梭菌致病机制、制备疫苗及评估新治疗方案等提供体内实验工具；（2）利用 Hiseq 高通量测序平台对小鼠粪便标本中细菌 16S rRNA 基因 V4 区进行测序分析，揭示肠道菌群失衡与 CDI 之间的相互关系，为依赖肠道菌群调节手段进行 CDI 防治提供理论依据。
方法 （1）使用艰难梭菌产毒标准菌 RT 027 对 C57BL/6 小鼠进行灌胃，观察记录小鼠一般情况、体重变化，收集粪便进行细菌培养与质谱鉴定，并对培养阳性的艰难梭菌进行毒素基因检测与核糖体分型，采集小鼠肠组织和血液标本分析小鼠肠道炎症病变及感染情况。（2）利用 Hiseq 高通量测序平台对模型组和对照组小鼠粪便标本中细菌 16S rRNA 基因 V4 区进行测序，通过 OTU 分析及物种注释、样品内多样性分析、两组间多样性参数比较和基于 Spearman 距离的 PCoA 分析、两组间物种组成聚类分析及组间显著性差异分析研究 CDAD 模型小鼠和对照组小鼠的粪便菌群结构差异。
结果 （1）建模期间模型组 C57BL/6 小鼠体重明显减轻，7 只小鼠出现稀便，腹泻发生率达 58.3%，其粪便艰难梭菌培养均为阳性，为产毒素的 RT 027，肠组织病理学检查显示所有腹泻小鼠均出现中至重度炎症，模型组小鼠 WBC、中性粒细胞百分率（N%）以及 hs-CRP 均有所升高，但差异无统计学意义。对照组小鼠各项指标均未见明显异常。（2）CDAD 模型较对照组小鼠的肠道菌群多样性及表达丰度显著降低。在门水平上 CDAD 小鼠较对照组拟杆菌门和厚壁菌门细菌比例明显减少，而变形菌门在模型组中比例显著增多。CDAD 小鼠与产丁酸相关的毛螺菌科和瘤胃球菌科等厌氧菌比例显著降低，与产乳酸相关的乳杆菌科等细菌比例则显著升高，与产内毒素相关的肠道条件致病菌如埃希菌属、摩根菌属、克雷伯菌属、变形杆菌属和耶尔森菌属等肠杆菌科细菌比例显著增加，与宿主肠黏膜及抗炎症相关的 Mucispirillum schaedleri 丰度降为 0。
结论 （1）经混合抗菌药物连续灌胃后予以克林霉素腹腔注射诱导处理，采用核糖体 027 型产毒艰难梭菌菌株灌胃，可成功建立稳定的小鼠艰难梭菌相关性腹泻模型。（2）CDAD 模型小鼠较对照组小鼠的肠道菌群组成及表达丰度显著降低，毛螺菌科和瘤胃球菌科等厌氧菌可能成为肠道菌群拮抗艰难梭菌的关键细菌，但需进一步研究。

PO-0921

纳米孔测序技术在感染性疾病中的应用

付宇[1]、赵瑾[2]、田宏攀[2]、周俊英[2]、陈良君[2]、李一荣[2]
1. 武汉大学中南医院
2. 武汉大学中南医院检验科

目的 近年来火热的纳米孔靶向测序技术（nanopore targeted sequencing, NTS）属于第三代测序技术，又被称做单分子测序技术。纳米孔测序技术的原理是当长的单链 DNA 稳定穿过纳米生物孔的时候，因为不同碱基有不同的电导率，会使电荷发生变化，从而短暂地影响纳米孔的电流强度，根据电流强度的改变，就能读出核酸分子序列。长期以来，感染性疾病诊断的金标准是实验室培养，但是病原体培养的方法耗时长，阳性率低且极容易被污染，不能及时指导临床。因此，本研究对包括脑脊液，胸腹水等在内的六个标本类型采用纳米孔测序技术，同时结合病人的临床表现，培养结果等综合判断纳米孔测序技术在临床运用中的可行性。
方法 我们收集了 2020 年 1 月-2021 年 3 月 1046 个病人的总共 1226 个临床标本（包括 129 个脑脊液标本，149 个胸腹水标本，448 个纤支镜灌洗液标本，87 个尿液标本，327 个血液标本，76 个伤口分泌物标本），采用纳米孔测序的方法检测这些标本中可能存在的病原微生物。同时，我们也收集了这些病人相应的临床表现，感染指标和用药信息进行总体分析。对于培养结果为阴性以及不相符合的标本，我们为了验证纳米孔测序结果的准确性，还专门设计了种特异性引物进行普通 PCR 以及巢式 PCR 扩增，且扩增产物进行了一代测序。
结果 根据病例和临床表现，所有病人可以分为感染性疾病组(infectious disease, ID, 720/1046, 68.8%)和非感染性疾病组（non-infectious disease, NID, 316/1046,31.2%）。ID 组中，肺部感染的病人占大多数（400/720, 55.56%），接下来是泌尿系统感染（76/720，10.56%），血流感染（72/720，10%）等。纳米孔测序的灵敏度和特异度分别是 88.49%（1076/1216），53.48%（238/445）。在感染性疾病中，纳米孔测序结果与 PCR 和一代测序验证的符合率为 73.98%（253/342），其中纤支镜灌洗液的符合率最高（84.05%，137/163），其次是胸腹水（75%，48/64）；在脑脊液中，符合率最低，为 52.63%（10/19），可能是由于脑脊液是无菌体液，微生物载量很低，所以检出率不高。
结论 纳米孔测序技术在病原体鉴定方面较培养来说具有更高的灵敏性，并且受抗生素使用的影响较培养小得多。纳米孔测序技术在不同的标本类型中针对不同微生物的灵敏度不同，未来可以根据具体临床标本类型和潜在的病原微生物种类做出相应改进，以使纳米孔测序技术更好地应用于临床中。

PO-0922

Trends in antimicrobial resistance in bloodstream infections at a large tertiary-care hospital in China: a 10-year retrospective study (2010-2019)

Cailin Liu
The First Affiliated Hospital of Zhengzhou University

Objectives Bloodstream infections (BSIs) are considered as a major cause of morbidity and mortality all over the world. The purpose of this study was to explored the distribution and antimicrobial resistanc trends of pathogens causing BSIs at a large tertiary-care hospital in Henan province, east-central China.
Methods In this surveillance study, blood culture specimens were routinely taken from patients with fever or suspicion of sepsis from 2010 to 2019 at the First Affiliated Hospital of Zhengzhou University. Identification of organisms was carried out using the VITEK 2 Compact system and/or the VITEK MS system. Antimicrobial susceptibility tests were carried out by the minimum

inhibitory concentration (MIC) method and/or the disk diffusion according to Clinical & Laboratory Standards Institute guidelines.
Results A total of 18180 strains were isolated from blood culture specimens, the most common pathogen was E. coli (21.6%), followed by CoNS (18.8%), K. pneumoniae (13.0%), S. aureus (6.6%), E. faecium (5.0%), A. baumannii (4.4%), and P. aeruginosa (3.8%). The resistance rates of E. coli to ceftazidime, cefotaxime, cefepime and aztreonam showed a significant declined trend, and the frequency of carbapenem-resistant E. coli was below 6.0% over time. It is noteworthy that the proportion of carbapenem-resistant K. pneumoniae exhibited sharp upward trend during the ten years (from 6.7% to 56.7%). The prevalence of carbapenem-resistant A.baumannii has remained at a high level (>75%). In contrast, the resistance rates for P. aeruginosa against all tested agents were lower than 25%, and the resistance rates to aminoglycosides and fluoroquinolones showed a significant downward trend. The frequency of methicillin-resistant CoNS maintained a high level over the past decade (>70%), however, the isolation rate of MRSA ranged from 58.0% to 34.9%, showed a significant decline.
Conclusions It was particularly noteworthy that the dramatic and consistent increase in carbapenem-resistance in K. pneumoniae during the 10-year surveillance period and effective infection control measures and stewardship efforts should be taken to prevent the spread. Our results indicate the the importance of active surveillance for bacterial etiology and their antibiotic resistance causing BSIs.

PO-0923

Etiological characteristics and change of cerebrospinal fluid related measurements in HIV/AIDS patients with central nervous system infection in Chongqing

Ming Luo[1]、Xiaofeng Li[1]、Xiaoying Wang[2]、Jing Wang[1]
1. Chongqing publpic health center
2. 重庆医药高等专科学校

Objective To analyze the characteristics of pathogens and cerebrospinal fluid (CSF) related measurements in HIV/AIDS patients with central nervous system (CNS) infection in Chongqing, and provide guidance for effective diagnosis and treatment of these patients.
Methods A total of 173 HIV/AIDS patients with CNS infection and 198 HIV/AIDS patients with non-CNS infection that hospitalized in the Chongqing Public Health Medical Center were enrolled. CSF and blood from the patients were collected for microbiological pathogen identification and drug susceptibility testing. CSF related measurements were determined and compared between different groups.
Results Of the 173 microbiological pathogens that isolated from the CSF of HIV/AIDS patients with CNS infection, the most prevalent one was Cryptococcus neoformans (58.38%), followed by Mycobacteria tuberculosis (22.54%), and coagulase negative staphylococci (11.5%). While for HIV/AIDS patients with non-CNS infection, Talaromyces marneffei was the dominate pathogen in blood culture (40.91%), followed by coagulase negative staphylococci (11.5%), and Cryptococcus neoformans (10.61%). Cryptococcus neoformans was sensitive to mostly commonly used anti-fungi agents. 7.69% of HIV/AIDS patients infected with Mycobacteria tuberculosis in CNS was resistant to rifampicin. Compared with the blood samples of HIV/AIDS patients with non-CNS infection, significantly higher protein levels, and lower levels of chloride and glucose were observed in CSF of HIV/AIDS patients with CNS infection (all $P < 0.011$). Moreover, the levels of protein, adenosine deaminase (ADA) and lactic dehydrogenase (LDH) in CSF samples were significantly increased in HIV/AIDS patients infected with mycobacteria tuberculosis than other groups (all $P < 0.037$).
Conclusion The distribution and antimicrobial susceptibility of pathogens causing CNS and blood infection in HIV/AIDS patients were variant. The CSF related measurements varied with different

pathogenic infection, which could be benefit for early pathogenic diagnosis of CNS infection in HIV/AIDS patients.

PO-0924

Isolation and characterization of a lytic Staphylococcus aureus phage WX 2 against Staphylococcus aureus biofilm

郑瑞
云南省第一人民医院

Staphylococcus aureus is a Gram-positive pathogen bacteria which causes a wide range of symptoms in human. Bacteria biofilm is the multicellular community of microorganisms that attached to non-biological and biological surfaces. In this study, a virulent phage WX was isolated from slaughter house. It was belonged to the Myoviridae family and Phage WX has ability of sterilize most clinical strains of S. aureus which were isolated from clinical patients in the first people's hospital of Yunnan province. Phage WX has better anti-biofilm effect than streptomycin in high concentration S. aureus culture of. Collaboration of phage WX and streptomycin have better anti-biofilm effect than alone of WX or streptomycin in low concentration S. aureus culture and phage WX has better anti-biofilm effect than streptomycin in high concentration S. aureus culture. The data of this study provided a strong evidence of application phage for reduce S. aureus biofilm growth and was important for replace of antibiotics in clinic.

PO-0925

Enhanced antimicrobial and antibiofilm activity of colistin combined with resveratrol against colistin-resistant Pseudomonas aeruginosa in vitro and in vivo

Lingbo Wang
Department of Clinical Laboratory, The First Affiliated Hospital of Wenzhou Medical University

Multidrug-resistant (MDR) Pseudomonas aeruginosa infections pose a serious threat to public health. Colistin is considered as the last resort antimicrobials, but in recent years, colistin-resistant strains is increasing. This study aimed to investigate the antimicrobial and antibiofilm activity of resveratrol in combination with colistin against colistin-resistant Pseudomonas aeruginosa isolates in vitro and in vivo. Antimicrobial susceptibility tests, checkerboard assays, and time-kill assays were performed to investigate the antibacterial and synergistic activity of resveratrol combined with colistin in vitro. The neutropenic mouse thigh infection model and G. mellonella infection model were used to investigate the combined antimicrobial activity in vivo. Biofilm formation assays and Scanning electron microscopy (SEM) were used to evaluate the antibiofilm efficacy. The susceptibility testing showed that the MIC of resveratrol was >512 μg/mL, which showed no antimicrobial activity against Pseudomonas aeruginosa. Checkerboard assay indicated that the combination of resveratrol and colistin showed great synergy effect. Furthermore, biofilm formation assays and SEM showed synergistic antibiofilm activity. The synergy of this drug combination partially disrupts the bacterial cell envelope resulting in a decreased number of bacteria. Further in vivo treatment experiments demonstrated that this combination could decrease the number of bacteria ≥2log10 CFU/ml after 24 h of therapy in mice infection model and the survival rate of G. mellonella improved obviously compared with single drug and control group. The combination of resveratrol and colistin is a valuable prototypical combination that has a high clinical potential, suggesting an attractive option for the treatment of MDR Pseudomonas aeruginosa infections

PO-0926

Genetic analysis of KPC-2-producing Klebsiella pneumoniae ST11 from Respiratory Departments of a Tertiary Care Hospital in Beijing, China, 2010-2018

Ling Guo
First Medical Center of Chinese PLA General Hospital

Background Carbapenem-resistant Klebsiella pneumoniae (CRKP) belonging to sequence type 11 (ST11) is a significant pathogen causing hospital-associated outbreaks in China and a major contributor to the spread of carbapenemases. This genetic lineage emerged several decades ago and remains a major global health care challenge.
Methods A total of 155 ST11 type KPC-2-producing K. pneumoniae isolates were collected from a respiratory departments between 2009 and 2018 from a tertiary care hospital in China. The genome sequencing of these isolates was performed on a HiSeq X Ten sequencer using a paired-end library with an average insert size of 350 bp. Single-nucleotide polymorphism (SNP) analysis was performed using the SNP-based CSI-Phylogeny-1.4 tool on the web site of the Center for Genomic Epidemiology. The tree file was visualized by iTOL. Plasmid replicon types and resistance genes were identified using PlasmidFinder, and ResFinder, respectively. The multilocus sequence type (MLST) was determined using the MLST 1.8 server. Fifteen isolates were selected for subsequent single-molecule real-time (SMRT) sequencing with a sheared DNA library with average size of 10 kb on a PacBio RS II. Genome sequences were annotated with the Rapid Annotations using Subsystem Technology (RAST) pipeline, combined with BLASTP/BLASTN searches. Alignment of the complete sequences of the *bla*$_{KPC-2}$-carrying plasmids and virulence-carrying plasmids f was performed by using BRIG and Easyfig.
Results In this study, genomic epidemiology was used to investigate the emergence, evolution, and persistence of different ST11 KPC-2 producing CRKP outbreak-causing clones at respiratory departments of a tertiary care hospital over 9 years. ST11 CRKP emerged in 2012 in these departments, then caused several outbreaks and persisted in the whole respirotary departmens. The phylogenetic analysis of 155 ST11 isolates demonstrated three genetically distinct clades (A, B, C). Except five strains belonging to KL25, most of clade A strains belonging to KL47 serotype (n=120, 77.4%) emerged firstly in 2012 and could been divided into nine subclades, A1-A9. Clade B belonging to KL64 serotype newly emerged in the end of 2016 and could be divided into subclade D1 and D2. Clade C belonging to KL16 serotype emerged only between 2013 and 2016. Although clade C did not persist but 62.5% (5/8) isolates co-possessed the *bla*$_{KPC-2}$ and *bla*$_{OXA-48}$ genes. The *bla*$_{KPC-2}$-carrying plasmids documented diversity, which included multireplcons: IncFII(pHN7A8)/IncpA1763-KPC (5/15), IncFII(pHN7A8)/IncR (6/15) , IncR(1/15) and IncpA1763-KPC (1/15),and unnamed type (1/15). The analysis of genetic environment of blaKPC-2 genes showed nine IS*26*-based composite transposons which had a basic core structure IS*Kpn27*-*bla*$_{KPC-2}$-ΔIS$_{Kpn6}$ structure forms. WGS revealed that the strains harboured a plasmid, which carried multidrug resistance genes and virulence-encoding genes
Conclusions In this study, twelve clone transmissions of KPC-2-producing-ST11 were observed within the same respiratory departments over nearly a decade. Findings in this study provide evidence of active plasmid evolution in K. pneumoniae and suggest that surveillance of multidrug-resistant and hypervirulent *K. pneumoniae* is urgently needed.

PO-0927

宏基因组测序对血液病患者合并毛霉菌病的诊断价值

许颖出、徐春晖、朱国庆
中国医学科学院血液病医院（血液学研究所）

目的 探讨宏基因组测序技术（metagenomic next-generation sequencing, mNGS）对血液病患者合并毛霉菌病的诊断效果及临床用药提示。
方法 回顾性分析中国医学科学院血液病医院 2020 年 6 月至 2021 年 6 月期间，采用 mNGS 技术检出的毛霉感染患者的实验室和临床特征，分析 mNGS 技术对血液病患者合并该类真菌感染的应用价值。
结果 一年期间共 242 例患者送检外周血 mNGS 检测，10 例患者检出毛霉，检出率为 4.1%，其中 6 例为米黑根毛霉，3 例为米根霉，1 例为小孢根霉。10 例患者中男性 8 例（80%），中位年龄为 43（20-57）岁。6 例为急性髓系白血病，3 例为再生障碍性贫血，1 例为急性淋系白血病。临床表现主要为发热（100%，10/10）、肺感染（80%，8/10）等。8 例（80%）患者新发斑片影，磨玻璃影，团状、片状实变影。实验室数据显示，10 例患者中粒缺者占 40%（4/10）, 1,3-β-D-葡聚糖均未增高，PCT 增高见于 4 例（40%）患者，Crp 增高见于 7 例（70%）患者。mNGS 检出毛霉 reads 的中位数为 167（6-6500）。10 例患者均据 mNGS 结果被调整抗生素用药，7 例好转，平均发热时间为 10 天；3 例病情加重后放弃治疗，平均发热时间为 12 天。
结论 血液病患者外周血 mNGS 检出毛霉具有较高的临床符合度，其无偏倚、报告周期短的特征可作为难以培养，实验室特异性检查缺乏的毛霉感染诊断的方法之一。

PO-0928

成都地区淋球菌耐药监测结果分析

罗才会、李春花、李红霞
电子科技大学附属医院·四川省人民医院

目的 了解 2013-2019 年成都地区淋病奈瑟菌对 5 种抗生素的耐药趋势及产 β-内酰胺酶淋球菌(PPNG)和质粒介导的高度耐四环素淋球菌(TRNG)的流行状况，为本地区淋病治疗方案的制定及预防控制措施的制订提供科学依据。
方法 收集自 2013-2019 年从我院性病门诊患者的泌尿生殖道分泌物中分离得到的 719 株淋病奈瑟菌，用琼脂稀释法测定头孢曲松、青霉素、大观霉素、环丙沙星、阿奇霉素和四环素的最小抑菌浓度(MIC)，用纸片酸度法检测 β-内酰胺酶，按 WHO 西太区淋病奈瑟菌耐药监测指南推荐的标准判断药物敏感性，采用 SPSS20.0 软件进行统计学分析。
结果 2013-2019 年共收集 719 株淋病奈瑟菌，检测出 PPNG 366 株 50.90%)、TRNG 315 株(43.81%)；青霉素、环丙沙星和阿奇霉素的耐药率分别为 90.54%、99.58%、24.61%；2018 年偶发现一株耐大观霉素菌株；未发现头孢曲松耐药菌株，但是其中敏率从 11.82%上升到 46.34%。7 年间，青霉素、环丙沙星的 MIC50 和 MIC90 均已超过耐药标准，大观霉素、头孢曲松的 MIC50 和 MIC90 均在敏感范围，阿奇霉素的 MIC50 在敏感范围，但 MIC90 超过耐药标准。
结论 持续监测淋球菌的耐药性十分重要，头孢曲松和大观霉素在成都地区可以作为治疗淋病的优选药物，具有良好疗效。发现的一株大观霉素耐药菌株和头孢曲松的中敏率逐年递增，应该引起临床医生的高度警惕及相关部门的高度重视，在临床上规范用药，加强对大观霉素和头孢曲松的耐药监测，及时发现耐药菌株的情况，防止耐药菌株的爆发流行。

PO-0929

抗生素治疗如何加重器械相关感染

何磊、李敏
上海交通大学医学院附属仁济医院

目的 器械相关感染经常在医院发生。由于器械上很容易形成生物被膜，而生物被膜对宿主本身和抗生素等具有强大的抵抗力，因此这种感染治疗起来特别困难。然而人们对器械上生物被膜形成的动态过程和调控机制仍知之甚少。
方法 我们收集了三年内临床器械相关金黄色葡萄球菌感染的同一组病人的连续分离株；并对这些分离株进行了溶血能力/生物被膜形成能力等体外表型研究，同时进行了基因组二代测序；接着基于构建的遗传分析工程菌，通过体外模拟和体内动物模型证实二代测序所筛选基因变异在调控生物被膜形成的机制；最后通过体内外实验找到可以有效针对生物被膜靶标的抗生素作为器械感染的有效治疗手段。
结果 在所有被调查的连续追踪病例中，群体感应功能失调的突变体在感染过程中超过了整个人群，强烈地促进了生物被膜的形成，从而增强了抗生素耐药性和细菌的持续感染能力。我们进一步在器械相关感染的小鼠模型中表明，用常用的糖肽和氟喹诺酮类抗生素治疗可提高群体感应功能失调突变的发生率并加重疾病。与此形成鲜明对比的是，利福平并未引发群体感应功能障碍，这为临床观察到的利福平治疗葡萄球菌感染的异常疗效提供了解释。
结论 我们的结果表明，器械相关感染是一个动态的过程，涉及特定的遗传适应，增加细菌的传染性。此外，通过揭示抗生素对这一过程的重要影响，我们的研究为此类感染的管理提供了重要建议。

PO-0930

产单核细胞李斯特菌致糖尿病性尿毒症患者严重脓毒血症 1 例并文献复习

肖华亮[1]、陈宗耀[2]、刘晓[2]、邹彦矫[2]、袁成良[2]
1. 德阳市人民医院检验科
2. 德阳市人民医院检验科

目的 为加强医务工作者对产单核细胞李斯特菌的认识，促进检验科与临床科室之间的沟通交流，更好的为患者服务。
方法 通过 MALDI-TOF MS 质谱鉴定技术快速对血培养中分离出的产单核细胞李斯特菌进行鉴定，并再次用 16S rRNA 基因测序检测技术进行验证。根据欧洲抗菌药物敏感性试验委员会标准，运用纸片扩散法（K-B 法）进行药敏试验，结合患者的病史及临床症状进行病例讨论，并对相关发病机制和文献进行复习讨论。
结果 经过鉴定该患者血培养所分离出的细菌为产单核细胞李斯特菌，药敏结果显示对氨苄西林敏感。由于患者有食用过夜剩饭剩菜的习惯，加上长期血液透析治疗，抵抗力低下，结合患者糖尿病病史，因此推测可能存在产单核细胞李斯特菌由胃肠道感染的途径。入院后最初经验性给予头孢哌酮舒巴坦抗感染治疗，但疗效差，相关炎症指标持续上升，达到严重浓度血症标准。待检验科血培养结果回报后，根据指南《热病：桑福德抗微生物治疗指南（第 44 版）》同时结合药敏结果更换为氨苄西林抗感染治疗，患者降钙素原、超敏 CRP 等指标持续降低，同时积极控制血糖、规律透析，患者住院期间总共进行了 17 天静脉及口服氨苄西林抗感染治疗最终治愈出院。已有大量文献提出针对产单核细胞李斯特菌不适当的经验性抗生素治疗会导致病情加重。因此，一旦证实或高度怀疑是产单核细胞李斯特菌感染，应当尽快调整治疗方案，使用合适的抗生素进行治疗。于是对产单核细胞李斯特菌的快速鉴定显得尤为重要，同时相关研究显示了 MALDI-TOF MS 系统可对产单

核细胞李斯特菌进行有效检测和鉴定，因此能使临床医生至少提前 24 小时获得准确的鉴定结果，为临床合理用药提供有力的支持。
结论 1、感染性疾病要重视病原学的搜寻，积极运用血培养、血浆降钙素原等检查手段来提高临床工作者的诊疗正确性，基层医院要从自身实际情况出发选择合适的治疗方案；2、病原学的鉴定要重视时效性，微生物工作者应不断提高自身的水平，灵活配制各种检查技术及时准确的鉴定出病原菌；3、加强检验科与临床的沟通，若检出少见菌、罕见菌要及时主动通知临床，积极的进入到临床疾病的诊治中，结合病史资料、临床症状等共同判断，更好的为患者服务。

PO-0931

淋病奈瑟菌的检出情况及药敏结果分析

徐优耀、张桂华
中国医科大学附属第一医院鞍山医院

目的 通过对全院淋病奈瑟菌分离情况和耐药性的研究，旨在为临床合理用药及有效治疗提供依据。
方法 统计 2015 年 4 月 1 日-2019 年 4 月 1 日全院分离诊断的淋病奈瑟菌，用淋病奈瑟菌检测试剂盒行药敏试验的检测。
结果 67 株淋球菌对头孢曲松耐和对头孢克肟耐药率为 0(0 /67) ，对阿奇霉素耐药率为 8.95%(6 /67)，对四环素耐药率为 38.8% (26 /67) ，对大观霉素耐药率为 11.94% (8/67)，对环丙沙星及青霉素耐药率均为 100% ，这与淋球菌的全国的耐药情况相一致。
结论 通过分离出的 67 株淋球菌对头孢曲松、头孢克肟、阿奇霉素敏感，对环丙沙星、青霉素、四环素、大观霉素耐药，旨在研究本院淋病奈瑟菌的分离情况，为临床合理用药及有效治疗提供依据。

PO-0932

质粒介导新生儿产 NDM-5 酶肺炎克雷伯菌分子耐药机制研究

张欢欢、杨晋
连云港市第一人民医院

目的 产新德里金属 β-内酰胺酶（NDM-5）肺炎克雷伯菌不断的出现，给全球公共健康带来了巨大威胁。本研究通过收集连云港市第一人民医院新生儿病房 2018 年 9 月-2019 年 9 月携带 blaNDM-5 基因肺炎克雷伯菌，分析新生儿病房菌株主要克隆群以及耐药机制。
方法 本研究通过 MALDI-TOF MS 进行菌株鉴定。通过药敏试验和 PCR 技术来分析菌株耐药性和耐药基因携带情况。通过多位点序列分型和脉冲场凝胶电泳分析菌株同源性。对携带 blaNDM-5 基因菌株进行质粒接合试验和 Southern blot 印迹，分析耐药质粒的特征；通过全基因组测序更加深入的了解 blaNDM-5 基因上下游基因环境，明确耐药基因的传播机制。
结果 本研究收集 12 株产 NDM-5 酶肺炎克雷伯菌。菌株均为多重耐药菌，其对碳青霉烯类、单环 β-内酰胺酶类、头孢菌素类、酶抑制剂复合制剂类均耐药。12 株耐药菌均携带 blaSHV-11 基因和 blaTEM-1 基因。同源性分析显示菌株均为 ST337 型，并属于 PFGE 同一克隆型。接合实验均成功，说明携带 blaNDM-5 基因的质粒具有高度的自主转移性。质粒分析显示 blaNDM-5 基因均位于约 47kb IncX3 质粒上。进一步的全基因组测序结果显示携带 blaNDM-5 基因的质粒序列完全一致，该质粒长度为 47, 474bp，与经典型质粒 pNDM-MGR194 核苷酸相似度超过 99%，blaNDM-5 基因位于典型的 ISAba125-IS5-blaNDM-5-bleMBL-trpF-IS26 结构中。
结论 该研究首次报道了产 NDM-5 酶 ST337 型肺炎克雷伯菌在新生儿病房的克隆传播，blaNDM-5 基因均位于约 47kb IncX3 型质粒，与经典型质粒 pNDM-MGR194 高度同源，该型质粒是传播 blaNDM-5 的重要载体，在新生儿病房有扩散风险。

PO-0933

Anti-psychotic drug thioridazine acts as a potent anti-microbial agent for MDR: a clinical strains-based study

Lin Yin
The Second People's Hospital of Hunan Province

Purpose The multidrug resistant (MDR) strains are emerging worldwide as a public health threat. The aim of the study was to comprehensively investigate the effect of anti-psychotic drug thioridazine on common MDR clinical isolated strains, and provide new strategies for the therapeutics of MDR infections.
Methods Bacteria were isolated from the clinical patients. The identification and susceptibility testing of isolated strains in this study were completed by MALDI-TOF mass spectrometry and VITEK 2 Compact analysis system, respectively. The antibacterial efficacy of thioridazine in vitro was assessed by agar dilution method.
Results A total of 156 strains were isolated from the clinical patients. Samples mainly come from blood, sputum, bronchoalveolar lavage, urine, cerebrospinal fluid, puncture fluid and wound secretion. Among these strains, 63 were susceptible strains and 93 were MDR strains. Specifically, MDR Gram-positive coccus included 3 methicillin-resistant Staphylococcus aureus (MRSA) and 7 MDR Enterococcus. MDR Gram-negative bacilli included 66 non-fermentative bacilli (17 Pseudomonas aeruginosa and 49 Acinetobacter baumannii) and 17 enterobacteriaceae (11 Klebsiella pneumoniae and 6 Escherichia coli). MRSA, MDR Enterococcus and MDR Acinetobacter baumannii were significantly inhibited by thioridazine at low concentrations (20 μM). MDR Pseudomonas aeruginosa and MDR Escherichia coli were inhibited by thioridazine at middle concentration (40 μM). MDR Klebsiella pneumoniae were inhibited by thioridazine at high concentration (100 μM). Moreover, all of susceptible strains were also inhibited by thioridazine at different concentration, except for susceptible Escherichia coli. Notably, common MDR clinical isolated strains shown susceptibility against thioridazine regardless of sample source.
Conclusion The present study shows that thioridazine is an effective drug against common MDR clinical isolated strains, which provides an alternative strategy for MDR and has a highly translational value.

PO-0934

中国血流感染金黄色葡萄球菌优势克隆种群特点研究

陈凤宁、陈宏斌、尹玉瑶、王辉
北京大学人民医院

本研究旨在调查中国血流感染金黄色葡萄球菌的种群结构及特点，探究优势克隆形成及传播机制。我们回顾性收集了全国各地区 16 家大型教学医院 2019-2020 年共 484 株血流感染金黄色葡萄球菌，并对 142 株优势克隆（ST59,ST5,ST398,ST239）进行了全基因组测序和比较基因组、体内外表型实验分析。
基于最大似然法构建的系统发育树表明，各 ST 被精确划分为不同的 lineage，且各 ST 内部又被划分为 3 个主要的 subgroup；进一步的 spa、*SCCmec*、Agr 和 IEC 分型发现优势克隆 ST59 主要是 t437-IVa(2B)-agrI-IEC type B；VFDB 和 Resfinder、CARD 数据库的分析表明各 ST 具有特异的毒力和耐药基因；基于 Scoary 的全基因组关联分析表明 ST5 的种群特异基因与肠毒素、ESAT-6 分泌系统相关，ST59 主要和细胞壁合成蛋白相关，ST398 主要和寡肽转运系统相关。142 株菌对氟喹诺酮类药物的敏感性在各 ST 差异最大；ST398 和 ST59 以及具有较强的溶红细胞能力，其中 ST398-MRSA 比 MSSA 具有更强的蛋白酶水解和溶红细胞能力，说明 ST398 在获得耐药性的同时不发生适应性代价，但 ST5-MRSA 的蛋白酶水解能力和溶红细胞能力却弱于 MSSA。这可能与其

特异的毒力和耐药基因组合相关。ST398 的蛋白酶水解能力明显强于其它 STs，但生物被膜形成能力弱于其他 STs，可能是由 ST398 特异的寡肽转运酶造成。总之，我们通过基因组和表型研究发现中国血流感染金黄色葡萄球菌呈现多克隆趋势，且各 ST 在基因组和体外适应性具有不同特点，基于全基因组测序的比较基因组和 GWAS 分析有助于找到各 ST 的特异性关键分子，从而对感染性疾病的精准诊疗提供指导。

PO-0935

二代测序技术应用于中枢神经系统感染的研究进展

杨传坤
东南大学附属中大医院

中枢神经系统（central nervous system,CNS）感染可引起严重的并发症和后遗症，由于临床实验室检测手段的限制，超过一半的 CNS 感染病例最终都无法明确诊断。早期快速明确 CNS 感染的病原体，对于降低 CNS 感染的病死率和减少后遗症都有重要的作用。目前临床应用最广泛的 CNS 感染病 原体检测方法主要包括：脑脊液病原体形态学鉴定、外周血或脑脊液培养、脑脊液和血清的病原体抗体检测以及脑脊液的基因检测；但总体阳性率较低，使 CNS 感染的诊治面临极大的困难。 本文综述了以二代测序（NGS）为基础的宏基因组测序技术以确诊 CNS 感染的研究，因其具有高通量、高灵敏度等特点，在微生物检测方面具有显著的优势。并对 NGS 在 CNS 感染病原体诊断及其所面临的问题与挑战等方面进行总结，作为一种分子诊断手段，二代测序技术为确定 CNS 感染的病原体提供了精准的结果，具有重大的意义。

PO-0936

Phenotypic and genotyic methods for detecting methicillin-resistant Staphylococcus aureus

Peiyao Jia、Qiwen Yang
Department of Clinical Laboratory, Peking Union Medical College Hospital, Peking Union Medical College, Chinese Academy of Medical Sciences

Objective The aim of this study was to evaluate and compare the phenotypic and genotypic methods for detection of Methicillin Resistant Staphylococcus aureus (MRSA), and investigate the prevalence of clinical isolated MRSA in China.
Materials/Methods Non-repetitive 1190 S.aureus were collected from 16 hospitals from 2014 to 2015. Antimicrobial susceptibility testing was performed by the broth dilution method accoding to CLSI. Cefoxitin susceptibility was determined by Disk diffusion method. All the Staphylococcus aureus were screened for the presence of the genes mecA, mecC and nuc, and 38 S.aureus were selected for the dectection for the expression of mecA gene.
Results The susceptibility of these 1190 isolates of Oxacilin and Cefoxitin were52.2%(621/1190) and 52.4%(623/1190), respectively. All the S.aureus were susceptible for Linezolid, Tedizolid, Vancomycin, Teicoplanin, Dptomycin. Among 1190 isolates from S. aureus, 621 (52.4%) isolates were positive for mecA gene by PCR method. The results of cefoxitin disk diffusion method with 100% sensitivity and 99.65% specificity was the same as PCR method. Oxacillin broth dilution method had 99.68% sensitivity and 99.65% specificity.
Conclusions Among the three laboratory diagnostic methods of MRSA, result of cefoxitin disk diffusion method with high sensitivity and specificity was the same as PCR method for detection mecA gene. Cefoxitin disk diffusion method can be used as an alternative method to PCR especially at those microbiology laboratories without molecular facilities. Mutiple real-time PCR has the advantage of high isolation rate and high sensitivity. It is one of the effective methods for the detection of MRSA.

PO-0937

基于 EUCAST 判读标准的血培养快速药敏实验评价

颜令
重庆市人民医院

目的 评价按 EUCAST 折点，血培养阳性瓶培养细菌为临床常见革兰氏阴性杆菌时（大肠埃希菌、肺炎克雷伯菌、铜绿假单胞菌和鲍曼不动杆菌），K-B 直接药敏实验适用性。
方法 本实验共收集培养细菌为大肠埃希菌、肺炎克雷伯菌、铜绿假单胞菌和鲍曼不动杆菌血培养瓶 168 例。168 例血培养瓶从仪器取出时均做血培养直接药敏实验，同时转种至血平板，培养过夜后作 K-B 法药敏实验，血培养直接药敏实验和 K-B 法药敏实验均按 EUCAST 要求进行。分别在血培养直接药敏实验 6 小时和 8 小时对结果进行读数，并按 EUCAST RAST 折点进行结果判读。K-B 法药敏实验在培养 16-18 小时进行读数，结果按 EUCAST 折点进行判读。对血培养直接药敏实验 6 小时和 8 小时判读结果与 K-B 法药敏实验结果进行比较。
结果 在本次实验，大肠埃希菌、肺炎克雷伯菌和鲍曼不动杆菌 92%抑菌圈在 6 小时可测定，几乎所有抑菌圈在 8 小时均可测定。对于铜绿假单胞菌培养 6 小时虽然抑菌圈仍较薄，但可以勉强测量，在 8 小时则抑菌圈非常清晰。在 6h 时大肠埃希菌、肺炎克雷伯菌、鲍曼不动杆菌和铜绿假单胞菌的药敏分类一致性分别为 96.54%、97.74%、93.98%和 94.03%，8h 时药敏分类一致性分别为 98.88%、98.53%、94.63%和 96.11%。在 6 小时判读时，大肠埃希菌、肺炎克雷伯和鲍曼不动杆菌各有 2 个非常严重错误，铜绿假单胞菌有 3 个非常严重错误。在 8 小时则未出现非常严重错误。
结论 基于 EUCAST 对大肠埃希菌、肺炎克雷伯菌、铜绿假单胞菌和鲍曼不动杆菌的血培养直接药敏实验早期判读结果是可靠的。

PO-0938

儿童碳青霉烯类耐药肺炎克雷伯菌感染 80 例临床特征及分子流行病学分析

杨俊文[1]、高凯杰[1]、周娟娟[1]、李珂[1]、张嵘[2]、杨俊梅[1]
1. 河南省儿童医院郑州儿童医院
2. 浙江大学附属第二医院

目的 研究郑州大学附属儿童医院碳青霉烯类耐药肺炎克雷伯菌（CR-KPN）感染儿童临床特征及分子流行病学分析，为碳青霉烯类耐药肺炎克雷伯菌感染儿童诊治及预防提供参考。
方法 收集郑州大学附属儿童医院 2018 年 12 月--2019 年 3 月 CR-KPN 感染患儿 80 例病历信息，对其分离出的 85 株 CR-KPN 进行药敏试验、聚合酶链反应(PCR)法及测序检测碳青霉烯酶、ESBL 酶基因及多位点序列分析，并对其临床资料进行统计分析。
结果 研究期间 CR-KPN 检出率高达 52.4%；年龄分布主要以 1 岁以下新生儿、婴儿为主 74 例（92.5%），入住科室主要为新生儿诊疗中心（42 例，52.5%）及儿童重症监护室（25 例，31.3%），耐药菌株分离标本主要为呼吸道标本（67 株，78.8%）、血液（11 株，12.9%）；80 例患儿中 65 例（81.3%）应用三代头孢菌素、碳青霉烯类等广谱抗菌药物，75 例（93.8%）有入住 ICU 史，59 例（73.8%）存在气管插管等侵入性操作史；85 株细菌对 β-内酰胺类抗菌药物耐药性均超过 90%，对阿米卡星、氟喹诺酮类、四环素耐药性略低 79%左右，对复方新诺明、氯霉素等耐药率较低均低于 30%；ESBL 酶基因主要为 CTX-M（68 株，80.0%）、SHV（24 株，28.2%），碳青霉烯酶基因主要为 KPC-2（60 株，70.6%）、NDM-5（16 株，18.8%），MLST 分型主要为 ST11（60 株，70.6%）、ST188（10 株，11.8%）。
结论 儿童碳青霉烯类耐药肺炎克雷伯菌感染率较高，应当引起重视；感染患儿主要为新生儿、婴儿，入住科室主要为监护室，分布这类病人及病区应当积极采取措施有效防治；85 株肺炎克雷伯

菌对非 β-内酰胺类抗菌药物耐药性略低，碳青霉烯酶主要为 KPC，临床救治患儿可参考药敏实验及耐药机制结果合理选用抗菌药物；分离菌株亲缘关系较近，应注意控制医院感染发生。

PO-0939

Au NC@NDM-1@Au NC 电化学生物传感器的构建及超灵敏检测多重耐药菌的研究

张立群
陆军军医大学第二附属医院检验科

目的 构建金纳米笼/NDM-1 LNA 探针/金纳米笼（Au NC/NDM-1/Au NC）三明治型电化学传感器检测系统，实现临床样本中多重耐药菌（Multidrug-Resistant Organism，MDRO）的直接、快速、精准和定量检测。
方法 设计合成锁核酸(LNA)修饰的捕获探针和信号探针，两种探针的 5'端均修饰有巯基，并且与目标基因的部分序列互补。首先在电极表面静电吸附 ZnO 溶胶-凝胶及氧化石墨烯，通过恒电位沉积法将 Au NC 沉积到电极表面。然后将 NDM-1 特异性 LNA 探针固定于电极表面，当溶液中含有目标基因时，捕获探针和信号探针分别与其对应的互补序列进行杂交，形成 Au NC/NDM-1/Au NC 结构。核酸杂交复合物在电极表面发生氧化还原反应，从而产生电化学信号，利用循环伏安法（CV）、差分脉冲伏安法（DPV）和电化学阻抗图谱法（EIS)表征修饰电极的电化学行为。
结果 锁核酸探针可识别单个碱基的错配，与靶 DNA 分子结合具有很高的热稳定性和亲和力，可与待检的 NDM-1 基因直接结合，无需 PCR 扩增，在大肠杆菌等干扰细菌存在的条件下，抗干扰能力强，选择性好。该电化学生物传感器的检测线性范围为 1 pg/L~100 μg/L，检出限低至 1 pg/L。方法学比较结果显示，电化学生物传感器与 PCR 法检测结果的符合率 100 %。另外，该电化学传感器制备简单，操作简便，电极孵育和扫描检测在 30 分钟内即可完成。
结论 本研究创建的电化学检测新方法，可以直接、快速、特异、灵敏地检测 NDM-1，为多重耐药菌的快速特异提供了新策略。

PO-0940

IMP-38-producing high-risk ST307 Klebsiella pneumoniae strains

赵娟[1]、王思怡[1]、刘宁[2]、刘文恩[1]
1. 中南大学湘雅医院
2. 中南大学湘雅二医院

Objectives To investigate the prevalence of blaIMP-38 among carbapenem-resistant Klebsiella pneumoniae isolates from a tertiary care hospital in central China.
Methods CRKP collected in a Chinese tertiary hospital were detected blaIMP-38. MLST was performed for genetic background typing. PacBio and Illumina whole-genome sequencing was conducted on one representative IMP-38-producing K. pneumoniae strain.
Results Fourteen (2.72%) blaIMP-38-positive strains were detected from 515 clinical CRKP isolates. The 14 isolates all belonged to the high-risk clone ST307. Genome sequencing of an ST307 strain WCGKP294 showed that it contained a circular chromosome and two plasmids. Phylogenetic analysis placed WCGKP294 in the global ST307 cluster, WCGKP294 doesn't contain the chromosomal fluoroquinolone resistance-associated mutations and IncFIIK/IncFIBK plasmid associated blaCTX-M-15 that frequently found in other global ST307 strains.
Conclusions high-risk ST307 clone continues to acquire different antimicrobial resistance genes, which should be closely monitored.

PO-0941

青蒿琥酯联合头孢菌素类药物对 CRKP 抗菌活性的分析

晏国威[1]、向延根[2]、马小华[2]、潘建华[2]、喻容[2]、石国民[2]
1. 长沙市第一医院
2. 长沙市中心医院

为探讨青蒿琥酯(artesunate, ASN)单独或联合头孢菌素类药物对多重耐药(multidrug-resistant, MDR) 肺炎克雷伯菌的抗菌活性。本研究收集 2018 年长沙市中心医院临床分离的多重耐药肺炎克雷伯菌菌株 32 株。分为单独用药组：青蒿琥酯(ASN)组、头孢曲松钠(CRO)/头孢他啶(CAZ)组和联合应用组。采用细菌动 态生长曲线法观察青蒿琥酯联合头孢菌素类药物对多重耐药肺炎克雷伯菌的生长影响；采用微量肉汤稀释 法检测青蒿琥酯单独或联合头孢菌素类药物对多重耐药肺炎克雷伯菌的抗菌作用；采用 RT-PCR 技术检测 外排泵基因 A crB mRNA 以及其调控基因 MarA 和 A crR mRNA 的表达水平。结果显示，终浓度为 2 048 滋 g/mL ASN 联合头孢曲松钠、头孢他啶明显地抑制了多重耐药肺炎克雷伯菌的生长，曲线走向平缓；终浓度为 1 024 滋 g/mL ASN 联合头孢曲松钠、头孢他啶对多重耐药肺炎克雷伯菌的 MIC50 与单独用药组比较显著减 低，均有统计学意义(K=68.07, P 约 0.05; K=62.34, P 约 0.05)。1 024 滋 g/mL ASN 联合头孢曲松钠、头孢他啶均以 相加作用为主；2 048 滋 g/mL 青蒿琥酯和头孢曲松钠、头孢他啶联用时，可以抑制外排泵基因 A crB 的表达， 2 048 滋 g/mL 青蒿琥酯联合 512 滋 g/mL 头孢曲松钠明显抑制正向调控子 MarA 的表达，而对于负性调控子 A crR 的表达没有明显影响。青蒿琥酯能显著改善多重耐药肺炎克雷伯菌对头孢曲松钠以及头孢他啶的敏感 性，其机制可能与下调外排泵基因 A crB 的表达有关。

PO-0942

Phenotypic and Genotypic Characterization of Linezolid Resistance Coagulase-negative Staphylococci Possessing cfr-Carrying Plasmid

Fei Jiang[2]、Ping Ma[1]
1. Department of Laboratory Medicine, The Affiliated Hospital of Xuzhou Medical University
2. Department of Laboratory Medicine, the Affiliated Hospital of Xuzhou Medical University

Dependence on linezolid was recently described as significant growth acceleration of linezolid-resistant Staphylococcus epidermidis isolates upon linezolid exposure in German and Greece. This study aimed to investigate coagulase-negative Staphylococci (CNS) clinical isolates exhibiting linezolid resistance and possibility of dependence on linezolid in China. Resistance phenotypic and genotypic characterization of thirteen CNSs were investigated by antimicrobial susceptibility testing and polymerase chain reaction (PCR). Homology of isolates was estimated by pulsed field gel electrophoresis (PFGE). Characterization of cfr plasmids was carried out by S1 nuclease-PFGE, southern blotting and whole genome sequencing (WGS). Growth curve analysis was conducted with and without linezolid to determinate possibility contribution of linezolid dependence to linezolid resistance CNSs dissemination. All CNSs had linezolid MICs >256 μg/mL and were typed into three PFGE profiles. Mutation in 23S rRNA and cfr gene was identified in all isolates. Southern blotting and WGS indicated that cfr gene was located on a plasmid of 39.5 kb, revealing 99.98% and 99.99% identity to the sequence of the cfr-harbouring plasmid pSR01 and pH46-29 respectively. The cfr gene was flanked by two copies of an IS256-like element ISEnfa4 family transposase, with a downstream MerR family transcriptional regulator and a orf gene. Thirteen CNSs did not exhibit linezolid-dependent upon exposure from 8μg/mL to 128μg/mL. The clonal dissemination caused by plasmid harboring cfr gene in the CNSs need to be raised serious concerns. Linezolidine-dependent growth under linezolid selective pressure is not a common phenotype in Staphylococcus spp. at present.

PO-0943

Clinical Utility of In-house Metagenomic Next-generation Sequencing for the Diagnosis of Lower Respiratory Tract Infections and Analysis of the Host Immune Response

Si Liu、Yuyao Yin、Hongbin Chen、Hui Wang
Peking University People's Hospital

Background Only few pathogens that cause lower respiratory tract infections (LRTIs) can be identified due to limitations of traditional microbiological methods and the complexity of the oropharyngeal normal flora. Metagenomic next-generation sequencing (mNGS) has the potential to solve this problem.
Methods This prospective observational study sequentially enrolled 93 patients with LRTI and 69 patients without LRTI who visited Peking University People's Hospital in 2019. Pathogens in bronchoalveolar lavage fluid (BALF) specimens were detected using mNGS (DNA and RNA) and traditional microbiological assays. Human transcriptomes were compared between LRTI and non_x0002_LRTI, bacterial and viral LRTI, and tuberculosis and nontuberculosis groups.
Results Among 93 patients with LRTI, 20%, 35%, and 65% of cases were detected as definite or probable pathogens by culture, all microbiological tests, and mNGS, respectively. Our in-house BALF mNGS platform had an approximately 2-working-day turnaround time and detected more viruses and fungi than the other methods. Taking the composite reference standard as a gold standard, it had a sensitivity of 66.7%, specificity of 75.4%, positive-predictive value of 78.5%, and negative-predictive value of 62.7%. LRTI-, viral LRTI–, and tuberculosis-related differentially expressed genes were respectively related to immunity responses to infection, viral transcription and response to interferon-γ pathways, and perforin 1 and T-cell receptor B variable 9.
Conclusions Metagenomic DNA and RNA-seq can identify a wide range of LRTI pathogens, with improved sensitivity for viruses and fungi. Our in-host platform is likely feasible in the clinic. Host transcriptome data are expected to be useful for the diagnosis of LRTIs.

PO-0944

blaNDM-33, a novel variant of blaNDM in an Escherichia coli isolate from hospital sewage

Tao Wang、Hong Du
Department of Clinical Laboratory,TheSecond Affiliated Hospital of Soochow University,Suzhou,China

Objectives The prevalence of carbapenemase-resistant Enterobacteriaceae (CRE) has increased since the early 2000s, which represents a potential public health threat. Hospital sewage systems often become reservoirs of drug-resistant bacteria. blaNDM carrying strains pose a threat to the use of most clinically commonly antibiotics. Several variants of the NDM have recently been reported. The survey to characterize a blaNDM-33 we first found located in IncX3 plasmid from Escherichia coli in hospital sewage.
Methods The blaNDM-33 gene and its genetic background were determined by PCR and whole-genome sequencing. Conjugation experiment was performed to assess the horizontal transferability of the plasmid carried blaNDM-33. Cloning experiment was used pET28a plasmid for ligation then transformed into DH5α. The antibiotic susceptibility assay was determined by broth microdilution methods.
Results The HD6415, which we isolated from hospital sewage, showed multiple resistance and was highly resistant to meropenem, ertapenem, imipenem, ceftazidime, and gentamicin. The novel blaNDM-33 was existed in HD6415 isolate, which belonged to ST650. The blaNDM-33 gene just has a single nucleotide difference (G214A) encoding an amino acid substitution (A72T)

compared with blaNDM-5. The blaNDM-33 was located in the Tn125-related blaNDM-33 region from an IncX3-type plasmid pHD6415-NDM that can transferred horizontally. Additionally, blaNDM-33 was resistant to carbapenems, ceftazidime, piperacillin/tazobactam but susceptible to tigecycline, colistin, and aztreonam.
Conclusions This study report a novel blaNDM variant blaNDM-33, which is carried by a self-transmissible IncX3-type plasmid from an E. coli isolate in China. NDM-33 shows the similar activity against carbapenems as NDM-5. The rapid increase variants of "superbugs" from NDM-producing have become a worldwide concern for health workers. Hospital sewage systems may be a reservoir of multidrug-resistant bacteria, increasing the prevalence of drug-resistant bacteria.

PO-0945

ST11 型碳青霉烯耐药高毒力肺炎克雷伯菌分子流行病学研究

王伟
徐州医科大学附属医院

目的 对徐州市某院 ST11 型碳青霉烯耐药高毒力肺炎克雷伯菌进行分子流行病学调查。
方法 收集徐州医科大学附属医院 2018 年 1 月至 2018 年 12 月临床分离的 26 株碳青霉烯耐药高毒力肺炎克雷伯菌（carbapenemase resistant hypervirulent *Klebsiella pneumoniae* , CR-hvKP）。PCR 检测常见的碳青霉烯酶耐药基因 (*bla*$_{KPC}$, *bla*$_{NDM}$, *bla*$_{IMP}$, *bla*$_{OXA-48}$, *bla*$_{VIM}$)，超广谱 β-内酰胺酶基因 (bla$_{CTX-M}$, bla$_{TEM}$, bla$_{SHV}$), 荚膜血清型基因 (K1, K2, K5, K20, K54, K57) 和毒力基因 (rmpA, kfu, aerobactin, entB, ybtS, fimH, mrkD, allS)。采用多位点序列分型和脉冲场凝胶电泳对 CR-hvKP 进行同源性分析。
结果 26 株 CR-hvKP 菌株均为多重耐药菌，对 b 内酰胺类、喹诺酮类、氨基糖苷类抗菌药物均表现为 100%耐药，对四环素耐药率为 69.2%，未发现对替加环素和多粘菌素耐药的菌株。26 株 CR-hvKP 均携带碳青霉烯酶耐药基因，主要携带 *bla*$_{KPC-2,}$ 占 96.2% (25/26)。K1、K2 阳性率分别为 53.8%(14/26)和 7.7%(2/26)。常见毒力基因携带率均超过 50%，其中 entB (100%, 26/26), aerobactin (92.3%,24/26), mrkD (92.3%, 24/26), fimH (88.5%, 23/26), rmpA (80.8%, 21/26), iron (80.8%, 21/26), ybtS (57.7%, 15/26) 和 allS (57.7%,15/26)。在 26 株 CR-hvKP 中共鉴定出 5 种 ST 分型，以 ST11 为主，占 87.5%（21/26）。PFGE 结果显示， 26 株 CR-hvKP 分为 7 个不同的 PFGE 簇群。簇群 A 和 C 为主要的簇群，分别占分离株的 19.2%（5/26）和 53.8%（14/26）。同一时期内，在某重症监护室病房 5 位患者中分离出了 7 个属于簇群 C 的 ST11 分离株，且具有相同的耐药表型、碳青霉烯耐药基因，这表明在这个病区局部暴发了 CR-hvKP 感染。
结论 本院流行的 CR-hvKP 多是 ST11 型由质粒介导的产 KPC-2 酶的 CRKP 菌株，耐药机制与 CRKP 菌株高度相似，局部存在暴发流行，应当实施一种基于分子生物学检测方法的实时、有效的防控手段降低此类细菌的流行。

PO-0946

通过人群规模的横断面及队列研究发现肠道菌群与高血压的流行现状与未来风险均显著相关

郑慧敏[1]、何彦[1]、李泽文[1]、吴为[2]、周宏伟[1]
1. 南方医科大学珠江医院
2. 广东省疾病预防控制中心

目的 高血压患者肠道菌群发生显著的变化，且多项动物研究表明肠道菌群与高血压存在因果关系，可能是高血压的全新风险因子和干预靶标，但菌群在高血压中是否发挥关键作用尚需流行病学数据的支撑。本研究采用横断面及纵向队列研究数据，尝试回答两个问题：（1）高血压流行与肠道菌

群均存在显著的地域差异，那么菌群的地域差异与高血压流行现状是否显著相关？（2）肠道菌群与未来的高血压发病风险是否显著相关？

方法 通过分层整群随机抽样的方式调查广东省 14 个地区（包括 3 个高收入地区和 11 个中低收入地区）共 5379 人的高血压流行状况，采用统一标准化流程测量血压等体检指标以及全程冷链收集粪便样本，通过 16S rRNA 基因测序鉴定粪便肠道菌群。另外纳入一项针对广州市中老年社区人群的纵向随访队列，并对其中正常血压人群进行随访，探究肠道菌群与高血压发病风险的关联。

结果 研究首先通过 5379 人的横断面研究，分析正常血压、高血压前期、未经治疗高血压、经治疗高血压四类人群，发现高血压存在等级递进式的菌群变化规律，其中以大肠杆菌、拟杆菌、普氏菌、阿克曼菌等为主要变化特征，进而建立高血压菌群紊乱指数（HDI）来量化紊乱程度，HDI 与高血压的比值比（OR）为 1.82（95% CI: 1.68 to 1.97; P<0.001）。横断面研究所调查 14 个地区的平均 HDI 为 0.38 至 0.55，表明由于地域差异的存在，部分地区的肠道菌群比其他地区更具有高血压紊乱的特征，即“地区性菌群紊乱”，且地区 HDI 与高血压患病率显著相关（R=0.85，P<0.001），HDI 解释了 34%广东省高收入地区和中低收入地区的高血压患病率差异，高于年龄、水果摄入等因素。纵向队列共入组 1173 人，其中 309 人在入组时血压正常并完成平均 2.95 年的随访，分析发现在校正了年龄、性别和 BMI 后 HDI 与未来发生前高血压/高血压的风险显著相关（HDI 上四分位相对下四分位高血压风险：OR: 2.64, 95% CI: 1.13 to 6.12，P = 0.024；HDI 四分位由低到高，高血压风险逐渐上升, P-trend = 0.027）。

结论 本研究首次发现肠道菌群与高血压的流行现状及未来风险均显著相关，为研究菌群与高血压的关系提供了重要的人群支撑数据。同时研究也是首次提出地域性菌群紊乱（geographical dysbiosis）这一概念，提示靶向地区性菌群紊乱开展人群菌群干预可能是控制慢病流行的潜在公共卫生手段。

PO-0947

Co-occurrence of fosA5, blaSHV-145 and blaOXA-48 among a Klebsiella pneumoniae high-risk ST16 from a tertiary hospital in China: focusing on the phylogeny of OXA-48 genes from global Klebsiella pneumoniae isolates

xiaoli cao
Nanjing Drum Tower Hospital

An imipenem intermediate Klebsiella pneumoniae isolated from blood culture was subjected to whole genome sequencing analysis and the global evolutionary relationship of blaOXA-48 gene was constructed. We found that this OXA-48-producing isolate co-carried oqxAB, fosA5, and blaSHV-145, and MLST (Multi-locus sequence typing) assigned this isolate into an international high-risk clone ST16. Further analysis showed that fosA5, oqxAB, and blaSHV-145 were found in chromosome, whereas blaOXA-48 was carried on a conjugative IncL/M plasmid. The phylogeny of OXA-48 genes from global Klebsiella pneumoniae isolates displayed 2 clades, indicating a simple evolutionary history and a strong transmission ability of OXA-48-producing K. pneumoniae.To the best of our knowledge, this is the first report on the co-occurrence of fosA5, blaSHV-145 and blaOXA-48 among the K. pneumoniae ST16 in China and for the first time we prescribed the blaOXA-48 evolutionary phylogenomic of global -producing K. pneumoniae.

PO-0948

Exploring Microbial Diversity in Environment of Aseptic Ward with 16S rRNA Sequencing

Huafang Sheng、Liping Qu、Dingqiang Chen
Microbiome Medicine Center, Division of Laboratory Medicine, Zhujiang Hospital, Southern Medical University, Guangzhou, China

Exploring microbial community in hospital environment is important for patients' health.This study aims to explore the environmental microbial community of aseptic wards in a large teaching hospital. We collected samples from floors and walls of 6 aseptic wards and hands of patients, and set control samples for sampling process, DNA extraction and PCR during experimental process. Through the alpha and beta diversity analysis, we found that bacteria of the control group and the ward group were clustered separately, and each group had a unique microbial community structure. Most of the sequences in control group were derived from commonly reported contaminating bacteria from environment and showed low abundance in ward groups. While in ward group, *Staphylococcus* (14.23%) was significantly abundant. Specifically speaking, *Acinetobacter* (25.67%), *Streptococcus* (6.28%) and *Enterococcus* (14.26%) were mostly found in floor, wall and hand groups respectively. This study was helpful for revealing reliable microbiome of low biomass environment by setting control samples in every steps.

PO-0949

Characterization of fosfomycin resistance and molecular epidemiology among carbapenem-resistant Klebsiella pneumoniae strains from two tertiary hospitals in China

Haichen Wang 、Changhang Min、Mingxiang Zou
Xiangya hospital, Central South University

Background Fosfomycin has been proven to be a vital choice to treat infection caused by multidrug resistance bacteria, especially carbapenem-resistant *Klebsiella pneumoniae* (CRKP). However, fosfomycin resistant cases has been reported gradually. In this study, we reported the fosfomycin-resistant rate in CRKP strains and further revealed the molecular mechanisms in resistance gene dissemination.
Results A total of 294 non-duplicated CRKP strains were collected. And 55 fosfomyin-resistant strains were detected, 94.5% of which were clustered to sequence type (ST) 11 by PCR followed up sequencing. PFGE further revealed two major groups and four singletons. The positive rates of genes responsible to fosfomycin and carbapenem resistance were 81.8% (*fosA3*), 12.7% (*fosA5*) and 94.5% (bla_{KPC-2}), respectively. Genomic analysis confirmed insertion sequence (*IS*) 26 was the predominant structure surrounding *fosA3*. The *fosA3* genes in six isolates were located on plasmids which were able to transfer to *E. coli* J53 recipient cells by means of conjugation.
Conclusions Although the resistant rate of CRKP to fosfomycin is relatively low in our area, considering its gene is located on transferrable plasmid and inserted in IS structure, continuous monitoring is still needed.

PO-0950

基于比较基因组学研究不同来源表皮葡萄球菌的基因组特征以及识别眼源性菌株标志性致病基因

林舒丹
温州医科大学

目的 表皮葡萄球菌常定植于人类皮肤、粘膜以及眼表，是医院感染最常见病原菌之一。我们通过泛基因组分析和全基因组分析了解包括眼内等不同来源的表葡基因组特征，明确其致病性与生物膜形成以及耐药性的关系；经系统发育分析揭示不同来源表葡的进化关系；利用比较基因组学分析毒力基因和耐药基因在不同来源的表葡中富集情况，寻找与眼内炎致病相关的标志性基因。
方法 从眼外伤引起的感染性眼内炎患者中分离 11 株表葡，对其进行全基因组测序，获得外伤性眼内炎来源的表葡全基因组；加以整合公共数据库不同来源的表葡全基因组，最后共达 187 株。按不同生态位来源分为眼、呼吸道、皮肤、血液，以及宿主不同健康状态分为疾病组和健康组。用 BPGA 进行不同来源菌株的泛基因组分析；构建基于核心 SNP 位点的最大似然树；对所有基因组进行 ST、SCCmec 分型，毒力、耐药性分析，并分组进行 Fisher'exact 检验，FDR 校正，筛选与表葡致病、生物膜形成显著相关的基因，观察其在不同来源菌株中富集情况，寻找与感染性眼内炎相关的标志性基因，并进行 PCR 验证。特定耐药基因进行体外药敏试验验证。
结果 表皮葡萄球菌是一个开放的基因组，单独眼部来源的表皮葡萄球菌可以形成相对稳定的核心基因组。从进化上看，表皮葡萄球菌分为两个群体，健康皮肤来源分离株的集中于 I 簇，ST2 和 ST5 型的临床分离株集中于 II 簇，眼源性分离株较分散，且 ST 分型多为未知。我们筛选多个与疾病来源表皮葡萄球菌相关的关键基因，其中 icaABCDR，sdrF,sdrG,fbe，Uhpt 和 essD 被鉴定为毒力基因。生物膜形成相关的基因 icaABCDR、pgaC 在眼源性菌株中并不富集，在血液来源的菌株中显著富集，而 sdrG 在眼部显著富集，转录调控基因 lrpC,CysL 存在于所有感染性眼内炎来源的表葡中。分析菌株的耐药性基因发现，喹诺酮类基因 norA 存在于所有菌株中，94/187 株为 mecA 阳性菌，提示为耐甲氧西林表皮葡萄球菌，且 96.8%集中于进化分支 II 簇中，眼源菌株中 mecA 基因携带率 5/11，与体外药敏试验结果一致。
结论 表皮葡萄球菌的泛基因组呈开放性，从进化上看有两个致病差异显著的来源；本研究中分离的眼内炎相关表葡虽然在进化上较分散，但与临床致病菌株距离接近，证明其致病性；引起眼内感染的表葡与生物膜形成无直接关系，sdrG,CysL 或作为眼致病性表葡的标志性基因；菌株 mecA 基因携带率与体外药敏试验一致，且耐甲氧西林表皮葡萄球菌的致病性更强。

PO-0951

Genomic Features and Comparative Genomic Analysis of Streptococcus sp. v1. nov., Isolated from an Endophthalmitis patient

Yutong Kang[1]、Yongliang Lou[2]、Meiqin Zheng[1]
1. Eye Hospital of Wenzhou Medical University
2. 温州医科大学

Endophthalmitis is an acute inflammatory intraocular condition that can cause permanent vision loss. The treatment strategy and visual outcome partly depend on identification of the agents of pathogens. In the study, metagenomic sequencing was conducted to investigate the microbial and antibiotic resistance genes (ARGs) composition in vitreous (intraocular body fluid) of an endophthalmitis patient, whose progresses rapidly and accompanied by severe pain. Metagenomic sequencing data revealed that the vitreous sample was predominated by Streptococcus, with a low-diversity microbiome in the vitreous. Main ARG types contained Beta-

lactam, macrolide-lincosamide-streptogramin, and multidrug. At last, Metagenome-assembled genome sequence of Streptococcus sp. v1. nov. was isolated. The Tetra Correlation Search (TCS) analysis uncovered that the closest relative of the Streptococcus sp. v1. nov. was Streptococcus mitis SK321. Pan/core genome analysis for Streptococcus sp. v1. nov. and TCS top 25 hits strains revealed that most unique genes of Streptococcus sp. v1. nov. were linked to ABC Transport system, which could indicate unique virulence and pathogenic potentials of Streptococcus sp. v1. nov. In addition, a total of 7 virulence factors were identified, and the overwhelming of them were classified into “Offensive virulence factors”. The high pathogenicity of Streptococcus sp. v1. nov. could be a reason for the patient’s rapid disease progression. Our study was first isolated an ocular pathogen with highly virulent based on metagenomic sequencing and bioinformatics analysis, which has important reference value for revealing the composition and genome characteristics of pathogens in endophthalmitis patient in the future.

PO-0952

碳青霉烯耐药肠杆菌临床特征和分子流行病学：一项单中心前瞻性队列研究

黄世峰
重庆医科大学附属第一医院

背景 旨在描述中国西南地区碳青霉烯耐药肠杆菌（CRE）的临床特征和分子流行特征。
方法 我们进行了一项前瞻性队列研究，纳入 2018 年 6 月 1 日至 2019 年 12 月 31 日期间被诊断患有 CRE 感染患者的 CRE 菌株，并收集患者的基本信息。对 CRE 菌株进行了菌种鉴定和分子鉴定，包括菌株分型。采用多位点序列分型(MLST)对不同分离时间的菌株进行分子分型。使用 PHYLOViZ 软件分析菌株间的进化关系，评估菌株间的序列类型（ST）和相关流行病学数据之间的关系。
结果 在研究期间共纳入 128 株菌株。其中 CRE：产碳青霉烯酶的肠杆菌（CPE）71 株（55.5%），非 CPE 57 株（44.5%）。最常见的耐碳青霉烯肠杆菌株为肺炎克雷伯菌(69 株,53.9%)。肺炎克雷伯菌最常见的序列型别是 ST11 型（43 株，33.6%）。ST11 型肺炎克雷伯菌主要产 KPC-2。在 CRE 感染的 128 位患者中，CPE 和非 CPE 感染患者的 DOOR 没有显著性差异。在感染的第 30 天，这些患者中有 35 名（27.3%，95%CI20-35）死亡。在大多数产生 KPC-2 的肺炎克雷伯菌中，都鉴定出了克隆关系。
结论 CPE /非 CPE 鉴定和 CRE 耐药机制的鉴定对于更好地指导 CRE 感染患者的临床管理至关重要，特别是在有 ICU 入住史和有肝病史的患者中。不论是否产碳青霉烯酶，CRE 感染均与高死亡率和不良后果有关。

PO-0953

内蒙古包头地区金黄色葡萄球菌致病机制及分子流行病学研究

李雅倩、胡同平
内蒙古科技大学包头医学院第一附属医院

目的 了解内蒙古包头地区临床上金黄色葡萄球菌的分布情况、耐药情况、分子流行病学情况以及毒力基因携带情况，为预防和治疗金黄色葡萄球菌引起的感染提供参考。
方法 1.收集 2017 年 1 月-2019 年 12 月内蒙古包头地区 11 所上报全国细菌耐药监测网的三级医院的金黄色葡萄球菌临床分离株，对数据采用 WHONET 5.6 软件和 SPSS 20.0 软件进行统计分析。2.对用全自动微生物鉴定仪初筛为甲氧西林耐药的金黄色葡萄球菌(Methicillin-resistant Staphylococcus aureus ,MRSA)采用头孢西丁纸片扩散法、聚合酶链式反应（Polymerase chain

reaction，PCR）技术检测常见的耐药基因 mecA。随机选取 MRSA 25 株和甲氧西林敏感的金黄色葡萄球菌（MSSA）25 株作为试验菌株，并采用 PCR 技术进行葡萄球菌蛋白 A 基（SPA）因分型和多位点序列分型（MLST）,采用多重 PCR 技术进行葡萄球菌染色体 mec 盒子(SCCmec)分型，MLST 结果用 eBURST 软件进行遗传信息分析。3.对上述 50 株金葡菌通过 PCR 技术检测以下几种常见的毒力基因：hla、hld、pvl、lukED、seh、seb、eta、tsst。

结果 1.三年共收集金黄色葡萄球菌 2562 株，共检出 MRSA 347 株，检出率为 13.5%，主要的标本来源为伤口分泌物占 39.6%（1015/2562）。万古霉素、利奈唑胺和替加环素的敏感率为 100%，MRSA 的耐药率要显著高于 MSSA 的耐药率，且具有统计学意义（P＜0.05）。2.MLST 分型的优势型别为 ST59 共 26 株，其中 MRSA 15 株，MSSA 6 株；SPA 分型的优势型别为 t437 为主共 19 株，其中 MRSA 13 株，MSSA 6 株；SCCmec 分型以 SCCmec IVa 为主共 14 株。3. 溶血素 hld 和 hla 的检出率为 100%，表皮剥脱毒素 eta 的检出率为 0，至少同时携带 2 种毒力基因，同时携带 3 种以上毒力基因的占 82%。

结论 1.该地区金葡菌主要分离自皮肤软组织和呼吸道标本，与国内外报道一致；MRSA 的检出率较低，未发现耐万古霉素、利奈唑胺和替加环素的菌株。2.本地区 MRSA 的主要流行株为 ST59-MRSA IVa-t437,与国内流行趋势相同，MSSA 的主要流行株为 ST59 -t437。3.该地区 MRSA 的毒力较强，耐药趋势严峻，临床应严格监测耐药菌的产生，合理使用抗菌药物。

PO-0954

SARS-CoV-2 receptor ACE2 is expressed in human conjunctival tissue, expecially in diseased conjunctival tissue: the evidence of COVID-19 infection by ocular surface

Shengjie Li、wenjun cao
Eye & ENT Hospital, Shanghai Medical College, Fudan University

Coronavirus disease 2019 (COVID-19) virus has currently caused major outbreaks worldwide. The virus is mainly transmitted through respiratory droplets and by close contact with infected individuals. Angiotensin-converting enzyme 2 (ACE2) is a major cellular-entry receptor for the COVID-19 virus, whether it is expressed by the conjunctival tissue is largely unknown. In this study, human conjunctival tissues from 68 subjects were obtained, which included 10 subjects with conjunctival nevi, 20 subjects with conjunctivitis, 9 subjects with conjunctival papilloma, 16 subjects with conjunctival cyst, 7 subjects with conjunctival polyps, and 6 ocular traumas as normal subjects. Expression of ACE2 was evaluated by immunohistochemistry, immunofluorescence, reverse transcriptase-quantitative polymerase chain reaction assay, and western blot assay. We observed the expression of ACE2 by conjunctival tissues, expecially in conjunctival epithelial cells. ACE2 was also expressed in the conjunctival lamina propria lymphocytes and vascular endothelial cells. ACE2 was significantly ($p<0.001$) overexpressed in conjunctival cells obtained from subjects with conjunctivitis, conjunctival nevi, conjunctival papilloma, conjunctival cyst, and conjunctival polyps epithelial cells when compared to that in conjunctival epithelial cells obtained from control subjects. A significant difference in ACE2 expression between conjunctivitis tissues and other diseased conjunctival tissues was observed ($p<0.001$). ACE2 is present in conjunctival epithelia, especially in patients with diseased conjunctiva, which might provide a possible route of entry for the COVID-19 virus. Thus, increase the awareness of eye protection is necessary.

PO-0955

The mechanism of destroyed intestinal flora on EBV infected NPC through regulating SCFAs and inflammatory factors

Haiye Jiang、Xinmin Nie
The Third Xiangya Hospital of Central South University

Background Nasopharyngeal carcinoma (NPC) is a malignancy of nasopharynx with a sophisticated etiology that mostly arisen in southern China. There is a consensus that the occurrence of NPC is associated with Epstein-Barr virus (EBV) infection. Current studies uncovered that the imbalance of intestinal microbiota is associated with NPC. Meanwhile, it is found that the metabolites of intestinal microbiota, such as short chain fatty acids can promote the carcinogenesis of EBV.
Methods To compare the differences in intestinal microbiota compositions and biological functions among 10 patients with EBV-infected NPC (EBV_I), 25 patients with NPC who haven't detected EBV-DNA (EBV_0) and 25 healthy controls (HC), we compared the intestinal microbiota DNA sequencing and hematological testing results between every two groups using bioinformatic methods. Meanwhile, short-chain fatty acids (SCFAs) were used to treat EBV-infected NPC cell lines.
Results Compared to EBV_0 and HC group, the intestinal microbiota structures of the patients in the EBV_I showed significant changes. In EBV_I, Ruminococcus gnavus, Clostridium symbiosum, Clostridium hathewayi and Clostridium ramosumwere significantly increased, while Gemmiger formicilis and Alistipes onderdonkii were significantly decreased. Several kinds of SCFAs and inflammatory factors were significantly increased in EBV_I, and it was found that these SCFAs and inflammatory factors were significantly positively correlated with bacteria. R. gnavus was significantly positively correlated with EBV-DNA (P=0.035, R=0.27), propionic_acid (P<0.001, R=0.64), butanoic_acid (P<0.001, R=0.55), valeric_acid (P<0.001, R=0.66), TNF_alpha (P<0.001, R=0.70), while was significantly negatively correlated with IFN_gama (P<0.001, R=0.53). After treated with SCFAs, EBV-DNA was increased significantly EBV-infected NPC cell (P<0.01).
Conclusion This research discovered that EBV infected NPC were associated with structural imbalances in the intestinal microbiota, with R. gnavus and opportunistic pathogens that promoted the elevation of SCFAs and inflammatory factors being significantly increased, while probiotics significantly decreased. Based on these findings, we can regulate the target intestinal flora and its metabolites to improve the occurrence and development of NPC.

PO-0956

mNGS 检测技术在儿童重症社区获得性肺炎中的应用

张鹏、刘勇、邹红雁、姜艳芳
吉林大学第一医院

目的 分析宏基因组二代测序技术（metagenomics next-generation sequencing, mNGS）在儿童重症社区获得性肺炎中的诊断价值。
方法 选取 2018 年 1 月至 2021 年 3 月在吉林大学第一医院儿科住院治疗的 37 例重症社区获得性肺炎患儿，留取肺泡灌洗液（Bronchoalveolar lavage fluid，BALF）标本同时进行 mNGS 病原检测和传统病原检测。比较两种技术的病原体检出结果及阳性率。
结果 37 例患儿的 BALF 同时进行传统病原检测和 mNGS 检测,细菌检出率 mNGS 明显高于传统检测方法（75.7% vs. 20.6%）,差异有统计学意义（P＜0.05）。病原菌阳性率与 2 种以上病原体感染上,mNGS 明显高于传统检测方法（94.6%vs. 54.1%, 42.9% vs. 8.1%）,差异有统计学意义

（P<0.05）。在 mNGS 检测与传统检测结果不一致的病原体、细菌与真菌中,培养阴性多于 mNGS 阴性结果。在复合感染中,mNGS 明显高于传统检测方法（67.6%vs. 24.3%）,差异有统计学意义（P<0.05）。

结论 在儿童重症社区获得性肺炎中，BALF mNGS 对病原菌的检出率高于传统检测方法，尤其是复合感染时诊断价值更高，能够对重症社区获得性肺炎提供早期诊治依据。

PO-0957

CRISPR 核酸检测技术与常规实验室检查诊断儿童结核病的效能分析

吕纯阳、李明远、江咏梅
四川大学华西第二医院

目的 探究和比较基于规律间隔成簇短回文重复序列（Clustered regularly interspaced short palindromic repeats，CRISPR）的新型核酸检测技术和常规实验室检查方法诊断儿童结核病的诊断效能

方法 纳入四川大学华西第二医院疑似结核病住院患儿 143 人，采集入院用药前第一次标本提取核酸，协同阴阳性对照以 IS6110 插入序列为靶标，经重组酶聚合酶扩增（RPA）后以 Cas12a 检测，制定前后荧光变化的差值或倍数值阴阳性判断 cutoff 值，以微生物学阳性和临床诊断为标准分别计算 CRISPR 技术的灵敏度、特异度。再计算 CRISPR 技术在不同部位结核、不同治疗情况结核下的诊断阳性率，相同标本进行 qPCR、MGIT 液体培养、涂片抗酸染色并计算上述诊断效能指标，与 CRISPR 技术比较。

结果 以诊断为标准，CRISPR 技术差值和倍值敏感度均为 73.3%，高于 qPCR（48.8%）、MGIT 液体培养（17.4%）、涂片抗酸染色（3.5%）。CRISPR 技术差值和倍值特异度分别为 83.9%和 89.3%，低于 MGIT 液体培养、涂片抗酸染色（均为 100%）。该技术在有微生物证实的患儿中灵敏度提升为 81.3%，特异度则为 53.2%，低于 qPCR（67.5%）。CRISPR 技术在肺泡灌洗液标本中灵敏度最高（差值 78.9%，倍值 89.5%），高于 qPCR(78.9%)和微生物学方法。该技术在痰液中的灵敏度为 73.3%、80.0%，在胃液中的灵敏度为 73.5%、67.6%，高于 qPCR 和微生物学方法。肺外标本 CRISPR 技术灵敏度为 66.7%。CRISPR 技术在呼吸道、胃液、肺外标本的特异度为 75~90.5%，低于微生物学方法。CRISPR 技术（差值）在肺结核、肺外结核、肺内外均结核中的阳性率分别为 71.1%、75%、75.8%，倍值则为 71.1%。87.5%、72.7%。qPCR 上述阳性率为 37.5%~60.6%，培养则为 13.3%~37.5%。CRISPR 核酸检测技术（差值）在初治、复治结核中阳性率为 72.1%、76%，倍值则分别为 70.5%、80.0%，均高于 qPCR 和微生物学方法。

结论 基于 CRISPR 的核酸检测技术灵敏度高于常规实验室诊断方法，特异性较好，是诊断儿童结核病较好的新型实验室检查方法。

PO-0958

益生菌来源的肽聚糖水解酶靶向 MDP-NOD2 调节肠稳态并治疗炎症性肠病

高杰、周宏伟
南方医科大学珠江医院

背景和目标 益生菌因其调节肠稳态的作用而具有治疗的炎症性肠病的潜力，但活菌定植能力差异、作用机制不明等原因限制其临床疗效。近年研究发现益生菌的代谢产物（后生元）也能发挥类似益

生活菌的功效，成为治疗炎症性肠病药物开发的重要方向。因此，鉴定具有治疗作用的后生元，具有重大临床需求。
方法和结果 通过系统文献检索，筛选出 4 种在临床研究中对炎症性肠病具有治疗效果的益生菌单菌（鼠李糖乳杆菌，干酪乳杆菌，副干酪乳杆菌，罗伊氏乳杆菌）；分析了这 4 个菌种下 10 个菌株的基因组，发现其中 8 株菌均编码一种分泌型的蛋白（相似度>75%），这里命名为 L.PH。利用多个肠炎模型及前期发表的结肠蛋白递送系统，证明了 L.PH 对肠炎小鼠的治疗效果。进一步生物信息学分析及实验鉴定发现 L.PH 是一种肽聚糖水解酶，能高效水解大分子肽聚糖生成胞壁酰二肽（MDP），一种 NOD2 配体。通过构建活性位点突变蛋白，及产物回补实验，明确了 L.PH 通过水解肽聚糖产生 MDP 改善肠炎。最后通过 NOD2-/-小鼠，阐明了 L.PH 通过 MDP-NOD2 调节肠稳态并治疗肠炎的机制。
结论 我们发现了 L.PH 是多个益生菌共有效应蛋白，并阐明了其靶向 MDP-NOD2 调节肠稳态并治疗炎症性肠病的效果及机制。

PO-0959

Resistance mechanism of Carbapenem-resistant Klebsiella pneumoniae in a tertiary hospital in Hunan, China

Xuan Liu、Wenen Liu、Mao Zhou、Xin Li、Qianqian Qi、Zijuan Jian、Xia Chen、Qun Yan
Department of Clinical Laboratory Xiangya Hospital, Central South University

Background The increasing prevalence of carbapenem-resistant Klebsiella pneumoniae (CRKP) brings severe challenges to the clinical anti-infection diagnosis and treatment. However, there were few comprehensive analyses of multiple resistance mechanisms in Central and Southern China, especially lack of research on porin deficiency. This study aimed to analyze the multiple antibiotic resistance mechanisms of CRKP and characterize CRKP isolates.
Methods The CRKP isolates at a tertiary hospital in central China from January 2018 to December 2018 were collected. Clinical characteristics and drug resistance of CRKP in this study were analyzed. Sixteen kinds of carbapenem resistance related genes including blaKPC-2, blaNDM-1, blaVIM, blaIMP, blaGES, blaOXA-48, blaCIT, blaCTX-M-9, blaDHA, blaCTX-M-25, blaACT, blaMOX, blaFOX, blaEBC, OmpK-35 and OmpK-36 were detected by polymerase chain reaction (PCR). Comparative analysis of distribution of resistant genes in departments were performed.
Results A total of 152 CRKP strains were collected, which had low resistant to tigecycline (3/152, 2.0%), amikacin (74/152, 48.7%), trimethoprim-sulfamethoxazole (75/152, 49.3%). The PCR detection rates of blaKPC-2 (119/152, 78.3%) ranked top one in resistance genes and negative rate of OmpK35 / 36 was 21.1% (32/152). The distribution of blaKPC-2, blaNDM-1 and blaCIT were different between departments ($p<0.05$), and pediatric wards had a high carrying rate of blaNDM-1. Production carbapenemase may be the main resistance mechanism.
Conclusions The main resistance genotypes of CRKP are blaKPC-2 (119/152,78.3%). And the resistance mechanism of most CRKP may be carbapenemase production. And some departments, such as pediatrics, are prevalent in NDM-KP, which should be paid great attention to prevent its further spread in hospitals.

PO-0960

高通量测序技术在结核性脑膜炎诊断中的临床应用研究

林敏涛、邓颖颖
南方医科大学珠江医院

目的 探究高通量测序技术（mNGS）在结核性脑膜炎（TBM）诊断中的价值。

方法 回顾性纳入 2017 年 8 月至 2019 年 5 月本院外送进行的 mNGS，筛选出送检标本类型为脑脊液（CSF）的病例进行分析，以 2010 年 TBM 诊断标准作为诊断依据，查阅并记录其辅助诊断结果，比对 mNGS、抗酸染色法、培养法、结核分枝杆菌核酸定量（TB-PCR）、WBC 镜检、CSF 糖、CSF 蛋白检查结果，计算出灵敏度（Se）、特异度（Sp）、阳性似然比（+LR）、阴性似然比（-LR）的差异，并比较不同方法的诊断价值。
结果 观察组 mNGS 阳性率 100%，Se、Sp、+LR、-LR 分别为 100%、88.9%、9.01、0，均优于其它检验方法。
结论 CSF 的 mNGS 检测可作为早期诊断 TBM 的重要指标。

PO-0961

一种艰难梭菌检测、治疗后动态监测和预测高毒力流行的多重数字 PCR 方法的建立

秦娟秀、李敏
上海交通大学医学院附属仁济医院

目的 艰难梭菌是抗生素相关腹泻最重要致病菌，且国内流行菌株与国外多不同。然而，目前缺乏高灵敏的动态监测和高毒力菌株预测方法。因此拟通过新建一种多重数字 PCR 方法（CD-DDPCR），进行艰难梭菌检测、治疗后动态监测和预测高毒力菌株流行。
方法 本研究搜集三家医院（上海交通大学医学院附属仁济医院，上海杨浦区中心医院和上海交通大学医学院附属同仁医院）腹泻标本 50 例，同时进行艰难梭菌谷氨酸抗原和毒素（A+B）检测，毒素培养、艰难梭菌数字 PCR 方法和艰难梭菌荧光 PCR 方法检测。艰难梭菌数字 PCR 和艰难梭菌荧光 PCR 并进行相关统计学分析。
结果 成功建立艰难梭菌多重检测体系，通过不同毒素型别的艰难梭菌和 11 种临床常见致病菌检测，证明该体系没有交叉反应，有很好的特异性。菌株 CFU/mL 从 105 to 102 ，DDPCR DNA 的含量（copies/ul）与其有很强的线性关系（R2>99.5）；同时将新的方法学和传统毒素培养及 GDH 检测方法学比较，灵敏度、特异性和符合率分别为 94.4%、87.5%和 90.0%。且与艰难梭菌感染的严重性呈正相关。通过对一例病人的动态监测，发现该方法能更早法发现艰难梭菌的再感染。同时本方法也检测一株高毒力菌株（tcdA+,tcdB+、ctdB+和 tcdC18bp 缺失），MLST 测序方法鉴定为 ST197。
结论 新建的同时检测艰难梭菌毒素 A，毒素 B 和二元毒素 B 以及调控基因 tcdC 多重 PCR 体系，能更灵敏的进行艰难梭菌检测、治疗后动态监测和预测高毒力菌株流行。

PO-0962

临床常见多重耐药阴性菌主动筛查方法的建立

徐成钰
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 所谓的多重耐药菌指的是三种或以上的抗菌药物同时存在耐药的菌株。抗生素的广泛使用以及临床上常见的介入治疗，使得细菌的耐药性越来越高，甚至出现了“超级细菌”，其中碳青霉烯耐药的革兰阴性杆菌最为常见，包括 CRE、耐碳青霉烯类鲍曼不动杆菌、亚胺培南耐药铜绿假单胞菌、美罗培南耐药的铜绿假单胞菌和唑类耐药念珠菌等。越来越多的研究把主动筛查作为防控临床常见多重耐药阴性菌出现的一项干预措施。分析探讨临床常见的多重耐药阴性菌的种类并建立主动筛查机制，及时为临床提供精准的检验报告和用药指导。

方法 对从苏州某三甲医院各科室中采集的临床标本，如咽拭子、肛拭子和痰液等进行培养。利用不同菌株发酵产物和对药物的敏感性的不同，将其置于不同的药物选择培养基中培养，观察其生长情况，进行筛查。EDTA 作为 MBL 的络合剂，可以对金属酶进行筛选。
结果 常见的多重耐药阴性菌有耐碳青霉烯类的肠杆菌科、铜绿假单胞菌还有其他碳青霉烯耐药阴性杆菌如洋葱伯克霍尔德菌、鲍曼不动杆菌、嗜麦芽窄食单胞菌、和黄杆菌。加有美罗培南的中国蓝平板中可筛选出耐碳青霉烯类肠杆菌科，十六烷三甲基溴化铵培养基中加入亚胺培南或者美罗培南可以筛查出铜绿假单胞菌。
结论 通过对检出多重耐药菌的分析，为控制医院院内感染和临床合理使用抗菌药物提供了可靠的科学依据。

PO-0963

一种用于快速检测隐球菌脑膜炎病原体的环介导等温扩增微流体模块

田月如
复旦大学附属华山医院

目的 隐球菌性脑膜炎具有高发病率和高死亡率，对全球构成公众威胁。目前用于隐球菌性脑膜炎诊断的整合性检测信息仍然有限。本研究开发一种具有实用性的整合性微流体模块用于隐球菌性脑膜炎诊断。
方法 我们采用 4 个重复过滤膜结构来提高目标捕获并简化富集过程，结合裂解酶消化、碱裂解和加热方法来优化微流控模块上隐球菌的核酸提取，联合环介导等温扩增检测单元进行靶标基因扩增，最后选择便携式紫外线手电筒照射扩增产物以获得肉眼可见的视觉检测结果。
结果 整合性检测模块降低了直接处理隐球菌样本的暴露风险。它无需任何额外的仪器，提供了一种简单、可靠且高效的检测备选方法。
结论 该整合性微流控模块具有实用前景，可作为辅助方法用于疾病诊断。有望在隐球菌性脑膜炎治疗期用于辅助疗效评估和随访。

PO-0964

Genetic Characteristics of OXA-48-producing Enterobacterales from China

Lifeng Wang、Ling Guo、Kun Ye、Jiyong Yang
Chinese PLA General Hospital

Background In China, OXA-48-producing Enterobacterales have been identified sporadically, causing only small-scale outbreaks in certain regions. This study aimed to investigate the molecular epidemiology, transmission and evolution of OXA-48-producing Enterobacterales and pOXA-48 from mainland of China.
Methods We conducted a multi-center bacterial resistance monitoring project from 2013 to 2018. The genome sequencing of OXA-48-produicng isolates was performed. Single-nucleotide polymorphism (SNP) was analysed. Eleven isolates were selected for subsequent single-molecule real-time (SMRT) sequencing. Genome sequences were annotated, and alignment of the complete sequences of the blaOXA-48-carrying plasmids from a subset of isolates that underwent long read sequencing was performed.
Results A total of 41 OXA-48-producing Enterobacterales were involved in this study, including 34 K. pneumoniae, 3 E. coli, 3 E. cloacae and one K. oxytoca. OXA-48-produicng K. pneumoniae (OXAKp) ST383, ST147 and ST11 caused outbreaks of different scales in our hospital. In

addition, OXA-48-producing E. coli ST156 and ST648, E. cloacae ST414 and ST418, and K. oxytoca ST34 were also identified. The blaOXA-48 gene was embedded in a Tn1999.2 structure, which was located in IncL plasmids with different sizes (63.58~109.14 kb). Importantly, K. pneumoniae ST11 co-producing KPC-2 and OXA-48 has been identified in our hospital and it was possible that KPC-2-producing K. pneumoniae ST11 obtained the blaOXA-48-carrying plasmid during the spread. A novel blaOXA-48-carrying IncL plasmid with size of 109 kb has been identified from OXAKp ST11. It was possible that two plasmids in OXAKp ST383 were integrated to form this larger plasmid.
Conclusions The OXA-48-produicng Enterobacterales were sporadic in China. Importantly, K. pneumoniae ST11 co-producing KPC-2 and OXA-48 has emerged and caused outbreak in China. This high-risk multidrug-resistant clone exhibited high compatibility and strong integration ability with foreign resistant plasmids.

PO-0965

重症监护病房住院患者艰难梭菌分离株的微生物学特征研究

崔颖超、董丹凤、苏同轩、江岑、倪琪、王道盛、陈炜、彭奕冰
上海交通大学医学院附属瑞金医院

目的 艰难梭菌（Clostridioides difficile，CD）已经成为全世界最常报道的医源性腹泻的主要病原体。研究表明，艰难梭菌感染是一种毒素介导的疾病，尽管毒素是最关键的致病因素，但细菌粘附、定植并形成对环境有抵抗力生物膜的作用已逐渐得到重视。本研究对上海交通大学医学院附属瑞金医院重症监护病房（Intensive Care Unit，ICU）患者分离得到的 58 株艰难梭菌菌株进行一系列微生物学特征试验，以探究中流行株的表型优势与致病情况的关联性。
方法 对 58 株艰难梭菌分离株进行毒素基因检测，并通过多位点序列分型技术进行菌株基因分型。进一步进行菌株生物膜形成试验、菌株动力试验、菌株对细胞粘附能力试验及菌株抵抗吞噬杀伤能力试验。
结果 该时间段内 ICU 中艰难梭菌分离株毒素型检测结果以 A+B+型为主、多位点序列分型以 ST81 和 ST2 为主。其次，发现 ST129、ST35 型别菌株表现出相对较高形成生物的膜能力、较高粘附力及较强抵抗吞噬杀伤的能力。此外，流行占比最高的 ST81 型别菌株显示出较强的形成生物膜及运动方面的能力。
结论 本研究表明流行菌株存在致病表型上的相应优势，也提示了临床检测菌株分型的重要性。因此，对入住 ICU 病房的高危易感人群实行 CD 的常规监测十分必要，其次对已患有 CDI 的患者检测其菌株型别，掌握菌株的表型特征，对其治疗和预后更有价值。

PO-0966

传统药敏试验与 HAIN 线性探针技术在结核分枝杆菌药敏中的方法学比较

孙月荣、陶贵华
德州市第二人民医院

目的 以传统药敏试验为金标准，比较 HAIN 线性探针(HAIN LPA)技术在耐多药结核分枝杆菌检测中检测方法的优劣。
方法 分别收集 2013 年-2014 年抗酸涂片阳性的痰标本和经培养阳性的结核分枝杆菌菌株各 379 份，用传统的结核菌比例法药敏试验和 HAIN 线性探针技术两种实验方法检测痰标本和菌株对异烟肼（INH）、利福平（REF）的敏感性。

结果 对 379 例痰涂片抗酸杆菌阳性的标本用 HAIN LPA 技术和传统药敏试验检测异烟肼、利福平敏感性，结果显示两种方法对 INH 耐药的检测结果无统计学意义（χ2=1.43, P>0.05），灵敏度为 65.15%，特异度为 96.49%，阳性预测值为 79.63%，阴性预测值为 92.92%，一致性为 91.03%。对 REF 耐药的结果无统计学意义（χ2=0.36, P>0.05），灵敏度为 98.21%，特异性为 97.83%，阳性预测值为 88.71%，阴性预测值为 99.68%，一致性为 97.89%。用 HAIN 线性探针技术检测痰标本中结核分枝杆菌对异烟肼耐药的检出阳性率与传统药敏试验相比较阳性率无差异（χ2=3.56，P>0.05），对利福平耐药的检出阳性率无差异（χ2=3.13，P>0.05）。对 379 例结核分枝杆菌菌株用 HAIN LPA 技术检测检测异烟肼、利福平的敏感性与传统药敏试验结果进行对照分析，HAIN LPA 技术与检测 INH 耐药的的结果无统计学意义（χ2=3.25, P>0.05），灵敏度为 68.33%，特异性为 98.75%，阳性预测值为 95.35%，阴性预测值为 94.31%,一致性为 94.46%。对 RFP 检测结果无统计学意义（χ2=0.51, P>0.05），灵敏度为 96.23%，特异度为 97.24%，阳性预测值为 85%，阴性预测值为 99.37%，一致性为 97.10%。用 HAIN 线性探针技术检测结核分枝杆菌菌株对异烟肼耐药的检出阳性率与传统药敏试验相比较阳性率有差异（χ2=12.19，P<0.05），对利福平耐药的检出阳性率无差异（χ2=3.27，P>0.05）。

结论 与传统药敏试验相比，应用线性探针技术检测痰标本及菌株对异烟肼、利福平的敏感性，检出率差异无统计学意义，加之线性探针技术检测药敏实验较之传统法的快速性，线性探针技术适合在临床上广泛应用。

PO-0967

MALDI-TOF MS 联合 VITEK@ 2 Compact 对阳性血培养样本病原菌快速鉴定和直接药敏试验的研究

张灏旻[1]、何志亮[2]
1. 上海交通大学医学院附属仁济医院
2. 广州中医药大学第三附属医院

目的 评估一种基于基质辅助激光解析电离飞行时间质谱(MALDI-TOF MS)联合梅里埃 VITEK@ 2 Compact 全自动药敏分析系统直接对阳性血培养瓶中细菌沉淀快速鉴定及直接药敏试验方法的临床应用价值。

方法 使用 MALDI-TOF MS 对 Triton X-100 裂解法富集的菌体进行快速鉴定，同时 VITEK@ 2 Compact 全自动药敏分析系统对分离胶促凝管富集的菌体进行直接药敏试验。以 CLSI M52 为参考文件，将快速鉴定和直接药敏试验的结果与纯培养菌落的 MALDI-TOF MS 鉴定和 VITEK@ 2 Compact 药敏试验的结果进行对比。

结果 快速鉴定法对 100 株革兰阳性菌、140 株革兰阴性菌和 19 株酵母菌的鉴定符合率分别为 84.00%、92.14%和 68.42%。与常规方法 AST 结果相比，直接药敏试验法对 125 株革兰阴性菌的 CA 为 97.98%(1944/1984)，VME 为 0.40%(8/1984)，ME 为 0.59%(3/1984)；62 株革兰阳性菌的 CA 为 96.89%(717/740)，VME 为 0.27%(8/740)，ME 为 1.89%(3/740)。

结论 MALDI-TOF MS 联合 VITEK@ 2 Compact 直接对细菌沉淀快速鉴定和直接药敏试验方法可以快速准确的鉴定出病原体和药敏结果，对提高实验室检验效率和提前指导临床使用抗生素有重要意义。

PO-0968

A TTP-incorporated Scoring Model for Predicting Mortality of Solid Tumor Patients with Bloodstream Infection Caused by Escherichia coli

Qing Zhang
Tianjin Medical University Cancer Institute and Hospital

Objective Mortality is a well-recognized complication of Gram-negative bloodstream infection (BSI). Few mortality-scoring model is currently available for solid tumor patients who are predisposed to develop Escherichia coli-caused bloodstream infection (ECBSI). We aimed to develop a mortality-scoring model by using information from blood culture time to positivity (TTP) and other clinical variables.
Methods A cohort of 509 solid tumor patients who were admitted to hospital with ECBSI and received empirical antimicrobial therapy was retrospectively enrolled. Survivors and non-survivors were compared to identify the risk factors of 30-day in-hospital mortality. Univariable and multivariable regression analyses were adopted to identify the mortality-associated predictors. Risk scores were assigned by weighting the regression coefficients with corresponding natural logarithm of the odds ratio for each predictor.
Results 315 and 194 solid tumor patients with ECBSI were distributed in the development and validation groups, respectively. Six mortality-associated predictors were identified and included in the scoring model: acute respiratory distress (ARDS) (8.777 [2.337-3.296]; 2) (odds ratio [95% confidence interval]; assigned score point), TTP ≤ 8h (2.788 [1.360-5.716]; 1), inappropriate antibiotic therapy (3.667 [1.921-7.000]; 1), blood transfusion (2.849 [1.499-5.414]; 1), fever ≥ 39 ℃ (3.034 [1.448-6.357]; 1) and metastasis (3.385 [1.67-6.861]; 1). Prognostic scores were categorized into three groups that predicted mortality: low-risk (<10% mortality, 0-1 points), medium-risk (10%–20% mortality, 2 points), and high-risk (>20% mortality, ≥3 points). The TTP-incorporated scoring model showed excellent discrimination and calibration for both groups, with AUC being 0.833 versus 0.844, respectively, and no significant difference in the Hosmer-Lemeshow test (6.709, P=0.48) and the Chi-square test (6.993, P=0.46). Youden's index showed the best cut-off value of ≥3 with 76.11% sensitivity and 79.29% specificity. TTP-incorporated scoring model had higher AUC than no TTP-incorporated model (0.837 vs 0.817, P<0.01).
Conclusion Our TTP-incorporated scoring model was associated with improving capability in predicting ECBSI-related mortality. It can be a practical tool for clinicians to identify and manage bacteremic solid tumor patients with high risk of mortality.

PO-0969

中枢神经系统酵母菌感染的临床和免疫特征分析

李正康
广东省人民医院

目的 从临床和免疫的角度分析中枢神经系统真菌感染的特征。
方法 收集 2012 年-2019 年间在广东省人民医院脑脊液培养的结果，设置酵母菌感染组和细菌感染组进行病例对照研究。
结果 满足纳入和排除标准的酵母菌感染组 49 例，细菌组 25 例。常见枢神经系统酵母菌感染病原体是新型隐球菌感染（35 例，占 71.43%），其次是白色念珠菌和无名假丝酵母菌（各 3 例），男女感染率没有差别，以成年人感染多见。体外药敏试验发现，绝大部分酵母菌对常见五类抗真菌药物（两性霉素 B、5-氟胞嘧啶、氟康唑、伊曲康唑和伏立康唑）敏感。与细菌感染进行组间比较发

现，酵母菌感染组具有系统性红斑狼疮基础疾病的比例（11/49，22.45%）显著高于细菌感染组（1/25，4.00%）（χ2=4.147，P=0.042）；酵母菌感染组有 3 例 HIV 感染患者（6.12%），细菌组为 0，但两组无统计学差异。酵母菌感染组血常规的淋巴细胞值、脑脊液生化中的氯化物浓度、患者体内 CD3+CD4+/CD3+CD8+和 CD3+CD4+的比例均显著低于细菌感染组（P 值均<0.05）；但脑脊液常规中的白细胞数值和免疫细胞检测中 CD3+CD8+的比例则相反，酵母菌组更高。
结论 机会性真菌感染与患者的免疫功能低下或失调有关。

PO-0970

腿伤凯斯特菌生物学特性及质谱自建库方法的建立

吴伊雪
中国人民解放军南部战区总医院

目的 了解腿伤凯斯特菌（Kerstersia gyiorum）的特点，结合鉴定结果、生长属性和药敏结果分析其病原学特征。同时应用基质辅助激光解吸电离飞行时间质谱（MALDI-TOF MS）系统 SARAMS Preminu 软件建库，为今后临床诊断提供依据。
方法 采用回顾性分析方法，收集本院临床患者呼吸道标本中分离出来的 17 株细菌，通过 16S rRNA 测序鉴定为腿伤凯斯特菌；采用生化反应管检测这些细菌的生化特性;测定菌株最低抑菌浓度（MIC）并分析药敏结果；同时用其中的 13 株菌进行蛋白指纹图谱数据采集，应用 MALDI-TOF MS 系统 SARAMS Preminu 软件完成 13 株菌进行自建库，并用另外 4 株菌进行验证。
结果 收集的 17 株细菌在 Vitek 2 全自动微生物鉴定仪和 MALDI-TOF MS 都不能鉴定出来，后经 16S rRNA 基因测序鉴定为腿伤凯斯特菌，该菌的生长特点与粪产碱菌(Alcaliges Faecalis)相似，都会蔓延生长，但部分生化特性不同；药敏试验结果显示该菌对阿米卡星、头孢他啶、亚胺培南、美罗培南、粘菌素和哌拉西林-他唑巴坦等多种抗菌药物呈现出高度敏感，而环丙沙星呈现中介或耐药；本研究还对这 13 株菌进行蛋白指纹图谱数据采集，建立菌株数据库，相关质谱数据通过菌株在相同培养环境下所得蛋白指纹图谱数据进行优化。用另外 4 株进行验证应用自建腿伤凯斯特菌数据库，可正确鉴定腿伤凯斯特菌，置信度大于 90%。
结论 Vitek 2 全自动微生物鉴定仪和 MALDI-TOF MS 都不能鉴定出腿伤凯斯特菌，本研究可以通过自建菌库准确鉴定该菌，与其他亲缘关系较近的鲍特菌属（Bordetella）、无色杆菌属（Achromobacter）可较好区分。同时本研究的腿伤凯斯特菌的鉴定准确性高，适用于临床直接检测，从而有利于临床工作者对患者的诊治。本研究结果更新了已有的数据库，同时也为其他细菌菌库的建立提供了很好的借鉴。

PO-0971

利用合成生物学抗消化道肿瘤大肠杆菌工程菌株的构建

高冬芳
山东大学第二医院

癌症是目前人类致死率最高的疾病之一，传统的癌症治疗主要为放疗和化疗。但是传统的治疗手段无法准确的定位于目标肿瘤、不能有效穿透肿瘤组织并且对正常组织细胞具有杀伤作用，导致治疗效果有限、副作用明显。随着合成生物学的发展，构建可特异性杀伤肿瘤细胞的工程菌是肿瘤生物治疗的全新发展方向。由于静脉注射的安全性及机体耐受性尚缺乏保证，口服是生物工程菌肿瘤治疗的理想给药方式，但细胞因子易受消化酶降解影响其应用。因此，用基因工程技术编辑非致病性细菌表达细胞因子，保护其不受胃酸降解, 进入肠道直接释放细胞因子到效应部位, 从而减少细胞因子剂量, 减轻全身副作用，在应用于消化道肿瘤的治疗时具有良好的前景。

本实验选取益生菌 E. coli Nissle 1917 作为平台菌株。利用前期工作中构建的大肠杆菌融合表达平台（Cel-CD），融合表达细胞因子 IL-18(携带肠激酶酶切位点)，一方面借助细菌载体融合表达可以减少胃内酸性环境及蛋白酶的降解；同时 Cel-CD 的分泌特性使 IL-18 被工程菌株分泌到胞外。到达肠道后，在肠激酶的作用下分离融合蛋白 Cel-IL 得到活性 IL-18，IL-18 与肠上皮细胞的细胞因子受体结合，激发一系列的机体抗肿瘤免疫应答。 利用 E. coli Nissle 1917 在消化道肿瘤组织处聚集生长的特性，借助来源于海洋发光细菌费氏弧菌(Vibrio fischeri) 的 LuxI/LuxR 群体感应系统构建大肠杆菌工程菌。通过感应菌体密度启始来源于假结核耶氏菌（Yersinia pseudotuberculosis）侵袭素 inv 的表达，侵染肿瘤组织并借助内源性 CDase 杀伤肿瘤细胞。

1) 构建大肠杆菌细胞因子 IL-18 融合分泌系统；2）群体感应（Quorum Sensing, QS）模块的构建 ；3）单质粒的靶向性平台菌株的构建；4）工程菌对消化道肿瘤杀伤作用的检测

本实验将 Cel-CD 融合表达平台应用于生物治疗工程菌的构建，提高了细胞因子的药物利用率，为肿瘤细菌治疗提供了全新的应用实例，具有良好的临床应用前景。

PO-0972

高毒力肺炎克雷伯菌的毒力特性及其对 RAW264.7 细胞炎症相关因子表达的影响

毕建蝶、杜艳、刘淑敏（通讯作者）
昆明医科大学第一附属医院

目的 比较分离自本院病人的一株高毒力肺炎克雷伯菌（hypervirulent Klebsiella pneumoniae，hvKP）和一株碳青霉烯类耐药的高毒力肺炎克雷伯菌（Carbapenem-resistant hypervirulent Klebsiella pneumoniae，CR-hvKP ）的毒力特性，探讨不同毒力的肺炎克雷伯菌对鼠源巨噬细胞 RAW264.7 炎症相关因子表达的影响。

方法 首先对收集的两株高毒力菌株进行黏液拉丝实验、PCR 扩增高毒力质粒和荚膜血清型相关基因（rmpA、rmpA2、iucA、iutA 等）及多位点序列分型(MLST)；随后进行细菌抗吞噬实验：以标准菌株 BAA1706 为对照，分为标准菌株组、 hvKP 组、CR- hvKP 组，将培养至对数生长周期的三组细菌按感染复数（multiplicity of infection,MOI)100:1 比例与 RAW264.7 细胞共培养 4h,分别计数细胞内细菌的存活率；最后取 4h 共培养上清液进行 ELISA 实验检测 TNF-α、IL-6、IL-1β 的表达情况。

结果 两株临床菌株均为高黏液表型，表达高毒力质粒相关基因，判定为高毒力菌株，其中 hvKP 的 MLST 为 23，荚膜血清型为 K1，CR-hvKP 的 MLST 为 36，荚膜血清型为 K62。在感染 4h 后，巨噬细胞 RAW264.7 内各组细菌存活情况为标准菌株>hvkp>CR-hvkp，差异均有统计学意义（P 均<0.001）。与标准菌株相比，TNF-α 的表达水平在 hvkp（P=0.007）和 CR-hvkp（P=0.009）感染后显著升高,而 IL-6 的表达水平在 hvkp（P=0.002）和 CR-hvkp（P=0.033）感染后略微升高,且与 CR-hvkp 相比 hvkp（P=0.036）更能促进 IL-6 的表达而对 TNF-α 的表达无显著差异。IL-1β 的表达在三株菌中均无显著差异。

结论 相对于标准肺炎克雷伯菌,高毒力肺炎克雷伯菌具有高黏液表型及抗巨噬细胞吞噬能力强的特性,且感染鼠源巨噬细胞 RAW264.7 细胞后,主要通过释放促炎因子 TNF-α 和 IL-6 引起更严重的炎症反应。

PO-0973

sIgA 在糖尿病的发生进程中与肠道微生态的初探

曾通旭
兰州市第二人民医院

目的 通过高脂饮食来制备前期糖尿病（Pre-DM）模型及高脂饮食联合小剂量多次注射链脲佐菌素（STZ）制备 2 型糖尿病（T2DM）模型,观察在糖尿病发生过程中肠道微生态与 sIgA 的相关性。
方法 通过前期预实验,将 C57BL/6J 试验小鼠随机分为 6 组：正常组（A 组）、Pre-DM 20 天（B 组）、Pre-DM 40 天（C 组）、Pre-DM 60 天（D 组）、Pre-DM 80 天（E 组）,在 80 天之后高脂饲喂联合小剂量多次注射链脲佐菌素制备 T2DM 模型（F 组）。各实验组测定空腹血糖腹腔注射糖耐量实验（IPGTT）,取粪便进行 16SrRNA 测序，采用 ELISA 法测定 sIgA 及胰岛素水平,胰腺做抗胰岛素抗体免疫组化实验,采用比浊法做 hs-CRP、应用流式细胞术检测 CD3+、CD3+CD8+、CD3+CD4+等 T 淋巴细胞亚群的比例。
结果 通过成功构建动物模型，16SrRNA 高通量二代测序发现 T2DM 发病进程中厚壁菌门、梭菌门、变形菌门、蓝藻菌门的菌群丰度等随着血糖的升高出现不同的变化趋势，胰岛素抵抗伴随着整个发病过程，可能慢性炎症与终胰岛素抵抗具有相关性。发现 T2DM 发病进程中细胞免疫与体液免疫出现不同程度的紊乱。
结论 肠道菌群丰度的变化伴随着 T2DM 的整个发病进程中，提示肠道菌群丰度与 SIgA 及部分免疫指标与 T2DM 的整个发病进程中具有一定的相关性.

PO-0974

Multiple carbapenemases genes clonal dissemination in carbapenem-resistant Enterobacterales strains mediated by multiple plasmids in China

Jun Li[1]、Mingxiang Zou[2]
1. Department of Clinical Laboratory, Xiangya Hospital, Central South University
2. Xiangya Hospital

Background The spread of carbapenem-resistant Enterobacterales (CRE) is an emerging clinical problem. The aim of this study was to investigate the molecular epidemiology of CRE isolates from China.
Methods CRE isolates were collected from 11 hospitals (three primary hospitals, seven general hospitals and one children's hospital) between October 2015 to July 2018. These isolates were subjected to multiple phenotypic and molecular tests, including in vitro antimicrobial susceptibility testing, PCR, pulsed-field gel electrophoresis (PFGE), and multilocus sequence typing (MLST).
Results Among the 399 CRE isolates, 51.6% (206/399) carried carbapenemases genes, and three carbapenemase genes were detected, including blaKPC-2, blaNDM-1 and blaIMP, with the rate of 29.8% (119/399), 17.5% (70/399), and 4.0% (16/399), respectively. The blaKPC-2 (33.4%, 117/350) and blaNDM-1 (61.5%, 16/26) were the predominat genes in K. pneumoniae and E. coli, respectively. The main genes in CRE isolated from adults and children were blaKPC (85.5%) and blaNDM-1 (76.5%), respectively. Notablely, blaKPC-2-positive ST11 K. pneumoniae carried by IncFII plasmids distributed not only in general hospital, but primary hospital, suggesting that it was clonal transmission. In addition, clonal distribution of blaNDM-1-positive ST2407 K. pneumoniae located on IncX3 plasmids and blaIMP-38-positive ST307 K. pneumoniae were also detected in the children's Hospital.
Conclusions The distribution of carbapenemase genes were different in species and also in adults and children. Multiple carbapenemase genes in CRE strains were clonal dissemination in

our regions mediated by multiple plasmids. Therefore, CRE monitoring should be strengthened and measures should be adopted.

PO-0975

6 例人型支原体致手术后感染的临床回顾性分析

唐朋[2]、邱宗文[1]、全念[1]、黄微微[1]、王晶晶[1]、陈奎[1]、李涛[1]、张立群[1]
1. 陆军军医大学第二附属医院检验科
2. 陆军军医大学第二附属医院检验科

目的 分析总结人型支原体（Mycoplasma hominis，Mh）引起的外科手术后感染病例的临床特征、治疗策略、实验室检测及其药物敏感性，以期对其引起的非典型感染的临床诊断和治疗用药有一定指导意义。
方法 收集本院 2019 年 1 月至 2020 年 8 月 Mh 致术后感染病例共 6 例，对病例资料进行数据汇总并对 Mh 的药物敏感性进行分析。
结果 6 例患者均为手术部位切口感染，表现为：手术部位积液，切口红肿、疼痛、不易愈合，多数患者低热。患者感染症状普遍较轻，容易被临床忽视，使用 β-内酰胺类药物经验性治疗效果不佳，感染周期长达 11-27d。实验室检测中，C-反应蛋白（CRP）升高明显，52.4-200 mg/L；中性粒细胞比例（NEUT %）升高，76.0%-94.8%；白细胞计数（WBC）基本正常；降钙素原（PCT）正常，其他指标无异常。Mh 对强力霉素、美满霉素等四环素类药物普遍敏感（6/6，100%）；氨基糖苷类药物，壮观霉素敏感性较好（5/6，83.3%）；大环内脂类药物中，交沙霉素敏感性较高（5/6，83.3%），而罗红霉素、阿奇霉素、克拉霉素均不敏感（0/6，0%）；喹诺酮类药物中，加替沙星敏感性较好（4/6，66.7%），左氧氟沙星敏感性较低（1/6，16.7%），氧氟沙星、环丙沙星、司帕沙星均不敏感（0/6，0%）。
结论 Mh 可引起泌尿生殖系统之外的外科手术后切口感染，一般发生在手术后 4-14 d，感染症状较轻，主要表现为切口红肿热痛等炎症反应，一般使用 β-内酰胺类药物经验性治疗效果不佳；Mh 感染主要引起 CRP、NEUT %升高明显，而 WBC、PCT 等指标基本正常；Mh 对四环素类药物普遍敏感，可作为临床治疗首选，但对其他种类抗菌药物敏感性不等，需结合药敏试验结果选择使用。

PO-0976

Aggregation of MPBA-AuNPs based rapid photothermal detection of foodborne pathogens

Wenjia Dong、Laibao Zheng、Yongliang Lou
Wenzhou Medical University

Rapid and portable detection of foodborne pathogens is of great significance for food safety and public health. The colorimetric methods based on naked-eye have been demonstrated to be a suitable qualitative method for point-of-care testing (POCT). However, analytical instruments like a microplate reader must be needed for the quantitative assay. To overcome its limitation, we herein report a novel photothermal method for foodborne pathogens based on the photothermal effect of aggregated mercaptophenylboronic acid-functionalized AuNPs (MPBA-AuNPs) induced by MPBA to translate the colorimetric detection into a simple temperature measurement using thermometers as the readout.

The working principle of the thermometric detection method for bacteria based on the photothermal effect of aggregated MPBA-AuNPs induced by excess MPBA is shown in Scheme 1. The well-dispersed MPBA-AuNPs appear red with maximum photothermal conversion efficiency at about 520 nm. However, when excess MPBA was added into MPBA-AuNPs, more MPBA could attach to AuNPs through Au-S, which results in the neutralization of the repulsion among

MPBA-AuNPs and the aggregation of MPBA-AuNPs through the formation of cyclic ester among the boronic acid group of MPBA(J. Huang et al., 2020). And, the color of aggregated MPBA-AuNPs will change to blue with maximum photothermal conversion efficiency at about 660 nm. When added excess MPBA, MPBA-AuNPs will turn aggregated and the color of the solution will change to blue, showing a larger temperature increase under 660 nm irradiation. However, bacteria could absorb MPBA-AuNPs onto its surface through the boronic acid of MPBA and the cis-diol groups of polysaccharides of bacteria(Liu et al., 2012). Then, if the excess MPBA were added to the mixed solution, MPBA-AuNPs will remain separated due to the protection of bacteria. Therefore, the color of the solution remains red and the temperature change is not obvious. And the degree of the aggregation has some relationship with the number of bacteria. Thus, the bacteria concentration can be detected by the temperature change using a pen-style digital thermometer easily.In conclusion, using *E. coli* O157:H7 as a model target, a good linear relationship is observed between temperature increase and bacteria concentration from 10^5-10^9 cfu mL^{-1} (R^2 = 0.9877) with a detection limit of 1.97×10^4 cfu mL^{-1}, which is three orders of magnitude lower than of the MPBA-AuNPs-based colorimetric assays. The proposed photothermal method provided a universal platform for rapid and portable detection of broad-spectrum bacteria strains in real samples.

PO-0977

Nanoparticle-enzyme complexes and the personal glucose meter based potable detection and antimicrobial susceptibility testing of pathogens

Yunqiu Shen、Laibao Zheng、Yongliang Lou
Wenzhou Medical University

Rapid detection of pathogens and assessment of antimicrobial susceptibility is of great importance for public health, especially in resource- limiting regions. Herein, we developed a simple, portable, and quantitative detection method for bacteria using AgNPs-invertase complexes and PGMs without multiple washing and rinsing steps. In the presence of bacteria, the invertase could be released from AgNPs-invertase complexes where its enzyme activity of invertase was inhibited. Then, the enzyme activity of invertase was restored and could convert sucrose into glucose measured by a commercially PGM. There was a good linear relationship between PGM signal and concentration of E. coli (from 1×10^2 cfu/mL to 1×10^7 cfu/mL) or S. aureus (from 1×10^3 cfu/mL to 1×10^7 cfu/mL), with the limit of detection of 2.99 cfu/mL and 7.59×10^2 cfu/mL respectively. Our proposed biosensor was proved to be a rapid and reliable method for antimicrobial susceptibility testing within 4 h with consistent results of MIC testing.
The detection principle of our designed potable and sensitive biosensor for bacteria detection using nanoparticle-enzyme complexes and the PGM is schematically illustrated in Scheme 1. The biosensor combines three main components: (a) invertase, an anionic enzyme, to provide signal amplification and convert sucrose into glucose measured by PGMs; (b) sucrose, a catalytic substrate of invertase; (c) PEI-AgNPs, a cationic nanoparticle, which could recognize bacteria and reversibly bind to invertase, inhibiting the catalytic activity. The catalytic activity of invertase is inhibited without denaturation by forming AgNPs-invertase complexes through electrostatic interaction. However, in the presence of bacteria, the cationic AgNPs competitively binds to the anionic surface of bacteria to displace the invertase with the recovery of enzyme activity. The active invertase converts sucrose into glucose, which could be measured by a commercially PGM. Thus, the concentration of bacteria could be quantified using a PGM.

PO-0978

In vitro activity of aztreonam–avibactam against metallo-β-lactamase-producing Enterobacteriaceae—A multicenter study in China

biying zhang、hong du
the Second Affiliated Hospital of Soochow University

Carbapenem-resistant Enterobacteriaceae (CRE) has increasinglybecome an significantincreasinglypublic health problemconcern. CRE is now detected in almost every province in China., including both metallo-β-lactamase (MBL) (e.g. NDM) andserine carbapenemases (e.g. KPC). Here, MBL-producer are particularly problematic as theyweren't inhibited by novelβ-lactamase inhibitors (e.g. avibactam). In this study, weaim toevaluate the in vitro susceptibility of aztreonam-avibactam, a novel monobactam andβ-lactamaseinhibitor combination, against MBL-producingEnterobacteriaceae in China.we collected161 metallo-β-lactamase (MBL) producing Enterobacteriaceae isolates were collected from six multi-centertertiarycare hospitals in Chinaresearch cities frombetweenOctober2016 toandSeptember2017. All isolates were identifiedcharacterizedby mass spectrometry for speciation, molecular detection (for sequence types, carbapenemase gene, andESBL-CTXgenes,mcr-1), and antibiotic susceptibility testing test. Klebsiella pneumoniae was simultaneously identified sequence types, serotype types, common virulence genes by multiplex PCR. Klebsiella pneumoniae (n=73, 45.4%) and Escherichia coli (n=53, 32.9%) accounted forthe first two of the isolateswere the most common species,. theTheisolates were collectedfrom respiratory tract (n=51, 31.7%), andurinary tract (n= 46, 25.6%) were the majority., withmore than half of the isolates (n = 94, 58.4%) carrying two or more of the screen antibiotic resistance genes. Multiplex PCR of Klebsiella pneumoniae showed ST11 type (n=13, 17.8%), K64 serotype (n=11, 15.1%), K47 serotype (n=2, 2.7%) with two isolates carrying virulence genes. Clinical common antibiotic Antimicrobialsusceptibility testing showed 81.4% isolateswere resistant tothat the resistance rate of aztreonam, and was as high as81.4%,which as a targeted treatment for MBL-Enterobacteriaceae ,the resistance rate of cefazolin, ceftazidime, ceftriaxone, cefotaxime, ampicillin-sulbactam, amoxicillin-clavulanic acid and piperacillin-tazobactam were all over 90%. After the combined use of aztreonam-avibactam, significantly reduced the MIC of the aztreonam-resistant isolates by more than 8-fold (range: ≤ 0.125 to 4μg/ml), withexceeding96.9% of theisolates wereinhibited at aztreonam-avibactam concentration ≤ 1/4μg/ml, suggesting that the combinedcombinationuseof aztreonam-avibactam mayis highly potent against become a new dawn as a candidate for the treatment ofMBL-producing Enterobacteriaceae infections, especiallyin China.

PO-0979

MALDI-TOF 质谱机器学习法进行微生物识别和药敏试验的相关性研究

赵亚楠
内蒙古自治区内蒙古人民医院

目的 基质辅助激光解吸/电离质谱飞行时间质谱(MALDI TOF MS)用于临床微生物实验室，以满足快速、低成本和准确鉴定微生物的需求。最近，机器学习技术被用来最大限度地利用 MALDI-TOF MS 中包含的信息。本文系统性地回顾和评价使用机器学习法分析 MALDI-TOF MS 质谱，从而细化物种鉴定和简化抗菌素耐药性的测定。

方法 我们利用 PubMed/Medline、Scopus 和 Web of Science 检索了已有的基于机器学习的 MALDI-TOF 质谱用于微生物种类鉴定和抗菌药物敏感性鉴定的文献。根据 PRISMA 指南进行系统评价，并对学习模型机器进行质量评估。纳入标准 查阅利用机器学习 MALDI-TOF 质谱法进行微生物种类和抗菌药物敏感性鉴定的原始研究的相关文献，研究以单一蛋白质和多肽为重点，排除相关案例研究和综述文章。

结果 在符合我们纳入标准的 36 项研究中，27 项采用机器学习进行物种鉴定，9 项采用抗生素敏感性测试。支持向量机法、基因演算法、人工神经网络法和快速分类器是最常用的机器学习算法。这些研究的质量介于差和很好之间。大多数研究报告了如何解释这些预测因素(约 88.89%)，同时提出了这些算法在临床应用的可能(100%)，但只有 4 项研究(11.11%)在外部数据集上验证了机器学习算法。

结论 基质辅助激光解吸/电离和飞行时间质谱(MALDI-TOF MS)技术通过促进精确和快速的物种鉴定，使微生物领域发生了革命性的变化。最近，越来越多的研究利用机器学习法优化 MALDI TOF MS 质谱分析。然而，这篇综述表明，目前的机器学习支持方法存在一定的缺陷，必须加以解决，使其广泛可用，并将其纳入临床常规。能够更好的解决相关问题，更好的服务于临床。

PO-0980

无背景耐甲氧西林金黄色葡萄球菌超敏检测技术研究

胡孝林[1,2]、罗阳[1,2]
1. 重庆大学医学院智慧检验与分子医学中心
2. 重庆大学医学院公共实验中心

Methicillin-resistant Staphylococcus aureus (MRSA), as one of the most common multidrug-resistant bacteria in hospital acquired infections, is mainly transmitted between patients and medical staff, patients and patients. Sensitive and accurate identification of Methicillin-resistant Staphylococcus aureus (MRSA) is of great significance. Due to the limitation of detection technology, most methods have background signal, which affects the interpretation of results. Herein, we describe an background-free sensing strategy based on aptamer-functionalized magnetic beads (AFMBs) and molybdenum disulfide (MoS2) nanosheets. AFMBs, as a tool to capture MRSA, are in charge of signal convertion, while MoS2 nanosheets are responsible for readout with near-zero background fluorescence. The detection signal was found to be linear from 10 to 106 CFU/mL with a detection limit of 6.4 CFU/mL. Besides, the method is highly specific and has good consistency with the culture method. This strategy provides a new road for establishing a universal pathogen detection platform.

PO-0981

环介导恒温扩增技术在呼吸道感染常见细菌临床检测中的应用评价

卫清[1,2]、李荷楠[2]、彭秋生[2]、杨硕[2]、王启[2]、王占伟[2]、王知任[2]、王辉[2]
1. 深圳市中医院
2. 北京大学人民医院

背景 传统的细菌培养为下呼吸道感染诊断的金标准，但其检验周期长且敏感性低。环介导恒温扩增技术（Loop-mediated isothermal amplification，LAMP）方法简单、检测快速，可应用于临床呼吸道感染常见细菌的快速检测。

目的 评估环介导恒温扩增技术对呼吸道感染常见 7 种细菌的检测能力。

方法 回顾性分析 2019 年 11 月至 2021 年 3 月 240 例北京大学人民医院疑似下呼吸道感染患者的呼吸道标本（痰和肺泡灌洗液）。利用自动化核酸提取仪提取 DNA 后，利用特异性引物进行环介导恒温扩增，检测呼吸道感染常见 7 种病原菌，肺炎克雷伯菌（KP）、鲍曼不动杆菌（AB）、金黄色葡萄球菌（SA）、铜绿假单胞菌（PA）、肺炎链球菌（SP）、卡他莫拉菌（MC）和流感嗜血杆菌（HI）。检测结果与常规细菌培养结果进行比较，分析环介导恒温扩增的灵敏性和特异性，评估优化不同菌种的阳性判断值（CT 值），探讨环介导恒温扩增技术在临床上的应用价值。
结果 本研究共检测 218 例痰和 22 例肺泡灌洗液样本，其中基于培养方法含有 7 种目标菌的样本 178 例，采用环介导恒温扩增法检测出 7 种目标菌的样本共 176 例。从提取核酸到环介导恒温扩增结果检出的平均检测时间为 2~3 小时，可同时检测多个样本。对 7 种常见呼吸道病原菌 HI、KP、AB、MC、SA、PA、SP 的最佳 CT 值分别为 18.5、20、20、15、25、19 和 18。检测灵敏度和特异性分别是：KP（90.7%，94.1%），AB（84.0%，94.2%），PA（90.8%，89.1%），MC（75.0%，99.2%），SA（81.8%，97.4%），HI（75.0%，90.3%），SP（33.3%，95.4%）。KP，AB 和 PA 的环介导恒温扩增技术结果与痰培养半定量结果具有较好的符合率，R2 值分别是 0.8557，0.8044 和 0.9243。
结论 环介导恒温扩增技术操作简单、快速。与培养方法相比，环介导恒温扩增检测的特异性较高（89.1%-99.2%），对于肺炎克雷伯菌、鲍曼不动杆菌、金黄色葡萄球菌和铜绿假单胞菌的检测灵敏度较高（81.8%-90.8%），可用于临床呼吸道感染病原菌的快速诊断。环介导恒温扩增技术结果与痰培养半定量结果符合率较好。流感嗜血杆菌和肺炎链球菌由于培养阳性标本量较少，有待进一步评估。

PO-0982

Outbreak of KPC-producing Klebsiella pneumoniae ST15 strains in a Chinese tertiary hospital: resistance and virulence analyses

Jiansheng Huang[1]、xiuying chen[2]、yunan zhao[1]、yang shi[1]、hui ding[1]、jianfen xu[1]、xinmi zhao[1]、rongzhen wu[1]、zhigang zhao[1]
1. Lishui Central Hospital, Lishui, Zhejiang, China
2. 丽水市疾控中心

Carbapenem-resistant Klebsiella pneumoniae (CRKP) is a major cause of clinical infection. However, KPC-producing K. pneumoniae ST15 strains are occasionally identified and have never been reported to cause hospital outbreaks in China. In this study, pulsed-field gel electrophoresis (PFGE) and whole-genome sequencing (WGS) were used to characterize 32 KPC-producing K. pneumoniae ST15 strains, which were collected at a Chinese tertiary hospital. Susceptibilities, resistance genes, virulence factors and clinical performances of the ST15 strains were comparatively analysed with corresponding ST11 strains. The ST15 strains were distributed in 7 wards, mainly in the intensive care unit (ICU, 24/32, 75%). PFGE results from 24 strains covering all the wards presented a similarity of more than 92%, indicating clonal spread. In 84% of the ST15 strains, the imipenem (IPM) and meropenem (MEM) minimum inhibitory concentrations (MICs) were ≤ 8 and ≤ 16 μg/mL, respectively, both of which were 4-fold lower than those of the ST11 strains. The infection rates of the ST15 and ST11 strains were 28.1% and 43.9%, respectively (P=0.018). PCR evaluation and WGS indicated that all the CRKP strains shared a 100% identical blaKPC-2 genetic structure, though a synonymous mutation and a Gly115-Asp116 (GD) insertion in the OmpK36 were identified in the ST15 and ST11 strains, respectively. None of the ST15 strains were positive for hypervirulence factors; however, the positive rate was 92.7% (38/41) in the ST11 isolates. To the best of our knowledge, this is the first description of nosocomial outbreaks caused by KPC-producing K. pneumoniae ST15 strains in China.

PO-0983

基于组织透明技术的脑胶质瘤中微生物三维可视化研究

孙海涛[1]、赵佳佳[1]、贺电[1]、李婷[1]、骆韵豪[1]、柯以铨[1]、郭琳琅[1]、周宏伟[1]、郭洪波[1]、吴武田[2]
1. 南方医科大学珠江医院
2. 暨南大学粤港澳中枢神经再生研究院

目的 运用组织透明技术和荧光标记结合光学显微成像及图像三维重建技术以及胶体金免疫电镜技术，验证人脑胶质瘤中微生物存在的可能性及其分布情况。
方法 在本研究团队前期建立的组织透明技术体系（OPTIClear pipeline）基础上进一步优化，以人脑胶质瘤为主要研究对象，选择 3 例我院人脑胶质瘤手术样本，并切取大小为 1cm×1cm×0.5mm 的胶质瘤组织块作为实验样本，以小鼠脑组织和小肠组织样本分别作为阴性和阳性对照，选择细菌细胞壁脂多糖(lipopolysaccharide,LPS)和磷壁酸(lipoteichoic acid, LTA)的特异性抗体进行标记，将实验样本整体组织透明化处理后在激光扫描共聚焦显微镜下扫描，选择组织块深部厚度为 100μm 的区域进行扫描和三维重建，在排除样本表面微生物污染的前提下，明确脑胶质瘤中是否存在微生物及其分布情况。并应用多种传统组织形态学**方法** 荧光原位杂交（FISH）、免疫组织化学（IHC/IF）和胶体金免疫电镜进行检测，对同一组织中是否存在微生物进行进一步验证。
结果 成功建立了人脑组织样本中微生物组织病理学三维可视化的研究体系，并通过此方法检测到脑胶质瘤组织深部存在 LPS 特异性信号，结合细菌 16S rRNA FISH 和免疫组化及胶体金免疫电镜检测结果显示，胶质瘤组织样本肿瘤中存在细菌的特异性信号，常定位于细胞内，散在分布，呈不规则形态，可为梭形或圆形。
结论 本研究提供了脑胶质瘤中存在细菌的有利证据，本团队的发现和建立的基于组织透明技术的完整大尺寸样本三维可视化的方法结合特异性荧光标记技术有望揭开脑胶质瘤中微生物的全貌，有助于更好地理解胶质瘤微环境中微生物群体与肿瘤细胞的直接交互作用。

PO-0984

米诺环素对白念珠菌的体外抑制作用分析

邹莉、梅昭、关涛、邓群
宜昌市第一人民医院

目的 初步探讨米诺环素对白念珠菌的体外抑制作用及其机制，为进一步研究米诺环素对抗白念珠菌的机制提供实验基础，为临床抗真菌治疗提供依据。
方法 收集分离的 46 株酵母菌临床样本，其中白念株菌 17 株、热带念珠菌 7 株、葡萄牙假丝酵母菌 4 株、近平滑念珠菌 4 株、光滑念珠菌 10 株、拟平滑假丝酵母菌 4 株。使用纸片扩散法对 46 株临床菌株进行药物敏感实验；采用电镜观察米诺环素对白念珠菌在 YPD 固体培及液体陪养基中的形态学变化；XTT 法检测白念珠菌生物膜和浮游细胞代谢活性；检测比较白念珠菌 caspase 3 的活化程度，对比分析各组之间差异。
结果 46 株酵母菌临床菌株中，米诺环素对白念珠菌表现出最强的抑制作用；与空白对照组比较，米诺环素处理后的白念珠菌的菌丝增长明显受抑制，在米诺环素浓度 256μg/ml 时展示出最佳抑制效果，随着米诺环素浓度增高，菌丝增长缓慢仍明显受抑制(P<0.01)。米诺环素处理后的白念珠菌生物膜活性显著降低(P<0.01)，且随着米诺环素浓度的增加，抑制作用更加明显，而米诺环素对白念珠菌浮游细胞活性没有明显改变；与对照组相比，256μg 组胞内 Caspase 3 酶活化程度升高，有显著性差异(P<0.05)，512μg 和 1024μg 组胞内 Caspase 3 酶活化程度明显高于对照组(P<0.01)，而三个实验组间的 Caspase 3 酶活化程度并无显著性差异(P>0.05)。
结论 米诺环素可抑制体外白念珠菌的生长，主要表现在菌量减少、激活 Caspase 3 酶活性从而诱导白念珠菌生物膜活性下降和凋亡，这可能与生物膜和 caspase 酶活性相关。

PO-0985

Outer membrane vesicles from Hypervirulent Klebsiella pneumoniae mediate virulence factor transfer

Yuneng Hua
southern medical university

Objective Hypervirulent Klebsiella pneumoniae(HvKp) has emerged as an important nosocomial pathogen, which is more virulent than classical Klebsiella pneumoniae (CKp) and carbapenem-resistant Klebsiella pneumoniae (CRKP). Hypervirulent Klebsiella pneumoniae can naturally secrete outer membrane vesicles, which are potent virulence factors, may acting as mediators of inter- and intra-species communication. It is crucial to determine the pathogenic mechanism of outer membrane vesicles from Hypervirulent Klebsiella pneumoniae.
Design Outer membrane vesicles from Hypervirulent Klebsiella pneumoniae and classical Klebsiella pneumoniae are isolated, characterized and verified by sequential differential centrifugation, transmission electron microscopy, NanoSight analysis and Western blotting. Virulence factors relates to Hvkp-OMVs and their intra-species communication are analyzed by transwell, reverse transcription-PCR, flow cytometry, enzyme linked immunosorbent assay and proteome analysis. To identify the role of Hvkp-OMVs in bacteria-bacteria interactions in vitro and in vivo.
Results we indicate that Hvkp-OMVs may promote virulent plasmids and proteins transfer from HvKp to CKp or CRKP, contribute to potential dissemination of virulence-encoding elements among Klebsiella pneumoniae.
Conclusion To date, this work demonstrates that HvKp OMVs are mediating virulence factors transfer and allowing increase the virulence level of CKP or CRKP.

PO-0986

头孢地尔联合其他抗菌药物对碳青霉烯耐药肠杆菌目细菌的体外活性研究

邹俊扬、王晓娟
北京大学人民医院

目的 本研究旨在探讨头孢地尔联合其他抗菌药物对碳青霉烯耐药肠杆菌目细菌的体外抗菌作用，为临床提供以头孢地尔为基础的联合治疗的体外活性证据。
方法 收集 2018 年 1 月至 2020 年 7 月期间北京两家三级医院病毒性肺炎合并碳青霉烯耐药肠杆菌目细菌（Carbapenem-resistant Enterobacteriales，CRE）感染患者分离出的 13 株非重复 CRE，从中筛选出 5 株 CRE，3 株携带 *bla*$_{KPC}$ 的肺炎克雷伯菌和 1 株携带 bla$_{NDM}$ 的大肠埃希菌和 1 株携带 *bla*$_{NDM}$ 的阴沟肠杆菌。在 2016 年至 2018 年 CRE network 监测项目筛选 4 株肺炎克雷伯菌，包括 1 株携带 *bla*$_{NDM-9}$，1 株携带 *bla*$_{IMP-4}$ 的，1 株携带 *bla*$_{OXA-48}$ 和 1 株同时携带 *bla*$_{KPC-2}$+*bla*$_{NDM-1}$，1 株携带 *bla*$_{VIM-1}$ 的阴沟肠杆菌，共计 10 株 CRE。检测乏铁的阳离子调节（iron-depleted Cation adjusted Mueller-Hinton broth，ID-CAMHB）和阳离子调节肉汤（Cation adjusted Mueller-Hinton broth，CAMHB）对头孢地尔、美罗培南、替加环素、多粘菌素 B 和左氧氟沙星抗菌药物敏感性试验是否存在影响。采用棋盘法检测以头孢地尔为基础联合美罗培南、替加环素、多粘菌素 B 或左氧氟沙星的两药联合药敏试验对携带不同碳青霉烯酶基因型的 CRE 的体外抗菌协同能力。
结果 ID-CAMHB 对替加环素和美罗培南发挥体外抗菌活性有影响，ID-CAMHB 中 80%的实验菌株 MIC 相比于 CAMHB 上升 1～3 个稀释度。在 ID-CAMHB 中，头孢地尔联合替加环素抗菌活性最好，该方案对 80%（8/10）的实验菌株表现出协同作用。其次为头孢地尔联合美罗培南或美罗培南联合左氧氟沙星，分别对 40%（4/10）和 30%（3/10）的实验菌株具有协同作用。头孢地尔联合多

粘菌素 B 仅对 1 株 CRE 中表现协同作用。在 CAMHB 中，头孢地尔联合美罗培南或头孢地尔联合替加环素分别表现出 10%（1/10）和 20%（2/10）的协同作用。在 ID-CAMHB 中，各种抗菌药物组合对 100%产 *bla*$_{KPC}$、*bla*$_{IMP}$、*bla*$_{VIM}$和 *bla*$_{OXA-48}$的 CRE 表现出较好的协同和相加作用。对于共产 *bla*$_{KPC}$ 和 *bla*$_{NDM}$ 的菌株，头孢地尔联合替加环素、美罗培南、多粘菌素或左氧氟沙星在两种肉汤中均未表现出协同作用。

结论 头孢地尔与替加环素联合使用可提高抗菌活性，是治疗 CRE 感染的一种有潜在价值的选择，仍需更多试验去验证。

PO-0987

碳青霉烯耐药铜绿假单胞菌分子流行病学和耐药机制研究

宋贵波、周飞
昆明医科大学第一附属医院

目的 了解昆明市两家医院微生物室分离的碳青霉烯耐药铜绿假单胞菌（CRPA）的分子流行病学特点和耐药机制。

方法 收集两院 2017 年 1 月至 2021 年 2 月微生物室分离的 81 株 CRPA，采用 MIC 法和 K-B 法检测其对常用抗菌药物的敏感性；采用多位点序列分型（MLST）检测其序列型（ST）并绘制最小生成树，进行同源性和遗传进化分析；聚合酶链式反应（PCR）扩增碳青霉烯酶酶基因（bla KPC、bla GES、bla IMP、bla VIM、bla SPM、bla NDM 和 bla OXA-40），经测序和 BLAST 比对确定其基因型；采用 PCR 扩增 oprD 基因全长，Sanger 测序并与标准菌株铜绿假单胞菌 PAO1 的 oprD 序列进行比对分析其突变；PCR 扩增 MexAB-OprM 外排泵过表达菌株的外排泵调节基因 mexR、nalC 和 nalD，结果进行 BLAST 比对分析其突变；应用微量滴定板试验检测其生物膜形成。

结果 81 株 CRPA 菌株对常用抗菌药物均表现出较高的耐药性；MLST 分型结果分为 36 种不同的 ST，其中 ST3645、ST3646、ST3647、ST3648 和 ST3649 为本研究中新发现的 ST，ST3390 为最常见的类型，占 41.98%（34/81）；碳青霉烯酶基因检测结果显示，其中 30 株携带 bla IMP-9 基因，22 株携带 bla VIM-2 基因，1 株携带 bla NDM-1 基因，未检出 bla KPC、bla GES、bla SPM 和 bla OXA-40 耐药基因；oprD 的突变分析显示，仅 3 株未发生任何形式的突变，在 78 株发生 oprD 突变的类型中，以碱基的插入或缺失造成的移码突变最常见（68/81），其中 nt109 位置缺失碱基 A 是最常见的突变之一（37/68），且 34 株 ST3390 均发生该突变；外排泵过表达的菌株有 17 株，占 20.99%，其调节基因蛋白的突变分析显示 NalC 蛋白的突变最常见，其突变类型有 G71E、A145V、Q182K、L206V 和 S209R；MexR 蛋白的突变类型有 V115E、L119K、V126E 和 L135H，其中菌株 CRPA51 发生 mexR 基因 nt135-146 的碱基缺失；NalD 蛋白的突变类型有 W49S 和 N130S，其中菌株 CRPA04 发生 nalD 基因 nt89 缺失碱基 A；微量滴定板形成试验检出形成生物膜的菌株有 74 株，占 91.35%。

结论 ST 型别丰富多样且 ST3390 耐药菌株存在院内播散和克隆传播，提示须严格做好耐药菌株的来源及传播的持续监测和感染防控措施；孔蛋白 OprD 的缺失或突变伴随生物膜形成是 81 株 CRPA 菌株的主要耐药机制。

PO-0988

基于熵驱动无酶扩增系统构建新型荧光传感器用于快速检测 HPV-18 E6/E7 mRNA

许伟、吴国球
东南大学附属中大医院

目的 本研究基于核酸链置换反应（熵驱动）的无酶扩增系统，以 HPV-18 E6/E7 mRNA 为链置换反应起始触发物，通过循环扩增反应生成大量信号产物；通过荧光纳米微球捕获信号产物，并构建荧光检测系统，实现对 HPV-18 E6/E7 mRNA 的快速、灵敏检测。本方法可应用于临床人乳头状瘤病毒感染的快速筛查。

方法 1.熵驱动扩增系统的构建：通过 NCBI 数据库对 HPV-18 基因组进行分析，选取保守区段的特异序列作为目标检测序列；在目标序列的基础上设计构建一种基于熵驱动的无酶扩增循环体系；利用数学模型分析该方法的理论可行性，并用非变性聚丙烯酰胺凝胶电泳验证核酸链间的程序性杂交方案；通过调整体系中各核酸链间的比例，以及改变反应的时间、温度、以及缓冲体系，获得最佳反应条件；研究核酸单、多点突变对检测结果的影响，评价该系统的灵敏度、特异度等。2.荧光传感器的构建及初步评价：在核酸链上标记生物素和地高辛，使其能被标记有亲和素的荧光纳米微球所捕获，从而实现信号的二次放大；使用修饰过抗地高辛抗体的试纸条对核酸-纳米微球复合物进行捕获；通过层析试纸条中的荧光纳米微球，将产物转化成荧光信号，并将信号进一步放大，以小型荧光扫描仪检测荧光信号，构建了一种基于熵驱动无酶扩增系统的荧光传感器。

结果 1.熵驱动扩增系统的构建：通过 NCBI 数据库查询到 HPV18 的全基因序列，并从其 E6/E7 基因保守序列中筛选出特异序列作为检测靶标；通过核酸计算软件 NUPACK 辅助设计了一套基于链置换反应的无酶等温扩增循环系统；理论计算结果显示产物转化效率可达到 99%；非变性凝胶电泳结果证实了核酸链之间可以实现程序性核酸置换，最终生成可与荧光纳米微球结合的核酸产物；；体系最佳反应条件为：100 nM 复合物 SBO、100 nM 链 F，避光恒温 37℃反应 60 min；在最优反应条件下靶标浓度在 100 pM 到 10 nM 之间时，该扩增体系中荧光强度与待测靶标浓度的对数呈线性关系，线性相关方程为 Y=395042logC-276257, R2=0.9753，最低检测下限约为 5 pM；该系统特异度高，单碱基错配可致荧光信号下降 95%以上；探针冻干 30 天内检测结果无统计学差异，（P=0.08）。、

结论 本研究成功构建了一种基于熵驱动的核酸无酶扩增系统，可实现扩增产物的信号放大，并通过偶联基于侧流免疫层析的荧光纳米放大系统，可实现目标 RNA 分子的有效检测。该传感器具有灵敏度高、特异度好、方法简便、成本低廉、快速检测等优点，可对 HPV-18 E6/E7 mRNA 进行快速检出，在临床 HPV 快速筛查中具有良好的应用前景。

PO-0989

ICU 念珠菌血流感染患者的临床特点及死亡的相关危险因素

陈霞、李艳明、刘文恩、杨勇文
中南大学湘雅医院

目的 分析重症监护病房（Intensive Care Unit，ICU）念珠菌血流感染的病原菌分布、患者临床特点及死亡相关危险因素。

方法 采用回顾性分析法，收集中南大学湘雅医院 2016 年 1 月至 2020 年 12 月 ICU 念珠菌血流感染患者的临床资料，感染相关指标以及预后情况，分析念珠菌血流感染病原菌分布及患者的临床特点。并根据预后将患者分为死亡组和生存组，采用单因素卡方检验及多因素 logistic 回归分析其死亡相关危险因素。

结果 在 80 例血流念珠菌感染患者中，白念珠菌感染率最高（36.3%）。药敏结果表明各种念珠菌均为野生型，对两性霉素 B 相对敏感。白念珠菌对氟康唑、伊曲康唑、伏立康唑相对敏感（均≥96.6%），非白念珠菌对氟康唑、伊曲康唑、伏立康唑有一定程度的耐药。80 例患者中死亡 29 例(36.3%)。单因素分析显示急性生理学与慢性健康状况 II（Acute Physiology and Chronic Health Evaluation II，APACHEⅡ）评分≥20、糖尿病及机械通气与念珠菌血流感染患者死亡相关。多因素 logistic 回归分析提示 APACHEⅡ评分≥20 是念珠菌血流患者死亡的独立危险因素（OR=0.220,95%CI：0.078~0.619，P=0.004）。

结论 白念珠菌是 ICU 患者念珠菌血流感染最常见的菌种。APACHEⅡ评分≥20 是念珠菌血流感染患者死亡的独立危险因素。

PO-0990

脆弱拟杆菌通过下调 NF-κB 信号通路抑制 TNF-α 诱导的结肠上皮细胞炎症反应

何秋月[1]、杜艳[2]、牛敏[2]
1. 昆明医科大学第一附属医院检验科
2. 昆明医科大学第一附属医院检验科

目的 探讨脆弱拟杆菌抑制 TNF-α 诱导的结肠上皮细胞 hcoEPIC 炎症反应的机制,以期发掘脆弱拟杆菌作为新一代益生菌的益生功能，为 CRC 的预防和治疗提供新的益生菌疗法。

方法 以 TNF-α 为诱导剂建立体外细胞炎症模型并分为 4 组, 即对照组、BF 组、TNF-α 诱导组、BF+TNF-α 组。首先用 BF 与正常结肠上皮细胞 hcoEPIC 共培养 4 小时，分别检测 BF 对 hcoEPIC 的粘附和侵袭能力；随后先用 TNF-α 诱导 hcoEPIC 细胞 4 小时后加入 BF 共培养，24 小时后分别用 CCK8 实验和 Annexin V-FITC/PI 法检测细胞存活率和凋亡情况情况；进一步采用 Western bloting 从蛋白水平检测不同处理组中 hcoEPIC 细胞内 NF-κB 信号通路关键蛋白 P-NF-κBp65 和 p-IκBα 的变化，再用 qPCR 方法从分子水平验证 NF-κB 和 IκBα mRNA 水平；最后用 ELISA 法检测该通路下游细胞因子 IL-1β、TNF-α、IL-10 的表达。

结果 脆弱拟杆菌能够粘附于正常结肠上皮细胞 hcoEPIC 上，但并不侵袭损伤细胞。与正常对照组相比，脆弱拟杆菌单独处理并不影响 hcoEPIC 细胞的细胞存活率和凋亡（P>0.05），但能显著降低由 TNF-α 诱导的细胞损伤和凋亡（P<0.05）；与 TNF-α 单独处理组相比，BF+TNF-α 组中 P-NF-κBp65 和 p-IκBα 蛋白表达水平和 NF-κB mRNA 和 IκBα mRNA 水平显著降低（P<0.05），细胞上清液中 IL-1β、TNF-a 的生成减少，IL-10 的释放增加（P<0.05）。

结论 脆弱拟杆菌能在体外增加 TNF-α 诱导的结肠上皮细胞存活率、抑制细胞凋亡和损伤；下调 NF-κB 信号通路、减少促炎性细胞因子 IL-1β、TNF-α 释放，增加抗炎性细胞因子 IL-10 的产生来对抗 TNF-α 诱导的炎症反应。

PO-0991

艰难梭菌感染的影响因素和治疗情况分析

高红林
广东省人民医院

目的 了解艰难梭菌感染的影响因素和分析艰难梭菌感染患者的治疗情况。

方法 回顾性分析广东省人民医院 2016 年 1 月 1 日-2020 年 12 月 31 日期间的 39 例艰难梭菌感染患者的基本资料，治疗方案以及预后情况；共有 39 例艰难梭菌 感染病例，其中男性患者占 79.49%，年龄大于 65 的患者占 56.41%，经检验， 对照组和病例组的大便性状、慢性肾脏损伤、

过去 3 月内有住院史、头孢菌素、喹诺酮类、侵入性机械通气、患者结局、年龄、治疗使用的抗生素个数有显著差 异（P<0.05），慢性肾脏损伤、过去 3 月内有住院史和治疗使用的抗生素个数是艰难梭菌感染的独立危险因素。39 例患者中，以甲硝唑治疗的患者为主占比 35.90%，其中治愈率 78.57%，未针对艰难梭菌使用抗菌药物的患者治愈率 83.33%。

结论 相比起其他患者，长期住院、高龄且患有基础疾病患者更易患艰难梭菌感染，应该控制存在独立危险因素患者的住院时间，且应严谨使用抗生素，对于已经艰难梭菌感染的患者医生应该先考虑调节肠道菌群，合理使用抗生素。

PO-0992

金属酶非泵出机制导致按蚊伊丽莎白菌对碳青霉烯类和氨曲南/阿维巴坦耐药

张晓兵、常彦斌、张代琴
重庆医科大学附属第一医院

目的 近年来，按蚊伊丽莎白菌感染日趋增加，且有爆发的报道，由于耐药模式存在地区差异性，本文回顾性分析该菌感染临床特征及可能的耐药机制。

方法 1）收集我院菌株，16S rRNA 鉴定。2）回顾性分析该菌感染患者临床资料,回归分析感染和死亡危险因素。3）测定该菌常用抗生素 MIC。4）检测该菌碳青霉烯酶和超广谱 β 内酰胺酶基因。5）碳青霉烯酶和五种外排泵基因克隆转化工程菌，测量转化株和空载质粒转化株 MIC，分析可能耐药机制。

结果 1）16S rRNA 鉴定：40 株脑膜炎伊利莎白菌 39 株应为按蚊伊丽莎白菌。2）Logistic 回归分析表明：39 例感染患者，冠心病、慢性阻塞性肺病、6 个月内手术史、贫血和全身性激素使用是感染独立危险因素；脑血管疾病、慢性阻塞肺疾病、鼻胃管置入、贫血是院内死亡危险因素，而贫血是死亡唯一独立危险因素。3）药敏实验**结果** 米诺环素 100%敏感、头孢他啶、头孢他啶/阿维巴坦、氨曲南、氨曲南/阿维巴坦、粘菌素均耐药。4）39 株按蚊伊丽莎白菌 blaGOB、blaBlaB、blaCME 基因阳性率分别为 94.9%、94.9%和 92.3%，未检出其他常见碳青霉烯酶基因和超广谱 β 内酰胺酶基因。5）基因功能显示：两种金属酶 BLAB 和 GOB 与碳青霉烯类耐药有关，blaCME 与头孢菌素类和单环类耐药有关；五种假定外排泵与该菌耐药并没有直接关系。

结论 1）传统微生物鉴定法易将按蚊伊丽莎白菌鉴定为脑膜炎伊丽莎白菌；该菌感染患者死亡率较高，冠心病、慢性阻塞性肺病、6 个月内手术史、贫血和全身性激素使用是该菌感染独立危险因素，贫血是死亡独立危险因素贫血是死亡的独立危险因素，应该高度重视。2）根据体外药敏试验结果，建议将米诺环素作为治疗该菌感染的首选抗生素。3）金属酶 BLAB 和 GOB 导致了该菌对碳青霉烯类和氨曲南/阿维巴坦耐药，而五种假定外排泵在耐药性方面没有发挥作用。

PO-0993

耐消毒剂基因 qacEΔ1-sul1 在 CRE 中的流行病学分析及其机制研究

陈丹丹
宁德市闽东医院

目的 检测耐碳氢酶烯类药物的肠杆菌科细菌（以下简称 CRE）中的的 qacEΔl-sull 基因，并对该基因在 CRE 的流行情况进行分析

方法 采用全自动微生物分析系统 VITEK 2-COMPACT 的鉴定卡、药敏卡进行细菌鉴定和药敏试验，应用 PCR 扩增法对 qacEΔ1-sul1 基因进行扩增，并测序分析

结果 检测 15 株耐碳氢酶烯药物的肺炎克雷伯杆菌中有 14 株携带 qacEΔI-sull 耐消毒剂基因，检出率的阳性率为 93%（14/15）
结论 耐消毒剂 qacEΔI-sull 基因极高的检出率表明肠杆菌科细菌对消毒剂的抗性极高,这种高抗性可导致医院常规消毒剂在正常规定使用浓度下无效,从而对环境耐药菌造成污染严重，此现象应引起医务人员对消毒剂浓度使用和医院感染的高度重视 。

PO-0994

创伤弧菌赖氨酸乙酰化的蛋白质组学分析

卢兆莲
山东大学第二医院

创伤弧菌(V. vulnificus)是一种嗜盐的河口细菌，可引起伤口坏死性感染或败血症，死亡率很高。赖氨酸乙酰化作为一种普遍的翻译后修饰(PTM)，几乎在细胞的各个方面发挥着重要的调控作用。在这里，我们使用抗乙酰赖氨酸免疫沉淀富集低丰度的 PTM 蛋白，然后进行 LC-MS/MS 分析。总的来说，我们在 841 种蛋白中检测到 2035 个赖氨酸乙酰化位点，占细胞总蛋白的 18.5%。乙酰基的生物信息学分析表明其在代谢调节中具有重要作用。更确切地说，参与碳代谢和生物合成的蛋白质是乙酰化的潜在目标。此外，通过对乙酰化组的研究，我们发现了两种乙酰化基序，一种是赖氨酸或精氨酸在+4/+5 位置，另一种是酪氨酸、组氨酸或苯丙氨酸在-1/+1 位置。此外，蛋白质相互作用网络分析表明，蛋白质乙酰化可以调节多种相互作用。本研究是创伤弧菌中的第一个乙酰基，为深入探讨创伤弧菌中赖氨酸乙酰化的生理作用提供了重要的开端。

PO-0995

Acquired mucoid phenotype of Acinetobacter baumannii: impact for the molecular characteristics and virulence

Wulin Shan、Huanhuan Zhang、Jinsong Kan、Meiling Yin、Jiayun Zhang、Lingling Wan、Renliang Chang、Ming Li
The First Affiliated Hospital of University of Science and Technology of China

Background Acinetobacter baumannii (A. baumannii), a major hospital-acquired pathogen, is a serious health threat and poses a great challenge to healthcare providers. Presently, limited studies focus on mucoid A. baumannii. The aim of this study was to analyze molecular characterization, virulence and its regulatory mechanism of mucoid A. baumannii.
Methods All strains, including multidrug-resistant mucoid (AB-R-M), multidrug-resistant non-mucoid (AB-R-NM) and carbapenem-susceptible non-mucoid A. baumannii (AB-S-NM), were isolated from different patients. The biofilm-forming ability was detected by crystal violet staining. Multilocus sequence typing (MLST) was performed on A. baumannii strains, and the virulence was determined in Balb/c mice injected by intraperitoneally (i.p.). mRNA sequencing was carried out to compare whole transcriptomes of mucoid and non-mucoid strains.
Results We observed the colonies of mucoid A. baumannii were moist, irregular round, with an elevated surface, and the wire drawing was positive. Gram staining data showed no difference in the morphology between mucoid and non-mucoid A. baumannii, and all strains were gram-negative coccidiella. Mucoid phenotype of A. baumannii could stably inherit regardless of transmitting these mucoid strains to 15 generations in the blood agar or 5 generations in the broth. Antibiotic susceptibility testing showed that all mucoid strains were multidrug-resistant. Notably, mucoid phenotype and antibiotic resistance weren't correlated with the amount of biofilm produced by A. baumannii. MLST data demonstrated that types of mucoid A. baumannii were ST2. Most (82.6%, 38/46) multidrug-resistant non-mucoid strains also belonged to the molecular type, ST2, and other types including ST129, ST158, ST195, ST80 and ST3. Additionally, mucoid

A. baumannii were more virulent than non-mucoid isolates in mouse model. Finally, our comparative transcriptomic data showed that the significantly altered 720 genes were mainly involved in six processes, including metabolic, cellular process, membrane, membrane part, catalytic activity and binding. Based on the GO enrichment, these genes are mainly enriched in transposon- and DNA-associated processes with significant q-values as calculated by the Benjamini-Hochberg procedure (q-values < 0.05). Bioinformatics analysis and literature review suggested that 15 genes, especially for IX87_RS16955 (acnA), IX87_RS10800 (XanP), IX87_RS12875 (GlmM), IX87_RS00885 and IX87_RS12395 (bfr), were possibly associated with the phenotype and virulence of mucoid A. baumannii.
Conclusions Our study comprehensively describes the molecular characterization, virulence and candidate regulatory genes of mucoid A. baumannii. Mucoid phenotype was adaptive response of A. baumannii to external stress and could be inherited stably. The morphology of mucoid A. baumannii was significantly different from non-mucoid strains. Besides, mucoid A. baumannii were resistant to most antibiotics, showed no biofilm-forming ability, belonged to ST2 type, and had high virulence. Notably, ST2 strains, associated with multidrug-resistance, potentially have spread in Anhui, China. Furthermore, our comparative transcriptomic data indicated that 15 genes were possibly associated with mucoid formation and virulence regulation of mucoid A. baumannii. The data would improve our understanding of phenotypic characteristics and the virulence of mucoid A. baumannii, and also provide novel insights in the prevention and therapeutics against these strains-related infections.

PO-0996

基于表面增强拉曼光谱鉴定志贺菌四种血清型

李佳
南京大学医学院附属鼓楼医院

背景 志贺菌感染形势严峻，但其检测与药敏需 3 天以上，无法满足临床需求。表面增强拉曼光谱(SERS)技术具有快速、高灵敏度和指纹特征光谱等优势，但对临床样本分析处于探索阶段。
目的 我们尝试将 SERS 技术用于志贺菌快速检测，并建立志贺菌四种主要血清型的数据库。
方法 首先制备纳米银溶胶，通过透射电镜、紫外可见分光光度仪对所制备的纳米材料进行分析表征。筛选出 SERS 增强效果最佳的材料作为检测志贺菌的活性基底，分别检测福氏志贺菌、宋内志贺菌、痢疾志贺菌、鲍氏志贺菌的拉曼信号，并通过 SIMCA 软件对所测得的数据进行正交偏最小二乘法判别分析(OPLS-DA)，结合十折交叉检验验证此方法的准确性。
结果 在拉曼位移为 550～1800cm-1 光谱内，福氏志贺菌有 6 处明显的拉曼谱峰，宋内志贺菌有 7 处明显的拉曼谱峰，痢疾志贺菌有 8 处明显的拉曼谱峰，鲍氏志贺菌有 5 处明显的拉曼谱峰。四种不同血清型志贺菌的拉曼谱峰位置以及强度区别明显。志贺菌四种不同血清型之间在 OPLS-DA 得分图中虽有一些重叠，但有明显的分离趋势，而且 R2X(cum)=0.983，表明重新组合的几个变量所能解释的 X 变量的比例已达 98.3%，说明该模型预测能力较好。通过十折交叉检验得到测试集的正确率为 95.22%。
结论 初步研究表明表面增强拉曼光谱结合 OPLS-DA 统计分析可作为临床志贺菌四种血清型检测的一种手段。

PO-0997

临床白色念珠菌感染诱导人气道上皮细胞损伤的作用研究

史清梅、孟繁君、王利新
宁夏医科大学总医院

目的 探究临床白色念珠菌感染对人气道上皮细胞的免疫损伤作用。
方法 分离临床白色念珠菌菌株并进行产膜能力分析；体外构建原代人气道上皮细胞培养损伤模型。酶标法检测细胞 ROS 和 LDH 水平；ELISA 法检测细胞 LDH 和细胞因子 hBD2、GM-CSF、G-CSF 的释放；Western blot 法检测细胞紧密连接蛋白 ZO-1 以及 MAPK 信号通路中 ERK1/2、JNK 和 p38 总蛋白及磷酸化蛋白表达水平。
结果 对临床分离的白色念珠菌进行产膜能力分析，并成功构建人上皮细胞损伤模型，与对照组相比，白色念珠菌感染可明显诱导上皮细胞 LDH 释放，促使胞内活性氧 ROS 的累积、细胞因子表达增加，进而下调细胞紧密连接蛋白 ZO-1 的表达，激活 MAPK 信号通路相关蛋白 p38、ERK1/2 的表达。
结论 白色念珠菌感染人气道上皮细胞造成免疫损伤主要通过激活 MAPK 信号通路 p38、ERKs 介导的氧化应激发挥作用。

PO-0998

尿路感染 B 群链球菌的耐药特征与 CAMP 试验敏感性分析

时翠销、王刚、黄颖、李亚娟、徐元宏
安徽医科大学第一附属医院

目的 研究尿路感染 B 群链球菌的耐药特点、耐药基因分布情况及 CAMP 试验敏感性和编码 CAMP 因子的 cfb 基因的表达情况。
方法 采用纸片扩散法和 Vitek 2 Compact 仪器法测定抗菌药物的敏感性，D 试验检测红霉素诱导的克林霉素耐药，PCR 法检测抗生素相关耐药基因；进行 CAMP 试验，通过检测 16 S rRNA 基因片段及 cfb 基因、生化试验、MALDI-TOF MS 鉴定菌株。
结果 51 株 B 群链球菌对氨苄西林、达托霉素、利奈唑胺、呋喃妥因、青霉素、奎奴普丁/达福普汀、替加环素、万古霉素耐药率为 0，对红霉素、四环素、克林霉素、左氧氟沙星、莫西沙星、环丙沙星耐药率分别为 66.7%、66.7%、49.0%、47.1%、49.0%、47.1%。红霉素和四环素主要耐药基因为 ermB 和 tetM, 喹诺酮类抗生素耐药基因 gyrA 和 parC，它们的检出率都为 78.4%。CAMP 试验结果显示 3 株阴性、9 株弱阳性、39 株阳性，经生化试验、cfb 基因、16 S rRNA 检测、MALDI-TOF MS 鉴定，除 2 株阴性株及 2 株弱阳性株未检测出 cfb 基因，其余方法鉴定均符合为 B 群链球菌的特征。
结论 尿路感染的 B 群链球菌对多种抗生素敏感，对红霉素、克林霉素、四环素、喹诺酮类抗生素耐药性高，耐药基因携带情况与耐药性具有一定相关性；CAMP 试验及 cfb 基因对于 B 群链球菌的鉴定缺乏敏感性。

PO-0999

小檗碱对耐甲氧西林金黄色葡萄球菌体外抑菌作用及其机制的研究

周芳芳、王蕾
上海市第八人民医院

目的 观察中药单体成分小檗碱及联合三种抗生素（庆大霉素、左氧氟沙星、阿米卡星对耐甲氧西林金黄色葡萄球菌的抑菌效果；探究小檗碱对 MRSA 的抑菌机制，为中药单体成分小檗碱在抗菌中的临床应用奠定基础。
方法（1）采用微量肉汤稀释法测定小檗碱、GEN、LEV、AMI 对 26 株临床分离的 MRSA 的最低抑菌浓度（Minimum Inhibitory Concentration，MIC），同时采用棋盘法测定小檗碱联合 GEN、LEV、AMI 对 MRSA 的 MIC，观察小檗碱对 MRSA 的抑菌效果；（2）采用时间杀伤曲线研究小檗碱联合抗生素对 MRSA 的抑菌动力学；采用培养基电导率实验观察小檗碱对 MRSA 通透性的改变；透射电子显微镜观察不同浓度小檗碱作用后 MRSA 形态学的变化。
结果 小檗碱对 26 株 MRSA 的 MIC 范围为 32~256 μg/mL。小檗碱分别联合庆大霉素、左氧氟沙星、阿米卡星对 MRSA 均有明显的抑菌效果。8 μg/mL、16 μg/mL、32μg/mL、64 μg/mL、128μg/mL 小檗碱作用菌体 4 小时后，电导率分别增加了 24.49% 、34.59%、50.34%、89.12%、91.84%。透射电子显微镜观察发现低浓度（8μg/mL；1/8 MIC）小檗碱对细菌无明显破坏作用，MRSA 菌体结构完整；高浓度（512 μg/mL；8 MIC）小檗碱诱导 MRSA 的细胞壁结构大量破坏溶解，菌体内容物大量外泄，导致细菌裂解死亡。
结论 小檗碱对 MRSA 有较理想的抑菌效果；小檗碱分别联合庆大霉素、左氧氟沙星、阿米卡星对 MRSA 均有明显的抑菌作用；低浓度小檗碱通过改变细胞膜通透性，从而达到抑制细菌的作用；而高浓度小檗碱通过破坏和溶解 MRSA 细胞壁的结构，从而达到杀灭细菌的作用。

PO-1000

Characterization of a novel B1 subclass metallo-β-lactamase gene, blaAFM-1, located on an IncW-type conjugative plasmid in Alcaligenes faecalis

Yingcheng Qin
Southern medical universty Nanfang hospital

Background and objective Metallo-β-lactamases (MBLs), due to the strong hydrolysis and plasmid-mediated properties, make carbapenems resistance widely spread, and due to the lack of effective carbapenemase inhibitors of carbapenem-resistant bacteria, carbapenem-resistant bacteria cause us great attention.
The novel type of MBLs, blaAFM-1 gene (GenBank accession number: MK143105.1) was first discovered in an Alcaligenes faecalis strain by us. It is quite different from other currently known acquired B1 MBLs genes, and the highest necleotide homology with NDM-type genes is only 85%. Like the other MBLs, AFM-1 enzyme also has two metal ions, and the AFM-1 enzyme has the ability to hydrolyze carbapenems. This research focuses on the genomics study of different strains carrying the blaAFM-1 gene from different species, which provides a theoretical basis for future research on the blaAFM-1 gene.
Methods Whole-genome sequencing (WGS) technology was used to sequence a Alcaligenes faecalis strain AN70 including blaAFM-1 gene. Conjugation assay was performed. Cloning and expressing of blaAFM-1 were designed to verify the function of AFM-1 to hydrolyze carbapenems and common β-lactamase substrates. CarbaNP was conducted to confirm AFM-1 belongs to

carbapenemase. Homology modeling was applied to predict the spacial structure of AFM-1. We also screened out strians that carried blaAFM-1 gene by conventional PCR and sequencing.
Results Through the analysis of WGS data of AN70 strain, blaAFM-1 was identified on a conjugative IncW-type plasmid, and one novel class 1 integron gene cassette array arranged as aacA3-blaOXA-21-catB3-dfrA1b was found on the AN70 chromosome. Transfer of the blaAFM-1-bearing plasmid from AN70 to E.coli J53 conferred meropenem resistance to the transconjugants at a frequency of 1.3×10−5, transconjugator also demonstrated reduced susceptibility of carbapenems and common β-lactamase substrates. Cloning of blaAFM-1 (pET-28a-AFM-1-Top10) was inhibited by imipenem-EDTA in MBL Etest experiment and it showed resistance to carbapenems and common β-lactamase substrates. AN70 and its clone (pET-28a-AFM-1-Top10) can hydrolyze imipenem. AFM-1 enzyme was composed of an αβ/βα sandwich structure, with two zinc atoms at its active site, similar to other B subclass metallo-β-lactamases. Through the conventional PCR, we also screened out 4 strains that carried blaAFM-1 gene.
Conclusions BlaAFM-1 is a novel B1 subclass carbapenemase gene, which could render the carbapenems and common β-lactamase antibiotics ineffective. What's more, the horizontal transfer of blaAFM-1 via plasmid conjugation allows antibiotic resistance to spread widely in bacteria. Further kinetic parameters and prokaryotic expression of AFM-1 enzyme are needed to study.

PO-1001

基于高通量测序探究复发性流产人群生殖道核心菌群

赵付菊[1]、陈艺升[2]、高晶[2]、李翠[2]、王志恒[2]、杜美蓉[2,3,4]、应春妹[2]
1. 复旦大学附属华东医院
2. 复旦大学附属妇产科医院
3. 国家人口和计划生育委员会计划生育药具重点实验室
4. 上海市女性内分泌相关疾病重点实验室

目的 复发性流产（recurrent spontaneous abortion，RSA）发病机理复杂，至少一半人群病因不明，对于该病诊断和治疗仍是临床医生面临的棘手难题。本研究拟探究 RSA 人群阴道微生物群特征，分析是否存在疾病相关核心菌群，以期为该病辅助诊断及病因提供新思路。
方法 2009 年 9 月至 2020 年 1 月共招募 RSA 患者 120 例及分娩 2 次或以上活胎健康对照人群 20 例，采集其阴道分泌物，利用 Illumina MiSeq PE300 高通量测序平台对样本中细菌 16S 核糖体 RNA 进行 V3-V4 区测序，过滤和拼接后获得有效序列，通过 RDP 贝叶斯算法对其进行物种注释，采用 Chao 及 Shannon 指数分析样本中微生物丰度及多样性，主坐标分析法分析组间样本微生物群落构成，运用曼-惠特尼 U 检验分析两组人群阴道微生物群物种差异，最后利用线性回归分析鉴别核心菌群。
结果 RSA 人群阴道微生物群丰度及多样性较对照人群有所下降，其中菌群丰度下降有显著统计学差异。两组人群菌群构成有显著差异，共发现 34 种差异菌属，RSA 人群阴道巨球型菌属相对丰度显著升高；而沙雷氏菌属及嗜血杆菌属等 11 种菌属在该人群中缺失；余 22 种菌属相对丰度较对照组有所降低，其中 5 个菌属包括棒状杆菌属、红球菌属、假单胞菌属、鞘氨醇单胞菌属及伯克霍尔德菌属为组间差异核心菌群。
结论 基于二代测序方法发现 RSA 人群与健康对照人群相比阴道微生物群物种丰度及组成存在显著差异，其中棒状杆菌属、红球菌属、假单胞菌属、鞘氨醇单胞菌属及伯克霍尔德菌属为疾病相关核心菌群，而巨球型菌属可能与病因有关。

PO-1002

新冠肺炎疫情中呼吸道常见病原体 IgM 抗体联合检测结果分析

高春波、苏丽菊
哈尔滨市第一医院

目的 对疑似新冠肺炎病例的诊断提供鉴别诊断依据，以便及时进行临床分类、隔离和治疗；掌握新型冠状病毒疫情下，我院发热门诊疑似新冠肺炎患者和普通呼吸道感染性疾病患者主要病原体感染的流行情况及新型冠状病毒确诊者有无其他病原体的合并感染情况，为临床精准治疗提供新的依据。

方法 分析自 2020 年 1 月 21 日~2020 年 3 月 3 日，我院 1479 例患者血清中呼吸道主要病原体 IgM 抗体联合检测结果，其中包括新型冠状病毒确诊者 9 例，发热门诊疑似新冠肺炎患者 741 例和普通呼吸道感染性疾病患者 729 例。我们采用间接免疫荧光法同时检测 9 项呼吸道感染病原体的 IgM 抗体，包括嗜肺军团菌(LP)、肺炎支原体(MP)、肺炎衣原体(CP)、Q 热立克次体(COX)、腺病毒(ADV)、呼吸道合胞病毒(RSV)、甲型流感病毒(IFA)、乙型流感病毒(IFB)及副流感病毒(PIVs)，并对结果进行分析比较。

结果 1479 例患者血清 9 项病原体 IgM 抗体总阳性率为 24.14%，混合感染检出率为 6.02%，其中肺炎支原体检出率最高（11.50%），和其他病原体阳性率比较差异均具有统计学意义(P<0.05)，其次为乙型流感病毒(5.0%)；9 例新型冠状病毒肺炎感染者 9 项呼吸道感染病原体的 IgM 抗体均为阴性；741 例发热门诊疑似新冠肺炎患者 9 项呼吸道病原体检出率为 16.46%，其中乙型流感病毒阳性检出率最高为 7.69%；729 例普通呼吸道感染性疾病患者阳性率为 32.24%，其中肺炎支原体(MP)阳性检出率最高为 18.66%。

结论 本时期我院新型冠状病毒肺炎感染者与 9 项呼吸道病原体无合并感染；呼吸道感染主要病原体为肺炎支原体，发热门诊疑似新冠肺炎患者的呼吸道主要病原体为乙型流感病毒。

PO-1003

碳青霉烯耐药肺炎克雷伯菌基因组流行病学特征及耐药机制研究

孙青阳
中国人民解放军联勤保障部队第 903 医院

目的 肺炎克雷伯菌（Klebsiella pneumoniae）是一种常见的医院感染性病原体，随着碳青霉烯类抗生素在临床的广泛使用，碳青霉烯类耐药肺炎克雷伯菌（CRKP）的分离率逐年上升。本研究旨在明确多重耐药肺炎克雷伯菌的分子流行病学特征与耐药机制，并应用全基因组测序（WGS）溯源本院分离的 CRKP 同源性及传播途径，为 CRKP 感染的治疗和医院感染控制提供科学依据。

方法 收集本院 2016 年 4 月 1 日～2018 年 3 月 31 日期间，分离自两院区不同标本类型的 138 株肺炎克雷伯菌，对常见抗生素采用平板稀释法和肉汤稀释法测定最低抑菌浓度（minimum inhibitory concentrations, MICs），聚合酶链反应（PCR）明确菌株是否携带碳青霉烯耐药基因，采用脉冲场凝胶电泳（Pulsed-field gel electrophoresis, PFGE）分析菌株间的同源性，利用 Illumina Hiseq X10 与 PacBio RS II 高通量测序平台进行全基因组测序，通过菌株基因组相似性分析本院 CRKP 暴发流行株，追踪这些菌株的可能传播途径。

结果 138 株肺炎克雷伯菌中有 47 株为 CRKP，47 株 CRKP 除对磷霉素（耐药率 38.3%）、替加环素（耐药率 10.6%）、多黏菌素（耐药率 2.1%）相对敏感外，对其余 18 种抗菌药物（耐药率>74.5%）。47 株 CRKP 均检出 blaKPC-2 基因；PFGE 分型检测出 16 株 CRKP 属于同一克隆，其余 PFGE 型别菌株分布离散性较大，散发于不同时期和不同病区。利用菌株间核心基因组 SNP 序列差异构建系统发生树，可将 16 株 ST11 型菌分成 2 簇，未发现两院区之间的传播流行。

结论 CRKP 可通过获得携带多重耐药菌的质粒促使耐药菌在院内传播与暴发流行，全基因组测序可为追踪 CRKP 院感暴发流行与传播提供更为准确的研究手段。

PO-1004

蚯蚓小分子量抗菌肽对革兰阴性菌抑菌效果研究

聂兆超
山东大学第二医院

目的 通过应用大孔树脂对蚯蚓小分子量的抗菌肽进行初步分离纯化，研究所提取抗菌肽对临床常见革兰阴性菌的抑菌作用，探索应用大孔吸附树脂对蚯蚓小分子量的抗菌肽进行分离纯化的可行性。
方法 将蚯蚓匀浆，反复冻融，浸提，高速离心，经过超滤柱超滤截留，得到低分子量的多肽。100℃加热法除去杂蛋白，用大孔吸附树脂吸附，解吸。有机溶剂丙酮沉淀解吸物质，初步纯化了蚯蚓低分子量的抗菌肽。用微量肉汤稀释法检测所提取的抗菌肽对广泛耐药型和非广泛耐药型铜绿假单胞菌、鲍曼不动杆菌、粘质沙雷菌等的抑菌作用，并统计最小抑菌浓度。采用 SPSS 进行统计学分析。
结果 蚯蚓在匀浆、磷酸盐缓冲液浸提后，经过超滤柱超滤截留，得到了一部分抗菌肽，经过 100℃加热灭活后，除去了一部分不耐热的杂蛋白，剩余含量约占 21.7%。后经大孔树脂进一步纯化得到的抗菌肽对广泛耐药型和非广泛耐药型铜绿假单胞菌、鲍曼不动杆菌、粘质沙雷菌均有不同程度的抑制作用。虽然不同菌种其 MIC 的范围有所不同，但是菌种间的 MIC_{50} 较为集中。
结论 应用大孔树脂对蚯蚓小分子量抗菌肽的初步分离提取有一定的可行性，采用本研究方法提取的抗菌肽，对临床常见革兰阴性菌具有广谱的抗菌活性。

PO-1005

2019-2020 年临沂地区耐碳青霉烯类肠杆菌耐药基因型及耐药性分析

高春海、孙淑红
临沂市人民医院

目的 了解我院耐碳青霉烯类肠杆菌（CRE）的产酶类型及头孢他啶-阿维巴坦（CZA）对该类细菌的药物敏感性，为临床合理用药提供依据。
方法 选取 2019 年 1 月～2020 年 12 月临床标本分离获得的 179 株 CRE，用改良碳青霉烯灭活试验（mCIM 试验）和乙二胺四乙酸（EDTA）协同碳青霉烯灭活试验（eCIM 试验）和 GeneXpert 两种方法检测碳青霉烯酶，用 K-B 法检测 CZA 的药物敏感性。
结果 179 株 CRE 中，mCIM 阳性 174 株（97.2%），eCIM 阳性 147 株（84.5%）；产丝氨酸酶 27 株（15.5%），金属酶 147 株（84.5%）。GeneXpert 检测结果与 mCIM、eCIM 表型检测结果一致。174 株 mCIM 阳性菌株对 CZA 的敏感率为 33.3%（58/174），其中 27 株产丝氨酸酶菌株敏感率为 96.3%（26/27），147 株产金属酶菌株 100%耐药。
结论 CZA 对产丝氨酸酶 CRE 有较高敏感性，检测 CRE 是否产碳青霉烯酶以及产酶类型有利于指导临床对该药物的合理利用。

PO-1006

诺卡菌菌种分布及耐药状况分析

于嘉崴
滨州医学院烟台附属医院

目的 本实验旨在研究 2017 年至 2019 年从中国烟台分离出的 19 株诺卡氏菌的物种分布和药物敏感性。

方法 通过对 16SrRNA 基因片段(1480bp)的测序和布鲁克微生物质谱(MALDI-TofMS)进行明确的物种鉴定。用微溴稀释法检测分离物对 15 种常用抗生素的敏感性。
结果 运用上述两种方法，将 17 株诺卡氏菌分离株从 19 个标本中鉴定了出来，并且证实出了五个物种，然而这两种方法还存在一些漏洞，MALDI-TofMS 常常将盖尔森基兴诺卡菌的两株菌株误认为是豚鼠诺卡菌。在鉴别出的物种中最常见的是鼻疽诺卡菌。在本次试验中，所有分离出来的菌株均对甲氧苄啶/磺胺甲恶唑和阿米卡星敏感，其次是利奈唑胺和替加环素。某些抗生素的敏感性和最低抑菌浓度与该物种显著相关。
结论 这些关于诺卡氏菌菌种分布和抗生素耐药性检测的结果进一步加深了我们对中国烟台地区诺卡氏菌多样性的理解，从而支持更准确的经验治疗的实施。

PO-1007

MALDI TOF MS 快速检测产碳青霉烯酶肺炎克雷伯菌的应用

袁晨燕
东南大学附属中大医院

目的 快速检出产碳青霉烯酶的肺炎克雷伯菌可为临床相关感染用药及控制医院感染提供依据，利用基质辅助激光解吸电离飞行时间质谱(matrix-assisted laser desorption/ionization-time of flight mass spectrometry, MALDI-TOF MS）建立鉴定产碳青霉烯类肺炎克雷伯菌的试验平台可对产碳青霉烯酶的肺炎克雷伯菌进行快速筛选。
方法 收集我院 2019 年 4 月 1 日至 2019 年 5 月 20 日分离肺炎克雷伯菌，依据对碳青霉烯类的活性可分为 CRKP 和 CSKP，对碳青霉烯类耐药的肺炎克雷伯菌 CRKP 进行改良的碳青霉烯灭活试验（mCIM），用水解底物法检测碳青霉烯酶的活性，其与 0.5mg/ml 美罗培南共孵育 1 小时候后以 MALDI TOF MS 检测特征水解蛋白峰。
结果 共分离得到肺炎克雷伯菌 210 株，其中 109 株为 CRKP（51.9%），109 株 CRKP 中 mCIM 试验阳性率为 80.07%；MALDI TOF MS 底物水解法阳性率为 78%；基于 MALDI TOF MS 的筛选模型在 CRKP 和 CSKP 中得到 3 个差异蛋白峰，分别位于 6100m/z, 11108m/z 和 13048m/z。
结论 基于 MALDI TOF MS 的 CRKP 快速筛选技术有望缩短筛选时间，为临床感染用药和院内感染控制提供有力的支持

PO-1008

呼吸道感染病原体检测方法的选择

公衍文
山东大学第二医院

目的 了解呼吸道感染病原体检测方法优缺点，选择最合适的检测策略。
方法 病原学诊断对呼吸道感染性疾病尤其重要，针对病原体抗原、抗体、核酸等通开展了一系列检验项目，将不同检测项目异同比较，以及不同检测方法/组合的选择建议如下。
结果 （1）门急诊社区获得性肺炎（CAP）患者：怀疑病毒性肺炎，如条件允许首选“甲型/乙型流感及呼吸道合胞病毒核酸联合快速检测”， 其次是“呼吸道病原体抗原检测”，可选择“呼吸病原体 IgM 抗体检测”作为辅助诊断。以上检验项目优势是检验周期短（0.5-1h），在急诊检验就可完成检测。（2）需要住院或需要进一步明确病原的 CAP 患者，如条件允许，建议做细菌培养+“13 种呼吸道病毒核酸检测”或“呼吸道病原体谱抗体，有助于及时确认感染病原体。（3）医院获得性肺炎（HAP）患者，如条件允许，可选择 13 种呼吸道细菌核酸检测，或细菌/真菌培养（可获得药敏结果）。（4）对病原体难以明确的急危重症患者，可选择外送做 mNGS，但最好能与微生物室沟通，排除正常菌群和定植菌，选择合适的常规方法对可疑病原菌做进一步确认。（5）对疑似结核杆菌

感染患者，抗酸染色、结核培养、结核杆菌 DNA 检测、Gene-Xpert 的检出限分别是 10^5CFU/mL、10^4CFU/mL、10^3CFU/mL、10^2CFU/mL，可以根据临床需要以及患者经济能力进行选择。结核感染 T 细胞检测能反映患者是否接触或感染过结核杆菌（不能确定是否为现症感染），阴性预测值大且有助于不易获得标本的肺外结核感染诊断。
结论 呼吸道疾病的诊断往往需要“组合拳”，不同检验项目或检验方法各有其优缺点，选择最合适的某一项或某些检验项目，才能较为准确的实现疾病的诊断、疗效监测、预后判断等目的。

PO-1009

去泛素化酶 USP24 促进 TBK1 的降解调控 EV71 感染的机制研究

顾锦[2]、史伟峰[1]
1. 苏州大学附属常州市第一人民医院
2. 苏州大学附属常州市第一人民医院

Objective We used loop-mediated isothermal amplification (LAMP) to detect the nucleic acid of EV71, and provide the basis for the rapid diagnosis of EV71 infection in clinic. EV71 possesses a complex immune escape mechanism that hinders the innate immune response of host cells. Innate immunity is the body’s first line of defense against infection by pathogenic microorganisms. When they invade host cells, the host recognizes pathogen-associated molecular patterns (PAMPs) through its pattern recognition receptors (PRRs). The downstream aptamer protein cascades are then stimulated to activate the corresponding signaling pathways in host cells and induce the production of type I interferon (IFN-I) and various pro-inflammatory cytokines to resist the infection of pathogenic microorganisms. Previous studies have shown that deubiquitinating enzymes play an important role in antiviral innate immunity. This paper aims to explore the regulatory mechanism of deubiquitinating enzyme USP24 in the innate immune response caused by EV71 infection, so as to provide a new idea for clinical treatment of hand, foot and mouth disease.
Methods Fourteen pharyngeal samples were collected, EV71 as well as 19 kinds of common respiratory viruses were detected by LAMP. Human rhabdomyosarcoma (RD) cells were infected with EV71 for 8 h postinfection (poi). The total RNA of the cells was extracted and the expressions of 88 deubiquitinating enzymes were analyzed by PCR microarray. USP24 knockdown plasmids (shUSP24) were transfected into RD cells at 48 h, and total RNA was extracted from the cells. The replication level of EV71 and the expression of USP24 mRNA were detected by RT-qPCR, and then the production of IFN-β was further detected. The phosphorylation level of transcription factor IRF3 was detected by Western blot. The interaction between USP24 and TBK1 was detected by immunocoprecipitation method.The overexpressed plasmids of TBK1 with Ub, Ub-K48 or Ub-K63 mutated plasmids were co-transfected into HEK293T, respectively, and the effects of USP24 on TBK1 ubiquitination and protein stability were analyzed.
Results Among the 14 pharyngeal samples, 22 viruses were positive by LAMP, including 2 cases of human rhinovirus combined with EV71, 4 cases of human rhinovirus, 6 cases of human rhinovirus combined with coxsackie virus A6, 2 cases of human parainfluenza virus type 1 or 3. Whereas, EV71 and coxsackie virus A6 were further confirmed using q-PCR by Changzhou CDC. EV71 infection promoted the expression of USP24. Immunoprecipitation assay showed that endogenous USP24 could interact with TBK1, and USP24 specifically removed the K63 ubiquitin chain of TBK1 molecule to reduce its stability, thereby inhibiting downstream type I interferon expression and antiviral immune response. The level of p-IRF3 in RD cells was not significantly increased after EV71 infection. However, the level of p-IRF3 was distinctly upregulated after knockdown of USP24 gene, and the mRNA and protein levels of IFN-β were remarkably increased. Knockdown of USP24 promoted the nuclear translocation of IRF3 by

immunofluorescence antibody detection, and inhibited EV71 replication and reduced the cytopathic effect.
Conclusion LAMP method can quickly detect EV71 in clinical samples, and provide the basis for clinical diagnosis of EV71 infection. EV71 infection can upregulate the expression of USP24. Subsequently, USP24 specifically removes the K63 ubiquitin chain on TBK1 molecule and redues the stability of TBK1 protein, which negatively regulates the TBK1-mediated IFN-I innate immune signaling pathway.

PO-1010

Mechanism of Notch Signal Regulating Alveolar Epithelial Cell Autophagy in Klebsiella Pneumoniae

Zhiyun Shi 、Wei Jia
Medical Experimental Center, General Hospital of Ningxia Medical University

Objective To investigate the molecular mechanism of Notch signaling regulating alveolar type II epithelial cell autophagy in Klebsiella pneumoniae infection.
Methods Klebsiella pneumoniae (KPN) -infected human alveolar type II epithelial cells (ACEII) A549 cell model was constructed. The autophagy inhibitor 3-Methyladenine (3-MA) and γ-secretase inhibitor (DAPT) were used to 24 hours, 48 hours, and 72 hours of action on A549 cells. Real-time fluorescent quantitative PCR was used to detect the mRNA expression of autophagy-related genes LC3 and Notch signal pathway Notch1. Western blot was used to detect the protein expressions of LC3 and Notch1. ELISA was used to detect the cell supernatant INF-γ, TNF-α and IL-1β.

Result The results showed that human alveolar typeⅡ epithelial cell A549 model infected with Klebsiella pneumoniae could significantly up-regulate the expression of Notch1 and autophagy-related protein LC3 and promote the production of inflammatory factors (IL-1β, TNF-α, INF-γ) at 24h, 48h and 72h after infection. The inhibition of autophagy by 3-MA can down-regulate the expression of autophagy-related proteins LC3 and Notch1 and the production of inflammatory cytokines. DAPT inhibition of Notch signal can down-regulate the expression of Notch1 and LC3 and the production of inflammatory factors.

Conclusion Klebsiella pneumoniae infection of typeⅡ alveolar epithelial cells can activate Notch signal and induce autophagy. Autophagy-related proteins LC3 and Notch1 have the same trend at transcriptional and protein expression levels. Autophagy and Notch signals play an important role in Klebsiella pneumoniae infection of alveolar typeⅡ epithelial cells.

PO-1011

MALDI-TOF MS 对临床侵袭性丝状真菌的快速鉴定技术的研究

谢良伊
湖南省人民医院

目的 评价基质辅助激光解吸电离飞行时间质谱（MALDI-TOF MS）技术在临床常见丝状真菌鉴定中的应用价值。
方法 收集 2017 年 4 月-2019 年 7 月本院各种类型临床标本中分离培养的 65 株丝状真菌，以及某三甲医院惠赠的 26 株丝状真菌。对这 91 株丝状真菌通过传统形态学鉴定、DNA 测序及 MALDI-TOF MS 鉴定方法后，以 DNA 测序结果为标准，与另外 2 种方法的鉴定结果进行统计学比较，评价 MALDI-TOF MS 在临床丝状真菌鉴定上的应用。

结果 在 28℃和 35℃条件下培养的菌株经质谱仪鉴定后，χ2 检验显示 P>0.05，提示培养温度差异对结果无统计学意义；以 DNA 测序结果为金标准，传统形态学方法的正确鉴定率为 81.3%（74/91），而基于 MALDI-TOF MS 技术的正确鉴定率可达 97.8%（89/91）；研究中，使用“甲酸乙腈提取法”提取蛋白后，丝状真菌质谱鉴定的正确率为 90.1%（82/91），而“磁珠研磨法”提取蛋白后的质谱鉴定率则为 97.8%（89/91）。
结论 临床常规工作中使用质谱仪鉴定常见丝状真菌时，培养温度不会影响质谱鉴定结果；改良“磁珠研磨法”提取蛋白后质谱仪鉴定的正确率优于质谱仪推荐“甲酸乙腈提取法”；MALDI-TOF MS 技术在常见丝状真菌的鉴定上，相比于传统形态学鉴定来说，该技术更快速、客观、高效及准确。

PO-1012

Pleural fluid GSDMD is a novel biomarker for the early differential diagnosis of pleural effusion

Pu Li[1]、jing shi[2]
1. Second Affiliated Hospital, Chongqing Medical University
2. First Affiliated Hospital, Chongqing Medical University

Objective Gasdermin D (GSDMD), controlling pyroptosis in cells, has multiple physiological functions. The diagnostic role of GSDMD in pleural effusion (PE) remains unknown.
Methods Sandwich ELISA kits that we developed were applied to measure the level of GSDMD for 335 patients with the definite cause of PE, including transudative pleural effusion, tuberculous pleural effusion (TPE), parapneumonic pleural effusion (PPE), and malignant pleural effusion (MPE). The diagnostic accuracy of the Light’s criteria vs the new marker GSDMD was performed. Clinical follow-up of 40 cases of PPE was conducted and divided into efficacy group and non-efficacy group according to therapeutic outcome. Nucleated cells (NCs) in pleural effusion were isolated and further infected with bacteria to verify the cell source of GSDMD.
Results The diagnostic accuracy of GSDMD for the diagnosis of PE were 96% (sensitivity) and 94% (specificity). The receiver operating characteristic (ROC) curve indicated that GSDMD can be an efficient biomarker for differential diagnosis of transudative pleural effusion and other groups (all AUC ＞ 0.973). Noteworthily, the highest AUC belonged to tuberculosis diagnosis of 0.990, and the cut-off value was 18.40 ng/mL. Moreover, the same cut-off value of PPE and MPE was 9.35 ng/mL. The combination of GSDMD, adenosine deaminase (ADA) and lactate dehydrogenase (LDH) will further improve the diagnostic efficiency especially between TPE and PPE (AUC = 0.968). The AUC of GSDMD change at day 4 could predict the therapeutic effect at an early stage was 0.945 (P < 0.0001). Interestingly, bacterial infection experiments further confirm that the pleural fluid GSDMD was expressed and secreted mainly by the NCs.
Conclusions GSDMD and its combination not only candidates as the potentially novel biomarker to separate PEs early and effectively, but also monitor disease progression.

PO-1013

碳青霉烯类耐药肺炎克雷伯菌耐药基因型及分子流行病学研究

谢强
安徽省滁州市第一人民医院

目的 分析本院耐碳青霉烯肺炎克雷伯菌（CRKP）的耐药情况及耐药基因型及分子流行病学情况，为临床治疗提供依据。
方法 收集并鉴定临床分离非重复 CRKP28 株。采用 VITEK-2 compact 全自动微生物鉴定药敏分析仪鉴定和药敏试验，碳青霉烯酶抑制剂增强试验检测 A 类丝氨酸碳青霉烯酶和 B 类金属 β 内酰胺

酶，使用全基因组测序技术（WGS）检测常见的耐药基因，采用多位点序列分析（MLST）和核心基因组多位点序列分析（cgMLST）软件对序列进行分析，并构建最小生成树（MST）。
结果 28 株肺炎克雷伯菌对碳青霉烯类和头孢菌素类抗菌药物的耐药率为 100%。碳青霉烯酶抑制剂增强试验显示 25 株 A 类丝氨酸碳青霉烯酶阳性，2 株 B 类金属 β 内酰胺酶阳性，1 株阴性。全基因组测序结果显示，28 株 CRKP 检出的耐药基因较多，其中超广谱 β 内酰胺酶 SHV 和 CTX-M 基因的携带率为 100%，TEM-1 的携带率为 85.71%；碳青霉烯类抗菌药物的耐药基因分布情况为：25 株携带 KPC-2 基因，2 株携带 NDM-5 基因，1 株携带 OXA-48 基因。MLST 分型显示，共有 6 个 ST 型，其中 ST15 型（20 株，71.43%）为我院主要流行型,另有 ST11 型（4 株，14.29%），ST110（1 株，3.57%）,ST306（1 株，3.57%），ST447（1 株，3.57%），ST5328（1 株，3.57%）；cgMLST 分型显示，CC1 簇（16 株，57.14%）为院内流行株,另有 CC2 簇（3 株，10.71%）和 CC3 簇（3 株，10.71%）。
结论 本院分离的 CRKP 对抗菌药物的耐药率较高，其中 ESBLs 的检出率为 100%，对碳青霉烯类抗菌药物的耐药机制主要是携带 KPC-2 基因，以 ST15 型为主要流行型，同时 CC1 簇亚型在院内有小范围的播散。

PO-1014

A Case of Invasive Disseminated Fusariosis in a Child with Acute Leukemia

Hong He、Yongxian Cao
The Affiliated Hospital of Qingdao University

Objective To investigate the clinical and pathological characteristics, diagnosis and treatment of invasive disseminated fusariosis with hematological malignancies, and to illustrate the correlation between initial fungal treatment and therapeutic effect.
Method A 16-year-old boy with invasive Fusarium disease after allogeneic stem cell transplantation for his acute lymphoblastic leukemia was selected, who was admitted to the hematological ward of Affiliated Hospital of Qingdao University on June 20, 2019, and his clinical manifestation and treatment was studied and analyze. Then we searched PubMed database by the key words of "malignant", "hematological diseases", "invasive Fusarium disease" and "invasive fuasriosis" January 1, 2010 to December 31, 2019, to summarize the clinical characteristics, diagnosis and treatment of hematological malignancies combined with invasive Fusarium disease. This study was approved by the medical ethics committee of Affiliated Hospital of Qingdao University.
Results Skin papules, erythema, vesicles and other changes occurred right on the day of bone marrow transplantation of the 16-year-old boy. Then, local light scab formed, the color became darker after scratching, followed by local sclerosis, pain, accompanied by central necrosis, scab and fever and other systemic infection, the area of skin changes expanded gradually spread to the whole body., Spores and hyphae were found in the smears of exfoliated cells by microscopically, the blood culture was positive, and the smear of blood culture positive specimens showed Fusarium megaconidia. DNA of the strain was extracted and was amplified by PCR, and its internal transcribed spacer of gene fragment was sequenced and compared, and the strain was identified as Fusarium oxysporum. Voriconazole was given for treatment, and the skin lesions slightly improved 2 weeks later. The boy was advised to continue treatment and was followed up for one month. Then he was lost to follow up. Among the 18 reported cases of invasive Fusarium infection, 12 were males and 6 females; The age ranged from 12 days to 69 years with a median of 16 years. The main clinical manifestations were persistent fever, ineffective to chemotherapy and anti-infection treatment, and poor prognosis; Skin lesions are common in limbs and buttocks, trunk and head and face. 12 cases were treated with systemic antifungal therapy, and 6 cases (33.33%) were treated with surgery, including surgical debridement (2 cases) and local excision (4 cases). 10 cases (55.56%) were cured, 1 case

(6.00%) was improved, 3 cases (16.70%) were lost to follow-up, and 4 cases (22.00%) died of the disease, all of them were disseminated infection.
Conclusion Patients with hematological malignancies have low immunity, those got Fusarium infection have high mortality of disseminated infection, thus early diagnosis and reasonable treatment was necessary. During the treatment of hematological malignancies, effective and sufficient antifungal therapy is the key to successful treatment. Amphotericin B combined with posaconazole can be used as one of the options for the treatment of invasive Fusarium disease.

PO-1015

新型质粒相关替加环素耐药基因 tet(Y)在鲍曼不动杆菌中的鉴定

王知任、李荷楠、张建港、王晓娟、王辉
北京大学人民医院

目的 随着替加环素耐药鲍曼不动杆菌的发生与传播成为日益严重的全球健康威胁，质粒介导的耐药基因引起人们的关注，了解质粒介导的耐药基因的遗传结构、功能与可转移性变得更加重要。本研究旨在报道与鉴定一株中国临床鲍曼不动杆菌中的一种新型质粒介导的替加环素耐药基因 *tet*(Y)。
方法 通过药敏试验和全基因组测序筛选得到带有替加环素耐药基因 *tet*(Y)的鲍曼不动杆菌 2016GDAB1。对菌株进行了基因组生信分析以研究 *tet*(Y)的遗传环境和可能来源。进行质粒电转化构建 *tet*(Y)表达菌株并进行相关表型试验以验证 *tet*(Y)的功能，同时还通过接合试验和体外细菌传代检测了质粒的可转移性和稳定性。
结果 从一例医院获得性肺炎患者支气管肺泡灌洗液中分离到携带 MFS 外排泵编码基因 *tet*(Y)的替加环素耐药鲍曼不动杆菌 2016GDAB1。2016GDAB1 属于非流行的序列类型(ST)355^{oxf}，该 ST 多在动物中报导。*tet*(Y)位于一个 72,156 bp 的质粒上，遗传环境分析表明 Tn*5393* 可能在 *tet*(Y)传播中起作用，而与 GenBank 中携带 *tet*(Y)菌株的进化分析暗示 2016GDAB1 的 *tet*(Y) 来源可能为气单胞菌而非不动杆菌。通过电转化发现 *tet*(Y)在大肠埃希菌 DH5α 和鲍曼不动杆菌 ATCC17978 中的过表达使菌株四环素、米诺环素和多西环素的 MIC 增加了 8 到 128 倍而替加环素增加了 2 到 4 倍。接合实验发现携带 *tet*(Y)的质粒 p2016GDAB1 未能成功转移到替加环素敏感的受体菌株中。稳定性实验发现携带 *tet*(Y) 的质粒可以在宿主和非天然宿主菌株中稳定维持，不易丢失。
结论 本研究首次在鲍曼不动杆菌中鉴定出替加环素耐药基因 *tet*(Y)，可以介导低水平替加环素耐药，Tn*5393* 可能在其传播中发挥作用。

PO-1016

Droplet encoding and pairing-based microfluidic multiplex digital LAMP enables high-content detection of lower respiratory tract infection pathogens

Dongyang Cai、Jingjing Zou、Dayu Liu
Guangzhou First People's Hospital

Objective To develop a microfluidic multiplex digital LAMP assay for high-content detection of lower respiratory tract infection (LRTI) pathogens.
Methods We fabricated a microfluidic chip with 20,700 calabash-shaped microwells (one small microwell with a diameter of 90 μm, 65 μm in depth; one large microwell with a diameter of 135 μm, 110 μm in depth; set a 15 μm overlap; 50 μm spacing). The entire experiment procedure performed on the chip was as follows (Figure 1): 1) a volume of 50 μL LAMP reactant without primers was dispersed into 1 nL droplets (sample droplets, 124 μm in diameter) with a droplet-generation device. The droplets were infused into the chip via micropipette and then trapped into the large microwells by the resultant of drag force and buoyancy force; 2) Each input of LAMP

primers was pre-mixed with a unique ratio of three colorimetric indicators - cresol red, bromothymol blue, and orange G, and standardized to a final concentration of 400 μM. Each input was respectively dispersed into 0.268 nL droplets (primer droplets, 80 μm in diameter) with another droplet-generation device. A fraction of each set of primer droplets was pooled into a single tube to form a droplet library. After thoroughly mixing, the primer droplets were infused into the chip via micropipette and then randomly trapped into the small microwells. 3) Contents of primer droplets were decoded by bright-field imaging the whole chip and processed with a machine learning-based custom program. Afterwards, coalescence of the paired droplets was achieved via an electrical impulse. 4) Finally, the chip was submerged in 67 °C water bath to perform the LAMP reaction and the fluorescence signal was measured from each microwell at the assay end.
Results We successfully generated monodisperse sample droplets and primer droplets, which is essential for successful droplet trapping and LAMP reaction (Figure 2A, B). We observed high-efficient trapping of sample droplets and primer droplets at the effectiveness of 98.9% and 98.4%. The average droplet pairing and merging efficiencies were 96.9% and 98.0%, respectively (Figure 2E). As a proof-of-concept, we pre-mixed colorimetric indicators with three different primer pairs tarting dominating LRTI bacteria, namely *Escherichia coli* (cresol red), *Klebsiella pneumoniae* (orange G), and *Staphylococcus aureus* (bromothymol blue), respectively, and the sample was *Escherichia coli* genomic DNA (Figure 3B-D). After the LAMP reaction, only the droplets encoded with cresol red showed a significant increase in fluorescence intensity (Figure 3E).
Conclusions This manuscript describes a droplet encoding and pairing-based multiplex digital LAMP technology. We have performed a proof-of-concept study to validate its capability to rapidly develop highly multiplexed detection panels. We envision that this technology could serve as an alternative for rapid point-of-care detection of LRTI pathogens in source-limited settings.

PO-1017

BacT/ALERT VIRTUO 血培养系统和 FAN®Plus 血培养瓶的临床应用评估

刘素玲、赵云虎、周典荣、张鑫强、王蔚莎、顾兵、侯铁英
广东省人民医院

目的 评估 BacT/ALERT VIRTUO 血培养系统和 FAN®Plus 血培养瓶对于菌血症患者的实验室诊断效能。
方法 广东省人民医院 6 个 ICU 科室和 3 个普通科室 2020 年 6 月-2021 年 5 月临床疑似 1772 例菌血症患者进行血培养，每名患者采集 2 个部位（包括导管血），每部位采集 16-20ml 血量，一个部位注入 FA plus 和 FN plus 一套瓶，于 BacT/ALERT VIRTUO 系统培养，另一个部位注入 FX 树脂需氧瓶和溶血素厌氧瓶，于 BACTEC FX400 系统培养；培养时间均设置为 5 天。比对两种血培养系统的所有血瓶的采血量、报阳时间及菌种鉴定；其中阳性率比较包含 BacT/ALERT VIRTUO 血培养系统和 BACTEC FX400 系统培养系统的所有入组标本，报阳时间比较为 BacT/ALERT VIRTUO 血培养系统和 BACTEC FX400 系统培养系统均报同一种菌的 TTD 比较。
结果 BacT/ALERT VIRTUO 系统阳性复苏率高于 BACTEC FX400 系统，分别为 9.7%和 7.7%。在血培养上机培养 0-8h 初期阶段，BacT/ALERT VIRTUO 系统阳性复苏率显著高于 FX 系统（9.4%：1.9%）。
结论 BacT/ALERT VIRTUO 系统培养是一种可靠且可缩短菌血症实验室诊断 TAT 的有效血培养系统。

PO-1018

比对评估一种自配粪便样本保存液保持细菌活性的能力

陈晓娇、段卓、翁少娟、何彦、周宏伟
南方医科大学珠江医院

目的 探索一种能在室温条件下维持粪便中细菌活性的自配样本保存液，对其性能进行对比分析。
方法 采集 6 个健康个体的粪便样本，分别用一种商品化样本运送培养基（室温）、自配样本保存液（室温）及-80℃三种不同条件保存样本。每种保存方式均在样本采集后 3 小时、3 天、1 周三个时间点，通过 SYTO 9/PI 双色荧光染色剂分别对样本中所有的细菌和细胞膜受损的细菌（死菌）进行标记，通过 CytoFLEX 流式分析仪（Beckman）对样本进行细菌计数，并评估样本中活性细菌的比例。对三种不同保存方式在一定时间内维持细菌活性的能力进行评估。
结果 在样本采集后 3 小时、3 天和 1 周三个不同的时间点，商品化运送培养保存的样本均检测到最高的活性细菌比较(89.29±5.22，87.76±4.12，74，77±10.90)，自配样本保存液次之(82.84±8.19，79.39±6.68，70.69±9.49)，-80℃条件下（57.35±13.81，60.08±14.91，60.78±15.10）保存的样本中活性细菌比例最低；但在三个时间点下，自配样本保存液组细菌活性比例与商品化培养基组均无统计学差异（p=0.266，p=0.135, p=0.490）），而均显著高于-80℃组（p<0.001，p<0.001，p=0.001）。此外，自配保存液组与商品化培养基组在 1W 时，细菌活性比 3H 时的活性比例显著降低，而-80 度组三个时间点的细菌活性则无统计学差异。
结论 该自配样本保存液能在室温条件下较好的维持细菌活性，优于目前实验室样本保存金标准——-80℃保存，且与商品化样本运送培养基效果相当，或可用于缺乏冰箱等实验室保存条件下对样本进行暂存。

PO-1019

优化头孢哌酮/舒巴坦、替加环素、多黏菌素 B 在鲍曼不动杆菌血流感染患者中的给药方案：基于全国血流感染细菌耐药监测联盟（BRICS）的蒙特卡洛模拟研究

辛娜
西安医学院第一附属医院

目的 应用蒙特卡罗模拟研究头孢哌酮/舒巴坦、替加环素、多黏菌素 B 治疗鲍曼不动杆菌血流感染的疗效，预测和评价不同抗菌药物的抗菌效果，进而优化临床给药方案。
方法 借助全国血流感染细菌耐药监测联盟（Brics）平台收集 2018-2019 年血流感染来源的鲍曼不动杆菌 514 株,使用文献公开发表的头孢哌酮/舒巴坦、替加环素、多黏菌素 B 的药动学参数，基于药动学/药效学(PK/PD) 理论利用蒙特卡洛模拟法，计算不同给药方案在各特定的 MIC 值获得的目标概率，即达标概率（PTA）和累积反应分数（CFR），以 PTA 或 CFR≥90%作为临床疗效评价的指标。
结果 治疗鲍曼不动杆菌引起的血流感染，头孢哌酮/舒巴坦（2:1）给药方案 3g q6h、4.5g q8h、4.5g q6h 在最低抑菌浓度（MIC）为 32ug/ml 时，可获得大于 90%的目标 PTA 值；4.5g q6h 的给药方案在 MIC 为 64ug/ml 时，仍可获得大于 90%的目标 PTA 值。替加环素推荐剂量（50mg q12h）,在 MIC≤0.25ug/ml 时，可获得大于 90%的目标 PTA 值。多黏菌素 B 1.25mg/kg 1h 输注 q12h 给药方案，可使 MIC≤1ug/ml 的细菌的 PTA 达到 90%以上，高剂量的多黏菌素给药方案(负荷 2 mg/kg 2h 输注后 2.5 mg/kg/day 持续输注) 在 MIC 为 2ug/ml 时，可提供较高的 PTA（96.83%）。

结论 鲍曼不动杆菌对头孢哌酮/舒巴坦群体耐药率较高导致 CFR 值较低，临床治疗中可能需要使用其他抗生素或将头孢哌酮/舒巴坦与其他抗菌药物联合使用取得更好的治疗效果。替加环素建议使用 100mg q12h 的给药方案，多黏菌素 B 建议使用负荷 2.5 mg/kg 2h 输注后 1.5 mg/kg 1h 输注 q12h，负荷 2 mg/kg 2h 输注后 2.5 mg/kg/day 持续输注的给药方案。

PO-1020

三种结核分枝杆菌检测方法的临床诊断效能评价

姜长宏
南方医科大学珠江医院

目的 评价涂片抗酸染色镜检（简称“涂片法”）、荧光探针法聚合酶链式反应（简称“PCR-荧光探针法”）、利福平耐药实时荧光定量核酸扩增（Xpert MTB/RIF，简称“Xpert 法”）3 种结核分枝杆菌检测方法的临床诊断效能。
方法 收集 2020 年 1 月至 2021 年 4 月南方医科大学珠江医院收治的 76 例疑似结核病患者的相关标本，用涂片法、PCR-荧光探针法、Xpert 法同时进行检测。以临床诊断作为参考标准，分别计算 3 种检测方法的检出阳性率、灵敏度、特异度、阳性预测值、阴性预测值、总符合率，并计算 Kappa 值做一致性分析，绘制 ROC 曲线评价其临床诊断效能。
结果 参照最新版结核病分类标准（WS196-2017）以及肺结核诊断标准（WS288-2017），76 例疑似病例最终诊断为结核病患者 41 例，非结核病患者 35 例。涂片法、PCR-荧光探针法、Xpert 法的检出阳性率分别为：28.9%、44.7%、50.0%。以临床诊断作为参考标准，3 种检测方法的灵敏度分别为：48.78%、80.49%、92.68%，特异度分别为：94.29%、97.14%、100.0%，总符合率分别为：69.74%、88.16%、96.05%，Kappa 值分别为：0.41、0.77、0.92，ROC 曲线下面积分别为：0.709、0.878、0.952。
结论 以临床诊断为参考标准，Xpert 法对检测结核分枝杆菌的灵敏度、特异度高，其诊断准确度也最高，诊断效能较好，其次是 PCR-荧光探针法、涂片法。而涂片法联合 Xpert 法对检出非结核分枝杆菌具有一定提示意义。

PO-1021

lasB 基因对铜绿假单胞菌外膜囊泡的影响

张佳星
重庆市人民医院

背景 铜绿假单胞菌又称绿脓杆菌（Pseudomonas aeruginosa，PA）广泛分布于自然界及健康人的皮肤、肠道和呼吸道，可引起多种感染，全球 10-15%的院内感染与 PA 有关，在铜绿假单胞菌感染宿主时，会通过一些分泌系统分泌蛋白毒力因子损害宿主细胞，目前已知的铜绿假单胞菌分泌系统有五种，以Ⅲ型分泌系统（type III secretion system，T3SS）的研究最为广泛。与其他分泌系统不同，铜绿假单胞菌通过分泌外膜囊泡（onter membrane vesicle，OMV，）可以帮助铜绿假单胞菌分泌不可溶的分子并与可溶性的物质形成复合物，使可溶性物质在它的保护下更加专一的到达作用靶点。PA 的 lasB 基因编码的弹性蛋白酶 LasB 能降解 T3SS 分泌系统的分泌蛋白。本研究拟通过比较 lasB 缺陷株和正常株的外膜囊泡形态结构及生物学功能，证实 lasB 对 PA 外膜囊泡的影响。
目的 研究 lasB 基因对铜绿假单胞菌外膜囊泡形态、蛋白及生物学活性的影响。
方法 密度梯度超速离心提取并纯化铜绿假单胞菌标准株 PAO1 和 lasB 基因缺陷株 PAO1lasB-的外膜囊泡，负染电镜观测形态，聚丙烯酰胺凝胶电泳鉴定其蛋白构成；建立外膜囊泡和细菌感染正常

人外周血单个核细胞 PBMC 模型，检测 lasB 缺陷后，外膜囊泡保护细菌免遭 PBMC 的吞噬能力的变化及诱导炎性因子 IL-6、IL-8 的表达水平。
结果 lasB 缺陷后，PAO1 分泌的外膜囊泡形态无改变，其所含蛋白减少，保护细菌免受宿主细胞吞噬的能力降低，诱导 PBMC 表达炎性因子 IL-6、IL-8 的能力降低。
结论 lasB 对铜绿假单胞菌的外膜囊泡的生物学活性有重要影响。

PO-1022

我国多中心碳青霉烯耐药粘质沙雷菌耐药机制及分子流行病学研究

江振东、孟涵、王启、王辉
北京大学人民医院

目的 研究我国多中心碳青霉烯耐药粘质沙雷菌耐药表型、基因型、质粒转移性，通过全基因组测序和生物信息学手段分析同源性，以探究耐药机制和分子流行病学特征，为 CRSM 的临床诊治和耐药监测提供理论依据。
方法（1）收集 48 株来自 CRE Network 的粘质沙雷菌，利用基质辅助激光解析电离串联飞行时间质谱进行鉴定；利用微量肉汤稀释法及琼脂稀释法进行药敏试验；利用改良碳青霉烯灭活试验和 EDTA 协同改良碳青霉烯灭活试验对其产酶情况进行筛查；（2）利用聚合酶链式反应检测酶基因型，进一步比对确定亚型；（3）通过质粒接合实验探究菌株酶基因转移性；（4）基于 Illumina NextSeq 550 平台进行全基因组测序，分析菌株携带耐药基因，利用 Roary v3.11.2 提取核心基因组，在 RAxML v8.2.10 上通过 GTR 模型构建系统进化树。
结果（1）48 株碳青霉烯耐药粘质沙雷菌中，产碳青霉烯酶菌株占比 75%（n=36/48），其中 KPC 为主要酶型，占比 77.8%（n=28/36）；（2）质粒接合实验中三株分别携带 blaKPC-2、blaKPC-3 和 blaNDM-1 的菌株成功转移并得到接合子，接合子 PCR 扩增都检测到相应酶基因，接合子药敏显示其对碳青霉烯、头孢他啶耐药性都有所提高，且携带 blaNDM-1 耐药基因的质粒接合效率高于 blaKPC-2、blaKPC-3；（3）系统进化树显示可能存在同源性的菌株在地域分布上和发生时间上有所集中，可能存在地区内播散。
结论（1）48 株来自全国多家中心的 CRSM 主要耐药机制为产 KPC-2 型碳青霉烯酶；（2）48 株 CRSM 对碳青霉烯、头孢菌素、喹诺酮类药物敏感性较差，对阿米卡星、米诺环素和磷霉素敏感性较好；（3）同一时间、同一地域的菌株有一定的同源性，极有可能存在耐药株的播散；（4）blaKPC、blaNDM 都可以成功转移接合，且 NDM 的接合效率高于 KPC。

PO-1023

耐碳青霉烯肠杆菌科细菌头孢他啶/阿维巴坦的敏感性分析及疗效评价

许雨乔
江苏省人民医院（南京医科大学第一附属医院）

目的 分析非金属碳青霉烯酶耐碳青霉烯类肠杆菌科细菌（CRE）对头孢他啶/阿维巴坦（CAZ/AVI）敏感性及 CAZ/AVI 抗感染疗效。
方法 选取 2019 年 9 月-2020 年 5 月南京医科大学第一附属医院临床分离 CRE 菌株 170 株，采用 mCIM 联合 eCIM 检测碳青霉烯酶酶型，Kirby-Bauer 法检测 CAZ/AVI 敏感性，并用肉汤稀释法对抑菌圈直径为 20~22 mm 的菌株进行复核。根据患者是否使用 CAZ/AVI 治疗分为试验组和对照组，通过倾向性匹配获得 37 对患者，比较两组临床疗效。

结果 170 株 CRE 菌株中产丝氨酸酶 130 株，产金属酶 35 株。CAZ/AVI 总敏感率为 78.8%（134/170），产丝氨酸酶 CRE 菌株敏感率为 99.2%（129/130），产金属酶 CRE 菌株敏感率为 0。52 株 CAZ/AVI 抑菌圈直径为 20~22 mm 的菌株经肉汤稀释法复核一致率为 99.4%（51/52）。试验组和对照组患者基线值基本一致，试验组总有效例数和呼吸道感染有效例数均高于对照组（P<0.05）。

结论 产非金属碳青霉烯酶 CRE 对 CAZ/AVI 有较高敏感性，CAZ/AVI 可显著提高治疗 CRE 感染的有效率。

PO-1024

Mycoplasma pneumoniae lipids license TLR4 for activation of NLRP3 inflammasome and autophagy to evoke a proinflammatory response

Haodang Luo[1,2]、Jun He[1]、Xiaoxing You[2]、Yimou Wu[2]
1. 南华大学附属南华医院检验科
2. 南华大学衡阳医学院病原生物学研究所

Mycoplasma pneumoniae is an obligate pathogen that causes pneumonia, tracheobronchitis,pharyngitis, and asthma in humans. It is well recognized that membrane lipoproteins are

immunostimulants exerting as LPS and play a crucial role in the pathogenesis of inflammatory responses upon M. pneumoniae infection. Here, we report that the M. pneumoniae-derived lipids are another proinflammatory agents. Using an antibody-neutralizing assay, RNA interference, or specific inhibitors, we found that TLR4 is essential for M. pneumoniae lipid-induced TNF-α and IL-1β production. We also demonstrated that NLRP3 inflammasome, autophagy, and NF-κB-dependent pathways are critical for the secretion of proinflammatory cytokines, while inhibition of TLR4 significantly abrogates these events. Further characterisation revealed that autophagy-mediated inflammatory responses involved the activation of NF-κB. In addition, the activation of NF-κB also promoted lipid-induced autophagosome formation, as revealed by assays using pharmacological inhibitors, 3-MA and Bay 11-7082, or silencing of atg5 and beclin-1. These findings suggest that, unlike the response to lipoprotein stimulation, the inflammation in response to M. pneumoniae lipids is mediated by the TLR4 pathway, which subsequently initiates the activation of NLRP3 inflammasome and formation of a positive feedback loop between autophagy and NF-κB signalling cascade, ultimately promoting TNF-α and Il-1β production in macrophages.

PO-1025

Antioxidant and antibacterial study of 10 flavonoids revealed rutin as a potential anti-biofilm agent in Klebsiella pneumoniae strains isolated from hospitalized patients

Zhibin Wang[1]、Zixuan Ding[1]、Zhaoyinqian Li[1]、Yinhuan Ding[1]、Fan Jiang[2]、Jinbo Liu[1]
1. The Affiliated Hospital of Southwest Medical University
2. 山东大学

The emergence of multi-drug resistance(MDR) and extensively drug-resistance(XDR) of *Klebsiella pneumoniae* strains have brought great threaten to conventional antibiotics. Previous studies showed that plant-derived flavonoids have inhibitory functions on pathogens. However, In *K.pneumoniae*, the antibacterial activities of different flavonoids on the growth and biofilm

formation remain a mystery. The aim of the present study is to evaluate the antioxidant abilities of different flavonoids, to screen active ingredients and to identify their inhibitory effects on *K. pneumoniae* growth and biofilm formation.Totally 10 flavonoids representing 4 major categories were screened and used in this study. The antioxidant capacity of each flavonoid was evaluated through DPPH assay. Rutin showed highest level of free radical scavenging capacity, followed by kaempferol, luteolin, quercetin, apigenin, hesperidin, sinensetin, naringenin, naringin and 3,5,6,7,8,3',4'-heptamethoxyflavone. The inhibitory effects of rutin and naringin on bacteria growth were also compared.The lowest MICs of rutin were found against *K. pneumoniae* ATCC700603(1024μg/mL) and E.coli ATCC25922(512μg/mL). However, the MBICs were not found. Rutin showed strong inhibitory ability against both the growth curve and biofilm production. The expression profiles of 15 biofilm-related genes were analyzed in biofilm cells both with and without rutin treatment. The *luxS* gene and *wabG* gene were down-regulated significantly by rutin treatment. The correlation analysis showed the *mrkA* gene expression was positively correlated with the biofilm biomass accumulation.Our study indicated the biofilm production is correlated with several genes expression rather than one. The *mrkA* gene expression was positively correlated with the biofilm biomass accumulation. Our study screened rutin as a potential agent to inhibit the *K. pneumoniae* biofilm formation.

PO-1026

新型疫苗佐剂增强鹦鹉热衣原体多表位融合抗原抗感染保护作用研究

李育萌[1]、陈恩[1]、谢小平[1]、刘双全[1]、吴移谋[2]
1. 南华大学附属第一医院
2. 南华大学

目的 构建基于病毒样颗粒以及纳米颗粒的新型疫苗佐剂，进一步优化、完善 Cps 的多表位融合疫苗。

方法 基于 CNPs 以及 HBc-144 构建 CNPs/HBc-144 新型疫苗佐剂，通过理化性质检测分析新型佐剂的及稳定性以形态结构。免疫 7 d 后，取肺组织以及注射部位肌肉组织进 H&E 染色。分别收集每次免疫 BALB/c 小鼠的血清、鼻腔灌洗液以及生殖道灌洗液，检测血清 IgG、IgA 以及 sIgA 抗体水平；流式细胞术检测细胞内 CD4+、CD8+细胞水平以及 CD44/CD62 分泌水平，并检测细胞上清以及细胞内细胞因子水平；随后检测感染 BALB/c 小鼠的肺组织 Cps 载量、肺上清炎症因子水平以及病理损伤情况。qRT-PCR 检测心、肝、脾等组织中的 Cps 载量。

结果 经理化检测分析，CNPs/HBc-144-Ags 为大小相似的圆形颗粒结构，且分布均匀。连续免疫 7 d 后，BALB/c 小鼠体重平稳，注射部位肌肉以及肺组织结构完好。CNPs/HBc-144-Ags 在免疫 BALB/c 小鼠体内诱导产生的血清 IgG、IgA 水平均随免疫次数增加显著上升，CNPs/HBc-144-Ags 诱导的 sIgA 则显著高于对照组。免疫 BALB/c 小鼠脾细胞上清中 IFN-γ、IL-2 以及 IL-17A 分泌水平均显著上升，且细胞内 IFN-γ 水平也显著高于对照组。此外，CNPs/HBc-144-Ags 组 BALB/c 小鼠脾细胞中 CD44/CD62 的分泌水平要显著高于对照组。CNPs/HBc-144-Ags 能够有效降低 Cps 感染后 BALB/c 小鼠肺组织衣原体载量、减轻肺组织的炎性病理损伤，并有效减少 Cps 的含量。

结论 CNPs/HBc-144 新型疫苗佐剂能显著增强 Cps 多表位融合抗原诱导的黏膜免疫以及细胞免疫应答，同时促进记忆性 T 细胞分泌，形成记忆性免疫应答抵抗 Cps 体内感染。

PO-1027

重组可溶表达结核分枝杆菌新基因编码蛋白 Rv2742 的相互作用蛋白质组研究

王红[1]、万李[2]、武舒佳[3]、常蕾[4]、万康林[2]、张瑶[4]、徐平[4]、戴二黑[1]
1. 石家庄市第五医院
2. 中国疾病预防控制中心传染病预防控制所传染病诊治协同创新中心
3. 北京国家蛋白质科学中心； 武汉大学基础医学院；
4. 北京国家蛋白质科学中心

目的 Rv2742 是我们课题组基于蛋白质基因组学技术从结核分枝杆菌（Mycobacterium tuberculosis H37Rv）中发现并验证的遗漏注释基因。本研究旨在利用结核分枝杆菌自身的细胞裂解液和免疫亲和纯化质谱（IP-MS）在蛋白质通量鉴定上的优势，筛选遗漏注释基因编码蛋白质 Rv2742 在结核菌中的相互作用蛋白质，克服普通微生物学实验室对结核分枝杆菌使用的限制，实现 Rv2742 在结核分枝杆菌中的蛋白质相互作用网络，并据此探索其在结核分枝杆菌中所参与的生物学功能。
方法 首先对 pMAL-c2X 空载和已构建好的 pMAL-c2X-Rv2742 载体，经 IPTG（异丙基硫代半乳糖苷）诱导表达、直链淀粉树脂亲和纯化后获得麦芽糖结合蛋白（MBP）和 MBP-Rv2742 的融合蛋白作为诱饵蛋白；分别取等摩尔蛋白与 H37Rv 非变性全细胞蛋白质裂解物孵育，进行 MBP pull-down 实验；将两次生物学重复实验得到的与 MBP 和 MBP-Rv2742 诱饵蛋白结合的蛋白质复合物洗脱收集，10% SDS-PAGE 凝胶电泳验证，并通过液相色谱串联质谱法（LC-MS/MS）分析、筛选出 Rv2742 在结核菌中的互作蛋白质，然后将筛选到的蛋白质进行 GO（Gene ontology）和互作网络分析。
结果 本实验共筛选出 105 个 Rv2742 的潜在相互作用蛋白质，其定位主要分布在细胞壁、细胞质膜和细胞外区域等细胞组分中，功能上主要参与低氧应激、宿主共生、运输、毒力因子分泌等生物学过程。
结论 Rv2742 可能参与结核菌致病过程，侵入人体后，积极应对宿主低氧、一氧化氮环境，与宿主共生的同时释放毒力因子。

PO-1028

172 例新生儿及儿童脑脊液分离菌的分布及耐药性分析

闵亮、周树平、余晓君、周艳、杜琴、柯江维
江西省儿童医院

目的 了解江西省儿童医院 2015 年 1 月-2019 年 12 月连续 5 年临床送检脑脊液标本中分离菌的分布及对常用抗菌药物的耐药性。
方法 对 5 年间所有临床送检的脑脊液标本按《全国临床检验操作规程》进行细菌培养和分离鉴定，采用 BD 公司 PHONX-100 全自动细菌鉴定药敏系统对培养出的细菌进行鉴定和药敏试验，按 CLSI2020 版标准对药敏结果进行判断，并使用 WHONET5.6 软件进行统计。
结果 剔除重复菌株后自 15124 例脑脊液标本分离出 172 株菌，阳性率为 1.13%，其中革兰阳性菌 111 株，占 64.5%，革兰阴性菌 60 株，占 34.9%，真菌 1 株，占 0.6%。172 株菌中检出前 5 位的是肺炎链球菌 52 株（30.2%）、大肠埃希菌 37 株（21.5%）、无乳链球菌 19 株（11%）、屎肠球菌 15 株（8.7%）、 凝固酶阴性葡萄球菌 11 株（6.4%），检出新型隐球菌 1 株。小于 28 天新生儿检出第一位的细菌为大肠埃希菌，占 37%（27/73），药敏结果统计显示革兰阳性菌中屎肠球菌对氨苄西林的耐药率已达 100%，肺炎链球菌对青霉素非敏感率为 94.2%，未发现对青霉素不敏感的无乳链球菌，未发现对万古霉素、利奈唑胺和替考拉宁耐药的革兰阳性球菌。革兰阴性杆菌中检出最多的是大肠埃希菌，占所有检出阴性杆菌的 61.7%（37/60)，药敏结果统计显示其对氨苄

西林、哌拉西林耐药率较高，均在 80%以上，而对带有酶抑制剂药物如氨苄西林/舒巴坦、哌拉西林/他唑巴坦耐药率均为 11.4%，头孢噻肟及头孢吡肟的耐药率为 45.9%及 40.5%，碳青霉烯类抗生素亚胺培南及美罗培南耐药率均为 5.4%。
结论 本研究样本中阳性率较低，值得注意的是 PRSP 检出率极高、也有部分 CRE 的检出，应重点加强临床对特殊耐药菌如 PISP、PRSP、VRE、CRE、MRSA 等菌株的传播防范及其防控管理。

PO-1029

肺炎克雷伯菌头孢地尔耐药性的研究

鲍金凤[1,2]、顾兵[3]、王成彬[1]
1. 中国人民解放军总医院第一医学中心
2. 徐州医科大学
3. 广东省人民医院

背景 碳青霉烯耐药的肺炎克雷伯菌的检出率不断升高，有限的治疗药物给临床带来了极大的困难。头孢地尔是一种新型五代头孢菌素，对碳青霉烯耐药的肺炎克雷伯菌有良好的抗菌活性。
目的 探究肺炎克雷伯菌对头孢地尔的耐药机制，寻找头孢地尔的耐药靶点，为开发新的药物及遏制耐药性的发生做好准备。
方法 体外诱导肺炎克雷伯菌 NTUH-K2044 对头孢地尔由敏感到耐药，对耐药前后菌株进行生长曲线测定，生物膜形成能力检测，碳氮及 ATP 代谢能力检测，然后进行蛋白组学分析，比较耐药前后菌株差异表达蛋白，并对相关蛋白进行生信分析。
结果 肺炎克雷伯菌对头孢地尔耐药后，生长速率降低，生物膜形成能力减弱；发生上调蛋白 507 个，下调蛋白 428 个。GO 及 KEGG 分析结果显示，这些差异显著蛋白多参与亚麻酸代谢、蛋白运出、阳离子抗菌肽(CAMP)耐药性、磷酸肌醇代谢、赖氨酸降解等通路。差异蛋白聚类分析显示，下调显著蛋白聚焦于碳氮代谢、两组分系统、ABC 转运体等通路；上调显著蛋白聚焦于代谢、蛋白转运、细菌分泌、β 内酰胺酶抗性 CAMP 抗性等通路。
结论 肺炎克雷伯菌对头孢地尔耐药后，生物膜形成能力减弱，碳氮及 ATP 代谢能力降低，铁转运相关蛋白下调。ABC 转运体通路及两组分通路的共同调节了肺炎克雷伯菌对头孢地尔的耐药性。

PO-1030

结核分枝杆菌新基因编码蛋白抗原性研究及其在结核病诊断中的应用初探

王红、戴二黑
石家庄市第五医院

目的 结核分枝杆菌临床诊断缺乏高特异性、超灵敏的生物诊断标志物，本研究旨在筛选用于结核菌体液免疫检测的特异性基因编码蛋白抗原及抗原组合，为结核病的快速诊断研发提供技术支撑。
方法 首先分别筛选了 pGEX-4T-2、pET-28a、pET-32a、pMAL-c2X 四种表达载体构建目的基因的重组表达菌株；尝试目的基因密码子和表达条件优化，实现异丙基-β-D-硫代半乳糖苷诱导目的蛋白的可溶性表达后进行亲和纯化；对纯化获得的目的蛋白进行质谱验证；通过软件对这些新编码蛋白进行 B 细胞可信表位的预测；并用 ELISA 技术评估这些新编码蛋白在结核病体液免疫诊断中的潜在应用价值。
结果 1 pMAL-c2X 表达载体均有效实现了 22 个新编码蛋白的可溶性诱导表达。新基因编码蛋白经质谱检测，序列正确。2 通过软件进行 B 细胞表位预测，发现这些新蛋白均具有高可信的表位，且为先前尚未报道的表位。3 初步血清学比较发现，pMAL-c2X 空载在检测中背景干扰最小，适于后续融合表达蛋白的血清学抗原性筛选。对 pMAL-c2X 载体获得的融合蛋白进行了血清学检测，共筛

选到 2 个潜在抗原 TB38.76 和 TB26.88。抗原 TB38.76 在结核病患者的灵敏度是 68.33%，特异度为 72.5%。TB38.76 在菌培养阳性的患者中，灵敏度是 90%，特异度为 55%；抗原 TB26.88 在菌培养阳性患者中，灵敏度是 80%，特异度为 50%。4 TB26.88、TB38.76、38 kDa 蛋白和商品化试剂盒进行并联试验或串联试验后，具有互补性，可提高对结核病的诊断效率。

结论 1.利用大肠杆菌异源表达系统，成功构建了 22 个 MTB 新基因的重组质粒，且在 pMAL-c2X 载体中均实现了高可溶性诱导表达。2. 22 个新抗原筛选获得了 2 个潜在的新抗原 TB26.88 和 TB38.76，与已知抗原和商品化试剂盒在结核病诊断中呈现互补性。

PO-1031

乙醇脱氢酶在鲍曼不动杆菌群体感应及生物膜形成中的作用

张康见
山东大学第二医院

目的 多重耐药鲍曼不动杆菌(multiple drug-resistant Acinetobacter baumannii, MDR-AB)是导致临床感染治疗失败的主要原因之一。而群体感应 (quorum sensing, QS)在抗生素耐药形成中发挥重要的作用，但其具体机制仍未明晰。固本研究通过对浮游和生物膜状态下的鲍曼不动杆菌进行转录组测序，获得一系列差异表达基因，经生物信息学技术分析候选差异表达基因可能参与调控的细菌细胞组分、参与的代谢过程和具备的生物学功能。

方法 QRT-PCR 验证测序结果。建立群体感应分子检测体系，分析 C12-HSL 对生物膜形成的影响。以微孔板法定量，结晶紫染色和扫描电镜定性检测其生物膜的形成能力。

结果 转录组测序结果分析发现 A1S_0109、1S_0112~ A1S_0114 及乙醇脱氢酶基因 A1S_2098 与群体感应系统相关并表达上调。QRT-PCR 验证差异表达基因的表达情况，结果与测序数据一致。群体感应分子 C12-HSL 的加入使鲍曼不动杆菌生物膜的形成能力增强，且细菌运动性亦增强。双硫仑（200μM）处理后，鲍曼不动杆菌生物膜内细菌乙醇脱氢酶的活性减弱，群体感应相关基因的表达下调，生物膜形成能力下降。双硫仑对鲍曼不动杆菌生物膜形成的抑制作用在临床分离株中同样有效。

结论 鲍曼不动杆菌生物膜的形成与群体感应系统相关。群体感应增强，鲍曼不动杆菌的生物膜形成能力和细菌运动性增强。乙醇脱氢酶在鲍曼不动杆菌生物膜形成中发挥重要作用。双硫仑处理后鲍曼不动杆菌乙醇脱氢酶活性减弱，同时群体感应基因表达下调，生物膜形成能力下降。

PO-1032

A Smart Efficient Nanocomposite Serving Dual Roles Cruelly Combat Carbapenem-Resistance Acinetobacter baumannii, the Promising Alternative Therapy

Xisheng Li
the Third Xiangya Hospital, Central South University

Purpose In the face of the abundant production of various types of carbapenemases, the antibacterial efficiency of imipenem seen as “the last line of defence” is weakening. Following, the incidence of carbapenem-resistant *Acinetobacter baumannii* (CRAB), which can generate antibiotic-resistant biofilms, is increasing. Based on the superior antimicrobial activity for silver nanoparticles against multifarious bacterial strains compared with common antibiotics, we constructed the silver nanocomposite whose core was silver nanoparticle to tackle the current dilemma, and silver nanocomposite was able to function as a novel smart pH-sensitive nanodrug system.

Method Preparation of silver nanoparticles; Characterization and the release characteristics of silver nanocomposite; Assay for antibacterial effects and research on antibiofilm activity of silver nanocomposite in vitro; Assessing influence on CRAB-infection MLE-12 cells by counting, apoptosis evaluation and CLSM; A series of cell experiments to verify toxicity and biocompatibility in vitro; Constructing mice model of carbapenem-resistant *A. baumannii* pneumonia and studying therapy in vivo; Experiments of toxicity research in vivo; Statistical analysis.
Results 1. Smart pH-sensitive silver nanocomposite was effective in acidic infected environments to release more imipenem and Ag+, which can kill A. baumannii together. The release rates of imipenem and Ag+ at pH=7.4 within 48 h were 62.73 ± 0.97% and 52.37 ± 1.73%, respectively. However, at pH=5.0 and 48 h, imipenem and Ag+ released from the silver nanocomposite were 88.37 ± 0.83% and 86.73 ± 1.47%, respectively.
2. This platform significantly enhanced antibacterial efficiency, while increasing the generation of reactive oxygen species and the damage of oxidative membrane, as well affecting the cell wall formation and the metabolic pathways.
3. According to the results of crystal violet staining, LIVE/DEAD Backlight bacterial viability staining, and RT-qPCR, this silver nanocomposite downregulated the levels of ompA expression to prevent foramation of biofilms.
4. This nanocomposite could also inhibit cell death induced by carbapenem-resistant *Acinetobacter baumannii* infection. The percentage of dead MLE-12 cells was 91.28 % for treatment of PBS, instead the numbers of dead cells were negligible for treatment of the silver nanocomposite. The MLE-12 cell line treated with the silver nanocomposite did not exhibit remarkable apoptosis, and the ratio was only 7.74 ± 1.23%.
5. The nanodrug system had a crucial impact on the efficient therapeutic efficacy in vivo by cytokine regulation and tissues repair acceleration. The images from HE and TUNEL assay of lung tissue sections suggested outstanding therapeutic efficacy of silver nanocomposite against CRAB-infected mice. The values of TNF-α and IL-6 obtained with silver nanocomposite treatment (approximately 30 pg/mL) were lowest among all seven groups. The silver nanocomposite was optimal in promoting the expression of VEGF and PECAM1 compared with other treatments.
6. The silver nanocomposite not only had excellent biosafety, biocompatibility, and hemocompatibility but also produced fewer side effects.
Conclusion The sliver nanocomposite is regarded as the pH-sensitive efficient antibacterial nanocomposite, which plays an excellent role in revolting with carbapenem-resistance *Acinetobacter baumannii* in vitro and in vivo. For one thing, this functionalized nanodrug system can be devoted to synergistically killing A. baumannii; for another, it is able to protect the released imipenem from hydrolyzing by carbapenemase. It is undisputed that there are preeminent biocompatibility and hemocompatibility, as well as high biosafety for this nanodrug system. This platform significantly enhanced antibacterial efficiency, while increasing the generation of ROS and the damage of oxidative membrane, as well affecting the cell wall formation and the metabolic pathways. It makes contributions to affecting on host-pathogen interaction, regulating immune response, and accelerating tissues repair. In summary, the constructed nanodrug system not only is considered as a supernal clinical application but also provides a new efficient antimicrobial therapeutic strategy.

PO-1033

动态显色法测定真菌(1,3)-β-D-葡聚糖试剂盒性能验证评价

吕星
中南大学湘雅二医院

目的 在 ATI-320 LKM 动态试管仪上采用动态显色法检测真菌(1,3)-β-D-葡聚糖，评价真菌(1,3)-β-D-葡聚糖检测试剂盒性能指标。
方法 根据美国临床实验室标准化委员会制定的评价方案对湛江安度斯公司生产的真菌(1,3)-β-D-葡聚糖检测试剂盒进行了回收试验、精密度试验、分析测量范围验证实验、干扰试验及参考区间试验。

结果 湛江安度斯公司所生产的真菌(1,3)-β-D-葡聚糖检测试剂盒的两个浓度水平质控品的实验室精密度 CV 为 7.0%；回收率 95.2%~103.5%。有关于线性评价的相关系数 r=0.990,而线性的回归方程为 Y=0.95X+206；不同浓度的血红蛋白在干扰试验中均对测定(1-3)-β-D-葡聚糖产生严重干扰。数据表明低于 1450 度的乳糜对测定(1,3)-β-D-葡聚糖产生的干扰不明显，浓度为 1450 度的乳糜会造成大于 10%的负偏差；浓度为 0.072g/L 的结合胆红素标本对测定(1,3)-β-D-葡聚糖产生不明显干扰。浓度大于 0.144g/L 的结合胆红素标本对测定（1,3)-β-D-葡聚糖产生明显干扰。浓度为 0.01g/L 的非结合胆红素标本对测定(1,3)-β-D-葡聚糖产生不明显干扰。其他浓度的非结合胆红素标本对测定(1,3)-β-D-葡聚糖均产生明显干扰。

结论 安度斯公司在国内推出的 G 试验试剂盒在正确度及精密度、抗干扰、线性等方面的性能达到临床要求，值得推广应用。

PO-1034

Risk factors for carbapenemase-producing organisms among inpatients in Scotland: A national matched case-control study

Shengyuan Zhao[1,2]、Meghan Perry[3]、Sharon Kennedy[4]、Julie Wilson[5]、Margo Chase-Topping[6,7]、Eleanor Anderson[8]、Michael Lockhart[4]、Mark Woolhouse[2,9]

1. Department of Clinical Laboratory, Xiangya Hospital, Central South University, Changsha, Hunan, China
2. Usher Institute, University of Edinburgh, Edinburgh, United Kingdom
3. Regional Infectious Diseases Unit, Western General Hospital, Edinburgh, United Kingdom
4. Public Health Scotland, Glasgow, United Kingdom
5. Antimicrobial Resistance and Healthcare Associated Infection (ARHAI) Scotland, NHS National Services Scotland, Glasgow, United Kingdom
6. The Roslin Institute, University of Edinburgh, Edinburgh, United Kingdom
7. The Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, United Kingdom
8. NHS Greater Glasgow and Clyde, Glasgow, United Kingdom
9. Centre for Immunity, Infection and Evolution, School of Biological Sciences, University of Edinburgh, Edinburgh, United Kingdom

Aim To determine risk factors for carbapenemase-producing organisms (CPOs) and to determine the prognostic impact of CPOs.

Methods This is a retrospective matched case-control study. Inpatients across Scotland in 2010-2016 were included. Patients with a CPO were matched with 2 control groups by hospital, admission date, specimen type, and bacteria. One group comprised patients either infected or colonized with a non-CPO and the other group were general inpatients. Conditional logistic regression models were used to identify risk factors for CPO infection and colonization, respectively. Mortality rates and length of postisolation hospitalization were compared between CPO and non-CPO patients.

Results In total, 70 CPO infection cases (with 210 general inpatient controls and 121 non-CPO controls) and 34 CPO colonization cases (with 102 general inpatient controls and 60 non-CPO controls) were identified. Risk factors for CPO infection versus general inpatients were prior hospital stay (adjusted odds ratio [aOR], 4.05; 95% confidence interval [CI], 1.52-10.78; P = .005), longer hospitalization (aOR, 1.07; 95% CI, 1.04-1.10; P < .001), longer intensive care unit (ICU) stay (aOR, 1.41; 95% CI, 1.01-1.98; P = .045), and immunodeficiency (aOR, 3.68; 95% CI, 1.16-11.66; P = .027). Risk factors for CPO colonization were prior high-dependency unit (HDU) stay (aOR, 11.46; 95% CI, 1.27-103.09; P = .030) and endocrine, nutritional, and metabolic (ENM) diseases (aOR, 3.41; 95% CI, 1.02-11.33; P = .046). Risk factors for CPO infection versus non-CPO infection were prolonged hospitalization (aOR, 1.02; 95% CI, 1.00-1.03; P = .038) and HDU stay (aOR, 1.13; 95% CI, 1.02-1.26; P = .024). No differences in mortality rates were detected between CPO and non-CPO patients. CPO infection was associated with longer hospital stay than non-CPO infection (P = .041).

Conclusions A history of (prolonged) hospitalization, prolonged ICU or HDU stay; ENM diseases; and being immunocompromised increased risk for CPO. CPO infection was not associated with increased mortality but was associated with prolonged hospital stay.

PO-1035

16S rRNA 靶向测序联合荧光定量 PCR 对血流感染人型支原体的鉴定

曾童、张小团、刘卓然
南华大学附属第二医院

目的 对南华大学附属第二医院产妇血培养“假阳性”标本进行微生物学分子检测，以进一步明确导致孕妇产后不明原因发热的病原谱，并指导临床诊治。
方法 对患者报阳性的需氧和厌氧血培养瓶培养物涂片后革兰染色镜检，进行细菌形态学初级检查，同时转种普通培养基培养；根据初级结果及临床特征对血培养物做支原体培养及药敏试验；采用 16S rRNA 靶向测序技术鉴定血培养物中可能存在的病原菌，根据测序结果进行人型支原体荧光定量 PCR 作进一步证实，同时验证荧光定量 PCR 法检测血培养物的可行性。
结果 将源于同一患者的两瓶“假阳性”瓶内血样进行病原学鉴定。涂片染色后镜下观察，未见典型细菌。转种普通培养至哥伦比亚血琼脂平板、麦康凯平板等细菌培养平板 48 h 后未见菌落生长。将血培养物集菌后进行支原体培养，结果亦呈阴性。随后进行 16S rRNA 基因测序鉴定，显示此产妇血液中存在人型支原体（序列相似度 99.93%），荧光定量 PCR 证实血培养物中的病原体为人型支原体。
结论 造成该孕妇产后持续性高热的原因为人型支原体血流感染，采用荧光定量 PCR 法检查结果可靠。对于产科不明原因发热送检的血培养“假阳性瓶”，采用 16S rRNA 测序和/或联合荧光定量 PCR 可提高支原体血流感染的检出效率。

PO-1036

Mechanism of the emergence of hypervirulent and carbapenem-resistant Klebsiella pneumoniae: mobilization of virulence plasmids under the help of conjugative plasmids?

Dongxing Tian
Huashan Hospital, Shanghai Medical College, Fudan University

Hypervirulent and carbapenem-resistant Klebsiella pneumoniae (hv-CRKP) has emerged as a threatening pathogen puzzling many scientists and clinicians. The mechanism of the acquisition of pK2044-like virulence plasmid by carbapenem-resistant Klebsiella pneumoniae (CRKP) is still unknown. Hypervirulent NTUH-K2044, carbapenem-resistant JS187 and HS11286 strains have been completely sequenced before, and were selected as representative strains to explore the mechanism of the mobilization of pK2044-like virulence plasmids. The virulence and resistance phenotype experiments were also performed in these strains and their corresponding transconjugants. The conjugative KPC plasmid pKPHS2 of HS11286 could be transferred to hypervirulent NTUH-K2044, and transconjugant NTUH-K2044-pKPHS2 was obtained. Although KPC plasmid could be stable in NTUH-K2044 after 25 passages, NTUH-K2044-pKPHS2 didn’t exhibit the dual phenotype of hypervirulence and carbapenem-resistance for the fitness costs. The transconjugant NTUH-K2044-pKPHS2 could acquire carbapenem resistance during subculturing but lost hypermucoid phenotype. The mucoid NTUH-K2044-pKPHS2 remained

hypervirulence but did not obtain carbapenem-resistance, while non-mucoid NTUH-K2044-pKPHS2 acquired high carbapenem-resistance but had a decreased virulence phenotype. We speculated that the fitness costs of KPC plasmid in hypervirulent NTUH-K2044 possibly result in the less common detection rate of carbapenem-resistant and hypervirulent Klebsiella pneumoniae (CR-hvKp) in hospital than hv-CRKP strains. We further performed conjugation experiment which NTUH-K2044-pKPHS was as a donor and carbapenem-resistant JS187 as a recipient, and virulence plasmid pK2044 could be transferred to JS187 under the help of the conjugative KPC plasmid pKPHS2. The transconjugant JS187-pK2044 had the dual phenotype of hypervirulence and carbapenem resistance. S1-PFGE and draft plasmids genome sequencing confirmed the simultaneous mobility of pK2044 and pKPHS2. In conclusion, our study confirmed a pathway of the mobilization of pK2044-like virulence plasmid to CRKP strains and provided a possible explanation of the lower detection rate of CR-hvKp strains than hv-CRKP strains in clinical settings.

PO-1037

6353 份血培养检出病原菌的分布及耐药性分析

何天娇
西安医学院第一附属医院

目的 通过检测血培养中的病原菌，并分析其耐药性，旨在为临床提供合理的用药参考。
方法 对本院 2018 年 1 月至 2019 年 12 月的血培养标本进行回顾性分析，采用 K-B 或 MIC 法对分离的主要病原菌进行药敏试验，使用 WHONET5.6 软件对病原菌的分布和药敏结果进行分析。
结果 在本实验纳入的 6353 份血培养标本中，共分离出病原菌 327 株，阳性率为 5.1%（327/6353），其中革兰阴性菌 184 株（占 56.3%）；革兰阳性菌 139 株（占 42.5%）；真菌 4 株（占 1.2%）。排名前 5 位的病原菌依次为：大肠埃希菌（占 30.9%）、人葡萄球菌（占 12.8%）、肺炎克雷伯菌（占 10.1%）、表皮葡萄球菌（占 8.0%），以及溶血葡萄球菌（占 6.4%），其中大肠埃希菌和肺炎克雷伯菌检出产超广谱 β-内酰胺酶的菌株分别为 32.7%和 45.5%；耐甲氧西林金黄色葡萄球菌的检出率为 7.1%，检出了对碳青霉烯类药物耐药的肠杆菌科细菌，检出率为 4.7%，未检出对万古霉素、替考拉宁、替加环素耐药的葡萄球菌。
结论 本院血培养存在阳性率低问题，需要加强临床科室的沟通，提高血培养送检，定期对血流感染病原菌的分布及耐药性进行分析，为临床医生经验用药提供依据。

PO-1038

The recombinant protein TPF-1 upregulates the secretion of IL-6 and IL-8 and promotes endothelial angiogenesis through the ERS/PI3K/ Akt and ROS/ NF-κB pathways

Ting Cao、Jialun Cai、Shuangquan Liu
The First Affiliated Hospital of University of South China

Aims In this study, human umbilical vein endothelial cells (HUVEC) were used as target cells to investigate the role of Treponema pallidum recombinant protein TpF-1 in promoting angiogenesis, and to further explore the mechanism of ERS/PI3K/AKT and ROS/NF-κB signaling pathway in TpF-1 promoting angiogenesis, which laid a foundation for studying angiogenesis and vascular inflammation caused by Treponema pallidum infection.
Methods 1. After stimulating HUVEC with different concentrations of TPF-1, CCK8 was used to detect cell proliferation and activity. The endoplasmic reticulum structure of cells was observed by transmission electron microscope. The expression levels of IL-6, IL-8 and VEGF-A in HUVEC

were detected by RT-PCR and ELISA, and detection of angiogenesis by in vitro angiogenesis assay.
2. After stimulating HUVEC with different concentrations of TPF-1, WB test detected the expression of proteins related to HUVEC ERS/PI3K/Akt and ROS/NF-κB pathway. ROS production was detected by flow cytometry. Immunofluorescence assay was used to detect nuclear translocation of NF-κ B.
3.After ERS, PI3K, AKT, ROS and NF-κB inhibitors pretreated HUVEC, WB detected the expression of related pathway proteins. Flow detection of ROS production. The expression levels of IL-6, IL-8 and VEGF-A were detected by RT-PCR and ELISA. Transwell and in vitro angiogenesis assay were used to detect migration and tube-forming ability of HUVEC.
Results 1. After stimulating HUVEC with different concentrations of TPF-1, the cell activity was enhanced, the endoplasmic reticulum structure was obviously swollen and broken, and the expression of IL-6 and IL-8 in HUVEC was up-regulated in a dose-dependent manner, which promoted the in vitro angiogenesis of HUVEC, but the expression of VEGF had no obvious change.
2. TPF-1 can up-regulate the expression of ERS-related proteins BIP, PERK and IRE1-α in a dose-dependent manner, after ERS inhibitor is used, the expression of ERS-related proteins is significantly down-regulated and the in vitro angiogenesis ability of HUVEC is inhibited.
3. The expressions of PI3K and AKT, IL-6 and IL-8 were significantly down-regulated after adding inhibitors of PERK and IRE1-α.
4.TPF-1 can up-regulate the production of ROS, and after using ROS inhibitor, it can significantly reduce the expression of p-65, the nuclear translocation of NF-κB, the expression of IL-6 and IL-8, and finally inhibit angiogenesis.
Conclusions 1.TpF-1 can promote HUVEC to secrete IL-6 and IL-8 to induce angiogenesis.
2. TPF-1 can stimulate the formation of endothelial cell tubes via the ERS(PERK、IRE1α)/PI3K/Akt pathway.
3.TpF-1 can induce endothelial cell tube formation through ROS/NF-κB pathway.

PO-1039

苯唑西林敏感 MRSA(OS-MRSA)多中心研究

刘俊兰、李敏
上海交通大学医学院附属仁济医院

Oxacillin-susceptible mecA-positive MRSA represents an important issue, as its oxacillin susceptibility contributed to misidentification and potential therapeutic failure, but limited data on the current status of OS-MRSA infection in Chinese hospitals are available. This multicenter study revealed that OS-MRSA represented 1.8% of total isolates. Of 17 OS-MRSA, 10 were ST59, followed by ST965, and 11 carried SCCmec IV, while 5 carried SCCmec V, but only one was PVL-positive, 16 had point mutations within mecA promoter. VITEK 2 system exhibited deficiency, whereas cefoxitin disk diffusion should be supplemented in detecting S. aureus with borderline MICs. This study has characterized phenotypically and molecularly OS-MRSA in China, and provided insights into effective management of OS-MRSA.

PO-1040

葡萄球菌激酶 SAK 活化 NLRP3 炎性小体促进社区获得性金黄色葡萄球菌肺部感染

王亚楠
上海交通大学医学院附属仁济医院

目的 明确葡萄球菌激酶 SAK 在高毒力社区获得性金黄色葡萄球菌（CA-SA）中的作用及机制。为及时的诊断与感控措施的实施以及设计新的抗感染药物或疫苗提供潜在的药物靶标和依据。
方法 检测不同临床菌株的 SAK 表达和分泌水平。构建 sak 基因敲除株，通过半定量生物被膜实验检测 SAK 对生物被膜形成的作用。在野生小鼠与 CRAMP−/−小鼠上构建肺炎模型进一步明确 SAK 在 CA-SA 侵袭性感染中的作用。取小鼠肺组织抽提总 RNA，通过 RNA 测序探究 SAK 对宿主基因表达的作用。并通过体外实验进一步验证 RNA 测序的结果。
结果 SAK 在 CA-SA 流行株 ST398 和 ST59 中的表达水平明显高于医院获得性的金葡菌。SAK 对金葡菌生物被膜形成的抑制作用主要是通过促进纤溶来实现。此外，小鼠肺炎模型结果表明感染野生型 ST398 的小鼠，其肺部的充血水肿明显更严重，肺组织 CFU 计数更高，并表现出更严重的炎细胞浸润，推测 SAK 能够促进金葡菌的肺部感染；并通过 CRAMP−/−小鼠进一步证实 SAK 的抗菌肽中和作用并非其促进感染的主要机制。RNA 测序结果表明，SAK 可促进固有免疫相关基因的表达，还可促进 NLRP3 炎性小体的激活，并通过体内外实验进一步证实。此外，SAK 可促进细胞活性氧的生成，进而促进 NLRP3 炎性小体的激活，介导肺组织的炎症性损伤。
讨论 本研究强调了控制炎症反应在急性肺部感染中的意义，炎性-抗炎反应失衡是金葡菌肺炎的重要致病机制，高毒力 CA-SA 流行株 ST398 在早期肺炎感染过程中通过 SAK 促进活性氧的生成，从而促进宿主固有免疫炎症反应的激活，尤其是 NLRP3 炎性小体的激活，可促使细胞焦亡，增强炎症因子的释放，加剧炎症性组织损伤。

PO-1041

感染性病原菌宏基因组检测标本预处理方法探索

朱盈、杨启文
中国医学科学院北京协和医院

目的 近年来，血流感染发病率逐年上，而其诊断依赖于病原菌的鉴定，但由于血液中病原菌浓度极低，培养慢且阳性率低，将不受靶标限制的宏基因组学测序技术用于病原菌诊断能带来极大的便利。本课题主要针对宏基因组学测序技术一大难题——血流感染患者标本中大量人类核酸对病原菌核酸检测带来的干扰进行研究，设计了三种去宿主（人源）核酸方法皂素（Saponin）去宿主核酸法、SDS 去宿主核酸法和水洗法，从中选出最优方法。
方法 向无菌血液样本中分别注入金黄色葡萄球菌、肺炎克雷伯菌、白色念珠菌模拟临床血流感染患者血液标本，对标本进行去宿主核酸处理、核酸提取、qPCR，通过比较对照组及实验组样本的 Cq 值评价各方法的去人源核酸效果以及病原菌核酸丢失量。
结果 皂素去宿主法中，人源核酸去除效果较好：GAPDH 基因=10.13，s2=1.02；β-actin 基因=12.76，s2=0.63，而病原菌核酸发生富集：= -1.32，s2=6.79。SDS 去宿主法中人源核酸去除效果好：GAPDH 基因=11.13，s2=0.30；β-actin 基因=14.30，s2=1.29，但病原菌核酸也发生了丢失：= 2.46，s2=4.43。水洗法中人源及病原菌核酸发生了富集， GAPDH 基因=-4.23，s2=0.38；β-actin 基因=-4.05，s2=0.96；病原菌= -0.73，s2=4.84。
结论 综合考虑去宿主核酸及病原菌核酸丢失量两方面，使用皂素去宿主核酸法处理含菌血液样本效果最理想。

PO-1042

Iron-rich conditions induce virulence and OmpA changes of Acinetobacter baumannii

Hui Liu[1]、Chunyuan Cao[2]、Fu lan Qiu[1]、Haonan Huang[1]、xiunian Hu[1]
1. Fujian Longyan First Hospital
2. 福建省龙岩市疾控中心

Background Iron ions affect the expression of outer membrane protein A (OmpA), a major pathogenic protein in Acinetobacter baumannii.
Objective To analyze the effect of iron ions on the expression of the OmpA protein of A.baumannii and explore its association with the virulence of OmpA.
Methods Site-directed mutagenesis was used to construct OmpA gene deletion strains and gene repair strains. The OmpA protein expression of A. baumannii under culture with different contents of iron ions were detected. The virulence of A. baumannii with different OmpA protein expression levels was evaluated in macrophages and mice.
Results OmpA protein levels of the three strains were enhanced under iron-rich conditions and were reduced in the presence of the iron-chelating agent 2,2'-bipyridine. A. baumannii wild type and +OmpA had a remarkable toxic effect on RAW246.7 macrophages ($P<0.05$), while the ΔOmpA had a significantly reduced toxic effect on RAW246.7 macrophages ($P<0.05$). The levels of the inflammatory factors IL-1β, IL-6, IL-8, and TNFα in the mice spleen were significantly increased in the +OmpA strain treatment group compared with the ΔOmpA strain group (all $P<0.05$). In addition, the levels were higher in the presence of iron ions than in the presence of the chelating agent.
Conclusion Iron-rich conditions increase the OmpA protein expression of A. baumannii. Strains with high OmpA protein expression were more invasive, which may be a key determinant of A. baumannii infection and pathogenicity. Iron control strategies mightbe used for the management of A. baumannii.

PO-1043

Repurposing eltrombopag as an antimicrobial agent against multidrug-resistant Staphylococcus aureus

Pengfei She、Shijia Li、Linying Zhou、Yong Wu
The Third Xiangya Hospital of Central South University

Because of the excessive use of antibiotics, methicillin-resistant Staphylococcus aureus (MRSA) has become prevalent worldwide. Moreover, the persisters formed in S. aureus biofilms are protected to the action of antimicrobials and cause persistence and relapse of infections. Thus, the discovery of antibiotics with excellent anti-persister and anti-biofilm activities is urgently needed. In the present study, eltrombopag (EP), a classic thrombopoietin receptor agonist, exhibited potential antimicrobial activity against multidrug-resistant (MDR) S. aureus and its persisters, alone or in combination with vancomycin. Through our mechanistic studies, EP was found to disrupt the proton motive force and inhibit the transport of iron across S. aureus cell membranes. The in vivo anti-infective efficacy of EP was further confirmed in the MRSA infection models. In addition, the cytotoxicity of EP against mammalian cells and the in vivo toxicity of EP in animal models were not observed at the tested concentrations of EP. Collectively, these results indicate that EP could be considered a potential novel antimicrobial agent against recalcitrant infections caused by MDR S. aureus and its persisters.

PO-1044

抗高血压药对 MRSA 及其持留菌的抗菌作用和机制研究

徐兰兰、佘鹏飞、陈丽华、李诗佳、周林颖、Zubair Hussain、刘亚倩、伍勇
中南大学湘雅三医院

目的 探索抗高血压药坎地沙坦酯对金黄色葡萄球菌（MRSA）及其持留菌的抗菌作用和机制。
方法 通过微量肉汤稀释法检测坎地沙坦酯的抗菌谱；通过棋盘稀释法检测其和传统抗生素的联合抗菌效果；通过摇菌培养和菌落稀释计数测其时间-杀菌曲线；通过持留菌杀菌试验和膜渗透试验探索其对 MRSA 持留菌的杀菌效果及相应的机制；通过膜渗透试验、膜去极化测试、ATP 释放试验、扫描电镜和透射电镜探索其对 MRSA 的作用机制；通过 XTT 实验和结晶紫染色,探索对其生物膜抑制和根除效果；通过激光共聚焦显微镜（CLSM）探索其对生物膜结构和形态的影响；通过人红细胞溶血试验和 CCK-8 细胞毒性实验测其红细胞溶血率和细胞毒性；通过一步耐药法和连续耐药试验测其对细菌诱导耐药产生的能力；通过小鼠皮肤脓肿模型探索其体内抗菌效果。
结果 坎地沙坦酯对革兰氏阳性菌，尤其是金黄色葡萄球菌，具有较强的抗菌活性，且不易诱导产生耐药性，具有较弱的溶血率和细胞毒性。此外，棋盘稀释法结果表明，坎地沙坦酯联合庆大霉素和妥布霉素对金黄色葡萄球菌的协同抑菌指数值为 0.375，表现为协同抗菌作用。在联合时间杀菌曲线中，联用组在 12 h 时可使细菌数量相比对照组下降约 5 个 Log10。且坎地沙坦酯可以阻止金黄色葡萄球菌生物膜形成并杀死持留菌。通过对其作用机制分析，我们发现坎地沙坦酯可以破坏金黄色葡萄球菌细胞膜通透性,使膜电位和 ATP 下降,并引起膜结构改变。最后，小鼠皮肤脓肿模型证明坎地沙坦酯在体内具有相似的抗菌作用。
结论 坎地沙坦酯可能是治疗金黄色葡萄球菌相关感染的潜在抗菌剂。

PO-1045

Antimicrobial resistance, genetic characterization and molecular epidemiology of Ureaplasma species in males with infertility

Lihong Zhao
Tai'an City Central Hospital

Objectives This study aimed to study the antimicrobial resistance, genetic characterization and molecular epidemiology of Ureaplasma species in order to provide clinicians sufficient data to select optimal strategies of treatment for genitourinary tract infections of infertile male patients.
Methods Firstly, a total of 817 clinical semen specimens were detected for Ureaplasma species by molecular detection. Secondly, culture and identification of Ureaplasma species were achieved by using Mycoplasma ICS Test, and the antimicrobial susceptibility tests were determined by using broth microdilution assay. Then the tetracycline resistance genetic determinants in Ureaplasma species were identified by PCR and the fluoroquinolone and macrolide resistance genetic determinants were identified by DNA sequencing. Finally, the molecular epidemiology of Ureaplasma species was studied by both multilocus sequence typing (MLST) and expanded MLST (eMLST) schemes.
Results Among the 817 semen specimens, 320 (39.17%) specimens were positive for Ureaplasma species. The percentages of resistance in 320 isolates against LEV, MXF, TET and ERY were 47.5%, 39.38%, 19.69%, and 3.75%, respectively. The tet(M) and int-Tn genes were detected positive in all the tetracycline-resistant isolates. One macrolide-resistant UU isolate had a novel amino acid alteration (R66T) in L4 ribosomal protein and another UU isolate harbored a novel alteration (S109T) in L22. In fluoroquinolones-resistant isolates, S83L substitution in the ParC was predominant. In this area, ST22 and eST16 were most prevalent ST and eST, respectively. One ST and 3 eSTs were newly identified in this study.

Conclusions This study has demonstrated that ERY can be first line therapy for Ureaplasma species infections.

PO-1046

Developing two rapid protein extraction methods using focused-ultrasonication and zirconia-silica beads for filamentous fungi identification by MALDI-TOF MS

Yating Ning、Li Zhang、Yingchun Xu
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College

Filamentous fungi identification by Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) has been challenging due to the lack of simple and rapid protein extraction methods and insufficient species coverage in the database. In this study, we created two rapid protein extraction methods for filamentous fungi: an one-step zirconia-silica beads method (ZSB) and a focused-ultrasonication method (FUS). The identification accuracy of two methods were evaluated with the VITEK MS, as well as number of spectra peaks and signal-to-noise ratio with M-Discover 100 MALDI-TOF MS compared to the routine method. The better method was applied to build a filamentous fungi in-house spectra library for the M-Discover 100 MS, and then another one and routine method were performed in parallel to verify the accuracy and commonality of the in-house library. Using the two optimized methods, the dedicated operating time before MALDI-TOF MS analysis was reduced from 30 mins to 7 (ZSB) or 5 (FUS) mins per sample, with only a few seconds added for each additional strain. And both two methods identified isolates from most mold types equal to or better than the routine method, and the total correct identification rate using VITEK MS was 79.67%, 76.42% and 76.42%, respectively. On the other hand, the two rapid methods generally achieved higher maximum and minimum S/N ratios with these isolates tested as compared to the routine method. Besides, the ZSB method produed overall mean of maximum and minimum S/N ratio higher than that by FUS. An in-house library of M-Discover MS was successfully built from 135 isolates from 42 species belonging to 18 genera using the ZSB method. Analysis of 467 isolates resulted in 97.22% correctly identified isolates to the species level by the ZSB method versus 95.50% by the routine method. The two novel methods are time- and cost-effective and allow efficient identification of filamentous fungi while providing a simplified procedure to build an in-house library. Thus, more clinical laboratories may consider adopting MALDI-TOF MS for filamentous fungi identification in the future.

PO-1047

MKT-077 选择性清除外排泵高表达唑类耐药真菌的作用机理研究

张明
山东大学第二医院

目的 白色念珠菌是临床常见的致病真菌，抗真菌药物种类少以及耐药的多发严重制约着白色念珠菌感染的治疗，因而寻找新型、特别是针对耐药菌的抗真菌药物具有重要意义。
方法 微生物和肿瘤均存在旁系敏感现象，即某种耐药突变会增加对其它类型药物的敏感性。我们利用该特性，采用荧光标记的敏感菌和耐药菌共培养模型对天然分子和药物分子库进行筛选，发现对由外排泵 MDR1 高表达引起的唑类耐药菌具有选择性清除作用的小分子。并通过寻找 MDR1 高表达株与其母体菌株的差异揭示该化合物的选择性作用机制。

结果 高通量筛选发现具有抗肿瘤活性的花菁染料类分子 MKT-077 对由外排泵 MDR1 高表达引起的唑类耐药菌具有选择性清除作用，其最小抑菌浓度为唑类敏感株的 1/8。机制实验表明 MKT-077 的选择性与胞内药物含量累积差异有关，且 MKT-077 的摄取依赖于质子梯度。
结论 MKT-077 对由外排泵 MDR1 高表达引起的唑类耐药菌具有选择性清除作用。

PO-1048

利用细菌肽聚糖结构构建革兰阳性细菌的超灵敏检测方法

韩道宾[1]、丁世家[2]
1. 山东大学第二医院
2. 重庆医科大学

目的 病原微生物感染的早期鉴定对于临床感染性疾病的早期诊断、治疗指导具有重要的意义。目前临床上传统的微生物检测方法较为耗时，且灵敏性有待提高。因此，本课题整合了革兰阳性细菌自身肽聚糖结构和金属纳米材料的优点，以及两者之间的高度亲和作用，基于电化学平台开发了免二抗、无酶、快速的细菌检测新方法。
方法 首先在电极表面依次修饰碳纳米管和金纳米粒子，增强导电性和有效反应面积。接下来，修饰特异性抗体，并且通过抗体捕获靶细菌。而后再加入铂镍铜三金属纳米立方体，革兰阳性细菌的肽聚糖结构可以稳固的结合金属纳米立方。最后利用铂镍铜纳米立方体的自身电化学特性及类过氧化物酶作用实现细菌的快速灵敏检测。
结果 方法在 1.5×102 - 1.5×108 CFU/mL 的检测范围内具有良好的线性关系，并且最低检测限达到了 42 CFU/mL。本方法完全可以在加入靶物质后 2 小时内实现结果的输出，免去了传统细菌过夜培养的时间。此外，本检测方法具有较高的特异性，能选择性的对革兰阳性细菌进行快速灵敏的检测。以上结果说明该方法具有良好临床适用性。
结论 本文首次基于细菌肽聚糖结构和铂镍铜三金属纳米立方体的高度亲和作用构建了细菌检测的新方法，具有免二抗、无酶等优点，并且方法在快速检测的基础上具有较高的特异性。该方法为临床病原微生物的检测和即时检验（POCT）提供了新的技术支持，具有广阔的临床应用前景。

PO-1049

Clinical Epidemiology and Resistance Phenotype of Invasive Escherichia coli in Children

Yang Li、Wei Li、Yunzhen Tao、Yunzhong Wang、Xuejun Shao
苏州大学附属儿童医院，Children's Hospital of Soochow University

Objective To investigate the clinical epidemiology and drug resistance of invasive *Escherichia coli* (*E. coli*) isolates at a children's medical center in east China and provide guidance for clinical treatment and nosocomial infection control.
Methods 67 invasive *E. coli* strains were isolated in Children's Hospital of Soochow University from January 2018 to December 2019. The strains were identified by automatic mass spectrometer and the drug susceptibility were analysed by VITEK 2 compact system. PCR was also performed to detect the genes of carbapenemases, extended-spectrum β-lactamases (ESBLs) and AmpC β-lactamases.
Results 67 invasive *E. coli* strains were isolated from blood (88.06%) and cerebrospinal fluid (11.94%). They were mainly from the departments of neonatology (37.31%), hematology (31.34%), and intensive care units (10.45%). 65.67% of patients were boys and 34.33% were girls. Among them, 44.78% was younger than 1 month, 31.34% was between 1 and 12 months old, 23.88% was between 1 and 18 years old. The drug sensitivity results showed that 67 invasive *E. coli* strains were not resistant to imipenem, meropenem, ertapenem and amikacin.

Among them, 25 invasive *E. coli* strains produced ESBLs at the same time. PCR results showed that the carbapenemase genes of 67 invasive *E. coli* strains were *NDM-1* (2.99%) and *OXA-1* (1.49%). ESBLs genes were *TEM-1* (62.69%) and *CTX-M-14* (34.33%). Besides, AmpC β-lactamase genes were *ACT-1* (64.18%), *FOX-1* (44.78%), *CIT-1* (2.99%), *CMY-2* (2.99%) and *DHA-1* (1.49%).
Conclusion The drug resistant rate of invasive *E. coli* from children was not high and the carriage proportion of β-lactam antibiotic resistance genes was lower than invasive *Klebsiella pneumoniae*. The mechanism of β-lactam antibiotic resistance was mainly attributed to the genes of *TEM-1*, *CTX-M-14*, *ACT-1* and *FOX-1*.

PO-1050

不同血培养瓶对 4 种常见抗菌药物中和能力比较

杨会林、陈娟、闫津津、闫津津、文明明
北京大学深圳医院

目的 研究不同血培养瓶对 4 种临床常用抗菌药物的中和效果。
方法 选取 4 种临床常用抗菌药物亚胺培南、哌拉西林/他唑巴坦、万古霉素、卡泊芬净，分别使用推荐质控菌株配对，进行血培养瓶细菌生长模拟试验，观察上机培养后细菌能否报阳及报阳时间，评估不同血培养瓶对抗菌药物的中和能力。
结果 亚胺培南/大肠埃希菌组，梅里埃 FN plus 瓶报阳，报阳时间为 12.4±0.3h，梅里埃 FA plus、BD Aerobic、BD Anaerobic 均超过 5 天不报阳；哌拉西林/他唑巴坦/铜绿假单胞菌组，梅里埃 FA plus、BD Aerobic 均能报阳，平均报阳时间分别为 16.2±0.3h、18.1±0.4h；万古霉素/金黄色葡萄球菌组，梅里埃 FA plus、FN plus、BD Aerobic 能报阳，平均报阳时间分别为 16.7±0.4h、24.1±0.6h、31.3±3.9h，BD Anaerobic 超过 5 天不报阳。卡泊芬净/白色念珠菌组，梅里埃 FA plus、BD Aerobic 能报阳，平均报阳时间为 47.1±3.3h、42.9±2.0h。
结论 梅里埃 FA plus、BD Aerobic 具有中和万古霉素、哌拉西林/他唑巴坦、卡泊芬净的能力，FA plus 具有中和亚胺培南、万古霉素的能力；使用抗菌药物前采集血培养很重要，应根据临床抗菌药物使用习惯选择合适的培养瓶；

PO-1051

Effect of CAP10 gene on immune response in mice infected with Cryptococcus neoformans

liping lin、Shanshan Chen、Junhui Zhang、Xianghui Li、Juan Wu、Ni Lin
Fujian medical university

Objectives The capsule associated protein 10 gene (CAP10) is indispensable to the formation of the polysaccharide capsule, and is closely related to virulence of the Cryptococcus (C.) neoformans. However, the role of CAP10 in the pathophysiology of cryptococcosis is still not well understood. This study aims to investigate the association of CAP10 expression with the immune responses to infected mice with C. neoformans.
Methods The shRNA expression plasmid was designed to interfere with the synthesis of CAP10. The animal model was established with C. neoformans wt strain H99, cap10-shRNA C. neoformans and PBS control in the respiratory tract. On the 7 days and 21 days after infection, mice lung histopathological examination and homogenate culture were performed, and cytokines expression level in the serum of mice were quantitatively detected.
Results The cap10-shRNA group may alleviate pathological lesions in pulmonary C. neoformans infection, and a lower degree of inflammatory cells was observed in the cap10-shRNA group. The fungal burden was significantly lower in the cap10-shRNA group, indicating

that the clearance towards C. neoformans was somehow affected. In addition, interference with CAP10 altered the expression profile of Th1, Th2, Th17 and Treg type cytokine. Down-regulation of CAP10 was beneficial to the balance of Th1/Th2 and Th17/Treg ratios.
Conclusions Collectively, our results showed that the expression of CAP10 was associated with an antifungal immune response in mice, suggesting that CAP10 regulates the inflammatory response. Therefore, we expect that the CAP10 gene will become a new molecular therapeutic target in cryptococcosis treatment.

PO-1052

丝状真菌培养条件对质谱鉴定的影响因素研究

袁凯旋、陈晓丽、叶龙
广东省人民医院（广东省医学科学院）

目的 以 Vitek MS 为平台，探究丝状真菌在不同培养基、不同培养温度和不同培养时间对质谱鉴定正确率的影响，以筛选适合本实验室丝状真菌质谱鉴定的理想培养条件，提高鉴定正确率。
方法 将从临床分离到的经过测序和形态学确认的 100 株丝状真菌分别接种于沙氏葡萄糖培养基（SDA）、马铃薯葡萄糖琼脂培养基（PDA）及 28℃和 37℃共四种组合培养条件下进行培养。在确定其最佳培养条件之后，在其培养的第 2、3、4、5、7、8、9 天对其进行质谱鉴定，以鉴定正确率的差异性从而筛选出丝状真菌的最佳培养条件。
结果 不同培养基比较，SDA 鉴定正确率为 85.5%，PDA 鉴定正确率为 73%，两种培养基准确性的鉴定率有显著差异(c^2=9.503，P=0.003)，其中使用 SDA 鉴定率最高。不同温度进行比较，28℃下总鉴定正确率为 80%，37 度下总鉴定正确率为 78.5%，两种温度比较其鉴定正确率无显著差异(c^2=0.137，P=0.805)。菌株培养 2~9 d 的质谱鉴定正确率分别为 93%、90%、79%、68%、62%、62%、56%、55%，随着培养时间的延长正确率随着下降，比较不同培养天数下的鉴定正确率，差异有统计学意义(c^2=75.189，P=0.000），2d 和 3d 正确率最高，差异无统计学意义（c^2=0.084，P=0.772）。
结论 使用 SDA 培养基在 28℃或 37℃下培养丝状真菌 2~3 d 进行质谱鉴定能取得良好的鉴定结果。

PO-1053

Identifcation of a novel bocaparvovirus in a wild squirrel in Kunming, Yunnan Province, China

Jiali Wang
Yunnan Province Hospital of Infection Disease

In December 2017, a squirrel (Callosciurus phayrei) died 2 days after capture in Kunming, and its intestinal tract, heart, liver, spleen, lung, and kidney were subjected to metagenomics analysis. Reassembly and verifcation by reverse transcrip_x0002_tion PCR of contigs generated by next-generation sequencing yielded a 5176-nt sequence, which was designated "squirrel bocaparvovirus" (SQBOV). Phylogenetic trees based on the aa sequences of NS1, NP1, and VP1 showed that SQBOV formed an independent branch in the bocaparvovirus phylogenetic tree. The amino acid sequence identity of the NS1 of SQBOV to those of other bocaparvoviruses was below the threshold of 85% that is used to demarcate species within the genus, indicat_x0002_ing that it should be considered a member of a new bocaparvovirus species. To our knowledge, this is the frst report of a bocaparvovirus in squirrels. Our fndings will enable further studies of viral diversity in rodents and of the genetic diversity and host range of bocaparvoviruses.

PO-1054

糖尿病足患者金黄色葡萄球菌分离株毒力的初步研究

罗振[1]、黄卯[2]
1. 中南大学湘雅三医院
2. 中南大学湘雅医学院检验系

目的 确定糖尿病足患者金黄色葡萄球菌分离株的毒力及相关的毒力因子，为后续研究提供依据。
方法 收集中南大学湘雅三医院微生物室分离鉴定的来源于糖尿病足（31 例）、血流感染（22 例）、分泌物标本（31 例）的金黄色葡萄球菌；利用体外溶血实验检测金黄色葡萄球菌分离株的毒力；利用反向 CAMP 实验检测金黄色葡萄球菌是否产 β 溶血素（β-toxin）；利用蛋白水解实验鉴定胞外蛋白酶的活性。
结果 糖尿病足分离株金黄色葡萄球菌的溶血活性明显高于血流感染和分泌物分离株，而血流感染菌株和分泌物分离株的溶血活性无明显差异；反向 CAMP 实验将糖尿病足分离出金黄色葡萄球菌分为 β-toxin+ 和 β-toxin— 分离株；β-toxin+ 分离株的溶血活性明显高于 β-toxin— 分离株；血清能显著抑制 β-toxin+ 和 β-toxin— 分离株的溶血活性，但是高密度脂蛋白（HDL）仅能显著抑制 β-toxin+ 分离株的溶血活性，而不影响 β-toxin—分离株的溶血活性。基因敲除 PSM 或 agr 基因能显著降低 RJ-2（β-toxin+）的溶血活性。丝氨酸蛋白酶抑制剂（PMSF）和金属蛋白酶抑制剂（EDTA）并不影响 β-toxin— 分离株的溶血活性及蛋白分解能力。自溶素抑制剂（SPS）能显著抑制 β-toxin— 分离株的溶血活性及蛋白分解能力，而不影响 β-toxin+ 分离株；
结论 糖尿病足患者金黄色葡萄球菌分离株的毒力增加，PSM 是 β-toxin+ 分离株的主要毒力因子，而是自溶素是 β-toxin—分离株的主要毒力因子。

PO-1055

bla 系统在苯唑西林敏感 mecA 阳性金黄色葡萄球菌中发挥重要调控作用

简颖、李天铭、赵林、李敏
上海交通大学医学院附属仁济医院

目的 苯唑西林敏感 *mecA* 阳性金黄色葡萄球菌（OS-MRSA）在世界各地均有报道，临床重要性越发受到关注，然而其发生机制却仍不清楚。本研究通过高通量全基因测序技术来分析 OS-MRSA 与苯唑西林耐药 *mecA* 阳性金黄色葡萄球菌（OR-MRSA）野生株的基因差异，并构建突变菌株探索 OS-MRSA 的形成机制。
方法 对 9 株 OS-MRSA 以及 77 株 OR-MRSA 临床分离株进行二代测序，选择代表性 OS-MRSA 菌株 ET-13、ET-16 在苯唑西林培养基中逐步诱导为耐药表型并进行二代测序分析。使用 CLC Genomics Workbench 对测序数据进行分析，构建系统发育树，分析差异基因。选取 OS-MRSA 代表菌株 ET-16 及其诱导耐药菌株 ET-16I，使用二者构建的突变株来分析目标 *bla* 调控基因对苯唑西林敏感性的影响。E-test 方法用来测量苯唑西林 MIC，并使用 qRT-PCR 以及蛋白印迹实验来确定相关基因的表达情况。
结果 OS-MRSA 和 OR-MRSA 菌株在系统发育树上散在分布，无进化差异关系。差异基因分析时发现在多数 OS-MRSA 菌株（7/9）*blaR1* 基因存在第 488 位 A 碱基缺失，从而造成 BlaR1 蛋白残缺，无法发挥正常功能；为代表菌株 ET-16 过表达 OR-MRSA 来源的 *blaR1* 基因后，其转变为苯唑西林耐药表型。另外，OS-MRSA 诱导耐药菌株测序发现大部分耐药株（5/6）*bla* 调控基因所在的质粒丢失，为代表菌株 16I 回补 OS-MRSA 来源的 *blaR1-blaI* 后，其恢复为敏感表型。

结论 *blaR1* 的碱基缺失造成苯唑西林敏感表型的出现，而在诱导耐药过程中其携带 *bla* 调控系统的质粒丢失后从而转变为耐药表型。*bla* 调控系统在 OS-MRSA 菌株苯唑西林耐药表型的调控中发挥了重要作用。

PO-1056

42 株多重耐药阴沟肠杆菌超广谱 ß-内酰胺酶的检测及基因型分布情况

崔兰英、刘文博、宋熙嫄
哈尔滨医科大学附属第一医院

目的 本文旨在研究临床分离出的多药耐药阴沟肠杆菌产生超广谱 ß-内酰胺酶情况，为临床合理用药提供依据，并对其基因型进行分析。
方法 收集 2020.1—2020.12 期间我院临床分离的 42 株非重复细菌菌株, 采用纸片扩散法（K-B 法）或自动化仪器法进行药物敏感试验, 按美国临床和实验室标准协会的标准判读药物敏感试验结果, 测定 42 株多重耐药阴沟肠杆菌的抗生素耐药情况，采用表型确证试验检测超广谱 ß-内酰胺酶，PCR 方法提取超广谱 ß-内酰胺酶待测基因，并对 PCR 产物进行测序分析。基因引物设计为 TEM，CTX-M-1，CTX-M-2，CTX-M-8，CTX-M-9 及 SHV。
结果 药物敏感试验结果显示 42 株待测阴沟肠杆菌，皆对一代，二代，三代，四代头孢菌素类药物耐药（100%，42/42），11 株对碳青霉烯类抗生素耐药（26.2%，11/42）；替加环素敏感性较高，敏感率占 95.2%（40/42），其次为阿米卡星，敏感率为 57.1%（24/42）。42 株多重耐药阴沟肠杆菌，共有 28 株检测出产超广谱 ß-内酰胺酶，占 66.7%（28/42）。 最常见基因型为 SHV-12，占 60.7%（17/28）；其次为 CTX-M-9，占 21.4%（6/28）。
结论 多重耐药阴沟肠杆菌耐药机制复杂，存在多种耐药机制。其中产生超广谱 ß-内酰胺酶仍然是导致其多重耐药的重要原因，基因型以 SHV-12 为主。

PO-1057

First Report of Oxacillin Susceptible mecA-Positive Staphylococcus aureus in Pediatric Patients in Kunming, China

Mingbiao Ma 、Minjun Chu、Lvyan Tao、Jue Li、Xiaojuan Li、Hailin Huang、Kexuan Qu、Haiping Wang、Li Li、Tingyi Du
Kunming Children's Hospital

Purpose The present study investigated the prevalence characteristics of oxacillin susceptible, *mecA*-positive *Staphylococcus aureus* (OS-MRSA) in pediatric patients in Kunming from January 2019 to December 2020.
Methods A total of 499 *S. aureus* strains were included in the study. All strains were first tested for oxacillin sensitivity using the VITEK 2 Compact Automated Antimicrobial Susceptibility Test System, and all oxacillin-susceptible strains were confirmed to have *mecA* and *mecC* genes by real-time polymerase chain reaction (PCR). E-test susceptibility testing was used to compare the minimum inhibitory concentration (MIC) value distribution characteristics of methicillin-susceptible *S. aureus* (MSSA), methicillin-resistant *S. aureus* (MRSA), and OS-MRSA for oxacillin, cefoxitin, penicillin, vancomycin, erythromycin, and clindamycin. Molecular typing of OS-MRSA was performed by Multilocus sequence typing (MLST) and SCCmec typing. Real-time PCR was used to detect toxin genes of OS-MRSA strains.

Results A total of 45 OS-MRSA strains were detected, for an overall detection rate of 9.02% (45/499), and no mecC-carrying strains were found. E-test susceptibility testing showed that the distributions of MIC values of MSSA, OS-MRSA, and MRSA strains against oxacillin were mainly concentrated at 0.38, 0.38, and 12 μg/mL, respectively; the distributions of cefoxitin MICs of MSSA and MRSA were concentrated at 2 and 32 μg/mL respectively, and MICs of OS-MRSA were concentrated at 2 and 8 μg/mL; the distributions of penicillin, vancomycin and erythromycin MICs against MSSA, OS-MRSA, and MRSA strains showed same centralized points, and were 32, 1, and 256 μg/mL, respectively; the MICs of clindamycin against MSSA was 0.5 μg/mL, while that against OS-MRSA and MRSA were mainly concentrated at 256 μg/mL. All three strain types showed an increasing trend for oxacillin and cefoxitin MIC50 and MIC90, as well as for penicillin and clindamycin MIC50, and no vancomycin-resistant strains were found. The molecular typing of OS-MRSA strains was dominated by ST59-SCCmec IV followed by ST38-SCCmec IV. The carrier rates of hemolysin genes (*hl-a, hl-d*) and fibrinogen-binding clumping factor genes (*clfA, clfB*) were 100% in OS-MRSA strains, followed by 40% (18/45) for enterotoxin genes（*sea,seb*）. The carrier rates of toxic shock syndrome gene (*tsst-1*) and Panton–Valentine leukocidin gene (*pvl*) were low, at 6.67% (3/45) and 4.44% (2/45), respectively.
Conclusion OS-MRSA strains were detected at a high rate in pediatric patients in Kunming, and the molecular typing was mainly ST59-SCCmecIV. OS-MRSA has unique distribution characteristics for MIC values against commonly used antimicrobial agents. The identification ability of automated antibacterial drug sensitivity test detection systems for OS-MRSA is very limited. For children with S. aureus infections, clinicians should be vigilant regarding the presence of OS-MRSA. A combination of phenotypic analysis and molecular detection should be used to improve OS-MRSA identification.

PO-1058

氨溴索联合左氧氟沙星对不同耐药机制肺炎克雷伯菌生物膜形成能力的研究

余潇[1]、黄晨蕾[1]、曹若楠[1]、李婕[1]、朱国萍[2]、李小宁[1]
1. 皖南医学院弋矶山医院
2. 安徽师范大学

目的 研究氨溴索联合左氧氟沙星对不同耐药机制肺炎克雷伯菌生物被膜的形成抑制和清除作用，旨在为临床提供拮抗肺炎克雷伯菌生物膜形成和治疗的新策略。
方法 收集不同耐药机制肺炎克雷伯菌各 15 株，将其分为敏感组、ESBLs 组、CRE 组，采用结晶紫染色法进行生物被膜半定量检测，再从各组中选取 3 株生物被膜产量相近的菌株，采用微量肉汤稀释法测定氨溴索和左氧氟沙星对肺炎克雷伯菌的最低抑菌浓度（MIC）；棋盘稀释法测定不同浓度氨溴索对左氧氟沙星 MIC 的影响以及通过计算部分抑菌浓度指数（FIC）判断联合效果和选择最佳协同浓度；采用结晶紫法联合激光扫描共聚焦荧光显微镜研究不同浓度药物对肺炎克雷伯菌生物被膜的形成抑制试验和清除试验。
结果 3 组细菌生物被膜均在第 5 天达到成熟，两两比较发现敏感组较 ESBLs 组和 CRE 组更易形成且产量更多（F=3.725，P=0.032）；棋盘稀释法显示，随着氨溴索浓度的增加，3 组细菌左氧氟沙星 MIC 值的几何均数均明显下降，呈显著的负相关，且联合药敏结果显示，两药组合均呈现协同作用；在生物被膜形成抑制试验中，随着氨溴索浓度的增加，其抑制率均达到了 75%以上，但其生物被膜清除率却未达到 70%。
结论 氨溴索联合左氧氟沙星对临床早期抑制肺炎克雷伯菌生物被膜形成具有指导意义，且其最佳协同浓度为 0.49mg/ml 氨溴索+4μg/ml 左氧氟沙星。

PO-1059

Comparative genome analysis of multidrug-resistant Pseudomonas aeruginosa JNQH-PA57, a clinically isolated mucoid strain with comprehensive carbapenem resistance mechanisms

Yujiao Wang、Mingju Hao、Wanshan Ma、Xiutao Dong、Xiaofeng Li、Fang Cheng
山东第一医科大学第一附属医院（山东省千佛山医院）

Background The prevalence of clinical multidrug-resistant (MDR) Pseudomonas aeruginosa has been increasing rapidly worldwide over the years and responsible for a wide range of acute and chronic infections with high mortalities. Although hundreds of complete genomes of clinical *P. aeruginosa* isolates have been sequenced, only a few complete genomes of mucoid strains are available, limiting a comprehensive understanding of this important group of opportunistic pathogens. Herein, the complete genome of a clinically isolated mucoid strain *P. aeruginosa* JNQH-PA57 was sequenced and assembled using Illumina and Oxford nanopore sequencing technologies. Genomic features, phylogenetic relationships, and comparative genomics of this pathogen were comprehensively analyzed using various bioinformatics tools. A series of phenotypic and molecular-genetic tests were conducted to investigate the mechanisms of carbapenem resistance in this strain.

Results Several genomic features of MDR *P. aeruginosa* JNQH-PA57 were identified based on the whole-genome sequencing. We found that the accessory genome of JNQH-PA57 including several prophages, genomic islands, as well as a PAPI-1 family integrative and conjugative element (ICE), mainly contributed to the larger genome of this strain (6,747,067 bp) compared to other popular *P. aeruginosa* strains (with an average genome size of 6,445,223 bp) listed in *Pseudomonas* Genome Database. Colony morphology analysis and biofilm crystal staining assay respectively demonstrated an enhanced alginate production and a thicker biofilm formation capability of JNQH-PA57. A deleted mutation at nt 424 presented in *mucA* gene, resulted in the upregulated expression of a sigma-factor AlgU and a GDP mannose dehydrogenase AlgD, which might explain the mucoid phenotype of this strain. As for the carbapenem resistance mechanisms, our results revealed that the interplay between impaired OprD porin, chromosomal β-lactamase OXA-488 expression, MexAB-OprM and MexXY-OprM efflux pumps overexpression, synergistically with the alginates-overproducing protective biofilm, conferred the high carbapenem resistance to *P. aeruginosa* JNQH-PA57.

Conclusion Based on the genome analysis, we could demonstrate that the upregulated expression of *algU* and *algD*, which due to the truncation variant of MucA, might account for the mucoid phenotype of JNQH-PA57. Moreover, the resistance to carbapenem in *P. aeruginosa* JNQH-PA57 is multifactorial. The dataset presented in this study provided an essential genetic basis for the comprehensive cognition of the physiology, pathogenicity, and carbapenem resistance mechanisms of this clinical mucoid strain.

PO-1060

Apramycin resistance in epidemic carbapenem-resistant Klebsiella pneumoniae ST258 strains

Mingju Hao[8]、Jessica Schuyler[1]、Haifang Zhang[2]、Derrick Fouts[3]、Michael Satlin[4]、Michael Satlin[5]、Barry Kreiswirth[6]、Liang Chen[6,7]

1. School of Graduate Studies, Rutgers University, Newark, NJ, USA;
2. Department of Clinical Laboratory, The Second Affiliated Hospital of Soochow University, Suzhou, Jiangsu, China
3. The J. Craig Venter Institute (JCVI), Rockville, MD, USA
4. The J. Craig Venter Institute (JCVI), Rockville, MD, USA;
5. Division of Infectious Diseases, Department of Medicine, Weill Cornell Medicine, New York, NY, USA;
6. Center for Discovery and Innovation, Hackensack-Meridian Health, Nutley, NJ, USA
7. Department of Medical Sciences, Hackensack Meridian School of Medicine, Nutley, NJ, USA
8. The First Affiliated Hospital of Shandong First Medical University & Shandong Provincial Qianfoshan Hospital

Background Recent studies indicated that the monosubstituted deoxystreptamine aminoglycoside apramycin is a potent antibiotic against a wide range of MDR Gram-negative pathogens.
Objectives To evaluate the in vitro activity of apramycin against carbapenem-resistant Klebsiella pneumonia (CRKp) isolates from New York and New Jersey, and to explore mechanisms of apramycin resistance.
Methods Apramycin MICs were determined by broth microdilution for 155 CRKp bloodstream isolates collected from 2013 to 2018. MLST STs, wzi capsular types and apramycin resistance gene aac(3')-IV were examined by PCR and Sanger sequencing. Selected isolates were further characterized by conjugation experiments and WGS.
Results Apramycin MIC50/90 values were 8 and >128 mg/L for CRKp isolates, which are much higher than previously reported. Twenty-four isolates (15.5%) were apramycin resistant (MIC 64 mg/L) and they were all from the K. pneumoniae ST258 background. The 24 apramycin-resistant K. pneumoniae ST258 strains belonged to six different capsular types and 91.7% of them harboured the apramycin resistance gene aac(3')-IV. Sequencing analysis showed that different ST258 capsular type strains shared a common non-conjugative IncR plasmid, coharbouring aac(3')-IV and blaKPC. A novel IncR and IncX3 cointegrate plasmid, p59494-RX116.1, was also identified in an ST258 strain, demonstrating how apramycin resistance can be spread from a non-conjugative plasmid through cointegration.
Conclusions We described a high apramycin resistance rate in clinical CRKp isolates in the New York/New Jersey region, mainly among the epidemic K. pneumoniae ST258 strains. The high resistance rate in an epidemic K. pneumoniae clone raises concern regarding the further optimization and development of apramycin and apramycin-like antibiotics.

PO-1061

碳青霉烯类耐药肠杆菌科细菌基因型检测及耐药性分析

甘龙杰、杨滨
福建医科大学附属第一医院

目的 了解本院碳青霉烯类耐药肠杆菌科细菌（carbapenem resistant Enterobacteriaceae,CRE）的基因型分布及耐药情况。
方法 收集本院临床标本分离的 613 株 CRE,用基质辅助激光解吸电离飞行时间质谱仪进行鉴定,MIC 法进行药敏试验。随机选取 68 株 CRE 进行 PCR 扩增,检测 blaKPC、blaIMP-1、blaVIM-1、blaOXA-48 及 blaNDM-1 等碳青霉烯酶基因;PCR 阳性结果进行 DNA 测序和 BLAST 比对,确定其基因型。

结果 出的 613 株 CRE 中,对临床常用抗菌药物如青霉素类、氟喹诺酮类、头孢菌素类及酶抑制剂的耐药率超过 90%,仅对复方磺胺甲噁唑和阿米卡星的耐药率较低,为 50%左右。68 株 CRE 经 PCR 扩增和 DNA 测序,blaKPC-2 检出 58 株、blaNDM-15 株和 blaIMP-15 株,但未检出 blaVIM-2 和 blaOXA-48 耐药基因。
结论 本院 CRE 常呈现为多重耐药,甚至是泛耐药。CRE 的基因型以 blaKPC-2 型为主,提示须加强院感监测,预防和控制 CRE 菌株在院内扩散传播流行。

PO-1062

ICU 患者艰难梭菌分离培养与流行病学特征研究

曾勇彬、杨滨
福建医科大学附属第一医院

目的 了解 ICU 患者艰难梭菌的定植和感染情况,为预防艰难梭菌的流行提供参考。
方法 收集 2016 年 9 月至 2017 年 6 月福建医科大学附属第一医院 ICU 中 139 例住院时间>7d 的患者的粪便样本,对其进行选择性厌氧培养和质谱鉴定。对艰难梭菌培养阳性标本进行毒素基因（tcdA、tcdB、cdt A、cdtB）的 PCR 检测以及毒素 A、B 表型检测。收集所有患者的临床资料,并对艰难梭菌培养阳性患者的临床特征和实验室检查结果进行单因素分析和多因素回归分析。
结果 艰难梭菌检出率为 17.27%（24/139）。其中,14 株艰难梭菌的 tcdA 和 tcdB 基因检测阳性,占 58.3%（14/24）;10 株为 tcdA 和 tcdB 基因检测阴性,占 41.7%（10/24）。所有菌株二元毒素基因（ctdA/ctdB）均未检出。单因素分析提示,高龄、长时间住院、高淋巴细胞数、使用 β-内酰胺类抗生素是艰难梭菌定植的高危因素;多因素回归分析提示,使用 β-内酰胺类抗生素是艰难梭菌定植的独立危险因素（OR=3.881,P=0.039）。
结论 我院 ICU 可能存在艰难梭菌感染和传播的风险,对具有高龄、长期住院以及使用抗生素等高危因素的患者应进行艰难梭菌的监测,以防艰难梭菌的传播、感染和艰难梭菌相关性腹泻的发生。

PO-1063

肺腺癌与肺鳞癌患者肠道菌群结构分析

安瑞[1,2]、何大强[1]、赵丰[3]、王丽倩[1]、王贤军[1]
1. 浙江大学医学院附属杭州市第一人民医院
2. 南京医科大学附属杭州医院
3. 浙江中医药大学附属第四临床医学院

探讨肺腺癌和肺鳞癌患者肠道菌群结构的多样性及构成。采用单中心病例对照研究， 连续入组 2018 年 9 月至 2020 年 10 月就诊于浙江大学医学院附属杭州市第一人民医院的肺癌患者共 27 例，其中男性 15 例，女性 12 例，同期招募健康体检者作为对照组(HC) 共 20 例，其中男性 9 例，女性 11 例。收集研究对象新鲜粪便样本及相关临床资料，根据病理诊断结果将肺癌患者分为肺腺癌组(AC，纳入 19 例患者，其中男性 8 例，女性 11 例)和肺鳞癌组(SCC，纳入 8 例患者，其中男性 7 例，女性 1 例)。提取粪便样本基因组 DNA，对 16SrDNA V3-V4 区域进行 PCR 扩增，通过 Illumina MiSeq 高通量测序平台进行测序，应用 QIIME 分析肠道菌群结构。采用方差分析、χ2 检验、K-W 检验等方法分析 3 组人群间性别、年龄、α 多样性、菌群相对丰度差异等的差异。AC、SCC 和 HC 三组的年龄分别为(58.74±9.27)岁、(63.38±6.12)岁和(55.65±7.79)岁;AC、SCC 和 HC 三组间在性别、年龄上差异无统计学意义(性别和年龄分别为:χ2=5.155 P=0.076;F=2.598，P=0.086)。三组间肠道菌群 α 多样性无显著性差异，β 多样性分析显示 AC、SCC 与 HC 三组间肠道菌群结构存在显著性差异(P=0.001)。物种差异分析显示，AC 与 SCC 组均存在优势菌属，巨球型菌属和 Erysipelatoclostridium 菌属在 AC 患者肠道中富集，而肠球菌属、韦荣球菌属和

Eubacterium_eligens_group 菌属在 SCC 患者肠道中富集。肺癌患者存在明显的肠道菌群失调，肺腺癌与肺鳞癌患者肠道菌群结构无显著性差异，但肺腺癌与肺鳞癌具有各自独特的菌群。这种肠道微环境的失衡，对研究不同病理类型肺癌的发生发展具有重要意义。

PO-1064

尿液病原菌种类分布和耐药性分析

牛瑜
山东大学第二医院

目的 分析 2016 年-2020 年本院临床科室尿标本中病原菌的种类分布和耐药情况，为临床治疗尿路感染提供理论依据。
方法 按照标本采集规范要求收集清洁中段尿并定量接种培养，使用安图微生物质谱仪对可疑病原菌进行鉴定，并使用 BD M50 全自动药敏仪和西门子 MicroScan Walkaway-96 Plus 全自动药敏仪进行药敏试验，然后使用 WHONET 5.6 软件统计，分析尿液中病原菌菌株种类分布和耐药情况等。
结果 自 2016 年至 2020 年本院尿培养病原菌共计 3938 株，其中大肠埃希菌 1530 株、屎肠球菌 691 株、肺炎克雷伯菌 440 株、粪肠球菌 196 株、奇异变形杆菌 187 株、铜绿假单胞菌 119 株等。尿液中碳青霉烯耐药的鲍曼不动杆菌 70 株、铜绿假单胞菌 25 株、肺炎克雷伯菌 128 株、大肠埃希菌 17 株，碳青霉烯耐药率分别为 72.9%、21.0%、29.1%、1.1%。万古霉素耐药的肠球菌 19 株，均为屎肠球菌，万古霉素耐药率为 2.7%。苯唑西林耐药的金黄色葡萄球菌 15 株，耐药率为 26.8%。
结论 尿液分离菌株以大肠埃希菌占绝大多数（38.9%），其次为屎肠球菌（17.5%）。碳青霉烯耐药率以鲍曼不动杆菌和肺炎克雷伯菌为主。万古霉素耐药的肠球菌均为屎肠球菌。随着诊疗技术的发展、方式的增多，增加了各类机会致病菌引起尿路感染的风险，应在各类治疗过程中注意手卫生，防止交叉感染，尽量避免院内感染的发生。

PO-1065

阴道分泌物革兰染色涂片自动化镜检及形态学人工智能分析系统准确性评估

王瑶、孙宏莉、赵颖、张丽、朱任媛、窦红涛、原英、刘亚丽、刘文静、徐英春
中国医学科学院北京协和医院

目的 评估仕达思 Comet-60au 高倍镜检分析系统对阴道分泌物革兰染色涂片自动化镜检及形态学人工智分析的准确性。
方法 收集 2020 年 1-5 月来自妇产科门诊或健康体检女性患者阴道分泌物标本 400 例，涂片革兰染色，以人工镜检半定量评分结果为对照，评估仕达思 Comet-60au 高倍镜检分析系统自动化镜检及阴道微生态形态学人工智能分析性能。人工镜检由 2 名研究人员分别独立进行并取半定量评分平均值，两人结果差异较大的由第三人镜检并取相近的两次结果均值为对照结果。
结果 与人工镜检结果相比，Comet-60au 系统对阴道菌群密集度、乳杆菌样革兰阳杆菌、阴道加德纳菌或拟杆菌样革兰阴性杆菌、弯曲杆菌的评分基本一致率为 93.3~100%，菌群多样性基本一致率为 85.3%，对酵母样孢子和假菌丝阴阳性一致率为 96.8~98.0%，对白细胞>10 个/每高倍镜视野一致率为 70.5%。对 Nugent 评分分类总符合率为 90.8%，Kappa 值为 0.861（P<0.001）。对真菌镜检总符合率为 97.0%，Kappa 值为 0.929（P<0.001）。
结论 Comet-60au 高倍镜检分析系统能够较为准确、快速地进行阴道分泌物革兰染色涂片自动化镜检及形态学人工智能分析，可大幅提高实验室检测效率并降低人工镜检工作负荷。

PO-1066

Using Routine Laboratory Markers and Immunological Indicators for Predicting Pneumocystis jiroveci Pneumonia in Immunocompromised Patients

Guoxing Tang
Department of Laboratory Medicine, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Background Pneumocystis jirovecipneumonia (PJP) is the most common opportunistic infection in immunocompromised patients. The accurate prediction of PJP development in patients undergoing immunosuppressive therapy remains challenge.
Methods Patients undergoing immunosuppressive treatment and with confifirmed pneumocystis jiroveci infection were enrolled. Another group of matched patients with immunosuppressant treatment but without signs of infectious diseases were enrolled to control group.
Results A total of 80 (40 PJP, 40 non-PJP) participants were enrolled from Tongji Hospital. None of the patients were HIV positive.The routine laboratory indicators,such as LYM, MON, RBC, TP, and ALB, were signifificantly lower in PJP patients than in non-PJP patients. Conversely, LDH in PJP patients was signifificantly higher than in non-PJP controls. For immunological indicators, the numbers of T, B, and NK cells were all remarkably lower in PJP patients than in non-PJP controls, whereas the functional markers such as HLA-DR, CD45RO and CD28 expressed on CD4+ or CD8+ T cells had no statistical difference between these two groups. Cluster analysis showing that decrease of host immunity markers including CD3+, CD4+ and CD8+ T cells, and increase of tissue damage marker LDH were the most typical characteristics of PJP patients. A further established model based on combination of CD8+ T cells and LDH showed prominent value in distinguishing PJP from non-PJP,with AUC of 0.941 (95%CI, 0.892-0.990).
Conclusions A model based on combination of routine laboratory and immunological indicators shows prominent value for predicting the development of PJP in HIV-negative patients undergoing immunosuppressive therapy.

PO-1067

中国临床微生物实验室多黏菌素药物敏感性检测系统性能评估

刘晓妤
北华大学
北京协和医院

目的 自《多黏菌素药物敏感性检测及临床解读专家共识》发布以来，临床实验室所使用的多黏菌素药物敏感性检测系统尚未进行过全面的性能评估，本文旨在对目前国内临床实验室常用的几种药物敏感性检测系统进行评估。
方法 随机选取的 367 株革兰阴性菌，使用微量肉汤稀释法 (BMD)检测菌株对多黏菌素 B/ E 的 MIC，并从中选取 MIC 范围从 0.25 mg/L ->64 mg/L 的 102 株菌（大肠埃希菌 59 株，肺炎克雷伯菌 39 株，不动杆菌属 5 株）对中国目前临床实验室常用的多黏菌素药物敏感性系统进行检测。主要检测的系统和试剂包含 PhoenixTM M50（Becton Dickinson）、多黏菌素 B 药敏条（安图生物）、多黏菌素 B 药敏试剂（康泰生物）、肠杆菌/氧化酶/非发酵菌/氧化酶阳性阴性革兰阴性杆菌鉴定药敏板（迪尔生物）及粘菌素 Etest 药敏条（Liofilchem）。对所有药敏系统使用基本一致率（EA）,分类一致率（CA），非常重大错误（VME）及重大错误（ME）进行评估。
结果 康泰生物系统的 CA、EA 均最高，分别为 98%和 85%，且 VME 最低，迪尔生物系统 CA 最低，为 71.6%，并且 VME 也略有欠缺，为 61.7%。两种 Etest 试带中，安图生物 Etest 条的 CA、EA、VME、ME 分别为 93.1%、78.2%、13.3%和 3.5%，Liofilchem 的 MTS 整体 MIC 偏低，

VME 为 57.8%，相比于 Liofilchem,国产 Etest 条的 MD 为 26.5%。BD 公司的两种板卡纳入研究，分别为 NMIC/ID-4 及 NMIC-413，两种板卡一致性较好，CA、VME 均为 95.1%和 10.6%。
整体而言，康泰系统在本实验中性能较好，PhoenixTM 系统最为稳定，而 Liofilchem MTS 对国内临床菌株并不适用，不能作为临床判断使用。

PO-1068

Species identification and antifungal susceptibility testing of Aspergillus strains isolated from patients with otomycosis in northern China

Ran Jing[1]、Wen-Hang Yang[1]、Meng Xiao[1]、Ying Li[2]、Gui-Ling Zou[3]、Cheng-Ying Wang[4]、Xiu-Wen Li[5]、Po-Ren Hsueh[6]、Ying-Chun Xu[1]
1. Peking Union Medical College Hospital
2. 首都医科大学宣武医院
3. 哈尔滨医科大学附属第四医院
4. 大庆油田总医院
5. 牡丹江市第一人民医院
6. 国立台湾大学医院

Background/Purpose There are limited studies on species distribution and susceptibility profiles of *Aspergillus* strains isolated from patients with otomycosis in China.
Methods A total of 69 confirmed *Aspergillus* species isolates were obtained from ear swabs of patients diagnosed with otomycosis from 2017 to 2018 in northern China. Identification of these *Aspergillus* isolates at the species level was performed using conventional morphological methods and MALDI-TOF MS in combination with molecular sequencing, and *in vitro* susceptibility to nine antifungal agents was evaluated using the Sensititre YeastOne system.
Results The *Aspergillus* section *Nigri* had the greatest distribution of *Aspergillus* isolates. *A. welwitschiae* (n=25) was the most predominant isolate in section *Nigri*, followed by *A. tubingensis* (n=12) and *A. niger* (n=11). Other *Aspergillus* species were also isolated, including *A. terreus* (n=11), *A. flavus/A. oryzae* (n=8), and *A. fumigatus* (n=2). Amphotericin B, posaconazole, and echinocandins were highly *in vitro* active against all the isolates tested. 2.9% (2/69) of the isolates were resistant to azoles in our study, including one *A. niger* isolate with a high MIC value for itraconazole (ITR) (16 mg/L) and one *A. tubingensis* isolate cross-resistant to both voriconazole (VOR) (MIC >8 mg/L) and ITR (MIC >16 mg/L). One *A. welwitschiae* and one *A. niger* isolate both had increased MIC values of 4 mg/L against VOR.
Conclusions *A. welwitschiae* was the most prevalent *Aspergillus* species isolated from patients with otomycosis. Our findings also indicated that the azole-resistant *Aspergillus* section *Nigri* should be utilized to guide clinical medication for otomycosis.

PO-1069

耐甲氧西林金黄色葡萄球菌的临床分布及危险因素分析

王丽、李凯、刁彤、李晓玲、刘正祥
新疆军区总医院

目的 分析某军队医院 2018 年耐甲氧西林金黄色葡萄球菌（MRSA）的临床分布特征及危险因素，为治疗及预防金黄色葡萄球菌（SA）感染提供全面、准确的依据。
方法 收集 2018 年 1—12 月我院临床送检标本中分离出的 SA 作为研究对象。采用梅里埃公司 VITEK MS 微生物质谱检测系统和 VITEK 2 系统进行细菌鉴定和药敏试验，结果判读遵循 2016 年版美国临床实验室标准化协会（CLSI）标准进行判定。应用 WHONET5.6 软件进行耐药性分析。

针对本次住院时间（>5 天）、反复入院、手术、糖尿病、高血压、使用抗生素、年龄（>60 岁）、性别、科室（ICU）等因素，使用 SPSS13.0 统计软件对上述各因素进行 Logistic 分析。首先将各个指标作为自变量，是否感染 MRSA 作为因变量，进行单因素 logistics 回归分析，得出未调整的 OR 值和 P。将经单因素 logistics 回归分析显示显著（p<0.05）的指标纳入多因素 logistics 回归分析，最终得出影响患病的因素，即调整后的 OR 和 P。

结果 2018 年 SA 共分离出 148 株，其中 MRSA 45 株，占 30.41%，重症治疗科病区和骨三科病区比例相对较高。分离出 MRSA 最多的标本来源为分泌物（20 株）和痰液（17 株），占全部分离菌株的 82.22%。中青年组（≤45 岁）是感染占的比例最高的年龄段，达到 48.89%。MRSA 对苯唑青霉素和青霉素（G）耐药率高达 100%，对红霉素、克林霉素、四环素耐药率均达到了 50%以上，未检出对万古霉素、替加环素、利奈唑胺和喹奴普汀/达福普汀耐药的菌株。多因素 Logistic 回归分析显示，住院时间（>5 天）、手术是 MRSA 感染的独立危险因素。

结论 医院需加强对 MRSA 的持续监测，做好 MRSA 的主动筛查工作，合理选择抗菌药物治疗方案，预防 MRSA 的产生和传播，加强抗菌药物合理应用。

PO-1070

碳青酶烯耐药肺炎克雷伯菌的全基因组测序结果分析

赵苏瑛
江苏省中医院

目的 基于基因组学研究碳青酶烯耐药肺炎克雷伯菌的耐药机制和传播机制，深入阐明其产生的原因，为临床的治疗和预防提供实验室依据。

方法 收集一株临床分离的碳青酶烯耐药的泛耐药肺炎克雷伯菌 KPX，测定对常用抗生素的 MIC，MLST 进行基因分型后提取全基因组 DNA 进行全基因组测序和基因功能注释。根据测序结果，选择相关耐药基因在临床收集的另外 50 株碳青酶烯耐药的肺炎克雷伯菌中进行扩增检测，验证其携带情况。

结果 该株 KPX 细菌对除粘菌素和替加环素外的抗生素全部耐药，对获得菌株的基因组进行全基因组测序，最终确定该菌染色体基因序列全长 5,468,925 bp，含有 4 个质粒 ，共有 5984 个蛋白质编码基因，85 个 tRNA 基因和 25 个 rRNA 操纵子。此外，该菌携带有大量耐药基因。MLST 结果显示，该菌基因型为 ST11 型，接近的是一株编号 SCKP020029 (NCBI Accession number: CP029384)的肺炎克雷伯菌，同样为 ST11 型，分离自四川某病人标本。收集的另外 50 株碳青酶烯耐药的肺炎克雷伯菌均产 ESBLs，其中 97%为 ST11 型。PFGE 结果显示分属 3 个克隆。在这些菌株中 ，耐药基因检出率分别为 KPC-2 (98.0%), SHV-11 (98.0%), TEM-1 (76.0%), CTX-M (76.0%), Oqxb1(66%), qnrS (70%), Int1 (42.0%), sul1 (82.0%), sul2 (96.0%), iutA (88%), iucABCD(10%)和 rmpA2 (100%)。

结论 试验结果揭示了院内碳青酶烯类耐药肺炎克雷伯菌的基因组学和流行病学特点。抗生素耐药结果提示了细菌耐药中选择性抗生素耐药压力的作用效应。同时质粒耐药基因在细菌中的传播提示有效的院内感染监测，隔离和控制是减少细菌耐药传播必不可少的措施。

PO-1071

角膜共聚焦显微镜检查联合实验室检测体系在真菌性角膜炎中的应用

金丽丽、郑美琴
温州医科大学附属眼视光医院

目的 分析浙南地区真菌性角膜炎患者的人口学及临床特征，并进一步研究角膜共聚焦显微镜检查、刮片镜检及培养鉴定在诊断真菌性角膜炎上的符合率，探讨联合使用在诊断中的应用价值。
方法 回顾性研究。收集 2016 年 1 月至 2020 年 12 月于温州医科大学附属眼视光医院拟诊为真菌性角膜炎的患者 562 例（562 眼），分析其人口学特征、致病因素、致病菌属、用药史、临床体征及治疗方式，并统计首诊时均行角膜共聚焦显微镜检查、刮片镜检及培养鉴定这三项检查的患者的结果，采用 χ2 检验对这三种病原学检查方法的阳性检出率进行比较,并分析联合使用的诊断效率。
结果 角膜共聚焦显微镜，培养鉴定，刮片镜检阳性检出率分别为为 80.0%，67.6%，42.9%。共聚焦显微镜（χ2=12.153,P<0. 01），培养鉴定（χ2 =6.967,P<0. 01）阳性检出率均高于刮片镜检。联合共焦显微镜检查与刮片镜检，阳性检出率为 93.3%；联合角膜共焦显微镜、刮片镜检、培养鉴定，阳性检出率为 95.7%。农民为主要患病人群，共 332 例（59.1%）。主要分布地区为温州市鹿城区 65 例（11.6%）。植物伤为主要致病因素，共 225 例（40.0%）。9 例（1.6%）为混合感染，其中 5 例（0.8%）合并细菌感染，4 例（0.7%）合并病毒感染。主要致病菌属依次为镰刀菌属 163 例（41.6%）。413 例（73.5%）可见明显溃疡灶，157 例（27.9%）可见前房积脓。69 例（12.3%）来院首诊前使用过糖皮质激素，130 例（23.1%）接受了手术治疗，其中 13 例（2.3%）剜除了眼内容物。
结论 秋季为浙南地区真菌性角膜炎高发期，中老年男性农民为主要患病人群，镰刀菌属是主要的致病菌属. 角膜共聚焦显微镜阳性检出率最高，联合角膜共聚焦显微镜，刮片镜检，培养鉴定这三者检查能提高阳性检出率，有利于真菌性角膜炎的诊断。

PO-1072

银金属有机框架药物联合万古霉素治疗耐甲氧西林金黄色葡萄球菌感染

黄蓉、聂新民
中南大学湘雅三医院 检验科

目的 构建一种具有良好抗菌性的新型的纳米递药系统，通过双重抗感染机制治疗耐甲氧西林金黄色葡萄球菌（MRSA）感染。
方法 以 2-甲基咪唑作为配体，硝酸银提供银离子，制备纳米金属有机框架 Ag-MOF。利用 Ag-MOF 负载万古霉素，形成新型纳米粒子 Ag-MOF-Vanc。检测 Ag-MOF-Vanc 抗菌能力及机制。
结果 Ag-MOF-Vanc 是一种具有 pH 响应性的纳米递药系统，对常见临床菌株有较好的抗菌作用，优于单纯万古霉素，可有效减少万古霉素的用量。Ag-MOF-Vanc 可通过干扰细菌细胞内新陈代谢、催化产生 ROS、破坏细胞膜完整性、抑制生物被膜的形成等多种机制杀伤 MRSA。
结论 Ag-MOF-Vanc 为一种新型有效的药物载体系统，有望用于 MRSA 的抗感染治疗。

PO-1073

Evaluation of Autof MS 1000 and Vitek MS MALDI-TOF System in Identification of Close-Related Yeasts Species Causing Invasive Fungal Diseases

Qiaolian Yi、Meng Xiao、Ying-Chun Xu
Peking Union Medical College Hospital

Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) has been accepted as a rapid, accurate, and less labor-intensive method in the identification of microorganisms in clinical laboratories. However, there is limited data on systematic evaluation of its effectiveness in the identification of phylogenetically closely-related yeast species.

In this study, we evaluated two commercially available MALDI-TOF systems, Autof MS 1000 and Vitek MS, for the identification of yeasts within closely-related species complexes. A total of 1,228 yeast isolates, representing 14 different species of five species complexes, including 479 of Candida parapsilosis complex, 323 of Candida albicans complex, 95 of Candida glabrata complex, 16 of Candida haemulonii complex (including two Candida auris), and 315 of Cryptococcus neoformans complex, collected under the National China Hospital Invasive Fungal Surveillance Net (CHIF-NET) program, were studied.

Autof MS 1000 and Vitek MS systems correctly identified 99.2% and 89.2% of the isolates, with major error rate of 0.4% versus 1.6%, and minor error rate of 0.1% versus 3.5%, respectively. The proportion of isolates accurately identified by Autof MS 1000 and Vitek MS per each yeast complex, respectively, was as follows; C. albicans complex, 99.4% vs 96.3%; C. parapsilosis complex, 99.0% vs 79.1%; C glabrata complex, 98.9% vs 94.7%; C. haemulonii complex, 100% vs 93.8%; and C. neoformans, 99.4% vs 95.2%.

Overall, Autof MS 1000 exhibited good capacity in yeast identification while Vitek MS had lower identification accuracy, especially in the identification of less common species within phylogenetically closely-related species complexes.

PO-1074

The “Same-Day” AST Report of Pathogens form Urine by A Simple MALDI-TOF MS-based Protocol

Wei Li、Enhua Sun、Yi Zhang
Department of Clinical Laboratory, Qilu Hospital of Shandong University

Backgroud and Purposes In the past years, Matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) has been considered as a rapid and reliable method for identification of microorganisms from positive blood cultures and other clinical specimens such as urine, which from culture plates and positive blood cultures, and also on other clinical specimens such as urine . Previous studies have shown that urine is an optimal sample for direct MALDI-TOF MS identification by MALDI-TOF MS, and some studies have been carried out to improve urine processing and to enhance the direct identification sensitivitycapability of MALDI-TOF MS from urine by improve the urine processing. However, most of these studies just mainly focused only on the direct identification, and there areis limited researchfew studies on methods for the direct AST from urine, especially to determine accurate minimum inhibitory concentrations (MICs). Furthermore, direct AST is more important than pathogen identification itself for fast and precise antibiotic treatment.for determining appropriate antibiotic treatment than bacterial identification itself, and could greatly shorten the time to the final microbiological report. In this study, we investigated a whole MALDI-TOF MS-based workflow to shorten the time of pathogenic diagnosis and effective treatment of UTIs by

combining the flow cytometry for screening, MALDI-TOF MS for microbial identification, and the VITEK 2 system for AST directly from urine samples.
Methods A total of 1,638 consecutive urine samples were submitted to the Clinical Microbiology Laboratory, Department of Clinical Laboratory, Qilu Hospital of Shandong University during September and December 2018 for culture without any chemical preservatives from inpatients and outpatients. Each urine sample had a volume of approximately 30 ml, which was divided into three aliquots using 15ml sterile centrifuge tubes. The first aliquot was used for culture by the Walk Away Specimen Processor (WASP, Copan, Brescia, Italy), and then for UF-1000i screening (Sysmex, Kobe, Japan). If the result of bacterial counts of ≥ 5000 bacteria/μL, the other two aliquots were subsequently processed to prepare bacterial pellets. The second and third aliquot (10 mL urine in a 15-mL sterile centrifuge tube) was vortexed and centrifuged for 1 min at 2,000 g for 1 min to remove leukocytes, cellular debris, leukocytes, and mucus. The resulting supernatant was centrifuged for 5 min at 10,000 ×g for 5 min and then discarded. The resulting pellet was re-suspended in 1mL of 0.45% saline solution (bioMérieux, Marcy l'Étoile, France) to wash the bacterial cells and transferred into a 1.5-mL micro-centrifuge tube. The bacterial suspension was pelleted after centrifugation (10,000 × g for 2min) and washed again by 0.45% saline solution. The bacterial pellet of the second urine aliquot was directly identified by the MALDI-TOF MS (Bruker Daltonik GmbH, Bremen, Germany). Once the reliable direct identification was determined, the bacterial pellet of third urine aliquot was used for direct AST by the VITEK 2 system (bioMérieux, Marcy l'Étoile, France).
Results 307 of 1,638 urine samples were positive by UF-1000i screening. Among them, 265 samples had significant growth of single-microorganism. Two hundred and twenty-nineReliable direct identification was obtained in 229 (86.42%) out of these 265 samples were reliably identified directly from urine and no pathogensbacteria were misidentified. Moreover, species-level identification was obtained in 163 (88.59%) out of 184 samples with Gram-negative bacteria, and 27 (38.03%) samples out of 71 samples with Gram-positive bacteria. VITEK 2 AST was performed in 117 samples of single-microorganism. The data of Enterobacteriaceae showed an agreement rate of antimicrobial categories of 95.1% (1301/1368) with a minor error, major error, and very major error rate of 3.95% (54/1368), 0.88% (12/1368), and 0.07% (1/1368), respectively. For Enterococcus spp., the overall categorical agreement was 92.94% (158/170), with rates for minor errors of 2.94% (5/170) and major errors 4.12% (7/170). The turnaround time of this combined protocol to diagnose UTI was 1 hour for directbacterial identification and 6-24 hours for direct AST, especially 6-8 hours for the Enterobacteriaceae by the VITEK 2 system. Therefore, our MALDI-TOF MS-based combined protocol could provide reliable "same day" report including identification and AST for Enterobacteriaceae, and it would result in earlier and precise antibiotic selection.
Conclusion It was concluded that the simple combined protocol of the flow cytometry, MALDI-TOF MS and VITEK 2 provided a rapid and reliable identification and AST method for UTI patients directly from urine samples, especially in those with Enterobacteriaceae, and it provide reliable "same day" AST report.

PO-1075

纳米孔测序技术在中枢神经系统细菌感染诊断中的应用价值

田宏攀[1]、王维洁[2]、陈良君[1]、周俊英[1]
1. 武汉大学中南医院
2. 湖北中医药大学

目的 研究和评估纳米孔测序技术在中枢神经系统细菌感染中的临床诊断价值。
方法 收集 2019 年 10 月到 2021 年 3 月在武汉大学中南医院临床诊断为中枢神经系统细菌感染的 44 名住院患者的脑脊液标本及病例资料，应用纳米孔测序技术对其进行致病菌检测，并与传统临

床微生物检验（微生物培养和染色）的结果进行比较分析，分别从阳性率、一致性和病原菌种类分布等方面，研究和评估纳米孔测序技术在中枢神经系统细菌感染中的临床诊断价值。
结果 本研究共收集 44 例脑脊液标本进行研究，纳米孔测序结果显示，其中 38 例患者的脑脊液中检出至少一种细菌或真菌，阳性率为 86.36%（38/44）；传统微生物培养中，有 4 例患者培养阳性，阳性率为 9.09%（4/44）。采用 McNemar 检验比较两种检测方法结果的阳性率，两者差异有统计学意义（p=0.00000001518 <0.05），纳米孔测序的阳性率较传统微生物培养高。采用 McNemar 检验比较两种方法在不同科室中的检测结果，在神经内科（p=0.023<0.05）、神经外科（p =0.0000364<0.05）和感染科（p =0.028<0.05）中两种检测方法的阳性率均有显著差异。采用 Kappa 检验比较两种检测方法结果的一致性，结果显示 Kappa=0.03<0.4，一致性较差。统计病原菌种类分布，纳米孔测序检出的病原菌分布为革兰阳性球菌 32.79%（20/61），革兰阳性杆菌 3.28%（2/61），革兰阴性杆菌 42.62%（26/61），真菌 21.31%（13/61）。61 株致病菌中包含 7 株厌氧菌（11.48%）和 2 株苛养菌（3.28%）。脑脊液培养结果为肺炎克雷伯菌 2 株，粪肠球菌 1 株，表皮葡萄球菌 1 株。
结论 纳米孔测序技术相比于传统微生物培养具有快速、敏感度高的优势，在中枢神经系统细菌感染的诊断中具有重要价值。

PO-1076

Antibacterial effect of chitosan-modified Fe3O4 nanozymes on Acinetobacter baumannii

Lin Yu[3]、wenjun wang[1]、peng qin[2]
1. The First Affiliated Hospital of Guangzhou Medical University
2. Guangzhou Medical University
3. The First Affiliated Hospital of Guangzhou Medical University

Objective To determine whether the antibacterial activity of chitosan-modified Fe3O4 (CS@Fe3O4) nanomaterials against Acinetobacter baumannii (AB) is mediated through changes in biofilm and reactive oxygen species (ROS) production.
Methods The broth dilution method was used for bacteriostasis test CS@Fe3O4 Effect of nanoparticles on bacterial growth. The effects of CS@Fe3O4 nanoparticles on biofilm formation were measured using a semi-quantitative crystal violet staining assay. A bacterial ROS detection kit was used to detect the production of ROS in bacteria.
Results CS@Fe3O4 nanoparticles had a significant inhibitory effect on the colony growth and biofilm formation of drug-resistant AB bacteria ($P < 0.05$). The ROS stress assay revealed significantly higher ROS levels in AB subjected to CS@Fe3O4 nanoparticles treatment than the control group ($P < 0.05$).
Conclusion Here, we show that CS@Fe3O4 nanoparticles had an inhibitory effect on AB in vitro, and that this effect was more significant in drug-resistant strains than drug-sensitive ones. Our findings indicate that the antibacterial mechanism of CS@Fe3O4 nanoparticles on drug-resistant bacteria is probably mediated through inhibition of the AB bacteria biofilm and stimulation of AB bacteria to produce ROS. CS@Fe3O4 nanoparticles had no significant inhibitory effect on the biofilm of drug-sensitive bacteria, suggesting that in drug-sensitive bacteria, CS@Fe3O4 nanoparticles probably exert their inhibitory effect through the production of ROS.

PO-1077

Genomic insights into evolution of pathogenicity and resistance of a multidrug-resistant Raoultella ornithinolytica WM1

Meng Wang
Department of Clinical Laboratory, Tianjin First Central Hospital

Raoultella ornithinolytica is a poorly understood opportunistic pathogen, and the underlying mechanisms of its multidrug resistance and pathogenicity have not yet been comprehensively investigated. The multidrug-resistant (MDR) strain, WM1, was isolated from the blood of a male patient in Tianjin, China, in 2018. Here, we describe the complete genome and provide a genomic analysis of R. ornithinolytica WM1. The isolate was resistant to all tested antimicrobials, except for amikacin, tobramycin, and tigecycline. Two plasmids, pWM1-1 (IncHI5) and pWM1-2 (IncR), carried multidrug resistance regions, indicating a close relationship to antimicrobial resistance. A large antimicrobial resistance island (ARI) region resided on pWM1-1 and exhibited complex mosaic structures. These structures mainly resulted from the acquisition of complex integrations of variable regions, including genes conferring resistance to multiple classes of antimicrobials. Moreover, WM1 possessed virulence-related elements that encoded several virulence factors, including type I fimbriae, Escherichia coli common pilus, type II and VI secretion systems, yersiniabactin, enterobactin, and surface polysaccharide, indicating pathogenic potential. Furthermore, the core genome phylogeny and pan-genome analyses revealed extensive genetic diversity of the species R. ornithinolytica. Our analysis indicated the need for stringent infection control, antimicrobial stewardship, periodic resistance monitoring, and rational medication to address the threats posed by MDR R. ornithinolytica strains.

PO-1078

液滴数字化显色分析实现快速耐碳青霉烯细菌检测

王羽[3]、欧阳秀酝[2]、刘大渔[1]
1. 华南理工大学附属第二医院（广州市第一人民医院）
2. 华南理工大学食品科学与工程学院
3. 华南理工大学附属第二医院（广州市第一人民医院）

目的 利用液滴数字化显色分析实现耐碳青霉烯细菌（Carbapenem-resistant Organism, CRO）快速检测。
方法 利用自行设计和加工的流式液滴分析仪以及液滴微流控芯片进行液滴数字化显色分析。实验步骤包括：1.临床样本经过滤处理选择性富集细菌，然后加入碳青霉烯类抗生素美罗培南及细菌活性指示剂刃天青；2.使用微流控芯片对细菌样品进行液滴分散，并在 37 ℃下孵育进行显色反应；3.完成显色反应后，应用流式液滴分析仪检测液滴荧光信号，使用 Python 处理数据快速进行液滴分类识别和阳性率计算，进一步依据 Poisson 算法推算出实验组和对照组的细菌密度，依据细菌活性抑制率判断样本中微生物对于碳青霉烯类抗生素的响应，从而确定样品中是否存在 CRO。
结果 该方法仅需孵育 1 h 即可分辨大肠埃希氏碳青霉烯耐药和敏感质控菌。批量临床样品细菌分离株的活性分析结果显示，液滴数字化显色分析可以准确判定 CRO 与非 CRO，其检测结果与传统方法具有高度一致性。
结论 得益于液滴反应器对于显色因子的富集作用以及数字化分析的精准定量能力，液滴数字化显色分析可快速检测 CRO。这种检测方法有望为 CRO 感染诊断提供快速准确的信息。

PO-1079

Mycobacterium tuberculosis ManLAM binding to TLR2 from mast cells release exosomes to recruit and induce macrophage polarization towards the M2-type

xianru xia
Taihe hospital

Background/Purpose Our previous studies have found that there are more mast cells and more macrophages in pulmonary tuberculosis infection site from patients with chronic active Mycobacterium tuberculosis (M.tb) infection. Given that we speculated whether mannose-capped lipoarabinomannan (ManLAM), a high-abundance lipolysaccharide from M.tb that regulates immunity negatively from many reports, may induce the permanent mast cells (MCs) in tissue and have corss-talk with macrophage to recruit macrophage and cause the persistence infection via some remote signal, exosomes.
Methods We extracted ManLAM from M.tb H37Rv and analyzed the ManLAM bind to ligand of MCs using peptide mass fingerprint (PMF) and Western Blot (WB). Following, we have cultured with mast cell line HMC-1 with the ManLAM extracted from Mycobacterium tuberculosis H37Rv and harvested the exosomes from MCs for proteomics analysis. The target proteins of exosomes' content, cytokines associated with chemokines and polarization of macrophage, were identified and verified by WB, Trans-well, FCM and qRT-PCR respectively.
Results In this research, we found that MCs released exosomes containing high levels of IL-4, IL-13 and CCL-2 through ManLAM binding to TLR2 of MCs. Following, we proved that the exosomes of ManLAM-induced MCs could recruit Mj and promote expression of M2-like macrophage characteristic phenotypic molecules (CD163+) and cytokines (Arginase-1, IL-10 and FIZZ-1).
Conclusions Our research suggested that exosomes from ManLAM-induced MCs recruit macrophage and induce them to polarize towards M2 type to escape immune elimination. It may be another novel clue that M.tb evade immune elimination to cause chronic persistent infection.

PO-1080

东北某三甲医院血流感染碳青霉烯耐药肺炎克雷伯菌的主导序列类型由 ST11 转化为 ST15

陈静静
中国医科大学附属第一医院

目标 探讨我院耐碳青霉烯类肺炎克雷伯菌（CRKP）血流感染的临床特征和分子流行病学特征。
方法 2015.1 至 2020.12 期间，51 名患者被确定为 CRKP 血流感染，其中 42 名患者保存菌株可用于进一步实验。采用 MALDI TOF MS 和 VITEK 系统进行菌种鉴定和药物敏感性检测。聚合酶链反应检测碳青霉烯酶基因、毒力基因和 MLST 基因。此外，还进行拉丝试验和血清杀灭试验以评估 CRKP 分离株的毒力。
结果 随访 6 年间血流感染 CRKP 检出率呈上升趋势，主要涉及重症监护病房、血液内科、呼吸内科等科室。分子流行病学分析表明，KPC-2 是主导的碳青霉烯酶基因，CRKP 的主导序列类型从 ST11 转换为 ST15。与 ST11 CRKP 相比，ST15 CRKP 均对阿米卡星敏感，KfuB 毒力基因呈阳性，且对血清杀伤的抵抗力更强，但感染 ST11 和 ST15 CRKP 的患者死亡率无显着差异。
结论 2015-2020 年期间观察到我院血流感染 CRKP 的主要序列类型从 ST11 转换为 ST15。与 ST11 CRKP 相比，ST15 CRKP 表现出阿米卡星敏感性、KfuB 基因阳性和血清抗性，这提示其可能有更强的毒力。

PO-1081

Metatranscriptomic analysis of host response and microbiome in vagina of severe COVID-19 women patients

Meng Xiao[1]、Bo Lu[2]、Yingchun Xu[1]、Chengqi Yi[2]、Lan Zhu[1]
1. Peking Union Medical College Hospital
2. 北京大学

COVID-19 has become a global pandemic threats and its impact on women's health has drawn great attention. Whilst host response and vaginal microbiome changes in reproductive system of women patients, especially those underlying severe conditions, remained unknown.

In this study, a novel TRACE-seq-based meta-transcriptomic analysis were applied to simultaneously characterize host responses and vaginal microbiome in 16 women patients with COVID-19 in an intensive care unit and five healthy women individuals.

Notably, although SARS-CoV-2 was absent from reproduction system of COVID-19 women patients, indications of systematic immune and defense responses were found in patients' vaginal samples. Transcriptome analysis revealed that expression of IL-36 subfamily cytokines belonging to IL-1 superfamily were up-regulated, whilst IL-36 pathway were previously considered unaffected by COVID-19 in blood and other body sites, indicating that reproductive tract epithelial cells were invovled in defence and immune response. In addition, NF-κB and type I interferon signaling pathways downstream to IL-1/IL-36 pathway were activated in COVID-19 patients. Moreover, we found abnormal high proportion of putative pathogenic microorganisms in COVID-19 patient's vaginal microbiota, i.e., Mycoplasma hominis, Gardnerella vaginalis, Ureaplasma urealyticum, Bacteroides spp., Atopobium spp., Enterococcus faecium and Acinetobacter baumannii, whilst there were significant intra-individual variations. Expression of antimicrobial resistant genes were also high in COVID-19 patients. Our reports provide further understanding of COVID-19 threats to women, and for the first time characterized its implication on women's reproductive system.

PO-1082

传染性腹泻患者中 mcr-1 阳性沙门氏菌的流行情况、基因组特征和传播动态研究

马芙蓉
广州医科大学附属第三医院

目的 本研究旨在了解 *mcr-1* 在广东省不同来源沙门氏菌中的流行情况，通过全基因组测序分析等手段探究菌株的遗传特征，并揭示其耐药传播机制。

方法 本研究收集了 2015-2017 年来源猪、猪肉及沙门氏菌感染病人样本 1701 份。通过 PCR 对 *mcr-1* 阳性沙门氏菌进行鉴定与分离。运用琼脂稀释法或肉汤稀释法检测 *mcr-1* 阳性沙门氏菌对 16 种临床常用抗生素的药物敏感性。通过质粒接合、S1-PFGE 及核酸杂交检测 *mcr-1* 的可转移性和基因定位。对 19 株 *mcr-1* 阳性沙门氏菌进行全基因测序，分析 *mcr-1* 阳性沙门氏菌的群体结构和基因组流行特点。

结果 本研究共检出 19 株 *mcr-1* 阳性沙门氏菌，在猪粪便、猪肉、临床病人感染菌株中的 *mcr-1* 阳性率分别为 0.53%（5/936），1.80%（3/167）和 1.84%（11/598）。药物敏感性实验结果发现 *mcr-1* 阳性沙门氏菌株均为多重耐药菌。*mcr-1* 基因位于 ST3-IncHI2 质粒上，其中 12 株菌株的 *mcr-1* 基因可接合转移。全基因组测序分析发现，所有沙门氏菌为 ST34 型或其相近的 ST 型。核心基因的分布与样本来源显著相关；附属基因网络图表明，不同的克隆复合体可以共享高度相似的附属基因组。

结论 本研究发现 *mcr-1* 阳性沙门氏菌呈低流行状态，菌株表现较高耐药率和多重耐药性，给抗沙门氏菌感染治疗带来了威胁。基于全基因组测序分析，克隆传播可能不是 *mcr-1* 阳性沙门氏菌传播的主要原因，而可能与 ST3-IncHI2 质粒的水平转移有关。因此，持续地监测 *mcr-1* 阳性沙门氏菌在动物、食品、社区和医院的流行趋势对 *mcr-1* 的防控至关重要。

PO-1083

Four types of ST11 novel mutations from increasing carbapenem-resistant Klebsiella pneumoniae in Guangdong, 2016-2020

Yunhu Zhao[1]、yalong liao[1]、ni zhang[1]、suling liu[1]、jiao zhang[2]、雪姣 hu[1]、dianrong zhou[1]、qianyun deng[1]、yanping shi[3]、bing gu[2]、tieying hou[1]

1. Guangdong Provincial Peoples Hospital
2. 南方医科大学皮肤病医院
3. 南方战区总医院

Objectives This study aimed to explore changes in CR-KP isolates collected in Guangdong over the period of 2016 to 2020.

Methods Antibacterial susceptibility was quantified through VITEK 2 compact and K-B method. Carbapenemase phenotypes and genotypes were characterized by mCIM, eCIM, and PCR. Molecular characteristics and evolutionary trends were analyzed by multilocus sequence typing and evolutionary tree.

Results A total of 2847 isolates of Klebsiella pneumoniae were separated in 2016-2020, and the separate rate of CR-KP increased from 5.65% to 9.90% (P=0.009). The top 3 wards were ICU (21.92%), neonatal wards (13.70%), and respiratory wards (12.33%). Serine carbapenemase was the main phenotypes and KPC-2 was the main genotypes in 146 CR-KP strains, in which 57 were contained two resistant genes, 1 was contained three resistant genes. Four polygenic strains were first found: KPC+VIM, KPC+IMP, IMP+GES, and KPC+NDM+VIM, but all the phenotypes were metalloenzyme, indicated that metalloenzyme was usually the first choice for CR-KP resistance. In addition, all the ST54 of metalloenzyme type contains IMP, and all the ST45, ST37, and ST76 contain OXA-48. ST11 was the most prevalent (42.47%), a novel type of ST11 mutation, the rpoB was mutated from sequence 1 to sequence 146, was in an independent separate branch on the evolutionary tree, and resistant to all antibacterial agents. The other 3 mutants: rpoB 1 to 15, infB 3 to 148, infB 3 to 80, also resistant to all antibacterials. Notely, all the four mutants produced serine carbapenemase and contained KPC-2, indicated that the prevalent strain, ST11, has a serious consequence of mutation, will lead to an outbreak with the fully resistant, probably. What's more, the medical burden of patients with CR-KP infection was far greater than that of CS-KP.

Conclusions The infection rate of CR-KP has increased, ICU and neonatal wards have become the key infection areas. Producing serine enzyme, KPC-2 genotype and ST11 are the predominant CR-KP. Polygenic strains and ST11 mutation made clinical treatment difficult, may become a potential threat.

PO-1084

Drug resistant mechanism and homology analysis of carbapenem-resistant Enterobacteriaceae isolated from different sites of one patient in intensive care units

Jinyi Gu 、deyao deng、wenli yuan
The Affiliated Hospital of Yunnan University

OBJECTIVE To investigate the drug resistant mechanism and homology of carbapenem-resistant Enterobacteriaceae (CRE)isolated from different sites of one patient in the intensive care unit(ICU).
METHODS The active screening of CRE in fecal or anus swabs was carried out for the patients who were hospitalized the ICU of a grade-A tertiary hosipital in Yunnan from January 1, 2017 to December 30,2018. If CRE was colonized in fecal or anus swabs ,some specimens for example, urine, sputum, drainage fluid, wound tissue, etc from other parts of the patient during the same period were collected to screen CRE. The collected CRE were identified and tested for drug sensitivity and phenotypic validation, and the clinical data and laboratory results were analyzed. Carbapenems resistance genes were detected by Polymerase chain reaction(PCR)and sequenced.The homology of CRE isolated from different sites of one patient was analyzed by Randomly amplified polymorphism DNA(RAPD) technique.
RESULT There were 1518 hospitalized patients to the ICU during the study period,and 1502 patients involved in screening, The rate of active screening of CRE was 98.95%（1502/1518）, the rectum colonization rate of active screening of CRE was 4.73%（71/1502）, The rate of CRE was detected only in rectum was 25.35%（18/71）,The rate of CRE was detected in two parts was 11.27%（8/71）, The rate of CRE was detected in three parts was 49.30%（35/71）, The rate of CRE was detected in four parts was14.08%（10/71）, Carbapenem-resistant Klebsiella pneumoniae(CRKP) strains were dominant among the pathogens,accounting for 87.32%（62/71）, All the CRE screened from two or more parts were CRKP.The results of drug sensitivity and phenotypic validation of CRE isolated from different sites of one patient were same.The positive rate of carbapenems resistance genes KPC-2,NDM-1,VIM-2 and IMP respectively were 69.83% 、 17.32% 、 8.38% and 6.70%, the gene OXA-48was not detected.The type of carbapenems resistance genes of was same（92.45%）. 161 strains of CRE isolated from two or more sites of one patient were classified into seven different clones by the RAPD technique,and the clone D was epidemic strain. CRE isolated from different sites of 94.34% patients were from same clone.
CONCLUSION Carring KPC-2 gene is the main cause leading to the drug resistance of CRE isolated from patient, and the CRE isolated from different sites of one patient have higher relatedness. It is necessary to active screening CRE and Strengthen prevention and control measure in clinic, the therapy method for the patient of CRE colonization and infection by early detection, early intervention, early treatment.

PO-1085

肺移植术后病原菌感染的分布和耐药特征及风险因素

许书琳、娄加陶
上海市胸科医院

目的 回顾性分析肺移植术后感染的病原菌的分布和耐药特征及增加感染风险的因素，为指导临床合理选择抗菌药物、调整抗感染治疗方案提供依据。

方法 分析 2007 年 9 月~2019 年 8 月行肺移植手术的 50 例患者术后病原菌分布情况、发生时间、耐药特征和增加感染的危险因素，采用 VITEK2 COMPACT 全自动微生物鉴定与药敏系统鉴定菌株和检测药物敏感性，使用 SPSS 22.0 软件系统处理数据。
结果 肺移植术后受者感染率 74%（37/50），单一病原菌感染 9 例（24.3%），两种及以上病原菌混合感染 28 例（75.7%）。引起感染的主要病原菌是革兰阴性菌（铜绿假单胞菌、鲍曼不动杆菌、嗜麦芽窄食单胞菌和肺炎克雷伯菌），铜绿假单胞菌对头孢类、氟喹诺酮类和复方新诺明耐药率 66.7%~94.1%；鲍曼不动杆菌对多种抗菌药物高耐药，耐药率 72.7%~100%；嗜麦芽窄食单胞菌对头孢他啶耐药率 50%；肺炎克雷伯菌对碳青霉烯类、β 内酰胺类、头孢类和氟喹诺酮类耐药率 44.4%~71.4%。其次是革兰阳性菌（金黄色葡萄球菌、溶血葡萄球菌和粪肠球菌），对利奈唑胺、万古霉素敏感，可作为抗感染治疗的首选药物。单因素分析结果显示性别、年龄、入住重症加强护理病房（Intensive Care Unit，ICU）、氧分压、血红蛋白水平、血清白蛋白水平、他克莫司水平、吻合口瘘/支气管狭窄、机械通气和闭塞性细支气管炎综合征是术后肺部病原菌感染的危险因素（$P < 0.05$）。
结论 移植物本身的性质、患者营养状态和外界环境因素是造成肺移植受者不同时间段感染的危险因素，以革兰阴性菌尤其是非发酵菌感染为主，对多种抗菌药物表现为高耐药，临床需根据药敏结果选择抗菌药物和剂量，以提高患者生存年限。除病原菌的识别、控制和治疗至关重要外，术后营养支持、康复护理、环境消毒隔离亦扮演重要角色，直接影响移植物的功能和免疫抑制剂的应用。

PO-1086

16 例莫拉菌属角膜炎的临床特征及分离株耐药性分析

杨媛媛、王海鸥、陈鹏飞、李亚利、郑美琴
温州医科大学附属眼视光医院

目的 探讨莫拉菌属角膜炎的临床特征及分离菌株耐药情况。
方法 回顾性研究。收集 2013 年 12 月至 2020 年 6 月于温州医科大学附属眼视光医院诊断为莫拉菌属角膜炎的 16 例患者资料，对其临床特征、风险因素、治疗效果及病原菌的分布变化、耐药性趋势进行分析。应用半自动鉴定仪 ATB Reader 与质谱检测仪 MBT 鉴定莫拉菌种。
结果 纳入研究的 16 例莫拉菌属角膜炎均为经实验室检查的确诊病例。经临床特征分析得出，最常见的局部与系统性风险因素诱分别为既往眼部手术和糖尿病/高血压，患者最常见的症状是眼痛，最常见的体征是角膜溃疡。通过实验室检查发现所有患者中腔隙莫拉菌 7 例，非液化莫拉菌 4 例，奥斯陆莫拉菌 3 例，卡他莫拉菌 1 例，亚特兰大莫拉菌 1 例。细菌药敏试验结果显示分离到的致病菌对青霉素、头孢菌素、四环素、喹诺酮类和氨基糖苷类等眼部常用药物耐药性不高。
结论 在研究的 16 例莫拉菌属角膜炎患者中，以眼痛和角膜溃疡多见；腔隙莫拉菌和非液化莫拉菌为主要感染病原菌，其分离株对药物敏感性较高，得到了有价值的结论，为以后的临床治疗与研究提供了基础。

PO-1087

Species distribution and antifungal susceptibilities of clinical isolates of Penicillium and Talaromyces species in China

Lina Guo 、shuying yu、yingchun xu
Department of Clinical Laboratory, Peking Union Medical College Hospital, Peking Union Medical College, Chinese Academy of Medical Sciences, Beijing, China

Objective Penicillium species have been found in clinical samples, however their prevalence and significance in the clinical setting are still largely unknown. Epidemiological studies provide important information about the demographic characteristics, species diversity, and susceptibility data, which are critical for the management of Penicillium-associated diseases.
Methods Morphologically identified 103 Penicillium isolates and 8 Talaromyces marneffei isolates were collected from various clinical sources between 2016 and 2017 at a medical center in Beijing, China. Identification at the species level was confirmed via sequencing of the internal transcribed spacer (ITS) region, β-tubulin (BenA), and RNA polymerase II second largest subunit (RPB2) genes. The antifungal susceptibility profiles of the Penicillium species were also evaluated by CLSI broth microdilution method.
Results The ITS region could identify 64.9% (72/111) of the isolates to the species level and 35.1% (39/111) to the genus level. Both BenA and RPB2 genes could confidently identify 100% of the isolates tested to the species level. For identification of clinical important T. marneffei isolates, the ITS, BenA and RPB2 genes worked equally well. Of the 111 isolates, 56 (50.5%) were identified as Penicillium species, and 55 (49.5%) were Talaromyces species. A total of 11 Penicillium species were detected, of which P. oxalicum was the most common, accounting for 51.8% (29/56), followed by P. rubens (10.7%, 6/56) and P. citrinum (10.7%, 6/56). Among the 55 Talaromyces isolates, nine species were identified, with T. funiculosus (36.4%, 20/55), T. stollii (27.3%, 15/55), and T. marneffei (14.5%, 8/55) being the most common. Of note, 89.3% (50/56) of Penicillium isolates and 98.2% (54/55) of Talaromyces isolates exhibited growth at 37°C. The isolates were mainly recovered from patients with pulmonary disorders (56.8%, 63/111), autoimmune disease (12.6%, 14/111), and AIDS (5.4%, 6/111). The azoles and amphotericin B exhibited potent activity against T. marneffei isolates, while various levels of activity were observed against Penicillium and other Talaromyces species. The echinocandins had the lowest MECs (MEC90 ≤ 0.12 mg/L) against most Penicillium and Talaromyces species, with the exception of T. marneffei, whose MEC90 (4 mg/L) was five or more dilutions higher than that of the other species tested.
Conclusion The ITS appears to be useful targets for identification at the genus level, while BenA can be performed for species-level identification within Penicillium and Talaromyces in clinical microbiology laboratory. RPB2 was recommended for the description of new species due to difficulties in PCR amplification and sequencing. High species diversity was observed in 111 clinical isolates, with P. oxalicum, T. funiculosus, and T. stollii being the most prevalent species. The majority of Penicillium (89.3%) and Talaromyces (98.2%) isolates were able to grow at 37°C, which might indicate an opportunistic potential to become etiological agents of systemic mycosis. These data on species distribution and antifungal susceptibility expand the current clinical knowledge of Penicillium and Talaromyces species.

PO-1088

Performance Evaluation of the Etest and disc diffusion method for ceftazidime- avibactam against Enterobacterales and P. aeruginosa, a dual center study

Jingjia Zhang、Ge Zhang、Wei Kang、Simeng Duan、Tong Wang、Jin Li、Zhiru Huangfu、Qiwen Yang、Yingchun Xu、Hongli Sun
Peking Union Medical College Hospital

Objectives Ceftazidime-avibactam is a novel synthetic β-lactamase inhibitor combination. It had been used to treat infections caused by gram-negative bacilli for only a few years. However, no commercialized product had been approved to test the drug susceptibility of ceftazidime-avibactam in clinical laboratories in China. In this study, we evaluated the performance of Etest and the disc diffusion method for the determination of ceftazidime-avibactam against *Enterobacterales* and *P. aeruginosa*.
Methods Antimicrobial susceptibility testing of 302 clinical *Enterobacterales* and *P. aeruginosa* isolates from two centers were conducted by broth microdilution (BMD), Etest, and disc diffusion method for ceftazidime-avibactam. Using BMD as a gold standard, essential agreement (EA), categorical agreement (CA), major error (ME) and very major error (VME) were determined according to CLSI guidelines. CA and EA > 90%, ME < 3%, and VME < 1.5% were considered as acceptable criteria. Polymerase chain reaction and sanger sequencing were performed to determine the carbapenem resistance genes of all the 302 isolates.
Results A total of 302 strains (228 *Enterobacterales* and 74 *P. aeruginosa*) were enrolled, among which 182 strains were from center 1 (148 *Enterobacterales* and 34 *P. aeruginosa*) and 120 strains were from center 2 (80 *Enterobacterales* and 40 *P. aeruginosa*). 18.21% (55/302) of the enrolled isolates were resistant to ceftazidime-avibactam. The categorical agreement rates of Etest for *Enterobacterales* and *P. aeruginosa* were 100% and 98.65% (73/74), respectively, and the essential agreement rates were 97.37% (222/228) and 98.65% (73/74), respectively. The categorical agreement rates of the disc diffusion method for *Enterobacterales* and *P. aeruginosa* were 100% and 95.95% (71/74), respectively. No very major errors were found by using Etest, while the major error rate was 0.40% (1/247). No major errors were found by using the disc diffusion method, but the very major error rate was 5.45% (3/55). Therefore, all the parameters of Etest were in line with acceptable criteria. For 31 blaKPC, 33 blaNDM, 7 blaIMP, and 2 blaVIM positive isolates, both of the categorical agreement rates and essential agreement rates were 100%, no major error and very major error was detected by two methods. For 15 carbapenemase-non-producing resistance isolates, the categorical agreement rate and essential agreement rate of Etest were 100%. Whereas the categorical agreement rate of the disc diffusion method was 80.00% (12/15), the very major error rate was 20.00% (3/15).
Conclusions Both Etest and the disc diffusion method can meet the needs of clinical microbiological laboratories for testing the susceptibility of ceftazidime-avibactam drugs. By comparison, the evaluation of Etest was better than that of the disc diffusion method. The detection performance of *Enterbacterales* was better than that of *P. aeruginosa*.

PO-1089

Multiplex PCR system for the rapid diagnosis of blood stream infection: systematic review and meta-analysis

Mei Yang、chuanmin Tao、zhongyi Zhao、zhonghao Wang
Department of Laboratory Medicine, West China Hospital, Sichuan University

Background Bloodstream infections (BSIs) are a leading cause of patient mortality and high health care-related costs worldwide, which are among the most common healthcare-associated infections. Traditionally, diagnosis of BSI relied solely on blood culture, which has been considered the gold standard of pathogen detection. However, there are some shortcomings with blood culture for the diagnosis of BSI, such as low sensitivity, prolonged turnaround time (>48 hours), and labor intensive or operator dependent. Recent advances have emerged for rapid and specific identification of infectious pathogen from positive blood culture bottles, which include melting curve analysis, real-time PCR and nucleic acid amplification technologies. In 2013, the Food and Drug Administration (FDA) approved a rapid and automated multiplex PCR assay, the FilmArray blood culture identification (BCID), which directly identifies common pathogens, including 8 genera/ species of Gram-positive bacteria, 11 genera/species of Gram-negative bacteria, 5 species of Candida and 3 antimicrobial resistance genes in the positive blood culture bottles. The FilmArray blood culture identification (BCID) panel is a multiplex PCR assay to detect the most commonly pathogens in bloodstream infections (BSIs) leading cause of patient mortality and high health care-related costs worldwide with increased sensitivity and specificity. However, a major problem remains that BCID panel still produce false negative or positive results, which prevents a wider adoption of this panel by laboratories.
Objectives Hence, we need to know the actual effectiveness of the method before integrating into the workflow of laboratory's diagnosis aimed to enhance the accuracy and efficiency of the disease diagnosis, allowing to accelerate the clinical decision-making. Therefore, we aim to provide a summary of evidence for the diagnostic accuracy of BCID panel, on the detection of positive blood cultures.
Methods The flow chart of our study was based on the PRISMA (Preferred Reporting Items for Systematic Review and Meta-analysis) statement and the guidelines for systematic reviews of diagnostic tests proposed by the Cochrane Collaboration. The protocol was registered with the International Prospective Register of Systematic Reviews (PROSPERO) (registration number CRD42021239176). We searched the MEDLINE, EMBASE and Cochrane databases though Mar 2021 for studies assessing the diagnostic test efficacy of the BCID panel. The number of true positives, false positives, true negatives and false negatives of the BCID panel compared with the reference standards were also extracted to calculate the sensitivities and specificities of the target assays. Last, in order to better understand the analytical accuracy of the BCID panel, we analyzed the results of confirmation methods which were performed by the investigators of the studies in all blood culture specimens with each discrepant result occurring between BCID panel and the reference identification techniques.
Results Sensitivity across the 17 included studies varied from 89% to 100% with most of the studies being from 94% to 100% for Gram-positive bacteria, it is noteworthy that in the one study with low sensitivity (89%). Sensitivity across the 17 included studies varied from 88% to 100% with most of the studies being 100% for Gram-negative bacteria, it is noteworthy that in the single study with low sensitivity (88%). Sensitivity across the 14 included studies varied from 50% to 100% with most of the studies being from 95% to 100% for fungi, it is noteworthy that in the single study with low sensitivity (50%). On the other hand, specificity across the 17 studies varied from 95% to 100% for Gram-positive bacteria, 97% to 100% for Gram-negative bacteria and 99% to 100% for fungi. Positive predictive value of the BCID panel was 42.7%, 41.6% and 96.7% for Gram-positive bacteria, Gram-negative bacteria and fungi, respectively. In other words, a positive panel result has 42.7%, 41.6% and 96.7% possibility of being correct to identify Gram-positive bacteria, Gram-negative bacteria and fungi bloodstream infection. In addition, negative predictive value of the BCID panel was 97.1%, 99.5% and 99.7% for Gram-positive bacteria, Gram-negative bacteria

and fungi, respectively. That is, a negative panel result has 97.1%, 99.5% and 99.7% possibility of being correct to identify Gram-positive bacteria, Gram-negative bacteria and fungi bloodstream infection. Summary estimates are calculated from the included studies by pooling the studies in a meta-analysis. For sensitivity analysis, goodness of fit and bivariate normality showed that random effects bivariate model is suitable. By applying a bivariate random-effects model, the pooled estimates for sensitivities were 97.0%, 99% and 99% for Gram-positive bacteria, Gram-negative bacteria and fungi, respectively. The pooled estimates for specificities were 100%, 100% and 100% for Gram-positive bacteria, Gram-negative bacteria and fungi, respectively.Overall, 83 and 104 specimens were detected as false positive and false negative, respectively, by the BCID panel compared with reference identification techniques. After confirmation methods implemented by the investigators of the included studies for the discordant results, false positive and false negative results decreased to 49 and 36, respectively. The largest number of false positive and false negative results after discrepant confirmation was showed Klebsiella pneumoniae and Staphylococcus spp.

Conclusions Based on the published studies, we conclude that the BCID panel test has higher rule-in than rule-out diagnostic value. In populations in which the prevalence of systemic bacterial or fungal infection is low, the negative BCID panel still offer useful information for clinical decision. The major limitation of the BCID panel is its suboptimal sensitivity. Before newer technology is available, we recommend clinicians combine biomarkers, clinical findings, and the BCID panel to enhance the diagnostic accuracy.

PO-1090

肠道定植碳青霉烯耐药肠杆菌目细菌的主动筛查及分子流行病

储雯雯
安徽医科大学第二附属医院

目的 筛查住院患者肠道碳青霉烯耐药肠杆菌目细菌的定植率，并分析 CRE 菌株分子的流行病学特征。

方法 采集 2019 年 3 月至 12 月安徽医科大学 第二附属医院外科重症监护病房、内科重症监护病房和血液内科（移植病房 213 例住院患者粪便、直肠拭子或肛周拭子标本，应用含碳青霉烯类药物的麦康凯平板法筛查 CRE 菌株，并进行细菌鉴定、药物敏 感试验检测，选取重点菌株进行全基因组测序，并分析其多位点序列分型、荚膜血清型、耐药基因、毒力 基因及质粒携带特征。

结果 共检出 CRE 菌株 23 株，检出率为 10.8% ；其中碳青霉烯类耐药肺炎克雷伯菌 15 株(65.2%)、大肠埃希菌和阴沟肠杆菌各 3 株(13.0%)、弗氏柠檬酸杆菌 2 株(8.7%)。单核苷酸多态性聚类分析表明，15 株 CRKP 有两种主要克隆型，均在外科重症监护病房内流行。15 株 CRKP 均属于 ST11-K64 型，均携带 β-内酰胺类耐药基因产肺炎克雷伯菌碳青霉烯酶 2 型基因；80.0% (12 株)的 CRKP 携带毒力基因黏液表型调控基因 2 型、iutABCD-iutA。

结论 住院患者中肠道定植 CRE 检出率较高，以 ST11-K64 型 CRKP 为主，CRKP 菌株兼具多重耐药性和毒力特征，有医院传播风险。

PO-1091

Respiratory Haemophilus influenzae infection linked to particulate air pollution

Shaocheng Zhang[1]、Xi Chen[2]、Jing Wang[2]、Chunmei Dai[2]、Yeran Gou[3]、Huanhuan Wang[4]
1. Suining Central Hospital
2. 绵阳市中心医院
3. 成都市第二人民医院
4. 汕头大学医学院

Particulate air pollution is correlated with many respiratory diseases. However, few studies have focused on the relationship between air particulate exposure and respiratory Heamophilus influenzae infection. Therefore, we detected respiratory Heamophilus influenzae infection by bacterial culture of sputum of patients, and we collected particulate air pollution data (including PM2.5 and PM10) from a national real-time urban air quality platform to analyze the relationship between particulate air pollution and respiratory Heamophilus influenzae infection. The mean concentrations of PM2.5 and PM10 were 37.58 μg/m3 and 58.44 μg/m3, respectively, showing particulate air pollution remains a severe issue in Mianyang. A total of 828 strains of Heamophilus influenzae were detected in sputum by bacterial culture. Multiple correspondence analysis suggested the heaviest particulate air pollution and the highest Heamophilus influenzae infection rates were all in winter, while the lowest particulate air pollution and the lowest Heamophilus influenzae infection rates were all in summer. In a single-pollutant model, each elevation of 10 μg/m3 of PM2.5, PM10, and PM2.5/10 (combined exposure level) increased the risk of respiratory Heamophilus influenzae infection by 34%, 23%, and 29%, respectively. Additionally, in the multiple-pollutant model, only PM2.5 was significantly associated with respiratory Heamophilus influenzae infection (B, 0.46; 95% confidence interval, 0.05–0.87), showing PM2.5 is an independent risk factor for respiratory Heamophilus influenzae infection. In summary, this study highlights air particulate exposure could increase the risk of respiratory Heamophilus influenzae infection, implying that stronger measures need to be taken to protect against respiratory infection induced by particulate air pollution.

PO-1092

17 株耐万古霉素肠球菌耐药与分子分型及同源性分析

纵帅
徐州医科大学附属医院

目的 研究万古霉素耐药肠球菌（VRE）分离株的耐药谱，并通过多位点序列分型（MLST）分型和脉冲场凝胶电泳（PFGE）分析菌株间的同源性，分析耐药谱和分子分型之间有无关联性；为临床药物治疗和预防感染暴发提供依据。
方法 对收集自北京中日友好医院的 17 株 VRE 进行鉴定和药物敏感性试验（包括微量稀释法测定其 MIC 值和 E-test 检测万古霉素和替考拉宁 MIC 值）；MLST 试验进行 ST 分型； PFGE 试验进行分子克隆分型和同源性分析。
结果 全部 17 株 VRE 万古霉素 MIC＞256μg/mL，9 株 VRE 的替考拉宁 MIC＞256μg/mL，17 株 VRE 对利奈唑胺、替加环素和奎奴普丁/达福普丁 100%敏感，对青霉素 G、氨苄西林、左氧氟沙星、环丙沙星和呋喃妥因 100%耐药，对替考拉宁、红霉素、四环素、链霉素和高水平庆大霉素的耐药率分别为 82.4%、47.1%、35.3%、23.5%和 17.6%；17 株 VRE 分为 4 个 ST 行，其中 ST78 型 14 株，为主要型别，ST343、ST192 和 ST547 型各 1 株；相同 ST 型别菌株间耐药谱和不同 ST 型别菌株间耐药谱均不完全相同；PFGE 将 17 株 VRE 共分为 10 个不同的克隆来源，PFGE 克

隆分型和 ST 分型型别未发现在严格对应关系；相同克隆来源的菌株间和不同来源的克隆株间耐药谱均不完全相同。
结论 VRE 存在严重的多药耐药特性；MLST 分型、PFGE 克隆分型和 VRE 耐药谱之间没有必然的联系；分子分型不能用于 VRE 的耐药谱及其严重程度的评估和预测；药物敏感性试验的直观结果依然是临床 VRE 治疗的主要依据。

PO-1093

A case of thoracic brucellosis misdiagnosed as malignant tumor and literature review

Fengzhen Yang
Yantai Yuhuangding Hospital

Brucellosis remains a major public health problem worldwide. It is commonly found in most developed and developing countries, such as the Mediterranean region, the Middle East, and Latin America. In China, brucellosis is mainly distributed in some of the northern provinces and is relatively rare in Shandong province. Brucellosis has a variety of clinical manifestations, with fever, sweating, fatigue, and migratory joint pain being the most common. Due to the non-specific clinical symptoms, brucellosis is often misdiagnosed as other diseases. Here, we report a rare case of brucellosis of thoracic vertebrae misdiagnosed as thoracic malignant tumor and present a review of related literature.

PO-1094

Based on transcriptome sequencing：clinicians need to pay attention to fever caused by common respiratory pathogens during the global outbreak of COVID-19

Sheng Yin、min wang、Wenlong Wang
The Second Xiangya Hospital of Central South University

Objectives During the COVID-19 pandemic, clinicians and public health decision-makers especially focus on fever patients. Other common pathogens that may cause fever are easily overlooked. We aimed to describe the pathogen infection and epidemic trend of non-SARS-CoV-2 occurring in hospitalized patients.
Methods An observational cohort study of 733 consecutive patients admitted to Hospital Clinic of the Second Xiangya Hospital for COVID-19. All samples of a pharyngeal swab from patients with fever have been tested for nucleic acid and immune antigens of SARS-CoV-2 and Influenza A/B virus. 649 fever patients have been tested for nucleic acid in ten respiratory pathogens. Macrotranscriptome sequencing was performed on 26 samples.
Results Of a total of 733 patients with fever, 2.05% patients had confirmed SARS-CoV-2 infections. Fever patients with common respiratory pathogens in fever patients was 8.78%. There is no integration phenomenon between SARS-Cov-2 and the human genome. SARS-CoV-2 positive samples will also be infected with other viruses, especially adenovirus. Macrotranscript analysis showed that there was no significant difference in the species and genus levels of pathogens between Covid-19 patients and other fever patients. The main pathways that affect human metabolism after SARS-Cov-2 infection are the Calvin-Benson-Bassham cycle, pyrimidine deoxyribonucleotides de novo biosynthesis I and D-galactose degradation V.
Conclusions Most patients have a fever caused by common respiratory pathogens. Clinicians still need to pay more attention to infections of common respiratory pathogens in addition to

SARS-CoV-2. China's public health measures to stop the spread of the epidemic have proven effective.

PO-1095

危重病科患者合并血流感染的影响因素及病原菌分析

陈凌娟、彭晓飞、李玉珍、徐令清、张中文
清远市人民医院

目的 探讨危重病科患者合并血流感染的影响因素及病原菌。
方法 选择 2020 年 1 月至 6 月我院危重病科收治的 162 例合并血流感染患者为观察组，162 例未合并血流感染患者为对照组，收集资料，分析危重病科患者合并血流感染的影响因素及病原菌。
结果 年龄≥60 岁、脑血管疾病、糖尿病、机械通气时间＞5d、入院前 30d 内使用抗菌药物是危重病科患者合并血流感染的高危因素（OR＞1 且 P＜0.05）；观察组中 162 例患者的血培养样本中分离出病原菌 251 株，其中革兰阴性菌 155 株（61.75%），革兰阳性菌 86 株（34.27%），真菌 10 株（3.98%）。
结论 危重病科患者合并血流感染与年龄、机械通气时间、使用抗菌药物和合并脑血管疾病、糖尿病有关，革兰阴性菌是其主要致病菌，临床需针对各危险因素加强护理干预，以减少血流感染发生。并根据病原菌实施药敏试验，按照试验结果合理选择抗菌药物，提高治疗效果。

PO-1096

川东某院 Gene Xpert MTB/RIF 在结核病早期诊断中的应用分析

王芬、王翠、刘家瑞、陈林
遂宁市中心医院

目的 探讨 Gene Xpert MTB/RIF 检测技术在基层医疗机构中对结核病早期诊断的应用价值，为该技术在川东地区的推广应用提供参考。
方法 收集 2020 年 3 月-2021 年 2 月遂宁市中心医院门诊及病区收治的疑似结核病患者送检标本 368 例，分别采用抗酸染色、荧光定量 PCR、Gene Xpert MTB/RIF、固体培养法进行检测，比较四种方法的阳性率。以固体培养法为金标准，分析 Gene Xpert MTB/RIF 对结核分枝杆菌的检测效能；以比例法药敏试验为金标准，分析 Gene Xpert MTB/RIF 对利福平耐药性的检测效能。
结果 抗酸染色、荧光定量 PCR、Gene Xpert MTB/RIF、固体培养法的阳性率分别为 14.13%、34.24%、49.46%和 50.82%，Gene Xpert MTB/RIF 检测的阳性率高于抗酸染色法和荧光定量 PCR 法，差异有统计学意义（P＜0.05）；固体培养法与 Gene Xpert MTB/RIF 检测阳性率差异无统计学意义（P＞0.05）。以固体培养法为金标准，Gene Xpert MTB/RIF 检测结核分枝杆菌的敏感度、特异度、阳性预测值、阴性预测值分别为 96.79%、99.45%、99.45%和 96.77%，两种方法的符合率为 98.10%，Kappa 值为 0.961；以比例法药敏试验为金标准，Gene Xpert MTB/RIF 检测利福平耐药性的敏感度、特异度、阳性预测值、阴性预测值分别为 88.89%、99.71%、96.00%和 99.13%，两种方法的符合率为 98.91%，Kappa 值为 0.884。
结论 Gene Xpert MTB/RIF 检测结核分枝杆菌和利福平耐药性的敏感度高、特异性好、对生物安全要求低，适合在川东生物安全防护薄弱的基层实验室推广使用。

PO-1097

Identification of New Peptide Biomarkers for Bacterial Bloodstream Infection

Yating Ma、Chengbin Wang
301 PLA Hospital

Background Due to a lack of effffective early diagnostic measures, new diagnostic methods for bacterial bloodstream infections (BSIs) are urgently needed. A protein–peptide profifiling approach can be used to identify novel diagnostic biomarkers of BSIs.
Methods In this study, MALDI-TOF MS and nano-LC/ESI-MS/MS are used to analyze serum peptides. In addition, GO and network analyses are conducted as a means of analyzing these potential protein markers. Finally, the potential biomarkers are verifified in independent clinical samples via ELISA.
Results m/z 1533.8, 2794.3, 3597.3, 5007.3, and 7816.7 reveal an identical trend; the intensity of m/z 1533.8, 2794.3, and 3597.3 are higher in the infection group relative to controls, whereas the intensity of m/z 5007.3 and 7816.7 are lower in the infection group. Four peaks are successfully identifified including ITIH4, KNG1, SAA2, and C3. GO and network analyses fifind these proteins to form an interaction network, which may be correlated with BSI. ELISA results indicate that ITIH4, KNG1, and SAA2 are effffective in diffffferentiating infected from normal control group and the febrile group.
Conclusions These biomarkers have the potential to offffer new insights into the signaling networks underlying the development and progression of BSI.

PO-1098

Excretory/Secretory Products From Trichinella spiralis Adult Worms Attenuated DSS-Induced Colitis in Mice by Driving PD-1-Mediated M2 Macrophage Polarization

Zixia Wang[1,2]、Chunyue Hao[2]、Qinghui Zhuang[2]、Bin Zhan[3]、Ximeng Sun[2]、Jingjing Huang[2]、Yuli Cheng[2]、Xinping Zhu[2]
1. Department of Clinical Laboratory Medicine, Guangdong Provincial People's Hospital, Guangdong Academy of Medical Sciences
2. Department of Medical Microbiology and Parasitology, School of Basic Medical Sciences, Capital Medical University, Beijing, China
3. Department of Pediatrics, National School of Tropical Medicine, Baylor College of Medicine, Houston, TX, United States

Helminth-modulated macrophages contribute to attenuating inflammation in inflammatory bowel diseases. The programmed death 1 (PD-1) protein plays an important role in macrophage polarization and is essential in the maintenance of immune system homeostasis. Here, we investigated the role of PD-1-mediated polarization of M2 macrophages and the protective effects of excretory/secretory products from Trichinella spiralis adult worms (AES) on DSS-induced colitis in mice. Colitis in mice was induced by oral administration of dextran sodium sulfate (DSS) daily. Mice with DSS-induced colitis were treated with T. spiralis AES intraperitoneally and pathological manifestations were evaluated. Macrophages in mice were depleted with liposomal clodronate. Markers for M1-type (iNOS, TNF-α) and M2-type (CD206, Arg-1) macrophages were detected by qRT-PCR and flow cytometry. Macrophage expression of PD-1 was quantified by flow cytometry; RAW 264.7 cells and peritoneal macrophages were used for in vitro tests while PD-1 gene knockout mice were used for in vivo investigation of the role of PD-1 in AES-induced M2 macrophage polarization. Macrophage depletion was found to reduce DSS-induced colitis in mice. Treatment with T. spiralis AES significantly increased macrophage expression of CD206 and Arg-

1 and simultaneously attenuated colitis severity. We found T. spiralis AES to enhance M2 macrophage polarization; these findings were confirmed studying in vitro cultures of RAW264.7 cells and peritoneal macrophages from mice. Further experimentation revealed that AES up-regulated PD-1 expression, primarily on M2 macrophages expressing CD206. The AES-induced M2 polarization was found to be decreased in PD-1 deficient macrophages and the therapeutic effects of AES on colitis was reduced in PD-1 knockout mice. In conclusion, the protective effects of T. spiralis AES on DSS-induced colitis were found to associate with PD-1 up-regulation and M2 macrophage polarization. Thus, PD-1-mediated M2 macrophage polarization is a key mechanism of helminth-induced modulation of the host immune system.

PO-1099

上海市 29 所医疗机构口腔综合治疗台用水非结核分枝杆菌检测及相关因素分析

鲍容、胡必杰、高晓东、郭玮
复旦大学附属中山医院

目的 了解上海市医疗机构口腔综合治疗台治疗用水水路非结核分枝杆菌（NTM）污染现状。
方法 对医疗机构口腔综合治疗台治疗用水进行现场采样，同时通对问卷调查收集治疗台水路消毒情况等相关基础资料。采集水样用滤膜过滤法进行处理，滤膜接种 7H10 培养基培养，疑似菌落经抗酸染色确认后，通过基质辅助激光解析/电离飞行时间质谱（MALDI-TOF MS）方法进行细菌鉴定。
结果 共调查 29 所医疗机构 204 份综合治疗台治疗用水水样，包括超声用水 40 份，手机用水 53 份，三用枪用水 55 份，以及漱口水 56 份。NTM 总检出率为 15.2%（31/204），以产粘液分枝杆菌（17 株，50.0%）和龟分枝杆菌（13 株，38.2%）为主。不同部位 NTM 检出率存在统计学差异（P=0.021），三用枪用水 NTM 检出率最高，为 25.5%；超声用水 NTM 检出率最低，为 2.5%。消毒频率小于 3 个月的水管路 NTM 检出率明显低于其它频率（P＜0.001）。
结论 上海市 29 所医疗机构口腔综合治疗台用水 NTM 检出率为 15.2%。水管路消毒频率是重要影响因素。

PO-1100

评估 EDTA 改良碳青霉烯灭活试验和碳青霉烯酶抑制增强试验检测肠杆菌目细菌产碳青霉烯酶的临床价值

黄声雷、周春妹、曹锦楠、马艳、单玉璋、沈佳瑾、胡必杰、郭玮
复旦大学附属中山医院

目的 评估 EDTA 改良碳青霉烯灭活试验和碳青霉烯酶抑制增强试验检测肠杆菌目细菌产碳青霉烯酶的临床价值。
方法 收集 2020 年 1-12 月碳青霉烯类耐药的肠杆菌目细菌共 195 株，使用微量肉汤稀释法进行体外药敏试验，然后分别用 EDTA 改良碳青霉烯灭活试验和碳青霉烯酶抑制增强试验检测对碳青霉烯类耐药的肠杆菌目产生的碳青霉烯酶进行检测并分型，同时使用 PCR 方法作为金标准检测碳青霉烯酶。
结果 除了对替加环素和粘菌素的敏感率高于 95%外，耐碳青霉烯类的肠杆菌目细菌对其它常见的抗菌药物敏感率均低于 50%。和 PCR 方法比较，EDTA 改良碳青霉烯灭活试验对肠杆菌目产生的碳青霉烯酶分型的特异性和敏感度分别为 95.7%和 100%，碳青霉烯酶抑制增强试验检测的特异性和敏感度分别为 97.5%和 100%。

结论 EDTA 改良碳青霉烯灭活试验和碳青霉烯酶抑制增强试验都能较好区分不同类型的碳青霉烯酶，其中碳青霉烯酶抑制增强试验可以同时检测产 KPC 和金属酶菌株，且操作较 EDTA 改良碳青霉烯灭活试验更为简便，更适合基层微生物实验室常规开展。

PO-1101

荧光染色法与 KOH 湿片法在诊断甲真菌病中的效果比较

王有为、李雪茹、李红霞、赵薇、杨阳
电子科技大学附属医院•四川省人民医院

目的 探索甲真菌病诊断的新方法，提高诊断的准确率和阳性检出率。
方法 87 例疑似甲真菌病的病甲进行处理后分别采用真菌荧光染色法和 KOH 湿片直接镜检，并对检测结果进行比较。
结果 荧光染色法共检出 52 例真菌阳性，而 KOH 湿片法只有 44 例阳性，荧光染色法的阳性检出率明显高于 KOH 湿片法（P<0.05）。
结论 荧光染色法是一种快速、准确的真菌检测方法，值得在皮肤科对真菌感染诊断的推广使用。

PO-1102

miRNA 在革兰阴性菌相关脓毒症中的诊断价值探讨

赵卫东、谢可心、李福兴、王黎、樊玉娟
大理大学第一附属医院

目的 探究 miRNA 在革兰阴性菌(Gram negative, G-)相关脓毒症中的诊断价值，为临床诊断和治疗提供新思路。
方法 选取 2018 年 9 月-2020 年 9 月就诊于大理某医院的 7 名 G-脓毒症患者及 7 名健康体检者作为筛选队列，进行 miRNA 测序及生物信息学分析，并选取 34 名 G-脓毒症患者及 16 名健康体检者作为验证队列，对上调的 miRNA 进行 qRT-PCR 验证，探讨差异表达 miRNA 对 G-脓毒症的诊断价值；根据预后，将 G-脓毒症患者分成生存组(n=18)和死亡组(n=16)，绘制 ROC 曲线，同时与 PCT、CRP、SOFA 评分等经典感染指标做相关性分析，探讨 miRNA 对 G-脓毒症患者的预后诊断价值。
结果 筛选队列中 G-脓毒症组的 hsa-miR-1202、hsa-miR-16-5p、hsa-miR-1299、hsa-miR-486-5p 和 hsa-miR-451a 的表达显著高于对照组(P<0.05)；验证队列中 G-脓毒症患者组 hsa-miR-16-5p、hsa-miR-1202、hsa-miR-486-5p、hsa-miR-451a 水平显著高于对照组；ROC 结果表明 hsa-miR-16-5p 的 AUC 最大为 0.74。对患者预后的判断，死亡组 hsa-miR-16-5p、hsa-miR-486-5p、hsa-miR-451a 水平显著高于生存组(P<0.05)。相关性分析表明，miR-451a 和 SOFA 评分呈正相关(r=0.43, P=0.01)。
结论 血清 hsa-miR-16-5p、hsa-miR-1202、hsa-miR-486-5p、hsa-miR-451a 可能是 G-脓毒症早期诊断的生物标志物，其中 miR-16-5p 的诊断性能最佳；hsa-miR-16-5p、hsa-miR-486-5p、hsa-miR-451a 与 G-脓毒症患者的预后有关，有可能是 G-脓毒症治疗的潜在靶点。

PO-1103

PCT、hs-CRP 及血培养对布鲁氏杆菌感染临床诊断研究

张弛[1]、林国跃*[1]、何雯雯[1]、蔺志强[1]、王子璠[1]、秦莹[1]、段丽[1]、许珺[1]、高辉[1]、张蕊[1]、王钒[1]、姜海[2]
1. 新疆医科大学第八附属医院
2. 中国疾病预防控制中心传染病预防控制所，传染病预防控制国家重点实验室，感染性疾病协同诊治协同创新中心，

目的 探讨新疆地区布鲁氏杆菌感染患者体内炎症因子 PCT、hs-CRP 免疫反应水平和 RF、ESR、ASO 及血培养的临床诊断意义。
方法 采用血培养、“琥”红平板和试管凝集试验等技术对我院住院患者 191 例及正常对照人群进行实验诊断，使用流式及电化学发光法等技术检测多种炎症因子等血液指标，应用 Stata 15.0 软件进行 χ2、t 检验统计处理。
结果（1）hs-CRP、PCT 和血培养阳性率在急性组明显高于慢性组（P<0.05），并且伴有布病脊柱炎和关节炎的患病率在慢性组明显高于急性组（P=0.035）。（2）基于布病感染发病程度的抗体滴度大小与外周血炎症因子免疫反映水平关系中 PCT、hs-CRP、RF、ESR 和血培养阳性率在高滴度组明显高于低滴度表达（P<0.001）。
结论 PCT、hs-CRP 等是布鲁氏菌感染急性期的重要炎症指标，与血培养结合有助于临床早期快速明确诊断、预估病情进展分期和机体免疫状况，对牧区布鲁氏杆菌感染患者及时治疗和防疫具有重要意义。

PO-1104

Combining comparative genomic analysis with machine learning reveals some promising diagnostic markers to identify five common pathogenic nontuberculous mycobacteria

Xinmiao Jia[1]、Linfang Yang[2]、Cuidan Li[3]、Yingchun Xu[1]、Qiwen Yang[1]、Chen Fei[3]
1. Medical Research Center, Peking Union Medical College Hospital
2. 邢台市人民医院
3. 中国科学院北京基因组研究所

Objectives Nontuberculous mycobacteria (NTM) can cause various respiratory diseases and even death in severe cases, and its incidence has increased rapidly worldwide. To date, it’s difficult to use routine diagnostic methods and strain identification to precisely diagnose various types of NTM infections. Thus, it’s essential to search for new diagnostic markers to precisely identify various species of common pathogenic NTMs.
Methods We combined systematic comparative genomics with machine learning (pan-genome/random forest model/ensemble classification) to select diagnostic markers for precisely identifying five common pathogenic NTMs (Mycobacterium kansasii (Mka), Mycobacterium avium (Mav), Mycobacterium intracellular (Min), Mycobacterium chelonae (Mch), Mycobacterium abscessus (Mab)) based on 81 complete genomes (discovery set) and 548 draft genome sequences (validation set).
Results A panel including six genes and two SNPs (nikA, benM, codA, pfkA2, mpr, yjcH, rrl_C2638T, and rrl_A1173G) was selected to simultaneously identify the five pathogenic NTMs with high accuracy. Notably, the panel only containing the six genes also showed a good classification effect on the five NTMs. Additionally, the two panels could precisely differentiate the five NTMs from M. tuberculosis (accuracy > 99%). We also revealed some new marker genes/SNPs/combinations to accurately discriminate any one of the five pathogenic NTMs separately, which provided the possibility of how to diagnose one certain NTM infection precisely.

Conclusions Our research not only reveals novel promising diagnostic markers to promote the development of precision diagnosis in infectious caused by NTMs, but also provides an insight into precisely identifying various genetically close species of pathogens through comparative genomics and machine learning.

PO-1105

基于催化发夹自组装信号放大系统的 SARS-CoV-2 核酸快速检测方法

邹明园[1,2]、吴国球[1,2]
1. 东南大学附属中大医院
2. 东南大学医学院

目的 自新型冠状病毒(SARS-CoV-2)疫情爆发以来，RT-PCR 方法检测 SARS-CoV-2 核酸一直是疑似病例确诊的病原学依据之一，也是确诊病例出院标准的重要参考。然而，RT-PCR 方法在实际应用过程中也暴露出许多缺点和不足。因此，开发一种操作简单、对仪器设备依赖性低、灵敏度高、可实现即时检验的核酸检测方法对疫情防控具有重要意义。
方法 利用催化发夹型 DNA 自组装反应（catalytic hairpin assembly，CHA）与免疫侧向层析试纸条（lateral flow immunoassay strip，LFIA）联合，建立了一种等温无酶、操作简单、快速经济的 SARS-CoV-2 病毒核酸检测方法（CHA-LFIA）。CHA 是一种等温无酶核酸信号放大系统。根据已公开的 SARS-CoV-2 序列进行多序列比对，筛选出 Orf1ab 基因和 N 基因中长度为 21 个碱基的保守序列作为检测靶标，并根据靶向序列设计了两组相应的发夹型 DNA 探针(H1 和 H2)。并分别在探针 H1 的 5’端标记地高辛（Digoxin），在 H2 探针的 5’端标记生物素（Biotin）。最后，利用侧向免疫层析试纸条检测地高辛-生物素双标记的 H1-H2 双链 DNA
结果 该方法的最低检测极限（limit of detection，LoD）为 10aM（≈6000 copies/ml）。该方法对 15 例 SARS-CoV-2 阳性的咽拭子标本均报告为阳性，对 15 例健康人群的咽拭子标本均报告为阴性。与实时荧光 RT-PCR 检测结果的一致性达 100%。
结论 CHA-LFIA 方法无需对样品进行核酸提取等前处理，所需的仪器简单，仅需恒温水浴锅和荧光试纸条定量分析仪。整个检测过程（从采样到报告结果）可在 90 分钟内完成

PO-1106

临床感染患者肠球菌药物敏感性分析

王立新[1]、何正原[2]
1. 天津市天津医院
2. 天津医科大学 临床医学院

目的 了解 2009 年 1 月-2020 年 12 月两年期间临床分离的粪肠球菌和屎肠球菌对多种抗菌药物的敏感性特点及标本来源和临床分布特点，为临床肠球菌感染患者的经验性用药治疗提供依据。
方法 采自法国梅里埃公司的 vitek-2 型全自动细菌鉴定仪、身分证和药敏卡进行细菌鉴定和药敏试验。数据分析用 whonet 5 软件进行分析。
结果 共分离出粪肠球菌 164 株，其中粪肠球菌 99 株，屎肠球菌 65 株。粪肠球菌来源主要源自于肢体矫形器的第二病房和足踝创伤的第二病房。屎肠球菌标本来源主要在肢体矫形二病区和外科 ICU，其标本类型也是以尿和伤口为主。164 株菌株中没有出现对万古霉素中介或耐药的菌株，其粪肠球菌对利奈唑胺、呋喃妥因、替加环素、左氧氟沙星、氨苄西林、环丙沙星、阿莫西林、青霉素和浓度庆大霉素等抗菌药物的敏感率均大于 50%。

结论 对万古霉素和替加环素耐药的肠球菌对利奈唑胺均较敏感，对多种抗生素的耐药率均高于对屎肠球菌粪肠球菌。在临床医治肠球菌感染时，应通过肠球菌感染的结果，酌情使用抗生素，以此来减缓细菌耐药性的发展。

PO-1107

新冠病毒入侵辅助受体 SR-B1 的发现及验证

曹源
解放军第九六〇医院

高密度脂蛋白（High-density lipoprotein，HDL）是脂蛋白的一种，是由蛋白质和脂质组成的大分子复合物。借由 SR-B1 受体，HDL 能够参与胆固醇的逆向转运，将胆固醇从细胞外组织转运到细胞内。在前期的研究中，我们发现 HDL 水平在新型冠状病毒（SARS-CoV-2）感染患者中显著降低，且与疾病的严重程度相关。

在本研究中，我们对新冠病毒 S 蛋白的一级序列进行分析，发现六个可能的胆固醇结合基序。借助微量热泳动（MST）、表面等离子共振（SPR）等技术发现，S 蛋白能够与 HDL 结合。通过流式细胞术等发现 HDL 能显著增强新冠病毒的 S 蛋白与宿主细胞表面结合。当新冠病毒感染体系中加入 HDL 之后，新冠病毒能够与宿主细胞表面的 SR-B1 结合，显著促进新冠病毒与细胞的结合和入侵。此外，敲低 SR-B1 能够抑制新冠病毒对细胞的感染；而将 SR-B1 过表达之后，新冠病毒对细胞的感染显著增强。而且，SR-B1 的抑制剂能够有效抑制新冠病毒对细胞的感染。

本研究揭示了 SR-B1 是新冠病毒的辅助受体，明确了新冠病毒与脂代谢之间的联系，扩展了对新冠病毒感染细胞机制的认识，也为筛选和开发抗新冠病毒感染药物提供了理论基础。该研究成果作为封面文章在 Nature Metabolism 期刊发表。

PO-1108

前带后带现象对虎红凝集试验结果的影响分析

都基爽
吉林金域医学检验所有限公司

目的 布鲁氏菌病是布鲁氏菌侵入人体后引发的以红斑点或瘙痒性丘疹为主要症状的传染病，同时，布鲁氏菌病具有容易传染，病症缺乏特异性等特点。因此，布鲁氏菌的早期发现对于患者的及早治疗以及临床上收集布鲁氏菌病患者的流行病学资料、临床表现等提供有利帮助。以试管凝集试验和 IgG 结果作为参考，分析前带后带现象对虎红凝集试验的影响。

方法 选取 2021.01.01-2021.03.31 期间送检我公司的 1700 例标本进行检测。实验前将冷藏保存的试剂平衡至室温，将试剂充分摇匀后，在室温（18-25℃）条件下进行布鲁氏菌病抗体三项试验。选出虎红凝集试验与其他两项试验结果不相符的结果可疑标本 139 例进行虎红凝集试验复查。复查试验采用 3 种比例，即 30 微升试剂分别与 10 微升、30 微升和 50 微升血清进行凝集试验，结果不同即认为结果受到前带后带现象的干扰。

结果 挑选出的 115 例进行虎红凝集试验进行复查标本中，其中 10 微升血清与 30 微升试剂混合后结果改变的 2 例，50 微升血清与 30 微升试剂混合后结果改变的 89 例，3 种比例结果相同的 16 例，3 种比例结果不完全相同的标本占总数的 79.13%，$P<0.05$,有统计学意义。

结论 前带后带现象会引起布鲁氏菌病虎红凝集试验结果的改变，前带后带现象是免疫学中一种由于抗体或抗原过量而导致所形成的免疫复合物减少，不发生凝集反应的现象。在布鲁氏菌病虎红凝集试验中，也会因为前带后带现象而出现假阴性，故需要在虎红凝集试验结果与其他试验结果不相符时，进行血清与试剂比例的修改，避免因前带后带现象造成的假阴性。

PO-1109

An enzyme-free electrochemiluminescence biosensor for ultrasensitive assay of Group B Streptococci based on self-enhanced luminol complex functionalized CuMn-CeO2 nanospheres

Jiaji Ling
West China Second University Hospital, Sichuan University

Purpose Group B Streptococcus (GBS) is an important pathogen with a high infection rate among adults worldwide, especially pregnant women. Early neonatal infection is usually caused by GBS carried by his or her mother asymptomatically, and it is transmitted vertically to the baby during delivery. Due to the low immunity of the newborn, the infection can cause neonatal sepsis and even death. Thus, early screening of GBS is of vital importance in clinical cases. Therefore, this research is committed to establishing a sensitive and efficient method for early monitoring of GBS, so as to improve the detection rate of GBS in pregnant women and newborns.
Method Based on the self-enhanced PEI-luminol functionalized CuMn-CeO2 signal tag and MNAzyme-mediated target-recycling amplification strategy, an enzyme-free electrochemiluminescence (ECL) biosensor for ultrasensitive detection of GBS was constructed in this work. First, CuMn-CeO2 nanomaterials prepared by hydrothermal method were encapsulated with PEI to make the CuMn-CeO2 endow mass amino groups, which further cross-linked with luminol viaglutaraldehyde to obtain the self-enhanced PEI-luminol functionalized CuMn-CeO2 nanocomposites. Then the resultant CuMn-CeO2-PEI-luminol was served as tracing tag by immobilizing signal probe to obtain the CuMn-CeO2-PEI-luminol-SP. Meanwhile, the thiol-modified capture probe was assembled on the Au modified electrode through Au-thiol bond. In the presence of target DNA, the two partzymes co-recognized with target DNA to form a stable active MNAzyme which further combined with hairpin substrate for cleavage with the assistant of Mg2+ cofactor. After the cleavage reaction, the HP substrate was cleaved into two segments (trigger fragment and the other part), releasing the activated MNAzyme for next cycle. The obtained trigger fragment as a mediator hybridized with SP bioconjugates and CP, making the SP bioconjugates assembled onto the modified electrode. When the modified electrode was detected in the test solution containing H2O2, a high ECL signal was achieved, attributing to the intramolecular enhancing of efficient PEI-luminol luminophore and the intermolecular enhancing of highly catalytic CuMn-CeO2 toward H2O2 oxidation.
Result The developed enzyme-free ECL biosensor showed ultra-sensitivity for target DNA detection with detection limits of 68 aM (synthetic DNA) and 5×102 CFU mL-1 (genomic DNA extracted from GBS strain). More importantly, this biosensor was successfully applied for detection of genomic DNA of GBS extracted from clinical vaginal/anal swabs as low as 320 copies.
Conclusion This proposed strategy not only achieve highly sensitive and efficient detection of target DNA, but also provides a new practical platform for ultra-sensitive detection of GBS in clinical vaginal/anal swabs, and provides a potential universal tool for nucleic acid analysis and clinical diagnosis.

PO-1110

建立一种在碱基淬灭探针技术基础上的二维 PCR 技术检测病人粪便中 4 种微生物实现对 IBD 进展的快速、低成本动态监测

吴璇、李月颖、刘维薇
上海市第十人民医院

目的 通过结合不同荧光基团的探针序列以及多个分别扩增的微生物靶基因带标签和不带标签的引物序列进行单管检测从而实现多通量检测。通过检测梭菌ⅩⅧ等细菌可实现 IBD 患者早诊筛查或者 IBD 进展动态监测和确诊的一个潜在的检测指标，有助于提示患者及时调整饮食结构，合理安排饮食，这将极大的有助于 IBD 患者长期疾病管理和干预。
方法 建立了一种在碱基淬灭探针技术的基础上开创的二维 PCR（Two-dimensional PCR, 2D PCR）技术进行单管闭管检测病人粪便标本中的 4 种微生物，可在单管闭管的反应条件下，结合 PCR 以及熔解曲线分析方法实现同时检测五种微生物，操作简单，反应时间短，成本低，无需额外的产物鉴定仪器设备和复杂的处理过程，结果可靠稳定。
结果 2D PCR 技术实现对 IBD 患者粪便微生物梭菌 XVIII，分支梭菌，螺旋梭菌和噬糖梭菌的检测，快速、低成本动态监测 IBD 患者的菌群微生物变化。
结论 实现一个荧光通道的单管闭管试验同时检测多个靶基因，通过荧光发射波长和 TM 值对每个靶基因进行鉴定。此技术可在单管闭管的反应条件下，结合 PCR 以及熔解曲线分析方法实现同时检测梭菌 XVIII，分支梭菌，螺旋梭菌和噬糖梭菌等 4 种微生物，操作简单，反应时间短，成本低，无需额外的产物鉴定仪器设备和复杂的处理过程，结果可靠稳定。

PO-1111

Prevalence and Antifungal Susceptibility of Candida parapsilosis Species Complex in Eastern China: A 15-Year Retrospective Study by ECIFIG

Jian Guo[1]、min zhang[1]、dan qiao[2]、lingbing zeng[3]、heping xu[4]、wenjuan wu[1]
1. Department of LaboratoryMedicine,Shanghai East Hospital, Tongji University School of Medicine, Shanghai, China
2. 上海交通大学附属瑞金医院
3. 南昌大学第一附属医院
4. 厦门大学附属第一医院

Candida parapsilosis complex is one of the most common non-albicans Candida species that cause candidemia, especially invasive candidiasis. The purpose of this study was to evaluate the antifungal susceptibilities of both colonized and invasive clinical C. parapsilosis complex isolates to 10 drugs: amphotericin (AMB), anidulafungin (AFG), caspofungin (CAS), micafungin (MFG), fluconazole (FLZ), voriconazole (VRZ), itraconazole (ITZ), posaconazole (POZ), 5-flucytosine (FCY), and isaconazole (ISA). In total, 884 C. parapsilosis species complex isolates were gathered between January 2005 and December 2020. C. parapsilosis, Candida metapsilosis, and Candida orthopsilosis accounted for 86.3, 8.1, and 5.5% of the cryptic species, respectively. The resistance/non-wild-type rate of bloodstream C. parapsilosis to the drugs was 3.5%, of C. metapsilosis to AFG and CAS was 7.7%, and of C. orthopsilosis to FLZ and VRZ was 15% and to CAS, MFG, and POZ was 5%. The geometric mean (GM) minimum inhibitory concentrations (MICs) of non-bloodstream C. parapsilosis for CAS (0.555 mg/L), MFG (0.853 mg/L), FLZ (0.816 mg/L), VRZ (0.017 mg/L), ITZ (0.076 mg/L), and POZ (0.042 mg/L) were significantly higher than those of bloodstream C. parapsilosis, for which the GM MICs were 0.464, 0.745, 0.704, 0.015, 0.061, and 0.033 mg/L, respectively ($P < 0.05$). The MIC distribution of the bloodstream C.

parapsilosis strains collected from 2019 to 2020 for VRZ, POZ, and ITZ were 0.018, 0.040, and 0.073 mg/L, significantly higher than those from 2005 to 2018, which were 0.013, 0.028, and 0.052 mg/L ($P < 0.05$). Additionally, MIC distributions of C. parapsilosis with FLZ and the distributions of C. orthopsilosis with ITZ and POZ might be higher than those in Clinical and Laboratory Standards Institute studies. Furthermore, a total of 143 C. parapsilosis complex isolates showed great susceptibility to ISA. Overall, antifungal treatment of the non-bloodstream C. parapsilosis complex isolates should be managed and improved. The clinicians are suggested to pay more attention on azoles usage for the C. parapsilosis complex isolates. In addition, establishing the epidemiological cutoff values (ECVs) for azoles used in Eastern China may offer better guidance for clinical treatments. Although ISA acts on the same target as other azoles, it may be used as an alternative therapy for cases caused by FLZ- or VRZ-resistant C. parapsilosis complex strains.

PO-1112

Synergistic activity and biofilm formation effect of colistin combined with PFK-158 against colistin-resistant Gram-negative bacteria

Liqiong Chen[1]、Kaihang Yu[2]、Lijiang Chen[1]、Xiangkuo Zheng[1]、Na Huang[1]、Yishuai Lin[2]、Huaiyu Jia[1]、Wenli Liao[1]、Jianming Cao[2]、Tieli Zhou[1]

1. Department of Clinical Laboratory, the First Affiliated Hospital of Wenzhou Medical University, Wenzhou, Zhejiang province, China

2. 温州医科大学

Purpose The emergence of colistin resistance among Gram-negative bacteria (GNB) poses a serious public health threat. Therefore, it is necessary to enhance the antibacterial activity of colistin through the combination with other drugs. In this study, we demonstrated the synergistic activity and the possible synergy mechanism of colistin with PFK-158 against colistin-resistant GNB, including non-fermenting bacteria and *Enterobacteriaceae*.

Method 31 colistin-resistant GNB, including *Pseudomonas aeruginosa* (n = 9), *Acinetobacteri baumanni* (n = 5), *Escherichia coli* (n = 8) and *Klebsiella pneumoniae* (n = 9), were collected as the experimental strains and the minimum inhibitory concentrations (MICs) of colistin, other routine antimicrobial agents and PFK-158 against all strains were determined by the broth microdilution method. The synergistic activity of colistin with PFK-158 was assessed by the checkerboard assay and time-kill assay. The biofilm formation assay and scanning electron microscopy were used to demonstrate the biofilm formation effect of colistin with PFK-158 against colistin-resistant GNB.

Results The results of the checkerboard assay showed that when colistin was used in combination with PFK-158, synergistic activity was observed against the 31 colistin-resistant GNB. The time-kill assay presented a significant killing activity of colistin with PFK-158 against the 9 colistin-resistant GNB selected randomly, including *Pseudomonas aeruginosa* (n = 6), *Acinetobacteri baumanni* (n = 1), *Escherichia coli* (n = 1) and *Klebsiella pneumoniae* (n = 1). The biofilm formation assay and scanning electron microscopy showed that colistin with PFK-158 can effectively suppress the formations of biofilms and reduce the cell arrangement density of biofilms against most experimented strains.

Conclusion The results of the performed experiments suggest that the combination of colistin and PFK-158 may be a potential new choice as a new antibiofilm group for the treatment of infections caused by the colistin-resistant GNB.

PO-1113

Clinical Study of Innovative Antifungal susceptibility Test

Yehuan Zheng[1]、Guangyu Fu[1]、Yi Zhang[2]、Yi Li[3]
1. Zhengzhou Autobio Diagnostics Co., Ltd.
2. 郑州市中心医院
3. 河南省人民医院

Introduction With the aging of the population and the improvement of organ transplantation and anti-tumor treatment, Candida infection may become one of the main factors threatening the health of susceptible people. The non-standard application of antifungal drugs has led to an increase in drug-resistant strains.
Aim To evaluate the clinical accuracy Innovative Antifungal susceptibility Test.
Methodology A total of 218 strains of Candida were isolated from Henan Provincial People's Hospital and Zhengzhou Central Hospital from April 2019 to September 2019. Ten antifungal drugs are tested respectively by Autobio Fungal Antimicrobial Susceptibility Test and broth microdilution method. Minimum Inhibitory Concentration (MIC) value of Essential Agreement (EA) and Categorical Agreement (CA) are applied for analysis and result interpretation.
Results For 10 of antifungal drugs, Minimum Inhibitory Concentration (MIC) value of Essential Agreement (EA) between Fungal Antimicrobial Susceptibility Test and Broth Micordilution Method is 98.81% (95.41% - 99.54%). CA of Anidulafungin (ANI) is 98.10%; CA of Caspofungin (CAS) is 95.73%; CA of Micafungin (MIF) is 97.63%; CA of Amphotericin B (AMB) is 98.56%; CA of Itraconazole (ITR) is 94.71%; CA of Fluconazole (FLU) is 97.01%; CA of Voriconazole (VOR) is 99.44%; CA of Posaconazole (POS) is 97.05%.
Conclusion Autobio Fungal Antimicrobial Susceptibility Test generates accuracy and reliable Minimum Inhibitory Concentration (MIC) value and in vitro sensitivity, which can fully meet the requirements of clinical and laboratory.

PO-1114

Update on laboratory detection methods for brucellosis

Fengfeng Zhao
Department of Clinical Laboratory of Zhongda Hospital, Southeast University

Obejective The persistent worldwide prevalence of human brucellosis causes serious public health concerns and economic loss to communities. The multisystem involvement and the protean and unusual clinical presentations of the disease pose significant diagnostic challenges. The clinical features are non-specific and can overlap with a wide spectrum of other infectious and non-infectious diseases, leading to brucellosis being labelled the 'disease of mistakes'. Protracted chronicity and serious complications can result and mislead physicians onto a path of costly laboratory and radiological investigations.
Medthod To reach a diagnosis clinicians must use a wide range of non-specific routine haematological and biochemical tests in addition to Brucella-specific assays. The latter are microbiological (culture), serological (e.g. slide or tube agglutination, Coombs test, immunocapture agglutination, Brucellacapt, immunochromatographic lateral flow, enzyme-linked immunosorbent assays and the indirect fluorescent antibody test) and molecular (e.g. polymerase chain reaction (PCR) and real-time PCR).
Results Each of these tests has advantages and limitations, and thus requires careful interpretation. Since brucellosis can have several presentations and phases(acute, subacute, chronic, relapsed, active and inactive), the search for reliable, discriminatory diagnostic and prognostic markers, especially for monitoring disease evolution, are ongoing.
Conclusion Although much progress has been made, further challenges remain to the accurate diagnosis of this historic but still common global zoonotic disease.

PO-1115

Alifax HB&L 微生物培养联合质谱技术快速鉴定血培养阳性菌的方法学研究

李晓杰
中山大学附属第三医院

目的 建立 Alifax HB&L 微生物培养联合质谱技术（MALDI-TOF MS）达到快速增菌鉴定血培养阳性菌的方法并评估其符合率。
方法 收集 2019 年 8 月～2020 年 1 月中山大学附属第三医院 Versa TREK 全自动快速微生物培养系统报阳性的血培养标本 101 例，从血培养瓶中提取内容物到 Alifax HB&L 微生物培养仪配套的体液培养基中，放进 Alifax HB&L 微生物培养仪中进行增菌培养。Alifax HB&L 微生物培养仪报阳，采用 MALDI-TOF MS 技术对待测菌株进行快速鉴定；同时采用常规实验室鉴定流程对待测菌进行转种培养及鉴定，比较两者之间的鉴定符合率。
结果 101 例血培养标本中，有 98 例单菌株血液感染，其中有 84 例（85.7%）鉴定正确，无准确鉴定结果的有 6 例（6.1%），鉴定不出的有 7 例（7.1%），错误鉴定的有 1 例。1 例两种菌株混合感染，两种菌株均鉴定至“种”水平。有 2 例鉴定结果与镜检结果不相符；Alifax HB&L 微生物培养联合 MALDI-TOF MS 较常规法用时缩短约 629 分钟，其中革兰阴性菌采用该方法鉴定菌种更具有优势，能缩短的培养鉴定时间更多。
结论 血培养阳性菌快速培养鉴定技术较常规培养方法快速、操作步骤简单，单一菌种鉴定结果准确，对革兰阴性菌的鉴定符合率高，可大幅缩短培养鉴定时间。

PO-1116

耐碳青霉烯类肺炎克雷伯菌的耐药基因及消毒剂的研究

谢屿平、曹颖平
福建医科大学附属协和医院

目的 分析福建医科大学附属协和医院 2014 年-2015 年收集的耐碳青霉烯类肺炎克雷伯菌（CR-KP）的耐药基因及消毒剂基因，为 CR-KP 的流行与传播提供实验室依据，并指导临床科学用药与消毒。
方法 通过 PCR 及测序法检测 CR-KP 碳青霉烯酶基因，并进行多位点序列分型（MLST），采用 PCR 扩增耐消毒剂基因，采用微量肉汤稀释法检测常用耐消毒剂的最低抑菌浓度（MIC）。
结果 对 101 株耐碳青霉烯类肺炎克雷伯菌进行碳青霉烯酶基因的检测发现，KPC-2 检出率最高，阳性率为 67.3%（68/101）；其次为 IMP-4 基因占 5.0%（5/101）；NDM-1 阳性率为 1.0%（1/101），其中有 1 株 CR-KP 同时携带 KPC-2 和 NDM-1 基因。101 株 CR-KP 中未发现 SME、GES、IMI、VIM、SIM、GIM、SPM 和 OXA-48。在 MLST 的检测结果中，68 株产 KPC-2 酶的肺炎克雷伯菌均为 ST11；在 5 株产 IMP-4 的肺炎克雷伯菌中，3 株为 ST26，2[1]株为 ST334。耐消毒剂基因检测结果中，检出 qacE△1 95 株(94.1%)， qacF/H/I 53 株（52.5%）,qacC 34 株（33.7%）,qacE 2 株（2.0%）。
结论 本院临床分离的 CR-KP 耐药基因主要是 KPC-2 和 IMP-4 基因。耐消毒剂基因的高检出率可能使菌株对消毒剂产生抗性，需引起临床重视。

PO-1117

2016-2019 年南疆三地州铜绿假单胞菌耐药性监测

热那古·艾山、玛依拉·阿布都热依木、党楠
喀什地区第二人民医院

目的 了解 2016 年 2019 年南疆三地州临床上铜绿假单胞菌的分布及耐药变迁，为临床合理使用抗生素提供依据。
方法 通过全自动细菌鉴定分析仪 VITEK-2 compact 和 VITEK-MS 对临床分离株进行菌株鉴定并进行药敏试验，K-B 纸片法做补充。
结果 4 年间共检出铜绿假单胞菌 2131 株，占全部标本检测总阳性率的 5%（2131/39767），占革兰阴性杆菌的 7.9% (2131/26964)。4 年来铜绿假单胞菌分离率位于革兰阴性菌的第四位，以痰标本为主，约占 61.9%，其次为尿标本，约为 11.4%。对铜绿假单胞菌有较高活性的抗生素包括头孢哌酮/舒巴坦、哌拉西林/他唑巴坦、头孢他啶、头孢吡肟、阿米卡星、庆大霉素 、环丙沙星、左旋氧氟沙星敏感率均大于 82%。
结论 铜绿假单胞菌已成为临床最常见的致病菌之一， 南疆三地州检出的铜绿假单胞菌耐药情况十分严峻，为了提高抗菌药物的治疗效果，应连续监测本地区的抗菌药物的耐药情况，根据药敏结果合理选用抗菌药物。

PO-1118

A Real-time Duplex Reverse Transcription Multienzyme Isothermal Rapid Amplification Assay for Detecting Severe Acute Respiratory Syndrome Coronavirus2 (SARS-CoV-2)

Jin Li
Department of Clinical Laboratory Medicine, Institute of Surgery Research, Daping Hospital, Army Medical University

Until now, there is still no effective cure for coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus2 (SARS-CoV-2). A rapid and simple method is necessary for testing suspected specimens and screening population. In order to better monitor sample effectiveness, this study describes a method to detect nucleocapsid protein gene (N gene) of SARS-CoV-2 and human ACTB gene employing a real-time duplex reverse transcription multienzyme isothermal rapid amplification (RT-MIRA) assay. Cross-reactions were not observed to other pathogens and the detection limit was 100 copies/reaction. Using simulated clinical samples to further test established assay and the amplification process can be completed within 20 min at 42℃. The above results showed that the real-time duplex RT-MIRA assay is expected to be further optimized and evaluated in the detection of SARS-CoV-2 confirmed cases.

PO-1119

MALDI-TOF MS 快速检测耐甲氧西林金黄色葡萄球菌的方法研究

唐克文、汤冬玲、汪倩钰、李从荣
武汉大学人民医院

目的 评价基质辅助激光解吸电离飞行时间质谱（Matrix-assisted laser desorption ionization time-of-flight mass spectrometry，MALDI-TOF MS）快速检测 MRSA 的应用价值，寻找辨别 MRSA 和 MSSA 的质谱特征峰。

方法 收集 2018 年 4 月至 2019 年 6 月自武汉大学人民医院临床患者分离的 214 株金黄色葡萄球菌作为实验菌株，采用头孢西丁纸片扩散法和 mecA 基因检测法区分 MRSA 和 MSSA 菌株。利用 MALDI-TOF MS 采集菌株蛋白指纹图谱，采用三种分组方式分别结合 ClinProTool 软件中遗传算法（Genetic Algorithm，GA）、监督神经网络算法（Supervised Neural Network algorithm，SNN）和快速分类算法（Quick Classification algorithm，QC）建立 MRSA 快速检测模型，利用软件进行峰值统计和计算，获得辨别 MRSA 和 MSSA 的特征峰并优化模型，同时验证模型对 MRSA 的检测效果。

结果 三种分组方式分别结合三种机器学习算法共获得九个基于 MALDI-TOF MS 的 MRSA 检测模型，其中 GA 算法获得最高交叉验证值和识别能力值，分别为 95.82%、98.13%。分析九个基础模型共获得 3 056m/z、4 322m/z 等九个特征峰，采用九个特征峰结合 GA 算法优化模型，最终优化模型交叉验证值由 95.82％增加为 96.68％。经验证，最终优化模型的特异性由 90.00％提高到 98.33％，准确性由 88.89％提高到 91.98％。

结论 MALDI-TOF MS 与机器学习算法的结合是一种高效而客观的分类工具，可应用于 MRSA 的快速筛查且具有很高的检测性能，与常规药物敏感实验相比具有快速、低成本等明显优势。

PO-1120

某院 4 年引起血流感染的念珠菌分布与阳性报警时间的应用分析

曹敬荣、王岩、陈典典、谢威、李文军、段园园、刘云屹、闵嵘、王培昌
首都医科大学宣武医院

目的 了解引起血流感染的念珠菌的分布及阳性报警时间（TTP）特点，为临床及早抗真菌治疗提供依据。

方法 Whonet5.6 软件回顾性分析某院 4 年血培养分离的念珠菌的菌种分布等临床资料，分析不同念珠菌的 TTP 特点。

结果 4 年间共收到血培养 45466 瓶，真菌阳性报警 226 瓶，阳性检出率为 0.51%，其中单一菌阳性 218 瓶，复数菌 8 瓶；患者年龄 26-92 岁（平均 64.67±16.03 岁），≥60 岁者占 70.33%（64/91），男女比例 2.6:1；共分离出念珠菌 234 株，以白念珠菌（39.74%，93/234）、热带念珠菌（26.50%,62/234）、近平滑念珠菌（22.22%，52/234）和光滑念珠菌（8.97%,21/234）为主。所有念珠菌的平均 TTP 为 36.9±18.04h，其中热带念珠菌 TTP 最短（25.85±12.00h），显著短于近平滑念珠菌（34.27±13.50h）、白念珠菌（41.14±17.80h）和光滑念珠菌的 TTP 53.26±24.90h（t=3.76，p=0.025）；不同念珠菌在性别、年龄及各科室的构成比均有显著差异，在外科和外科 ICU 的分离率显著高于内科和内科 ICU（x2=19.14、4.66，p=0.03,0.025）；4 年中各念珠菌构成比由白念珠菌为主变迁为非白念珠菌为主；热带念珠菌在 24h 内报警阳性占 50.0%，其 TTP 明显短于其它念珠菌（x2=16.80，p=0.03），近平滑念珠菌和热带念珠菌＞90%菌株在 48h 内报警阳性，而光滑念珠菌则在≥72h 报警阳性占 33.33%，TTP 显著长于其它念珠菌（x2=6.42，p=0.02）。

结论 我院念珠菌血流感染病原菌构成比中非白念珠菌增加，TTP 对初步判断血培养念珠菌菌种有一定的提示意义，对及早正确的抗真菌治疗尤为重要。

PO-1121

The response of PD-1–based immunotherapy for non-small cell lung cancer altering by gut microbiome

Daqiang He[1]、Xing Li[2]、Rui An[1]、Lihong Wang[2]、Yun Wang[2]、Mingfeng Jiang[2]、Xueqin Chen[2]、Xianjun Wang[1]
1. Affiliated Hangzhou First People's Hospital, Zhejiang University School of Medicine
2. 浙江大学医学院附属杭州市肿瘤医院

Purpose To identify a group that has specific effects of gut microbiome on PD-1 based immunotherapy for non-small cell lung cancer (NSCLC).
Methods We performed a study on patients with advanced NSCLC who received PD-1 mAb 6 months after one or several prior therapies, and we combined blood immune-related factors of the participants and fecal 16s rRNA sequencing at baseline to investigate the diversity and composition of the gut microbiota. We also compare the differences in relative abundancies at the genus level of gut microbiome, and we used spearman rank correlation coefficient analysis of genus abundance in relation to blood immune-related factors.
Results 16s rRNA sequencing showed that a clear difference between the bacterial community diversity and compositions of stable disease (SD) and disease progression (PD) patients. Comparison of the differences in relative abundances at the genus level showed that Escberichia-Shlgella, Akermansia and Olsenella in SD groups were significantly higher compared to the PD group. SD groups had significantly higher IL-12 and INF-γ than those in the PD groups. Interestingly, numbers of white blood cells as well as sorted cells in SD groups were higher than those in the PD groups. Spearman rank correlation coefficient analysis showed that Escberichia-Shlgella was positively correlated with IL-12，INF-γ and BASO. Akermansia was positively correlated with monocytes.
Conclusions The response of PD-1–based immunotherapy for NSCLC altering by gut microbiome diversity and composition. Escberichia-Shlgella and Akermansia may have specific effects on PD-1 inhibitory immunotherapy for NSCLC.

PO-1122

基质辅助激光解吸电离飞行时间质谱技术对分枝杆菌液体培养系统菌种鉴定的临床研究

杜岩青
天津市海河医院

目的 应用基质辅助激光解吸电离飞行时间质谱(matrix assisted laser desorption ionization time of flight mass spectrometry，MALDI-TOF MS)对 BactecTM MGITTM 960 液体培养出的阳性培养物进行高通量、快速、准确的菌种鉴定，为临床早期、精准治疗提供病原学依据。
方法 选取我院 BactecTM MGITTM 960 分枝杆菌快速液体培养的阳性培养物为研究对象，通过不同的孵育时间、不同大小的研磨珠处理、不同的破壁方式摸索出 MALDI-TOF MS 对 BactecTM MGITTM 960 阳性培养物鉴定的“最优处理方法”，并将所有结果与基因芯片法菌种鉴定做参照进行比对，鉴定不一致的结果通过基因测序确认。
结果 BactecTM MGITTM 960 液体培养报阳性后增加孵育时间可提高检出率及鉴定分值，同时使用 0.5mm 的氧化锆珠研磨，使用超声震荡混匀处理，鉴定效果最佳。鉴定结果方面，液体系统报阳

的 420 份阳性标本，基因芯片法鉴定结果为结核分枝杆菌占 69.05%(290/420)，非结核菌占 28.81%(121/420)，9 例未鉴定出，未鉴定占 2.14%（9/420），错误鉴定占 0.95%（4/420），总鉴定率为 97.86%（411/420）；采用 MALDI-TOF MS 质谱鉴定 420 份阳性标本中鉴定出 419 例，其中结核分枝杆菌占 69.05%(290/420)，非结核占 30.00%(126/420)，星型奴卡菌 0.48%（2/420），巴西奴卡菌占 0.24%（1/420），1 例未鉴定出，总鉴定率为 99.76%。两种方法比较 p 值>0.05 没有统计学意义。

结论 质谱做为高通量的微生物鉴定手段对实验室工作起到了一个巨大的推动作用，广泛应用能助力结核病的快速诊断。

PO-1123

MALDI-TOF MS 自建数据库对丝状真菌临床分离株鉴定能力的评估

李颖、曹敬荣、王培昌
首都医科大学宣武医院

目的 评估 MALDI-TOF MS 自建数据库对丝状真菌临床分离株的鉴定能力。

方法 分子测序技术明确 41 株拟建库丝状真菌的种属信息；采用标准提取法分别对拟建库菌株幼稚菌落和成熟菌落进行 MALDI-TOF MS 自建数据库处理；另采用 236 株丝状真菌临床分离株评估该自建数据库的鉴定能力。

结果 41 株建库丝状真菌分属于 10 属 25 种；自建数据库包含 82 张参考质谱峰图。采用 MALDI-TOF MS 自建数据库可将评估菌株种水平鉴定率由商业数据库的 29.2% (69/236) 提升至 67.5% (159/236) ；将自建数据库与商业数据库联合后，评估菌株种水平鉴定率为 76.3% (180/236) 且无错误鉴定情况。与形态学方法相比，MALDI-TOF MS 自建数据库对临床常见曲霉分离株的鉴定无优势，对于曲霉少见种和非曲霉丝状真菌，其种水平鉴定率为 61.8% (34/55)，显著优于形态学方法 (16.4%，9/55)。

结论 MALDI-TOF MS 自建数据库有助于提高实验室丝状真菌鉴定能力，在形态学方法鉴定困难的少见丝状真菌鉴定方面其作用更为显著。

PO-1124

分枝杆菌快速诊断实验室方案-大数据回顾性研究

彭静、汪峰、孙自镛
华中科技大学同济医学院附属同济医院

背景 肺结核（PTB）的及时准确诊断仍是临床实践的一大难题。本研究旨在建立一种在真实环境下优化的 PTB 快速诊断策略。

方法 回顾性分析同济医学院附属同济医院 28171 例疑似 PTB 的成人住院患者的病历资料。支气管肺泡灌洗液（BALF）和/或痰用于抗酸杆菌（AFB）涂片、Xpert MTB/RIF（Xpert）检测和培养，外周血单个核细胞（PBMC）用于 T-SPOT.TB 检测。以分枝杆菌培养阳性作为参考标准，我们分析了标本类型对检测结果的影响，分析了诊断 PTB 所需的涂片次数，并评价上述检测方法单独或联合检测诊断 PTB 和非结核分枝杆菌（NTM）感染的能力。

结果 痰和 BALF 在 AFB 涂片或 Xpert 检测中具有中等至较高的一致性，BALF 的阳性检出率较高。3-4 次涂片的敏感性高于 1-2 次涂片。同时联合应用 AFB 和 Xpert 可将 44/51 例 AFB+/Xpert+和 6/7 例 AFB+/Xpert-分别正确诊断为 PTB 和 NTM 感染。当与 AFB/Xpert 序贯联合使用时，T-Spot 在 AFB+或 Xpert+的患者中作用有限。对于 AFB-/Xpert-患者，T-SPOTMDC（厂家给定的阳性判断值）显示高的阴性预测值（99.1%）和次佳敏感性（74.4%），而 TBAg/PHA（结核分枝杆菌特

异性抗原与植物血凝素斑点形成细胞的比值，一种改进的计算 T-SPOT.TB 检测结果的方法）≥0.3 显示高的特异性高（95.7%）和相对较低的敏感性（16.3%）。
结论 在结核高负担的真实环境中，同时对痰和/或 BALF 进行 AFB 涂片（至少 3 次）和 Xpert 检测有助于快速诊断 PTB 和 NTM 感染。如果可以，BALF 是 AFB 涂片和 Xpert 检测的首选样本类型。此外，PBMC T-SPOTMDC 和 TBAg/PHA 比值对 AFB-/Xpert-患者的 PTB 诊断具有辅助作用（分别具有中度排除 PTB 和判定 PTB 的作用）。

PO-1125

Comprehensive pathogen identification, antibiotic resistance and virulence genes prediction directly from simulated blood samples and positive blood cultures by Nanopore metagenomic sequencing

Menglan Zhou、Qiwen Yang、Yingchun Xu
Peking Union Medical College Hospital

Bloodstream infection is a major cause of morbidity and mortality worldwide. We explored whether MinION Nanopore sequencing could accelerate diagnosis, resistance and virulence profiling prediction in simulated blood samples and blood cultures. One milliliter of healthy blood samples from direct spike (sample 1), anaerobic (sample 2) and aerobic (sample 3) blood culture with initial inoculation of ~30 CFU/ml of a clinically isolated Klebsiella pneumoniae strain, were subjected to DNA extraction and Nanopore sequencing. Hybrid assembly of Illumina and Nanopore reads from pure colonies of the isolate (sample 4) was used as a reference for comparison. Hybrid assembly of the reference genome identified a total of 39 antibiotic resistance genes and 77 virulence genes through alignment with the CARD and VFDB database. Nanopore correctly detected K. pneumoniae in all three blood samples. Fastest identification was achieved within 8h from specimen to result in sample 1 without blood culture. However, direct sequencing in sample 1 only identified seven resistance genes (20.6%) but 28 genes in sample 2-4 (82.4%) compared to reference within 2h sequencing time. Similarly, 11 (14.3%) and 74 (96.1%) of the virulence genes were detected in sample 1 and sample 2-4 within 2h sequencing time, respectively. Direct Nanopore sequencing from positive blood cultures allowed comprehensive pathogen identification, resistance and virulence genes prediction within 2h which is promising to be used in point-of-care clinical settings.

PO-1126

临床常见四种曲霉菌的分子检测方法的建立及其临床验证

许婉怡、杨洋、张磊、陈敬贤
广州金域医学检验中心

各种曲霉菌一直是免疫低下病人出现致死性感染的重要病原体。 高危人群包括长期粒细胞减少、造血干细胞移植、实体器官移植、先天或后天免疫缺陷、糖皮质激素使用者等。曲霉感染主要有侵袭性曲霉病、多种慢性曲霉病以及过敏性曲霉病三种临床类型，它们的实验诊断方法包括真菌培养、抗原检测（G 试验）、分子诊断、组织病理。由于侵袭性曲霉病病情进展快，给诊断只留取狭窄的时间窗。因此快速、准确、敏感的分子检测方法为临床所需要。不同曲霉菌对抗真菌药物的敏感性不尽相同，譬如临床最常见的烟曲霉近年来对唑类抗真菌药物耐药的报道不断增加，而土曲霉对各种二性霉素制剂均不敏感。因此我们在建立了能够检出各种曲霉菌的泛曲霉分子检测法以后，进一步研发了临床常见的四种曲霉菌（烟曲霉、黄曲霉、黑曲霉和土曲霉）各自的分子检测方法。

它们均为基于 Taqman 探针的实时荧光 PCR 方法，反应条件一致，因此可以选择几种同时应用，以便一次采样一次鉴定到菌种。泛曲霉检测法的线性范围 10^3～10^8 拷贝/微升（最小检测浓度 1000 拷贝/微升）。烟曲霉，黄曲霉，黑曲霉，土曲霉分子检测方法的线性范围在 10^2～10^8 拷贝/微升（最小检测浓度 100～1000 拷贝/微升）。干扰实验表明，B 族链球菌、肺炎链球菌、化脓链球菌、卡他链球菌、表皮葡萄球菌、金葡、肺炎克雷伯菌、铜绿假单胞菌、百日咳杆菌、D 群沙门氏菌、白念、光滑念、近平滑念、结核杆菌、烟曲霉、黄曲霉、黑曲霉、土曲霉，以及腺病毒、鼻病毒、副流感病毒、呼吸道合胞病毒对这几个曲霉菌的实时荧光 PCR 都没有干扰。这些检测方法的临床验证正在进行之中。

PO-1127

1976 例 β-半乳甘露聚糖和 2012 例曲霉菌抗原结果分析

陈振朋、张维
西安金域医学检验所有限公司

目的 β-半乳甘露聚糖（G 试验）和曲霉菌抗原（GM 试验）作为真菌早期感染的血清学标志，在真菌早期感染的筛查中，有着重要的应用价值。
方法 统计了陕西省的 2012 例曲霉菌抗原和 1976 例 β-半乳甘露聚糖的病人检测结果。曲霉菌抗原使用竞争法检测，β-半乳甘露聚糖使用显色法检测，所用试剂由丹娜生物提供。并对以上统计结果进行分类分析。
结果 2012 例曲霉菌抗原结果，阳性结果为 408 例，占比为 20.3%；1976 例 β-半乳甘露聚糖，阳性结果 304 例，占比 15.4%。同时送检曲霉菌抗原和 β-半乳甘露聚糖的病人为 508 例，曲霉菌抗原结果阳性、β-半乳甘露聚糖阴性者 72 例，占比 14.2%，曲霉菌抗原结果阴性、β-半乳甘露聚糖阳性者 56 例，占比 11%，两项试验均阳性者 32 例，占比 6.3%。
结论 血清中的 β-半乳甘露聚糖在某些侵袭性真菌感染时升高，尤其是对念珠菌血症，是首选的筛查指标；半乳甘露聚糖（GM）从薄弱的菌丝顶端释放，曲霉菌感染的患者血液内存在 GM，而且常于临床症状和影像学出现异常之前数日出现。因此，GM 试验可用于曲霉菌感染的早期诊断的筛查指标。两个相试验同时进行，有助于进一步明确感染类型：G 试验阳性、GM 试验阳性：曲霉菌和青霉感染；G 试验阳性、GM 试验阴性：排除 GM 假阴性后，念珠菌，镰刀菌属；G 试验阴性、GM 试验阳性：排除 G 试验假阴性后，隐球菌属感染。

PO-1128

Multilocus Sequence Typing Reveals Clonality of Fluconazole-Nonsusceptible Candida tropicalis: A Study From Wuhan to the Global

Qianyu Wang
Renmin Hospital of Wuhan University

Candida tropicalis is a globally distributed human pathogenic yeast, and its increasing resistance to azoles makes clinical treatment difficult. In this study, we investigated the clinical features, azole resistance and genetic relatedness of 87 C. tropicalis isolates from central China and combined with the global database to explore the relationship between genetic information and fluconazole susceptibility. Of the 55 diploid sequence types (DSTs) identified by multilocus sequence typing (MLST), 27 DSTs were new to the C. tropicalis MLST database. Fluconazole-nonsusceptible (FNS) isolates were genetically closely related. goeBURST analysis showed that DST225, DST376, DST506, and DST546 formed a distinct and unique FNS clonal complex (CC) in Wuhan. The local FNS CC belongs to the large FNS CC (CC2) in China, in which the putative

founder DST225 has been reported from the environment. The three most prevalent types (DST506, DST525, and DST546) in Wuhan had high minimum inhibitory concentrations (MICs) for antifungal azoles, and the six possible nosocomial transmissions we captured were all FNS strains, most of which were from CC2. Unique FNS CCs have been found in Singapore (CC8) and India (CC17) and are close to China's CC2 in the minimum spanning tree. There were no FNS CCs outside Asia. This study is the first to reveal a significant correlation between genetic information and fluconazole susceptibility worldwide and to trace geographical locations, which is of great value for molecular epidemiological surveillance and azole-resistance study of C. tropicalis globally.

PO-1129

三叶青提取物 TH-w3 对金黄色葡萄球菌微生物膜的抑制和清除作用

孙丹[1]、翁远珍[2,3]、祝宇翀[2]、刘军权[2,3]、单宇[2]
1. 乔司街道社区卫生服务中心
2. 杭州金域医学检验所有限公司
3. 杭州下城区中西医结合医院

探究三叶青提取物 TH-w3 对金黄色葡萄球菌微生物膜形成的抑制和清除作用。**方法** 从本实验室临床分离培养并保存的 300 株金黄色葡萄球菌中选取各 20 株成膜能力阳性的 MRSA 和 MSSA 菌株，菌落计数法绘制金黄色葡萄球菌生物膜形成曲线，二倍稀释法肉眼观察加吸光度检测测定最小抑菌浓度，结晶紫法研究三叶青提取物 TH-w3 对金黄色葡萄球菌生物膜的抑制及清除作用。**结果** 有 MRSA 菌株 202 株（67.3%），MRSA 菌株成膜阳性率 60.9%，有 MSSA 菌株 98 株（32.7%），MSSA 菌株成膜阳性率 20.4%，两者差异比较有统计学意义；三叶青提取物 TH-w3 对"MRSA(+)组"和"MSSA(+)组"菌株的 MIC 均为 8.00μg/mL；三叶青提取物 TH-w3 对"MRSA(+)组"和"MSSA(+)组"菌株生物膜的抑制和清除作用均具有浓度依赖性，在 2MIC 浓度下抑制率和清除率最高，可达 90%以上。**结论** 三叶青提取物 TH-w3 对金黄色葡萄球菌微生物膜有一定的抑制和清除作用，有重要的研究开发和临床应用价值。

PO-1130

恶性肿瘤患者合并胆道感染的病原菌分布和耐药性分析

张秀色
天津医科大学肿瘤医院

目的 分析 2010-2017 年恶性肿瘤患者胆汁中分离病原菌的分布及耐药性，为临床合理应用抗生素提供帮助。
方法 细菌、真菌鉴定及细菌药敏试验均采用 Vitek2-Compact 系统，真菌药敏试验采用 ATB FUNGUS 试剂盒，采用 Whonet 5.6 软件对数据进行统计分析。
结果 2010-2017 年 678 份胆汁培养阳性标本共分离出 80 种 1079 株病原菌。胆道感染患者主要分布于肝胆肿瘤科（223，47.1%）、胰腺肿瘤科（103，21.8%）、介入治疗科（73，15.4%）、生物治疗科（22，4.7%）和消化肿瘤内科（17，3.6%）。革兰阴性菌、革兰阳性菌和酵母菌的构成比为 48.6%（524/1079）、44.5%（480/1079）、6.9%（75/1079）。革兰阳性菌对万古霉素、替加环素、利奈唑胺高度敏感。凝固酶阴性葡萄球菌（CNS）和金黄色葡萄球菌耐甲氧西林（MRCNS 和 MRSA）分别占 47.6%和 33.3%。大肠埃希菌和肺炎克雷伯菌产 ESBLs 率分别为 46%和 24.8%。革兰阴性菌对碳青霉烯类、阿米卡星及哌拉西林/他唑巴坦高度敏感。所有真菌对常用抗真菌药物的耐药率均较低。

结论 恶性肿瘤患者胆汁中分离的病原菌种类复杂，定期进行耐药性分析能够为临床合理使用抗生素提供帮助。

PO-1131

中国西部人群 7p21.3 基因座的遗传多态性与肺结核合并肺外结核的进展相关性分析

刘国烨[1]、梁渊[3]、王茜[1]、董惠霞[1]、汪强虎[3]、严虹[2]
1. 南京医科大学附属脑科医院
2. 南京医科大学第二附属医院
3. 南京医科大学

背景 结核病（TB）仍然是主要的公共卫生问题。众所周知，肺结核合并肺外结核（PTB＆EPTB）会增加临床诊疗的难度。在这项研究中，我们探索了新的遗传基因位点促进 PTB＆EPTB 的易感。
方法 本研究纳入了中国西部汉族人群的 900 TB 患者和 1,534 名健康个体。在 900 例 TB 中，有 657 例仅肺结核（PTB），93 例仅肺外结核（EPTB）和 150 例 PTB 合并 EPTB（PTB＆EPTB）。在我们的研究中还收集了实验室指标。总共通过数据库 1000 Genomes Project 和软件 Haploview V4.2 选择了三个单核苷酸多态性（SNP）（rs12333784，rs6463794 和 rs720964），并通过定制的 2×48-Plex SNPscan™试剂盒进行了基因分型。
结果 我们观察到 rs12333784 的次要等位基因型（G 携带者）使 PTB 和 EPTB 发生的风险增加（pBonferroni = 0.03878），并且在显性模型分析下观察到了类似但更显着的影响（pBonferroni = 0.013，OR = 1.349），95％CI = 1.065-1.709）。我们发现具有 rs12333784 GG + GA 基因型（在显性模型中）的患者与葡萄糖（GLU）（P = 0.03），γ-谷氨酰转移酶（GGT）相关（p = 0.05 ）和红细胞沉降率（ESR）（P = 0.05）实验室指标显著相关。
结论 我们的发现初步探究了一个新的 7p21.3 基因座，该基因座可促进 PTB 和 EPTB 的进展，并提示 AC007128.1 基因是 7p21.3 基因座的功能靶标。

PO-1132

二氧化碳嗜纤维菌引起的血流感染两例

许晶晶
徐州医科大学附属医院

二氧化碳嗜纤维菌引起血流感染的相关报道国内比较少见。它属隶属于黄杆菌科，为兼性厌氧无动力的革兰阴性杆菌。它也是人口腔里的正常菌群，经常分离自成人牙周病患者。二氧化碳嗜纤维菌已经被报道可引起免疫功能正常或低下（尤指中性粒细胞缺乏）患者败血症及其他内源性的感染（心内膜炎、子宫内膜炎，腹膜炎，骨髓炎等等）。该类菌能够抑制中性粒细胞趋化和淋巴细胞增殖。2020 年 11 月份，我院微生物室从两位血液病患者血培养中分别分离出两株二氧化碳嗜纤维菌。

二氧化碳嗜纤维菌属的细菌通常对广谱头孢菌素类。碳青霉烯类、克林霉素、大环内酯类、四环素和氟喹诺酮类抗菌药物敏感，但是对氨基糖苷类耐药，有时候可检出多重耐药菌株。虽然二氧化碳嗜纤维菌为人类口腔正常菌群，一般不致病，但分离自无菌体液和血液时可能有临床意义，临床医生可结合患者情况和临床资料综合分析，合理选择抗生素。

PO-1133

mNGS 在沙门氏菌感染中的临床应用研究

赵倩雯
南方医科大学珠江医院

背景 临床上常用的传统的检测沙门氏菌感染的检测技术多是进行粪便或血液的培养，培养出可疑病原体后再进行细菌鉴定的药敏检测，至少需要花费 2-3 天的时间。而且血培养的阳性率还很低，对于一些疑难危重症病人来说，时间就是生命，较长的检测时间会贻误患者的病情和临床诊疗，也不一定能得到相应的阳性结果。现如今 mNGS 已经逐渐在临床上广泛应用，其检测时间短，敏感性高，有较高的阳性率，具有广泛的临床应用前景。本研究的目的就是为了探索 mNGS 在沙门菌感染中的临床应用价值。
方法 对粪便和血液中沙门氏菌临床检测阳性的患者，收集其血浆标本，观察是否可以利用 mNGS 技术快速检测出其血浆标本中的沙门氏菌序列，提高沙门氏菌患者的诊疗效率。同时分析粪便标本沙门氏菌阳性的患者血浆标本中的阳性率。
结果 在本研究收集得到的粪便和血液标本沙门氏菌阳性患者的血浆标本中，血液培养沙门氏菌阳性的患者标本中经过 mNGS 的检测得到沙门氏菌序列的阳性率可达 85%以上。而粪便标本阳性患者的血浆标本经过 mNGS 的检测得到沙门氏菌序列的阳性率也可达 67%以上。
结论 mNGS 可成功地从沙门氏菌感染患者的标本中快速检出沙门氏菌序列，且检出阳性率较高，有望应用于急危重症和疑难感染患者中沙门氏菌感染的检测和诊断。

PO-1134

MALDI-TOF MS 鉴定马尔尼菲篮状菌的实验条件优化

刘俞谷、王艳芳
南方医科大学珠江医院

目的 构建用于质谱鉴定的马尔尼菲篮状菌数据库，并探索用于马尔尼菲篮状菌质谱鉴定的最佳培养条件和前处理方案。
方法 利用 8 株马尔尼菲篮状菌构建自建质谱库，比较不同培养基（SDA、SDB）、培养温度（28℃、35℃）、培养时间、前处理方法（甲酸乙腈法、直涂法）对谱图质量及鉴定结果准确度的影响。
结果 在 VITEK MS RUO 模式中成功构建马尔尼菲篮状菌质谱自建库。SDA 平板较 SDB 液体培养基更适合马尔尼菲篮状菌质谱鉴定，后者采集谱图中干扰峰较多。两种温度培养采集谱图的特征峰相似，但 35℃菌落的鉴定准确率略高。培养 3-5 天时的菌落鉴定准确率高于 71.4%，其中 5 天时鉴定准确率最高，为 100%。甲酸乙腈法的提取效果优于直涂法。以上最优培养条件和前处理方案，对于形态不典型的马尔尼菲篮状菌，同样适用。
结论 为提高 VITEK MS RUO 模式鉴定马尔尼菲篮状菌的准确率，较优的条件为：SDA 平板 35℃培养 3-5 天内，经甲酸乙腈法前处理可得到较高的准确率，需要更多的菌株进一步扩大数据库及评价。

PO-1135

粪便标本溶组织内阿米巴原虫 Real-Time PCR 检测方法的建立及初步评价

张春莹[1]、孟妍明[1]、刘成玉[2]、马莹[1]
1. 四川大学华西医院
2. 成都市妇女儿童中心医院

建立粪便标本溶组织内阿米巴原虫 Real-Time PCR 检测方法，并评价该方法在临床粪便标本中检测溶组织内阿米巴原虫的应用价值。基于溶组织内阿米巴原虫小亚基核糖体 RNA（SSU rRNA）基因设计特异性引物，使用 Real-Time PCR 方法对溶组织内阿米巴原虫标准株 DNA 进行扩增，建立溶组织内阿米巴原虫感染的 Real-Time PCR 技术；同时收集临床腹泻病人粪便标本 221 例，分别采用镜检法检测病原体、ELISA 方法检测原虫抗原、Real-Time PCR 法扩增粪便标本中的溶组织内阿米巴原虫 DNA，以临床诊断为判断阳性的依据，比较三种方法的检测性能。本研究成功建立粪便溶组织内阿米巴原虫 Real-Time PCR 检测方法，模板 DNA 最低检测限为 0.05 fg/uL，可用于临床腹泻患者粪便标本溶组织内阿米巴原虫检测，检测灵敏性和特异性好，而镜检法易漏检，不同方法检测临床粪便标本的结果比较中，PCR 方法最优，镜检法易漏检，本研究使用的 ELISA 试剂盒在检测我国西部地区肠道溶组织内阿米巴原虫感染时特异性低于 PCR 方法。本研究为建立临床溶组织内阿米巴原虫感染的 Real-Time PCR 检测方法提供了可靠的实验基础，同时也为临床检测其他致腹泻原虫的分子生物学检测方法提供参考。

PO-1136

Novel long noncoding RNA and LASSO prediction model to better identify pulmonary tuberculosis: A case-control study in China

Zirui Meng
West China campus of sichuan university

Introduction The insufficient understanding and misdiagnosis of clinically diagnosed pulmonary tuberculosis (PTB) without an aetiological evidence is a major problem in the diagnosis of tuberculosis (TB). This study aims to confirm the value of lncRNA n344917 in the diagnosis of PTB and construct a rapid, accurate and universal prediction model.
Methods A total of 536 patients were prospectively and consecutively recruited, including clinically diagnosed PTB, PTB with an aetiological evidence and non-TB disease controls, who were admitted to West China hospital from Dec 2014 to Dec 2017. The expression levels of lncRNA n344917 of all patients were analyzed using reverse transcriptase quantitative real-time PCR. Then, the laboratory findings, electronic health record (EHR) information and expression levels of n344917 were used to construct a prediction model though the Least Absolute Shrinkage and Selection Operator (LASSO) algorithm and multivariate logistic regression.
Results The factors of n344917, age, CT calcification, cough, TBIGRA, low-grade fever and weight loss were included in the prediction model. It had good discrimination (AUC = 0.88, cutoff = 0.657, sensitivity = 88.98%, specificity = 86.43%, positive predictive value = 85.61%, negative predictive value = 89.63%), consistency and clinical availability. It also showed a good replicability in the validation cohort. Finally, it was encapsulated as an open-source and free web-based application for clinical use and is available online at https://ziruinptb.shinyapps.io/shiny/.
Conclusions Combining the novel potential molecular biomarker n344917, laboratory and EHR variables, this web-based prediction model could serve as a user-friendly, accurate platform to improve the clinical diagnosis of PTB.

PO-1137

2014-2015 年广州 759 例儿童肠道病毒感染病原谱调查

赵崇泉
南方医科大学珠江医院

目的 调查 2014-2015 年我院 759 例儿童感染肠道病毒血清型的分布，了解广州地区肠道病毒（enterovirus, EV）病原谱。
方法 采集手足口病等疑似肠道病毒感染患儿肛拭子标本，采用荧光逆转录多聚酶联反应法(reverse transcriptase polymerase chain reaction, RT-PCR)检测通用型、EV71 型、CA16 型核酸，巢式 PCR 法扩增 VP1 基因测序分型。
结果 1 060 例疑似感染者检出 759 例 EV 阳性（检出率 71.6%）；两年均检出 11 种血清型，2014 年科萨奇病毒 A 组 16 型(Coxsackie virus A group 16，CA16)、肠道病毒 71 型（enterovirus 71, EV71）、科萨奇病毒 A 组 4 型(Coxsackie virus A group 4，CA4)、科萨奇病毒 A 组 10 型（Coxsackie virus A group 10，CA10）和科萨奇病毒 B 组 5 型（Coxsackie virus B group 5，CB5）列前五位，CA16 和 EV71 占 77.1%；2015 年科萨奇病毒 A 组 6 型（Coxsackie virus A group 6，CA6）、EV71、CA10、CA16 和科萨奇病毒 A 组 2 型（Coxsackie virus A group 2，CA2）列前五位，CA6 占 51.7%；性别比 1.8～5.3；感染以<3 岁儿童为主（60.1%，456/759）；全年均可检出，4～7 月达高峰，5 月 CA16、EV71、CA10 和 CA2 达高峰，7 月 CA6 达高峰。由于病原谱不同，2015 年病情普遍较 2014 年轻，两年均无死亡病例。EV71 感染重症病例比率最高（12.7%），CA16、CA10、CA4 和 CA6 偶见重症病例。
结论 广州主要流行十余种肠道病毒，两年病原谱不同，大部分病情较轻感染引起疾病较轻。

PO-1138

ST5-t2460-SCCmecII 型耐甲氧西林金黄色葡萄球菌与高死亡率相关

李雪寒
郑州大学第五附属医院

目的 自 2013 年以来，ST5-t2460-SCCmecII MRSA 在中国大量出现并迅速增加，而关于该型别菌株的特征及其与感染者临床预后的关系的研究也非常有限。因此，我们收集了 ST5-t2460-SCCmecII MRSA 感染者的部分临床特征，研究 ST5-t2460-SCCmecII MRSA 对感染者临床预后的影响。
方法 91 株 MRSA 来源于 2018 年 1 月至 2019 年 12 月期间于武汉大学中南医院住院患者的不同临床标本。提取菌株染色体 DNA 进行 spa，MLST 和 SCCmec 分型。收集感染者的年龄、性别、基础疾病、血常规指标、PCT 水平、药敏试验结果、感染 30 天后的结局、感染来源、感染前 1 个月内进行的侵入性操作等资料，采用 SPSS 22.0 进行统计分析。
结果 筛选出 34 株 ST5-t2460-SCCmecII MRSA 和 57 株非 ST5-t2460-SCCmecII MRSA 菌株。与非 ST5-t2460-SCCmecII MRSA 相比，ST5-t2460-SCCmecII MRSA 是一种小菌落突变体，其生长速度慢、菌落小、无色素沉着、在血琼脂平板上溶血环较弱。ST5-t2460-SCCmecII MRSA 对大多数抗生素的耐药率明显高于非 ST5-t2460-SCCmecII MRSA。感染 ST5-t2460-SCCmecII MRSA 和感染非 ST5-t2460-SCCmecII MRSA 的患者其性别、年龄、基础疾病和感染源无显著差异，但感染 ST5-t2460-SCCmecII MRSA 的患者白细胞计数、PCT 水平及 30 天死亡率较高，且感染者入住 ICU 的频率更高，一个月内接受侵入性手术的频率也更高。
结论 ST5-t2460-SCCmecII MRSA 是一种金葡菌小菌落突变体，在医院环境内可能具有更大的竞争优势，预示着严重的感染，其感染者通常预后较差。

PO-1139

由产 ESBLs 肠杆菌引起的术后脑膜炎的表型、分子特征和危险因素分析：一项为期六年的多中心队列研究

郑光辉
首都医科大学附属北京天坛医院

背景 为了解我国产超广谱 β-内酰胺酶 (Extended-spectrum β-lactamase，ESBL) 肠杆菌科 (ESBL-producing Enterobacteriaceae，EPE) 术后脑膜炎的表型、分子特征及危险因素。
方法 2014 年 1 月至 2019 年 12 月，我们对中国 4 个神经外科感染中心的肠杆菌感染引发的术后脑膜炎患者进行的多中心队列研究。对分离菌株的表型和分子特征进行了分析，并用 logistic 回归分析了 EPE 脑膜炎的独立危险因素。
结果 本研究中，共检出肠杆菌 220 株，包括 EPE 78 株。其中有 85.6% (67/78) 的菌株中检测到 ESBL 相关基因，包括 blaSHV (14.9%) 和 blaSHV+blaTEM+blaCTX-M-9 (20.9%) 是肠杆菌感染最常见的单基因和复合基因。logistic 分析显示，开颅术 (OR. 2.583，95%C.I. 1.274-5.235，P=0.008) 和恶性肿瘤 (OR. 2.406，95%C.I. 1.299-4.456，P=0.005) 为 EPE 诱发脑膜炎的独立危险因素。
结论 据我们所知，这是迄今为止我国开展的最大的与 EPE 脑膜炎相关的危险因素分析研究。开颅手术和恶性肿瘤是 EPE 脑膜炎的独立危险因素。危险因素的鉴别可进一步应用于临床实践和研究中，以降低感染患者的死亡率。

PO-1140

Listeria monocytogenes infections: Analysis of 59 patients

Xingbing Lu
west china hospital

Objective Various conditions increase the risk of meningitis caused by Listeria monocytogenes. However, the relative importance of these risk factors has not been well established. We describe and analyze the demographics and clinical features of 59 cases of L. monocytogenes to determine the predisposing conditions for severe meningitis infections.
Methods A retrospective study was conducted to use positive isolated L. monocytogenes from blood, cerebrospinal fluid（CSF）, and other organic fluids. Electronic medical record data were used to determine the epidemiological and clinical characteristics of L. monocytogenes infection. Multiple logistic regression analysis was used to predict the risk factors for Listeria meningitis.
Results A total of 59 cases and 133 controls were enrolled. Three major groups were identified: minors (3.39%), pregnant women (3.39%), and adults (93.22%). The outbreak was mainly concentrated in the spring and summer, and the indices of cerebrospinal fluid and blood increased in varying degrees. Twenty-five patients (42.37%) developed a neuroinvasive infection. In univariate and multivariate analyses, the use of hormonal drugs (odds ratio =3.207) and use of immunosuppressive agents (odds ratio=3.058) were associated predictors of severe meningitis, and the presence of headache (odds ratio=7.296) and pain symptoms (odds ratio=3.898) were the major independent risk factors for the occurrence of severe nervous system infection with L. monocytogenes. The 47 patients (79.66%) were treated with ampicillin (27.12%), carbapenems (18.64%), quinolones (11.86%), and β amidase inhibitors (11.86%) as the main target of antimicrobial treatment. Thirty-four patients (57.63%) improved clinically, five patients (8.47%) had a poor prognosis, and two patients (3.39%) died.
Conclusion In addition to pregnancy and foodborne factors, long-term use of immunosuppressants and hormones is the main risk factor for severe adult forms of Listeria-related infections. The headache and pain are independent risk factors for severe neurological

infections. In the early empirical treatment of L. monocytogenes, sensitive antibiotics such as penicillins and carbapenem should be added or replaced.

PO-1141

云南省抗病毒治疗后死亡 HIV/AIDS 患者基因型耐药情况调查

李健健
云南省传染病医院

目的 调查云南省 2011-2019 年间接受抗病毒治疗后死亡 HIV/AIDS 患者基因型耐药率、耐药程度、突变位点分布及其与非死亡患者的耐药差异。
方法 采用横断面研究方法，收集患者耐药相关流行病学信息。通过 In house 方法，运用 RT -PCR 扩增患者 HIV-1 pol 基因序列，测序后进行比对分析，阐明和对比两组患者耐药率及三类抗病毒药物耐药情况。
结果 纳入全省 HIV/AIDS 致死亡患者 415 人，扩增阳性 345 例，发生耐药突变 221 例（64.1%），在抗病毒治疗失败的死亡患者中耐药率较非死亡患者 73.5%（169/230）低，粗略估计 HIV-1 在死亡人群中总体耐药率为 1.5%（221/14603）。死亡患者耐药发生的影响因素包括性别、年龄、感染途径、初始 CD4+细胞计数和治疗方案（P<0.05）,死亡患者核苷类抑制剂（NRTIs）、非核苷类抑制剂（NNRTIs）以及蛋白酶抑制剂（PIs）的耐药率分别为 64.2%(142/221)、85.5%（189/221）、5.0%（11/221）；三类药物出现频率最高的突变位点依次为 NRTIs -M184V（59.1%），NNRTIs-K103N/S（28.7%），PIs-L23I（1.3%）。
结论 云南省死亡 HIV/AIDS 患者耐药呈现低流行水平，耐药率相对较低与患者发现较晚、治疗时间短、病毒在药物压力作用下变异程度小有关，三类药物中，各种药物耐药率和突变位点出现频率与非死亡组患者略有差异。我们应加强对 HIV/AIDS 危重症患者抗病毒治疗的管理和基因型耐药的检测，控制耐药毒株的产生，进一步降低患者死亡率。

PO-1142

脑脊液 MyD88L265P 基因突变在原发性中枢神经系统淋巴瘤预后影响分析

陈锟[1,2]、关明[1]、陈波斌[1]
1. 复旦大学附属华山医院
2. 复旦大学附属华山医院北院

目的 原发性中枢神经系统淋巴瘤（PCNSL）是一种预后较差的侵袭性结外淋巴瘤，常规检测诊断价值不高，脑脊液的液体活检成为首选。本文拟探讨脑脊液髓样分化因子 88L265P 突变（MyD88L265P）和白细胞介素 10（IL-10）在 PCNSL 预后的关系，为临床治疗提供依据。
方法 收集 39 例 PCNSL 患者的病例资料、脑脊液检测（包括细胞学、细胞计数、蛋白及 IL-10）及治疗经过进行回顾性分析。采用数字 PCR 检测 39 例石蜡组织和 35 例脑脊液标本中 MyD88L265P 基因突变，分析与 PCNSL 相关的预后因素，应用 Log-rank 检验进行单因素分析和 Cox 回归进行多因素分析。
结果 39 例 PCNSL 患者中位年龄 59 岁，30.1%的患者在初诊及治疗过程中出现眼内受累。组织 MyD88L265P 突变率为 74.4%（29/39），脑脊液 MyD88L265P 突变率为 40.0%（14/35），组织、脑脊液同时检测到该突变率为 51.9%（14/27），单因素分析显示眼内累及、脑脊液高 IL-10（≥45pg/mL）及脑脊液 MyD88L265P 突变中位无进展生存期（mPFS）均有明显统计学差异（p＜0.05）。多因素分析显示：眼内累及（HR=2.4，95%CI 1.3～7.8，p＜0.05）和脑脊液 MyD88L265P 突变（HR=2.1，95%CI 1.1～5.7，p＜0.05）均是影响患者 PFS 的独立预后因素。

结论 PCNSL 患者中出现眼内累及和脑脊液 MyD88L265P 突变是预后不良的因素，检测脑脊液 MyD88L265P 突变有希望成为肿瘤微残留的监测指标。

PO-1143

LGALS3 异常剪接体及空腹血糖水平与 CML 疾病进展的相关性研究

赵翠、李书琪、刘静、姚芳苡、徐颜美、张静、林晋、秦婷玉、钟芳敏、李美勇、黄波、王小中
南昌大学第二附属医院

研究背景及目的 慢性髓系白血病(Chronic myelogenous leukemia, CML)是一种与费城染色体 t(9;22)相关的造血干细胞恶性肿瘤。CML 分为慢性期（CP）、加速期(AP)及急变期（BP)三个不同的临床阶段。尽管伊马替尼（IM）的引入使 CML 患者的疗效及预后得到了极大改善，但是 IM 原发性或继发性耐药和不耐受的情况出现导致急变期，其预后极差，故而探究 CML 疾病进展相关机制意义重大。观察发现 CML 急变期（Blastic phase-CML, BP-CML）患者易出现高糖现象。同时，课题组 CML 转录组测序结果表明，CML 患者 LGALS3 基因存在 3 号内含子保留（LGALS3 intron 3 retention, LGALS3-R）的异常选择性剪接。因此，本研究拟探索 LGALS3 异常剪接体表达水平、空腹血糖（Fasting blood glucose, FBG）水平与 CML 疾病进展的相关性，旨在为 CML 疾病进展预测、治疗提供新的思路。
方法 在这项回顾性研究中，我们根据纳入和排除标准最终纳入 CML 慢性期（Chronic phase-CML, CP-CML）患者 304 名和 BP-CML 患者 117 名。采用受试者工作特征(ROC)曲线分析、倾向得分匹配法(PSM)分析和实时荧光定量 PCR (qPCR)检测的方法，比较 BP-CML 组和 CP-CML 组患者的 FBG 水平和 LGALS3 基因及其异常剪接体的表达水平，并使用相关性分析变量之间的相关性。
结果 FBG 水平在 CP-CML 组和 BP-CML 组分别为 3.74 ± 1.52mmol/L 和 5.81 ± 1.94 mmol/L。BP-CML 组 FBG 水平明显高于 CP-CML 组($P < 0.001$)。经 PSM 分析，未经靶向治疗的 BP-CML 组的 FBG 水平高于 CP-CML 组($P < 0.001$)。FBG 诊断 BP-CML 的曲线下面积（Area under the curve, AUC）为 0.785，FBG 的最佳临界值为 5.08 mmol/L，敏感性为 61.9%，特异性为 83.3%。LGALS3 基因 BP-CML 组表达量较 CP-CML 组表达量低($P < 0.001$)，与 FBG 水平呈负相关性($R = -0.552$, $P < 0.001$)。进一步分析显示与 CP-CML 组相比，BP-CML 组中异常剪接体 LGALS3-R 表达显著下调($P < 0.001$)。
结论 本研究结果表明，FBG 高水平和 LGALS3-R 低表达水平可能是 CML 疾病进展的潜在标志，对 BP-CML 和 CP-CML 的鉴别诊断具有较高的临床价值。

PO-1144

γδT 细胞、Th17 细胞和 IL-17 在慢性乙型肝炎患者外周血中表达的意义

王雅姝[1]、晋红梅[2]、王克强[2]
1. 泰安市中心医院
2. 山东第一医科大学第二附属医院检验科

目的 了解 γδT 细胞、Th17 细胞和 IL-17 在慢性乙型肝炎（CHB）患者外周血中的表达情况，探讨 γδT 细胞、Th17 细胞和 IL-17 在 CHB 发病机制中可能的作用。
方法 用流式细胞仪检测 20 例健康人、20 例 CHB 无症状携带者（AsC）、20 例 CHB 轻度患者和 20 例 CHB 中、重度患者外周血中 γδT 细胞和 Th17 细胞的数量，用 ELISA 法检测各组血清中 IL-17 细胞因子的含量。

结果 健康人、AsC、CHB 轻度患者和 CHB 中、重度患者，γδT 细胞的表达量分别为 1.258±0.1348、2.178±0.1946、4.160±0.0693、7.058±0.9699，差异具有统计学意义（F＝498.35, P＝0.000）；Th17 细胞的表达量分别为 1.252±0.1545，1.714±0.1031、2.338±0.2337、3.826±0.4884，差异具有统计学意义（F＝310.65, P＝0.000）；IL-17 的浓度（pg/ml）分别为 16.307±19.25、92.706±16.85、147.635±6.32、391.787±28.52，差异具有统计学意义（F=349.41，P＝0.000）。Pearson 相关性分析显示，CHB 患者外周血中 γδT 细胞和 Th17 细胞的百分率存在正相关（r=0.978，P=0.000）；γδT 细胞的百分率和 IL-17 存在正相关（r=0.959，P=0.000）；Th17 细胞的百分率和 IL-17 存在正相关（r=0.954，P=0.000）。
结论 随着 CHB 病情程度的加深，外周血 γδT 细胞、Th17 细胞和 IL-17 表达也随之升高，表明 γδT 细胞和 Th17 细胞可能参与了机体感染病毒后引起的免疫反应和组织损伤过程；γδT 细胞和 Th17 细胞表达呈正相关，提示 γδT 细胞可能对 Th17 细胞具有调节功能，并在免疫系统的发病机制中可能起着关键的作用。

PO-1145

外周血异常红细胞形态联合血常规红细胞参数在缺铁性贫血和地中海贫血诊断中的价值探讨

吴昊
电子科技大学附属医院·四川省人民医院

目的 探讨外周血异常红细胞形态联合血常规红细胞参数在缺铁性贫血和地中海贫血鉴别诊断中的价值。
方法 选取 2018 年 1 月至 3 月本院收治的 40 例地中海贫血患者，58 例缺铁性贫血患者，54 例健康体检者作为研究对象。对各组入选样本进行血常规检测，并制作血涂片分类计数 1000 个红细胞。将各组红细胞参数 HGB、MCV、MCH、MCHC，10 种异常红细胞（靶形红细胞、球形红细胞、椭圆形红细胞、泪滴形红细胞、低色素性红细胞、盔形红细胞、红细胞碎片、嗜多色性红细胞、嗜碱性点彩红细胞、其它异常红细胞）检出率共计 14 项指标进行比较分析。
结果 与对照组相比，缺铁贫组除嗜碱性点彩红细胞检出率无统计学差异外，其余 13 项指标均有统计学差异；与对照组相比，地贫组 14 项指标均有统计学差异；与缺铁贫组相比，地贫组除 MCH、低色素性红细胞检出率、嗜多色性红细胞检出率 3 项指标外，其余 11 项指标均有统计学差异。
结论 外周血异常红细胞形态联合血常规红细胞参数在缺铁性贫血和地中海贫血的鉴别诊断中具有一定的价值，提高检验人员外周血红细胞形态识别能力有助于向医生和患者提供更多有意义的信息。

PO-1146

红细胞体积分布宽度新型计算公式对地中海贫血和缺铁性贫血鉴别诊断的价值

杨卓、甘勇、吴洁、伊洁、陈雨、陈倩、王斐、吴卫
中国医学科学院北京协和医院

目的 初步探讨利用血常规中红细胞参数的新型运算公式【（MCV2×RDW-CV）/Hb*10】对缺铁性贫血与地中海贫血进行鉴别诊断的实用价值。
方法 使用全自动血细胞分析仪 Advia 2120 对 68 例缺铁性贫血和 62 例地中海贫血样本的红细胞参数进行检测，α-地中海贫血缺失型采用 GAP-PCR 法确诊，α-地中海贫血点突变和 β-地中海贫血采用 PCR-反向点杂交法确诊，排除其他合并疾病。缺铁性贫血诊断标准：

小细胞低色素贫血：男性 Hb<120g/L, 女性 Hb<110g/L, MCV<80 fl， MCH<26pg，MCHC<300g/L，有明确的缺铁病因和临床表现，血清铁蛋白<12μg/L。统计数据采用 SPSS 软件进行 t 检验分析。
结果 地中海贫血组红细胞数值为(5.06±1.07)×1012/L，包含 α-地中海贫血标本 12 例，β-地中海贫血标本 48 例，α-地中海贫血复合 β-地中海贫血 2 例。缺铁性贫血组红细胞数值为(4.19±0.57)×1012/L，地中海贫血组的 RBC 数值高于缺铁性贫血组，两者具有统计学差异（p=0.000）。采用两组变异差别较大的红细胞体积分布宽度百分比（RDW-CV,单位%）、平均红细胞体积（MCV，单位 fL）和血红蛋白(Hb,单位 g/L)参数，组合多种公式进行分析，结果发现采用公式【（MCV2×RDW-CV）/Hb*10】，地中海贫血组数值为 86.02±39.87,缺铁性贫血组数值为 109.41±26.81,地中海贫血组明显低于缺铁性贫血组，两者具有统计学差异（P=0.015）。
结论 利用常规红细胞参数进行组合运算，有助于初步推导低色素小细胞性贫血的类型，对疾病的鉴别诊断和进一步临床处理具有重要的参考价值。

PO-1147

利用 CD38/CD58 的 MFI 比率可以在 B-ALL 诊断样本中更容易区分出白血病细胞

王清晨
北京大学第一医院（北京大学第一临床医学院）

目的 急性 B 淋巴细胞白血病（B-ALL）是儿童常见的血液系统肿瘤。微小残留病（minimal residual disease；MRD）是儿童 B-ALL 的独立预后标志，对于预测预后和选择进一步治疗策略的强度至关重要。目前 MRD 的测量方法主要包括流式细胞术及 PCR 技术。本研究目的是通过流式细胞术分析我院儿童 B-ALL 初诊免疫表型，探讨在儿童急性 B 淋巴细胞白血病(B-ALL)诊断中最具鉴别能力的抗原组合。
方法 病例组为 22 例初诊 B-ALL 患者骨髓细胞，对照组选取 6 例患有血液系统疾病但已达到完全缓解患儿的骨髓细胞。采用多参数流式细胞术分析八种标记物的平均荧光强度(MFI):CD45、CD19、CD10、CD34、CD38、CD20、CD58、CD117，并在白血病细胞和正常 B 祖细胞上获得的 MFI 进行对比。利用 ROC 曲线的 AUC 值分析标记抗原组合的敏感性和特异性。
结果 抗原的定性表达模式显示,相比较正常 B 祖细胞，CD58、CD34、CD10 在白血病淋巴细胞上过度表达，而 CD45、CD38 表达不足。使用 ROC 曲线分析，相比较 CD38 与 CD58 单独进行免疫表型分析（CD38 AUC：0.61；CD58 AUC：0.665），CD38/CD58 的抗原平均荧光强度比率在 0.32 时，ROC 曲线下面积达到最大，此时灵敏度为 0.824，特异度为 0.8。
结论 CD38/CD58 的 MFI 抗原比率可以更好区分白血病细胞和正常的未成熟 B 祖细胞。

PO-1148

ABCB1 和 CES1 基因多态性对 达比加群酯治疗脑卒中患者抗凝效果的影响

张琳、郑绪雅、张俊峰、许军秀
郑州大学第五附属医院

目的 探究 ABCB1 SNP（rs1045642）与 CES1 SNP（rs2244613）基因位点多态性对服用达比加群酯的脑卒中患者的抗凝疗效的影响，以进一步推进达比加群酯的个体化治疗，改善抗凝效果。
方法 选取 2020 年 11 月至 2021 年 6 月在郑州大学第五附属医院住院治理的脑卒中患者 60 例作为研究对象。利用 Taqman®荧光探针法检测患者全血标本中 ABCB1 SNP（rs1045642）与 CES1 SNP（rs2244613）的基因型，HTI 凝血分析法来测定患者服用达比加群后的血浆浓度谷峰值，凝

血分析仪检测患者服药后的凝血指标，包括活化部分凝血活酶时间(APTT)、凝血酶时间(TT) 、凝血酶原时间（PT）和国际标准化比值（INR），并在患者治疗期间观察记录出血事件。统计分析基因多态性对服用达比加群的患者血浆浓度、凝血指标和出血风险的影响。
结果 ABCB1 SNP（rs1045642），CES1 SNP（rs2244613）两个位点的基因型和基因频率均无显著性差异（P>0.05）。rs1045642 多态性与达比加群血浆浓度、凝血指标均无显著关联；此位点上不同基因型的房颤患者在治疗期间的出血事件发生率，差异无统计学意义（P>0.05）。rs2244613 位点多态性与达比加群浓度峰值无显著关联，但等位基因(A)携带者较非携带者有更高的达比加群血药浓度谷值(AA 与 CC 基因型，P<0.05；CA 与 CC 基因型，P<0.05)；不同基因型间峰值水平的凝血指标均无统计学意义，在谷值水平测得的凝血指标中，只有 APTT 值差异有统计学意义，两两比较显示 CC 基因型患者的 APTT 值高于 CA 基因型患者与 AA 基因型患者；等位基因携带者与非携带者相比，具有轻微出血的危险性。
结论 ABCB1 SNP（rs1045642）基因位点可能不会影响脑卒中患者口服达比加群酯后的抗凝疗效。CES1 SNP（rs2244613）上的次要等位基因可以使接受达比加群治疗的脑卒中患者的血药浓度谷值增高，并且增加轻微出血风险。

PO-1149

CircPVT1 promotes acute myeloid leukemia cell proliferation, migration and invasion via the miR-455-3p/MCL1 axis

Kun Wu 、Yuntao Li、Bo Nie、Yun Zeng、Mingxia Shi
First Affiliated Hospital of Kunming Medical University

Background Circular RNAs (circRNAs) play a crucial role in acute myeloid leukemia (AML) progression. Recently, accumulatingstudies have confirmed that circPVT1 participates in diverse pathological processes, especially tumorigenesis. However, the function and mechanism of circPVT1 in AML remain unclear.
Methods The mRNA expression levels of circPVT1, miR-455-3p and MCL1 in 42 adult AML patients andhealthy subjects were determined by RT-qPCR. Cell Counting Kit-8 (CCK-8)andTranswell assays were conducted to identify the roles of circPVT1 in the growth and migration/invasion, respectively, of NB4 and HL-60 cells. Bioinformatic analysis and in vitro experiments were conducted to clarify the mechanism of circPVT1-mediated gene regulation in NB4 and HL-60 cells.
Results CircPVT1 expression was significantly increased in primary AML samples and cell lines. CircPVT1knockdown significantly reduced the proliferation, migration and invasion of NB4 and HL-60 cells and impaired tumor growth in vivo. Bioinformatic analysis and luciferase reporter assays demonstrated that circpvt1 promoted MCL1 expression by interacting with miR-455-3p. Moreover, the inhibitory effects of MCL1 knockdown on AML progression were partially reversed by decreasing miR-455-3p levels or enhancing circPVT1 expression.
Conclusions In summary, our findings suggested that circPVT1 might be a therapeutic target for the treatment of patients with AML since targeting circPVT1 suppressed AML progressionin vitroand in vivo.

PO-1150

The important clinical role of minimal residual disease detection by flow cytometry in childhood acute lymphoblastic leukemia and its prognostic significance

Kun Wu 、Shenju Cheng、Yanhong Li
First Affiliated Hospital of Kunming Medical University

B cell acute lymphoblastic leukemia (B-ALL) is a malignant neoplastic disease which causing great burden to children's health and family life. Aiming to explore possible risk factors for B-ALL relapse, we conducted a retrospective cohort study from October 2016 to March 2018. Flow cytometry was used to minimal residual disease (MRD) detection. 192 children with B-ALL were divided into groups according to the level of MRD (MRD≥0.01% and MRD<0.01%) and different periods (end of the induction remission period and maintenance treatment period). Each group was followed-up in different times. The results showed that the cumulative recurrence rate of children with MRD+ was significantly higher than MRD- (P=0.0293) during the maintenance treatment period, while the cumulative recurrence rate was not statistically different at the end of the induction remission period (P=0.419). With Cox risk proportional regression model, we found that prednisone insensitive, bone marrow characteristics on day 15 and the MRD level after remission (≥0.01%) may be high-risk factors for the B-ALL recurrence. Our 4-color fluorescent labeled B lymphocyte antibody combination template for flow cytometry could well distinguish B-ALL children with MRD+ and MRD- and negative after chemotherapy. Our present study confirmed the important clinical role of MRD in B-ALL in Chinese population and provided the 4-color fluorescent labeled B lymphocyte antibody combination template for other researchers.

PO-1151

多发性骨髓瘤患者外周血肿瘤教育血小板的研究

张娟[2]、蒋黎[1]
1. 电子科技大学医学院·四川省人民医院
2. 电子科技大学医学院·四川省人民医院

目的 肿瘤教育血小板（Tumor-Educated-Platelete,TEP）是指血小板吞噬了肿瘤来源的 RNA 而形成的特殊的血小板。本研究主要探讨多发性骨髓瘤(Multiple Myeloma, MM)患者外周血是否存在肿瘤教育血小板及其形态特征和机制研究。

方法 收集 2020 年 10 月-12 月在四川省人民院确诊的多发性骨髓瘤患者 50 例和 50 例正常人外周血血小板进行了密度梯度离心分离纯化，并按试剂说明书提取了血小板中的 RNA，进行了二代测序。同时对提取出的血小板进行透射电镜和扫描电镜观察。对多发性骨髓瘤患者和正常人外周血进行血涂片瑞氏染色观察。

结果 测序结果显示，MM 患者与正常人外周血血小板中 RNA 表达是有差异的，即 MM 具有特异的 TEP RNA。扫描电镜结果显示，MM 患者外周血血小板形态较不规则，形态变化较大，而正常对照组血小板相对较为规则。透射电镜结果显示，MM 患者血小板多呈不规则形，胞浆中可见线粒体、粗面内质网和颗粒结构，部分线粒体有轻度肿胀，偶见少量脂滴。正常对照组血小板形态结构多呈规则形，胞浆中可见线粒体、粗面内质网和颗粒结构。瑞氏染色结果显示，与正常人对照相比，MM 患者外周血易见大血小板，部分血小板胞浆边缘可见长短不一绒毛状的突起，部分血小板胞浆边缘可见明显"环状"结构。可能与 MM 患者外周血血小板被激活，伸出伪足有关。"环状"结构可能与血小板中微管与驱动蛋白有关。

结论 MM 患者外周血肿瘤教育血小板可能与 MM 的发生有关，其具体机制有待进一步深入研究。

PO-1152

基于柔性等离子活性琼脂糖薄膜的便携 SERS 平台用于血清中尿酸的快速检测

陈嘉明[1,2]、洪国焌[1,2]
1. 厦门大学附属第一医院 检验科
2. 厦门市基因检测重点实验室

目的 复杂体液样品的检测中容易受到其他生物大分子的干扰，影响检测结果。如何快速分离样品和实现目标物的快速检测成为目前的研究热点。我们针对这一问题，利用表面增强拉曼散射（SERS）技术的高灵敏、无损快速检测的优势，并结合琼脂糖凝胶的筛分能力，构建了基于柔性等离子活性琼脂糖薄膜的便携 SERS 平台并用于体液样品的即时诊断。

方法 采用贵金属纳米粒子和琼脂糖水凝胶溶液作为前驱体，调控温度和湿度，大规模制备等离子活性琼脂糖薄膜。整个制备过程温和、简单而且低廉。通过琼脂糖凝胶的微纳米孔道，对样品中生物大分子进行初步分离，再结合便携拉曼光谱仪进行指纹图谱的识别、分析。

结果 首先，对该 SERS 薄膜的多项 SERS 性能进行考察。实验结果表明，该 SERS 薄膜具有极高的 SERS 灵敏度和均一性。以罗丹明 6G 作为模型探针，得到检测限可以达到 10 fM，检测线性范围 1.0 pM 至 10 nM。然后，该等离子凝胶珠作为 SERS 基底被用于对尿酸进行定量检测，其线性检测范围为 1.0 μM∽1000 μM，检测限为 0.1 μM，并成功应用于人血清中的尿酸检测。

结论 基于柔性等离子活性琼脂糖薄膜的便携 SERS 平台方法具有制备温和简单，大批量制备的优点。并且，可以利用琼脂糖特点分离生物大分子快速、灵敏地检测复杂生物样品中目标分子，配合便携拉曼光谱仪有望应用于即时检验等领域。

PO-1153

Falsely elevated platelet count in a ITP infant with unusual finding of megakaryocytes in peripheral blood

Qingzhou Chen
The First Affiliated Hospital of Zhengzhou University

An 11-month-old infant had the platelet count of 63×10^9/L. After Wright-Giemsa stain, we almost could not see platelets in the peripheral blood by smear microscopy (panel A&B, black arrow, original magnification×1000). Apart from that, mature erythrocytes were of varying sizes, the cells were mainly small and hypochromic, and the central portion of the cells was lightly stained, and target cells were visible (panel A&B, red arrow, original magnification ×1000). After correction with Mindray BC-6800Plus instrument, the final platelet count was 5×10^9/L, the number of erythrocytes increased from 4.8×10^12/L to 4.86×10^12/L. The number of increased erythrocytes (60×10^9/L) was almost equal to the decreased platelets (58×10^9/L) via calculation. Considering of the value (57.0fL) of erythrocyte mean corpuscular volume (MCV), we considered that the cause of false increase of platelet count was the interference of small erythrocytes. The peripheral venous blood was collected by a routine venipuncture procedure. Peripheral smear showed above is consistent with clinical history of ITP and hypochromic microcytic anemia. So we need to take microscopic examination as the gold standard, and make full use of various scientific and technological means to solve the difficult problems.

Immune thrombocytopenia (ITP), an autoimmune disorder characterized by autoantibody production which can inhibit proplatelet formation by megakaryocytes and impair platelet production in vitro. Because of low platelet, the majority of patients have the risk of haemorrhage and require treatment. The etiology of ITP is complex. Of note, we found two typical granular megakaryocytes at the end of the slide(panel C&E, arrow, original magnification×40, panel D&F,

original magnification×1000). Such accidental discovery has been rarely reported in literature. Generally speaking, megakaryocytes appearing in peripheral blood are common in diseases including chronic lymphoblastic cytic leukemia (CLL), chronicmyelomonocyticleukemia (CMML), myelodysplastic syndromes (MDS), myeloproliferative (MPN), primary myelofibrosis (PMF) and acute megakaryocytic leukaemia (AMeL). Clinical significance of this finding is unknown, the mechanism may be the increased gap of sinus wall after treatment of the infant, then megakaryocytes enter peripheral blood from bone marrow. In addition, a manifestation of ITP is the maturation disorder of megakaryocytes in bone marrow,

we speculate that megakaryocytes appearing in peripheral blood smears are almost immature, so the granular megakaryocytes we found is consistent with the explanation. What's more, this case teaches us an inspiration to use the end of the slide as an significant area for finding large cells of diagnostic importance such as tumor cells, atypical lymphocytes, or in this case granular megakaryocytes can be found.

PO-1154

Performance evaluation of PA-990, a novel automated Lifotronic specific protein analyzer, in detecting C-reactive protein

Fan Zhang 、Mianyang Li 、Chengbin Wang
Chinese People's Liberation Army General Hospital

Background PA-990 is a new automated Lifotronic specific protein analyzer that can detect C-reactive protein (CRP). The aim of this study was to investigate the analytical performance of PA-990.
Methods The analytical performance of PA-990 was evaluated on the basis of the following parameters, including the limit of blank (LoB), carryover, precision, accuracy, linearity, and reference interval. Additionally, channel comparison and method comparisons were performed.
Results LoBs satisfy the manufacturer's statement (≤0.5 mg/L). No significant carryover (≤0.5%) was observed in this study. The precision and accuracy for all parameters fell within acceptable criteria. The channel comparison analysis and reference interval fell within acceptable criteria. The method comparison analysis demonstrated strong agreement between PA-990 results and those of PA-990, and those of Siemens–BN-II automated specific protein analyzer. Excellent measurements were observed in the dilution linearity (coefficient of determination, r2≥0.95).
Conclusion The analytical and clinical performance characteristics of PA-990 were demonstrated satisfactory, which made it well suited for routine use in clinical laboratories and emergency departments.

PO-1155

2 例 X 染色体非随机灭活导致女性血友病 A 的机制

徐扬
上海交通大学医学院附属瑞金医院

目的 X 染色体非随机灭活是女性血友病 A 的主要发病机制之一，但 X 染色体非随机灭活机制不清，本文主要研究了 X 染色体非随机灭活导致女性血友病的分子发生机制。
方法 检测相关凝血指标；进行基因相关检测，包括 PCR 扩增及测序分析 FVIII 和 XIST 基因的各外显子及其侧翼序列、拷贝数检测、FVIII 基因内含子 1 和 22 倒位检测；针对 HUMARA 基因和 RP2 基因进行 X 染色体灭活率的检测；采用 G 显带法分析外周血细胞核型。

结果 诊断 2 名女性为血友病 A 患者，检测发现患者 1 FVIII 基因存在第 22 内含子远端倒位，患者 2 FVIII 基因存在 c.592T>A:p.Cys198Ser 杂合突变；HUMARA 检测发现两名患者 X 染色体为非随机灭活；XIST 基因分析显 2 名女性血友病 A 患者存在相同位点的 XIST 突变，但该突变与患者的 X 染色体非随机灭活无关；G 显带核型分析显示先证者染色体核型未见明显异常。
结论 这 2 名患者均携带单 FVIII 基因杂合突变，且均由 X 染色体非随机灭活导致的女性血友病 A；排除了 XIST 基因 11150 位 A 到 G 的突变对 X 染色体非随机灭活的影响。X 染色体非随机灭活与细胞选择有关，推测存在 X 染色体大片段缺失导致细胞生存劣势，从而造成 X 染色体非随机灭活现象的产生；也可能存在另外未知的 X 染色体突变，而且该突变不利于接下来的细胞的繁殖，造成该 X 染色体灭活。这也将是后续深入研究的方向。

PO-1156

乳腺粘液癌的针吸细胞学形态分析

朱玉秋
徐州医科大学附属医院

目的 乳腺粘液癌是一种发生于乳腺导管的少见浸润性特殊型乳腺癌，发生率仅占乳腺肿瘤的 1-6%。肿块多呈膨胀性生长，生长缓慢，境界清楚，质地较软，因此，容易被临床体格检查、超声等影像学检查误诊为纤维腺瘤。针吸取细胞学检查是术前早期鉴别诊断乳腺肿瘤良恶性的重要方法之一。但由于乳腺黏液癌的发病率低、肿瘤细胞形态异型性不明显、针吸细胞学文献报道少、缺乏诊断标准等原因，给术前诊断带来了困难和挑战。本文旨在探讨乳腺粘液癌的针吸细胞学的形态学特征，提高对乳腺粘液癌针吸细胞学的诊断率。
方法 对乳房肿块进行针吸细胞学检查，结合组织病理学结果，分析乳腺粘液癌的细胞形态学诊断特征。
结果 以病理学结果为金标准，5 例乳腺黏液癌针吸细胞学诊断结果与病理组织学结果一致，准确率为 100%。5 例乳腺黏液癌针吸物均为半透明胶冻样粘稠物，镜下形态学特点：1.中等至大量的透明、半透明黏液物质背景；2.肿瘤细胞体积略增大、轻度异型；3.紧密排列呈乳头状或三维立体球团样，如同小岛漂浮在粘液湖中，亦可与黏液交织存在；4.未见或极少见肌上皮细胞。
结论 乳腺黏液癌针吸细胞形态学特征较鲜明，可以作为乳腺粘液癌术前诊断的一种常规检查方法。

PO-1157

Quantitative proteomic analysis of plasma exosomes to identify the candidate biomarker of Imatinib Resistance in Chronic Myeloid Leukemia patients

Meiyong Li、Bo Huang、Xiaozhong Wang、Cui Zhao、Fangmin Zhong、Ying Cheng、Shuai Xu、Fangyi Yao、Junyao Jiang、Yulin Yang
The Second Affiliated Hospital of Nanchang University

Background Imatinib (IM), a tyrosine kinase inhibitors (TKIs), has markedly improved the survival and life quality of chronic myeloid leukemia (CML) patients. However, IM resistance and lack of specific biomarkers remain a serious clinical challenge for a subset of patients. Recently, growing evidence has suggested that exosomes-harbored proteins were involved in tumor resistance and could be novel biomarkers for the diagnosis and prediction of cancer. Therefore, we aimed to investigate the proteomic profile of plasma exosomes derived from CML patients to identify ideal biomarkers for IM resistance.
Methods We extracted exosomes from pooled plasma samples of 9 imatinib-resistant CML and 9 imatinib-sensitive CML by Total Exosome Isolation Reagent. Then, we identified the expression

levels of exosomal proteins by liquid chromatograph-mass spectrometer (LC-MS/MS) based label free quantification, and bioinformatic analyses were used to analyze the proteomic data. Finally, the western immunoblotting (WB) and Parallel reaction monitoring (PRM) analyses were applied to validate the candidate proteins in an independent cohort.
Results A total of 2812 proteins were identified in plasma exosomes from imatinib-resistant and imatinib-sensitive CML patients, including 279 differentially expressed proteins (DEPs) with restricted criteria ($p<0.05$, fold change>1.5). Compared with imatinib-sensitive CML, 151 proteins were up-regulated and 128 proteins were down-regulated. Bioinformatics analyses revealed that the main function of upregulated proteins was to participate in the protein synthesis, while the downregulated proteins were mainly involved in lipid metabolism. The top 20 hub genes were obtained using STRING and Cytoscape, most of which are the components of ribosomes. Moreover, we found that RPL13 and RPLP2 exhibited especially marked differences between imatinib-resistant and imatinib-sensitive CML patients, which were further confirmed by WB and PRM in respective independent cohorts.
Conclusion Proteomic analysis of plasma exosomes provides new ideas and important information for the study of imatinib resistance in CML. Especially the exosomal proteins (RPL13 and RPLP2), which may have great potential as biomarkers of imatinib resistance.

PO-1158

达比加群酯在非瓣膜性房颤抗凝治疗中基因多态性的研究进展

张帆、王成彬
解放军总医院第一医学中心检验科

房颤是临床上最常见的快速心律失常，致死率高，非瓣膜性房颤已成为心血管病中最常见的疾病之一。房颤易发生血栓栓塞事件，尤其是脑动脉栓塞和外周动脉栓塞。因此，房颤患者为预防脑卒中，抗凝剂的应用是最重要的治疗方案。如今传统抗凝剂、新型口服抗凝剂等常规剂量的应用仍面临着出血与栓塞的问题。为了实现个体化治疗，减少出血风险，对基因多态性研究显得尤为重要，本研究主要针对此方面做一综述。

达比加群酯作为新型口服抗凝药，其疗效与安全性较为肯定，与华法林相比具有诸多优势，预防脑卒中的效果明显优于华法林; 目前临床上使用的达比加群酯普遍存在个体差异，基因的多态性对于达比加群酯的影响主要包括药物代谢及药物动力学方面。国外研究普遍接受 CES1 和 ABCB1 基因可以作为接受达比加群酯治疗的非瓣膜性房颤患者发生不良心脑血管事件的独立预测因子，对于携带等位基因 CES1 SNP rs2244613 而导致出血不良事件，可以选用低剂量达比加群酯; ABCB1 与 CES1 SNP rs8192935 可能会有小概率缺血性事件的发生，可适当予以提高剂量; 杂合子 143G/E 基因型对于达比加群酯的激活、活化速率有影响，如今并没有确切相关试验表明会引起不良事件的发生。

基于 CES1、ABCB1 基因多态性的指导更好地提高药物的疗效与安全性。然而现在相关临床研究主要集中在西方人群中，由于基因多态性的差异，在不同人种及个体中达比加群酯的药代动力学及药效动力学存在较大差异。因此，尚需进一步在亚洲人群中开展相关研究，并推动中国基因多态性检测指导临床工作，提升抗凝药物使用的安全有效性，减少不必要的不良事件发生，有助于临床进一步权衡达比加群剂量，使抗凝治疗更合理安全，从而实现个体化治疗。

PO-1159

结合机器学习和血常规分析揭示中性粒细胞过度激活在 SARS-CoV-2 感染重症化中的作用

秦士杰、夏欣一
中国人民解放军东部战区总医院

目的 目前已知有 7 种冠状病毒可感染人类：四种只引起轻度呼吸道疾病（HCoV-229E、HCoV-OC43、HCoV-NL63 和 HCoV-HKU1），而另外三种（SARS-CoV、MERS-CoV、SARS-CoV-2）可引起严重呼吸道疾病甚至死亡。重型冠状病毒相较于轻型冠状病毒具有更强的促进细胞因子风暴的能力，导致严重的呼吸系统疾病、多器官衰竭等。系统构建人体内的信号转导网络对揭示 COVID-19 的病因学和传播特点十分必要。
方法 检索获得 7 种冠状病毒的基因组、基因和蛋白序列。病毒感染后的人类基因表达数据来自 GEO 数据库。2979 例 COVID-19 患者血液中性粒细胞及临床资料来源于武汉火神山医院。使用 edgeR R 包计算病毒感染后转录组差异表达基因。利用 GEO 数据库计算芯片表达差异基因。用 BLAST 软件比较并计算 7 种病毒的蛋白质编码基因相似性。所有患者均在实验室采用咽拭子进行 RT-qPCR 方法确诊。全自动血细胞分析仪检测所有患者血细胞比率和计数。
结果 核衣壳磷酸化蛋白在重型冠状病毒中表现出显著的保守性，但在不同的轻型冠状病毒中存在差异，表明核衣壳磷酸化蛋白参与致病反应。感染 SARS-CoV-2 后，宿主应答基因（HRG）、HRG 富集以及富集后 KEGG 通路的生物学过程与 SARS-CoV 和 MERS-CoV 略有重叠，但与四种轻型冠状病毒不同，并且 HRGs 对中性粒细胞过度激活的富集只在重型冠状病毒感染中常见，轻型冠状病毒中则没有。此外，临床数据表明，重症患者中性粒细胞的过度激活可能是 SARS-CoV-2 感染与其他两种严重冠状病毒（SARSCoV 和 MERS-CoV）感染相似临床症状的一个主要因素。
结论 本文揭示了 SARS-CoV-2 编码蛋白的特征和宿主对其感染的反应，为 SARS-CoV-2 的致病机制提供了开创性见解，强调了中性粒细胞失调在 SARS-CoV-2 致病的关键作用，揭示了宿主对 SARS-CoV-2 感染反应的信号转导网络和关键转录因子，揭示了为 SARS-CoV-2 可能的致病机制。（本文部分内容已发表于 Bioinformatics，IF=5.61）

PO-1160

恢复期血浆治疗 COVID-19 患者的安全性与有效性研究: 来自匹配病例对照研究和荟萃分析的证据

蒋卫军、夏欣一
中国人民解放军东部战区总医院

目的 新型冠状病毒（COVID-19）自大流行以来，已造成全球数千万人的感染。鉴于 COVID-19 快速传播，目前没有针对 COVID-19 的特定治疗制剂或疫苗。一些临床治疗方法，如托珠单抗疗法和恢复期血浆疗法(CPT)，正在研究中。CPT 是较有前景的治疗方法之一，受到越来越多国家研究人员青睐。但 CPT 在 COVID-19 中的临床疗效和安全性尚不清楚。
方法 本病例对照研究所有被纳入患者均经 qRT-PCR 确诊为新冠肺炎病例，所有患者都接受了其他标准治疗，实验组还接受恢复期血浆治疗。我们对 2020 年 8 月 31 日之前发表的研究进行关键词检索，检索数据库包括 PubMed，Web of science 和 MedRxiv，并手动检索纳入文章的参考文献以获取其他相关文章。
结果 我们纳入共 326 例患者研究（CPT 组 163 例和对照组 163 例）。发现 CPT 组患者住院天数明显高于对照组(P < 0.0001)。CPT 组与对照组在年龄、病情严重程度、出院情况、基础疾病、ICU 人数等方面无显著差异。我们荟萃分析 498 例 CPT 治疗患者和 557 例标准治疗患者，评估 CPT 在 COVID-19 患者中临床疗效和安全性。发现与标准治疗对照组相比，接受 CPT 治疗患者组

死亡率显著降低 (OR= 0.496, 95%CI= 0.342-0.719, P< 0.0001)，序贯性分析也发现这是真阳性结果。在不良事件方面，虽然荟萃分析发现，相比于对照组，CPT 治疗患者不良事件发生率显著增加，序贯性分析发现其是假阳性结果。而在住院时长，临床症状改善和出院率方面，未发现两组之间差异性。

讨论 CPT 作为较有前景的治疗方法之一，其临床疗效和风险仍不清楚。John Mair-Jenkins 等人分析 CPT 治疗 SARS 冠状病毒感染的研究发现 CPT 能显著降低死亡率，特别是在症状出现后早期给予 CPT 治疗。我们也发现 CPT 能显著降低 COVID-19 患者死亡率(4.91% vs. 9.20%)。本文首次在最大样本量系统回顾和荟萃分析 CPT 治疗 COVID-19 患者的有效性和安全性研究。表明 CPT 可以显著降低 COVID-19 患者死亡率，且不良事件发生率无明显增加。这为 CPT 治疗 COVID-19 患者的有效性和安全性提供了证据。（本文部分内容已发表于 Blood, IF=17.543，ESI 高被引和 Clin Transl Med，IF=7.919 上）

PO-1161

Clinical values of combined analyses of blood routine ratio parameters in patients with acute ischemic stroke

Jia Wu、Junjun Wang
Department of Clinical Laboratory, Jinling Hospital, Medical School of Nanjing University, Nanjing 210002, Jiangsu, China

Objective To analyze the blood routine ratio parameters, systemic immune inflammation index (SII), neutrophil to lymphocyte ratio (NLR) and platelet to lymphocyte ratio (PLR) of patients with acute ischemic stroke (AIS), and assess its severity with AIS and explore its value in predicting the prognosis of AIS.

Methods A total of 116 AIS patients and 57 healthy controls were selected, Albumin (ALB), platelet count (PLT), neutrophil percentage [N(%)] and lymphocyte percentage [L(%)] were detected in AIS patients and healthy controls, respectively. SII, NLR, PLR were calculated and analyzed the level of other blood lipids and coagulation parameters at the same time as well as assessed the National Institutes of Health Stroke Scale (NIHSS) on admission and the modified Rankin Scale (mRS) and modified Barthel Index (mBI) on discharge of AIS patients.

Results Compared with the control group，Patients with AIS had a significantly increased SII (Z=-2.740, P=0.006)、NLR (Z=-3.752, P<0.001)、PLR (Z=-8.076, P<0.001). Correlation analysis showed that in AIS patients, SII were significantly positively correlated with NLR (r=0.932, P<0.001) ; SII and NLR were both significantly positively correlated with NIHSS(SII: r=0.364, P<0.001; NLR: r=0.395, P<0.001)、mRS(SII: r=0.228, P=0.019; NLR: r=0.236, P=0.015), but both were significantly negatively correlated with mBI(SII: r=-0.318, P<0.001; NLR: r=-0.375, P<0.001). multiple stepwise regression analysis showed that after correcting for the effects of age, sex, blood lipids, and coagulation parameters, SII (corrected R2=0.228, β=0.526, P=0.030) remained significantly independent of the NIHSS score. According to ROC curve analysis, the area under the ROC curve AUC of the combined SII, NLR, and PLR three parameters to distinguish the AIS group and the control group was 0.903(95% CI: 0.858 ~0.948, P<0.001). Logistic regression analysis showed that SII(OR=2.287, 95%CI: 1.120~4.670, P=0.023) 、PLR(OR=2.090, 95%CI: 1.118~3.905, P=0.021) can still be used as independent predictors of AIS after adjusting for the effects of age, gender, and blood lipid , coagulation parameters; During the follow-up of 2 years, 24 patients with AIS developed cerebrovascular diseases, their SII (Z=-3.455, P=0.001) and NLR (Z=-3.262, P=0.001) were significantly higher than those without occurrence. Multivariate Cox regression analysis showed that after adjusting for the effects of age, gender, blood lipids and coagulation parameters, SII(HR=1.284, 95%CI: 1.105~1.493, P=0.001) can still be used as an independent predictor of AIS.

Conclusion The levels of blood routine ratio parameters NLR, PLR and SII in AIS patients are significantly increased; Combined analysis of SII, NLR and PLR can be used as a new indicator for evaluating the severity and prognosis of acute ischemic stroke.

PO-1162

建立和验证预测非小细胞肺癌患者接受 PD-1 单抗治疗疗效和预后的列线图

夏艳、袁世进、谢鑫友、张钧
浙江大学医学院附属邵逸夫医院

背景 程序性细胞死亡蛋白-1（PD-1）单抗显著改善晚期非小细胞肺癌（NSCLC）患者的预后。但是缺乏简便可靠的预测标志物。本研究旨在探究 NSCLC 患者的临床特征和外周血实验室指标与 PD-1 单抗治疗疗效及生存的相关性，并建立相应的预测模型。
方法 纳入浙江省内 8 家医院共 203 例接受 PD-1 单抗单药治疗的 NSCLC 患者，其中 92 例作为训练队列，111 例作为验证队列。此外，纳入 124 名接受化疗的患者作为对照队列。收集患者治疗前的临床资料和实验室指标。在训练队列中，多因素 Logistic 和 Cox 模型分别确定与疗效和生存显著相关的因素，并在对照队列中探索这些因素与化疗疗效和生存的相关性。以训练队列中的显著因素为基础，构建列线图预测治疗有效、疾病无进展和生存的概率。C 指数、曲线下面积（AUC）和校准曲线评估列线图的预测效能，并在验证队列中进行验证。
结果 训练队列中，多因素 Logistic 模型确定吸烟和淋巴细胞高与 PD-1 单抗治疗有效显著相关；多因素 Cox 回归模型确定女性、年龄＞65 岁和乳酸脱氢酶高与无进展生存期较短显著相关；乳酸脱氢酶高和衍生中性淋巴比率高与总体生存期较短显著相关。在对照队列中，这些相应的因素与化疗的疗效和生存均无相关性。基于上述训练队列中明确的显著相关的因素，构建了三个列线图分别用于预测患者 PD-1 单抗第 6 周治疗有效的概率（列线图 1）、第 6、12 和 18 个月疾病无进展的概率（列线图 2）以及第 6、12 和 18 个月生存的概率（列线图 3）。列线图 1 的 C 指数和 AUC 均为 0.706；列线图 2 的 C 指数为 0.728，第 6、12、18 个月的 AUC 分别为 0.782、0.702 和 0.661；列线图 3 的 C 指数为 0.741，第 6、12、18 个月的 AUC 分别为 0.836、0.717 和 0.691；提示三个列线图均具有良好的预测效能。在验证队列中，列线图 1 的 C 指数和 AUC 均为 0.701（95%CI 0.613-0.722）；列线图 2 的 C 指数为 0.701（95%CI 0.638-0.764），第 6、12、18 个月的 AUC 分别为 0.767、0.680 和 0.634；列线图 3 的 C 指数为 0.709（95%CI 0.612-0.806），第 6、12、18 个月的 AUC 分别为 0.818、0.700 和 0.667；提示三个列线图在验证队列中依然保持良好的预测效能。同时，校准曲线展示出了每个列线图的预测概率和实际结果有良好的一致性。
结论 基于 NSCLC 患者临床特征和外周血中简便可靠的标志物建立三个列线图来预测 PD-1 单抗治疗的疗效和生存，可以帮助临床医生早期评估患者的治疗效果和预后。

PO-1163

一种血细胞形态学室间质评新方式的探索

宋颖
上海市临床检验中心

目的 采用全自动细胞图像采集设备将血涂片数字化，通过网络服务器和专用软件实现网络化阅片。改变传统的形态学室间质评单张图片识别的考核方式，用数字化血细胞图片进行检测人员阅片能力考核。
方法 此新方式使用莱卡 Aperio CS2 扫片机在油镜下选取目标识别区域进行区域扫描。得到区域细胞数字图像后，用箭头指出待考核的所有细胞。后台随机配置一定数量的考核血细胞，参加考核的

人员通过网络打开电子图片，并点击目标箭头，进行细胞识别。2019 年至 2020 年共进行 5 次调查。调查所选用的图片来源为正常体检人员的血涂片样本。
结果 调查所选取的形态识别类型包括：中性粒细胞、嗜酸性粒细胞、嗜碱性粒细胞、小淋巴细胞、大淋巴细胞、异形淋巴细胞、单核细胞、红细胞、血小板、杂质。其中，识别率较高的细胞为中性粒细胞、嗜酸性粒细胞、小淋巴细胞和杂质。交易混淆的细胞为淋巴细胞有假核仁、反应性淋巴细胞/大淋巴细胞/单核细胞、正常红细胞/小红细胞/球形红细胞、镰状红细胞/泪滴红细胞/裂红细胞、巨大血小板/小血小板。同年形态学室间质评新方式考核回报结果为 70 至 80%，而传统考核回报结果为 98%。传统考核方式照片和照片之间的联系不够，和细胞形态学的实际检验工作相距甚远，无法使用量化指标对参与者进行考核。新方式的好处在于细胞形态的室间质评和细胞形态的实际检验工作相一致，并且能够采取量化指标对参与者进行考核。
结论 运用此新方式，参加者可以随时比较箭头所指细胞与整张片子中其他细胞的形态差异，结合所给图片信息作出正确的判断。此方式为随机抽取考核，参加室间质评的各实验室考核内容各有所异，不同于旧方式次序不同但内容相同。血细胞形态学室间质评新方式改变了传统的形态学室间质评考核模式，室间质评结果更加公平公正，具有说服力。若被应用在细胞形态学的室间质评中，可提供较为一致的质评，且更能体现公平和公正原则。

PO-1164

不明原因血细胞减少症中 MDS 的早期鉴别诊断模型的初步建立

常青
中国人民解放军总医院第一医学中心

目的 血细胞减少症（blood cytopenia）是指血液中红细胞、白细胞及血小板一系或多系减少，其原因包括营养性、免疫性、理化因素、肿瘤性等。在不明原因血细胞减少症中，临床最关注的是一类是骨髓增生异常综合征（myelodysplastic syndrome，MDS），MDS 是一组克隆性造血干细胞肿瘤，其特征是造血细胞存在不同程度的病态造血（dysplasia），外周血呈一系或多系的血细胞减少。约 60%以上的患者，因骨髓或外周血中髓系原始细胞并未明显升高，又缺乏特异性诊断标志物，多数病例混于不明原因血细胞减少症中，其早期鉴别诊断一直是个难题，且对于该病的及时治疗干预至关重要。本研究旨在将 MDS 从不明原因血细胞减少症中更准确地鉴别出来，为临床尽早进行血液专科治疗提供依据。
方法 对该实验入选的患者信息收集，进行单因素和多因素分析。包括性别、年龄、症状与体征、病史，临床常规检查结果；进行血液专科检查及数据收集，包括血液常规、血细胞形态、生化指标（铁代谢、叶酸/B12）、骨髓细胞形态、骨髓活检病理、免疫分型、染色体核型，38 种髓系肿瘤相关基因突变（包含了 WHO 2016 诊断标准列出所有髓系肿瘤相关基因突变）。
预期结果和结论 综合利用患者的临床信息、血液指标、骨髓细胞形态学与骨髓活检病理、流式免疫分型 CD 分子、染色体核型，以及 38 种髓系肿瘤相关基因突变。建立不明原因血细胞减少症早期鉴别诊断指标和参数的数据库，用于进一步模型建立与疾病诊断分析。以期实现对不明原因血细胞减少症中 MDS 的早期精准鉴别诊断，并进一步优化 MDS 诊断指标和诊断模式。

PO-1165

血小板活化功能异常性疾病发病机制探究

张驰昊、戴菁
上海交通大学医学院附属瑞金医院

目的 对 3 名血小板功能障碍的患者及其家系成员进行深入研究，明确患者的临床表型，并结合基因检测结果，尝试对患者的发病机制进行探究。

方法 采用血小板聚集试验观察血小板在多种刺激剂作用下的聚集反应；采用流式细胞术检测血小板表面功能受体的表达水平，以及经凝血酶刺激后活化标记（CD62p）的阳性率；采用血块收缩试验与血小板铺展试验评估血小板表面受体与细胞骨架蛋白的功能；同时对患者进行全外显子组基因测序，初步筛选其基因组中具有潜在致病可能的突变，并使用 Sanger 测序对可疑突变进行验证。
结果 患者 1 血小板对多种刺激剂诱导的聚集减低，其血块收缩率与血小板平均铺展面积均低于正常对照。患者 2 血小板对 ADP（2μM）诱导的聚集减低，血块收缩率低于正常对照，流式分析显示经凝血酶（0.05U/mL）活化后其血小板表面 CD62p 阳性率低于正常对照；患者 2 及其父亲均在 HPS5 基因上存在一个杂合的错义突变（c.3122C>T, p.Thr1041Met）。患者 3 血小板对 ADP（2μM）诱导的聚集减低，流式分析显示经凝血酶（0.05U/mL）活化后其血小板表面 CD62p 阳性率低于正常对照；患者 3 及其母亲、外祖父均在 ITGA2B 基因上存在一个杂合的错义突变（c.1212C>A, p.Asp404Glu）。
结论 血小板功能通常受到多种因素的影响，故血小板相关疾病的临床表型和发病机制往往较为复杂。本文对 3 名血小板功能障碍的患者进行了研究与分析，后续可进一步探究患者存在的可疑突变对蛋白功能的影响，这将有助于阐明疾病的发病机制，为血小板相关疾病的诊断与研究提供新的参考。

PO-1166

miR-181c 增加可调节 GATA2 缺陷细胞的存活率

陈锐[1]、王文新[2]
1. 首都医科大学附属北京同仁医院
2. 美国国立卫生研究院

GATA deficiency is caused by germline mutations in GATA, leading to loss of function or haploinsufficiency of the GATA transcription factor. GATA deficiency is manifested by severe cytopenias of multiple cell lineages, susceptibility to opportunistic infections and strong propensity to develop myelodysplastic syndrome (MDS) and acute myeloid leukemia. In this study, miRNA profiles were evaluated and eight miRNAs were found to be differentially expressed ($p \leq 0.05$) in patient derived GATA deficiency cell lines in comparison to controls. Cell death assays indicated that miR-181c potently induces cell death. GATA expression led to significant repression of miR-181c expression in transfection experiments. Conversely, knock-down of GATA by RNA interference led to increased miR-181c expression. These findings indicate that miR-181c expression is increased in GATA deficiency cells, and that GATA represses miR-181c transcription. Increased miR-181c may contribute to elevated cell death, in GATA deficient cells.

PO-1167

Development of an ultrasensitive fluorescent immunochromatographic assay based on multilayer quantum dot nanobead for simultaneous detection of SARS-CoV-2 antigen and influenza A virus

Wanzhu Shen、Chongwen Wang、Rui Xiao
Beijing Institute of Radiation Medicine

Background The ongoing coronavirus disease 2019 (COVID-19) pandemic, which is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has rapidly spread to over 214 countries since December 2019 and resulted in more than 104 million infected individuals and over 2.27 million deaths. The early symptoms (mainly cough and fever) of SARS-CoV-2 infection

mimic those of common respiratory viruses, such as influenza A virus (FluA); as such, controlling the epidemic spread and guiding clinical treatment are difficult. Thus, methods for accurate and rapid diagnosis of FluA/SARS-CoV-2 are urgently needed.
Methods Here, we developed a two-channel fluorescent immunochromatographic assay (ICA) for ultrasensitive and simultaneous qualification of the two viruses in biological samples. A high-performance quantum dot nanobead (QB) was fabricated by adsorption of multilayers of dense quantum dots (QDs) onto the SiO2 surface and used as the highly luminescent label of the ICA system to ensure the high-sensitivity and stability of the assay. The combination of monodispersed SiO2 core (~180 nm) and numerous carboxylated QDs formed a hierarchical shell, which ensured that the QBs possessed excellent stability, superior fluorescence signal, and convenient surface functionalization. The fluorescence signals of SiTQD labels on the two T lines could be easily observed using a UV light source for qualitative detection and quickly measured by a commercial fluorescent reader for quantitative analysis of SARS-CoV-2 and FluA.
Results Under the optimal conditions, the SiTQD-ICA simultaneously detected SARS-CoV-2 NP and FluA H1N1 in throat swab samples with LOD values of 5 pg/mL and 50 pfu/mL, respectively. The compared test results verified that the sensitivity of SiTQD-ICA was improved by about 100 times than that of traditional AuNP-based ICA method and over 20 times than that of ELISA kits. Moreover, our method showed high accuracy and specificity in throat swab samples.
Conclusions To the best of our knowledge, this work is the first to develop a two-channel ICA for simultaneous detection of SARS-CoV-2 and FluA. The proposed method is a promising and convenient tool for detection of respiratory viruses.

PO-1168

红细胞碎片参数在不同基因型地贫中诊断价值的探讨

李轶勋、武坤、郭翀、斯南卓玛、陈睿
昆明医科大学第一 附属医院

目的 探讨红细胞碎片参数（Fragmented red blood cells FRC）针对不同基因型的地中海贫血，其诊断价值的大小。
方法 收集 2018 年 2 月至 2021 年 2 月间到院就诊的地中海贫血疑似病例 724 例，采集其样本进行血液细胞分析及地中海贫血基因检测，记录红细胞碎片及常规红细胞参数结果，地贫基因分析结果。通过构建受试者工作特征曲线(Receiver operating curve ROC) ，分析比较红细胞碎片参数以及常规的 HGB、HCT、MCV、MCH、MCHC、RDW 等参数针对不同基因型地贫的诊断运用价值。
结果 （1）724 例疑似病例中，野生型 473 例（65.33%），非野生型 251 例（34.37%）。地贫基因阳性病例中，占比较高的基因型如下：aa/--SEA 基因型共 64 例（25.50%），aa/-3.7a 基因型 48 例（19.12%），βO 型 CD41-42(-TCTT)共 28 例（11.16%），βO 型 CD17 A>T 共 25 例（9.96%），β+型 CD26 G>A 共 27 例（10.76%），β+型 IVS II-654 C>T 共 23 例（9.16%）。（2）野生型和非野生型 FRC 参数均值比较 P＜0.05，差异有统计学意义。（3）在 aa/--SEA 型、βO 型 CD41-42(-TCTT)型、βO 型 CD17 A>T 型三种亚型中，FRC 绝对值 ROC 曲线下面积（AUC）分别为 0.916、0.916、0.915，FRC 百分比 AUC 分别为 0.908、0.929、0.917；在 β+型 IVS II-654 C>T 型、β+型 CD26 G>A 型、aa/-3.7a 型三种亚型中，FRC 绝对值 AUC 分别为 0.897、0.704、0.579，FRC 百分比 AUC 分别为 0.910、0.740、0.579。常规血液细胞分析参数（HGB、HCT、MCV、MCH、MCHC、RDW）AUC 均未超过 0.5。（4）若 FRC 参数联合 MCV、MCH，在 β+型 IVS II-654 C>T 型、βO 型 CD41-42(-TCTT)型、aa/--SEA 型、βO 型 CD17 A>T 型四种亚型中，AUC 可达 0.972、0.959、0.947、0.939，在 β+型 CD26 G>A 型、aa/-3.7a 型两种亚型中，AUC 可提升至 0.913、0.807。
结论 FRC 参数在本地区常见的地中海贫血基因型中的诊断价值明显优于 MCV、MCH、MCHC 等常规血液分析的筛查指标，且针对不同基因型其诊断效用不同。若将 FRC 参数与 MCV、MCH 联合运用，可提高地中海贫血筛查的效用，为地贫筛查拓展了新思路，新方法。

PO-1169

Isolation of circulating tumor cells in patients undergoing surgery for esophageal cancer and a specific confirmation method

Yingjie Chen
Department of Clinical Laboratory, Second Hospital of Shandong University

The clinical significance of circulating tumor cells (CTCs) in patients with esophageal squamous cell carcinoma (ESCC) who have undergone radical surgery was investigated. A novel confirmation method for identifying CTCs or circulating tumor microemboli (CTM) in ESCC was also investigated. Blood samples from 55 patients with ESCC were collected 1-3 days prior to surgery and 7 days post-surgery. All patients underwent curative thoracic esophagectomy and lymphadenectomy. Blood samples from 20 healthy volunteers were obtained as controls. Isolation by size of epithelial tumor cells was also performed. The overall CTC detection rate was 52.7% preoperatively and 49.1% postoperatively. The presence of CTCs correlated with the Tumor-Node-Metastasis stage and the Log odds of positive lymph nodes. No significant difference in perioperative CTC transformation was discovered between the thoracoscopic and laparoscopic approach, and the open approach. The P40+/cluster of differentiation (CD)45- phenotype was confirmed in the CTCs and CTM. The isolation by size of epithelial tumor cells method appeared to have high sensitivity for detecting CTCs within ESCC patients. Immunofluorescence staining for CD45 and P40 was a specific, accurate and conve_x0002_nient method for confirming the presence of CTCs or CTM in patients with ESCC, and is strongly recommended as a supple_x0002_ment to morphological analysis.

PO-1170

The significance of coagulation and fibrinolysis-related indexes in predicting venous thrombosis after breast cancer surgery

Lijie Su
The Second Hospital of Jilin University

Background We aimed to explore the expression level of coagulation and fibrinolysis-related indexes in the plasma of breast cancer patients after surgery, and analysis their predictive value for deep venous thrombosis (DVT).
Methods From May 2016 to May 2019, 65 patients with lower extremity DVT after radical mastectomy in our hospital were selected as the thrombus group, and 74 patients without venous thrombosis after radical mastectomy were selected as the control group. The levels of D-dimer (D-D) and fibrinolytic product (FDP) were measured by latex enhanced immunoturbidimetry, Fibrinogen (FIB) levels were measured using the von Clauss method, thrombin antithrombin complex (TAT) levels were measured by enzyme-linked immunosorbent assay (ELISA), and the evaluation value of coagulation markers on tumor thrombosis was analyzed by receiver operating characteristic curve (ROC) curve analysis.
Results There were significant differences in blood pressure, platelet count (PLT) level, and tumor metastasis between the two groups ($P<0.05$). The levels of PT, D-D, FDP, and TAT in the thrombus group were significantly higher than those in control group ($P<0.05$). The area under the curve (AUC) of D-D, FDP, and TAT were 0.790, 0.881, and 0.672, respectively and there was a marked difference among the indexes ($P<0.05$). The AUC of FDP was the largest, and the sensitivity and diagnostic value of FDP were the highest.

Conclusions The plasma levels of FDP, D-D, and TAT in breast cancer patients with DVT after radical mastectomy were significantly increased, which is related to imbalanced coagulation and fibrinolysis functioning in patients. FDP had the highest predictive value for DVT after radical mastectomy.

PO-1171

Clinical applications of monitoring immune status with 90 immune cell subsets in human whole blood by 10-color flow cytometry

Weiwei Wang[1]、Haibo Li[2]、Lihua Zhang[1]、Wenli Jiang[1]、Lisong Shen[1]、Guang Fan[2]
1. Clinical laboratory, Xinhua hospital, Shanghai Jiaotong University of Medicine School, Shanghai,200092,China
2. Department of Pathology, Oregon Health and Science University, Portland, Oregon, USA.

Introduction The immune system may involve and predict the different prognosis and therapy consequences. So, it's important to monitor and evaluate the immune status before and after treatments.
Methods Flow cytometry is the best technology to perform immune monitoring, because it can detect immune cells using small amount of sample in a short time. The whole blood is the ideal sample for immune status monitoring, since it includes almost all the immune cells and it's relatively easy to obtain and less invasive than bone marrow or lymph node.
Results Here we developed and validated a 10-color panel with only four tubes containing 29 antibodies to monitor 90 immune cell subsets in 2 ml whole blood samples. The major immune cell populations detected by our panel included T cell subsets (CD3+total T, Th, Tc, Treg, CD8hi, CD8low, αβTCR, γδTCR, naïve, and memory T), T cell activation markers (CD25, CD69, and HLA-DR) and one immune checkpoint PD1, B cell subsets (B1, switched memory, non-switched,naïve B, and CD27-IgD B cells),neutrophils, basophils, four monocytic cell subsets, dendritic cells (pDCs and mDCs),and four NK cell subsets. These panels of antibodies had been applied to monitor immune status (percentage and absolute number) in total 303 cases with various diseases, such as leukemia (AML, CML, MM, and ALL), lymphoma (B cells and NK/T cells), cancers (colon, lung, prostate, and breast), immune deficiencies, and autoimmune diseases.
Conclusion We provided proof of feasibility for clinical monitoring immune status and guiding immunotherapy by multicolor flow cytometry testing.

PO-1172

Perioperative change in neutrophil count predicts worse survival in esophageal squamous cell carcinoma

宋倩
中国科学院大学附属肿瘤医院（浙江省肿瘤医院）

Background This study aimed to investigate the relationship between perioperative change in neutrophil count and survival of patients with esophageal squamous cell carcinoma (ESCC).
Methods Neutrophil change (Nc) (Nc=Post-Neutrophil–Pre-Neutrophil) was counted according to data within one week before surgery and two weeks after surgery. All patients were divided into two groups (Nc≥2.60 and Nc<2.60) according to the median of Nc.
Results Multivariate analysis revealed that neutrophil change(Nc)(≥2.60 vs.<2.60) was an independent prognostic marker for overall survival (OS). Subgroup analysis suggested that OS of male patients, age≤60 patients, patients without vessel invasive and patients without nerve infiltration were dramatically worse for those with neutrophil change(Nc)(<2.60).

Conclusions Perioperative change in neutrophil count predicts worse survival in ESCC after the operation.

PO-1173

Impairment of proliferation and hematopoietic support function in bone marrow mesenchymal cells derived from myelodysplastic syndrome patients

Juan Wu[1]、Jiadi Chen[2]、Xuchun He[3]、Yanfang Lin[2]、Huifang Huang[2]
1. Fujian Medical University
2. 福建医科大学附属协和医院
3. 福建省卫生职业技术学院

Myelodysplastic syndrome (MDS) is characterized by a group of heterogeneous clonal disease derived from hematopoietic stem cells (HSC) and a high risk of transforming to leukemia. Bone mesenchymal stromal cells (BMSCs), as an important component of bone marrow microenvironment, play a pivotal role in the pathogenesis of MDS. Some previous studies have shown that the BMSCs derived from patients with MDS (MDS-BMSCs) exhibited the genetic abnormalities, biological and functional alterations. However, the knowledge of MDS-BMSCs is still limited and controversial. In the present study, we investigated the genetic, biological and functional characteristic of MDS-BMSCs. Although we failed to found the chromosome abnormalities which was reported in some previous literature, we found MDS-BMSCs exhibited defective proliferation and more prone to senescence partly due to the activation of p53/p21 pathway. Moreover, our study suggested MDS-BMSCs displayed significantly diminished ability to support hematopoiesis and dysregulation of some key hematopoietic cytokines gene expression including IL-6, TGF-β, GM-CSF and G-CSF. Taken together, our data showed that defective proliferation and dysfunctional hematopoietic support capacity of MDS-BMSCs.

PO-1174

Single-cell multi-omics analysis reveals the Leydig cells developmental obstacles and related mechanisms in non-obstructive azoospermia patients

Haihong He、Fan Yu、Yiwen Zhou
Clinical Laboratory Medical Center, Shenzhen Hospital, Southern Medical University

Non-obstructive azoospermia is an important factor that prevents couples from acquiring offspring naturally. We constructed a single-cell multi-omics map of NOA and normal people and found that testicular cells of NOA patients are mainly composed of somatic cells. MYC and TSSK6 were identified as hub genes among the 301 differentially expressed genes. We further focused our research on LCs and identified ACTA2, CDKN1A, SOD2 and TNFAIP3 as key genes. The pseudo-chronological analysis showed that ACTA2 increased rapidly in the later stages of cell development, while the developmental trajectories of the other 3 genes were basically the same. For the first time, we found transitional LCs between the NOA group and the normal group and the most important marker genes are CDH1, GREM1 and ABCG1. Gene Set Enrichment Analysis showed that the male gamete generation gene set was highly expressed in transitional LCs. Transcription factor analysis showed that EGR1 (975g) and JUND (156g) play an important role in the development of LCs. Gene set variation analysis showed that the NGF and Wnt signaling pathways are the key pathways that affect the development of LCs. Further analysis of the interaction between testicular cells showed that the NGF signaling pathway has

close interactions in LCs and other testicular cells, especially the NGF-NGFR ligand receptor pair. Our research reveals that LCs has developmental obstacles in NOA and further reveals the key genes, transcription factors and key signaling pathways that affect the development of LCs, filling the related knowledge and mechanism of LCs and NOA.

PO-1175

一个遗传性蛋白 C 缺陷症家系的表型与基因型分析

丁红香、 李姗姗、 朱丽丹 、徐晓杰 、倪莉 、 江明华
温州医科大学附属第二医院

目的 探讨 1 个遗传性蛋白 C 缺陷症家系的分子致病机制。
方法 对先证者及家系成员（共 3 代 7 人）进行血浆蛋白 C 活性（PC:A）、蛋白 C 抗原（PC:Ag）含量及其他凝血指标检测。用 PCR 法对先证者蛋白 C 基因（PROC）9 个外显子及侧翼序列进行扩增，PCR 产物纯化后进行直接测序；对可疑的突变用反向测序进行验证，并对家系其他成员相同突变位点进行检测。分别用生物信息学软件 MutationTaster、PolyPhen-2、PROVEAN 及 FATHMM 和 ClustalX-2.1-win 分析突变的致病性和保守性；用 Swiss-PdbViewer 软件分析蛋白质三维模型和突变氨基酸之间的相互作用。
结果 先证者及其祖母、父亲和哥哥 PC:A 和 PC:Ag 分别降至 55%、52%、48%、51%和 53%、55%、50%、56%，均明显降低。基因分析显示，上述 4 名成员 PROC 第 9 号外显子均存在 c.1318C>T（p.Arg398Cys）杂合错义突变。有三个生物信息学软件对该突变的预测评分结果一致：MutationTaster 为 0.991 分，PROVEAN 为-3.72 分，FATHMM 为-2.49 分，均显示为有害的突变；保守性分析显示，Arg398 在同源物种间高度保守。蛋白质模型分析显示，在野生型 PC 蛋白质中，极性带正电的 Arg398 与 Glu341 和 Lys395 各形成 1 个氢键；当突变为极性不带电的 Cys398 后，其链变短，与 Glu341 的氢键消失，与 Lys395 增加了 1 个氢键，使蛋白质的空间结构发生了改变。
结论 c.1318C>T 杂合错义突变是该家系遗传性蛋白 C 缺陷症的分子致病机制。

PO-1176

两种不同采血方式的临床应用价值对比分析

杨丽思、尹利民、潘永圣
昆明市第一人民医院

目的 探讨不同采血方式的临床应用价值对比分析。
方法 选取昆明市第一人民医院检验科 2017 年、2018 年、2019 年至 2020 年门诊采血患者共 751421 例为研究对象，比较 2017 年、2018 年、2019 年、2020 年的检验科门诊患者采血数据、采血等待时间、采血速度和针刺伤风险率的情况。
结果 2017 年均采用蝶翼针采血，全年采血量为：152873 例，2018 年开始采用直针采血技术以后，2018 年至 2020 年门诊采血量分别为 186554 人次、220668 人次、191146 人次，采血量的增长率分别为 22%、18.2%、44%。我科 2017 年、2018 年每天平均 6 名采血人员在工作，2019 年减少到平均每天 5 名采血人员，2020 年平均每天 4 名采血人员即可完成采血工作，使用直针技术后提高了采血速度，同比 2017 年蝶翼针采血数据每人日采血量分别增加了 22%、73.2%、86.7%；同比 2017 年的碟翼针针刺伤数据，2018 年直针采血针刺伤率风险率下降 33%，2019 年下降 50%，2020 年下降 66.7%。
结论 直针采血技术的运用提高了采血人员的采血速度，缩短了患者采血等待时间，提高了工作效率，显著降低了针刺伤风险。

PO-1177

ADAMTS13 基因突变所致低活性与血栓事件发生风险的关联

陈俊捷、李蕾、梁茜、陆晔玲
上海交通大学医学院附属瑞金医院

目的 探讨发生血栓疾病的人群中 ADAMTS13 基因突变所导致 ADAMTS13 低活性之间的关联，以及临床检测 ADAMTS13 是否具有一定的诊断价值。
方法 收集来自上海交通大学医学院附属瑞金医院的 24 例血栓病人血浆标本以及 40 例正常对照血浆标本，对病人的血浆标本进行 ADAMTS13 活性及抗原检测，以及 ADAMTS13 基因测序，筛选出 ADAMTS13 基因上存在突变的患者，以 ELISA 法检测 ADAMTS13 的抗原，FRET 法检测 ADAMTS13 的活性。
结果 对携带 ADAMTS13 基因突变患者的血浆进行 ADAMTS13 活性及抗原分析，发现较正常人群差异不大，但对 14 个 ADAMTS13 活性检测低值的标本分析后，发现除 ADAMTS13 活性降低，同时也存在 VWF 抗原升高，而 VWF 活性无明显升高，进一步检测发现这些样本的 ADAMTS13 突变位点多集中在 ADAMTS13 的 Disintegrin 结构域和 tsp1-5 结构域。
结论 本次对 24 例血栓病人进行 ADAMTS13 基因分析及 ADAMTS13 活性及抗原分析显示，携带 ADAMTS13 基因中位于 Disintegrin 结构域和 tsp1-5 结构域中的突变可导致 ADAMTS13 活性降低及 VWF 抗原水平升高，可能是与 Disintegrin 结构域包含的外泌体能够增强 MP 结构域的蛋白水解功能以及 tsp1-5 结构域能够调节 ADAMTS13 蛋白结合 VWF 的能力有关。因此，若患者携带了 ADAMTS13 该结构域的突变，其发生血栓性疾病的风险升高。而在 tsp1-8 结构域、tsp1-3 结构域、富半胱氨酸结构域和 cub-2 结构域存在突变的患者血浆的 ADAMTS13 活性及抗原水平与正常对照相比未见明显异常，其血栓发生与 ADAMTS13 突变的关系有待进一步探究。本研究显示检测 ADAMTS13 活性较检测 ADAMTS13 抗原更有意义，对临床更具有诊断价值。

PO-1178

缺血性脑卒中患者凝血和纤溶系统标志物的临床意义

宋佩佩[1]、李伟[2]、赵灵芝[1]、尤崇革[1]
1. 兰州大学第二医院
2. 中南大学湘雅医院

目的 探讨新型血栓标志物血栓调节蛋白（TM）、凝血酶-抗凝血酶复合物（TAT）、纤溶酶-α2 抗纤溶酶复合物（PIC）、组织型纤溶酶原激活物-纤溶酶原激活物抑制剂-1 复合物（t-PAI-C）在缺血性脑卒中患者中的临床意义。
方法 采用化学发光酶免疫法检测 176 例确诊的缺血性脑卒中患者初次入院时血浆 TM、TAT、PIC、t-PAI-C 水平，比较缺血性脑卒中患者与 60 名健康对照组之间的差异，同时分析这些标志物在动脉粥样硬化型卒中与腔隙型卒中之间的表达差异；短期随访三个月，记录 mRS 量表评分、卒中复发和死亡率。
结果 缺血性脑卒中患者组血浆 TM（9.83±3.14 vs 8.29±2.30 TU/ml）、TAT（3.70±3.48 vs 1.39±0.77 ng/ml）、PIC（0.70±0.56 vs 0.48±0.17 ug/ml）和 t-PAI-C（8.10±3.07 vs 6.14±2.71ng/ml）水平均明显高于正常对照组，且差异均存在统计学意义（$P < 0.01$）。动脉粥样硬化型卒中相比腔隙型卒中患者有更高的 TAT（4.07±3.12 vs 2.55±1.65 ng/ml，$P < 0.05$）和 PIC（0.75±0.53 vs 0.59±0.20 ug/ml，$P < 0.05$），TAT 的 ROC 曲线下面积为 0.649，敏感度 56.9%，特异度 76.1%。三个月有效随访患者 168 例，无死亡事件，预后不良的患者复发率更高（13/72 vs 5/96）；短期预后不良（mRS > 2）较预后良好患者血浆 TAT（5.58±4.81 vs 2.37±1.47 ng/ml，$P < 0.05$）和 PIC（0.86±0.57 vs 0.56±0.25 ug/ml，$P < 0.05$）更高，而 TM 和 t-PAI-C 在卒中亚型和预后中无明显差异。

结论 缺血性脑卒中患者存在血管内皮损伤及凝血和纤溶系统功能紊乱，初次血浆 TAT 和 PIC 水平与卒中亚型和患者预后相关，可作为缺血性卒中鉴别诊断及预后判断的辅助指标。

PO-1179

NAGL 和 IL-8 用于儿童早期尿路感染快速诊断的实验研究

余抒、李如飞
重庆市重钢总医院

目的 探讨尿液中 IL-8 和 NAGL 的表达变化与尿路感染 (urinary tract infection, UTI)以及在早期肾损伤的关系。POCT 具有“快速、便携、操作简单”等优势，突破了诸多限制，在医院检验科、急诊科、社区门诊、家庭健康管理、疫情控制等多个领域得到充分应用和推广，解决了传统大型医疗设备的使用局限，尤其是在医院资源相对落后的地区实现检验指标的快速实施。
方法 选取 6 周龄以下儿童 150 例，根据 UTI 临床诊断分为 3 组：A 组为初次诊断为尿路感染未实施临床治疗的患儿 50 例；B 组为既往尿路感染实施治疗后复发的患儿 50 例；C 组为未发生急慢性感染的儿童 50 例。为了进一步研究 NGAL 在肾损伤中的表达变化，将 UTI 标本分为 D 和 E 组，其中 D 组为 UTI 且包含合并症 44 例；E 组为单纯性 UTI 56 例。采用干化学技术分别检测入组标本尿液中 IL-8 和 NAGL 的浓度，分析两者在不同临床分组中的表达变化，结果进行统计学分析。
结果 通过对 IL-8 和 NAGL 的检测分析，IL-8 在尿路感染中呈现显著性高表达，p 值分别为 0.007 和 0.0015，并且初次感染表达明显高于再次感染；NAGL 不仅在尿路感染中呈现高表达(*p=0.008)，同时在伴有合并症的尿路感染中表达显著性升高(#p=0.005)。通过 Mann-Whitney U 检验分析得出：UTI 组中 IL-8 表达显著高于正常对照(*p=0.007)，差异显著；同时复发组中 IL-8 表达也高于对照(#p=0.0015)，差异显著，说明 IL-8 可以作为初次以及复发性尿路感染的重要提示(如图 1A 所示)。尿液 NAGL 在 UTI、复发性 UTI 均呈现高表达，且与正常对照差异显著(p 值分别为 0.008，0.005)，说明 NAGL 在尿路感染的不同阶段均具有指示性作用。
结论 本研究通过对 IL-8、NGAL 在 UTI 诊断中的分析，探讨两种指标在尿路感染发生以及合并症出现时 IL-8 和 NGAL 的表达变化。以便辅助临床快速筛查 UTI 患儿，为及时诊断治疗儿童 UTI 提供简便、准确、可靠的实验依据，减少或避免 UTI 迁延不愈、肾脏瘢痕结局的发生，达到快速诊断儿童早期尿路感染的实验目的。

PO-1180

Value of TAT, PIC with D-dimer for Cancer Patients with Metastasis

juan Cui
Chinese Academy of Medical Sciences and Peking Union Medical College

Introduction The hypercoagulability of blood is related to the development and metastasis of cancer. High levels of D-dimer have been reported to be associated with the metastasis and poor prognoses of cancer. Here, we investigated the performance of biomarkers—TAT, PIC, TM, and tPAI·C by new method—for monitoring cancer patients with metastasis.
Methods A total of 197 cancer patients were enrolled. TM, TAT, PIC, and tPAI·C were detected by the chemiluminescence immunoassay.
Results Results showed that the levels of TAT and PIC were higher in the metastasis group than those in the nonmetastasis group (P < .01). In the nonmetastasis group, there were 16 patients with elevated levels of D-dimer. But, TAT and PIC in these 16 patients were all at normal level (<0.55 mg/L FEU). After dilution, D-dimer was also decreased to normal levels in these 16 patients. The ROC was used to show the performance of D-dimer, TAT, and PIC on indicating cancer with metastasis. The AUC of PIC was higher than that of D-dimer (0.825 vs. 0.770). The

specificity and PPV of TAT and PIC were higher than those of D-dimer. Serial test of TAT, PIC, and D-dimer improved the specificity and positive predictive value to 90.91% [80.61%, 96.25%] and 89.29% [77.45%, 95.57%], respectively.
Conclusion Combining TAT and PIC with D-dimer could be useful surveillance biomarkers for cancer with metastasis.

PO-1181

细菌、真菌及 EB 病毒感染性疾病中外周血单核细胞亚群和 HLA-DR 活性的研究

刘基铎[1]、林浩颐[2]
1. 广州中医药大学第一附属医院
2. 广州中医药大学

目的 探讨不同感染性疾病的患者外周血中单核细胞及其亚群的占比和相应 HLA-DR 活性的表达是否具有统计学差异以及是否可以为相应的感染性疾病的诊断、鉴别诊断、疗效监测及预后评估提供实验室依据。
方法 收集 2020 年 8 月至 2021 年 2 月本院感染性疾病病例共 230 例，其中革兰氏阳性菌感染 47 例，革兰氏阴性菌感染 42 例，真菌性感染 46 例，EB 病毒感染 43 例，健康对照 52 例，做流式细胞学检查。
结果 实验组指标分别两两比较之后：①G+组：与对照组比较得出在总单核活性、经典型占比及其活性中表达下降，在中间型占比中表达升高；与 EB 病毒组比较得出在总单核活性、经典型活性中表达下降；与 G-组比较得出在总单核占比中表达升高，以上均具有统计学差异（P<0.05）。②G-组：与对照组比较得出在总单核活性、总单核占比、经典型占比及其活性中表达下降，在非经典型占比、中间型占比中表达上升；与 EB 病毒组比较得出在总单核活性、总单核占比、经典型活性和非经典型活性中表达下降，以上指标具有统计学差异（P<0.05）。③真菌组：与对照组比较得出在总单核活性、经典型占比及其活性、中间型活性中表达下降；与 EB 病毒组比较得出在总单核活性、经典型活性、非经典型活性、中间型活性中表达下降，具有统计学差异（P<0.05）。其余实验指标没有得出具有统计学意义的结果。
结论 不同感染性疾病的患者外周血中总单核细胞的占比和 HLA-DR 活性以及经典型、中间型、非经典型的单核细胞亚群占比和 HLA-DR 活性等的表达是不同的。分析不同感染性疾病的单核细胞及其亚群的占比和 HLA-DR 活性变化可以为相应的感染性疾病的诊断、鉴别诊断、疗效监测、预后评估提供实验室依据。

PO-1182

三种心脏病患者的外周血单核细胞亚群及 HLA-DR 的表达水平研究

刘基铎[1]、张雨欢[2]
1. 广州中医药大学第一附属医院
2. 广州中医药大学

目的 探讨三种心脏病（冠状动脉粥样硬化性心脏病 CHD、慢性肺源性心脏病 CPHD、高血压性心脏病 HHD）中单核细胞及其亚群比例和表面 HLA-DR 活性表达的差异，为临床进一步诊断、指导治疗心血管疾病提供良好的依据。

方法 收集 2020 年 7 月至 2021 年 3 月本院收治的确诊为 CHD 患者 30 例、CPHD 患者 28 例和 HHD 患者 30 例以及健康人 43 例，通过流式细胞术分别检测外周血单核细胞及其亚群的比例和表面 HLA-DR 活性。

结果 与对照组相比，HHD 组和 CHD 组外周血单核细胞比例明显升高（P<0.05），HHD 组、CHD 组、CPHD 组外周血单核细胞、CD14++CD16-单核细胞、CD14++CD16+单核细胞表面 HLA－DR 活性表达均明显降低（P<0.05），CHD 组外周血 CD14+CD16++单核细胞表面 HLA－DR 活性表达明显降低（P<0.001），。HHD 组外周血 CD14+CD16++单核细胞表面 HLA－DR 活性表达明显高于 CHD 组（P<0.001）。CHD 组外周血 CD14++CD16-单核细胞比例与对照组、HHD 组和 CPHD 组相比明显降低（P<0.001），而外周血 CD14+CD16++单核细胞比例明显升高（P<0.001）。CHD 组外周血 CD14++CD16+单核细胞比例高于 CPHD 组（P<0.05）。

结论 HHD、CHD 及 CPHD 的外周血单核细胞及其亚群比例和表面 HLA-DR 活性表达的差异与心血管疾病的疾病进程、炎症发展机制相关。

PO-1183

应用凝血酶生成试验评估胰腺癌患者高凝状态风险的研究

赵一晨[1,2]、陆晔玲[1]
1. 上海交通大学医学院附属瑞金医院
2. 上海交通大学医学院检验系

目的 评估凝血酶生成试验(thrombin generation test, TGT)在预测胰腺癌(Pancreatic cancer)患者高凝状态中的应用价值。

方法 选取 2021 年 1 月至 2021 年 3 月就诊于上海交通大学医学院附属瑞金医院的胰腺癌患者 38 例，并将胰腺癌患者的标本根据常规凝血功能试验（Routine coagulation test，RCT）结果分为 RCT 高值组[纤维蛋白原（Fibrinogen，FIB）、纤维蛋白原降解产物（Fibrin degradation products，FDP）、D 二聚体（D Dimer，DD）中至少一项高于正常值]和 RCT 正常组（FIB、FDP、DD 各项结果均正常）。另选同期相同年龄段的 60 名健康体检者作为正常对照组。在患者知情同意的情况下，采集患者乏血小板血浆，首先进行常规凝血功能试验各项检测，同时检测患者与正常对照者在 5 pmol/L TF（tissue factor, TF）试剂激活下的凝血酶生成能力的差异。分析患者 RCT 高值组与患者 RCT 正常组、患者 RCT 高值组与正常对照组、以及患者 RCT 正常组与正常对照组之间 TGT 各参数[凝血酶生成峰值(Peak)、凝血酶生成潜力（endogenous thrombin potential, ETP）、达峰时间（time to peak, ttPeak）]的差异。

结果 在 5 pmol/L TF 激活下，RCT 高值组的 Peak、ETP 显著高于正常对照组（P<0.01）；LT、ttPeak 在 RCT 高值组与正常对照组之间无统计学意义（P>0.05）。RCT 正常组的 Peak、ETP 显著高于正常对照组（P<0.01）；LT 在 RCT 正常组与正常对照组之间无统计学意义（P>0.05）。ETP、ttPeak、Peak 在 RCT 高值组与 RCT 正常组之间差异均无统计学意义（P>0.05）。

结论 胰腺癌患者中，在 5pmol/L TF 激活下，Peak 和 ETP 是 TGT 的 4 个参数指标中评估胰腺癌患者高凝状态风险的最佳指标；且 TGT 能够在常规凝血功能试验各参数结果正常的情况下，提示胰腺癌患者存在高凝状态的风险，有助于为患者制定合理的抗凝方案提供参考。此外，研究发现 TGT 中 LT 与常规凝血实验项目（PT、TT、INR、DD、FDP、FIB）具有相关性。

PO-1184

外周血白细胞绿色包涵体合并疟色素的临床和实验室检查回顾分析

郭平
上海交通大学医学院附属瑞金医院

目的 本文旨在回顾分析一例外周血白细胞绿色包涵体合并疟色素病例的临床和实验室检查，以加深广大医务工作者对该现象的认识。
方法 研究对象为尼日利亚归国务工人员，因反复高热伴关节酸痛就诊，经确诊为恶性疟感染，后因多脏器衰竭、感染性休克等并发症，经全力救治不幸逝世。实验室检查包括血常规、C 反应蛋白、生化肝肾功能检查、免疫胶体金疟原虫抗原检测、外周血细胞形态学观察。疟原虫厚、薄血膜制备与染色，油红 O 染色。
结果 入院时血常规及生化检查结果示血小板严重减少，中性粒细胞百分比升高；C 反应蛋白升高；肝、肾功能异常，胆红素升高。入院时外周血涂片见疟原虫环状体，虫体密度高。免疫胶体金抗原检测提示恶性疟感染。治疗期间疟原虫虫体密度逐渐下降，但至治疗后期仍未完全消失，外周血及脑脊液均可见虫体残留。患者病情恶化后外周血涂片中性粒细胞出现中毒颗粒，在大约 16%的中性粒细胞以及少数单核中观察到绿色包涵体及疟色素，油红 O 染色后包涵体呈橘红色，疟色素未染色。
结论 外周血白细胞的绿色包涵体及疟色素对重症疟疾预后不佳患者病情的发展具有重要提示作用。

PO-1185

急性炎症患者联合检测 CRP 和 SAA 结果分析

王白石
天津医科大学中新生态城医院

目的 急性炎症一般起病急，持续时间短，早期症状不明显。通常是由于细菌感染、病毒感染所引起。严重的细菌感染会导致脓毒血症或脓毒性休克，容易导致儿童死亡。若能在细菌感染发病早期使用抗生素，能够明显降低死亡率；而病毒感染时，不需服用抗生素。
方法 通过分组对临床标本急性炎症期 C-反应蛋白（CRP）、血清淀粉样蛋白 A（SAA）水平和正常人群水平进行动态分析比较。
结果 各组研究对象与正常对照组 CRP、SAA 水平检测结果及 SAA/CRP 的比值比较细菌感染组患者急性期的 CRP、SAA 水平明显高于病毒感染组和正常对照组，而 SAA/CRP 比值明显低于正常对照组，差异具有统计学意义（$P<0.05$）。病毒感染组患者急性期的 SAA 水平及 SAA/CRP 比值明显高于正常对照组，差异具有统计学意义($P<0.05$)，但 CRP 水平与正常对照组相比无明显变化（$P>0.05$），差异无统计学意义。
结论 1.CRP 及 SAA 均可作为细菌感染的早期诊断指标，CRP 的特异度高于 SAA，SAA 的敏感度高于 CRP。2.SAA 在判断病毒感染方面的敏感性高于 CRP，可作为病毒感染的诊断指标。3.计算 SAA/CRP 的比值，对于病毒感染早期诊断的敏感性高于单独检测 SAA，因此 SAA/CRP 的比值对于病毒感染更具有研究价值。4.CRP 与 SAA 两种感染性标记物联合检测，有利于提高早期诊断急性炎症病因的准确性，为疾病的治疗及预后提供准确有效的实验室参考指标。

PO-1186

光镜下的凋亡细胞、胀亡细胞和焦亡细胞形态学研究

沈兴娅、赵广明、李德来、杨立顺
天津市北辰区中医医院

目的 ：用显微照片形式描述和分析光镜下凋亡细胞、胀亡细胞、焦亡细胞形态，以利于临床检验操作及临床应用。

方法 将工作中收集的复检血涂片、精液涂片、脑脊液涂片及阴道/宫颈细胞涂片经瑞-姬氏染色在光镜、油镜下拍照的显微照片，利用文献中描述的细胞程序性死亡形态学理论进行分类，对不同疾病组进行分析和总结。

结果 1.凋亡细胞形态：细胞体缩小，细胞核固缩、核碎裂、核丝断裂、核融合、凋亡小体形成；①在少精子症或畸形精子症患者精液中常可检到凋亡精子细胞和凋亡初级精母细胞，②在炎性脑脊液中常可检到凋亡中性粒细胞；③在健康体检者血涂片中凋亡中性粒细胞比例较高；④在绝经期以后妇女阴道/宫颈脱落细胞涂片中常可检到凋亡鳞状上皮细胞；⑤在含有阴道毛滴虫的阴道分泌物中，可检出凋亡的阴道毛滴虫；2.胀亡细胞形态：细胞体及细胞核胀大，细胞核边聚并胀出胞体外，核染色质分散，常出现核染色质均质化溶解和不全均质化溶解，细胞膜通透性增强，可见胞浆内有泡状物，并可见胞浆内容物渗透到胞体外；①在少精症患者精液中可检到胀亡生精细胞；②在围产期妇女血涂片中常可检到较多胀亡淋巴细胞；③在 IM 组病例中，胀亡淋巴细胞检出率达（45.7%）；3.焦亡细胞形态：细胞核类似于凋亡细胞的核固缩、核碎裂，细胞质类似于胀亡细胞的细胞质胀大，细胞膜通透性增强。

结论 凋亡细胞、胀亡细胞、焦亡细胞均属于程序性死亡，是临床检验中比较常见细胞，凋亡细胞最终被巨噬细胞吞噬，不会引起周边组织炎症，属于静默性死亡；而胀亡细胞和焦亡细胞最终会出现细胞解体，将细胞内容物等炎性因子释放，引起周边组织炎症。

PO-1187

中国表观健康老年人群外周血白细胞随龄变化趋势研究

王双、陈思、江虹
四川大学华西医院

目的 探讨外周血白细胞参数及中性粒细胞淋巴细胞比(Neutrophil to lymphocyte ratio，NLR)、血小板淋巴细胞比(Platelet to lymphocyte ratio, PLR)、淋巴细胞单核细胞比（Lymphocyte to monocyte ratio ，LMR)在中国老年人群中的性别、年龄分布特征，以了解外周血白细胞的随龄变化趋势；

方法 2018 年 4 月至 12 月，对不同地区 9 家医院招募的 14331 例健康受试者进行血液常规检测，其中 40-49 岁组 3941 例（男 2012 例，女 1929 例)、50-59 岁组 3346 例（男 1947 例，女 1399 例) 、60-69 岁组 3808 例（男 2103 例，女 1705 例) 、70-79 岁组 2222 例（男 1376 例，女 846 例)、80-89 岁组 1014 例（男 677 例，女 337 例)，对各组受试者外周血白细胞参数及血细胞比值结果进行组间比较，分析不同性别及年龄组白细胞参数与血细胞比值差异，探索年龄与 NLR、PLR 及 LMR 的相关性及其随龄变化趋势；

结果 各年龄组组间比较显示淋巴细胞计数、单核细胞计数、NLR 及 PLR 四项参数结果组间比较差异具有统计学意义（P＜0.05）；通过 Pearson 相关分析显示， NLR 与年龄呈正相关、LMR 与年龄呈负相关（P＜0.01）；NLR 随受试者年龄增加缓慢上升，LMR 随受试者年龄增长缓慢下降，PLR 无明显的随龄变化趋势；各年龄组男性白细胞、中性粒细胞、嗜酸性粒细胞计数和 NLR 均高于女性，淋巴细胞计数、PLR 和 LMR 均低于女性，差异具有统计学意义（P＜0.05）。

结论 老年人群白细胞参数及全血 NLR、PLR、LMR 结果可随受试者性别、年龄发生变化，将其应用于疾病诊断或预后评估时应充分考虑年龄及性别的影响。

PO-1188

应用外周血细胞相关指标构建重症感染评分进行感染预测研究

王双、陈思、江虹
四川大学华西医院

目的 探讨外周血细胞检测参数在感染性疾病中的变化，构建重症感染评（Intensive Care Infection Score，ICIS），应用 ICIS 进行感染早期预测评估。
方法 选取脓毒症患者 140 例，纳入脓毒症病例组；单纯感染患者 160 例，纳入感染病例组；随机选取健康体检者 100 例，纳入对照组。对研究纳入者进行血常规检测，获得外周血细胞参数结果，进行非参数分析组间比较，选取指标构建 ICIS，应用受试者工作曲线（ROC）评估 ICIS 预测感染的诊断效能。
结果 组间比较可见中性粒细胞计数（NEUT）、幼稚粒细胞计数 (IG)、高荧光强度大细胞计数（HFLC）、平均中性粒细胞侧向荧光强度(NE-SFL)、成熟红细胞与新合成红细胞间血红蛋白差异（Delta-He）五项参数结果具有明显统计学差异（P＜0.001), 脓毒症与单纯感染组 NEUT、IG、HFLC、NE-SFL 结果明显高于健康组，Delta-He 结果则低于健康组，绘制感染预测 ROC 曲线，NEUT、IG、HFLC、NE-SFL、Delta-He 曲线下面积分别为 0.830、0.872、0.630、0.837、0.804；应用 NEUT、IG、HFLC、NE-SFL、Delta-He 五项参数构建 ICIS（0-5 分），感染预测临界值为 3 分，用于感染早期预测时灵敏度为 83.6%，特异度为 72.1%。
结论 由外周血细胞参数构建的 ICIS 可作为一种简易方法预测患者感染情况，将 ICIS 与外周血炎性因子等其他感染预测指标结合使用可辅助提高临床对感染性疾病的诊断效能。

PO-1189

危重症慢性呼吸衰竭患者淋巴细胞免疫分型变化研究的临床价值

张文佳
重庆市人民医院三院院区

目的 探讨外周血淋巴细胞免疫分型在危重症慢性呼吸衰竭患者中的变化及临床价值。
方法 选取本院 64 例危重症慢性呼吸衰竭患者，根据病因将其分为肺实质炎症组、肺间质炎症组、慢性阻塞性肺疾病组和其它疾病组，同时选取 30 例健康人作为正常对照组，采用流式细胞法检测外周血 CD3+、CD3+CD4+、CD3+CD8+T 淋巴细胞绝对计数及其百分比，同时计算 CD3+CD4+/CD3+CD8+比值，比较各亚组间淋巴细胞绝对计数及其百分比差异，同时与对照组比较分析。
结果 危重症慢性呼吸衰竭患者较正常人外周血 CD3+、CD3+CD4+、CD3+CD8+T 淋巴细胞绝对计数均极显著降低（P≤0.01），当肺部疾病与其它疾病比较时，前者 CD3+CD4+/CD3+CD8+淋巴细胞比值明显升高（P≤0.05），后者明显降低（P≤0.05），其中肺实质炎症组 CD3+CD8+%极显著降低（P≤0.01），肺间质炎症组 CD3+CD8+T 淋巴细胞绝对计数明显降低（P≤0.05），慢性阻塞性肺疾病组 CD3+CD4+%明显降低（P≤0.05）和 CD3+CD4+/CD3+CD8+淋巴细胞比值明显升高（P≤0.05）；当与正常对照组的外周血淋巴细胞免疫分型比较时，肺实质炎症组和肺间质炎症组变化一致，即 CD3+、CD3+CD4+、CD3+CD8+T 淋巴细胞绝对计数极显著降低（P≤0.01），CD3+%、CD3+CD8+%明显降低（P≤0.05），CD3+CD4+/CD3+CD8+淋巴细胞比值明显升高（P≤0.05），慢性阻塞性肺疾病组无 CD3+%显著升高；三组肺部疾病之间外周血淋巴细胞免疫分型变化均无明显差异（P≥0.05）。

结论 危重症慢性呼吸衰竭患者淋巴细胞数量均较低，存在明显的细胞免疫功能紊乱，对比其他严重病因，CD3+CD4+T 淋巴细胞数量的升高，可用于鉴别诊断肺部炎症和慢性阻塞性肺疾病。但是相较于正常人，引起危重症慢性呼吸衰竭的各种肺部疾病之间的差异，有待进一步研究。

PO-1190

数字 PCR 检测血流感染病原菌的临床应用研究

吕琳婷、刘芳瑞
上海交通大学医学院附属仁济医院(东院)

背景 血流感染是指细菌、真菌等病原微生物入侵血循环，在血液中繁殖,释放毒素和代谢产物,并诱导细胞因子释放,引起全身感染性疾病。目前血流感染的主流病原菌有大肠埃希菌、肺炎克雷伯菌、鲍曼不动杆菌、铜绿假单胞菌以及各类葡萄球菌。大多入侵为呼吸道感染、泌尿系统感染以及腹腔感染。近些年由于抗生素和介入治疗的使用，血流感染的发病率呈持续增高趋势。目前检测血流感染最重要的检查手段是血培养。但血培养周期时间长、用血量大、且无法定量，早期诊断及准确的抗菌治疗对降低疾病死亡率至关重要。
目的 运用领航数字 PCR 系统检测临床血浆样本中的病原菌，以测评该技术的临床应用价值。
方法 采用领航基因五色荧光数字 PCR 系统检测 169 份临床血浆样本，并与传统血培养方法进行比较，计算数字 PCR 技术检测血流感染的敏感度、特异性和符合率。
结果 本次实验检测的 169 份样本中，血培养阳性 27 例，阴性 142 例，阳性率 16%；数字 PCR 阳性 15 例，阴性 154 例，阳性率 8.9%。与传统血培养鉴定技术相比，领航五色荧光数字 PCR 系统检测血流感染样本的敏感度为 24%，特异性为 97.2%，阳性预测值为 60%，阴性预测值为 88%，总体符合率为 88.8%。数字 PCR 系统鉴定阳性的病原菌包括绿假单胞菌（1 例）、大肠埃希菌（5 例）、肺炎克雷伯菌（4 例）、鲍曼不动杆菌（2 例）、屎肠球菌（3 例）、粪肠球菌、嗜麦芽窄食单胞菌（5 例）、表皮葡萄球菌（3 例）。但由于血培养阴性而数字 PCR 检测阳性的病原菌主要集中在嗜麦芽假单胞菌和表面葡萄球菌，所以不能排除污染的可能性。
结论 数字 PCR 技术是一种新型血流感染的检测技术，检测时间短，具有较好的特异性，但敏感性还有待提高，未来或许可以成为临床早期诊断与优化感染治疗的新方法。

PO-1191

117 例多发性骨髓瘤流式细胞术免疫表型分析

陈雪
吉林金域医学检验所有限公司

目的 探讨多发性骨髓瘤(MM)免疫表型的特点和临床意义。
方法 选取 2020 年 1 月至 2020 年 12 月送检我公司的多发性骨髓瘤分型样本 117 例，使用十色流式细胞仪,按照多发性骨髓瘤分型十色方案添加抗体,对样本进行免疫分型检测,并分析抗原表达情况。
结果 117 例样本中，浆细胞呈单克隆性共 83 例,占 70.9%,胞内免疫球蛋白 Kappa 轻链限制性表达的为 38 例(45.7%),胞内免疫球蛋白 Lambda 轻链限制性表达的为 45 例(54.3%),各类抗原的表达情况依次为 CD38 强阳性 33 例(39.7%),阳性 50 例(60.2%);CD138 阳性 59 例(71.0%),部分阳性 23 例(27.7%),少量阳性 1 例(1.2%);CD19 阳性 17 例(20.4%),部分阳性 13 例(15.6%),少量阳性 1 例(1.2%),阴性 52 例(62.6%);CD56 阳性 47 例(56.6%),部分阳性 1 例(1.2%),阴性 35 例(42.1%);CD20 阳性 15 例(18.0%),阴性 68 例(81.9%);CD27 阳性 7 例(8.4%),部分阳性 14 例(16.8%),阴性 62 例(74.6%);CD81 阳性 16 例(19.2%),部分阳性 3 例(3.6%),少量阳性 1 例(1.2%),阴性 63 例(75.9%);CD28 阳性 10 例(12.0%),部分阳性 5 例(6.0%),少量阳性 3 例(3.6%),阴性 65 例(78.3%)。浆细胞呈多克隆性共 27 例,占 23.0%,各类抗原的表达率依次为 CD38 阳性 27 例(100%);CD138 阳

性 19 例(70.3%),部分阳性 8 例(29.6%);CD19 阳性 27 例(100%);CD56 阴性 27 例(100%);CD20 阳性 3 例(11.1%),阴性 24 例(88.8%);CD27 阳性 15 例(55.5%),部分阳性 7 例(25.9%),阴性 5 例(18.5%);CD81 阳性 24 例(88.8%),阴性 3 例(11.1%);CD28 阴性 27 例(100%)。无浆细胞共 7 例,占 5.9%。

结论 流式细胞术免疫分型能快速、多参数、客观地测定细胞膜和胞浆中多种抗原的表达,准确地判断多发性骨髓瘤的类别,结果重复性好,从而能够更加准确的判断出多发性骨髓瘤,为多发性骨髓瘤的预后和治疗方案的选择提供了科学的依据。

PO-1192

尿液分析中如何快速解决携带污染问题的探讨

何秋阳、马顺高、钟国梁
大理州人民医院（云南省大理白族自治州）

目的 探讨日常工作中如何快速解决尿液分析中携带污染问题。

方法 将 200 名我院 2020 年 1 月-2020 年 12 月期间住院患者的肉眼血尿标本和当天健康体检尿液标本作为研究对象，研究对象分为 2 组，即肉眼血尿组 100 例和健康体检组 100 例。采用希森美康 UF5000 和 UF3500 分别对其连号（即 1 号为肉眼血尿，2 号为健康体检）和隔号（1 号为肉眼血尿，2 号为生理盐水，3 号为健康体检）进行分析。

结果 相同标本的隔号分析结果和连号分析结果做比对，肉眼血尿标本无显著差异、健康体检标本隔号检查结果与连号检查结果有显著差异。

结论 隔号检测可以有效避免高浓度标本给低浓度标本带来的携带污染问题。此方法在标本量大且时间紧迫的三甲医院日常工作中非常实用，既可以保证检验结果的准确性，又可以按时出具报告。

PO-1193

CRP/ALB 联合 ALB/PLT、NLR 和 PLR 对克罗恩病的辅助诊断价值

江烊州
中国人民解放军陆军军医大学第二附属医院

目的 探讨血清 C-反应蛋白 / 白蛋白值（CRP/ALB）、白蛋白 / 血小板值（ALB/PLT）、中性粒细胞与淋巴细胞比值（NLR）及血小板与淋巴细胞比值（PLR）联合指标对克罗恩病(Crohn disease，CD)的辅助诊断价值。

方法 收集来源于陆军军医大学第二附属医院的 218 例样本，其中健康组：健康者 68 例；疾病组（CD 组）：克罗恩病患者 86 例；鉴别对照组（UC 组）：溃疡性结肠炎患者 64 例进行回顾性分析。比较各组中 CRP/ALB、ALB/PLT、NLR 和 PLR 的变化，采用受试者工作特征(ROC) 曲线评价单项及联合分析对 CD 的诊断及鉴别诊断价值。

结果 与健康组相比，疾病组 CRP/ALB、NLR 和 PLR 水平均显著升高，而 ALB/PLT 水平显著性降低，差异均有统计学意义（P<0.05）。与鉴别对照组相比，疾病组 CRP/ALB、ALB/PLT、NLR 和 PLR 水平显著升高且差异具有统计学意义（P<0.05）；四项指标联合检测 CD 的 ROC 曲线下面积（AUC）为 0.867，明显高于单项检测（AUC 分别为 0.703、0.718、0.791、0.839）。联合检验的灵敏度为 79.1%，特异度为 86.6%；CRP/ALB、ALB/PLT、NLR 和 PLR 四项指标单独检测鉴别诊断 CD 和 UC 的 AUC 分别为 0.575、0.527、0.658、0.659。联合检测下鉴别诊断的 AUC 为 0.716。

结论 CRP/ALB、ALB/PLT、NLR 和 PLR 联合指标对 CD 的辅助诊断有较高价值，可用于 CD 的辅助诊断和鉴别诊断。

PO-1194

男性患者精液分析及疾病分布探讨

陶亚
中南大学湘雅医院

目的 通过分析男性患者精液常规检测结果，探讨临床上导致精液异常的疾病分布以及男性不育症患者的精液质量现状，为临床上男性不育等男科疾病的诊疗提供依据。
方法 对 2020 年 7 月 1 日-2021 年 2 月 28 日在中南大学湘雅医院首次进行精液常规检测的 1280 例患者，利用 SQA-V 自动化精子质量分析系统进行精液常规检测。
结果 1280 例患者中，精液检测各项参数完全正常患者 479 例，一项或多项参数异常患者 801 例。精液异常患者主要表现在精子总活动力、前向活动精子率及形态正常精子率异常，分别占 63.4%、78.5%、41.1%；其中 532 例患者已被确诊为男性不育症，188 例存在前列腺炎，147 例有精索静脉曲张，140 例罹患泌尿生殖系统感染，51 例存在性功能障碍，28 例存在生殖系统炎症，18 例存在泌尿生殖系统器质性病变，7 例有内分泌系统疾病，12 例为其他疾病患者。对 814 例临床已诊断明确的男性不育患者的精液进行常规分析，其中完全正常者 283 例(34.8%)，异常者 531 例(65.2%)。各参数分析显示：精子总活动力异常 343 例(占 42.1%)；前向活动精子率异常 430 例(占 52.8%)；形态正常精子率异常 244 例(占 30.0%)。
结论 男性患者的精液异常主要表现在精子活力的下降及精子畸形率高，与男性不育症患者精液异常表现一致。精索静脉曲张，前列腺炎及泌尿系统感染对男性生育有较大的影响，临床上应及时采取有效的治疗措施。

PO-1195

snoRD4A 作为肾透明细胞癌新型标志物及调控其生物学行为的研究

张倩茹、宋兴国、尚晓玲、宋现让
山东省肿瘤医院

肾细胞癌（Renal Cell Carcinoma，RCC，简称肾癌）是起源于肾小管上皮的恶性肿瘤，占肾脏恶性肿瘤的 80%-90%，其最常见的病理类型为透明细胞癌，近年来肾癌的全球发病率以每年 2%-3%的速度持续增长，已经成为全球男性第六大常见癌症。 多项研究表明 snoRNAs 的异常表达直接影响着肿瘤的发生、发展及预后。在多种肿瘤中普遍存在有 snoRNAs 异常表达，但在特定肿瘤中只有特定 snoRNAs 表达异常，这表明 snoRNAs 表达却具有肿瘤类型特异性。
目的 验证尿沉渣中 snoRD4A 作为肾透明细胞癌（Clear cell renal cancer cell, ccRCC）新型标志物能力，并探索 snoRD4A 对 ccRCC 发生发展的驱动作用。
研究方法（1）通过肾癌组织 TCGA 数据，筛选出与肾癌发生发展效密切相关的 snoRNAs，RT-PCR 验证肾癌患者和健康志愿者之间血浆、尿沉渣 snoRNAs 分子表达差异情况，计算诊断效能；（2）进行肾癌恶性生物学行为体外功能实验，包括 CCK8 实验，克隆形成实验，细胞凋亡实验等；（3）慢病毒构建过表达或沉默表达 snoRD4 稳筛细胞株，进行裸鼠皮下成瘤实验；（4）蛋白质谱分析差异蛋白，WB 验证差异蛋白表达。
结果 （1）snoRD4A 在肾癌石蜡组织、血浆以及尿沉渣中表达升高。（2）在肾癌细胞中沉默 snoRD4A 表达，细胞的增殖、克隆形成能力减弱，凋亡能力增强；在肾癌细胞中过表达 snoRD4A，细胞的增殖和克隆形成能力增强，凋亡能力减弱；（3）在动物体内沉默 snoRD4A 的表达，肿瘤体积明显减小；（4）蛋白质谱实验、western blot 实验以及拯救实验表明 snoRD4A 可能通过 Wnt 信号通路调控肾癌恶性生物学行为。

结论 尿沉渣 snoRD4A 可作为 ccRCC 的一种无创性诊断标志物。且 snoRD4A 通过 Wnt 信号通路调控 ccRCC 恶性生物学行为。

PO-1196

血小板活化及功能评估参数在静脉血栓栓塞性疾病诊断中的价值

肖贺欣、吕晓艳、王言
吉林大学第二医院

目的 血小板在静脉血栓栓塞（VTE）中的角色和参与程度目前仍未明确。本研究的目的是评估 VTE 患者血小板活化和功能状态。通过对 VTE 患者外周血中不同血小板参数，包括未成熟血小板分数（IPF）、未成熟血小板计数（IPC）、P-选择素、血小板计数（PLT）及血小板聚集（PA）参数的检测，探索未成熟血小板以及血小板的活化和功能在静脉血栓栓塞疾病中的作用及对疾病进程的影响。
方法 选取超声检查显示有特发性深静脉血栓形成（DVT）和/或因固定引起的肺栓塞（PE）或 VTE 的 46 位 VTE 入院患者为观察组。选取 50 名健康体检者作为对照组。IPF、IPC、PLT 计数由 Sysmex XN-2000 分析仪检测，P-选择素由 Beckman 流式分析仪检测，PA 使用血小板聚集分析仪检测。
结果 与对照组相比，VTE 组 IPF、IPC 均无明显差异(P>0.05)。PLT 计数和诱导剂刺激下 PA 与对照组相比均有不同程度的下降(P<0.05)，且 ADP、胶原及 AA 诱导的 PA 降低与血小板计数之间呈正相关。血小板 CD62p 与对照组相比呈显著增高（P<0.01）。
结论 VTE 患者血小板绝对计数及聚集功能显著降低，且二者呈相关性，这可能与 VTE 中血小板的消耗相关。但血小板活化程度明显增高，提示血小板的活化在 VTE 疾病发生中发挥重要作用。

PO-1197

冠心病患者同型半胱氨酸水平与血小板聚集功能的相关性探讨

李洁、张云平
哈尔滨医科大学附属第一医院

目的 探讨冠心患者同型半胱氨酸水平(Homocysteine，HCY)与血小板聚集功能之间的关系。
方法 检测 112 例冠心死患者及正常的健康体检者 91 例的 HCY 及以二磷酸腺苷（ADP）和花生四烯酸（AA）为诱导剂的血小板聚集功能，进行统计对比分析。
结果 冠心病组的 HCY 水平、血小板聚集功能与对照组比较有显著差异(P<0.05)；高 HCY 患者组的血小板聚集功能与正常 HCY 患者组比较有显著差异(P<0.05)。
结论 HCY 水平增高可引起血小板聚集功能增强，是冠心病反复发作的高危因素。

PO-1198

骨髓间充质干细胞来源的外泌体 miR-10a 通过 RPRD1A 激活的 Wnt 信号通路保护急性髓系白血病细胞免受化疗

张雅琴[1]、吴娟[2]、李小玉[1]、陈玲[2]、陈加弟[1]、黄慧芳[1]、曹颖平[1]
1. 福建医科大学附属协和医院
2. 福建医科大学医学技术与工程学院

Exosomes derived from acute myeloid leukemia(AML)-bone mesenchymal stem cells(AML-BMSCs-Exos) has been proposed as one of the important factors for promoting tumor development and drug resistance on AML. However, the molecular mechanism remains unclear. In this study, We found that the level of miR-10a in AML-BMSCs-Exos was increased compared with that of healthy donor BMSCs exosomes(HD-BMSCs-Exos), and miR-10a can protect AML cells from chemotherapy. MiR-10a derived from AML-BMSCs-Exos can down-regulate RPRD1A expression, which can activate Wnt signaling pathway and mediated AML cells drug resistance.

PO-1199

房颤患者 CRP、D-2 聚体水平与脑血管病认知障碍的相关性分析

朱冉
资阳市第一人民医院

目的 研究房颤患者 CRP、D-2 聚体水平与脑血管病认知障碍的相关性。
方法 选取我院 90 例房颤患者，根据出现脑血管病及认知功能障碍，分为研究组（N=30）和观察组（N=30）以及参考组（N=30），对三组都进行 CRP、D-2 聚体水平的检测，分析房颤患者 CRP、D-2 聚体水平与脑血管病的相关性分析。
结果 研究组以及观察组均出现不同程度的脑血管病并伴一定程度认知功能障碍，CRP、D-2 聚体升高率明显高于参照组（P<0.05），分析其相关性发现，CRP、D-2 聚体水平与脑血管病认知障碍呈负相关（r=-0.621，-0.51，p<0.01）。
结论 房颤患者 CRP、D-2 聚体水平与脑血管病认知障碍呈负相关，对于房颤患伴 CRP、D-2 聚体水平升高的患者具有早期预防诊断作用。

PO-1200

妊娠合并血小板减少的病因分析及产后母儿影响

袁秋艳
资阳市第一人民医院

目的 观察和分析妊娠合并血小板减少的病因及不同程度血小板减少对母婴结局的影响。
方法 回顾性分析 2010 年 1 月 1 日至 2020 年 12 月 31 日本院收治的妊娠合并血小板减少病例 X 例,分析血小板减少的不同病因和血小板降低的不同程度对母儿结局的影响。
结果 妊娠合并血小板减少的病因主要为妊娠期血小板减少症(GT)、免疫性血小板减少性紫癜(ITP)、先兆子痫(PE)、HELLP 综合征及弥散性血管内凝血(DIC).五组患者的早产率、胎死宫内发生率、产后出血发生率等妊娠结局存在组间差异(P<0.05).依血小板降低程度分为轻 PLT(50～100)×109/L、中 PLT(30～50)×109/L、重,PLT＜30× 109/L 三组,随血小板减少程度的增加,三组间剖宫产率、早产率、死产率、产后出血率均存在统计学差异(P<0.05).
结论 不同程度血小板减少对母婴结局均有不良影响..血小板计数<50×109/L 对不良妊娠结局有重要的提示作用.

PO-1201

血 NLR、β2-MG 和 Cys-C 对初诊多发性骨髓瘤患者合并肾损伤预测价值的探讨

厉吉霞
烟台市烟台山医院

目的 探讨血中性粒细胞/淋巴细胞比值（NLR）、β2-微球蛋白(β2-MG）及胱抑素 C（Cys-C）对初诊多发性骨髓瘤（MM）患者合并肾损伤的预测价值。
方法 回顾性分析 2013 年 1 月至 2020 年 12 月烟台市烟台山医院收治的初诊为 MM 的患者 97 例，按照血肌酐水平将 MM 患者分为肾损伤组 22 例（血肌酐＞176.8mmol/L）及非肾损伤组 75 例（血肌酐≤176.8mmol/L）。比较肾损伤组和非肾损伤组的性别、年龄、临床分型及实验室指标。采用二元 Logistic 回归法单因素及多因素分析 MM 发生肾损伤的危险因素，应用受试者工作特征曲线（ROC），评估各危险因素对 MM 患者发生肾损伤的预测价值。
结果 97 例初诊 MM 患者发生肾损伤者占 22.70%。MM 肾损伤组与非肾损伤组比较性别、年龄，红细胞分布宽度（RDW）、血浆纤维蛋白原含量（FIB）、血清白蛋白（ALB）检测水平差异不具有统计学意义（P 值均＞0.05）；临床分型 IgG-λ 型，IgA-κ 型、IgA-λ 型、不分泌型差异不具有统计学意义（P 值均＞0.05），临床分型轻链型、IgG-κ 型差别具有统计学意义（P 值均＜0.001）。MM 肾损伤组外周血白细胞（WBC）、中性粒细胞/淋巴细胞比值（neutrophil to lymphocyte ratio,NLR），单核细胞与淋巴细胞比值(mtolymphocyte ratio,MLR)、血清碱性磷酸酶（ALP）、血清唾液酸（SA）、血清胱抑素 C(CysC)、血清 β2-微球蛋白(β2-MG）水平高于非肾损伤组，红细胞（RBC）、血红蛋白（HB）含量低于非肾损伤组。差别均有统计学意义（P 值均＜0.05）。WBC、NLR、MLR、ALP、HB、RBC、β2-微球蛋白、Cys-C 是多发性骨髓瘤肾损伤的危险因素。NLR≥1.92，β2-MG≥6.66mg/L，Cys-C≥1.66mg/L 是多发性骨髓瘤肾损伤的独立危险因素，P 值均＜0.05。ROC 曲线分析显示，NLR、β2-MG、Cys-C 曲线下面积（area under the curve,AUC）分别为 0.758、0.929、0.921；NLR、β2-MG 和 Cys-C 联合检测预测价值更高，曲线下面积 AUC 值为 0.968。
结论 NLR≥1.92，β2-MG≥6.66mg/L，CYS-C≥1.66mg/L 是多发性骨髓瘤肾损伤的独立危险因素。提示临床联合检测 NLR、β2-MG、Cys-C 可提高 MM 患者肾功能损伤的早期检出率。

PO-1202

妊娠期贫血患者的血常规检验结果分析

王菊
资阳市第一人民医院

目的 结合临床意义，对妊娠期妇女的血常规检验结果进行回顾性分析。
方法 选取 2019 年 1 月至 2021 年 1 月到资阳市第一人民医院就诊的 150 例妊娠期贫血患者，另收集同期就诊的 150 例非贫血孕妇，对两种人群的血常规检验结果进行分析比较。
结果 孕中期及孕早期小细胞性贫血发生的几率较高，分别为 35.53%和 39.47%，孕晚期大细胞性贫血发生率较高，为 60.29%，组间差异有统计学意义（P<0.05）。小细胞贫血孕妇的 MCV、MCH、MCHC 等指标均低于对照组，大细胞贫血孕妇的 MCV、MCH 等指标均高于对照组，而 RBC 低于对照组，组间差异有统计学意义（P<0.05）。
结论 孕妇贫血的几率较高，应加强对孕妇生理健康的定期体检和长期管理，避免影响到胎儿出生后的健康状态。

PO-1203

行人工全髋关节置换术后高凝状态患者凝血因子活性变化及D-二聚体水平相关分析

唐笛娇
重庆医科大学附属第一医院

目的 凝血因子活性是临床凝血项报告中最常见的一种参数，反映了参与血液凝固过程中各种蛋白质组分的活性。已有研究表明，凝血因子活性检测可能对有效评估出血风险等有积极作用。D-二聚体可作为血栓的排除指标。本研究旨在探讨行人工全髋关节置换术后呈高凝状态患者的凝血因子活性变化情况以及与术后 D-二聚体水平是否存在一定关系。
方法 本研究共收集了 2019 年 1 月至 2020 年 1 月重医附一院骨科的 63 例人工髋关节置换术患者的相关临床资料并进行了相关分析。利用血栓弹力图数据判断术后高凝状态的患者。
结果 通过配对样本 t 检验发现，手术前后活性变化有统计学意义的有凝血因子Ⅱ、凝血因子Ⅷ和凝血因子 XⅡ，并通过 Spearman 相关性分析得到，在 D-二聚体≤3.4mg/L 时，凝血因子 XⅡ与 D-二聚体有显著相关（P＜0.05）。以 TEG 指标作为高凝状态的诊断标准做 ROC 分析，凝血因子Ⅱ(AUC=0.507,P=0.954), 凝血因子 XI（AUC=0.447，P=0.643）、FXII（AUC=0.414，P=0.451）。
结论 在 D-二聚体较低时，凝血因子 XⅡ与 D-二聚体有显著相关。术后单独 FⅡ、FXI、FXII 活性对高凝状态的预测作用并不显著，可以选择联合应用提高预测效果。

PO-1204

AKA、CCP、MCV、RF 和 CRP 联合诊断在类风湿关节炎中的临床价值

张彬、李智洋
南京鼓楼医院

目的 探究抗环瓜氨酸肽抗体（ anti-CCP ）、抗角蛋白抗体（ AKA ）、C 反应蛋白(CRP)、抗突变型瓜氨酸波形蛋白抗体（ anti-MCV ）联合类风湿因子(RF)在类风湿关节炎(RA)诊断中的价值。
方法 选择 2018 年 10 月- 2019 年 11 月南京鼓楼医院纳入类风湿关节炎（ RA ）临床确诊病例 173 例，归为 RA 组；另外选取同期非类风湿关节炎病例 99 例，为非 RA 组。抗 CCP 抗体和抗 MCV 抗体采用 ELISA 法检测，抗角蛋白抗体（ AKA ）采用间接免疫荧光法，(RF)和(CRP)采用速率散射比浊法检测。采用 t 检验及 ROC 曲线等统计方法，分析两组结果差异及其相关性。比较两组之间抗 CCP 、AKA 、CRP 、抗 MCV 、 RF 单独检测与联合检的阳性率；比较抗 CCP 、CRP 、抗 MCV 、 RF 检测的灵敏度、特异性。
结果 RA 组患者抗 CCP 、抗 AKA、 CRP 、抗 MCV 和 RF 的阳性率明显高于非 RA 组的阳性率，差异均有统计学意义（P<0.05）；联合检测的阳性率明显高于单一检测的阳性率，差异有统计学意义（P<0.05）。血清抗 CCP、抗 MCV 和 RF 诊断 RA 的曲线下面积（ AUC ）分别为 0.7827、0.7904 和 0.7372；在最佳诊断临界条件时，敏感度分别为 65.32％、65.90％和 58.72％；特异度分别为 89.90％、89.90％和 87.88％。 RA 组患者血清 RF 与 CRP 呈正相关（ y = 4.170 x + 174.2， r = 0.2482， P = 0.0010 ）。抗 CCP 和抗 MCV 与 CRP 均无相关性（均 P > 0.05）。
结论 抗 CCP 、抗 AKA 、 CRP 、抗 MCV 及 RF 对 RA 均具有一定的辅助诊断价值，5 项联合检测可提高 RA 的检出率，有助于风湿科临床医师对 RA 患者采取及时有效的治疗、干预措施。

PO-1205

Lymphocyte-Monocyte-Neutrophil index: a Predictor of Severity of Coronavirus Disease 2019 Patients Produced by Sparse Principal Component Analysis

Jianan Jia
The 901th Hospital of Joint Logistics Support Force of Chinese People's Liberation Army

Background It is important to recognize severe ill coronavirus disease 2019 (COVID-19) patients from moderate ones and more effective predictors should be developed.
Methods Clinical indicators of COVID-19 patients from two independent cohorts (Training data: Hefei Cohort, 82 patients;Validation data: Nanchang Cohort, 169 patients) were retrospected. Sparse principal component analysis (SPCA) using Hefei Cohort was performed and prediction models were deduced. Prediction models were evaluated by receiver operator characteristic curve and decision curve analysis (DCA) in above two cohorts.
Results SPCA using Hefei Cohort revealed that the first 13 principal components (PCs) accounted for 80.8% of the total variance of the original data. The PC1 and PC12 were significantly associated with disease severity with odds ratio of 4.049 and 3.318 respectively and were used to construct predication model, named Model-A. In disease severity prediction, Model-A gave the best prediction efficiency with area under curve (AUC) of 0.867 and 0.835 in Hefei and Nanchang Cohort respectively. Model-A's simplified version, named as LMN index, gave comparable prediction efficiency as classical clinical markers with AUC of 0.837 and 0.800 in training and validation cohort respectively. In DCA, Model-A gave slightly better performance than others and LMN index showed similar performance as albumin or neutrophil-to-lymphocyte ratio.
Conclusions Prediction models produced by SPCA showed robust disease severity prediction efficiency of COVID-19 patients and have the potential for clinical application.

PO-1206

罗湖区孕期 D-二聚体、FDP 参考区间的建立及在产后出血的应用

唐丽姣
深圳市罗湖区妇幼保健院

目的 初步建立深圳市罗湖区孕妇不同孕期 D-二聚体、FDP 的参考区间，并探讨动态检测 D-二聚体、FDP 对产后出血早期预测价值。
方法 收集研究组孕妇 1138 例，按孕期分为早孕（386 例）、中孕（351 例）、晚孕组（401 例），对照组健康体检非孕妇 300 例；疾病组：选取产后出血 84 例。采用免疫比浊法检测 D-二聚体、FDP 的含量。不同孕期 D-二聚体、FDP 之间比较采用 Kruskal-Wallis 检验，$P < 0.05$ 为差异有统计学意义；不同孕期组之间 D-二聚体、FDP 的两两比较同样采用非参数 Kruskal -Wallis 检验，并应 Bonferroni 方法进行 P 值的校正。D-二聚体、FDP 参考区间均采用 95%作为参考区间上限，采用单侧百分位数法，计算 95%参考区间。
结果 D-二聚体、FDP 水平随孕期增加有上升趋势，呈正相关（$r = 0.80$、$r = 0.77$，$P < 0.05$），且明显高于对照组 （$P<0.05$）。孕早期妇女血浆 D-二聚体、FDP 的参考区间分别为<1.5μg /ml、<4.45μg /ml，孕中期 D-二聚体、FDP 的参考区间为<2.53μg /ml、<8.75 mg/ml，孕晚期孕妇血浆 D-二聚体、FDP 的参考区间分别 为<4.35μg /ml、<13.6μg /ml。疾病组明显高于参考区间（$P<0.05$）

结论 本研究通过初步建立罗湖区孕妇 D- 二聚体、FDP 参考区间，提高凝血功能在产后出血的应用价值。

PO-1207

外周血中性粒细胞膜碱性磷酸酶在骨髓增生异常综合征分型中的应用价值

朱立梅、王然、张丽
连云港市第一人民医院

目的 本研究应用流式细胞术检测骨髓增生异常综合征(myelodysplastic syndrome，MDS)患者外周血中性粒细胞膜碱性磷酸酶(Alkaline phosphatase expression on the membrane of neutrophils，mNAP)的表达，探讨其在 MDS 分型中的价值。
方法 收集 2018 年 8 月至 2019 年 12 月连云港市第一人民医院收治初诊 MDS 患者 32 例,通过骨髓细胞形态学诊断，入选患者符合 2016 版 WHO-MDS 分型标准。以同期医院体检中心 50 名健康体检者作为对照组。 采用流式细胞术检测 MDS 患者和对照组外周血 mNAP 水平。
结果 32 例 MDS 患者中，MDS 伴单系发育异常（MDS-SLD）15 例，MDS 伴多系发育异常（MDS-MLD）8 例，MDS 伴环状铁粒幼红细胞（MDS-RS）3 例，MDS 伴有原始细胞过多（MDS-EB）2 例，MDS 不能分类（MDS-U）4 例，其中 15 例 MDS-SLD 患者 mNAP 水平显著升高，最低值为 11650AB/c, 最高值为 18687AB/c，均值 13937 AB/c，高于健康对照组 1831 AB/c（1371-2411 AB/c）和 MDS 其他组 1851 AB/c（1124-3001 AB/c），差异有统计学意义(P<0.01）。其他型 MDS 患者中，除 2 例 MDS-EB 结果为 634AB/c、910AB/c，低于正常参考均值 1831AB/c 外，其他组 mNAP 水平均在正常参考值范围内，与健康对照组比较，差异无统计学意义(P>0.05）。
结论 mNAP 在 MDS-SLD 中的高水平表达，对 MDS 的分型有提示作用，可通过检测外周血 mNAP 水平对 MDS-SLD 的分型起到诊断价值。

PO-1208

Autophagy regulates glycolytic metabolism of acute myeloid leukemia cells in bone marrow stroma

min huang
Shandong Provincial Hospital Affiliated to Shandong First Medical University

To investigate the relationship between glycolytic activity and autophagy in acute myeloid leukemia (AML), and the changes of autophagy when co-culture AML cells with bone marrow-derived mesenchymal stromal cells (BMSCs), we detected the expression of Autophagy-related E1 ligase 7 (ATG7), hexokinase II (HKII), glucose transporter 1(GLUT1) and lactate dehydrogenase A (LDHA) in bone marrow from healthy samples and AML patients. In this study, we further detected the changes of glycolysis and chemosensitivity in AML cells after ATG7 knockdown. We co-culture AML cells with BMSCs, then research the level of glycolysis and autophagy. The data suggests that over expression of ATG7 is associated with the prognosis of AML, the decrease of glycolysis followed autophagy inhibition due to the decrease of HK-II, GLUT1 and LDH. ATG7 knockdown sensitizes AML cells to cytarabine (Ara-C). Co-culture with BMSCs enhanced autophagy in AML cells, this effect can be partially reversed the decrease of glycolysis in ATG7 knockdown cells and protects AML cells from Ara-C induced cytotoxicity. These results indicate autophagy plays a role in regulating glycolysis, and the inhibition of autophagy could improve outcomes in AML therapy.

PO-1209

质谱流式临床应用——17 markers 淋巴细胞精细分群方案

王世佳
上海宸安生物科技有限公司

背景 流式细胞术是临床样本检测的重要技术手段。通用的 TBNK 分型一般采用 6 色或 8 色方案。荧光流式技术可选的检测通道有限，且存在通道间信号干扰，难以满足日益增长的临床检测需求。质谱流式技术结合了荧光流式高效的单细胞研究能力和飞行时间质谱的全谱高分辨率优势，采用金属标记抗体对样本进行染色，可以实现单个样本 50+指标检测，并且克服了荧光基团光谱重叠的问题。
目的 为开发下一代单细胞诊断技术，完善质谱流式临床应用，上海宸安生物科技有限公司自主研发了 17 markers 质谱流式淋巴细胞精细分群检测方案。
方法 将人外周血单个核细胞与含有金属标记抗体的冻干微芯混合；经孵育、洗涤、DNA 染色、洗涤、重悬后上样；收集 8 万个细胞后分析淋巴细胞的分群情况。
结果 在本方案中，去除碎片和死细胞后，我们对 CD45 阳性的细胞进行分析：采用 CD3 和 TCRγδ 标记 γδT 细胞；采用 CD25 和 CD127 标记 Treg 细胞；采用 CD3, CD4, CD8, CD45RO, CD45RA, CCR7 区分不同 T 细胞亚群；采用 CD19, CD27, IgD, CD24, CD38 区分不同 B 细胞亚群；采用 CD16 和 CD56 区分 NK 细胞和 NKT 细胞（图 1）。
结论 宸安生物自主研发的质谱流式淋巴细胞精细分群检测方案，可以实现单份样本 17 个生物标志物检测，超越了荧光流式相同样本量下的检测能力，获取更加精确的诊断信息。

PO-1210

应用骨髓涂片 FISH 技术回顾性鉴别诊断 ALL 与 CML 急淋变一例

熊克梅
四川金域医学检验中心有限公司

目的 探讨一例 3 年前诊断为急性淋巴细胞白血病(Acute lymphoblastic leukemia，ALL)患者初诊时的骨髓涂片进行荧光原位杂交（fluorescence in situ hybridization，FISH）检测，回顾性鉴别诊断 ALL 与 CML 急性变。
方法 对陈旧的骨髓涂片进行去油、褪色，再在新鲜配置的固定液（甲醇：冰乙酸=3:1）中固定 10 分钟，胃蛋白酶消化 15 分钟,用磷酸缓冲盐溶液（phosphate buffer saline，PBS）处理三次，每次 10 分钟，依次在 70%、85%、100%的无水乙醇中脱水各 3 分钟，然后加 BCR/ABL1 双色融合探针进行荧光原位杂交，最后荧光显微镜下分析结果。
结果 对进行荧光原位杂交的骨髓涂片进行计数，计数 200 个细胞，检测到 BCR/ABL1 融合细胞占 52.0%（104/200），其中淋巴细胞和粒细胞均出现阳性。细胞信号模式为：1G1R2F 26.0%,1GIR1F 14.0%,2G1R2F 8.0%,1G2F 2.0%,1G1R3F 2.0%,2G2R 44.5%,3G2R 1.5%,3G3R 2.0%。
结论 特殊情况下可以应用骨髓涂片直接进行荧光原位杂交检测，并可以基于形态学鉴别诊断急性淋巴细胞白血病与慢性粒细胞白血病急淋变。

PO-1211

髓系肿瘤浸润浆膜腔积液的临床和实验室特征研究

龚旭波
浙江大学医学院附属第二医院

背景 髓系肿瘤浸润浆膜腔积液的研究报告在国内外少见，本研究旨为研究此类患者的临床与实验室特征。
方法 回顾性分析 2004 年 1 月 1 日至 2021 年 1 月 1 日之间，在浙江大学附属第二医院收治的髓系肿瘤浸润浆膜腔积液的患者临床资料。疾病诊断参照 2016 年《WHO 造血与淋巴组织肿瘤》的标准，浆膜腔积液中检出髓系原始细胞（>3.0%），即判为髓系肿瘤累及。
结果 在此期间，检出髓系血液肿瘤浸润胸水 8 例（8/4637，0.1725%），浸润腹水 2 例（2/2096，0.0954%），未检出浸润心包积液病例(0/372)。这 10 例标本中，以 CGL 急变为主（n=4，40%），M5 次之（n=2，20%），另有 M2、M4、MDS-EB2、髓系肉瘤各一例。对于 8 例浸润胸水的病例，自发现胸水累及时计算，中位生存时间仅 3.5 月，而对照组（n=25）中位生存时间为 21 个月，两组比较具有统计学差异（P = 0.03）。
结论 髓系肿瘤浸润浆膜腔积液的占比极低，疾病类型以 CGL 急变为主，几乎均累及双侧胸腔，且预后较差。

PO-1212

登革热患者 NLR、d-NLR、白细胞值测定的临床意义

严建新
温岭市第一人民医院

目的 探讨登革热患者血常规相关参数的变化特点，为登革热的诊断与鉴别诊断提供参考。
方法 收集 2019 年 4 月至 11 月在本院住院治疗的登革热患者 38 例，收集同期甲型流感抗原筛查阳性患者 102 例作为甲型流感病毒感染组，，收集 2020 年 1 月-2 月在本院就诊的新型冠状病毒核酸 RNA 阳性患者 54 例作为新型冠状病毒感染组，并收集 2019 年 9 月-10 月在本院健康体检者 69 例作为对照组，分别做血常规检测。
结果 登革热病毒感染组与健康对照组相比，白细胞、淋巴细胞、血小板计数下降，单核细胞、中性粒细胞/淋巴细胞比值（NLR）、血小板/淋巴细胞比值、衍生中性粒细胞/淋巴细胞比值（d-NLR）升高；与甲型流感病毒感染组相比，白细胞、中性粒细胞、血小板、平均红细胞体积、中性粒细胞/淋巴细胞比值、SⅡ、CRP 下降，淋巴细胞/单核细胞比值、淋巴细胞/CRP 比值升高；与新型冠状病毒感染组相比，淋巴细胞、淋巴细胞/单核细胞比值、衍生中性粒细胞/淋巴细胞比值下降。
结论 NLR、d-NLR、白细胞、血小板、淋巴细胞等感染性指标的组合，不仅可以减少个体差异和不稳定，而且反映了机体炎症反应和免疫状态之间的平衡关系，为登革热病毒感染的早期诊断与鉴别诊断提供参考。

PO-1213

The expression of SWI/SNF subunits BRG1 is increased in clinical acute myeloid leukemia patients and associated with Wnt/β-catenin pathway

Shuo Gao[1]、Xuejing Xu[1]、Wanqing Zhou[1]、Junhao Chen[1]、Jun Han[2]、Han Shen[1]
1. Nanjing Drum Tower Hospital, the Affiliated Hospital of Nanjing University Medical School
2. Children's Hospital of Nanjing Medical University

SMARCA4/BRG1, a core component of the SWI/SNF ATP-dependent chromatin-remodelling complex, plays an important role in cell cycle regulation, DNA repair and tumor development. Unlike the evidences as tumor suppressor genes in the past reports, latest researches show that BRG1 plays an important role in sustaining the growth of leukemia cells in acute myeloid leukemia (AML). Here we observed the expression of BRG1 in clinical AML patients and investigate the relationship between BRG1 and β-catenin, an important protenin in Wnt/β-catenin pathway. The expression level of BRG1 was increased in 50 of 70 AML patients（71.43%）, with the positive rate was only 36.73% in other hematological diseases detected by qRT-PCR and Western blot. Clinical data analysis showed that the expression of BRG1 was highly correlated with the myeloblast proportion in bone marrow of AML patients (P=0.0329), but had no relevance with other clinical pathological factors, including age, gender, FBA types and fusion genes. Moreover, there was a positive correlation between BRG1 and β-catenin expression，and the two genes were decreased significantly in patents in complete remission after clinical treatment. Our results showed that the expression of BRG1 is increased in clinical AML patients and associated with Wnt/β-catenin pathway, which indicates BRG1 as a biomarker or therapeutic target of AML.

PO-1214

Establishment of APTT critical value based on coagulation factor deficiency

莫喜明[1]、屈天吉[1,2]
1. 中南大学湘雅二医院
2. 中南大学医学检验系

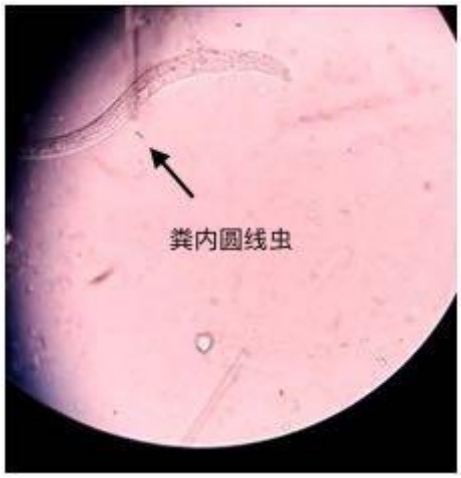
Purpose To evaluate the sensitivity of different APTT reagents in the laboratory to endogenous coagulation factors, and to provide a scientific basis for the establishment of the APTT critical value in the laboratory.
Methods According to the critical value of endogenous coagulation factor recommended by the guidelines, an in vitro single coagulation factor deficiency model was established. APTT values were measured in Sysmex FSL, Sysmex Actin, Stago PTTA and Wolfen HenosIL SynthAsil, respectively .
Results In the in vitro model established by using Stago deficiency single factor plasma, The 95% confidence intervals of APTT critical value obtained by Sysmex FSL, Sysmex Actin, StagoPTTA and Wolfen HenosIL SynthAsil detection systems respectively are: 43.8-47.2s, 62.7-72.7s, 54-60.3s, 74.3-75.0s.
Conclusion Different APTT detection systems have huge differences in factor sensitivity, and it is necessary to set the APTT critical value according to different instruments and reagents in clinical practice.

PO-1215

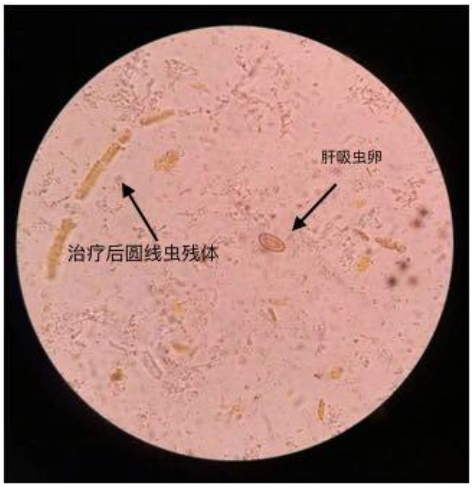
双虫混合感染（粪类圆线虫+肝吸虫）

兰萌
南方医科大学珠江医院

佛山市南海区的李阿伯（化名）因全身浮肿一个月，发热 10 天在当地医院治疗无缓解后被家人送往我院就医。初进院时李阿伯情况危急，精神差，食欲差，睡眠差，小便少，全身浮肿加重，面色苍白，重度贫血貌，并出现发热，不喜言语，还有现感染性休克。初进院的第 1 天，李阿伯的抽血检测项目肿瘤指标高，呼吸科邓教授查房指示不排除胃肠道及肺部肿瘤的可能，并于床边在局麻下行右锁骨下深静脉穿刺置管术，手术顺利。第 2 天李阿伯全身水肿减轻，但仍有发热，精神很差，睡眠差。第 3 天李阿伯留取粪便送检，粪便涂片于显微镜观察发现有活动的虫体，虫体细长，大小约为 0.6-0.7mm，咽管呈柱状，尾端尖而分叉。于当天粪检结果报查见粪类圆线虫，如下图：



继给予肠虫清治疗。余继续抗感染，营养支持，纠正贫血对症处理。第 4 日李阿伯水肿消退，发热状况有所好转，睡眠一般。继又留取粪便复检，接到此标本时是我当班，引起了我的好奇。我想看看有没有虫子排卵的可能。于是我往试管中加大粪量，用吸管吸取最底层的液体涂片，小心仔细的查看每个视野，生怕漏掉任何蛛丝马迹，圆线虫依旧还有，忽然，低倍镜下见到一个似曾相识淡黄色透亮的东西，内心无比的激动，转到高倍镜下，确认是肝吸虫卵，如下图：



于是报**结果** 查见粪类圆线虫、查见肝吸虫卵。并致电临床医生并了解到患者喜欢去河塘下水捞鱼和吃鱼生的习惯。这次的粪便检查又有了重大发现除了发现粪类圆线虫，又查见了肝吸虫卵。这一检查结果让呼吸科的医务人员振奋人心，夏教授查房听取病史汇报后，认为这是一例较少见的两种寄生虫同时感染。 增加抗寄生虫药物，继续肠虫清治疗，余治疗继续营养支持，纠正贫血处理。一直到了第 13 天，李阿伯无水肿，无发热，意识清楚，小便正常，感染休克已纠正。抽血检测结果大部分正常。面色较前红润，中度贫血貌。且粪便检查结果均未查见圆线虫和肝吸虫卵。李阿伯经历了两周的住院治疗症状好转后，家属满意签字出院。

心得体会：想起一位形态学专家说过：找到一个异常细胞容易，寻找第二个异常细胞有时需要 5 分钟或者几十分钟，粪便常规亦是如此。我们不担心找不到虫卵，我们只害怕找到一个虫卵，因为这样，你需要花费比其他标本多几倍的时间才能放心的发出报告。

PO-1216

凝血因子XII缺乏合并狼疮抗凝物阳性一例并文献复习

黄珣钡、刘超男、凌莉琴、廖娟、周静
四川大学华西医院

目的 通过分享 1 例凝血因子XII缺乏合并狼疮抗凝物阳性病例并复习相关文献，提高对该疾病的诊断及治疗水平。
方法 结合该患者的临床诊治过程及相关文献报道，对该疾病临床表现、实验室鉴别诊断及治疗特点进行讨论。
结果 分析实验室指标及临床表现，患者诊断为凝血因子XII缺乏合并狼疮抗凝物阳性。
结论 当患者凝血因子严重缺乏的时候，1:1APTT 纠正试验会掩盖低滴度抑制物的存在，合理选择 4:1 纠正试验有助于低滴度抑制物的识别。

PO-1217

尿液细胞学巴黎报告系统在泌尿系统肿瘤中的应用价值

朱立强
徐州医科大学附属医院

目的 探讨尿液细胞学巴黎报告系统对泌尿系统肿瘤的诊断价值。
方法 收集徐州医科大学附属医院泌尿外科 2017 年 5 月至 2019 年 2 月间疑似膀胱癌的住院患者 224 例。所有患者均在膀胱镜检查操作前，留取晨起第二次新鲜尿标本至少 30ml，制作液基细胞学薄片，分别用传统报告模式和更新的巴黎报告系统进行诊断。根据外科病理活检诊断结果这一“金标准”，分别计算传统模式与巴黎报告系统诊断的敏感性、特异性等评估诊断效能的指标，以 $P<0.05$ 为差异有统计学意义，以确定哪种诊断范式与病理活检诊断有更强的相关性。
结果 根据 224 例患者的最终病理结果和细胞学检查结果，我们的研究得到泌尿细胞学巴黎报告系统对尿路上皮细胞肿瘤诊断的敏感性(55.6％)和正确率(71.0％)均要明显优于传统细胞学的敏感性(24.7％)和正确率(58.0％)，而两者的特异性、阳性预测值和阴性预测值则没有显著差异;在不同级别尿路上皮癌中，泌尿细胞学巴黎报告系统对低级别尿路上皮癌的敏感性(84.6％)要显著高于传统细胞学的敏感性(19.4％);在高级别尿路上皮细胞癌的诊断中，2 者没有显著差异。
结论 泌尿细胞学巴黎报告系统通过规范性的诊断标准和术语提高了细胞学在尿路上皮细胞肿瘤的诊断效能，在膀胱癌的诊断中值得推广。

PO-1218

超声引导下经皮细针穿刺细胞学对肝脏占位性病变的诊断价值 --67 例细胞/组织病理分析

朱立强
徐州医科大学附属医院

目的 评估超声引导下经皮细针穿刺细胞学(FNAC)诊断可疑肝脏肿块的敏感性、特异性和准确性。
方法 结合临床及组织病理学资料，回顾性检索分析 2019 年 12 月至 2020 年 12 月接受超声引导下经皮 FNAC 联合肝肿块病理组织活检患者的细胞学和组织病理学数据库。所有患者均有一个或多个影像学检查出的肝脏占位性疾病。以肝活检组织病理学诊断为金标准，确定 FNAC 诊断肝病变的敏感性、特异性和准确性。

结果 67 例患者中，细胞学诊断为非肿瘤性的 8 例，怀疑肿瘤的 12 例，恶性的 47 例。在 8 例(11.9%)细胞学诊断为非肿瘤性患者中，最终病理诊断为非肿瘤性 4 例，恶性 4 例(50.0%)；在细胞学怀疑肿瘤的 12 例患者中，最终病理全部诊断为恶性(100.0%)；47 例细胞学诊断为恶性肿瘤患者中，15 例(31.9%)肝细胞癌(HCC)，6 例(12.8%)胆管细胞癌，21 例（44.7%)为转移性肿瘤，为转移性肿瘤，其余 5 例(10.6%)为其他原发性肝脏恶性肿瘤。总体而言，FNAC 诊断肿瘤性病变的敏感性为 93.7%，特异性为 100%，准确性为 94.0%，阳性预测值为 100%，阴性预测值为 50.0%。
结论 肝肿块 FNAC 是一种高准确性的技术，可用于鉴别大多数肝肿瘤的良恶性，具有较高的特异性。联合超声、细胞、组织病理学方法在肝肿瘤的诊断方面提供了更高的准确性，这可能会影响治疗决定。

PO-1219

Distinguishing patients presenting prolonged activated partial thromboplastin time with/without bleeding diathesis by comparison of immediate and post incubation mixing test

Yu Liu、Chao Zhu、Guanqun Xu、Fang Wu、Xuefeng Wang
Ruijin Hospital, Shanghai Jiao Tong University School of Medicine

Objectives To establish laboratory differentiation diagnosis of acquired hemophilia A (AHA) in patients presenting prolonged activated partial thromboplastin time (APTT) with and without bleeding diathesis by comparing the outcome of mixing test performed immediately and post incubation.
Methods The coagulation function profile of 186 patients from March 2013 through November 2019 with prolonged APTT, including 42 AHA patients and 144 asymptomatic individuals, was retrospectively investigated. The association of bleeding manifestation and outcome of mixing tests, both immediate and post-incubation as represented by Rosner index (RI 1,2), were analyzed. Novel parameter, Rosner index 3 and 4, calculated by minus or dividing RI 2 with RI 1 was adopted and its performance in laboratory differentiation diagnosis of AHA was also evaluated.
Results The correction immediately after mixture was more prominent in AHA patients as represented by RI 1 ($p<0.001$). The magnitude of correction was similar in AHA patients and asymptomatic individuals when the clotting assay was performed after incubation as shown by RI 2 ($p=0.277$). Both RI 3 and 4 had excellent performance (Youden Index>0.9).
Conclusion The blood coagulation interferences of AHA and asymptomatic individuals can be better characterized by RI 3 and 4 concerning outcome of both immediate and post-incubation mixing test.

PO-1220

外周血单个核细胞 DNA 甲基化标志物对乳腺癌和乳腺良性病变的鉴别诊断价值

张莹
山东大学第二医院

背景 到 2020 年，女性乳腺癌已成为全球癌症发病率最高的恶性肿瘤。同时，乳腺癌也是全球死亡率第 5 的恶性肿瘤。在女性中，乳腺癌占癌症病例的 1/4，占癌症死亡人数的 1/6，成为绝大多数国家女性发病率和死亡率最高的恶性肿瘤。在我国，由于经济增长带来的生活方式、社会文化的巨

大变化以及工业劳动力中女性比例的增加对乳腺癌发病率产生了影响——推迟生育和少生孩子，更大程度的超重和缺乏体力活动，乳腺癌发病率逐年缓慢升高。乳腺癌目前诊断方法（细针穿刺活检、影像学检查及血清标志物）各有其局限性。探索乳腺腺癌发生的机制，并寻找无创的兼具灵敏度和特异度的诊断乳腺癌的新型肿瘤标志物，是当前研究的焦点。

方法 通过密度梯度离心法分离乳腺癌和乳腺良性病变患者外周血 PBMC 通过 850K 芯片获得、乳腺癌 DMPs 差异表达谱，先后在 2 个独立样本集中验证筛选得到的的特异性 DMPs 和诊断模型，并研究其临床应用价值。

结果 对照组和肿瘤组差异 DMPs 建立的诊断模型检测 BC 具有较高的敏感性、特异性和总体准确性。

结论 PBMC 差异甲基化位点具有较好的鉴别能力。

PO-1221

mIPS 评分联合 T 淋巴细胞亚群对恶性血液病化疗粒细胞缺乏期并发血流感染的预测价值

武坤、罗珊、聂波
昆明医科大学第一附属医院

目的 探究 mIPS 评分联合 T 淋巴细胞亚群对恶性血液病化疗粒细胞缺乏期并发血流感染预测价值。

方法 选取 2015 年 4 月~2020 年 11 月我院血液科收治的 100 例首发恶性血液病成年（≥18 岁）化疗患者作为研究对象，根据血流感染结局分为感染组（n=33）和非感染组（n=67）。收集患者一般资料及化疗前、粒细胞缺乏期时感染可能性评分（IPS）及 T 淋巴细胞亚群（CD3+、CD4+、CD4+/CD8+）等指标并分析其变化。采用受试者工作特征曲线（ROC）评估血流感染的预测价值，logistic 进行多因素回归分析。

结果 粒细胞缺乏期 mIPS 评分与化疗前比较显著增加，且粒细胞缺乏期感染组高于非感染组；粒细胞缺乏期 CD3+、CD4+、CD4+/CD8+与化疗前比较显著降低，且感染组低于非感染组，差异均具有统计学意义（P<0.05）。mIPS 联合 T 淋巴细胞亚群对粒细胞缺乏期并发血流感染的预测能力最强（AUC=0.898），mIPS、CD 3+、CD4+、CD4+/CD8+单项指标 AUC 面积依次为 0.820、0.697、0.694、0.748，且多因素 logistic 回归分析 mIPS 为独立危险因素，CD3+、CD4+、CD4+/CD8+为保护因素。

结论 mIPS 评分联合 T 淋巴细胞亚群对恶性血液病化疗粒细胞缺乏期并发血流感染有较好的预测价值，可为后续血流感染预防用药提供依据。

PO-1222

Detection of pancreatic cancer-specific exosomes based on surface-enhanced Raman spectrum

yanru li
The Second Hospital of Shandong University

Exosomes have been proven to be important biomarkers for non-invasive diagnosis of cancer. However, the laborious process of separation and enrichment of exosomes hinders accurate quantification of exosomes. Here, we propose a simple method to capture and analyze GPC1-positive exosomes directly from the serum. First, connect streptavidin magnetic beads and biotinylated antibodies to construct functionalized exosomes capture magnetic beads, and use CD63 functionalized magnetic beads to enrich exosomes based on the antigen-antibody reaction. Secondly, an Ag@MBA SERS tag modified with anti-GPC1 antibody was added to label exosomes GPC1 for quantification. In addition, this method was used for quantification of GPC1

positive exosomes by using 20 μL of clinical serum samples.The system can quickly enrich and separate exosomes from the solution, with a separation efficiency of 60%~80%. Due to the specific signal amplification effect of the surface-enhanced Raman scattering substrate, the detection limit of exosomes is up to 10 particles/ml. Based on SERS signal analysis, it is possible to easily distinguish pancreatic cancer patients from healthy controls. More importantly, clarifying the amount of GPC1 positive exosomes will help distinguish patients with benign pancreatic disease and pancreatic cancer.

PO-1223

血小板相关参数与甲状腺肿瘤的相关性研究

朱莹、吴惠玲、高晓玲、乔焱源
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 研究外周血血小板相关参数对甲状腺肿瘤的临床病例特征关系及诊断与预后价值。
方法 回顾性分析 2019 年 12 月—2020 年 12 月在我院初次行手术治疗的甲状腺乳头状癌及良性肿瘤患者临床检验病理资料，分别讨论 PLR、PLT、PDW、MPV、PCT 及 P-LCR 与甲状腺乳头状癌患者临床病理特征的关系。
结果 与健康对照组相比，观察组 PLR、MPV、PCT 及 P-LCR 均升高，差异有统计学意义(P<0.05)。此外，PLR 最大曲线下面积(AUC)为 0.857，MPV 最大曲线下面积(AUC)为 0.845, PCT 最大曲线下面积(AUC)为 0.761, P-LCR 最大曲线下面积(AUC)为 0.809，联合预测因子最大曲线下面积(AUC)为 0.961，敏感度为 87.1%，特异度为 95.2%。
结论 术前检测血小板相关参数可辅助诊断甲状腺癌，对病情评估具有一定临床预测价值。

PO-1224

西南地区血红蛋白 H 病筛查分析

张玲、潘建华
广州金域医学检验中心

目的 回顾性分析西南地区筛查血红蛋白 H（HbH）病阳性类别占比情况。
方法 分析来自金域医学检验中心西南三省（昆明金域、贵州金域、四川金域）2020 年 1 月至 2020 年 10 月期间进行血红蛋白病筛查的孕前，产前，婚检、体检样本共 180624 例，其中，昆明金域 81633 例、贵州金域 50543 例，四川金域 48448 例。三个中心人群筛查年龄从 0 岁到 88 岁，平均年龄 29 岁。所有样本经 COULTER-DXH800 全自动血球分析仪进行血液学分析、四川和贵州金域采用美国 Helena 全自动电泳仪（SPIFE3000）和昆明金域采用法国 Sebia Capillarys3 进行血红蛋白电泳、Beckman AU680 全自动生化仪检测红细胞渗透脆性分析。对筛查出 HbH 病的所有样本均在报告中加建议进一步做地贫基因确诊试验证实，并从 LIS 系统查与该阳性患者相关联的 α 地贫基因缺失或点突变的类型。对少见或罕见类型的 α 地贫进行测序鉴定。同时取来自各子金域体检中心的健康人群作为正常对照组 100 例，平均年龄 35 岁，排除贫血或其他相关疾病。
结果 从 180624 例电泳筛查出 200 例 HbH 病患者，其中，昆明金域筛查出 HbH 病 130 例（HbH 型：130 例，HbBart's 型：0 例），阳性率为 0.16%（130/81633）；贵州金域筛查出 HbH 病 48 例（HbH 型：16 例，HbBart's 型：32 例），阳性率为 0.09%（48/50543）；四川金域筛查出 HbH 病 22 例（HbH 型：9 例，HbBart's 型：13 例），阳性率为 0.05%（22/48448）；昆明金域筛查出的 HbH 病患者阳性率明显高于贵州金域和四川金域人群，西南三省的金域实验室筛查 HbH 病的阳性率比较存在差异，具有统计学意义（P＜0.05);西南三省的金域实验室筛查出的 HbH 病阳性类型存在差异,昆明金域筛查的 HbH 病类型主要是 HbH 型为主，贵阳和四川金域筛查出的 HbH 病类型主要以 HbBart's 型为主，具有统计学意义（P＜0.05)。

结论 西南三省 HbH 病筛查出的阳性率不同地区存在差异，以云南发病相对较高，应加强优生优育的普检和健康人群血红蛋白电泳的体检，早发现早预防。

PO-1225

206 例各类贫血患者网织红细胞参数结果分析

吴惠玲、高晓玲、朱江贤
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨网织红细胞参数在贫血性疾病鉴别诊断中的价值。
方法 采用 Sysmex XN-9000 血细胞分析仪对 206 例七类贫血患者及 50 例健康体检者的网织红细胞百分率（RET%）、网织红细胞绝对值（RET#）、未成熟网织红细胞比率（IRF%）、低荧光网织红细胞比率（LFR%）、中荧光网织红细胞比率（MFR%）、高荧光网织红细胞比率（HFR%）及网织红细胞血红蛋白含量（RET-He）进行检测。
结果 七类贫血患者 RET%、RET#、IRF%、LFR%、MFR%、HFR%及 RET-He 与健康对照组比较，肾性贫血 RET%不增高（P>0.05)，RET#轻度降低，LFR%降低，IRF%、MFR%、HFR%增高（P<0.05)；溶血性贫血和失血性贫血 RET%、RET#、IRF%、MFR%、HFR%显著或明显增高，LFR%显著降低（P<0.05）；巨幼细胞性贫血和缺铁性贫血 RET%轻度增高，IRF%、MFR%及 HFR%明显增高，LFR%明显降低（P<0.05)，RET#不增高（P>0.05)；再生障碍性贫血 RET%、RET#明显降低（P<0.05)，LFR%略降低、IRF%、MFR%及 HFR%略增高(P>0.05)；白血病贫血 RET%、RET#、LFR%降低，IRF%、MFR%及 HFR%增高(P<0.05)。与健康组比较，肾性贫血、溶血性贫血和白血病贫血的 RET-He 差异无统计学意义(P>0.05)；缺铁性贫血和失血性贫血 RET-He 降低，巨幼细胞性贫血和再生障碍性贫血 RET-He 增高(P<0.05)。
结论 网织红细胞参数检测在贫血性疾病的诊断、鉴别诊断等方面具有重要价值。

PO-1226

Cysteine depletion induces ferroptosis in myeloid leukemia cells

Shuhan Liu、Qiaoqian Chen、Zhiyuan Zheng、Xiandong Jiang、Wei Wu、Donghong Lin
Fujian Medical University

Objective This study aimed to explore the effect of cysteine depletion on the induction of ferroptosis in different types of myeloid leukemia cells, and preliminarily explore its potential molecular mechanism.
Method We used 6 myeloid leukemia cells as experimental cell lines, including HL-60, Kasumi-1, U937, THP-1, K562, K562/G01. Firstly, experimental cell lines were cultured in the cysteine-free medium, and we detected the proliferation capacity of cells by MTS after 24 hours. Next, cells were treated with four cell death inhibitors such as apoptosis, necrosis, ferroptosis, and autophagy to determine the form of cell death. Meanwhile, we used transmission electron microscopy, micro-method, flow cytometry to detect cell mitochondrial morphology, MDA content, ROS level, respectively. Finally, we used qPCR and Western blot to detect the mRNA and protein expression levels of the cystine/glutamate reverse carrier (System XC-) subunits SLC7A11 and SLC3A2 of the corresponding cells.
Results In the absence of cysteine, the proliferation ability of HL-60, THP-1, K562 had no significant change, while the proliferation ability of Kasumi-1, U937, K562/G01 decreased significantly(P<0.001). Among them, only K562/G01 cells can be observed the changes of ferroptosis indicators: As to the four inhibitors, only ferroptosis inhibitors can reverse the cell proliferation inhibition of K562/G01 (P<0.001). After cysteine depletion, K562/G01 cells showed

characteristic ultrastructural changes of ferroptosis, such as the disappearance of mitochondrial cristae, incomplete mitochondrial membranes, and large numbers of lipid droplets in the cytoplasm under the transmission electron microscopy. Moreover, MDA and ROS levels of K562/G01 cells were also significantly increased(P<0.001). qPCR and Western blot results showed that the mRNA and protein expression levels of SLC7A11 and SLC3A2 in K562/G01 cells increased significantly(P<0.01) after cysteine depletion.
Conclusion Cysteine depletion can induce the death of K562/G01 in the form of ferroptosis. The underlying mechanism may be related to the redox metabolism regulated by SLC7A11 and SLC3A2. This study suggests that targeting cysteine metabolism to induce ferroptosis may become a new treatment for myeloid leukemia and it deserves further study.

PO-1227

联合检测 WBC、CRP、IL-6、PCT，SAA 及血培养在小儿败血症诊断中的临床价值

陈剑、张良艳、张大莲、周利、黄奕然、冯磊
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨联合检测 WBC、CRP、IL-6、PCT，SAA 及血培养在小儿败血症中的诊断价值。
方法 分析 2020 年 5 月-2020 年 8 月在我院接受诊疗的 47 例小二败血症患者的临床基本资料，作为试验组；再选取 50 例在本院同期健康体检者作为对照组。分析比较两组患者 WBC、CRP、IL-6、PCT、IL-6、SAA 水平。
结果 试验组患者 WBC、CRP、IL-6、PCT，SAA 水平均显著高于对照组，且差异均具有统计学意义（P<0.05）。试验组 47 例患者共分离出 45 株致病菌，其中 28 株革兰阳性菌（62.22%），主要为 16 株表皮葡萄球菌（35.56%）和 10 株溶血性链球菌（22.22%），2 株肠球菌（4.44%）；以及 17 株革兰阴性菌（37.78%），主要为 11 株大肠埃希菌（24.44%）和 5 株肺炎克雷伯菌（11.11%）,1 株鲍曼不动杆菌（2.22%）。
结论 WBC、CRP、IL-6、PCT，SAA 检测可以早期诊断小儿败血症而且可以提示疾病的严重程度，联合血培养观察患儿致病菌分布对患者的诊断和治疗具有重要的临床意义。

PO-1228

标本未离心放置对 D-二聚体(DD)及血浆纤维蛋白原降解产物(FDP)检测结果影响分析

曾超、陈佳益、刘寒、凌昉钦
上海市第一人民医院嘉定分院

目的 探讨标本未离心放置时间对 D-二聚体(DD)及血浆纤维蛋白原降解产物(FDP)检测结果影响，为规范分析前过程提供实验依据。
方法 随机选取我院 2021 年 6 月门诊采集的 100 份枸橼酸钠抗凝的外周血标本，所有标本均无溶血、脂血以及黄疸情况，采集之后分成 4 份，分别在室温下放置 0h、2h、4h、24h，在 3000r/min，持续离心 10min，使乏血小板血浆分离。离心之后立即检测，在室温条件下于分别对 D-二聚体(DD)及血浆纤维蛋白原降解产物(FDP)这两个指标进行测定。使用ＳＡＳ统计软件包对上述两项指标在放置 2h、4h、24h 后离心所得到的检测结果与 0h 后离心检测的结果进行配对ｔ检验。
分析 与 0h 后离心检测的结果相比，2h D-二聚体(DD)及血浆纤维蛋白原降解产物(FDP)无明显差异（P>0.05）； 4h 、24h D-二聚体(DD)及血浆纤维蛋白原降解产物(FDP)均明显升高（P＜0.05）；

结论 DD 是交联纤维蛋白在纤溶酶(Plasmin)作用下所产生的一种特异性纤维蛋白降解产物,是证实体内存在继发性纤溶的特异指标。FDP 是在机体发生纤溶亢进时纤溶酶作用于血浆中的纤维蛋白或纤维蛋白原产生的降解产物的总称,FDP 反映的是机体纤溶活性的总水平,原发性纤溶亢进或者继发性纤溶亢进时都为阳性。为了保证这两项检验结果的准确性，本实验说明 D-二聚体(DD)及血浆纤维蛋白原降解产物(FDP)的标本未离心的情况下，在室温存放一段时间后,对 D-二聚体(DD)及血浆纤维蛋白原降解产物(FDP)两项指标均造成一定影响，为保证凝血功能指标的检测结果更为精准，标本从采集到检测的整个过程必须控制在采血后 2h 内。超过 2h 未送检或者未完成检测的标本，均需重新采集后检测。

PO-1229

Identification of a serum lncRNA panel for the diagnosis and recurrence prediction of bladder cancer.

Weili Duan、chuanxin wang
The Second Hospital of Shandong University

Purpose The involvement of circulating lncRNAs in cancer and their potential as biomakers of diagnosis and prognosis biomakers are becoming increasingly appreciated. However, little is known about dys-regulated circulating lncRNAs in bladder cancer (BC). The purpose of present study was to identify a panel of circulating lncRNAs capable of differentiating BC patients from controls, and determining their clinical applications in BC recurrence prediction.
Methods We examined the expression of 13 candidate lncRNAs in 80 BC and matched adjacent normal tissues via quantitative real-time PCR. Eleven dys-regulated lncRNAs were evaluated in serum from 120 BC
patients and 120 controls (training set). A three-lncRNA panel was established based on logistic regression model using training set date. Then, the panel was validated in an independent cohort of 100 BC patients and 100 controls
(validation set). Meanwhile, the relationship between lncRNAs and BC recurrence was further assessed in the validation set.
Results We identified a three-lncRNA panel (MEG3, SNHG16 and MALAT1) that provided a high diagnostic accuracy of BC in training and validation set. The satisfactory diagnostic performance of lncRNA panel persisted regardless of disease status. Furthermore, Kaplan-Meier analysis was applied for BC patients and identified that non muscle invasive BC (NMIBC) patients with low MEG3 level had worse recurrence-free survival. Univariate and multivariate Cox analysis indicated that MEG3 was an independent predictor for the recurrence of NMIBC.
Conclusion This study indicated that a three-lncRNA panel can act as a novel blood-based biomarker for the diagnosis of BC. Furthermore, MEG3 was identified as an independent factor for BC recurrence.

PO-1230

凝血功能指标在热射病中的临床应用

邢丽丽
西安医学院第一附属医院

目的 中暑是指人体在高温环境下，由于水和电解质丢失过多，散热功能障碍引起的以中枢神经系统和心血管功能障碍为主要表现的热损伤性疾病。其中热射病是中暑中最为严重的类型。出凝血功能障碍在中暑发病后最早出现并对患者的预后起决定性作用，继发的其他器官功能损害也与凝血功能的异常有密切的联系。热射病合并凝血功能异常的发病机制，目前研究认为可能的发病机制，其一血液浓缩学说：高温使机体失水增加，血液浓缩，血液黏滞度变高，这些因素增加了血栓形成的

风险； 其二炎性反应因子学说：高温导致的热应激可以直接激活炎性反应系统，诱导大量中性粒细胞、巨噬细胞及单核细胞的活化，释放多重炎性反应介质和氧自由基，而诱导炎性反应级联反应的产生。在缺氧、应激时，激发“瀑布样”炎性反应可以促发凝血反应，反之凝血反应也会加重炎性反应；其三内皮细胞损伤学说：即高温产生的细胞高代谢、缺氧等一系列因素导致血管内皮细胞的损伤，使原本带有抗凝因子的血管内皮细胞表面变成促凝因素；凝血异常作为许多疾病的急性时相反应，包括急性感染、创伤等因素引起的 MODS。此类患者中普遍存在着凝血功能的异常，同时凝血异常会加重已发生的 MODS。因此本论文评价凝血功能指标在热射病中的临床应用的研究。

方法 一般资料选取 2015 年 7 月到 2018 年 7 月在本院急诊科接受治疗的 30 例热射病患者，其中男性 22 例，女性 8 例。年龄 28-55 岁，平均（43±7.5）岁。入院患者均排除其他疾病导致的凝血功能损害。30 例患者中存活组（24 例）及死亡组（6 例）。方法两组患者均进行血液检查，在入院后立即进行肘前静脉血的抽取，抽取量为 2.7ml，将其放于 3.2%柠檬酸钠抗凝的负压溶液试管中，轻摇试管，将血液与抗凝剂充分的混合，之后采用 3000r / min 进行离心，时间 10min。采用全自动血凝分析仪进行凝血功能指标的检测，将测试结果进行记录.同时采集 2ml 前肘静脉血放于 EDTA-K2 抗凝真空管中，采用全自动血细胞分析仪进行 PLT 计数，将测试结果进行记录。观察指标对比 DD、FDP、PT、APTT、FIB、PLT 各项指标之间的差异。

结果 观察生存组和死亡组患者血小板、纤维蛋白原比较差异无统计学意义，但死亡组患者 PT 和 APTT 明显高于生存组（P=0.021）；DD、FDP 亦明显高于生存组（P=0.035），差异有统计学意义。

结论 本研究结果显示，死亡组 PT、APTT、DD、FDP 均显著高于生存组，证实凝血功能障碍是热射病患者死亡的高危因素,证明凝血功能相关指标可以作为热射病预后判断因子，为热射病临床干预提供指导。

PO-1231

中性粒细胞和单核细胞 VCS 参数在早期诊断细菌感染中的临床价值初探

简子娟、梁湘辉、刘文恩
中南大学湘雅医院

目的 探讨中性粒细胞和单核细胞 VCS 参数在早期诊断细菌感染中的临床应用价值。

方法 利用 Beckman Coulter DxH800 血液分析仪分析 40 例血流感染患者、47 例局部感染患者和 69 例健康对照者的 WBC、NE%（中性粒细胞百分比）和中性粒细胞、单核细胞的 VCS 参数，对以上参数进行组间差异比较。绘制差异有统计学意义指标的 ROC 曲线，计算灵敏度、特异性和 AUC 值。

结果 血流感染组和局部感染组与对照组比较时，MNV（中性粒细胞平均体积）、MNV-SD（中性粒细胞平均体积的标准差）和 MMV（单核细胞的平均体积）的差异均有统计学意义（P＜0.01）。中性粒细胞的光散射值只有 UMALS（高中位角光散射）、UMALS-SD 和 LMALS（低中位角光散射）的差异有统计学意义（P＜0.05）。单核细胞的光散射值只有 MALS（中位角光散射）、LMALS 和 UMALS 的差异有统计学意义（P＜0.05）。血流感染组的 MNV、MNV-SD 和 MMV 值显著高于局部感染组（P＜0.01），可用于鉴别诊断。MNV 用于鉴别血流感染与局部感染的临界值为 155.5 时，灵敏度和特异性分别为 0.85 和 0.723；MNV-SD 的临界值为 21.35 时，灵敏度和特异性分别为 0.9 和 0.681；MMV 的临界值为 185.5 时，灵敏度和特异性分别为 0.6 和 0.745。

结论 监测 MNV、MNV-SD 和 MMV 有利于细菌感染性疾病的早期诊断，较 WBC 和 NE%有更高的灵敏度和特异性，且可为临床鉴别血流感染和局部感染提供实验室指标。

PO-1232

Investigation on Reference Intervals of Complete Blood Count for Children Aged 0-6 Years Old in Shenzhen of China

Xiaoliu Liu
Medical Laboratory of Shenzhen Luohu Hospital Group

Objective To establish the RIs of CBC for healthy children aged 0-6 years old in Shenzhen city, China.
Methods The peripheral blood of 101797 healthy children aged 0-6 years old who underwent physical examinations from January 2016 to April 2019 were collected. Blood samples were grouped by genders and ages for CBC.
Results The 24 RIs of CBC for healthy children from 0 to 6 years old in Shenzhen city were provided, including 8 items in red blood cells, 11 items in white blood cells and 5 items in platelets. The 24 test items in different age or gender groups were all non-normal distributions. The developing trends of 24 items of CBC with age were clarified by comparing the differences between neighboring age groups of the same indicators. Besides that, the gender differences in 24 test items of CBC were provided.
Conclusions The RIs of CBC for healthy children aged 0-6 years old were established. The RIs can be utilized as a reference index of CBC for children from Shenzhen city

PO-1233

To detect roapoptotic effects of the novel proteasome inhibitor b-AP15 on multiple myeloma cells and natural killer cells

Xiaoli Feng
Clinical laboratory center of the second hospital of Shandong university

we show that b-AP15 triggers time- and dose-dependent apoptosis of the human multiple myeloma (MM) cell lines RPMI8226 and U266, as determined by phosphatidylserine exposure. Apoptosis was dependent on caspase activation and was partially dependent on cathepsin D. Furthermore, b-AP15 triggered processing of pro-caspase-3 and cleavage of poly (ADP-ribose) polymerase in MM cells. b-AP15 also induced caspase-independent apoptosis in primary human natural killer cells. We also demonstrate that b-AP15 induces activation of the mitochondrial apoptosis pathway in MM cells, with activation of the proap optotic protein Bax and a pronounced loss of the mitochondrial transmembrane potential.The latter events, however, appeared largely independent of caspase activation.

PO-1234

A Rapid and Fully Automated Mixing Test for Screening of FVIII Inhibitors in Hemophilia A Patients

Qiang Li
Department of Laboratory Medicine, Nanfang Hospital, Southern Medical University

BACKGROUND Coagulation factor VIII (FVIII) inhibitors are the most significant complication in the treatment of hemophilia A. Activated Partial Thromboplastin Time (APTT) correction test is commonly used as a screening method, which is manual, time-consuming and laborious. The purpose of this study is to develop a rapid and automated method for screening of FVIII inhibitors.
METHODS Protocols of immediate APTT correction test (APTT-I) and post-incubation APTT correction test (APTT-P) were set on the SYSMEX CA1500 analyzer. A total of 360 patients with hemophilia A and 94 patients with lupus anticoagulant were detected by the automated method and Bethesda method. A positive inhibitors value for Bethesda was defined as ≥0.6 BU/mL. The APTT difference (APTT-D) and APTT correction index (APTT-CI) were calculated to evaluate the diagnostic efficiency of the automated method in this study and the anti-interference ability of lupus anticoagulant.
RESULTS The positive rates of Bethesda, APTT-D, APTT-CI and APTT-D combined APTT-CI were 20.29%, 22.35%, 22.65% and 21.76%, respectively. The sensitivities of APTT-D, APTT-CI and APTT-D combined APTT-CI were 97.10%, 98.55% and 97.10, 96.68%, 96.68% and 97.42% for specificity, 99.24%, 99.62% and 99.25% for negative predictive values (NPV), 88.16%, 88.31% and 90.54% for positive predictive values (PPV), 96.76%, 97.06% and 97.35% for diagnose accordance rates (DAR), respectively. The positive rates of APTT-D, APTT-CI and APTT-D combined APTT-CI were not significantly different from that of the Bethesda.
CONCLUSIONS The fully method automated established and verified by this study is a simple, rapid and accurate method for screening of FVIII inhibitors, which can be widely used in medical laboratories.

PO-1235

2 型糖尿病患者血小板聚集功能水平的研究

黎海生、邱潇林、徐敏、蒋金梅、戚南昌、朱莹泉、赵晓丽
昆明市第一人民医院

目的 通过研究 2 型糖尿病（T2DM）患者的血小板聚集功能水平，为 2 型糖尿病患者血栓（及出血）防治提供客观的依据。
方法 入选 231 例该院住院的 T2DM 患者作为研究对象（研究组），以健康体检者 222 例作为对照组，利用 PL-12 型全自动血小板功能分析仪分别检测花生四烯酸（AA）和二磷酸腺苷（ADP）诱导的血小板聚集率。对研究组和对照组的血小板聚集率进行比较，收集并分析研究组血小板聚集率与糖化血红蛋白（HbA1c）、平均血小板体积（MPV）、病程之间的相关性，比较研究组有并发症和无并发症患者的血小板聚集率差异。
结果 研究组 AA 和 ADP 诱导的血小板聚集率均明显高于对照组，差异均有统计学意义（P<0.05）。研究组 AA 和 ADP 诱导的血小板聚集率与 HbA1c 水平和病程均无相关性（P>0.05，r>0）；研究组 ADP 诱导的血小板聚集率与 MPV 呈负相关（P<0.05，r<0），AA 诱导的血小板聚集率与 MPV 无相关性（P>0.05,r<0）。研究组 AA 和 ADP 诱导的无并发症患者的血小板聚集率与有并发症患者差异均无统计学意义（p>0.05）。
结论 T2DM 患者的血小板聚集功能水平与 HbA1c、MPV、病程和并发症无明显关联。动态监测 T2DM 患者的血小板聚集功能水平在预防血栓（及出血）事件中具有一定的临床应用价值。

PO-1236

Homozygous prothrombin-Tyr510Asn mutation causes severe dysprothrombinemia with no abnormal bleeding due to antithrombin resistance

Yeling Lu 、Xi Wu、Qiulan Ding、Xuefeng Wang
Ruijin Hospital,Shanghai Jiaotong University School of Medicine

A patient with hematuria referred to our clinic was diagnosed with urolithiasis. Analysis of the patient's plasma clotting time indicated that both APTT (52.6 s) and PT (19.4 s) are prolonged and the prothrombin activity is reduced to 12.4% of normal, though the patient exhibited no abnormal bleeding phenotype. Genetic analysis revealed the patient is homozygous for prothrombin Tyr510Asn mutation. We expressed and characterized the prothrombin-Y510N variant in appropriate coagulation assays and found that the specificity constant for the activation of the mutant zymogen by factor Xa is impaired ~5-fold. Thrombin generation in the prothrombin-deficient plasma supplemented with either wild-type or prothrombin-Y510N revealed that the mutation has decreased the peak height and time to peak of thrombin generation without affecting the endogenous thrombin generation potential of the mutant prothrombin. Further analysis indicated that the thrombin mutant exhibits resistance to antithrombin and is inhibited by the serpin with ~12-fold slower rate constant. Protein C activation by thrombin-Y510N was also decreased ~10-fold, however, thrombomodulin overcame the catalytic defect. The Na+-concentration-dependence of the amidolytic activities revealed that the dissociation constant for the interaction of Na+ with the mutant has been elevated ~20-fold. These results suggest that Tyr510 (Y184a in chymotrypsin numbering) belongs to network of residues involved in binding Na+. A normal protein C activation by thrombin-Y510N suggests that thrombomodulin modulates the conformation of the Na+-binding loop of thrombin. The clotting defect of thrombin-Y510N appears to be compensated by its markedly lower reactivity with antithrombin, explaining patient's normal hemostatic phenotype.

PO-1237

降钙素原在急性淋巴细胞白血病化疗后感染中的应用价值

周泽杰
南方医科大学珠江医院

目的 研究降钙素原（PCT）在急性淋巴细胞白血病化疗后感染的诊断价值。
方法 选取在南方医科大学珠江医院出院诊断为急性淋巴细胞白血病（ALL）113 例，分为 3 组，分别为重症细菌感染组 27 例、局部细菌感染组 69 例，非细菌感染组 17 例为对照组。采用固相免疫层析技术测定各组降钙素原（PCT）水平。
结果 重症细菌感染组、局部细菌感染组及非细菌感染组之间患者降钙素原不全相等，具有统计学意义（P<0.05）。根据尤登指数， PCT>0.19 时为早期细菌感染的最佳诊断阈值，敏感度 62.5%, 特异度 100%。
结论 在急性淋巴细胞白血病化疗后细菌感染诊断中，降钙素原较 CRP 特异度高，是一种具有较高特异性新型诊断指标；严重细菌感染时，降钙素原水平异常升高，且与感染的严重程度及预后有关。

PO-1238

老年肺炎患者中 D-二聚体与降钙素原及中性粒细胞的相关性及临床意义

吕士玉
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 探讨老年肺炎患者外周血中 D-二聚体、中性粒细胞比例和降钙素原水平变化及临床意义。
方法 收集 2015 年 10 月至 2017 年 2 月在我院进行治疗的老年肺炎患者 56 例作为观察组，选取同期健康体检的健康老人 100 例作为对照组。两组研究对象，采集空腹静脉血，检测 D-二聚体（D-D）、降钙素原（PCT）水平、白细胞计数（WBC）和中性粒细胞比例（N%），比较两组间这些指标的变化情况。
结果 ①老年肺炎组与健康对照组相比，D-D、PCT、WBC 和 N%均升高（P<0.01）；②老年肺炎组中，D-D 与 PCT、N%之间均存在显著正相关性；
结论 在老年肺炎患者，随着炎症程度升高（炎症生物标志：降钙素原水平、白细胞计数及中性粒细胞比例），血栓风险增加（D-二聚体增高），及时检测 D-二聚体，采取预防和治疗措施，有助于减少血栓发生。

PO-1239

RBC、RET 系统参数在闽东地区地中海贫血和缺铁性贫血的鉴别诊断应用

陈丹丹
宁德市闽东医院

目的 探讨红细胞 3 项系统参数：红细胞计数（RBC）、平均红细胞体积（MCV）、平均红细胞血红蛋白量（MCH）；网织红细胞 6 项系统参数：网织红细胞百分率（RET％）、网织红细胞绝对值（RET＃）未成熟网织红细胞比率（IRF%）、低荧光强度网织红细胞百分率（LFR％）、中荧光强度网织红细胞百分率（MFR％）、高荧光强度网织红细胞百分率（HFR％）在地中海贫血（thalassemia trait，TT）和缺铁性贫血（iron deficiency anemia，IDA）的鉴别诊断中的应用。
方法 将 100 例 TT 患者设为地贫组，100 例 IDA 患者设为缺铁贫组，100 例健康人设为对照组，用希森美康 XN9000 系列全自动血液分析仪检测红细胞参数及网织红细胞参数，用 SPSS 23.0 统计软件分析各组参数间的差异，多组间数据采用单因素方差（one-way ANOVA）分析，多组间比较采用 Tukey 校正，同时采用受试者工作特征曲线（ROC）分析各参数曲线下面积（AUC）,评价各项指标的在鉴别 TT 和 IDA 中的诊断效能。
结果 TT 组和 IDA 组 RBC、MCV、MCH、RET%、RET#、IRF%、LFR%、MFR%、HFR%与对照组比较，其差异均有统计学意义（P＜0.05）；地中海贫血组 RBC、MCV、RET%、RET#、IRF%、LFR%、MFR%、HFR%与缺铁贫组比较，其差异均有统计学意义（P＜0.05）。α 地中海贫血与 β 地中海贫血在这些参数上进行比较，差异无统计学意义（P＞0.05）。用 ROC 分析各项指标时，HFR%的曲线下面积（AUC）=0.862，在各项指标中 AUC 下面积最大，在鉴别 TT 和 IDA 中 HFR%的 cut-off 值为<2.680。
结论 在 TT 和 IDA 的鉴别诊断中 HFR%的诊断效能最大，有望作为两者鉴别诊断重要的实验室指标。

PO-1240

红细胞分布宽度联合血清 D-二聚体水平对急性心肌梗死患者 PCI 术后心脏不良事件的预测价值

李宁
西安市第一医院

目的 探讨红细胞分布宽度联合血清 D-二聚体水平对急性心肌梗死患者 PCI 术后心脏不良事件的预测价值。
方法 选取 2016 年 10 月-2017 年 4 月期间入我院进行 PCI 术的急性心肌梗死患者 100 例，根据红细胞分布宽度是否≥16.0%分为高 RDW 组和低 RDW 组，根据 D-二聚体的水平是否＜1.0μg 分为低 D-二聚体组和高 D-二聚体组。
结果 高 RDW 组患者的 LVEF 明显低于低 RDW 组，LVEDD 和 LVESD 明显高于低 RDW 组（P＜0.05）；高 RDW 组的院内死亡、心力衰竭、再发性急性心肌梗死和恶性心律失常发生率明显高于低 RDW 组（P＜0.05）；低 D-二聚体组的死亡率明显低于高 D-二聚体组（P＜0.05）。
结论 红细胞分布宽度和血清 D-二聚体水平能够对急性心肌梗死患者 PCI 术后的心脏不良事件进行有效的预测，可以对预后效果进行一定程度的提示。

PO-1241

肾综合征出血热患者凝血及纤溶相关指标检测结果分析

李锐成、董轲
空军军医大学唐都医院检验科

目的 分析不同临床分期和不同严重程度肾综合征出血热（hemorrhagic fever with renal syndrome, HFRS）患者凝血指标和纤溶指标的检测结果，探讨 HFRS 在病情变化时凝血纤溶指标的改变规律。
方法 选取 2010 年 1 月至 2020 年 7 月期间在我院就诊的有明确分期和严重程度的 HFRS 患者 552 例，对其进行凝血、纤溶功能指标的检测，包括活化部分凝血活酶时间（APTT）、凝血酶原时间（PT）、纤维蛋白原含量（FIB）、凝血酶时间（TT）、纤维蛋白原降解产物（FDP）和 D-二聚体（D-D），对各项指标在临床分期和不同严重程度时的检测结果进行分析比较。
结果 PT、APTT、FIB 和 TT 四项凝血指标在低血压休克期时异常幅度最为明显，而 FDP 和 D-D 两项纤溶指标则在少尿期时最为明显。六项指标随着疾病的严重程度出现了异常率和异常水平的明显上升，差异均具有统计学意义(P 均<0.05)。
结论 六项凝血指标及纤溶指标在 HFRS 患者中出现明显异常，尤其处在低血压休克期和危重型。在低血压休克期前和重症时做到早期干预以纠正凝血和纤溶系统紊乱意义重大。

PO-1242

Hsa_circ_0006834 在非小细胞肺癌中的作用及机制研究

丁小鸽
江苏大学

目的 研究表明 CircRNA 在人非小细胞肺癌（non-small cell lung cancer, NSCLC）发生发展中起着重要作用。本文拟探究 Circ6834 在 NSCLC 中的表达模式及生物学功能，并探讨其潜在的作用机制。
方法 采用 qRT-PCR 检测 NSCLC 患者肿瘤组织及细胞系中 Circ6834 的表达水平。采用过表达及敲减 Circ6834 质粒转染 NSCLC 细胞，通过克隆形成、生长曲线、transwell 细胞迁移侵袭实验分

别观察过表达和敲减 Circ6834 对 NSCLC 细胞生物学功能的影响，采用荧光素酶报告基因实验、RNA 免疫共沉淀（RIP）及质谱分析探究 Circ6834 在 NSCLC 中的潜在作用机制。
结果 Circ6834 在 NSCLC 患者肿瘤组织中低表达。体外实验发现 Circ6834 过表达后能明显抑制 NSCLC 细胞增殖、迁移和侵袭能力，促进细胞凋亡；敲减 Circ6834 具有相反效果。同时，Circ6834 应答 NSCLC 细胞内转化生长因子 β（transforming growth factor-β,TGF-β）刺激，TGF-β 刺激后，Circ6834 在 NSCLC 细胞中表达下调且 TGF-β 可以部分逆转过表达 Circ6834 引起的 NSCLC 细胞的功能学改变；而过表达 Circ6834 可以抑制 TGF-β/Smad 信号通路的激活。荧光素酶报告基因实验发现 miR-873-5p 具有较强抑制 Circ6834 荧光素酶报告基因活性的作用，过表达 miR-873-5p 可以逆转 Circ6834 的抑癌作用。RIP 及质谱分析表明 Circ6834 可能通过与 AHNAK 蛋白结合调控 AHNAK 的表达从而抑制 NSCLC 的转移。
结论 Circ6834 在 NSCLC 中低表达，具有抑制 NSCLC 生长和转移的重要作用，可能作为一个潜在的生物标志物，为 NSCLC 的早期诊断及治疗提供新靶点。

PO-1243

初步探讨血浆 vWF 和 ADAMTS-13 在 VSD 患儿术后血管内皮损伤评估及预后的应用价值

王欣怡[1,2]、张琼文[1,2]、沈永明[3]、刘军锋[1]、李文正[1]、贾克刚[1,2]
1. 泰达国际心血管病医院
2. 天津医科大学心血管病临床学院
3. 天津市儿童医院

目的 动态观察先天性心脏病室间隔缺损（VSD）患儿围手术期血浆血管性血友病因子（vWF）、血管性血友病因子裂解蛋白酶（ADAMTS-13）的水平和活性变化，探讨 VSD 患儿术后血浆 vWF 浓度（vWF:Ag）和 ADAMTS-13 活性（ADAMTS-13:AC）反应内皮细胞损伤及预后的影响。
方法 收集泰达国际心血管病医院 2018 年 10 月至 2019 年 3 月期间行手术治疗的 VSD 患儿 74 例为实验组(单纯 VSD 组 28 例、VSD 合并肺动脉高压组 32 例、VSD 合并心脏瓣膜病组 14 例)。收集同期天津市儿童医院健康儿童 31 例为对照组。分别留取患儿入院时、心脏手术后当天、术后一天的外周静脉血血浆，记录入院时各项生化指标。进行 vWF 活性（vWF:AC）、vWF:Ag、ADAMTS-13 抗原(ADAMTS-13:Ag)、ADAMTS-13:AC 检测。
结果 ①实验组患儿血浆 vWF:Ag、vWF:AC 术前含量明显低于对照组（P<0.001），术后当天、术后 1 天均持续明显升高（P<0.001）；②实验组患儿血浆 ADAMTS-13:Ag 术前含量明显高于对照组（P<0.001），术后当天、术后 1 天较术前明显下降，但两者之间无显著差异（p=0.777）；③实验组患儿血浆 ADAMTS-13:AC 水平明显低于对照组（P<0.001），术后当天、术后 1 天均无明显变化（p=0.054，p=0.926）；④VSD 合并瓣膜病组术前 vWF 水平与对照组无明显差异，三亚组术后 vWF、ADAMTS-13 水平与实验组变化趋势相同；⑤vWF:Ag/ADAMTS-13:AC 比值曲线面积（AUC=0.798）高于 vWF:Ag 和 vWF:AC；术后 1 天 vWF:Ag/ADAMTS-13:AC 比值在反映血管内皮损伤中的敏感性及特异性最高。
结论 术后 vWF:Ag、vWF:AC 明显上升,ADAMTS-13:Ag 明显下降，呈明显相反的动

PO-1244

肝病发展阶段凝血六项的变化趋势研究

刘飞、徐运
陆军军医大学第二附属医院检验科

目的 探讨凝血六项联合检测在肝病的诊治、病情监测及指导用药中的临床价值。
方法 （1）样本选取 2010 年至 2020 年新桥医院消化内科 210 例不同病程的肝病患者（慢性肝炎 70 例、肝硬化 70 例，肝癌 70 例）及健康体检者 70 例；采用静脉全血检测，枸橼酸钠抗凝。（2）采用 ACL TOP 700 LAS 全自动凝血分析仪及其配套试剂检测患者凝血六项各指标水平,研究肝病发展进程与凝血六项的相关性。（3） 组间比较采用 t 检验或非参数 Wilcoxon 秩和检验，多组间比较采用单因素方差分析或非参数 Kruskal-Wallis H 秩和检验。P＜0.05，差异有统计学意义。
结果 1）不同发展阶段的肝病患者 PT、APTT、TT 较对照组均有不同程度的延长（P＜0.05）；FIB 含量较对照组均有不同程度的下降（P＜0.05）；AT-III 活性较对照组均有不同程度的下降（P＜0.05）；D-二聚体含量较对照组均有不同程度的上升（P＜0.05）。2）各型肝脏疾病 PT、APTT 呈现慢性肝炎组＜肝硬化组、肝癌组（P＜0.05）而肝硬化组和肝癌组相比差异无统计学意义（P＞0.05）；TT 呈现慢性肝炎组＜肝硬化组（P＜0.05），而慢性肝炎组与肝癌组、肝硬化组与肝癌组相比差异无统计学意义（P＞0.05）；FIB 含量呈现肝癌组＞慢性肝炎组＞肝硬化组（P＜0.05）；AT-III 活性呈现慢性肝炎组＞肝硬化组、肝癌组（P＜0.05），而肝硬化组和肝癌组相比差异无统计学意义（P＞0.05）；D-二聚体含量呈现慢性肝炎组、肝硬化组＜肝癌组（P＜0.05），而肝硬化组和慢性肝炎组相比差异无统计学意义（P＞0.05）。
结论 凝血六项的水平可客观地评价肝病患者的凝血纤溶状况，并且与肝病的严重程度一致。对临床肝脏疾病的诊断、治疗、动态检测和指导临床用药提供依据，具有重要的临床指导意义。

PO-1245

基于沃芬凝血系统的常规凝血项目结果自动审核规则建立与验证的多中心研究

苗林子[1]、李传宝[2]、戴菊华[3]、屈晨雪[1]、续薇[4]、曲林琳[4]、范庆坤[5]、汪润[1]、叶辉铭[6]、张晶[6]、王海[7]、芦慧霞[8]、赵艳丽[9]、李小侠[10]、沈阳[11]、伍佰清[12]、夏立娇[13]、朱传金[14]
1. 北京大学第一医院
2. 北京医院
3. 北京大学国际医院
4. 吉林大学白求恩第一医院
5. 武汉亚洲心脏病医院
6. 厦门市妇幼保健院
7. 吉林大学中日联谊医院
8. 东南大学附属中大医院
9. 吉林大学第二医院
10. 陕西省人民医院
11. 沃芬医疗器械商贸（北京）有限公司
12. 江西省人民医院
13. 民航总医院
14. 山东省肿瘤医院

目的 建立能够满足临床需要的基于沃芬凝血系统的凝血项目自动审核规则，在保证检验报告准确性的同时，减轻人工审核的人员支出，有效缩短实验室内周转时间。
方法 通过来自 9 个中心的包括凝血酶原时间(PT)，活化部分凝血活酶时间(APTT)，凝血酶时间(TT)、纤维蛋白原(FIB)、纤维蛋白原降解产物（FDP）以及 D 二聚体（D-D）6 项的凝血数据建立

了自动审核规则。自动审核规则包括质控检查、核对与医嘱一致性和结果的数字形式、标本性状检查、报警信息检查，危急值检查、历史结果查询及差值检验、限制范围判定、放宽条件判定以及逻辑关系判定，将自动审核规则设入模拟验证软件、仪器中间件中，进行了初步验证、一期验证及二期验证。规则验证通过自动审核通过率、真阳性率、真阴性率、假阳性率、假阴性率、敏感性和特异性进行评估；用实验室周转时间(TAT)评估自动审核规则的效率。
结果 收集 2020 年 1 月至 2020 年 3 月 9 家医院凝血检测样本 22072 份进行自动审核规则的建立。初步验证采用规则建立组数据，自动审核通过率为 68.83%，其中 6281 例假阳性病例，无假阴性病例。 在 2020 年 6 月进行了 32743 份样本的一期模拟验证，自动审核的总体率为 66.73%，其中 4650 例假阳性病例，无假阴性病例，敏感性为 100%，特异性为 85.80%。 在 2020 年 10-11 月将自动审核规则设入中间件和 LIS 系统，进行了 10176 例样本的二期验证。自动审核总体通过率为 69.50%，各家中心检验后平均实验室内周转时间（TAT）由 91min 降至 72min，差异具有统计学意义(P=0.006)。
结论 基于沃芬凝血系统的自动审核系统可以在保证医疗安全的同时，对大部分无异常的结果进行自动审核，减轻人工审核的负担，缩短 TAT，提高工作效率。

PO-1246

健康成人白细胞表面 CD64 和 HLA-DR 指标参考区间建立及其影响因素探讨

苗林子、陆遥、屈晨雪、由然、龚岩
北京大学第一医院

目的 建立健康成人白细胞表面 CD64 和 HLA-DR 及相关指标的参考区间，探讨其影响因素。
材料和方法 选取北京大学第一医院体检中心 126 例 22-60 岁的健康成人，分别采用抗 CD64、抗 HLA-DR 单克隆抗体标记白细胞表面 CD64 和 HLA-DR，采用流式细胞术检测二者的表达情况，计算白细胞表面 CD64 和 HLA-DR 相关指标并建立相应的参考区间，分析年龄、性别对白细胞表面 CD64 和 HLA-DR 相关指标的影响。
结果 健康成人白细胞表面多个 CD64 和 HLA-DR 相关指标检测结果显示，数据均呈偏态分布。CD64 相关指标在各年龄组间无统计学差异。单核细胞 HLA-DR 平均荧光强度、单核细胞 HLA-DR 荧光强度中位数、单核细胞与中性粒细胞 HLA-DR 比值(平均荧光强度）随年龄增加有逐渐上升趋势。18-29 岁组的单核细胞 HLA-DR 平均荧光强度低于 40-49 岁组和 50-59 岁组（P=0.023，P=0.007）；18-29 岁组的单核细胞 HLA-DR 荧光强度中位数低于 50-59 岁组（P=0.034），上述差异均具有统计学意义。男性与女性白细胞表面 CD64 和 HLA-DR 相关指标均无显著差异（P 均>0.05）。
结论 本研究首次建立了健康成人白细胞表面 CD64 和 HLA-DR 相关的多个指标的参考区间，对这些指标的临床应用提供了依据。年龄会影响健康成人白细胞表面 HLA-DR 相关指标检测结果。

PO-1247

XN9000 血细胞分析系统自动审核规则验证

刘中路
临沂市人民医院

目的 在血液分析中联合应用多项规则进行检验结果的自动审核，来验证多规则联合应用的有效性。
方法 利用临沂市人民医院检科 2020 年 8 月至 11 月期间的 EDTA-K2 抗凝的血常标本共 50659 例，联合应用标本性状检查、复检规则、多中心审核规则、IP 报警检查、Positive 检查等多项规则，对

XN9000 血液水线结果自动审核。对所选择验证的标本全部推片镜检，镜检阳性结果录入Labman6.0 系统，统计自动审核通过率、假阳性率、假阴性率、复检率及镜检率。
结果 自动审核验证通过率 68.78%（34845/50659）、假阳性率 15.58%（7982/50659）、假阴率 1.51%（765/50659）、复检率 18.51%（9379/50659）、镜检率 15.71%（7959/50659）。使用自动审核规则后，平均 TAT 缩短 3 分钟。
结论 使用 XN9000 配套的 Labman6.0 系统，联合应用多项规则进行血常规结果的自动审核，在满足假阴性要求的前提下，提高结果自动审核率（70%左右），保证工作人员集中精力复检异常标本，提高血常规的检验质量。

PO-1248

Establishment and Bleeding Assessment in Subarachnoid Hemorrhage Mice Model Based on Aggregation- Induced Emission Probe

Maliang Tao
Sourthern medical unniversity NanFang hospital

Background & Objective Subarachnoid hemorrhage (SAH) is a serious disease caused by the rupture of diseased blood vessels at the bottom of the brain or on the surface of the brain, with blood flowing directly into the subarachnoid space. The pathophysiological mechanisms involved in SAH brain damage, such as brain injury and cerebral vasospasm, is still unclear. As is considered to the closest imitation of human SAH, the endovascular perforation method for inducing SAH is frequently used in rodents for exploring the mechanisms involved in SAH brain damage and developing effective therapeutic strategies. However, the assessment of SAH severity by radiological technology is greatly limited, due to the difficulty on bleeding quantification, especially the micro bleeding (less than 40 μL) and diffuse bleeding in SAH rodents.
In order to overcoming these above shortcomings, we demonstrated a near-infrared (NIR) aggregation-induced emission (AIE)-active probes for in vivo bleeding indication, through binding blood to switch the fluorescence state from off to on. Based on the fluorescence signal in the subarachnoid space, we hope to identify the induction of SAH without euthanasia and establish a new grading system for the quantification of bleeding and the evaluation of SAH severity, providing a new visual bleeding quantitative tool and new animal model for the study of the pathological mechanism of SAH.
Methods 1. AIE-active fluorescent probe TTVP that can specifically respond to blood was obtained by constructing and screening the AIE molecular library. Its photophysical properties were studied by UV-absorption spectrum analysis, photoluminescence (PL) analysis, and other methods. Stability detection, selective-specificity experiment, tissue penetration experiment, and CCK8 assay were performed to determine the capacity of TTVP to work as an in vivo bleeding indicator.
2. To bring TTVP into the subarachnoid space of mice during the induction of SAH, a new injectable cannula was connected by the insulin needle and the ultra-fine capillary tube, which was used to replace the traditional No. 3 fishing line for puncturing the intracranial blood vessel and injecting TTVP.
3. The brain fluorescent signal of SAH mice with different levels of hemorrhage was detected by an In-Vivo FX PRO imaging system, and a new in vivo identification method and quantitative hemorrhage grading system were established. To evaluate the superiority and reliability of the fluorescent grading system, mouse brain anatomy and MRI were assessed at the same time.
Results 1. TTVP showed an absorption maximum at 480 nm and emitted red fluorescence with emission peak at 645 nm in THF, with maximum tissue penetration depth exceeding 0.75 cm. TTVP was completely unaffected with pH changes ranging from 3 to 12 and showed excellent stability in fresh cerebrospinal fluid over 24 h.

2. TTVP can specifically light up the blood through binding to albumin and hemoglobin in the blood and had a good linear response relationship with the blood volume in the range of 2-20 μL, with the lowest detection limit of 2 μL.
3. The new injectable device successfully brought TTVP into the subarachnoid space of mice and obtained the SAH mice model;
4. The brain fluorescent signal in the occipital region was used to determine the induction of SAH, and its intensity difference was proportional to the bleeding degree and severity of SAH in the mice, which could be divided into 5 levels from light to severe. The signal of the fluorescence imaging system based on TTVP was not only consistent with the brain anatomy and MRI results, but also far superior to MRI for the quantitative detection of bleeding, especially in diffuse bleeding and minor bleeding.
Conclusion In this study, we constructed and screened a near-infrared (NIR) aggregation-induced emission (AIE)-active probe TTVP for in vivo bleeding indication, through binding with albumin and hemoglobin in the blood to switch the fluorescence state from off to on. It has the advantages of near-infrared luminescence, high biological stability, and high tissue penetration. Based on the fluorescence signal in the subarachnoid space, we successfully identified the induction of SAH without euthanasia. Furthermore, a new fluorescence grading system based on TTVP has also been established for the quantification of bleeding and the evaluation of SAH severity. This fluorescence evaluation system provides a new visual bleeding quantitative tool and new animal model for the study of the pathological mechanism and novel therapeutic therapies of SAH.

PO-1249

不同检验原理血凝仪器检测结果可比性讨论

靳强强
山东大学第二医院

目的 探讨不同检测原理血凝仪器凝血常规四项检测结果可比性。
方法 收集 20 份检验结果覆盖线性范围的病人样本，离心获得乏血小板血浆后，均分成两份，并编成 A、B 两组。A 组为对照组：实验组检测仪器为沃分 TOP 700；B 组为检测仪器为思塔高 STAR Max。分别上机检测项目为 PT、APTT、TT、FiB，4h 之内检测完毕，并对检验结果进行比较分析。
结果 两台仪器检测原理：思塔高 STAR Max 为磁珠法，沃分 TOP 700 为光学凝固法。通过对 A、B 两组数据 20 份样本进行数据分析，利用数据一致性、相关性、符合性三个方面对检测结果进行分析。根据 WS/T406-2012 凝血检验批内精密度的检测要求推导得来，系统间比对偏倚应<1/2Tea，PT 正常标本允许偏差≤6.0%，异常标本≤16.0%；APPT 正常标本允许偏差≤8.0%，异常标本≤16.0%；TT 正常标本允许偏差≤10.0%，异常标本≤10.0%；FiB 正常标本允许偏差≤12.0%，异常标本≤24.0%。由于不同品牌仪器间试剂及检测原理差异，若比对结果不能满足相对偏差要求，则应对数据进行回归分析，计算 r2 满足 1±0.05 即可。若不满足相关性要求，则降级按照定性检验地要求进行结果符合率验证，符合率>80%即可通过。本次比对结果中，PT 检测结果具有符合性，符合率为 85%；APTT 检测结果具有相关性，APTT 回归方程 $y = 1.224x + 1.5505$，$r^2=0.9814$；TT 检测结果具有符合性，符合率为 100%；FiB 检测结果具有一致性。
结论 PT 检测结果具有符合性；APTT 检测结果具有相关性；TT 检测结果具有符合性；FiB 检测结果具有一致性。

PO-1250

探究布加综合征患者血小板活化情况

刘云
徐州医科大学附属医院

目的 探究布加综合征患者血小板活化百分比，为疾病的早诊断早治疗提供新思路。
方法 收集 BCS 患者外周血 10 例，同时采集正常人外周血 10 例作为对照，采用流式检测 CD62P、PAC-1 百分比以及 CD41a、AK2 的表达情况。
结果 BCS 患者 CD62P、PAC-1 以及 CD41a 与正常对照相比差异有统计学意义（1.236±0.14vs0.340±0.02，P=0.0004；1.946±0.42vs0.309±0.03，P=0.001；9305±436.1vs7604±500.6，P=0.025）。
结论 BCS 患者外周血血小板活化指标 CD62P、PAC-1 相对于正常对照均升高，提示在疾病诊断中具有较大临床应用价值。

PO-1251

新型尿液分析仪在疑似尿路感染病人中快速筛查应用研究

李江
湖南省人民医院

尿路感染（Urinary Tract Infections，UTI）是门诊和住院患者最常见的感染之一。如不能及时准确地诊断，延误治疗，可能导致患者逐渐发展为复发性难治性尿路感染，严重降低患者生活质量。在疑似尿路感染的病人中，大部分定量尿细菌培养的结果为阴性，阴性率可以高达 60%，甚至更高。此外，尿细菌培养程序至少需要 24 小时，并且需要临床实验室工作人员的大量手工操作。在临床诊断操作中，临床实验室无法快速提供尿细菌培养的病原体信息，临床医生基于其自身的技术和经验，采用经验性抗生素用药方法，可引起抗生素的过度使用，增加尿路感染细菌的耐药性风险。希森美康 UF-5000 尿有形成分分析仪采用 488nm 波长新型蓝色半导体激光器，同样基于荧光流式细胞术的检测原理，快速准确计数并分类尿液中有形成分如红细胞、白细胞、上皮细胞、管型及微生物等的全自动化尿液分析仪。UF-5000 能够更精准识别和鉴定细菌的特征。采用流式细胞术原理，基于革兰氏阳性菌和阴性菌细胞壁肽聚糖的含量差异，二者的前向散射光强度和荧光染色特性均有差异，从而区分出革兰氏阳性菌和革兰氏阴性菌，从而提供极其有价值的尿细菌学信息，为指导尿路感染患者抗生素的使用提供重要依据。最新研究表明，UF-5000 在检测尿有形成分颗粒计数、分类方面展现出良好的性能，但用于评估其在筛查疑似尿路感染患者的性能方面鲜有报道。

PO-1252

定量比值法测新生儿脐血 G6PD 临界值设定的探讨

刘均如
广东省人民医院

目的 通过高铁血红蛋白还原实验结合双酶定量比值法检测脐血 G6PD，探讨新生儿脐血双酶比值法测定 G6PD 的临界范围设定。
方法 用广州米基公司 G6PD 定量比值法试剂盒对本院产科 2018 年 7 月-2021 年 4 月共 2065 例女性新生儿脐血进行 G6PD 定量检测，同时进行高铁血红蛋白还原试验（肉眼观察呈明显棕红色、棕色或黑色为阳性）。

结果 2065 例女性新生儿中， G6PD 比值<1.10 有 52 例（双酶比值法脐血正常参考范围 1.10-2.50），高铁血红蛋白还原实验阳性 141 例，其中 52 例 G6PD 比值<1.10 新生儿脐血，两种方法符合率为 100%。另 89 例 G6PD 比值>1.10 而高铁血红蛋白还原试验阳性的脐血样本，结合父母亲 G6PD 缺陷情况，判定 87 例为 G6PD 杂合子。
结论 比值法测 G6PD 杂合子容易漏检，参照试剂说明书正常参考范围，脐血女性新生儿 G6PD 缺陷检出率为 2.5%；而根据本研究，比值法测脐血 G6PD 对女性杂合子的漏检率约为 4.2%，若比值法检测 G6PD 设定脐血临界参考范围在 1.05-1.40，则脐血女性新生儿 G6PD 缺陷检出率可达 6.7%，可大大降低新生儿脐血筛查 G6PD 女性杂合子漏检率。

PO-1253

The effects of storage on platelet proteome assessed by protein expression changes and lysine modification changes using TMT isobaric labeling

Li Wang、Zhicheng Wang
Department of Laboratory Medicine, Huashan hospital, Fudan University

Objective To provide the first insight into the proteomic dynamics during platelet storage.
Experiment design In this study, based on TMT-labeled LC-MS/MS analysis, combined with antibody-affinity enrichment and purification for acetylated and succinylated peptides, we performed quantification of global proteomics, acetylome and succinylome. Simultaneously, dynamic molecular changes and functional transformation of platelet were also characterized under proper conditions stored for 1, 3, 5, 7 days, respectively.
Results 3,100 proteins are quantified from a total of 3,609 proteins identified from platelets. Out of 1,308 acetylated sites identified in 648 proteins, 790 sites in 396 proteins are quantifiable. There are 1,947 succinylated sites in 959 proteins in which 1,279 sites in 661 proteins are quantifiable. We screened the differential expression changes of global proteins, acetyl- and succinyl- proteins, and systematically interpreted their molecular functions, biological processes, cellular components, pathways and motif characters to fully investigate the molecular dynamics and biological functions of platelets.
Conclusions This paper is the first systematic exploration of proteomes and modified proteomes of platelet dynamics during storage in the aim to improve our understanding of platelet biology, which may be a valuable reference for further research and clinical application.

PO-1254

OSA 患者血浆外泌体在促心肌细胞纤维化和肥大作用中机制研究

吕星、龚辉、张湘瑜
中南大学湘雅二医院

目的 研究阻塞性睡眠呼吸暂停（OSA）血浆外泌体在心肌细胞纤维化和肥大中的作用机制，为进一步研发新的无创诊断方法、新的诊断标记物和有效治疗的方法提供理论依据。
方法 将未经治疗的 OSA 患者(OSA-exos)和健康对照(非 OSA-exos)空腹血浆样本中提取的外泌体作用于心肌细胞 H9C2。采用 Western blotting、PCR 和免疫荧光染色观察 Col1A1、ANP、BNP 等纤维化和肥厚性标志的表达变化，此外，在 H9C2 中加入等量的 OSA-Exos,观察自噬和 Akt/mTOR 表达变化以及在其中的作用机制。

结果 与对照组相比，未经治疗的 OSA 外泌体导致 Col1A1、ANP 和 BNP 显著升高。并且自噬指标 LC3B 和 beclin1 在 OSA-Exos 组表达下降。OSA-Exos 处理组 p-Akt/Akt、p-mTOR/mTOR 水平高于对照组。
结论 OSA 血浆外泌体可能通过 Akt/mTOR 信号通路抑制自噬从而调控心肌细胞纤维化和肥大。

PO-1255

遗传性异常纤维蛋白原血症一家系纤维蛋白原含量及功能分析

吴雪莲、李孟韩、谢依杉、卢谊、潘娟、王逍遥、吴斯玮、邓昆
重庆医科大学附属第三医院

目的 对 1 个遗传性异常纤维蛋白原血症家系进行表型和基因型分析，阐述该家系成员的纤维蛋白原含量、纤维蛋白原功能之间的联系，探讨该家系分子发病机制。
方法 应用 ACL TOP 700 全自动凝血分析仪检测先证者及其家系成员三代 20 人的血浆活化部分凝血活酶时间（activated partial thromboplastin time, APTT）、凝血酶原时间（prothrombin time，PT）、凝血酶时间（thrombin time，TT）、纤维蛋白原（fibrinogen，Fg），分别采用 von-Clauss 法、PT 衍算法检测纤维蛋白原活性（Fg：C）；用贝克曼 AU 5800 全自动生化分析仪检测纤维蛋白原抗原水平（Fg：Ag）。应用血栓弹力图仪检测 9 名凝血功能异常家系成员的反应时间（R）、凝血形成时间（K）、最大振幅（MA）、弹力图最大切角（α-Angle），评估纤维蛋白原功能以及血小板功能。应用 BGISEQ-500RS 基因测序仪对先证者、先证者父母及先证者儿子 4 人进行全外显子测序，进行基因分析。
结果 凝血功能检测结果显示先证者以及包括先证者母亲和儿子在内的 10 名家系成员均存在凝血酶时间（TT）明显延长、Fg 活性（von-clauss 法）明显减低；血栓弹力图检测结果显示先证者弟弟 K 值延长， α-Angle 减低，先证者弟弟的儿子凝血 R 值缩短， α-Angle 减低；二代测序结果显示先证者、先证者母亲以及先证者儿子存在 FGA 基因 c.103C＞T 杂合突变。
结论 基于 FGA 基因的 c.103C＞T 突变是导致先证者、先证者母亲以及先证者儿子异常纤维蛋白原血症的分子发病机制；该突变所致异常纤维蛋白原的功能正常。

PO-1256

线粒体转移促进肿瘤发展的研究进展

张娟[1]、张柳芸[2]、向云会[2]
1. 电子科技大学附属医院·四川省人民医院
2. 电子科技大学医学院

细胞间线粒体转移（Mitochondria transfer）在多种血液系统肿瘤和实体瘤的发生、转移、侵袭力改变、化疗耐药等过程中都发挥了重要的作用。肿瘤细胞与其微环境中细胞之间的线粒体转移对肿瘤的发展至关重要，微环境中的细胞，如间充质干细胞、内皮细胞等，可以将线粒体转移至肿瘤细胞中，恢复肿瘤细胞的有氧呼吸，并为快速增殖的肿瘤细胞提供能量，从而促进肿瘤发展。不仅如此，肿瘤细胞也可以将线粒体转移至微环境中的细胞，从而降低自身线粒体的数量，避免线粒体氧化磷酸化中，呼吸复合物 I 和 III 产生过多的线粒体活性氧(Reactive Oxygen Species，ROS) 损伤肿瘤细胞。此外，肿瘤细胞之间有时也会发生线粒体转移。本综述主要讨论了截至目前研究报道的有关细胞间线粒体转移对肿瘤细胞增殖、化疗耐药和诱导凋亡等方面的影响，为将线粒体作为肿瘤治疗中的潜在靶标奠定理论基础。

PO-1257

新型冠状病毒感染的重症和非重症患者实验室指标的对比分析

李佳珊
哈尔滨医科大学附属第一医院

背景 2019 冠状病毒病(COVID-19)已威胁全球健康。冠状病毒的实验室特征对临床诊断和治疗具有重要意义。我们发现了可能最有效地预测非重症 COVID-19 患者发展为重症患者的指标。
方法 我们对检索的文献中 COVID-19 重症患者与非重症患者的实验室检查结果进行 meta 分析。
结果 通过分析 35 篇文献(5912 例)中 COVID-19 患者的实验室检查资料，我们发现重症病例具有更高的白细胞(1.20 倍)、中性粒细胞(1.33 倍)、CRP(3.04 倍)、PCT(2.00 倍)、ESR(1.44 倍)、AST(1.40 倍)、ALT(1.34 倍)、LDH(1.54 倍)、CK(1.44 倍)、CK-MB(1.39 倍)，总胆红素(1.14 倍)，尿素(1.28 倍)，肌酸(1.09 倍)，PT(1.03 倍)，d -二聚体(2.74 倍)，淋巴细胞(1.44 倍)，嗜酸性粒细胞(2.00 倍)，单核细胞(1.08 倍)，血红蛋白(1.53 倍)，PLT(1.15 倍)，白蛋白(1.15 倍)，APTT(1.02 倍)，与非重症相比较。重症组与非重症组的淋巴细胞亚群和炎性细胞因子序列也有所不同，在重症组中 CD4 T 细胞较低(2.10 倍)、CD8 T 细胞较低(2.00 倍)，而 IL-1β(1.02 倍)、IL-6(1.93 倍)、IL-10(1.55 倍)较高。
结论 部分实验室检查指标可预测 COVID-19 变化的进展，特别是淋巴细胞、CRP、PCT、ALT、AST、LDH、D -二聚体、CD4 T 细胞和 IL6，这些指标可能为预防疾病恶化提供有价值的信号。

PO-1258

贫血鉴别诊断中的血液检验效果观察

吕艳丽
南方医科大学珠江医院

目的 研究贫血鉴别诊断中血液检验的应用价值与有效性，为临床诊断提供必要指导。
方法 随机将 2017 年 3 月～2019 年 3 月本院 25 例贫血患者作为实验组，同期选择 25 例健康体检者作为对照组，对比两组参与者血液检验结果。
结果 实验组 MCV 为（74.79±0.48）、RBC 为（3.71±0.44）、MCH 为（10.11±1.32）、Hb 为（86.61±4.48）、RDW 为（22.46±1.57），前四项指标均比对照组高，最后一项指标高于对照组，差异具备统计学研究意义（P＜0.05）。
结论 诊断贫血的过程中，选择血液检验方式，可有效提高诊断结果的准确性，临床应用相对广泛。

PO-1259

血浆 D-二聚体诊断肺癌合并肺栓塞的最佳临界值研究

刘胜男、廖建枫、李广华、黄革、顾兵
广东省人民医院

目的 探讨血浆 D-二聚体诊断肺癌合并肺栓塞的最佳临界值。
方法 2010 年-2019 年广东省人民医院收治肺癌合并肺栓塞患者 158 例，随机选取 2010 年-2019 年广东省人民医院收治肺癌患者并肺栓塞阴性 158 例作为对照组。目前临床上普遍采用螺旋 CT 增强扫描作为肺栓塞的确诊依据[1]，因此以影像学诊断为主，结合临床医生诊断，收集患者诊断当天的 D-二聚体数值以拟合 ROC 曲线，确定其最佳临界值。

结果 经 ROC 曲线分析，D-二聚体诊断肺癌合并肺栓塞的灵敏度为 72.2%，特异度为 75.9%，阳性预测值为 79%，阴性预测值为 78.2%，Youden 指数为 0.481，AUC 值为 0.810，有较高的诊断价值；D-二聚体诊断肺癌合并肺栓塞的最佳临界值为 1950μg/L。
结论 肺癌患者体内 D-二聚体升高，临床上目前使用 500μg/L 作为肺栓塞阴性排查值并不适用于肺癌人群， D-二聚体取 1950μg/L 作为肺癌合并肺栓塞的最佳诊断值,有利于肺栓塞的早期诊断和治疗,对改善肺栓塞患者预后有重要意义。

PO-1260

Outcome of adolescent and adult T-cell acute leukemia and the prognostic significance of early T-cell precursor leukemia subtype

Hongyan Liao [1]、Qin Zheng[2]
1. Department of Laboratory Medicine, West China Hospital, Sichuan University
2. 四川大学华西医院实验医学科

Objective To evaluate the clinical characteristics of T-cell acute leukemia/lymphoma and explore the prognosis significance of early T-cell precursor leukemia/lymphoma.
Methods 160 patients diagnosed of T-ALL from 2008 to 2016 in West China Hospital, Sichuan University were enrolled in this study. They were further categorized by immunophenotype according to the expression of T-cell lineage markers CD1a, CD8, CD5 and one or more stem cell or myeloid markers. The laboratory indicators and prognosis factors were also statistically analyzed.
Results Of all patients, the ratio of male to female was 2.2:1, with the median age 26 years old (range 10 to 77). The percentage of ETP-ALL was as high as 44.4%. T-ALL patients showed higher ratio in first clinical remission rate (CR1) than T-LBL patients (64.4% vs 30.8%, P = 0.03). Group with WBC count higher than 50×109/L at presentation showed higher ration of achieving CR1 than those lower than 50×109/L (78.4% vs 50.9%, P = 0.009). In comparison with the Non-ETP-ALL, ETP-ALL patients had older age of onset (P < 0.001), lower WBC count (P < 0.001), lower risk of CNS involvement (11.3% vs 25.4%，P = 0.049) and slightly inferior overall survival (P = 0.053).Results between positive and negative expression of T-cell lineage markers CD1a-, CD8- ,CD4- and myeloid lineage markers CD33-, CD56-, there is no statistical significance of prognosis.
Conclusion Flow cytometry and associated markers for immunophenotyping is of significance in the diagnosis and prognosis monitoring of T-ALL/LBL. The percentage of ETP-ALL/LBL subtype is high in Chinese adolescent and adult T-ALL patients. ETP/ALL/LBL is a high risk subtype, which needs more precise standard for diagnosis and advanced therapies for better outcome.

PO-1261

一例少见异常 HbQ 的家系分析

葛艳芬
广东省人民医院（广东省医学科学院）

目的 报道一例异常 Hb Q 的家系分析结果。
方法 采集患者一家三口的外周血标本，进行常规血液学检测、血红蛋白电泳、变性珠蛋白小体（Heinz 小体）实验。
结果 先证者（新生儿）的血红蛋白电泳发现在 S 区含有 19.2%的区带,Hb Barts：0.5%，Hb A：21.0%，Hb F：59.3%。其父为异常 Hb Q 含量：29.0%，Hb A：68.6%,Hb A2：2.4%（偏低）。

其母 Hb A：97.1%,Hb A2：2.9%，未发现异常血红蛋白区带。其父 RBC:5.31*1012/L,Hb:136g/L,MCV:76.1fl,MCH:25.6pg，RDW-CV:0.14。其母血液学参数均正常。一家三口变性珠蛋白小体均阴性。

结论 根据家系遗传分析，推断先证者及其父的异常血红蛋白均为 α 链变异的 Hb Q。此异常血红蛋白是我国少见的一种异常血红蛋白变异体，且与 aa / -a4.2 缺失型的 α 地中海贫血连锁携带 。此家系的报道丰富了医务工作者对异常血红蛋白复合 α 地中海贫血的认知，对于优生优育、指导遗传咨询具有重要的意义。

PO-1262

侵袭性 NK 细胞白血病的实验室和临床特点分析

廖红艳[1]、金咏梅[2]、蒋能刚[2]
1. 四川大学华西医院
2. 四川大学华西医院实验医学科

目的 探讨侵袭性 NK 细胞白血病（Aggressive NK Cell Leukemia, ANKL）患者的临床病理特点。

方法 回顾性分析 2016 年 1 月-2016 年 12 月在我院确诊的 12 例 ANKL 患者的临床病理资料，包括骨髓细胞形态学、免疫表型及病理结果。

结果 12 例骨髓涂片中可见大颗粒淋巴细胞。流式细胞学示 ANKL 的免疫表型均为 CD2(+)sCD3(-)CD5(-)CD56(+)，6 例 CD7(+)，3 例 CDl6(+)。6 例行免疫组化检测，结果均为：EBER1/2 (+)、粒酶 B（+）。

结论 骨髓细胞形态学、免疫表型和免疫组化对于 ANKL 的及时诊断和鉴别诊断具有重要意义。

PO-1263

毛细管电泳技术在非缺失 α-地中海贫血中的筛查价值

葛艳芬
广东省人民医院（广东省医学科学院）

目的 分析毛细管电泳技术的电泳结果,评价其在非缺失 α-地中海贫血中的应用价值并对非缺失型 α-地中海贫血的基因型和表型进行分析。

方法 收集标本检测血常规，Hb 电泳以及地贫基因结果。设为 A 组非缺失 α-地贫杂合子（包括 HbCS、HbQS、HbWS），B 组 α-地贫 2（-α3.7/αα 或-α4.2/αα），C 组 α-地贫 1（--αSEA /αα），D 组为非缺失型复合 α-地贫 2，E 组为非缺失型复合 β-地贫，F 组为非缺失型复合 α-地贫 1。进行统计学分析。

结果 381 个病例：A 组 22 例，临床表现为静止型一轻型;B 组 116 例，临床表现为静止型;C 组 239 例，临床表现为轻型；D 组：2 例（-αWS/-α3.7），临床表现为轻型；E 组 2 例（ ααCS/αα 合并 β-28 杂合子），临床表现为轻型；F 组 1 例（ααWS/--SEA），临床表现为轻型一中间型。

结论 初步阐明非缺失 α-地贫杂合子表型比缺失型的 α-地贫 2 明显，毛细管电泳技术对筛查非缺失 α-地中海贫血具有较大的应用价值，提高了 α-地贫的检出率。

PO-1264

Optimization of pretreatment methods for cerebrospinal fluid metabolomics based on Ultrahigh Performance Liquid Chromatography/Mass Spectrometry

Zhiqiang Song[1,2]、Mian Wang[1]、Zhenyu Zhu[2]、Gusheng Tang[1]、Yue Liu[2]、Yifeng Chai[2]
1. Changhai Hospital
2. 第二军医大学药学系

Sample pretreatment of cerebrospinal fluid (CSF) in metabolomics plays an important role in metabolic profiling study, especially for samples related to central nervous system diseases. However, there is few study about optimization of CSF metabolomics pretreatment. Therefore, it is an urgent need to optimize CSF pretreatment in order to promote the extraction efficiency of metabolites. In this study, CSF samples were separately subjected to nine different protein precipitation solvents and five different reconstitution solvents to establish the most effective pretreatment method before hydrophilic interaction (HILIC) and reverse-phase (RP) ultrahigh performance liquid chromatography mass spectrometry (UPLC/MS) analysis. The optimal conditions for different sample pretreatment methods were analyzed based on coverage (number of detected potential metabolites), stability (the relative standard deviation (RSD) distribution of metabolites) and the reproducibility of the data. Our results suggested that using EtOH or MeOH-EtOH-ACN (1:1:1, v/v/v) as the protein precipitation solvents and H2O-MeOH-ACN (2:1:1, v/v/v) as the reconstitution solvent were optimal methods for T3 column analysis. For HILIC column analysis, using EtOH to precipitate protein and H2O-MeOH-ACN (2:1:1, v/v/v) to reconstitute or MeOH to precipitate and 5%ACN to reconstitute performed best. This developed UPLC/MS pretreatment method could provide better protein precipitation solvents and reconstitution solvents for global CSF metabolic analysis, potentially facilitating the comprehensive understanding of many central nervous system diseases.

PO-1265

Significance of plasma fibrinogen assay in risk assessment of retinopathy in patients with type 2 diabetes

Qinghua Huang[1,2]、Mingyi Wo[1,2]、Fan Han[1,2]、Yiran Wang[1,2]、Chaonan Li[1,2]、Xianming Fei[1,2]
1. Zhejiang Provincial People's Hospital
2. 杭州医学院附属人民医院

Objective To explore the clinical significance of plasma fibrinogen (Fbg) measurement in risk assessment of diabetic retinopathy (DR).
Methods The coagulation parameters of 307 patients with type 2 diabetes (T2D) was measured, the association of Fbg and DR was assessed, the risk factors of DR was analyzed by Logistic regression, and the ROC curve was used to evaluate the predicting power of risk factor for DR.
Results The level of Fbg in DR group was significantly higher than that in T2D group (P<0.001), and patients in DR with proliferative stage had a significantly higher Fbg level than that in non-proliferative stage (P<0.01). The area under ROC curve of Fbg predicting DR risk was 0.835 (95% CI:0.775-0.896, P <0.001)， and the sensitivity and specificity were 86% and 83%, respectively according to cutoff value of 2.95g/L. Moreover, the area under ROC curve for discriminating between was 0.778 (95% CI: 0.729-0.828, P <0.001), and the sensitivity and specificity were 82% and 75%, respectively, when the cutoff value was 3.23 g/L. Multivariate regression analysis revealed that Fbg was an independent risk factor for occurrence and progression of DR with OR values of (4.121, 95% CI: 2.332–8.430) and (8.516, 95% CI: 4.886–16.655) (P <0.01).

Conclusion Plasma fibrinogen can be used as an independent predictor of retinopathy and its progression in type 2 diabetes.

PO-1266

mir-155 与冠心病患者阿司匹林抵抗的相关性研究

徐成伟
山东大学第二医院

目的 研究 mir-155 与冠心病患者阿司匹林抵抗的相关性，统计分析 AR 的其他危险因素。
方法 入选 2016 年 3 月至 2017 年 1 月因冠心病入住山东大学第二医院心内科和干部保健科的患者 58 例，采用血栓弹力图的方法检测静脉血花生四烯酸(amchidonic acid，AA)诱导的血小板抑制率，将 AA 诱导的血小板抑制率≤50%，定义为阿司匹林抵抗（AR），血小板抑制率＞50%，定义为阿司匹林敏感（AS），收集临床资料分析。根据 TEG 结果分为 AR 组和 AS 组，利用患者血样提取 RNA，通过实时荧光定量 PCR（QRT-PCR）检测两组患者中 mir-155 的表达水平,利用多因素 logistic 回归分析 mir-155 与 AR 的相关性。
结果 所有患者中，20 例（34.5%）存在阿司匹林低反应，两组间性别、吸烟、高血压、糖尿病史、血清总胆固醇、甘油三脂、糖化血红蛋白、外周血小板计数差异无统计学意义，AR 组低密度脂蛋白水平均高于 AS 组，差异具有统计学意义。AR 组 mir-155 表达明显低于 AS 组，通过 logistic 回归分析得出 mir-155 表达水平下调可能是 AR 的危险因素。
结论 mir-155 在冠心病血小板低反应患者中的表达下调，是 AR 的危险因素。Mir-155 可能成为抗血小板药物个体反应的差异性新标志物，为临床医师治疗血小板低反应提供新的导向。

PO-1267

血清轻链和游离轻链在多发性骨髓瘤和淋巴瘤患者中的差异性表达研究

张娟、王加强、王智斌、蒋黎
电子科技大学附属医院·四川省人民医院

目的 探讨多发性骨髓瘤 MM 和淋巴瘤 LYM 患者血清单克隆免疫球蛋白轻链、游离轻链 FLC 与免疫球蛋白 IgG 及其亚类的表达水平差异，为辅助诊断及探讨疾病机理提供可靠依据。
方法 收集 2019 年 1 月-12 月在四川省人民院确诊的 MM 患者 229 例，LYM 患者 231 例，分别进行轻链、游离轻链和总 IgG 及其亚类的回顾性分析。各变量的组间比较采用非参数 Mann-Whitney U 检验。IgG 亚类与轻链的相关性采用 Spearman 相关分析。轻链在不同年龄段的分布采用独立样本克鲁斯卡尔-沃利斯检验。
结果 MM 患者轻链 κ 显著低于 LYM 患者(P=0.000)，而 FLCκ、FLCλ 显著高于 LYM 患者(P 分别等于 0.001，0.000)。血清轻链及亚型定性结果显示，MM 患者 κ、λ、IgGκ、IgGλ、IgAκ、IgAλ 阳性率显著高于 LYM 患者，而 IgMκ、IgMλ 显著低于 LYM 患者(P 分别为 0.001，0.000)。IgG 亚类分析显示，MM 患者 IgG3 显著低于 LYM 患者(P=0.024)，而 IgG1、IgG2、IgG4 差异没有显著性。不同性别、不同年龄组轻链、游离轻链的分布显示，男性 LYM 患者 FLCλ 含量明显高于女性患者，差异有统计学意义(P=0.045)，MM 患者的年龄显著高于 LYM 患者(P=0.000)，IgG 亚类含量与血清轻链、游离轻链的相关分析显示，随着 MM 总 IgG、IgG1 含量的增高，患者 λ 有增高的趋势，随着 IgG2、IgG3、IgG4 的升高，患者 κ 有增高的趋势。LYM 患者中，随着 IgG、IgG1、IgG2、IgG4 含量的增高，患者 λ 有增高的趋势，随着 IgG、IgG1 升高，患者 κ 有增高的趋势。
结论 血清轻链、游离轻链与 IgG 亚类结果在 MM 患者和淋巴瘤患者中存在差异，Ig 亚类与轻链的表达具有一定相关性，需要进一步的研究明确其在辅助诊断及发病机理的价值。

PO-1268

三种血凝分析仪检测 D-二聚体结果的比对分析

亓春玲
泰安市中心医院

目的 比较 3 种全自动血凝分析仪检测 D-二聚体结果的一致性。
方法 随机选取本院患者 219 例，其中包括门诊体检者 45 例和住院患者 174 例，分别用 Sysmex CS-5100 全自动血凝分析仪(CS5100), 日本积水 SEKISUI CP2000 全自动血凝分析仪(CP2000)、)、Biomerieux VIDAS 酶联免疫荧光分析仪及其配套试剂，检测患者血浆 D-二聚体水平并进行统计学分析。
结果 CS5100，CP2000、VIDAS 3 种仪器检测 D-二聚体的阳性率分别为 94.1%、91.3%、92.5%, 差异无统计学意义(P＞0.05)。3 种仪器检测 D-二聚体结果比较差异有统计学意义(P＜0.05)，CP2000 与 CS5100 检测 D-二聚体结果比较差异有统计学意义(χ2=8.89,P<0.05)；CP2000 与 VIDAS 检测 D-二聚体结果差异有统计学意义(χ2=9.3,P<0.05)；CS5100 与 VIDAS 检测 D-二聚体结果差异有统计学意义(χ2= 4 .33,P<0.05)，CS5100 与 VIDAS 检测 D-二聚体结果相关性比 CP2000 与 VIDAS 检测 D-二聚体结果相关性较好些。
结论 不同仪器检测 D-二聚体结果阳性率基本相同,但由于检测原理和检测试剂等的不同导致同一患者检验结果的可比性较差,难以进行方法间的比对。因此,在同一实验室内,建议连续对患者 D-二聚体水平进行检测时,尽可能使用同一机型及配套试剂进行检测，以便更好地动态观察病人病情变化。

PO-1269

Plasma miR-1273g-3p acts as a potential biomarker for early Breast Ductal Cancer diagnosis

苏海翔
甘肃省医学科学研究院，甘肃省肿瘤医院

Circulating miRNAs presenting in plasma in a stable manner have been demonstrated their potential role as a promising biomarkers in many human diseases, such as Alzheimer's disease, melanoma and ovarian carcinoma. However, few circulating miRNAs could be used for breast ductal cancer diagnosis. Here, we identified miR-1273g-3p as a biomarker for detecting breast ductal cancer. We detected miR-1273g-3p levels in the plasma. The results showed the plasma miR-1273g-3p level were significantly up-regulated in breast ductal cancer patients compared with healthy donors (p=0.0139). Taken together, miR-1273g-3p could represent as a potential biomarker for early breast ductal cancer diagnosis

PO-1270

极易误诊为母细胞性浆细胞样树突细胞肿瘤的以皮肤为首发表现的急性髓系白血病一例

杨利群[1]、唐梅[1]、潘建华[2]
1. 四川金域医学检验中心有限公司
2. 广州金域医学检验中心有限公司

目的 探讨极易误诊为母细胞性浆细胞样树突细胞肿瘤以皮肤为首发表现的急性髓系白血病一例。
方法 对 1 例急性髓系白血病的临床资料分析、皮肤活检组织形态学、免疫组化及骨髓流式细胞免疫表型特点进行分析。

结果 患者，女，25 岁，全身皮疹 8 月余，最大者直径 3CM，左后腰皮疹活检示：真皮内见原始/幼稚细胞呈弥漫性分布，易见嗜表皮性；免疫组化(IHC)示：原始/幼稚细胞 CD4（+）、CD56（+）、CD123（+）、TdT（+）、Ki-67（+、约 80%）、CD3（-）、CD5（-）、CD15（-）、CD30（-）、ALK（-）、CD20（-）、CD10（-）、CD117（-）、GrB（-）、MPO（-） 。骨髓流式细胞免疫表型（FCM)示：检测到异常细胞占有核细胞总数约 13.5%，表达 CD4，CD56，CD123，cMPO，CD13+33，HLA-DR，不表达 BDCA-2/CD303，BDCA-4/CD304，CD14，CD64，CD36，CD19，CD20，CD10，cCD79a，cCD3，CD61，CD38，CD138，CD200，CD117，CD34，CD2，CD3，CD5，CD7，CD8，综合骨髓 FCM、皮肤组织活检形态学及 IHC 综合诊断为急性髓系白血病（AML），倾向单核细胞来源。

结论 AML 累及皮肤与母细胞性浆细胞样树突细胞肿瘤（BPDCN） 具有相同的形态学和免疫表型特征（尤其是单核细胞分化的 AML，可共表达 CD4、CD56 和 CD123），鉴别诊断具有挑战性，因此在诊断 BPDCN 之前需要进行广泛的 IHC，并且一定要注意年龄及病史，CD303、CD304 为 BPDCN 的特异性标记，成为鉴别诊断要点之一，因 FCM 检测的是活体细胞，部分抗体表达保存更加完好，此例流式表达 cMPO，而免疫组化 MPO 阴性，FCM 在两者的鉴别诊断中发挥了关键作用。

PO-1271

细胞外囊泡与肿瘤发生发展的关系及其检测方法进展

黄蓉蓉
南京鼓楼医院

目的 了解细胞外囊泡在肿瘤发生发展中的作用及其检测方法

方法 在 web of science、springer、ACS 等数据库及杂志社检索相关文章并综述

结果 大量研究证实，肿瘤细胞分泌的细胞外囊泡数量相较正常细胞更多，这些细胞外囊泡是将肿瘤细胞产生的核酸、蛋白质等多种重要的生物活性分子运输到靶细胞的载体，是连接肿瘤原发部位和转移部位的桥梁，细胞外囊泡作为细胞间的通讯载体，能将来源于肿瘤细胞或肿瘤相关细胞和病毒的重要生物分子如蛋白质（包括酶类、粘附分子、转录因子、受体和膜转运蛋白等）、DNA、miRNA 以及长非编码 RNA 等进行细胞间转移，细胞外囊泡既能调控靶细胞的增殖、分化和凋亡，也能调节肿瘤细胞微环境，与肿瘤的获得性耐药、肿瘤细胞上皮-间质转化、肿瘤细胞侵袭力上升、血管渗漏性提高、肿瘤细胞免疫逃逸等息息相关。研究人员逐年开发出了越来越多的细胞外囊泡定量方法。基于细胞外囊泡物理性质进行定量的方法有动态光散射（Dynamic light scattering，DLS）、可调电阻脉冲传感（Tunable Resistive Pulse Sensing，TRPS）以及 Nanoparticle tracking analysis（NTA）。除去这些传统的方法，还有各种基于电化学、荧光、SPR 等检测原理的新型检测方法。

结论 细胞外囊泡是连接肿瘤原发部位和转移部位的桥梁，在作为肿瘤诊断和预后指标方面有着巨大的潜力，以细胞外囊泡作为肿瘤生物标志物有利于提高癌症诊断的精确性和便利性。深入探索与癌症发生和发展的过程密切相关的细胞外囊泡所特异性表达的蛋白和核酸等标志物，并将该类标志物作为检测靶标，有助于实现特定细胞来源细胞外囊泡的特异性分离和检测，为临床应用带来便利。

PO-1272

qSOFA 评分联合中性粒细胞 CD64 指数对恶性血液病患者血流感染早期诊断价值分析

武坤、祝艳翠、李艳红、聂波
昆明医科大学第一附属医院

目的 探讨 qSOFA 评分联合中性粒细胞 CD64 指数在恶性血液病患者血流感染的早期诊断价值。
方法 选择我院 2019 年 6 月-2020 年 6 月收治的 45 例恶性血液病血流感染患者为研究对象（血流感染组），另选择同期恶性血液病住院无感染患者 45 例（非感染组）作为对照。流式细胞仪测定中性粒细胞 CD64 指数及 TNF-α 水平，对患者进行 qSOFA 评分，并进行统计学分析。
结果 血流感染组患者 qSOFA 评分、中性粒细胞 CD64 指数明显高于非感染组（P＜0.05），血流感染组中死亡患者 qSOFA 评分、中性粒细胞 CD64 指数明显高于非死亡患者（P＜0.05）；血流感染患者 qSOFA 评分（r=0.410，P=0.005）、中性粒细胞 CD64 指数（r=0.380，P=0.010）与 TNF-α 呈显著正相关；qSOFA 评分诊断血流感染曲线下面积为：0.706（95%CI：0.682-0.755），P=0.037，中性粒细胞 CD64 指数诊断血流感染曲线下面积为：0.749（95%CI：0.695-0.813），P=0.028；qSOFA 评分联合 CD64 细胞指数诊断恶性血液病患者血流感染的曲线下面积为 0.874（95%CI：0.831-0.926），P=0.015。
结论 qSOFA 评分、中性粒细胞 CD64 指数联合应用对恶性血液病血流感染的早期诊断具有一定价值。

PO-1273

粪便钙卫蛋白在炎症性肠病诊断中的价值

熊志刚
四川省医学科学院·四川省人民医院

目的 探讨定性与定量粪钙卫蛋白检测在炎症性肠病诊断中的价值。
方法 选取 43 例正常体检患者作为对照组，114 例经临床检查诊断的消化内科及儿科的肠病患者作为炎症性肠病组。检查内容包括隐血，轮状病毒，血常规，CRP 检测等。本实验采用 SPSS 23.0 分析两组患者粪钙卫蛋白水平，因数据不满足正态分布，采用百分位数表示。
结果 炎症性肠病患者组与对照组的粪钙卫蛋白检测值【中位值（四分位数间距）】分别为 65.64（49.33-159.73）ug/g、56.27（43.83-102.04）ug/g，炎症性肠病组患者的粪钙卫蛋白水平明显高于对照组（P＜0.05）。根据 Kappa 一致性检验结果，可以认为定性与定量两种试验结果一致。
结论 定性与定量粪钙卫蛋白检测在炎症性肠病的诊断中具有重要意义。

PO-1274

SysmexXN-10 与迈瑞 BC-6900 全自动血细胞分析仪在有核红细胞干扰下相关研究

熊志刚
四川省医学科学院·四川省人民医院

目的 探讨外周血出现有核红细胞时,Sysmex XN-10 全自动血细胞分析仪与迈瑞 BC-6900 全自动血细胞分析仪的白细胞数是否存在相关关联.

方法 应用 Sysmex XN-10 全自动血细胞分析仪筛查有核红细胞阳性的 104 例标本,分别用迈瑞 BC-6900 和人工显微镜计数,分析显微镜检与两台仪器计数之间有无统计学差异,以及当出现 NRBC 情况下,两台仪器之间计数白细胞存在的关联.
结果 分别校正前后,显微镜检与迈瑞 BC-6900 计数外周血白细胞数量均有极好的相关性 (r=0.990), 2 种方法计数结果的差异无统计学意义 (P> 0.05).显微镜检与 XN-10 计数有极好的相关性(r= 0.988), 显微镜检（校正前）与 XN-10 计数差异有统计学差异（P＜0.05），而校正后与 XN-10 计数差异无统计学意义（P>0.05 ）.XN-10 与 BC-6900(校正前)白细胞计数差异有统计学差异（P＜0.05）, 两者存在线性关系（Peason 相关系数 r=0.992）,建立线性回归模型有极显著的统计学意义，线性回归方程:Y=1.044X-0.092，r^2=0.984，P＜0.05.
结论 当外周血出现 NRBC 时,根据一元线性回归方程,可由迈瑞 BC-6900 全自动血细胞分析仪 WBC 计数预测 Sysmex XN-10 全自动血细胞分析仪的 WBC 数值，有一定的实际实用价值.

PO-1275

PDCA 信息化闭环管理对血常规部分质量指标的影响

陈光意
河南省肿瘤医院检验科

目的 分析 PDCA 信息化闭环管理模式后对血常规部分质量指标的影响。
方法 选取我院 2020 年 10-12 月血常规非急诊门诊和住院患者标本检验前及实验室内 TAT 的中位数与实行 PDCA 信息化闭环管理模式后 2021 年 1-3 月份的数据作比较。
结果 前者非急诊血常规门诊标本检验前及实验室内 TAT 中位数分别为 25min 和 23min，住院患者非急诊标本检验前及实验室内 TAT 中位分别为 83min 和 75min，；后者血常规门诊非急诊标本检验前及实验室内 TAT 中位分别为 13min 和 14min，效率分别提高 48%和 39.2%,住院患者非急诊标本检验前及实验室内 TAT 中位分别为 60min 和 57min，效率分别提高了 27.8%和 24%。
结论 从 2021 年年初开始科室配合医院对血常规标本采用 PDCA 信息化闭环管理模式，严格标本每个环节的 TAT 时间，制定详细的实施计划，检查计划，及时反馈到院周会，按完成情况进行奖惩处罚，根据 2021 年第一季度与 2020 年最后一季度统计结果来看，非急诊的门诊和住院患者血常规标本检查时间 TAT 均有明显缩减，达到预期的目标，显著提高了检验工作效率。

PO-1276

低血红蛋白密度在缺铁性贫血疗效观察中的应用

师传帅
吉林大学第一医院

目的 通过观察口服铁剂后低血红蛋白密度（low haemoglobin density, LHD）的变化情况，动态监测缺铁性贫血患者对铁剂治疗后的疗效反应，为临床缺铁性贫血的诊治提供新的参考依据。
方法 动态观察 28 例缺铁性贫血患者口服铁剂治疗后 1 周、4 周、8 周、12 周的 LHD、RBC、HGB、血清铁、铁蛋白的变化情况。
结果 28 例缺铁性贫血患者口服铁剂治疗前 LHD 为 87.8%±12.8%，口服铁剂 4 周后降低至 67.1%±20.4%，差异有统计学意义。12 周基本降至正常水平 14.2%±7.2%。同时，血清铁水平升高、铁蛋白升高、RBC 和 HGB 亦恢复正常。
结论 缺铁性贫血患者口服铁剂后 LHD 恢复时间较晚，连续动态监测 LHD 可有效评估病情变化和铁剂治疗效果。

PO-1277

免疫细胞、细胞因子、凝血指标及血脂水平在肺癌分期中的应用价值

李丹、赵辰昊、何春燕
苏州大学附属第二医院

目的 探讨外周血免疫细胞、细胞因子、凝血指标及血脂水平与肺癌肿瘤分期的相关性，为临床诊断和治疗提供依据。
方法 选择 2020 年 6 月至 2021 年 5 月在苏州大学附属第二医院就诊的肺癌患者共 96 例。根据患者的临床表征，依据传统肿瘤分期方法（I/II/III/IV 期）进行分组。采用流式细胞术检测处于不同病程阶段的肺癌患者免疫细胞（CD4、CD8、NK、B 细胞，CD4/CD8 比值）及细胞因子（IL-2、IL-4、IL-6、IL-10、IL-17A、TNF-α、IFN-γ、IL-12）水平，同时对患者凝血指标（凝血酶原时间、活化部分凝血活酶时间、纤维蛋白原、抗凝血酶 III、D-二聚体）和血脂水平（总胆固醇、甘油三酯、总胆汁酸）的结果进行回顾性分析。
结果 随着病情的进展，肺癌患者血清中的细胞因子 IL-6、IL-17A 和 IFN-γ 水平明显上升（P<0.05）；晚期肺癌患者血清中抗凝血酶 III 和纤维蛋白原水平显著增加（P<0.01）；免疫细胞和血脂相关指标则与肺癌病程无关（P>0.05）。
结论 在肺癌诊断和治疗过程中，细胞因子 IL-6、IL-17A、IFN-γ 和凝血指标 ATIII、FIB 可以辅助临床对肺癌进行分期，有助于后续治疗。

PO-1278

中医气血虚证与丙种球蛋白及血红蛋白的相关性

唐芸
昆明市中医医院

目的 探讨 中医气虚、血虚患者的丙种球蛋白，血红蛋白值之间的相关性。
方法 选择 203 例中医辨证为气虚，血虚，气血双虚症患者为研究对象，采用证素辨证方法以其检查的丙种球蛋白及血红蛋白指标进行研究。
结果 气虚、血虚，气血双虚与丙种球蛋白、血红蛋白值之间均存在着相关性 (P <0.05)；而虚症病理改变程度之间无显著性差异(P >0.05)。
结论 不能单纯依靠丙种球蛋白及血红蛋白值来诊断气虚、血虚证的病理改变。

PO-1279

探讨ＥＤＴＡ依赖性血小板减少的最佳处理方法

张明珍
山东第一医科大学第一附属医院

目的 探讨ＥＤＴＡ依赖性血小板减少的处理方法，纠正血小板计数。
方法 用Ｓｙｓｍｅｘ XN-10 血液分析仪对标本进行检测、使用配套试剂及质控品仪器状态良好，每天均检测质控，且均在控。收集本院门诊就诊及住院的患者 20 例，仪器结果均显示血小板减少，同时报警提示血小板聚集，血小板直方图曲折不平滑，有翘尾现象；血涂片染色镜下见有大量血小板紧密聚集，一般为 10 个左右血小板聚集成堆，甚至出现大片聚集现象，散在的血小板少见。对这种血小板凝集的标本，采取两种方法进行复检：方法 1、用不加抗凝剂的采血管抽血后立即上机

检测。方法 2、使用含有枸橼酸钠抗凝剂蓝帽采血管抽血后上机检测，以人工显微镜检计数血小板为参考，寻找的最佳处理方法

结果 对于 EDTA 依赖性血小板减少的标本，采取方法 1 在仪器准备妥当的情况下，通知患者来门急诊化验室重新采血立即上机检测，结果是可靠的。采取方法 2 使用含有枸橼酸钠抗凝剂蓝帽采血管进行重新抽血上机检测，并记录 1 小时内不同时间段的检测结果，其结果可靠。

结论 使用含有枸橼酸钠抗凝剂蓝帽采血管的方法对于解决 EDTA 依赖性血小板减少的现象是非常有效可靠的，方便患者，防止因走动影响到患者的病情，也为临床诊治患者节约时间，是最佳处理方法。

PO-1280

一例伴免疫组化 BCL2 阴性的滤泡性淋巴瘤的诊断及鉴别诊断分析

姜山、杨利群、唐梅
四川金域医学检验中心有限公司

目的 探讨一例免疫组化 BCL2 阴性的滤泡性淋巴瘤的实验室检查结果分析并文献复习

方法 对一例免疫组化 BCL2 阴性的滤泡性淋巴瘤的临床资料、淋巴结活检、免疫组化、分子生物学检查的结果分析并鉴别诊断。

结果 患者，68 岁，女性，全身淋巴结肿大 2 年余，双侧颈部、腋窝、腹股沟区均可触及数个肿大淋巴结，最大者位于腹股沟，约 3*2cm，左腋窝淋巴结切除活检示淋巴结结构破坏，滤泡明显增生，套区变薄，呈现“背靠背”现象，符合滤泡性淋巴瘤病理形态特征；免疫组化结果提示：肿瘤性滤泡 CD20（+），CD79α（+），CD10（+），BCL2（-），Ki67（+，30%），MUM-1（-），IgD（+），Lambda（+），Kappa（-）；滤泡间区 CD3（+），CD5（+）；C-MYC（-），CyclinD1（-），CD30（-）；CD23 FDC 网（+）。B 细胞克隆性分析提示 IGK 的 Vk-Kde+intron-Kde 区间 267.76/280.60bp 处检测到单克隆重排；二代测序淋巴造血相关 175 基因中检测到 NOTCH2、BCL6、KMT2C、KMT2D、BTG1、CREBBP、BCL2、PHF6 基因突变；荧光原位杂交 IGH/BCL2 重排探针阳性，信号模式为 1G1R1F 21%,2G1F 8%,1G1F 15%,1R1F 6%,1G1R2F 3%,2G1R 10%,1G2R 2%,2G2R 35%；结合临床表现及病理诊断、免疫组化、分子生物学检测，综合诊断为滤泡性淋巴瘤(FL)，2 级。

结论 BCL2 蛋白阴性 FL 与反应性淋巴滤泡性增生鉴别诊断困难，BCL2 阴性仍不能除外滤泡性淋巴瘤，BCL2 蛋白在 1 级和 2 级 FL 约 85%-90%病例中表达，FL 缺乏 BCL2 表达可能是由 BCL2 基因突变引起的，应及时行荧光原位杂交、基因重排及相关基因突变检测，因为荧光原位杂交及分子生物学的检测可以极大地辅助诊断。

PO-1281

瑞氏染色检测结膜阿米巴包囊

黄小天
电子科技大学附属医院·四川省人民医院医学检验中心

目的 阿米巴角膜炎（Acanthamoeba keratitis， AK）是一种以阿米巴原虫感染导致的感染性角膜炎。阿米巴原虫为单细胞结构的生物，其生活于淡水、咸水、灰尘、泥土、污物、腐败植物及人畜粪便中。另外，又文献报道，再浴盆、空气过滤器、水冷却塔角膜接触镜、镜盒护理液中也分离出阿米巴原虫。致病性自生生活阿米巴不仅可以在自然界自生生活，而且可在温血宿主体内发育增殖，故又称为两栖型生物，属兼性寄生虫。本文收集到 1 例阿米巴角膜炎病例

方法 眼科检查，使用荧光素钠染色后，对患者的眼睑、角膜及晶状体进行观察；使用激光共聚焦显微镜观察患者角膜病变情况。
显微镜检查：刮取患者眼部分泌液，在载玻片上进行涂片，立即使用。
结果 VOD:CF/50cm，VOS:0.8。右眼眼睑无水肿，结膜混合充血，角膜中央区可见直径约 6mm 圆环状全层雾状水肿，上皮褶皱，周边角膜透明，角膜缘 3 点钟位可见一直径约 1mm，深度约 0.7mm 角膜溃疡，前房透明，KP(-)，Tvn(-)，周边虹膜纹理可见，中央区欠清，瞳孔圆，直径约 2mm，对光反射灵敏，晶状体及其后结构欠清。左眼眼睑无水肿，结膜无充血，角膜透明，前房清，虹膜纹理清，瞳孔圆，直径约 2mm，对光反射灵敏，晶状体透明，玻璃体轻混，眼底小瞳下未见明显异常
结论 瑞氏染色检测结膜病灶刮片，查见非常典型的车轮状外壁的阿米巴包囊。

PO-1282

红细胞分布宽度和红细胞分布宽度与血清钙比值是急性胰腺炎严重程度和死亡率的主要预测因子

黎青、陈颖
江苏省人民医院（南京医科大学第一附属医院）

目的 本研究的目的是评估 RDW 与其它预后评分系统相比在 AP 严重程度和死亡率方面的诊断价值。
方法 回顾性病例对照研究 2018-2020 年住院的 160 例 AP 患者。其中重度 AP 患者 80 例，轻度 AP 患者 80 例。
结果 与轻度 AP 患者相比，重度 AP 患者的 RDW 0h 较高（p<0.001），RDW 与血清钙的比值较高（p<0.001）。经过多变量和 ROC 曲线分析后，RDW 0h（AUROC：0.945；p<0.001）和 RDW 与血清钙比值（AUROC：0.969；p <0.001）是 AP 严重程度的主要预测指标，其临界值为 12.9 和 1.39。这些因素优于预后评分，例如 Ranson（AUROC：0.787； p<0.001；临界值：3.0），BISAP（AUROC：0.743；p<0.001；临界值：2.0）和改良 Marshall（AUROC：0.765；p<0.001；临界值：1.0）。死亡率为 9.4％（15/160），所有病例均与重度 AP 相关（18.8％；15/80）。非存活 AP 患者的 RDW 0h 和 RDW 0h 与血清钙比值较高（分别为 15.5±1.5；13.7±1.4；p<0.001 和 2.1±0.4，1.7±0.4；p<0.001）。
结论 RDW 是一个简单的常规参数，可在入院时检测。本 AP 队列显示，RDW 0h>12.9 和 RDW 0h 与血清钙比值>1.39 是较好的 AP 严重程度预测因子，RDW 0h>14.2 和 RDW 0h 与血清钙比值>1.72 是非常好的 AP 死亡率预测因子，优于传统的预后评分系统。

PO-1283

肺泡灌洗液检查对结缔组织病相关间质性肺疾病和特发性间质性肺病的诊断价值

周茂华、李文敏、冼璐桦、蓝名伟
广东省人民医院

目的 探讨支气管肺泡灌洗液(BALF) 细胞分类计数及 T 淋巴细胞亚群检测对结缔组织病相关间质性肺疾病(CTD-ILD)与特发性间质性肺病（IIP)的鉴别诊断价值。
方法 收集 2018 年 6 月～2019 年 12 月来我院行支气管肺泡灌洗液检查的 66 例间质性肺疾病患者的临床资料和实验室检查结果，包括 CTD-ILD 组 28 例和 IIP 组 38 例，比较两组患者 BALF 细胞分类计数和 T 淋巴细胞亚群的差异。

结果 CTD-ILD 组支气管肺泡灌洗液中中性粒细胞、淋巴细胞及嗜酸性粒细胞中位数分别为 31.98×104/ml、13.51×104/ml 及 4.32×104/ml，与 IIP 组相比无显著性差异 (P>0.05）；CTD-ILD 组巨噬细胞计数降低，差异有统计学意义(50.20×104/ml vs 14.04×104/ml，P<0.05）。两组患者 T 淋巴细胞亚群 CD3+、CD3+CD4+、CD3+CD8+和 CD4+/CD8+比值差异均无统计学意义 (P>0.05）。

结论 BALF 细胞分类计数对 CTD-ILD 与 IIP 的鉴别诊断具有一定的价值，巨噬细胞升高可能是 CTD-ILD 区别于 IIP 的特异性表现；BALF T 淋巴细胞亚群检测对 CTD-ILD 与 IIP 的鉴别诊断价值有限。

PO-1284

312 例儿童急性 B 淋巴细胞白血病免疫表型分析

周茂华、罗燕飞、林婷、周远
广东省人民医院

目的 研究儿童急性 B 淋巴细胞白血病(B-ALL)免疫表型特征，初步探讨髓系抗原 CD33、CD13 的表达在儿童 B-ALL 预后中的临床意义。

方法 回顾性分析广东省人民医院 2012 年 1 月至 2020 年 12 月收治的 312 例初治儿童 B-ALL 患者的临床资料，并分析其免疫表型特征。

结果 儿童 B-ALL 表达率最高的淋系抗原为 CD19（99.04%），其后依次为 CyCD79a、CD10、TDT、CD22、CD9、CD20 和 SIgM（分别为 98.08%、96.79%、96.15%、96.15%、92.63%、48.72%、14.74%），85.90%的病例表达 CD34，70.51%的病例表达 CD38。跨系抗原表达率最高的是髓系抗原 CD13 和 CD33，分别占 27.24%和 19.23%，其它抗原 CD15、CD71、CD11b、CD117、CD14 与 CD56 和 CD7 极少表达。临床特征上，CD33+ 儿童 B-ALL 组的临床危险度分级显著高于 CD33-组（P=0.031），但 CD33、CD13 的表达在泼尼松试验、第一阶段化疗后第 15 天和 33 天的完全缓解率（CR）上均无统计学差异。

结论 儿童 B-ALL 存在特征性的免疫表达谱，其临床危险度分级在 CD33+组中显著高于 CD33-组，提示 CD33 可能与长期预后不良有关，但 CD13、CD33 的表达与化疗第一阶段的临床特征及预后没有显著性关系。

PO-1285

Rinsing Sampling of Core Needle Biopsy for Flow Cytometric Analysis: a Favorable Method for Lymphoma Diagnosis

Peidong Chi、Yijun Liu、Yuhua Huang、Minjie Mao、Yu Wang、Zhiming Li、Jian Li
Sun Yat-Sen University Cancer Center, Guangzhou, Guangdong 510060, P.R.China

BACKGROUND Conventional protocols utilize core needle biopsy (CNB) or fine needle aspiration (FNA) to produce cell suspension for flow cytometry (FCM) is a diagnostic challenge for lymphoid malignancies. We aim to develop an alternative CNB rinsing technique (RT) to produce cell suspension for FCM during this mini-invasive procedure of CNB for lymphoma diagnosis.

METHODS FNA and CNB specimens from the same lesion of 93 patients with suspected lymphoma were collected under the guidance of B-ultrasound simultaneously. The fresh CNB samples were prepared to cell suspension by RT for FCM immunophenotyping analysis (Group CNB-RT). Then the CNB tissues after performing the RT process and the fresh FNA tissues were processed by conventional tissue cell suspension (TCS) technique to obtain the cell suspensions

(Groups of CNB-TCS & FNA-TCS) respectively as comparison. The diagnostic efficacies, as well as the concordances of the FCM results with reference to the morphologic diagnoses were compared in these three groups.
RESULTS RT could yield sufficient cells for FCM immunophenotyping analysis, though a lower cell numbers compared to TCS technique. The diagnostic concordance was comparable in group CNB-RT (91.1%) to the group CNB-TCS (88.9%) and group FNA-TCS (88.4%) (p=0.819). The diagnostic sensitivity and specificity of CNB-RT (91.1%; 100%) was not inferior to that of CNB-TCS (88.9%; 100%) and FNA-TCS (88.4%; 98.8%).
CONCLUSIONS This study shows the CNB-RT presented non-inferior diagnostic concordance and efficacy as compared to the TCS technique. CNB-RT has the potential to produce cell suspension for FCM immunophenotyping while preserving tissue for lymphoma diagnosis and research.

PO-1286

Potential diagnostic significance of Hsp90α and Neutrophil to Lymphocyte Ratio in Gestational Hypertension and Preeclampsia

Ning Wang[1]、Jun Zhang[2]、Ke Zhao[2]、Yaru Liu[2]、Hua Li[2]
1. 山东第一医科大学附属山东省肿瘤医院
2. 济南市妇幼保健院

Objective The objective of this study wasto evaluate the differences and the potential diagnosis significance of Hsp90α and Neutrophil to Lymphocyte Ratio（NLR）in normal pregnant women and patients with gestational hypertension (GH) or preeclampsia (PE).
Methods We recruited 131 normal pregnant women, 61 patients with GH and 97 patients with PE. The plasma concentration of Hsp90α was determined by enzyme-linked immunosorbent assay (ELISA)，and complete blood counts were measured by an automated hematology analyzer Sysmex XN-9000. The NLR was calculated as the absolute neutrophil count divided by the absolute lymphocyte count. A receiver operating characteristic (ROC) curve was employed to assess the diagnostic performance of Hsp90α and NLR.
Results Our study indicated that Hsp90α and NLR were increased in the middle and the third trimester of normal pregnancy than the first trimester of normal pregnancy; However, the level of Hsp90α but not NLR in the third trimester was significantly higher than the middle trimester of normal pregnancy. Hsp90α and NLR were increased in GH and PE compared to the normal pregnancy (NP). More importantly, Hsp90α and NLR served as the diagnostic biomarkers for GH and PE, the AUCs for GH were 0.749 and 0.658, for PE were 0.886 and 0.775, respectively. Moreover, their combination significantly elevated the diagnostic efficiency for GH and PE, possessing the AUC of 0.792 and 0.941, respectively.
Conclusions The new inflammatory marker Hsp90α and NLR might be the promising and effective markers for GH and PE. Hence, during prenatal follow-up, NLR and Hsp90α may be useful to predict GH and PE. However, these results must be supported by further prospective large scale.

PO-1287

一种导致复合杂合性遗传性凝血因子XI缺陷症的 F11 基因新突变

王欢欢、王明山、杨丽红、金艳慧
温州医科大学附属第一医院

目的 对一个复合杂合性遗传性凝血因子XI缺陷症家系进行基因突变分析，探讨其分子致病机制。
方法 用 STAGO-STA-R 自动血凝仪检测先证者及其家系成员的血浆凝血酶原时间（PT）、活化部分凝血活酶时间（APTT）、FXI活性（FXI:C）等指标；用 ELISA 法检测 FXI抗原（FXI:Ag）等指标，明确临床表型诊断。采用 DNA 直接测序法分析先证者 F11 基因，发现突变位点后用反向测序予以证实，并检测家系成员相应的突变位点区域。采用 ClustalX-2.1-win 软件分析氨基酸突变位点的保守性；用四个在线生物信息学软件分析突变对蛋白质功能的影响；用 Python-Pymol 软件对突变位点进行蛋白模型分析。
结果 先证者 APTT 为 89.2s，其 FXI:C 和 FXI:Ag 分别为 2%和 3.5%；其父亲、母亲和女儿 APTT 均稍延长，FXI:C 和 FXI:Ag 也均有不同程度下降；其姐姐 APTT 为 91.6s，FXI:C 和 FXI:Ag 分别为 2%和 3.1%。基因分析发现先证者 F11 基因第 7 号外显子存在 c.689G>T 杂合错义突变及第 13 号外显子存在 c.1556G>A 杂合无义突变。保守性分析结果表明，Cys230 在同源物种间高度保守。四个生物信息学软件对 p.Cys230Phe 突变的预测结果一致：均预示此突变很可能是有害突变。突变蛋白模型分析显示，在野生型 FXI蛋白质中，极性亲水性的 Cys230 与 Cys226、His233 和 Ser279 各形成一个氢键；当其突变为非极性疏水的 Phe230 后，原有的氢键没有改变，但增加了一个苯环，从而改变了蛋白质的结构。
结论 该先证者 F11 基因第 7 号外显子存在 p.Cys230Phe 杂合错义突变和第 13 号外显子存在 p.Trp519stop 杂合无义突变，其中 p.Cys230Phe 为一新发现的突变；p.Cys230Phe 遗传自父亲，p.Trp519stop 遗传自母亲，且与该家系 FXI水平减低有关。

PO-1288

Mis-judgement of a patient with Diffuse Large B-cell Lymphoma and the influence of uncapped-statue time on APTT mixing study

Hong Wang
Jiangsu Province Hospital

We reported a woman with the history of Diffuse Large B-cell Lymphoma. At first, she was misdiagnosed with multiple clotting factors deficiency of Factor VIII, Factor IX, Factor XI, and Factor XII. Through further examinations, such as APTT mixing study, diluted clotting factor activity assay, and antiphospholipid antibody test, the laboratory helped in making the correct diagnosis of antiphospholipid syndrome and Factor XII deficiency. New points of this case are: (1) Antiphospholipid antibodies can lead to false combined deficiency of Factor VIII, Factor IX, Factor XI and Factor XII, the true activity levels of which can be detected by dilution method. (2) APTT mixing study of this patient mistakenly indicated the presence of FVIII inhibitor. (3) Autoimmune disorders are frequently mentioned risk factors of APS. However, this patient was a case of APS secondary to hematological malignancy (especially lymphoid neoplasm) and there are less than 10 cases reported till now.

PO-1289

纤维蛋白丝对血细胞计数的影响及处理

赵媛、王妍、林婕、程翔、荆晶、贾晶缓、胡嗯亮
空军军医大学西京医院

目的 探讨外周血涂片中发现纤维蛋白丝对血细胞计数各个参数的影响，分析成因以妥善处理。
方法 1、收集外周血涂片发现纤维蛋白丝的标本 156 例，首先进行性状复检，剔除 9 例不合格标本（可见血凝块），统计剩余 147 例外周血涂片含有纤维蛋白丝的血细胞计数结果数据，简称数据组 1，同时将此 147 例标本当天重新抽血复测，统计复测推片后无纤维蛋白丝的结果数据，简称数据组 2；2、利用统计学软件 SPSS 26.O 对 2 组数据（组 1/组 2）进行配对样本 t 检验统计学分析，以 p〈0.005 为差异有统计学意义；3、调查 147 例患者采血情况，分析比较前后 2 次结果，寻找其他提示。
结果 1、本次试验数据显示纤维蛋白丝会引起 PLT 计数假性减低，RBC/HGB/HCT 计数假性增高，WBC 计数不同程度的变化；2、分析血细胞分析仪散点图直方图，147 例标本中 PLT-F 通道有 145 例散点图报警提示 PLT-Clumps，灵敏度为 98.6%。
结论 1、外周血涂片发现纤维蛋白丝可引起血细胞计数各参数发生变化，应重新采血进行检测；2、XN-9000 血细胞分析仪 PLT-F 通道散点图报警 PLT-Clumps 对于检出纤维蛋白丝有较高的灵敏度。

PO-1290

Clinical application of thrombelastography in patients with different types of coronary heart disease after percutaneous coronary intervention

Peng Zhang
Yijishan Hospital of Wannan Medical College

Objective To study the clinical application of Thrombelastography (TEG) in patients with different types of coronary heart disease after percutaneous coronary intervention (PCI).
Methods One hundred patients diagnosed as coronary heart disease and successfully treated with percutaneous coronary intervention in our hospital from June 2017 to January 2019 were included into the study. According to the type of coronary heart disease, patients were divided into three groups: acute myocardial infarction (AMI) group, unstable angina pectoris (UAP) group and stable angina pectoris (AP) group. We detected coagulation parameters, the degree of platelet inhibition and analyzed difference in the incidence of clopidogrel resistance in three types of coronary heart disease using TEG.
Results The proportion of men in the AMI group is more than in AP group and UAP group($p<0.01$). R and K indices were markedly reduced in the UAP and AMI groups, compared with the AP group, while MA,Angle and CI values significantly increased ($p<0.01$). Clopidogrel was more effective in the AMI group than in the AP group ($P<0.01$) , but the efficacy of clopidogrel in the UAP group was no different from that in the other two groups($p>0.05$).
Conclusions These results show that TEG has high clinical value in monitoring coagulation in patients with coronary heart disease. The coagulation parameters of TEG and clopidogrel effect were significantly different among the three groups at the same dosage of routine antiplatelet drugs, suggesting that clinicians should promote individual antiplatelet therapies based on the results of TEG.

PO-1291

流式荧光技术检测血清细胞因子常见问题与对策

张鹏、徐永新
郑州金域临床检验中心

目的 流式荧光技术检测细胞因子实验由于血清成份复杂，细胞因子含量差距大会对实验结果造成很大影响，且没有商业化质控品,室内质控难以建立。本研究分析流式荧光技术检测细胞因子的常见问题，探讨该项目的室内质控方法，提出处理对策供实验室同行参考。
方法 选取我中心 50 例病人（男 12 例，女 38 例）血清样本，其中高值标本 25 例，低值标本 25 例。每天用质控微球校正仪器，保证仪器光路运行良好。运用流式荧光技术法对血清中 Th1/Th2/Th17 相关十四项细胞因子进行检测，用 FCAP 软件对数据进行分析，发现并分析试验过程中的常见问题，探讨相关对策。
结果 根据不同标本的状态有选择的上调 FSC/SSC 的阈值，可以有效减少细胞碎片的干扰，降低背景噪音；在试验过程中加强对微球斡旋混匀可避免微球聚集现象，有利于微球和样本的结合，在上机前加强对细胞悬浮液的斡旋混匀可保证获取足够的可供分析的细胞数,提高数据有效性；建立标曲时通过增加标准品的稀释点数，扩大了检测范围，保证了对低浓度样本的检测，减少零值的结果；通过对空白微球的荧光强度动态监测，可实现对仪器电压的监测，有利于项目试验条件的标准化；通过用标准品自配高、低浓度的质控品，可实现项目的室内质量控制，保证实验的准确性和重复性。
结论 建立了流式荧光技术检测血清细胞因子常见问题的处理方法和对策,用自配两个浓度标准品的方法进行室内质控可帮助实验室及时发现问题，一定程度上保证实验结果的可靠。

PO-1292

慢加急性肝衰竭患者无临床症状消化道出血的凝血功能改变及预后分析

袁冲、刁艳君、刘家云、周磊、何娟、徐晓丽
空军军医大学西京医院

目的上消化道大出血是慢加急性肝衰的主要死亡原因，但无症状的消化道出血常常被大家忽略。本文探讨无临床症状的慢加急性肝功能衰竭出血患者的凝血功能改变和预后情况，方法收集 2015 年至 2020 年期间在西京消化病医院住院的 42 例慢加急性肝衰竭无出血症状，住院期间不少于 2 次大便潜血阳性病人作为观察组（排除其他原因的出血），另外，选取 42 例同时间段在我院住院的慢加急性肝衰竭大便潜血阴性病人作为阴性对照组。收集患者出凝血检测指标：凝血酶原时间（PT）、活化部分凝血活酶时间 (APTT)、纤维蛋白原（FIG）、凝血酶时间 (TT)、国际标准化比值（INR）、凝血酶原活动度（PT%）、D-二聚体、纤维蛋白/纤维蛋白原降解产物（FDP），并进行患者 4 周内生存时间分析。结果 PT、APTT、INR、D-二聚体、FDP 结果观察组与对照组差异无统计学意义（P>0.05）；PT%、FIG、TT 结果观察组与对照组差异有统计学意义（P<0.05），观察组 FIG 为 1.01±0.20、TT 为 21.84±2.62、PT%为 28.32±6.91;对照组 FIG 为 1.35±0.29、TT 为 19.28±1.74、PT%为 36.79±3.94。生存时间分析发现，观察组病人并发症多，生存时间短，两组差异有统计学意义（P<0.05）。

PO-1293

关于 D-二聚体假阴性与假阳性问题的探讨与分析

颜楠
空军军医大学西京医院

目的 探讨高浓度 D-二聚体（D-Dimer）在“抗原过量”情况下可出现假阴性结果，是否需要进行稀释处理与最适稀释倍数的选择；标本中由于出现异嗜性抗体（heterophilicantibody， HA）等因素干扰导致假阳性结果时，是否需要证明其为假阳性与干扰因素排除方法的选择。
方法 选取我院 2019 年 4 月～2020 年 10 月门诊与住院病例，分为 D-Dimer 假阴性组与 D-Dimer 假阳性组。其中假阴性组分别收集 D-Dimer〈5mg/L, 纤维蛋白/纤维蛋白原降解产物（FDP）<20ug/mL 范围内的结果 50 例，D-Dimer 为（5-10）mg/L, FDP>20ug/mL 范围内的结果 50 例，D-Dimer>10mg/L, FDP>20ug/mL 范围内的结果 50 例，将三种范围的 D-Dimer 结果分别进行各梯度稀释检测并计算回收率；假阳性组收集 D-Dimer 与 FDP 结果倒置的病例 35 例，将 D-Dimer 与 FDP 结果分别进行各梯度稀释检测并计算回收率。

PO-1294

Transient appearance of postchemotherapy pseudothrombocytopenia associated with eosinophilia in a child with acute promyelocytic leukemia

Li Chang 、Fang Liu、Yongmei Jiang
Department of Laboratory Medicine, West China Second University Hospital, Sichuan University

Pseudothrombocytopenia is a well known phenomenon, which is characterized by erroneous low platelet counts due to platelets in vitro clumping. We report a transient appearance of postchemotherapy pseudothrombocytopenia in a child with acute promyelocytic leukemia. Pseudothrombocytopenia and increased eosinophils were two major apparent abnormalities in this patient, and the appearance and disappearance of pseudothrombocytopenia was accorded with abnormal eosinophil counts in time. After excluding EDTA-dependant pseudothrombocytopenia by using alternative anticoagulant or incubating 30min at 37℃, a pseudothrombocytopenia likely induced by IgE-mediated immunologic mechanism associated with eosinophilia was considered. According to the history of disease and medicine, we concluded drug may be an important factor to induce increased eosinophils and IgE in this child. To avoid incorrect diagnoses and inappropriate treatment, pseudothrombocytopenia should always be considered as a possible cause of reported low platelet counts, and once EDTA-induced can be excluded, attention should be paid to drug-use or other causes which may activate platelets.

PO-1295

血小板与淋巴细胞比值对异常凝血酶原阴性肝细胞癌进展的诊断价值

刘京萍
江苏省人民医院

目的 血小板和血小板活化参与肿瘤细胞生长，转移和血管生成的关键步骤。在这项研究中，我们分析了异常凝血酶原阴性的肝细胞癌（HCC）中血小板与淋巴细胞比率（PLR）之间的相关性。
方法 本研究纳入 2017 年 1 月至 2019 年 10 月在江苏省人民医院就诊的 111 名异常凝血酶原阴性的 HCC 初诊患者，并选取 111 名健康体检者作为对照。采用 Mann-Whitney U 检验比较 HCC 和对照组之间实验室参数和临床病理特征的差异。绘制 ROC 曲线确定 PLR 在异常凝血酶原阴性肝癌（PIVKA-II-NHCC）患者中的诊断价值。使用单向方差分析计算 HCC 不同阶段 PLR 的差异。Spearman 相关分析用于分析肝癌患者 PLR 与相关实验参数之间的相关性。
结果 HCC 患者的绝对嗜中性粒细胞计数（N），平均血小板体积（MPV）和嗜中性粒细胞与淋巴细胞之比（NLR）高于对照组。 HCC 患者的血小板计数（PLT），绝对淋巴细胞计数（L），血小板分布宽度（PDW）和 PLR 明显低于对照组。在肝癌的四个阶段之间，PLR 存在显着差异。Spearman 相关分析表明，PLR 与癌症分期，甲胎蛋白（AFP），NLR 和 MPV 呈负相关，与 PLT 和 PDW 呈正相关。 PLR 的 ROC 特性曲线下的面积为 0.631（95％CI：0.591-0.662）。
结论 PLR 与异常凝血酶原阴性的 HCC 相关，可能是其进展的潜在标志。

PO-1296

血栓弹力图分析在妊娠高血压综合征中的应用价值

高丽钦、欧启水
福建医科大学附属第一医院

目的 通过观察妊娠高血压综合征（妊高征）患者血栓弹力图（TEG）与常规凝血项目各项指标之间的关联性,探讨 TEG 在妊高征诊断中的应用价值。
方法 选择 2015 年 11 月至 2018 年 3 月在福建医科大学附属第一医院门诊和住院治疗的妊高征患者 90 例,同时纳入正常妊娠女性（正常妊娠组）60 人和正常非妊娠女性（正常对照组）60 人,采集样本进行 TEG 及常规凝血指标检测,并进行统计学分析。
结果 与正常对照组、正常妊娠组相比,妊高征组凝血因子激活时间（R）、血块形成速率（K）明显减小,而最大血块强度（MA）及弹力图最大切角（α-Angle）明显增高（均 P<0.05）;与正常对照组比较,正常妊娠组和妊高征组凝血酶原时间（PT）、活化部分凝血活酶时间（APTT）、国际标准化比值（INR）、凝血酶时间（TT）明显降低（P<0.05）,而纤维蛋白原（Fib）浓度升高（P<0.05）。与正常对照组和正常妊娠组相比,妊高征组血小板计数（PLT）水平升高（P<0.05）。妊娠高血压组、轻度子痫前期组、重度子痫前期组间 R、K、α-Angle、MA 各指标差异有统计学意义（均 P<0.05）;与妊娠高血压组和轻度子痫前期组相比,重度子痫前期组血小板计数指标差异有统计学意义（P<0.05）;但常规凝血指标结果比较,差异无统计学意义（均 P>0.05）。TEG 各指标与常规凝血指标的相关性分析表明,R 值与 PT、APTT 呈正相关,α-Angle 与 Fib 呈正相关（r=0.701,P<0.01）、K 值与 Fib 呈负相关（r=-0.461,P<0.01）;MA 与 PLT 呈正相关（r=0.635,P<0.01）;但 K 值与 PLT、α-Angle 与 PLT、Fib 与 MA 相关性无统计学意义。
结论 TEG 对于鉴别妊高征患者以及区分妊高征的严重程度有一定的临床价值,其与常规凝血功能指标存在一定的相关性。

PO-1297

微流控芯片单细胞选择性扩增用于循环肿瘤干细胞检测

罗彦彰、刘洋、林冬果、陈晓、刘大渔
华南理工大学附属第二医院（广州市第一人民医院）

目的 利用肿瘤干细胞自我更新特性，发展一种微流控芯片单细胞选择性扩增方法用于循环肿瘤干细胞检测。
方法 设计并制作了一种包含 8000 个捕获池的微流控芯片；分散有结直肠癌 HCT116 细胞的血液样本去除红细胞后重悬于海藻酸钠溶液中，并引入微流控芯片。连续培养 7 天后，通过荧光呈像识别单细胞来源肿瘤球，提示肿瘤干细胞的存在。通过芯片反向灌流回收肿瘤球，利用流式细胞术、免疫荧光、连续传代和类器官培养进行肿瘤干细胞定性分析。
结果 芯片培养获得直径为 36.9 ± 6.8 μm 的单细胞来源肿瘤球，成球率约为 21.6%；肿瘤球的 LGR5、CD44、CD133、CD24、Nanog、OCT4 和 SOX2 等一系列干性标志物呈阳性，而上皮分化标志物 CK20 呈现阴性；芯片回收细胞中肿瘤干细胞标志物 CD133、ALDH、LGR5 阳性细胞比例显著高于悬浮培养所获细胞；在连续传代培养过程中，肿瘤球均呈现 CD133 和 LGR5 均质强阳性，表明细胞干性可稳定维持。
结论 本研究发展了一种微流控芯片单细胞选择性扩增方法，有望实现循环肿瘤干细胞检测，为开发循环肿瘤干细胞作为新型肿瘤标志物做出了有益的尝试。

PO-1298

术前炎症指标 NLR、MLR、SII 在甲状腺髓样癌中应用价值的探索

林琳、吴丽娜
中国医科大学附属盛京医院

目的 探讨外周血中性粒细胞与淋巴细胞比值、单核细胞与淋巴细胞比值、系统免疫炎症指数在甲状腺髓样癌中的应用价值。
方法 以中国医科大学附属盛京医院 2012 年 2 月至 2020 年 7 月收治的甲状腺髓样癌患者 50 例(MTC 组)、甲状腺乳头状癌患者 50 例(PTC 组)、健康体检者 50 例(HC 组)为研究对象，比较三组患者外周血 NLR、MLR、SII 水平的差异，并采用受试者工作特征曲线分析上述三个指标在 MTC 中应用价值，再根据上述三个指标的 ROC 曲线截点值分析其与甲状腺髓样癌临床病理特征的相关性。
结果 MTC 组 NLR 显著高于 PTC 组，差异有统计学意义(P<0.05)；MTC 组 MLR、SII 水平显著高于 PTC 组与 HC 组，差异有统计学意义(P<0.05)。通过 ROC 曲线分析发现，NLR、MLR、SII 的 ROC 曲线下面积分别为 0.620、0.681、0.634， NLR、MLR、SII 的 ROC 曲线截点值分别为: 1.92、523.10× 109 /L、0.26，据此分为将 MTC 组分为低 NLR 组(NLR<=1.92)、高 NLR 组(NLR>1.92)；低 SII 组(SII<=523.10× 109 /L)、高 SII 组(SII>523.10× 109 /L)；低 MLR 组(MLR<=0.26)、高 MLR 组(MLR>0.26)。MLR 指标高值组和低值组患者，性别、淋巴结转移的差异有统计意义(P<0.05)，年龄、肿瘤双侧性及多发性之间差异无统计学意义(P > 0.05)。NLR、SII 与年龄、性别、淋巴结结转移，肿瘤双侧性及多发性之间差异均无统计学意义(P > 0.05)。
结论 MTC 患者 NLR、MLR、SII 水平显著升高，可作为 MTC 辅助鉴别诊断指标。MLR 水平与 MTC 患者淋巴结转移显著相关。

PO-1299

联合检测纤维蛋白原、抗凝血酶Ⅲ对静脉血栓栓塞症的诊断价值

陈峻
武汉市第一医院

目的 探讨纤维蛋白原（FIB）联合抗凝血酶 III（AT-III）在静脉血栓栓塞症患者中的诊断效果。
方法 选择 2017 年 6 月-2018 年 5 月武汉市第一医院住院治疗的静脉血栓栓塞症患者 59 例作为对象，设为观察组；选择同期健康体检者 53 例设为对照组。观察组入院后次日早晨取空腹静脉血 3mL，对照组当天早晨取空腹静脉血 3mL，血清分离后采用发光底物法测定两组 AT-III 水平；采用凝固法测定两组 FIB 水平；绘制 ROC 曲线，分析 FIB 与 AT-III 在静脉血栓栓塞症患者中的诊断效能。
结果 观察组中肺血栓栓塞症与深静脉血栓 FIB、AT-III 水平比较差异无统计学意义（P>0.05）；观察组肺血栓栓塞症合并深静脉血栓患者 FIB、AT-III 水平，均低于单一肺血栓栓塞症与深静脉血栓（P<0.05）；观察组 FIB、AT-III 水平，均低于对照组（P<0.05）；单一 FIB、AT-III 在静脉血栓栓塞症患者中诊断敏感性、特异性差异无统计学意义（P>0.05）；FIB 联合 AT-III 在静脉血栓栓塞症患者中诊断敏感性、特异性，高于单一 FIB、AT-III（P<0.05）。
结论 FIB、AT-III 在静脉血栓栓塞症患者中呈低表达，二者联合检测能获得较高的诊断效能，值得推广应用。

PO-1300

血液检查指标在老年患者脊柱骨质疏松性压缩骨折的辅助诊断价值

霍青
徐州矿务集团总医院（徐州医学院第二附属医院）

目的 探讨血液检查指标能否对老年患者脊柱骨质疏松性压缩骨折提供辅助诊断价值。
方法 纳入 2019 年 10 月至 2020 年 10 月期间 326 例脊柱骨质疏松性压缩骨折老年患者为研究组，205 例腰腿疼患者为对照组，统计两组的性别、年龄、血沉、C 反应蛋白、PT (凝血酶原时间)、PTINR（国际标准化值），PT%（PT 活动度），APTT（活化部分凝血活酶时间），TT（凝血酶时间），FIB（纤维蛋白原），AT（抗凝血酶），D-二聚体的数据并进行比较，并分析两组数据之间的差异性。
结果 两组之间的性别没有差异，研究组的平均年龄 76.89 岁略高于对照组 74.94 岁。PT、PTINR、PT%、APTT、TT，这四个反映血凝的指标，虽然在研究组和对照组之间存在统计学的差异，但是都在正常参考值范围内。研究组血沉为 26.86 mm/h ，C 反应蛋白 9.66 mg/l ，FIB 为 4.27g/l ，D-二聚体 813.94 ng/ml，明显高于正常值，并且与对照组血沉为 18.94 mm/h ，C 反应蛋白<3.45 mg/l ，FIB 为 3.80g/l， D-二聚体 225.21 ng/ml，有统计学差异（P<0.001）。
结论 血沉、C 反应蛋白、FIB 及 D-二聚体的数值在老年患者脊柱骨质疏松性压缩骨折中均有不同程度的升高，对于患者的诊断有一定的辅助价值，其中 D-二聚体升高较明显，提示意义也最大，并且与患者骨折的病史长短有很大相关性。

PO-1301

血常规检测在 HFRS 和 SFTSV 诊断中的作用

张丽霞
江苏省人民医院（南京医科大学第一附属医院）

肾综合征出血热（hemorrhagic fever with renal syndrome，HFRS）我国主要以 HTNV 和 AMRV 感染为主，以鼠类为主要的传染源自然疫源性疾病。该病以全身小血管以及毛细血管损伤为主要病理变化，在临床上以发热、出血倾向、肾脏损伤为主要的三大症状，并可将病程大致上分为五期：发热期、低血压休克期、恢复期、少尿期、多尿期， 重症者可有多个时期重合出现，出血热不仅会造成肝肾功能的损害，严重者还可危及生命，死亡率可达到 10%。

发热伴血小板减少综合症（ fever with thrombocytopenia syndrome virus, SFTSV）我院检出率也非常高。SFTSV 俗称“蜱虫病”，是由新型布尼亚病毒引起的急性自然疫源性传染病，蜱虫为其传播媒介。好发人群主要为蜱虫疫源区的居民、旅游者，急性期患者的血液和血性分泌物具有传染性，感染者在临床上主要表现为发热、乏力、精神不振、恶心、腹泻等症状。

病毒感染确诊主要依靠病原学的检查，同时病毒感染时，外周血会发生非特异性的变化。对于某类病毒感染来说，血液学指标会具有一定的共性及特性，结合其病史，临床体征等信息，往往可以给疾病的诊断提供重要方向。我们根据本院临床多例 HFRS 和 SFTSV 感染的外周血基本特征，进行了分析和总结，发现两种病毒感染存在共同点为：红细胞正常或者升高，血小板进行性下降，外周血可见：核左移；各型反应淋巴细胞，浆样反应淋巴细胞增多；涂抹细胞增多。不同点为通常 HFRS 白细胞增高而 SFTSV 白细胞下降。

在血常规检测指标中，找到蛛丝马迹，及时给临床提供诊断思路，从而更好的为临床病毒感染的诊断、鉴别诊断及治疗提供依据。

PO-1302

新冠疫苗接种对 CPD 参数的影响

孙婷婷
陆军特色医学中心（大坪医院）

目的 白细胞群落参数（cell population data, CPD）是 UniCel DxH800 血细胞分析仪通过 VCS 技术对外周血进行检测,许多研究表明 CPD 参数可能具有临床诊断价值或者作为某些疾病的筛选指标。本研究通过检测接种了新冠疫苗志愿者外周血对 CPD 参数值的影响，为临床提供 CPD 参数潜在的有用信息。

方法 选取 2020 年 3 月-2020 年 4 月进行新冠病毒灭火疫苗接种的志愿者 20 名，年龄在 22-36 岁之间，男女比列为 12/8，分别在接种前 24 小时，第一次接种后 24 小时，第二次接种前 24 小时，第二次接种后 24 小时 四个时间段抽血志愿者的 EDTA-K2 抗凝全血标本，对所有全血样本采用 DxH800 血细胞分析仪检测获得 CPD 参数，观察 CPD 参数的变化趋势。

结果 接种前与第一次接种 24 小时后有显著差异的参数有 18 个，接种前与第二次接种前进行比较，有 12 个参数具有统计学差异，接种前与第二次接种后 24 小时进行比价，有 25 个参数具有统计学的变化，第二次接种前与第二次接种后 24 小时相比较，18 个参数具有统计学差异变化。

结论 新冠疫苗接种后，激活了人体的细胞免疫系统，导致细胞发生了不同程度的变化，第一次疫苗接种后机体的免疫细胞已经启动，也间接反映接种疫苗是成功的，这项研究提供了接种新冠病毒疫苗后 CPD 变化的重要信息，这些变化可能成为临床潜在的应用指标，为某些形态参数的变化做出量化的解释。

PO-1303

儿童继发性血小板增多与呼吸道感染病原体分析

徐丹
华中科技大学协和深圳医院

目的 通过分析患儿呼吸道感染病原体与血小板增多的关系，帮助临床从血小板计数结果对患儿呼吸道感染病原体作初步诊断与鉴别诊断。
方法 收集 2020 年 9 月至 2021 年 2 月住院患儿 163 例（血小板增多 45 例，血小板非增多 118 例）采集血清及 EDTA 抗凝血，应用间接免疫荧光法对九种呼吸道病原体 IgM 进行检测，用 SYSMEX XN-9000 血细胞分析仪对血小板进行计数。
结果 呼吸道感染患儿血小板水平显著高于健康儿童（P＜0.05），45 例呼吸道感染患儿发生血小板增多，其中，肺炎支原体 IgM 检出率最高，其次是副流感病毒；与血小板正常的患儿相比，肺炎支原体检出率显著高于正常组患儿（P＜0.05），而副流感病毒检出与正常组患儿无显著差异（P＞0.05）；乙型流感病毒则不易引发血小板增多；其他病原体检出率较低，差异均不显著（P＞0.05）。
结论 在九种呼吸道道病原体中，儿童对肺炎支原体普遍易感，并易发血小板增多，而乙型流感病毒感染不易引起血小板增多。

PO-1304

新型血栓标志物对恶性肿瘤患者围手术期并发 VTE 的预警效能

张金彪、曹蕾、马飞、代荣琴
河北省沧州中西医结合医院

目的 探讨新型血栓标志物对恶性肿瘤患者围手术期并发 VTE 的预警效能。
方法 回顾性分析自 2020 年 7 月 1 日至 2021 年 2 月 1 日我院收治恶性肿瘤手术患者 150 例，为观察组，围手术期内并发 VTE 者 30 例，为血栓组；未并发 VTE 者 120 例，为无栓组。另选同期健康体检者 60 例，为对照组。各组均检测血栓标志物，对照组检测一次，观察组术前 1d 和术后 1d 各检测一次。采用 SPSS23.0 作统计学处理，评价血栓标志物预警效能。
结果 ①肺癌（P=0.014＜0.05）、老龄（P=0.036＜0.05）、肥胖（P=0.000＜0.05）、转移（P=0.031＜0.05）、晚期（P=0.023＜0.05）是恶性肿瘤患者术后并发 VTE 的高危因素；②术前 1d，血栓组的 TAT 和 TM 高于无栓组，差异有统计学意义（P＜0.05），TM 预警效能最好（截断值 10.70，AUC=0.786，灵敏度 73.30%，特异度 81.70%，P=0.000），TAT 和 TM 联合可提升预警效能（AUC=0.796，灵敏度 80.00%，特异度 77.50%，P=0.000）；术后 1d，血栓四项均高于无栓组，差异具有统计学意义（P＜0.05），TAT 预警效能最好（截断值 16.50，AUC=0.887，灵敏度 82.36%，特异度 71.65%，P=0.000），四项联合可提升预警效能（AUC=0.913，灵敏度 90.00%，特异度 88.60%，P=0.000）；③PIC 作为纤溶激活标志物，与 TAT 均呈现良好的正相关（术前：r=0.665,P=0.000＜0.05；术后：r=0.638,P=0.000＜0.05）。
结论 新型血栓标志物在恶性肿瘤患者围手术期预测 VTE 中具有重要的预警价值；TM 相对 TAT 能更早提示 VTE 风险，截断值为 10.70TU/ml；可选用 PIC 把控 VTE 发生前的纤溶状态，评估出血风险。

PO-1305

Neutrophil Extracellular Traps (NETs) in Peripheral Blood Smear of a Patient with Septic Shock

Lixia Zhang
The First Affiliated Hospital of Nanjing Medical University

We present a patient with septic shock after mitral valve replacement. Examination of blood film revealed neutrophils with toxic granules and vacuole, immature granular cells and numerous smudge granulocytes. These smudge granulocytes might be identified as neutrophil extracellular traps(NETs). The peripheral blood smear analysis may be a simple method for identification of NETs.

A 73-year-old woman got septic shock after mitral valve replacement. CBC showed: white blood cell 8.62×109/L (neutrophil 89.2%), hemoglobin 102 g/L and platelet 26 ×109/L. The peripheral blood smear identified by CellaVision® Hematology Autoanalyzer showed neutrophils with toxic granules and vacuoles (Figure 1A, B [Digital microscopy; Cellavision, ×100 objective]), immature granular cells (Figure 1B, C) and numerous smudgegranulocytes (Figure 1D-I). The free granules near the nucleus, the secreted expulsion nuclear chromatin and network structure showed that these smudge cells might be identified as neutrophil extracellular traps(NETs).

NETs are extracellular, network structures composed of cytosolic and granule proteins that are assembled on a scaffold of chromatin. NETs trap, neutralize and kill pathogens. However, NETs can contribute to immune-related diseases when dysregulated. NET formation in the circulation promotes coagulation, vascular occlusion and thrombosis. NETs are also found in tumors and can promote tumor metastasis1-3. NETs can be analyzed by immunofluorescence. Recently, NETs are proved can be identified by peripheral smear autoanalyzers4-5. The peripheral blood smear analysis may be a simple method for identification of NETs.

PO-1306

The higher risk of severe thrombocytopenia in Escherichia coli comparing with Klebsiella pneumoniae and Pseudomonas aeruginosa

Yingying Diao
China medical university

Thrombocytopenia increases the mortality rate during sepsis. But there is no clear conclusion about which bacteria caused higher levels of thrombocytopenia. The goal of this study is to determine whether there is a difference in the incidence of thrombocytopenia pneumoniae caused by the three common bacteria, namely Escherichia coli (E. coli), Klebsiella (K. pneumoniae) and Pseudomonas aeruginosa (P. aeruginosa). Our data indicate that severe thrombocytopenia (P = 0.04) was a risk factor for bad clinical outcomes, OR were 3.20 (95% CI 1.06–9.68). Then we compared the difference of the risk of severe thrombocytopenia in E. coli as compared with bacteria with K. pneumoniae and P. aeruginosa. After adjusting for potential confounders, the risk of severe thrombocytopenia in E. coli was higher than that in K. pneumoniae and P. aeruginosa in a multivariable logistic regression model (P = 0.04) and OR was 3.30 (95% CI 1.04–10.53). But there was no statistically significant among the age subgroup, gender subgroup, organ dysfunction subgroup. In conclusion, the risk of severe thrombocytopenia in E. coli is significantly higher than K. pneumoniae and P. aeruginosa. For those infected with E. coli, the platelet count should be increased as soon as possible to reduce mortality.

PO-1307

尿液 κ 和 λ 轻链检测在糖尿病早期肾损伤中的价值分析

卢佩
空军军医大学西京医院

目的 探讨尿 κ 轻链、尿 λ 轻链、尿免疫球蛋白 G（IgGU）和尿转铁蛋白（TRFU）在糖尿病早期肾损伤评估中的临床价值。
方法 选择 56 例糖尿病早期肾损伤患者和 50 例同时期健康体检者作为观察组和对照组，分别检测两组的尿 κ 轻链、尿 λ 轻链、尿免疫球蛋白 G 和尿转铁蛋白，并对各组指标进行统计学分析。
结果 观察组尿 κ 轻链、尿 λ 轻链、尿免疫球蛋白 G 和尿转铁蛋白检测水平高于对照组，差异有统计学意义（P<0.05）；观察组尿 κ 轻链、尿 λ 轻链、尿免疫球蛋白 G 和尿转铁蛋白阳性率分别为 92.9%、82.1%、62.5%、64.3%，均高于对照组各指标阳性率，差异有统计学意义（P<0.05）。
结论 尿 κ 轻链、尿 λ 轻链、尿免疫球蛋白 G 和尿转铁蛋白检测，对糖尿病早期肾损伤监测及预测其发生发展有重要的临床价值。

PO-1308

IFN-γ Down-regulated CXCR2 Expression on Circulating Monocytes Results in Re-education of Tumor-Associated Macrophages in Colorectal Cancer

Huayang Wang
Qilu Hospital of Shandong Universtiy

Circulating monocytes are the main source of tumor-associated macrophages (TAMs), but their recruitment to tumor tissue and further differentiation remains unclear. Chemokine receptors play an essential role in cancer development and anti-tumor immunity. In the present study, we observed a significant decrease of CXCR2 expression on circulating monocytes of colorectal cancer (CRC) patients, which was associated with tumor stages, and systemic and local inflammatory status. Pro-inflammatory cytokine IFN-γ, which was over-expressed in CRC patients, was involved in CXCR2 downregulation by promoting GRK-2 expression in monocytes. Decreased CXCR2 expression hindered monocyte recruitment to the tumor site, and modified inflammatory polarization of CRC-educated TAMs. Comparing with humans, mice monocytic cells exhibited a different CXCR2 expression profile. The inhibition of CXCR2 signaling in CRC-bearing mice altered sub-population constitutions of circulating monocytes and TAMs. Interestingly, inhibiting CXCR2 decreased pro-inflammatory cytokine levels in peripheral blood, but increased their expression in xenograft tumor of mouse model. In summary, our findings suggest that CXCR2 expression on circulating monocytes reflects CRC stages, and has the potential to be an effective target of monocytic cell-dependent therapy. However, its effect on anti-tumor immunity should be carefully examined, as it exhibits different expression profiles between species, and seems to exert diverse influence on different myeloid cell types.

PO-1309

应用 CpG-OND 细胞培养添加剂提高 CLL 患者染色体核型分析阳性检出率的临床研究

谭鸿文[1]、毛翠[2]
1. 四川金域医学检验中心有限公司
2. 广州金域医学检验集团股份有限公司

目的 探讨应用含 CpG-ODN（CpG oligonucleotide, CpG 寡脱氧核苷酸）细胞培养添加剂提高慢性淋巴细胞白血病（chronic lymphocytic leukemia，CLL）患者染色体核型分析阳性检出率的临床价值。
方法 收集 2020 年 1 月至 2021 年 3 月送检至我实验室行染色体核型分析且明确诊断为慢性淋巴细胞白血病的初诊患者 143 例，同步进行双线培养，进行常规骨髓细胞培养为常规组；同时应用 CpG-ODN 刺激培养为 CpG 组。收获制备染色体，进行 G 显带染色体核型分析。
结果 143 例 CLL 患者中，染色体培养成功率（镜下可分析中期分裂相≥20 个）CpG 为 99.30%，常规组为 98.60%，培养成功率无明显差异；CpG 组检出异常核型 83 例（58.04%），其中检出 1 种染色体异常 33 例（39.76%），2 种异常 30 例（36.14%），≥3 种异常 20 例（24.10%），常规组仅检出异常核型 1 例（0.70%），其中检出≥3 种异常 1 例（0.70%），差异有显著性；CpG 组 83 例患者中，共检出 14 种 93 个异常，其中数目异常 14 例（16.67%），结构异常 8 例（9.52%），数目及结构异常 61 例（73.50%）。常规组 1 例患者中，数目及结构异常 1 例（0.70%），差异有显著性。
结论 染色体培养成功率无明显差异，但是应用 CpG-ODN 细胞培养添加剂刺激培养细胞，能显著提高在慢性淋巴细胞白血病中异常核型的阳性检出率，值得推广。

PO-1310

一例初诊为 BCR/ABL1 阳性 CML 治疗后转变为 BCR/ABL1 阴性伴复杂核型 AML 的病例分析及文献复习

杨涯梅
四川金域医学检验中心有限公司

目的 探讨一例初诊为 BCR/ABL1 阳性 CML 治疗后转变为 BCR/ABL1 阴性伴复杂核型 AML 的病例分析并文献复习。
方法 对一例为 BCR/ABL1 阳性 CML 治疗后转变为 BCR/ABL1 阴性伴复杂核型 AML 的病例的临床资料、骨髓细胞形态学、骨髓活检、流式细胞学及分子生物学检查的结果及临床诊疗经过分析。
结果 患者 2016 年 4 月初诊时表现为白细胞高、脾大；骨髓形态学提示：骨髓增生极度活跃，粒系占 91.5%，主要以中性中晚幼粒细胞为主；染色体检查提示：46,XY,t(9;22)(q34;q31)；BCR/ABL1(p210 型)融合基因阳性；流式细胞学检查符合 CML-CP 特征；临床诊断为 CML。给予伊马替尼维持治疗，并动态监测 BCR/ABL1(p210 型)融合基因，于 2018 年 7 月达完全细胞遗传学反应。2020 年 11 月，染色体检查提示：45,XY,-7；白血病融合基因检测提示 BCR/ABL1(p210 型)、EV11 基因阳性；流式细胞学查见 15.5%异常髓系原始细胞。2021 年 4 月染色体检查提示：49,XY,-7,+13,+20,+21,+21[3]/50,idem,+8[12]/50,idem,+10[3]/46,XY[2]；骨髓细胞形态学提示原始粒细胞占 53.0%；流式细胞学查见 24.52%异常髓系原始细胞；分子生物学 BCR/ABL1(p210 型)融合基因筛查为阴性；FISH 的 BCR/ABL1 融合探针为阴性；诊断为 AML 伴复杂核型。
结论 CML 疾病发生发展中可能存在 t(9;22)以外的获得性细胞遗传学变异，并可导致第二种髓系肿瘤，当 CML 疾病进展时，应对其进行遗传学与分子生物学评估，并注意与 CML 急变期相鉴别。

PO-1311

狼疮抗凝物在习惯性流产和系统性红斑狼疮中的应用

晋臻[1]、骆贵平[2]
1. 昆明医科大学第一附属医院
2. 昆明医科大学

目的 探索狼疮抗凝物（lupus anticoagulant，LA）在习惯性流产和系统性红斑狼疮（systemic lupus erythematosus，SLE）中的应用价值。
方法 选择 2020 年 12 月至 3 月昆明医科大学第一附属医院及 2020 年 1 月至 2021 年 3 月昆明医科大学第二附属医院临床诊断为习惯性流产或系统性红斑狼疮的患者 214 例，应用磁珠法检测患者血清中狼疮抗凝物，D-二聚体（D2）的数值，其中习惯性流产 98 例，系统性红斑狼疮 116 例。收集同期就诊未发生不良妊娠的患者 88 例,其他就诊的患者 91 例。将所得的四组数据分为系统性红斑狼疮组即 A 组和习惯性流产组即 B 组。
结果 根据 Spearman 相关性分析，在 A 组中 LA（r=0.166）、抗心磷脂抗体（r=0.341）、抗 β2 糖蛋白总抗体（r=0.374）与系统性红斑狼疮呈正相关（P<0.05）。在 B 组中 LA（r=-0.208）、D-二聚体（r=-0.293）与习惯性流产呈负相关（P<0.01）；抗心磷脂抗体（r=0.152），抗 β2 糖蛋白总抗体（r=0.329）与习惯性流产呈正相关（P<0.05）。根据 Logistic 回归分析，在 A 组中，抗心磷脂抗体（ACA）和抗 β2 糖蛋白总抗体（抗-β2）是系统性红斑狼疮的独立危险因素（P<0.05）；在 B 组中，抗 β2 糖蛋白抗体是习惯性流产的独立危险因子（P<0.05）。
结论 ACA 和抗 β2 糖蛋白总抗体可能是系统性红斑狼疮的独立危险因素；抗 β2 糖蛋白总抗体可能是习惯性流产的独立危险因素。

PO-1312

Red blood cell distribution width: a potential laboratory parameter for monitoring inflammation in rheumatoid arthritis

Yujue He、Qishui Ou
the First Affiliated Hospital of Fujian Medical University

Correlation analysis of red blood cell distribution width (RDW) and C-reactive protein (CRP), erythrocyte sedimentation rate (ESR), tumor necrosis factor α (TNF-α), interleukin (IL)-6, and IL-10 in rheumatoid arthritis (RA) to investigate whether RDW can serve as a potential parameter for indicating inflammation in RA patients. A total of 670 RA patients from October 2014 to April 2016 were enrolled in our study. The white blood cell (WBC), red blood cell (RBC), platelet (PLT), hemoglobin (HGB), RDW, CRP, and ESR in peripheral blood of patients with RA were retrospectively analyzed. The relative expression of TNF-α, IL-6, and IL-10 was detected by RT-qPCR. Correlation analysis between RDW and CRP, ESR, TNF-α, IL-6, and IL-10 in RA was conducted by Microsoft Excel. RDW level was significantly increased in RA patients compared to osteoarthritis (OA) patients (P < 0.001) and healthy donors (HDs) (P < 0.001), and RDW was positively associated with inflammatory markers, such as CRP and ESR. In ROC curve analysis, the area under the curve (AUC) of RDW for the identification of RA was 0.881, with a 95% confidence interval (CI) from 0.864 to 0.898. Moreover, correlation analysis showed that RDW level was positively associated with TNF-α and IL-6, however negatively associated with IL-10. RDW was increased in patients with RA which was associated with inflammation in RA, suggesting that RDW may be a potential auxiliary marker for indicating inflammation process in RA conveniently.

PO-1313

基于全基因组表达谱数据的弥漫大 B 细胞淋巴瘤 R-CHOP 方案预后标记物筛选及潜在分子机制研究

彭佳敏
浙江省立同德医院

目的 弥漫大 B 细胞淋巴瘤是最常见的 NHL 类型。R-CHOP 作为 DLBCL 的一线治疗方案，仍存在着相当比例的原发性耐药及缓解后复发。筛选治疗疗效预测标记物及新治疗靶点是临床医生面临的重大挑战。本文通过分析 884 例 DLBCL 表达谱数据结合临床标本验证，筛选疗效预测标记物，为早期预测 DLBCL 患者 R-CHOP 方案敏感性、制定精准化诊疗策略提供依据，并为开发具有临床应用潜力的药物奠定理论基础和研究依据。
方法 根据生存时间计算预后相关差异基因，并利用多基因列表韦恩图分析来筛选。对差异基因进行 heat map、聚类分析和功能网络分析，并对差异基因的预后价值进一步验证，筛选出预后价值最佳的目的基因，验证目的基因的表达水平与患者临床病理因素及预后的相关性，用免疫组化方法检测目的基因在 DLBCL 组织及正常淋巴结对照中的表达水平并进行统计学分析。对目的基因进行功能富集分析，构建相互作用蛋白网络，同时构建药物-目的基因调节网络。
结果 我们筛选出 HK2 等 25 个预后差异表达基因。发现 HK2 表达与患者 OS 及 PFS 显著负相关，并且 HK2 在 PD 组和 ABC 亚型患者中的表达均显著升高。免疫组化结果显示，HK2 在 DLBCL 组织中的表达显著升高。GSEA 分析发现，HK2 表达与肿瘤组织缺氧、侵袭转移、DNA 修复、化疗耐药、肿瘤干细胞通路等显著相关。蛋白相互作用网络分析发现 HK2 与 EGFR、BUB3 等蛋白的直接相互作用可能促进了 DLBCL 的耐药等恶性生物学表型。HK2-药物网络分析发现，JQ1、GKA50 等药物可抑制 HK2 表达。
结论 本研究通过对大样本者全基因组表达谱数据的分析及临床标本免疫组化验证，初步证实 HK2 是一个有效的 R-CHOP 方案疗效预测标记物和潜在治疗靶点，为制定精准化诊疗策略及开发具有临床应用潜力的 DLBCL 药物奠定理论基础和研究依据。

PO-1314

血栓弹力图-血小板图对蛛网膜下腔出血患者行预防性血小板输注的疗效评估

王妍、邹荣基、孟荣、马瑜婷、李卓
西安医学院第一附属医院

目的 运用血栓弹力图-血小板图 (TEG-Platelet Mapping) 评估预防性血小板输注对于服用抗板药物的蛛网膜下腔出血患者的出血倾向的纠正情况。
方法 2019 年 12 月至 2020 年 12 月间纳入的蛛网膜下腔出血患者 80 例，以是否服用抗血小板药物（氯吡格雷）将患者分成实验组（n=40）及对照组（n=40），实验组患者术前预防性输注个 1 治疗量血小板。使用常规血凝六项、TEG-血小板图对两组术前及预防输注后的出血风险进行评估，同时结合相关的临床数据进行分析，探讨预防性输注血小板的疗效。
结果 1、实验组患者的入院出血量、ADP 抑制率、ADPMA 均提示该组患者出血风险高于对照组（t=3.235/4.633/-7.63, P 值均<0.05）；2、血小板输注后，实验组患者的 ADP 抑制率及 ADPMA 较前有显著改善（t=0.068/0.072, P 值均<0.05）;且两组患者的术中出血率、术后发热率及血液相关检测数据均无显著差异（P 值均>0.05）。
结论 TEG-血小板图评估服用抗血小板药物的蛛网膜下腔出血患者的出血倾向有较好的预测力，预防性血小板的输注对于纠正出血风险及改善患者病程可能有一定作用。

PO-1315

Evaluation of inflammatory parameters in patients with hepatic hydatid disease

Zhijia Fan[1]、Hui Zhao[2]、Zhicheng Wang[1]
1. Department of Laboratory Medicine, Huashan Hospital, Fudan University, Shanghai
2. 新疆医科大学附属第一医院检验科

Background Hydatid disease (HD) is a zoonotic parasitic disease caused by the adult or larval stages of Echinococcus cestodes. Early diagnosis and treatment of hepatic HD are difficult owing to the lack of clinical symptoms in early-stage and awareness of the disease. The growth and proliferation of the hydatid were directly related to hosting immune-inflammatory reactions by the infiltration of inflammatory cells. And thus, some hematologic inflammatory factors which are simple and accessible in routine laboratory tests for use as auxiliary markers may be considered. However, the association of these inflammatory parameters with hepatic hydatid disease has not been investigated. We aimed to evaluate the potential value of inflammatory indices in this disorder.

Methods In this retrospective study, a total of 114 patients with hepatic HD and 114 healthy individuals were enrolled from January 2016 to November 2019. Clinical characteristics and laboratory data for all participants were collected and analyzed. The levels of inflammatory parameters were compared in the patient and control group. Univariate and multivariate logistic regression analyses, after correction for potential confounding factors such as age, gender, and ethnic minorities, were applied to evaluate the risk factors of hepatic hydatid disease. Odds ratios (ORs) with 95% confidence intervals (CI) were calculated for the estimated association. To observe the discriminative accuracy of inflammatory indices, receiver operating characteristic (ROC) analyses and the area under the curve (AUC) were analyzed, and differences between pre- and post-operation were compared by pair tests.

Results A total of 114 patients with hepatic HD including 57 males and 57 females were included in this study. Significantly higher levels of platelet distribution width (PDW) and eosinophil percentage (EOS %) were observed in patients than in healthy individuals, and we found significant inflammatory response in patients, as evidenced by the altered levels of inflammatory indices, the patient group had higher levels of neutrophil to lymphocyte ratio (NLR) ($P=0.047$), higher gamma-glutamyl transpeptidase to platelet ratio (GPR) ($P<0.0001$), and higher alkaline phosphatase to platelet ratio (APPR) ($P<0.0001$) and lower levels of the prognostic nutritional index (PNI) ($p<0.0001$) with statistical significance as compared to those in the control group. Multivariate analyses showed each parameter above was the potential risk factor of hydatid. To further evaluate the predictive accuracy of inflammatory indices as markers for HD, the ROC analyses with each parameter were performed. We found that APPR and PNI had better discriminative accuracy as compared to other parameters. After surgical treatment, the levels of PDW and APPR significantly decreased and no significant differences in PLT and EOS % were observed, while PNI still kept lower after surgery.

Conclusions In summary, our results presented the remarkable correlation between hepatic hydatid disease and inflammatory parameters. A significant increase in PDW, EOS, NLR, GPR, and APPR and a decrease in PLT and PNI were found in patients, particularly elevated PDW and APPR, which gradually returned to normal levels after surgical treatment. The alterations of levels in these parameters may be conducive to alerting physicians to the possibility of hepatic hydatid disease and useful to early detect the parasites. And further researches are needed to confirm if each factor combined with the other factors could have more diagnostic value.

PO-1316

MicroRNA-92a for colorectal cancer diagnosis: A systematic review with meta-analysis

Yiling Li[1]、Wei Cui[2]

1. Department of Clinical Laboratory, National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, China
2. Department of Clinical Laboratory, National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, China

Introduction Colorectal cancer (CRC) is the third most frequently diagnosed cancer. Aside from being the second leading cause of cancer death. MicroRNA-92a (miR-92a) functions as an oncogene and promotes tumorigenesis in several types of cancer, and miR-92a is also thought to be a viable biomarker for diagnosing colorectal cancer (CRC). However, there are two or three different sampling methods which are associated with varying degrees of diagnostic accuracy. This meta-analysis aimed to summarize the diagnostic value of miR-92a derived from blood (plasma and serum) and stool samples and for the first time, qualitative comparison of the two sample types' diagnostic accuracy.

Methods The relevant diagnostic studies were retrieved from PubMed, Embase, the Cochrane Library, and Web of Science, up until February 2021. Pooled sensitivity, specificity, and diagnostic odds ratio (DOR) were pooled to assess and compare diagnostic accuracies under random-effects. Data abstracted included first author, publication year, region, demographic information of patients, number of patients and controls, specimen type, TNM stage, screening methods, statistical analysis measure (AUC), and the number of true positive (TP), false positive (FP), false negative (FN) and true negative (TN). Overall test performance, both in plasma/serum and stool sample groups were estimated using summary receiver operating characteristic (SROC) curve analysis and area under the curve (AUC) using Meta-Disc (version 1.4). Besides, the risk of bias and applicability concerns of the inclusions was accessed according to QUDAS-2 (Quality Assessment of Diagnostic Accuracy Studies-2). Meta-regression analysis was also conducted using Deek's funnel plots and Fagan plots using Stata (version 15.1).

Results Initially, 174 were retrieved from the selected databases and through hand searching. 14 studies were included after reviewing the articles in detail and one piece of research data were finally included. There were ten plasma/serum studies and six which utilized stool sampling. In total there were 2,658 participants, consisting of 1,499 CRC patients and 1,159 controls. Comparative analysis found that, miR-92a identified in plasma/serum is superior with a pooled sensitivity of 73% as opposed to 63% although there was no difference in terms of specificity, both having 85% accuracy. Comparative AUC yielded 0.884 for plasma/serum samples versus 0.847 for stool samples. However, in terms of discriminative capacity, analysis of plasma/serum samples appears superior with a DOR of 16.35 compared to stool samples which had a DOR of.9.81.

Conclusions MiR-92a has good diagnostic accuracy for colorectal cancer although there appears to be fewer false positives/negatives when analyzing plasma/serum compared to stool samples.

PO-1317

A multicenter reference interval study of thromboelastography in the Chinese adult population

Xian-fei Zeng[1]、Xing-bin Hu[2]
1. 西安区域医学检验中心
2. 空军军医大学西京医院

Background Thromboelastography (TEG), a method of near-patient monitoring of coagulation, plays an essential role in the assessment of coagulation status, guiding component blood transfusion, and evaluating the effects of anticoagulants. Imprecise reference intervals (RIs) adversely impact the determination of the need for blood transfusion and clinical diagnosis and treatment of coagulopathy. However, there are few RI studies of thromboelastography (TEG) based on the protocols of the Clinical and Laboratory Standards Institute (CLSI) and International Federation of Clinical Chemistry and Laboratory Medicine, Committee on Reference Intervals and Decision Limits (IFCC/C-RIDL). The present multicenter study aimed to establish RIs for the adult Chinese population.
Methods Apparently healthy individuals who fulfilled the inclusion criteria were recruited by non-probability sampling (judgment sampling) at 6 medical centers in Xi'an City and Baoji City of Shaanxi.Based on the health questionnaire, physical examination, laboratory tests, and imaging examinations, inclusion criteria were determined according to the IFCC/C-RIDL and WS/T 402-2012 in China. Blood samples were subjected to laboratory TEG analysis for R, clot formation time (K), α angle (angle), maximum amplitude (MA), and coagulation index (CI). Based on the data distribution outliers were determined using the Dixon method or Tukey's fence, as appropriate. The Ichihara method, 2-level nested analysis of variance (ANOVA) (2N-ANOVA), and the latent abnormal values exclusion (LAVE) were used to define the RIs following recommendations of the Clinical and Laboratory Standards Institute and International Federation of Clinical Chemistry and Laboratory Medicine, Committee on Reference Intervals and Decision Limits. Multiple regression analysis was performed to explore sources of variation.
Results A total of 507 healthy participants were enrolled into the study cohort. Twenty-five individuals with potential coagulopathy were secondarily excluded by LAVE. Smoking was related to reaction time, α angle, and coagulation index in the TEG test ($P < 0.05$). Three test items (R, K, and angle) that did not follow a Gaussian distribution were subjected to Box-Cox transformation for 2N-ANOVA. 2N-ANOVA revealed that the RIs of all 5 test items of TEG needed to be partitioned by age and sex. Finally, TEG RIs were derived both parametrically and nonparametrically for males or females and different age Groups, respectively. Finally, given the clinical application of TEG RIs, RIs with differences < 5% between lower limits and simultaneously between upper limits were recommended to be merged.
Conclusions Few studies have reported RIs determined using TEG. The findings of previous studies with relatively small sample sizes did not significantly conform to the manufacturer's normal references' suggested and differed distinctly from each other. The oversensitivity in determining hypercoagulability where there is no risk for thrombosis and clinical presentation mainly arises from the imprecise TEG RIs, most of which originated from the manufacturer's data, which were not peer-reviewed. In our study, TEG RIs were established for the adult Chinese population using up-to-date methodology. The results will provide a useful and essential comparator for patients in the assessment of coagulation state, goaldirected blood transfusion therapy, and monitoring of the pharmacodynamic effects of anticoagulant drugs.

PO-1318

Prognostic value of pre-treatment LMR and NLR in patients with CD20 positive B cell non- Hodgkin lymphoma after immunochemotherapy

Xiaopeng Zhao、Li Ren
Tianjin Medical University Cancer Institute & Hospital

Objective To investigate the significance of peripheral blood lymphocyte/monocyte ratio (LMR) and neutrophil/lymphocyte ratio (NLR) in predicting the prognosis of CD20 positive B cell non-Hodgkin lymphoma patients after immunochemotherapy with rituximab.
Methods The clinical data of 220 patients with CD20-positive B-cell non-Hodgkin's lymphoma who were first diagnosed and treated in Tianjin Medical University Cancer Hospital from 2009 to 2013 were retrospectively analyzed. First, Pearson Chi-square test was used to study the relationship between pre-treatment LMR and NLR and the clinical disease characteristics of the patients. The cut-off values of LMR and NLR were determined according to the RECEIVER Operating Characteristic (ROC) curve, and the patients were divided into the high-value group and the low-value group according to the cutoff values of LMR and NLR respectively. Kaplan-meier survival curve analysis was performed to determine whether the difference between the high-value group and the low-value group was statistically significant. Then univariate and multivariate analyses were performed on the patients' total survival (OS) and progression-free survival (PFS) using Cox proportional hazard model to obtain the independent risk factors affecting the patients' OS and PFS.
Results The median age of 220 patients was 59 years old and ranged from 18 to 92 years old. At the last follow-up, 94 patients died, 126 survived, with a mortality rate of 42.7%. Pearson chi-square test results showed that NLR level was closely related to the number of extranodal involvement (P=0.002), LDH level (P=0.000) and IPI score (P=0.020). LMR level was closely related to B symptoms (P=0.020), clinical stage (P =0.003), the number of extranodal involvement (P = 0.009), the level of LDH (P = 0.000), β2 microglobulin level (P = 0.001) and the IPI score (P = 0.000). Survival analysis showed that patients with high NLR (≥3.0) had poorer OS and PFS than those with NLR<3.0. Compared with patients with LMR>2.4, patients with LMR≤2.4 had significantly lower OS and PFS. Multivariate analysis showed that NLR（HR 1.865,95%CI 1.196-2.910,P=0.006）and rituximab treatment（HR 0.587,95% CI 0.386-0.893, P=0.013）were independent risk factors affecting the overall survival of the patients. At the same time, statistical analysis showed that IPI score (HR 2.119,95%CI 1.188-3.780, P=0.011), NLR(HR 1.683,95%CI 1.095-2.587, P=0.018)and number of extranodal involvement（HR 2.340,95%CI 1.093-5.009,P=0.029） were independent risk factors affecting patients' progress-free survival.
Conclusions LMR and NLR at initial diagnosis can be used to predict the prognosis of patients with CD20-positive B-cell non-Hodgkin lymphoma, regardless of rituximab treatment.

PO-1319

调节性 B 细胞（Regulatory B cells,Breg）在 IGA 肾病发病机制中的功能作用

李涛
山东大学齐鲁医院

目的 研究调节性 B 细胞（Regulatory B cells,Breg）在 IGA 肾病发病起到的作用及意义。

方法 选取在 IGA 肾病确诊患者 37 名，排除继发性肾病，肿瘤等干扰因素，另取 17 名健康体检患者作为对照组(HCs)。收集所有参与者外周血抗凝标本进行流式细胞术（FCM）和酶联免疫吸附实验（ELISA）分析，检测外周血单个核细胞(PBMCs)中 Breg 细胞及相关亚群和血浆中 IL10 细胞因子水平的表达情况。同时收集所有参与者临床肾功能损伤指标进行统计学相关性分析。
结果 与正常健康对照组相比，IGA 肾病患者外周血单个核细胞(PBMCs)分析中：CD24hiCD38hiCD19+B 细胞，CD5+CD24hiCD38hiCD19+B 细胞,IL10+CD24hiCD38hiCD19+B 细胞水平低表达(P 值>0.05)，然而 CD138+CD9+B 细胞水平高表达(P 值>0.05)，其他 CD24intCD38intCD19+B 细胞，CD24hiCD38-CD19+B 细胞亚群未见显著性差异。ELISA 细胞因子分析中：IGA 肾病患者细胞因子 IL10 水平显著低于健康对照组。临床肾功能损伤指标中：IGA 肾病患者 24h 尿蛋白水平显著高于正常对照组(P 值>0.05)。Spearman 统计学相关性分析发现：CD24hiCD38hiCD19+B 细胞与细胞因子 IL10 水平，CD138+CD9+B 细胞与 24h 尿蛋白水平具有显著性正相关(P 值>0.05)，而 IL10+CD24hiCD38hiCD19+B 细胞与 CD138+CD9+B 细胞具有显著性负相关(P 值>0.05)。
结论 IGA 肾病发病过程中存在 Breg 细胞表达水平的降低，而 Breg 细胞的降低可能是功能性细胞因子 IL10 降低的原因，进而导致了 CD138+浆细胞的活化高表达。两者间的平衡失调可能参与了 IGA 肾病的免疫学发病机制

PO-1320

LPCAT3 regulates erastin-induced ferroptosis in AML cells via UPR pathway

Qiaoqian Chen、Zhiyuan Zheng、Shuhan Liu、Xindi Lin、Donghong Lin
Fujian Medical University

Objective To analyze the induction effect of erastin on the ferroptosis of AML cells; to study the effect of LPCAT3 and LPCAT3-UPR axis in the induction of ferroptosis of AML cells by erastin.
Methods 1. MTS method was used to detect the proliferation of AML cells, such as Kasumi-1, HL-60, K562/G01, K562 under different concentrations of erastin and different intervention times, and used apoptosis, autophagy, ferroptosis, and other cell deaths inhibitors to validate the mode of cell death. 2. The ferroptosis index was used to observe the morphology of mitochondria by transmission electron microscope, the content of ROS was detected by inverted fluorescence microscope and flow cytometry, and the content of MDA was detected by TBA method. 3. Detect PUFAs by GC-MS and analyze the content of oxidized fatty acids. 4. Lentiviral transfection of K562 cells mediates LPCAT3 overexpression. 5. qPCR, Western blot detection of molecular expression of LPCAT3 and UPR pathway.
Results 1. At an erastin concentration of 10μM/L for 24 hours, the proliferation of Kasumi-1 and HL-60 cells was inhibited and could be reversed by ferroptosis inhibitors, the contents of ROS and MDA increased significantly, mitochondria appeared vacuolization and the double membrane was dense, Lipid droplets and other changes; K562/G01, K562 did not appear the above changes. It is suggested that Kasumi-1 and HL-60 are susceptible strains to ferroptosis at an erastin concentration of 10μM/L for 24h, while K562/G01 and K562 are relatively insensitive strains. 2. The basic expression of LPCAT3 in Kasumi-1 and HL-60 cells was higher than that in K562/G01 and K562 cells. After erastin induction, the expression of LPCAT3 in Kasumi-1 and HL-60 cells increased, and the expression of K562/G01 and K562 cells did not change significantly. It is suggested that LPCAT3 is related to the ferroptosis of AML cells induced by erastin. 3. Up-regulation of LPCAT3 in K562 cells induced by erastin can inhibit their proliferation and increase the content of PUFAs, ROS and MDA, showing that K562 cells are relatively insensitive to erastin have ferroptosis. 4. Up-regulation of LPCAT3 in erastin-induced K562 cells can up-regulate the expression of UPR branch PERK-eIF2α-ATF4 protein and cause ferroptosis, and further intervention with UPR branch inhibitors, and inhibition of cell proliferation, reduction of ROS and MDA content, etc. The result of ferroptosis.

Conclusion 1. AML cells can be induced to ferroptosis by erastin, and different AML cell lines have different sensitivity to erastin-induced ferroptosis. 2. LPCAT3 may induce AML cell ferroptosis through UPR branch PERK-eIF2α-ATF4 regulation, cell oxidation sensitive fatty acid and lipid peroxidation regulation of erastin.

PO-1321

The coagulation analysis of reveals novel biomarkers for neonatal hyperbilirubinemia in full term newborn

Fangye Zhou、Li Liu、Rong Fu
Fujian Medical University Teaching Hospital, First Hospital of Putian,

Background The coagulation test is used to diagnose the hematological diseases. Little is known about correlation between the coagulation test and neonatal hyperbilirubinemia. The aim of the study was to determine the neonatal coagulation analysis value in infants with neonatal hyperbilirubinemia as reliable markers. .
Methods All newborns were born and inpatients in the newborn wards of the Chengdu Second People's Hospital. Measurement of serum bilirubin was done to diagnose hyperbilirubinemia. All neonates involved were full term of either gender without any significant illness or major congenital malformations. Data were collected from newborns who had neonatal hyperbilirubinemia and healthy in Chengdu Second People's Hospital. Prothrombin time(PT), Thrombin time(TT), Fibrinogen(Fbg), activated partial thromboplastin time(APTT), and calculated international normalized ration(INR) values were recorded. Linear relationship between INR and level of total bilirubin and indirect bilirubin were analyzed by linear regression. Comparisons of two groups were made by GraphPad Prism 8.
Results In this case-control study, the mean PT, APTT level were significant higher in the infants with hyperbilirubinemia group compared to the healthy infants. We found the correlation between INR and total bilirubin(R=0.3327; P<0.0001). There was also correlation between INR and indirect bilirubin(R=0.3402; P<0.0001).
Conclusions PT, APTT were significant high in neonatal hyperbilirubinemia group. Correlation were observed between the coagulation test and neonatal hyperbilirubinemia. Importantly, the study revealed coagulation test as novel biomarkers for diagnosis of neonatal hyperbilirubinemia in full term newborn.

PO-1322

血栓分子标志物在弥漫大 B 细胞淋巴瘤中的检测及临床意义

江秀娟、张正华、黄金晶、苏海翔
甘肃省肿瘤医院

目的 探讨血栓分子标志物在弥漫大 B 细胞淋巴瘤(Diffuse large B-cell lymphomaDLBCL)中的检测及临床意义。
方法 选择 2019 年 8 月至 2020 年 10 月间在我院住院的弥漫大 B 细胞淋巴瘤患者 60 例为淋巴瘤组，其中初治组 23 例，缓解组 24 例，未缓解组 13 例；选择同期健康体检者 46 例作为对照组。采用化学免疫分析法检测各组血浆中血栓调节蛋白(TM)、纤溶酶-α2 纤溶酶抑制剂复合物(PIC)、组织型纤溶酶原激活剂-抑制剂 1 复合物(t-PAIC)和凝血酶-抗凝血酶Ⅲ复合物(TAT)水平，全自动生化分析仪检测淋巴瘤组血清中乳酸脱氢酶（LDH）水平。比较各组血栓分子标志物之间差异和淋巴瘤患者并发血栓的可能及预后以及与 LDH 相关性。
结果 淋巴瘤患者血浆 TM、PIC 水平明显高于健康对照组（ P ＜0.05）；初治和治疗后未缓解组 TM、PIC 水平均明显高于缓解组（ P ＜0.05）；初治组与未缓解组间 TM、PIC、t-PAIC、TAT 各

指标均无显著差异（ P＞ 0.05）；淋巴瘤并发血栓组 TM、PIC、TAT 水平均明显高于未并发血栓组（ P ＜0.05）。血浆 TM、PIC 水平与淋巴瘤患者 LDH 预后指标有相关性（ P ＜0.01）。
结论 淋巴瘤患者血浆 TM、PIC 水平明显升高，有望作为弥漫大 B 细胞淋巴瘤疗效及预后判断指标。

PO-1323

血栓弹力图检测在评估肝癌患者凝血状态中的临床价值

闫彬、胡天喜、杜伟鹏
南阳市中心医院

目的 探讨血栓弹力图（TEG）在评估肝癌患者凝血状态中的应用价值。
方法 回顾性分析 2017 年 8 月至 2020 年 9 月在河南省南阳市中心医院肝胆外科就诊的 102 例肝癌患者和 48 例肝血管瘤患者。收集患者的 TEG 检测指标（R 值、K 值、Angle 值、MA 值、CI 值和 G 值）、常规凝血指标（PLT、PT、INR、APTT、FIB、TT）以及肝癌患者的基本临床资料。分析肝癌组和肝血管瘤组不同检测参数之间的差异性；分析 TEG 参数在不同肝癌患者亚组中的差异性，并采用 Spearman 秩相关分析肝癌患者 TEG 与常规凝血检测之间的相关性，并比较两种检测方法在判断肝癌患者凝血状态时敏感性的优劣。
结果（1）与肝血管瘤患者相比，肝癌患者 PLT 显著降低，而 PT 值、INR 值和 APTT 值则显著升高（*P*<0.001）；肝癌患者的 MA 值和 G 值则低于肝血管瘤患者（*P*<0.05）；（2）与初诊肝癌患者相比，复诊肝癌患者的 PLT 显著降低，R 值和 K 值显著升高，而 Angle 值、MA 值、CI 值和 G 值则显著降低（*P*<0.05）；（3）除 R 值外，TEG 其它参数在肝切除、经肝动脉栓塞化疗术和保守治疗之间的差异具有显著性（*P*<0.05）；（4）肝癌患者的 TEG 参数与其常规凝血指标之间具有一定的相关性（*P*<0.05）；（5）血栓弹力图检测对低凝状态的检出率为 18.63%（19/102），常规凝血指标对低凝状态的检出率为 7.84%（8/102），检出率之间的差异有统计学意义（*P*=0.001）。
结论 与初诊相比，复诊肝癌患者处于相对低凝状态。利用 TEG 能够更灵敏地诊断出肝癌患者凝血状态的变化，及时采取措施有利于降低出血风险。

PO-1324

LINC01255 combined with BMI1 to regulate human mesenchymal stromal senescence and acute myeloid leukemia cell proliferation through repressing transcription of MCP-1

qinghua Liu、Jing Dong、Jie Li、yanchao Duan、keqiang Wang、qiuhong Kong、hong Zhang
The Second Affiliated Hospital of Shandong First Medical University

Background Long non-coding RNAs (lncRNAs) govern fundamental biochemical and cellular biology processes, for exam_x0002_ple, participate in chromatin remodeling, imprinting, splicing, transcriptional regulation and translation. Dysregulation of lncRNA expression is act as a feature of various diseases and cancers, including hematopoietic malignancies. However, the clinical relevance of myelodysplastic syndrome (MDS) and acute myeloid leukemia preceded by MDS (MDS-AML) requires further research. Recently, lncRNAs have been demonstrated, which play an important role in hematopoiesis, thus, to further fnding more functional lncRNA seemed particularly important.

Methods Western blotting, real-time PCR, RNA-pulldown, RIP (RNA immunoprecipitation), Chromatin immunoprecipi_x0002_tation (ChIP), cellular compartments extraction assays, SA-β-gal staining, lentivirus transfection, cell viability assay and cell proliferation assays were used to examine the relationship between lncRNA LINC01255 and its regulation of p53–p21 pathway in human mesenchymal stromal and acute myeloid leukemia cells.
Results LncRNA LINC01255 is highly expressed in bone marrow cells of AML patients, CD34+ cells of MDS-AML patients and AML cell lines and the higher expression of LINC01255 is associated with poor survival rate of AML patients. LINC01255 can interact with BMI1 and repress the transcription of MCP-1 to active p53–p21 pathway, thus inhibiting the senescence of human mesenchymal stromal and proliferation of acute myeloid leukemia cell.
Conclusions We discovered a novel functional lncRNA LINC01255, which can regulate the senescence of human mesen_x0002_chymal stromal and the proliferation of acute myeloid leukemia cell through inhibiting the transcription of MCP-1.

PO-1325

Dysregulation of LINC00324 associated with methylation facilitates leukemogenesis in de novo acute myeloid leukemia

Guokang Sun[1]、dongming yao[2]、qiurong he[1]、jing zhang[1]
1. West China School of Public Health and China Fourth Hospital
2. 镇江市第一人民医院

Background LINC00324, long intergenic non-coding RNA 324, was found to be overexpressed and facilitated carcinogenesis in various solid malignant tumors such as gastric cancer, ovarian cancer, and lung cancer. However, the role of LINC00324 in leukemogenesis remains to be elucidated.
Methods In this study, bone marrow samples and corresponding clinical data were collected from 106 adult patients with de novo AML. The relative expression levels of LINC00324 was detected by real-time quantitative PCR (RT-qPCR) technology. The real-time quantitative methylation-specific PCR (RQ-MSP) technology was used to detect the promoter unmethylation levels of LINC00324 in bone marrow samples from healthy donors and AML patients. Cell proliferation was used to detect the proliferation of leukemia cell lines after overexpression of LINC00324. Flow Cytometer (FCM) was used to detect the change of apoptosis in leukemia cell lines after overexpression of LINC00324.
Results In de novo AML patients, lower LINC00324 expression was associated with significantly increased hemoglobin (Hb) and lower platelets (PLT). Moreover, Kaplan-Meier analysis suggested that patients with lower LINC00324 expression showed more prolonged overall survival (OS). Importantly, our experimental data showed that LINC00324 was significantly hypomethylated in whole-AML and non-APL patients. Furthermore, the paired sample experiment also showed that the low expression group's promoter region had lower unmethylation levels. Notably, overexpression of LINC00324 in leukemia cell lines promoted the proliferation of target cells and inhibited their apoptosis.
Conclusion Our findings firstly identified that the hypomethylation of LINC00324 was a common molecular event in de novo AML patients. Moreover, higher LINC00324 expression was associated with its promoter methylation and suggested an unfavorable prognosis in AML. Finally, the abnormally up-regulated LINC00324 promotes proliferation and inhibits apoptosis in leukemia cells.

PO-1326

妊娠期 D-二聚体、凝血系列、白细胞及血小板动态变化及临床意义

路静
山东省千佛山医院

目的 探讨妊娠期 D-二聚体、凝血系列、白细胞及血小板的动态变化及临床意义。
方法 选取 2014 年 10 月至 2015 年 5 月期间，在我院妇产科门诊就诊的 288 例健康妊娠期女性患者（按妊娠周期分为：早期妊娠组 116 例，中期妊娠组 85 例，晚期妊娠组 87 例；按妊娠年龄分为：≤30 岁组 166 例，>30 岁组 122 例），选取同期年龄相匹配、健康查体非妊娠女性 50 例作为对照组，观察不同妊娠期 D-二聚体水平（D-dimer，D-D）、凝血酶原时间（prothrombin time，PT）、活化部分凝血酶时间（activated partial thromboplastin time ，APTT）、纤维蛋白原含量（fibrinogen FIB）、白细胞（white blood cell ，WBC）及血小板（platelet，PLT）的变化。
结果 妊娠组与正常对照组比较，PT、APTT 时间缩短，PLT 降低，FIB、D-D 和 WBC 增高，差异有统计学意义（P<0.05），中期妊娠和早期妊娠比较，FIB、D-D 和 PLT 明显增加，差异有统计学意义（P<0.05），PT、APTT、WBC 无明显差异（P>0.05）。晚期妊娠和中期妊娠比较，PT 时间进一步降低，FIB、D-D 增加，差异有统计学意义（P<0.05），APTT 、WBC、 PLT 无明显差异（P<0.05）。晚期妊娠和早期妊娠比较，PT、APTT、PLT 明显减少，FIB、D-D 明显增加，差异有统计学意义，WBC 无明显差异。妊娠年龄≤30 岁和>30 岁女性的 D-D、PT、APTT、FIB 水平比较，差异无统计学意义（P>0.05）。
结论 妊娠期女性的 D-D、PT、APTT、FIB 与正常女性比较有显著性差异，且随着妊娠期的进展，FIB、D- D 在体内含量逐渐增加，而 PT、APTT 逐渐降低；但升高或降低程度均与年龄无关。

PO-1327

一个复合杂合变异导致的遗传性凝血因子Ⅹ缺陷症家系分析

蒋淑婷、王明山
温州医科大学附属第一医院

目的 对一个遗传性凝血因子Ⅹ（FⅩ）缺陷症家系进行表型和基因型检测，寻找致病基因并探讨其可能的分子致病机制。
方法 检测先证者及其家系成员血浆凝血酶原时间(PT)、活化部分凝血活酶时间（APTT）、纤维蛋白原（FIB）、FⅩ活性（FⅩ:C）和 FⅩ抗原（FⅩ:Ag）等指标来明确表型诊断。用 PCR 法对先证者 F10 基因所有外显子及侧翼序列进行扩增，PCR 产物经纯化后进行直接测序；对发现的疑似变异用反向测序予以验证，并对家系其他成员相同变异位点进行检测。通过凝血酶生成试验来评估先证者及其家系成员 FⅩ的促凝活性。运用 ClustalX-2.1-win 软件分析变异的保守性；用 PolyPhen-2、SIFT 和 Mutation Taster 三个在线生物信息学软件预测变异对蛋白质功能的影响；用 Swiss-PDB Viewer 软件对变异前后的蛋白进行模型分析。
结果 先证者 PT 和 APTT 明显延长，分别为 21.8s 和 57.1s；FⅩ:C 和 FⅩ:Ag 分别降低至 7%和 14%；其母亲、二姐、儿子和女儿 FⅩ:C 和 FⅩ:Ag 均下降为正常对照的 50%左右；先证者及家系成员其他相关凝血指标均在正常范围内。基因分析发现先证者 F10 基因第 4 外显子存在 c.361T>C 杂合错义变异及第 8 外显子存在 c.979C>T 杂合错义变异。先证者凝血酶生成潜力比值和峰高比值明显下降，而其延迟时间和达峰时间明显延长。保守性分析显示，p.Cys121 和 p.Arg327 位点在同源物种间均高度保守。生物信息学软件预示两种变异均为有害变异。变异蛋白模型分析显示，

p.Arg327Trp 变异后，Trp327 与 Glu306 之间产生分子碰撞力，原 Arg327 与 Tyr271 之间的氢键消失，导致蛋白质空间结构发生改变。
结论 该家系 F10 基因第 4 外显子 p.Cys121Arg 杂合错义变异和第 8 外显子 p.Arg327Trp 杂合错义变异与该家系 F X 水平减低有关。

PO-1328

云南省 4720 例新生儿溶血病检测情况分析研究

杨雯、陆艳红、李雪然、李玉芳、魏彩霞
昆明金域医学检验所有限公司

目的 探讨 2018 年 1 月至 2020 年 11 月云南省十四个地州市医院送昆明金域医学检验所有限公司共计 4720 例新生儿溶血病（Neonatal hemolytic disease，HDN）标本的发病情况。
方法 送检的 4720 例新生儿溶血标本进行 ABO 和 Rh 血型鉴定（采用玻片凝集法）及新生儿溶血病三项检测（含直抗抗人球蛋白试验、游离抗体试验和释放抗体试验，均采用微柱凝胶法检测），检测结果从性别结构、血型类型、发病率、出生天数阳性率和地区分布等因素进行统计分析。
结果 4720 例中男婴占比 52.4%，女婴占比 47.6%，出生性别比为 110.15:100，A 型血占比 39.3%，B 型血占比 31.4%，AB 型血占比 25.8%，O 型血占比 26.7%，Rh（D）阳性 99.7%，Rh（D）阴性 0.3%。ABO 系统引起的溶血发病率 22.38%远大于 RhD 溶血的发病率 0.43%，母婴血型为 O-A 型阳性率 67.96%大于 O-B 性阳性 31.91%，出生三天内检查阳性率最高达 26.46%，出生 7 天后检出阳性率明显降低仅 2.31%。滇中（辖昆明、玉溪、楚雄和曲靖）阳性率 12.36%，滇西（辖大理、保山和德宏）阳性率 23.00%，滇东南（辖红河和文山）阳性率 17.59%，滇东北（辖昭通）阳性率 32.70%，滇西南（辖普洱、版纳和临沧）阳性率 20.39%，滇西北（辖丽江、迪庆和怒江）没有阳性（送检标本例数仅 2 例）。
结论 使用微柱凝胶法可以微量准确的检出直接抗人球蛋抗体、游离抗体和释放抗体，HDN 检出阳性率三天内最高，母婴血型为 O-A 型阳性率占比高，HDN 尽早送检，做到早发现、早预防、早确诊、早治疗，避免核黄疸的发生危及患儿的生命健康。

PO-1329

全光谱流式细胞术检测 B 淋巴细胞白血病微小残留病单管 16 色组合方案的建立与验证

陈南[1,2]、兰山卉[1]、张静文[1,2]、潘建华[1,2]
1. 广州金域医学检验中心
2. 广州医科大学金域检验学院

目的 建立全光谱流式细胞术检测 B 淋巴细胞白血病微小残留病的单管检测方案。
方法 利用全光谱流式细胞仪，设计单管 16 色 17CD 组合方案检测 B 淋巴细胞白血病微小残留病，并对组合方案荧光染料组合可行性、抗体滴定等验证；同时收集传统流式 8 色组合方案检测的 B 淋巴细胞白血病微小残留病样本，应用单管 16 色组合方案进行全光谱流式细胞术检测，比对两种检测方案的结果，分析其可行性与优劣势。
结果（1）建立了一套基于本实验室的用于全光谱流式细胞仪检测 B 淋巴细胞白血病微小残留病的单管 16 色 17CD 组合方案的设计，其 16 色荧光染料组合的复杂性指数为 6.6。（2）对该组合方案的 17 个 CD 分子分别进行抗体滴定试验，根据染色指数分析，优化了基于该组合方案的最适合的抗体终浓度。（3）与传统流式 8 色组合方案检测结果相比，全光谱流式单管 16 色组合方案检测结果基本一致，表达异常的 CD 分子的比例无显著差异（4）同等条件下，全光谱流式收集的可分

析细胞数量多于传统流式，使用的标本量更少，而且一次性可对 17 个 CD 分子标记进行检测，覆盖较全面，对于微小残留病的检测敏感性更好。与传统流式细胞仪相比，光谱分析不用调整荧光补偿，对多色的分析更便捷。
结论 全光谱流式不用调整荧光补偿、检测灵敏性更好，本项目建立的单管 16 色组合方案可用于 B 淋巴细胞白血病微小残留病的检测。

PO-1330

3134 例早孕女性生殖道微生态检测结果分析

韦小妮
柳州市妇幼保健院

目的 了解本地区早孕女性生殖道微生态的状况，为本地区早孕女性生殖道感染性疾病的早期保健治疗提供科学依据。
方法 选取 2018 年 6 月至 2019 年 9 月在柳州市妇幼保健院就诊的 3134 例早孕女性为研究对象，对其生殖道分泌物进行生殖道微生态检测，检测项目包括盐水湿片显微镜检查、干片革兰染色检查菌群和病原微生物，评估其 Nugent 和 AV 评分，并依据相关标准进行全面微生态评价。
结果 生殖道微生态平衡者 1526 例，占比 48.7%；生殖道微生态失衡者 1608 例，占比 51.3%，其中 CCV 和 BV 感染率较高，分别为 403 例（25.1%）和 395 例（ 24.6%），混合感染者 85 例（5.3%），TV 感染者为 18 例（1.1%），不同年龄阶段早孕女性生殖道微生态失衡总体上无差异。
结论 早孕女性生殖道微生态失衡发生率较高，生殖道感染以 CCV 和 BV 最常见，应提高孕早期妇女的生殖道健康意识及加强其生殖道感染性疾病的早期保健治疗。

PO-1331

高效液相色谱串联质谱测定总睾酮及游离睾酮指数在多囊卵巢综合征诊断中价值

徐苏娟、曾玉、陈亚军
南京市妇幼保健院

目的 通过比较高效液相色谱串联质谱（LC-MS/MS）与化学发光法（CLIA）对多囊卵巢综合征（PCOS）患者及健康对照女性血清总睾酮的定量检测，探究高效液相色谱串联质谱与化学发光法诊断 PCOS 临床意义以期寻找更好的 PCOS 诊断指标。
方法 收集 PCOS 患者 114 例、正常对照 100 例，比较 PCOS 患者和正常对照 LC-MS/MS 和 CLIA 测定的血清总睾酮以及游离睾酮指数诊断效价。
结果 CLIA 方法显示 PCOS 组和对照组在年龄（$p<0.001$）、黄体激素（$p<0.001$）、胰岛素（$p=0.002$）、雌二醇（$p<0.001$）、总睾酮（$p<0.001$）、游离睾酮指数（$p=0.021$）、硫酸脱氢表雄酮（$p=0.021$）、胰岛素抵抗指数（$p=0.034$）以及空腹葡萄糖之间（$p=0.017$）均有差异，其中总睾酮诊断效价较好，曲线下面积为 0.766。我们进一步通过 LC-MS/MS 检测两组甾体类激素，结果显示雄烯二酮（$p<0.001$）、睾酮（$p<0.001$）以及 17-羟孕酮（$p<0.001$）具有显著差异。进一步通过 ROC 曲线显示三者诊断效能分别是 0.830、0.851 以及 0.714。Bland-Altman 法结果显示 LC-MS/MS 和 CLIA 检测的总睾酮一致性较差，因此，LC-MS/MS 检测更准确，且检测的总睾酮有最高的诊断效能。我们进一步分析了 LC-MS/MS 检测结果对于胰岛素抵抗诊断价值，结果显示游离睾酮指数具有最高的诊断价值，ROC 曲线显示三者诊断效能分别是 0.798。
结论 LC-MS/MS 法测定血清总睾酮以及游离睾酮指数较 CLIA 灵敏性高、准确度好。总睾酮对女性 PCOS 的诊断效能高，而游离睾酮对胰岛素抵抗诊断价值更高。

PO-1332

Effect of MT2A on apoptosis and proliferation in HL60 cells

Yuqing Pan、Yan Du
The First Affiliated Hospital of Kunming Medical University

Although accumulating evidence has revealed that metallothioneins (MTs) and its family member MT2A are strongly linked to the risk of various solid tumors, researches on the occurrence and development of acute myeloid leukemia (AML) have rarely been investigated. Here, we constructed a lentiviral vector with MT2A over-expression and the interfering plasmids with MT2A expression inhibition to study the influence of MT2A on the bioactivities of HL60 cells. After cells were infected with a lentiviral vector containing the MT2A gene, both transcription and translation levels of MT2A were significantly increased in the over-expressed group in comparison with control groups. In vitro experiments, all results demonstrated that cell reproductive capacity was inhibited, but cell apoptosis rate was significantly increased. Together, the expression of apoptosis-related protein Bcl2 was remarkably reduced, while a high expression level of Bax protein was detected. Further experiments revealed that up-regulation of MT2A induced cell apoptosis and promoted G2/M phase arrest. The mechanism may be associated with down-regulated p-IκB-α and cyclinD1 expression and up-regulated IκB-α expression in the nuclear factor-kappaB (NF-κB) pathway. On the contrary, MT2A expression was down-regulated by interfering plasmids. We found that cell proliferative potential was notably increased in the interfering group compared with the negative and untreated group. What's more, MT2A may be closely related to AML cell proliferation and function via the NF-κB signal pathway.

PO-1333

脑脊液实验室检测在原发性中枢神经系统淋巴瘤诊断中的价值探讨

赵晖、李虓、宋蓓、赵运转、刘扬、关春燕、张国军
首都医科大学附属北京天坛医院

目的 探讨原发性中枢神经系统淋巴瘤（PCNSL）患者脑脊液的实验室检测指标在 PCNSL 诊断及鉴别诊断中的价值。

方法 回顾性研究。2017 年 12 月至 2020 年 1 月在北京天坛医院诊断 PCNSL 的 46 例患者作为研究对象，选取同期就诊的中枢神经系统脱髓鞘疾病 44 例、中枢神经系统感染性疾病 37 例作为对照组。回顾性分析和比较 3 组患者的脑脊液细胞学、脑脊液有核细胞数、脑脊液糖、蛋白、氯及脑脊液细胞因子 TNF-α、IL-6、IL-8、IL-10、IL-10/IL-6 各指标表达水平，采用 F 检验或秩和检验分析组间水平差异，对有统计学意义的指标运用受试者工作曲线（ROC）评价指标的诊断价值。

结果 46 例 PCNSL 患者中有 15 例在脑脊液中发现淋巴瘤细胞（32.6%）；淋巴瘤组脑脊液蛋白［53.11(37.20,82.8) g/L］及脑脊液 TNF-α［9.1（6.20，12.55）pg/ml］明显高于脱髓鞘组［脑脊液蛋白：35.09(25.71,56.33) g/L；脑脊液 TNF-α：4.91（4.00，7.64）pg/ml］，诊断 PCNSL 的 ROC 曲线下面积分别为 0.630 和 0.631（P<0.05）；PCNSL 组脑脊液 IL-10 和 IL-10/IL-6 高于脱髓鞘组和脑膜炎组，诊断 PCNSL 的 ROC 曲线下面积分别为 0.729 和 0.735（P<0.05）；当 IL-10 的 cut-off 值选择 8.47 时，敏感度为 48.9%，特异度为 95.6%，但 IL-10/IL-6 的 cut-off 值选择 1.38 时，敏感度为 73.3%，特异度为 64.8%。

结论 脑脊液中发现淋巴瘤细胞是 PCNSL 的诊断的直接依据，脑脊液细胞因子 IL-10 及 IL-10/IL-6 对 PCNSL 有较高的诊断价值。

PO-1334

网织红细胞血红蛋白含量对缺铁性贫血诊断的临床价值

闫欣、周伟、孙沐新、安培莹
吉林大学第一医院

缺铁性贫血 (Iron-deficiency anemia, IDA) 为临床最常见的贫血疾病之一, 主要是指机体内贮存铁无法满足正常红细胞生成需要而引发的贫血。诊断步骤较为复杂，骨髓涂片检查是该病的金标准，但骨髓检查是有创性的、费时、操作技术要求较高且花费高，而其他用于诊断缺铁性贫血的生物学指标，例如：血清铁、血清铁蛋白、总铁结合力、可溶性转铁蛋白受体等，通常受炎症、慢性疾病和年龄影响。网织红细胞血红蛋白含量(CHr) 与上述这些指标相比，实用性较好，CHr 更能反映体内实时的 Hb 合成情况，且受炎症的影响较小，是治疗反应的早期预测因子。CHr 在诊断铁缺乏方面具有中等敏感性和特异性，CHr 是铁可用性的良好监测指标，也是缺铁红细胞的早期标记，还可用于铁治疗的监测。通过文献查阅，本文主要探讨 CHr 在缺铁性贫血临床研究中的应用价值。

PO-1335

Circulating Monosaccharide Composite-based Glycan Biomarker Diagnoses of early Hepatocellular carcinoma in patients with hepatitis B virus

Minghui Hu
Affiliated Hospital of Qingdao University

Background Hepatocellular carcinoma (HCC) is one of the most common malignancies in the world. As chronic hepatitis B (CHB) can progress to cirrhosis and HCC, predicting HCC development in high-risk patients with high viral replicative activity or advanced fibrosis is important. Detection of early HCC is critically important for treatment of these patients. Since developing glycan structure-based biomarkers is still ongoing worldwide after continuous effort for several decades, we decided to take the simpler circulatingglycan monosaccharide composite-based biomarker approach for HCC early detection.
Methods The blood samples of age- and gender-matched patients with CHB (n=82), cirrhosis (n=80), HCC in patients with hepatitis B virus (80) and healthy controls (n=82) were collected. The monosaccharide compositions of both free and hydrolyzed glycans were quantified by using an established HPLC method.Receiver operating characteristic (ROC) and logistic regression were used to assess the reliability of the biomarker. The K fold cross validation was applied to test the coefficients of the biomarker for HCC.
Results The circulating monosaccharides especially the mannose from hydrolyzed glycans and the free glucose to free mannose (G/M) ratio not only distinguished the HCC patients from healthy controls, but also distinguished the patients of patients with CHB, cirrhosis and HCC. Logistic regression analysis revealed that monosaccharide composite had better AUC (0.87) and accuracy (87.88%) for detecting HCC patients than the mannose or the G/M ratio alone. Moreover, the monosaccharide composite, the G/M ratio, or even mannose alone was better for HCC early detection than AFP.
Conclusions The monosaccharide composite was a novel circulating biomarker for HCC early detection and systems malfunction-information compounded in monosaccharide composite explained its molecular basis. Thus, systems malfunction-based biomarkers should be pursued for early diagnosis of HCC or other cancers in future.

PO-1336

炎症相关细胞因子与 Ph 阴性骨髓增殖性肿瘤的相关性研究

陈朴、马艳婷、程韵枫、潘柏申、郭玮、王蓓丽
复旦大学附属中山医院

目的 探讨经典型骨髓增殖性肿瘤（myeloproliferative neoplasms，MPN）患者血清中炎症相关细胞因子及部分急性时相反应蛋白水平及其临床意义。
方法 105 例 Ph（-）MPN 患者为 MPN 组，20 例体检健康者为对照组，2 组采用化学发光法及免疫透射比浊法检测造血及炎症相关细胞因子：促红细胞生成素（erythropoietin，EPO）、肿瘤坏死因子-α（tumor necrosis factor-α，TNF-α）、白介素（Interleukin，IL）-1β、IL-2 受体（IL-2R）、IL-6、IL-8、IL-10 及两种急性时相反应蛋白：高敏 C 反应蛋白（hypersensitive C-reactive protein，hs-CRP）和铁蛋白，分析 Ph（-）MPN 发病及疾病转化过程中细胞因子及 hs-CRP、铁蛋白的变化规律。
结果 MPN 患者血清 TNF-α、IL-2R、IL-6、IL-8、hs-CRP 和铁蛋白水平均显著高于对照组（P<0.001），IL-10 水平则显著低于对照组（P<0.001）。PMF 组 IL-2R 水平显著高于 PV 组和 ET 组（P<0.01），PV 组 EPO 水平低于其余各组（P<0.05）；网状纤维增生程度为Ⅲ级的 MPN 患者 IL-2R 水平高于Ⅱ级组（P<0.05），TNF-α 水平高于未增生组（P<0.05）。
结论 炎症相关细胞因子及 hs-CRP、铁蛋白在 MPN 患者中表达异常，且在三种疾病亚型中的表达水平也存在差异。相比既往的骨髓细胞学及病理活检等随访手段，细胞因子检测具有无创、便捷及经济的优点，有望成为 MPN 诊断分型及疾病进展随访的有效辅助指标，甚至在可能成为潜在的治疗及疗效监测的靶点。

PO-1337

初发骨髓瘤患者骨髓涂片与活检浆细胞数量的相关性研究

朱建锋、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 本研究用于评估初发骨髓瘤患者骨髓涂片和活检对计数浆细胞数量的相关性研究。
方法 我们回顾分析了 205 例骨髓瘤患者的骨髓涂片与骨髓活检中浆细胞数量，采用 fit curve 方法得到拟合曲线方程，并比较两者的相关性，探讨使用任意一种方法来预测浆细胞数量，以降低或避免临床漏诊。
结果 骨髓涂片与骨髓活检检查骨髓瘤患者的浆细胞数量的非线性曲线方程为 y=11.75x0.38（R2=0.163）。骨髓涂片浆细胞数量≦10%时，骨髓活检浆细胞数量≦10%的仅占 27.8%（5/18），而活检浆细胞>10%的占 72.2%（13/18）；骨髓涂片浆细胞数量>60%时，活检浆细胞数量≦10%占比为 0（0/20），而活检浆细胞>10%的占 100%（20/20），即涂片与活检浆细胞数量均大于 60%。对于浆细胞数量不高的患者，骨髓涂片与活检的结果一致性欠佳；浆细胞数量较高的患者，骨髓涂片与活检具有很高的一致性。
结论 实验结果显示对于初发骨髓瘤患者，需重视同时行骨髓涂片与活检检查的必要性，以避免将骨髓涂片作为评判浆细胞数量的标准判断，而忽视活检的重要性。反之亦然，武断地采用任何一种方法的浆细胞数量（10%）进行诊断是不可取的，引起不必要的漏诊。同时对未行骨髓涂片或活检的患者，可采用我们实验模拟的非线性曲线方程对任一方法浆细胞数进行合理估判，来评估预后疗效，如复查时的骨髓涂片与初诊时活检浆细胞量，两者可采用拟合曲线进行结果比对，从而判断患者骨髓浆细胞变化情况，对疾病进展进行判断。

PO-1338

一种基于流式细胞术原理的低值血小板检测方法建立与验证

朱捷、方佩琪、王蓓丽、郭玮
复旦大学附属中山医院

目的 利用流式平台建立一种检测低值血小板的方法并进行验证。
方法 在流式平台上使用绝对计数管检测不同浓度的低值血小板，并分析其在各个不同浓度下的检测精密度和准确度。同时用所得结果与人工镜检法进行比较。另外在实际实验操作中进行验证，通过检测巨核细胞培养体系内的血小板浓度，分析其与体系内巨核细胞数量的相关性。
结果 流式检测法检测低值血小板的的准确度和精密度均优于人工镜检法，其精密度的 CV 和准确度的偏倚值在检测同浓度血小板时均小于人工镜检法。在检测实际巨核细胞体外培养体系中的血小板浓度结果后发现，巨核细胞产生的血小板数量与巨核细胞数量呈显著正相关。
结论 基于流式细胞术原理检测低值血小板的方法，其精密度和准确度可满足实际实验需求，方法可行。

PO-1339

Rosner 指数在血浆纠正试验中的应用

罗磊、陈朴、朱建锋、王蓓丽、郭玮
复旦大学附属中山医院

目的 评估 Rosner 指数（Rosner index）在血浆纠正试验中的应用。
方法 收集 103 例血浆纠正试验标本，比较使用回归正常参考区间或 Rosner 指数结果<11%或 Rosner 指数结果<15%作为判断依据的结果。
结果 103 例血浆纠正试验结果，使用回归正常参考区间作为判断标准时，得出凝血因子缺乏 74 例、肝素或抗磷脂抗体存在 26 例、凝血因子抑制物存在 3 例。使用 Rosner 指数结果<11%作为判断标准时，得出凝血因子缺乏 75 例、肝素或抗磷脂抗体存在 25 例、凝血因子抑制物存在 3 例。使用 Rosner 指数结果<15%作为判断标准时，得出凝血因子缺乏 83 例、肝素或抗磷脂抗体存在 19 例、凝血因子抑制物存在 1 例。
结论 当 APTT 结果轻度延长或显著延长时，分别使用 Rosner 指数<11%或回归参考范围，作为血浆纠正试验的判断依据参考价值更大，能更好的为临床提供诊断思路。

PO-1340

18 例骨髓坏死临床特征及实验室结果分析

陈楠、朱建锋、陈朴、朱娜、王蓓丽、郭玮
复旦大学附属中山医院

目的 分析骨髓坏死的临床特征及实验室结果，加强对该类疾病的认识。
方法 本研究回顾了 2007 年 1 月至 2021 年 1 月于我院行骨髓涂片检查患者 29065 例，其中骨髓坏死患者 18 例，对 18 例骨髓坏死患者临床特征及相关实验室结果进行收集分析。
结果 18 例患者中男性占 61%，女性占 39%。年龄分布为 25~74 岁，中位年龄 54 岁。原发病为恶性肿瘤的患者占 83%，非恶性肿瘤患者占 17%。恶性肿瘤患者中实体肿瘤患者占 53%，其中胃肠道肿瘤患者 4 例，肝恶性肿瘤患者 1 例，肺部肿瘤患者 1 例，腹部结缔组织肿瘤患者 1 例，乳腺肿瘤患者 1 例；血液系统疾病患者占 40%，其中急性早幼粒细胞白血病患者 1 例，急性淋巴细胞白血病患者 1 例，B 细胞淋巴母细胞淋巴瘤/白血病患者 1 例，弥漫大 B 细胞淋巴瘤患者 1 例，慢性

淋巴细胞白血病/小淋巴细胞淋巴瘤患者 1 例，多发性骨髓瘤患者 1 例；另 1 例患者未确认肿瘤来源。非恶性肿瘤患者中消化道出血患者 1 例，心功能不全患者 1 例，不明原因的全血细胞减少患者 1 例。临床症状多种多样，其中最常见的为发热、骨痛、腰背酸痛。实验室结果中外周血涂片均能见到幼粒或者幼红细胞，贫血、血小板减低、白细胞减低及 LDH、ALP、纤维蛋白原、DD-二聚体、C 反应蛋白、血沉、ALT、AST、铁蛋白升高较常见。除外 3 例患者未行骨髓活检检查，其余患者中骨髓坏死程度分级 III 级 40%，II 级 13%，I 级无，无坏死 47%。骨髓纤维化程度 3 级 0%，2 级 20%，1 级 33%，0 级 27%。

结论 骨髓坏死较为少见，多继发于恶性肿瘤，死亡率高、预后较差，骨髓涂片细胞学检查是骨髓坏死诊断的重要方法之一，联合多种实验室检查加强对该类疾病的认识，减少漏诊、误诊的发生，做到早发现、早诊断、早治疗，以望改善预后，提高生存率。

PO-1341

高嗜酸粒细胞综合征的临床及实验室特征研究

张岚、朱建锋、陈朴、郭玮、王蓓丽
复旦大学附属中山医院

目的 高嗜酸粒细胞综合征（HES）是一组少见的异质性疾病。通过对我院 2014 至 2020 年间收治的 63 例 HES 患者的临床资料进行总结分析，了解各亚型的临床及实验室特点，尤其是骨髓及外周血中嗜酸粒细胞的形态学异常。

方法 回顾分析 63 例 HES 患者的临床和实验室资料，复阅外周血和骨髓涂片中嗜酸粒细胞的形态学特征。

结果 以男性多见（男：女=50：13），中位年龄 49（18-85）岁，按照病因分为反应性组 54 例，特发性组 9 例。反应性组的病因众多，主要继发于肿瘤（嗜酸粒细胞为非克隆性）、血管炎、感染性疾病及药物等。两组患者的临床表现均以皮肤受累最为常见，脾肿大及骨髓纤维化发生率接近。特发性组患者的外周血基线嗜酸粒细胞比例高于反应性组（P<0.05）。33%特发性组患者（3/9）外周血可出现幼稚阶段嗜酸粒细胞，而反应性组全部未见（P=0.000）。骨髓涂片中特发性组的嗜酸粒细胞更易出现形态学异常，其中以颗粒稀疏、胞浆嗜碱性颗粒及核分叶过多这三种异常特征的发生率高于反应性组（P<0.05）。

结论 特发性和反应性 HES 的临床及实验室特征相互重叠，但通过骨髓涂片中嗜酸粒细胞的异常形态学特征，能够为两组 HES 的鉴别诊断提供一定帮助。

PO-1342

Prognostic value of circulating tumor cells in patients with bladder cancer: A meta-analysis

Hui Jiang、Xiujuan Gu、Zhihua Zuo、Gang Tian、Jinbo Liu
The Affiliated Hospital of Southwest Medical University

Objective Circulating tumor cells (CTCs) have been considered as a diagnostic and prognostic biomarker for urothelial cancer. However, the prognostic role of CTCs in bladder cancer (BC) remains controversial. Here, we conducted a meta-analysis to evaluate the prognostic significance of CTCs for patients with BC.

Methods All studies relevant to this topic were searched in PubMed, Embase, and Web of Science databases. Hazard ratio (HR) and 95% confidence interval (95% CI) were set as effect measures. The outcomes were overall survival (OS), cancer-free survival (CSS), progression-free survival (PFS)/time to progression (TTP), and disease-free survival (DFS)/recurrence-free survival (RFS)/time to first recurrence (TFR). All analyses were conducted in STATA 15.1.

Results Eleven eligible studies comprising 1,062 patients with BC were included in this meta-analysis. Overall analyses showed that CTC-positive patients had poorer survival (OS: HR 3.88, 95% CI 2.52–5.96, p < 0.001; CSS: HR 3.89, 95% CI 2.15–7.04, p < 0.001) and more aggressive progression (PFS/TTP: HR 5.92, 95% CI 3.75–9.35, p < 0.001; DFS/RFS/TFR: HR 4.57, 95% CI 3.34–6.25, p < 0.001) than CTC-negative patients. Subgroup analyses according to number of patients, detection method, positive rate, and follow-up time revealed that the presence of CTCs predicted high risk of mortality and disease progression in most subgroups.
Conclusion The meta-analysis confirmed that CTCs are a promising prognostic biomarker of poor survival and aggressive tumor progression for patients with BC.
Prospero registration number: CRD42021224865.

PO-1343

APOBEC3B and SPAG5, the Target Genes of miR-539, Involved into Imatinib-Resistant of Gastrointestinal Stromal Tumors

Hongxing Wang
Qilu Hospital, Shandong University

Background Although imatinib can effectively treat gastrointestinal stromal tumor (GIST), some patients are still resistant to it or cannot tolerate the adverse reactions of the drug. This study aimed to investigate potential miRNAs, mRNA and tumor-infiltrating lymphocytes (TILs) associated with the prognosis of imatinib-resistant GIST.
Methods mRNA, miRNA sequencing data and patient clinic traits of primary (imatinib-naive) and imatinib-resistant GIST were obtained from GEO (Gene Expression Omnibus) database. A systems biology approach combining Weighted co-expression network analysis (WGCNA) and differential expression analysis were utilized to detect the imatinib-resistant-related miRNA and gene modules and construct a miRNA-gene network. Tumor-infiltrating immune cells were analyzed by Estimating the Proportion of Immune and Cancer cells (EPIC) and Tumor-Immune System Interactions (TISIDB). miR-539 was measured by qRT-PCR. SPAG5 and APOBEC3B was measured by qRT-PCR and WB. Transforming growth factor (TGF)-β and interleukin (IL)-10 were assessed with enzyme-linked immunosorbent assay (ELISA). The proportions of CD4+ T cells, CD8+ T cells , NK cells and B cells in tumor-infiltrating lymphocyteswere analyzed via flow cytometry (FCM).
Results Two gene modules (brown and yellow) and one miRNA module were associated with the imatinib-resistant. Two hub genes (APOBEC3B and SPAG5) were associated with the imatinib-resistant. Three hub miRNAs were identified to be related to imatinib-resistant (miR-539, miR-376b and miR-18b). G1/S transition of mitotic cell cycle, G2/M transition of mitotic cell cycle, and cell proliferation were common pathways of the gene modules and miRNA module. apolipoprotein B mRNA editing catalytic polypeptide-like 3B (APOBEC3B) and Sperm-associated antigen 5 (SPAG5), which were both target genes of miR-539 was located at the core of miRNA–gene network. APOBEC3B (rho=0.509, p < 2.2e-16) and SPAG5 (rho=0.468, p < 2.2e-16) was positive correlated with the infiltration levels of activated CD4+ T cells. he proportions of CD4+ T cells, and the mRNA and protein relative expression of APOBEC3B and SPAG5 in imatinib-resistant tumor samples significantly increased as compared with tumor samples in imatinib-naive group. Imatinib-resistant tumor samples exhibited significantly downregulation of miR-539 and TGF-β1. Over-expression of miR-539 sensitized imatinib resistant GIST48 cells and increased the secretion of TGF-β1 by inhibiting APOBEC3B and SPAG5.
Conclusion APOBEC3B and SPAG5, the target genes of miR-539 may play as key factor for imatinib-resistant GIST by increasing the proportion of tumor-infiltrated activated CD4+ T cells via TGF-β1. These findings help to advance the understanding of imatinib-resistant GIST and provide potential therapeutic targets.

PO-1344

新型自动粪便分析仪 FA280 检测性能评价

龙婷婷、邓山鹰、江虹
四川大学华西医院

目的 评价自动粪便处理分析系统 FA280 的性能指标，以保障其检测结果的准确性。
方法 对 FA280 进行本底测试，并对重复性、携带污染等性能以及便隐血试剂检测限等进行评价。同时对比 FA280 与 FA160 检测结果或与手工检测隐血结果的一致性。
结果 测试 FA280 的本底白细胞（WBC）、红细胞（RBC）、真菌孢子、脓细胞、虫卵和隐血结果均为阴性。重复 WBC、RBC、真菌孢子和隐血检测在第 2-11 次结果与第 1 次的结果完全一致。携带污染试验中，已知的 10 份阳性标本检测结果 WBC、RBC 及真菌孢子均为阳性，交叉其中的空白样本检测结果均为阴性。隐血试剂卡检测血红蛋白（Hb）浓度低于 0.05ug/ml 时结果为阴性，浓度为 0.1ug/ml 时结果为弱阳性，当 Hb 在 0.2-2000ug/ml 时隐血为阳性。FA280 与 FA160 仪器结果比对，所测 10 份标本 WBC、RBC、真菌孢子、脂肪滴和隐血试验结果全部一致，卡式便隐血试剂与艾博隐血试剂手工检测结果符合率达 96.2%。
结论 FA280 空白测试合格，重复性良好，携带污染试验符合要求。卡式便隐血试剂的检测限为 0.1ug/ml-2000ug/ml。且 FA280 检测结果与 FA160 结果及手工隐血试验比对均合格。仪器性能良好，用于临床检测结果准确。

PO-1345

富氧空位 WO3-x QDs 增强电化学发光的乳腺癌循环肿瘤细胞检测新方法研究

潘登
青岛大学附属医院

目的 近年来，乳腺癌成为威胁女性健康安全的一大重要因素，远处转移是乳腺癌的主要致死原因，循环肿瘤细胞检测在乳腺癌转移及预后判断方面发挥着重要作用，因此探索循环肿瘤细胞的高灵敏检测方法在癌症转移筛查中非常重要，本研究以期通过构建超灵敏检测 CTCs 电化学发光传感方法实现提高乳腺癌转移筛查水平。
方法 本研究提出以二硫化钨粉末为前驱物，通过超声剥离和温和的化学转化过程成功合成了富氧空位氧化钨量子点，利用 WO3-x QDs 高效地增强三联吡啶钌电化学发光的性质来提高乳腺癌循环肿瘤细胞的检测灵敏度，随后合成负载 WO3-x QDs 的磁性 ECL 探针用于高效富集循环肿瘤细胞以便进一步实现检测信号放大作用，本研究以 MUC1 蛋白作为选择性识别肿瘤血清中 CTCs 的标志物，修饰其适体在磁性 ECL 探针上对 CTCs 进行分离和富集，利用 EpCAM 抗体将循环肿瘤细胞固定在电极表面，通过调控电化学发光探针的功能化设计、界面组装及其与特异性 MUC1 适体间相互作用等实现电化学发光探针性能和结构的优化，筛选综合性能最佳组合方案构建用于超灵敏检测乳腺癌循环肿瘤细胞的电化学发光传感器。
结果 1、富氧空位 WO3-x QDs 被用于 ECL 共反应剂可提高 Ru(bpy)32+的 ECL 强度近 400 倍；2、基于富氧空位 WO3-x QDs/Ru(bpy)32+新发光体系的 ECL 效率可与传统 TPrA 标杆体系相媲美，但动物毒性比 TPrA 低约 300 倍；3、结合富氧空位 WO3-x QDs 增强电化学发光以及磁性探针高效富集双重信号放大机制的循环肿瘤细胞检测新方法，其检测限可达到 3 cell/mL。
结论 本研究所构建的电化学发光传感器可实现循环肿瘤细胞的高灵敏分析，为乳腺癌转移提供一种有效的筛查工具，以及其他癌症转移筛查和预后判断提供新方法和新思路。

PO-1346

Plasma SNORD42B and SNORD111 as potential biomarkers for early diagnosis of non-small cell lung cancer

Kangyu Wang、Xingguo Song、Li Xie、Xianrang Song
Shandong Cancer Hospital and Institute, Shandong First Medical University and Shandong Academy of Medical Sciences

Background Despite decades of efforts, non-small-cell lung cancer (NSCLC) remains the leading cause of cancer mortality globally primarily due to the challenge in early detection of the cancer. The aim of this study is to access the efficacy and reliability of plasma snoRNAs in early diagnosis of NSCLC.
Materials and Methods Differential snoRNAs of LUAD and LUSC were analyzed using the SNORic and TCGA databases, then SNORD42B and SNORD111 were selected and further verified in 48 FFPE NSCLC and adjacent normal tissues, as well as in plasma from 165 NSCLC patients and 118 health donors. Then, the diagnostic efficiency of plasma SNORD42B and SNORD111, as well as combined with CEA was determined by receiver operating characteristic (ROC) analysis.
Results SNORD42B and SNORD111 were significantly increased not only in tissues but also in plasma from NSCLC as well as from early-stage NSCLC compared to those from healthy donors. In addition, we validated plasma SNORD42B and SNORD111 were capable to act as promising diagnostic biomarkers for NSCLC and early-stage NSCLC. Moreover, the diagnostic efficiency of CEA was significantly evaluated for early-stage NSCLC when combined with the two plasma snoRNAs.
Conclusion SNORD42B and SNORD111 are significantly upregulated in NSCLC patients, and can serve as the promising and non-invasive diagnostic biomarkers for NSCLC and early-stage NSCLC.

PO-1347

tRNA 衍生片段 tRFs: tRF-Gly-CCC-046,tRF-Tyr-GTA-010 和 tRF-Pro-TGG-001 作为乳腺癌新型诊断生物标志物

张悦[1]、毕钊[1]、董晓菡[1]、于淼[2]、王康羽[1]、宋兴国[1]、谢丽[1]、宋现让[1]
1. 山东省肿瘤医院
2. 山东省立第三医院

目的 近年来，乳腺癌的发病率越来越高，一些晚期发生转移的乳腺癌患者预后仍然很差，因此，需要找到更有效的生物标志物，以达到乳腺癌的早期诊断,早期治疗和改善预后的目的。tRNA 衍生片段(tRFs)已被发现在多种肿瘤的发生和发展中发挥调节作用。本研究的目的是鉴定 tRFs 在乳腺癌中的表达情况及其作为乳腺癌诊断标志物的能力。
方法 本研究纳入了在 2017 年 9 月至 2019 年 9 月，于山东省肿瘤医院接受手术的 83 例患者的癌与癌旁组织，以及另外的 214 例乳腺癌患者与 113 例健康人的血清进行 tRFs 表达水平分析。组织与血清样本的总 RNA 分别用 Trizol 或 Trizol LS 试剂提取，然后采用 q-PCR 的方法检测 tRFs 在癌症组与对照组的相对表达量。通过 ROC 曲线分析，阐明三个 tRFs 作为乳腺癌诊断标志物的能力。
结果 与健康人相比，乳腺癌患者的组织和血清中 tRFs: tRF-Gly-CCC-046, tRF-Tyr-GTA-010 and tRF-Pro-TGG-001 均下调。更重要的是，这三个 tRFs 可以作为乳腺癌诊断和早期诊断的循环生物标志物，曲线下面积(AUC)分别为 0.7871 和 0.7987。
结论 tRFs: tRF-Gly-CCC-046, tRF-Tyr-GTA-010 and tRF-Pro-TGG-001 在乳腺癌中显著下调，可作为乳腺癌诊断和早期诊断的新型生物标志物。

PO-1348

Basophils in the cerebrospinal fluid from a case of central nervous system leukemia

Hongmei Ding
The First Affiliated Hospital of Nanjing Medical University

A 34-year-old man presented with headache, decreased vision, tinnitus, and weakness in both lower extremities. He was diagnosed with chronic myeloid leukemia in 2013 and progressed to acute basophilic leukemia in 2015. Since February 2016 to August 2019, he was diagnosed in the complete remission period (CR) with 0.0% BCR-ABL1 gene detected after a series of treatments including dasatinib.

In this case, an uncommon acute basophilic leukemia in the central nervous system was presented. A large number of basophils were seen in CSF but no obvious abnormalities in the peripheral blood and bone marrow.

This is a very rare case in which CML transforms into acute basophilic leukemia, which then further invades the central nervous system. The patient's first symptoms were blurred vision and ocular congestion for two months. They are essential clinical information that require vigilance for patient with CML in remission. Lumbar MRI and CSF laboratory examinations are very important for the diagnosis of this case of central system leukemia.

PO-1349

Usefulness of Mean Platelet Volume for Differential Diagnosis of Biliary and non-Biliary Acute pancreatitis

Fengfeng Zhao
Department of Clinical Laboratory of Zhongda Hospital, Southeast University

Objective To explore whether the mean platelet volume (MPV) can be used as a reference index for the differential diagnosis of bile-derived acute pancreatitis from non-bile-derived acute pancreatitis.

Method From August 2016 to May 2017, 132 inpatients with acute pancreatitis were diagnosed as acute pancreatitis in the Hospital affiliated to Southeast University, including 62 cases of biliogenic pancreatitis and 70 cases of non-biliogenic pancreatitis. The MPV values of blood routine were analyzed and compared.

Results There was significant difference in MPV between the two groups ($P < 0.05$). The working characteristic curve (ROC) of the subjects showed that the area under the MPV curve was 0.773 (95% CI:0.793-0.895) for distinguishing bile pancreatitis from non-bile pancreatitis. When the cut-off value of MPV was 8.41, the sensitivity and specificity of differential diagnosis of bile pancreatitis were 80.4% and 71.6%, respectively.

Conclusion MPV can be used as a simple and practical reference index to distinguish bile from non-bile acute pancreatitis.

PO-1350

嵌合抗原受体修饰的 T 细胞疗法（CAR-T）后血凝系统的活化

沈文红[1,2,3,5]、沙萍萍[1,2,3,5]、周志英[1,4]、崔庆亚[1,2,3,5]、张威[1,2,3,5]、白霞[1,2,3,5]
1. 苏州大学附属第一医院
2. 江苏省血液研究所
3. 国家血液系统疾病临床医学研究中心
4. 江苏省苏州市高新区（虎丘区）疾病预防控制中心
5. 卫生部血栓与止血重点实验室

目的 嵌合抗原受体修饰的 T 细胞疗法（chimeric antigen receptor T cell therapy， CAR-T 疗法）在血液系统恶性疾病治疗取得令人鼓舞的疗效，CAR-T 活化伴随着细胞因子释放综合征(CRS)，会引起血凝异常，并可能出现威胁生命的弥漫性血管内凝血（DIC）。目前常规开展的凝血系统检测仅能发现已存在血凝异常，对凝血异常前，血栓前状态、Pre-DIC 等的状态不敏感，不易发现凝血系统，纤溶系统，血管内皮功能早期发生的改变。
方法 我们分析 39 例血液系统恶性疾病 CAR-T 后发生 0-1 级 CRS，2-3 级 CRS，11 例急性白血病和 21 例血液系统恶性疾病合并 DIC 患者血栓分子标志物（TAT、PIC、TM、tPAI-C）和血凝指标发生的变化。
结果 39 例血液系统恶性疾病分别为 ALL20 例，AML15 例，MM4 例。CAR-T 的靶标有 CD19，CD19-CD22 双靶，CD38 和 BCMA。我们发现 0-1 级 CRS，2-3 级 CRS 的凝血指标（APTT，PT，TT）较治疗前没有差异。我们也发现发生 2-3 级 CRS 患者 FDP 和 D-dimer 明显升高，除此之外还发现 0-1 级 CRS，2-3 级 CRS 的患者 PIC 明显升高。CAR-T 治疗后合并 CRS 的 TAT 也有一定程度升高，但较治疗前升高并不明显。TM 和 tPAI-C 作为内皮细胞损伤的标志物，我们发生 2-3 级 CRS 的患者内皮损伤更加明显。
结论 我们发现 CAR-T 治疗后机体内凝血、纤溶、内皮系统明显活化，而内皮系统损害更加明显，常规的凝血指标并不能很好的反应 CAR-T 治疗后机体内出血和止血的状态，血栓分子标志物结合血凝指标判断 CAR-T 治疗后凝血和止血状态，可能为临床 CAR-T 后凝血异常的治疗提供更为真实可靠的依据，仍需较大样本的临床实验进一步证实以上结论。

PO-1351

Prediction of lymph node metastasis in oral tongue squamous-cell carcinoma using the neutrophil-to-lymphocyte ratio and platelet-to-neutrophil ratio

Bo Wang[3]、JunWen Liu[2]、Zhengrong Zhong[1]
1. Department of Clinical Laboratory, Shanghai Ninth People's Hospital, Shanghai JiaoTong University School of Medicine
2. Department of Clinical Laboratorial, The Children's Hospital of Fudan University
3. Department of Clinical Laboratory, Shanghai Ninth People's Hospital, Shanghai JiaoTong University School of Medicine

Background Lymph node metastasis in a variety of tumors is associated with systemic inflammatory markers. However, this association has not been reported in oral tongue squamous-cell carcinoma (OTSCC). This study aimed to investigate how the preoperative neutrophil-to-lymphocyte ratio (NLR) and platelet-to-neutrophil ratio (PNR) in OTSCC patients correlated with the occurrence of OTSCC and lymph node metastasis.
Methods The data of 73 patients with primary OTSCC who underwent surgical resection were retrospectively analyzed. Patients with other malignant tumors, patients who had received radiotherapy or chemotherapy before surgery, and patients with active inflammation were excluded. The enrolled patients were divided into groups N0 (no early-stage lymph node

metastasis) and N1 (early-stage lymph node metastasis). Venous blood samples were collected before surgery and at the third week after surgery and subjected to complete blood counting in a blood analyzer. Eighty-seven healthy people were included as a control group. In addition, the NLR and PNR in OTSCC patients were compared with those in the controls, and the postoperative NLR and PNR of group N0 were compared with those of group N1.
Results The NLR was significantly higher in the OTSCC patients than the controls ($P < 0.05$). The area under the receiver operating characteristic curve was 0.595. Further comparison of the NLR and PLR between group N0 and group N1 showed that when NLR was ≤ 1.622, the probability of early-stage lymph node metastasis in OTSCC patients was 73.3%, and when PNR was > 60.889, the probability was 86.7%. In re-examination 3 weeks postoperatively, the NLR and PNR were not significantly different between groups.
Conclusion The NLR has certain reference value for the diagnosis of OTSCC. The preoperative NLR and PNR can be used to predict early-stage lymph node metastasis in patients with histopathologically confirmed OTSCC.

PO-1352

去甲基化药物治疗骨髓增生异常综合征的最新进展

张婧玲
福建医科大学附属协和医院

近年来随着表观遗传学的深入研究，发现 DNA 甲基化在恶性血液肿瘤的发生、发展中起着重要的作用，并为治疗提供了新的靶点。表观遗传学异常尤其是 DNA 甲基化改变是骨髓增生异常综合征发病机制的研究重点，去甲基化药物作为一线治疗方案之一，已在临床取得了一定疗效。目前被批准用于 MDS 临床治疗的去甲基化药物主要有阿扎胞苷和地西他滨。通过对 MDS 患者中克隆细胞内 DNA 甲基化和去甲基化的研究，从而对去甲基化药物的机制有更深入的了解，为临床治疗提供更多的治疗策略。

PO-1353

Efficacy and Safety of Iron Chelator for Transfusion-Dependent Patients with Myelodysplastic Syndrome: A Meta-Analysis

张婧玲、曹颖平
福建医科大学附属协和医院

To systematically evaluate the efficacy and safety of iron chelators for transfusion-dependent patients with MDS. Thirteen cohort studies with 12,990 patients diagnosed with MDS were included in this study. Meta-analysis results showed that in transfusion-dependent MDS patients with secondary iron overload, OS was longer and LFS was longer in MDS patients receiving iron chelators than in MDS patients not receiving iron chelators and in patients with lower-risk MDS in a further subgroup analysis. Subgroup analysis of DFX showed that compared with patients not treated with iron chelator, the group receiving DFX monotherapy had significantly improved OS. In terms of tolerance, meta-analysis of the binary variables in CAEs showed that the occurrence of CAEs was significantly reduced by ICT.

PO-1354

对流式白血病免疫分型样本处理中最适离心力的探讨

董敏
四川省医学科学院·四川省人民医院

目的 找寻流式细胞前处理过程中最适合的离心力和洗涤次数，以保证在流式细胞分析过程中人为造成的异常细胞的选择性丢失最少。
方法 选取诊断正常标本和异常的标本各 10 例，加入 100ul 至流式管中；在流式管中加入 5ml 红细胞溶解剂（一般为 NH4CL），溶血 5min 并计时；溶血时间到后以 250g 的转速离心 5min，后弃去上清液；后加入与之前溶血剂等体积的 PBS（磷酸盐缓冲液）重悬沉淀，混合均匀，以 250g 的转速再次离心 5min 后弃去上清液，收集两次离心后的上清液。配制混合抗体：CD16-FITC，CD3-PE，CD14-ECD，CD19-PC5.5，CD45-PC7，CD33-APC，每种抗体 3ul，共 18ul。加入配好的混合抗体于重悬沉淀管和两次混合上清管中，避光孵育 15min，后上机检测。重新拿一支干净试管，重复上述步骤，只离心一次，收集上清，加入混合抗体孵育 15min，后上机检测。以上为一种离心力一次完整的检测方案。设置不同的离心力梯度：400g、550g、700g、850g，依次重复上述检测步骤，分别记录流式细胞仪收集细胞的速度和图形。
结果 离心次数为一次或者两次，离心力分别为 250g、400g、550g、700g、850g，上清液和重悬沉淀液的细胞的数目和类别是有差异的，且这种差异具有统计学意义（$p<0.05$）。
结论 不同的离心力和不同的离心次数对不同标本影响的差异是有统计学意义的。经统计学和流式细胞学分析，我们认为离心力为 550g，时间为 5min 且离心两次时，异常细胞的丢失（从数目和类别角度）是最少的，对于最终疾病结果判断的影响基本可以忽略不计。

PO-1355

Single and combined used of preoperative inflammatory biomarkers and CA199 in diagnosing pancreatic cancer

Yu Lu[1,2]、Hongli Yu[2]、Shanzi Qin[1]、Mingxing Chen[1]、Huaping Chen[1]、Zuojian Hu[1]、Shan Li[1]、Xue Qin[1]
1. Department of Clinical Laboratory, First Affiliated Hospital of Guangxi Medical University, Nanning 530021, Guangxi, China
2. Department of Clinical Laboratory, Liuzhou People's Hospital, Liuzhou 545006, Guangxi, China

Objective Pancreatic cancer (PCC) poses a significant diagnostic challenge due to the non-specific symptoms of the disease and the close proximity of major blood vessels, which can be easily invaded by the tumor. To improve its accuracy, combinations of CA199 with other indicators have been widely studied. However, the potential diagnostic value of inflammation-related biomarkers combined with CA199 in the diagnosis of PCC remains unclear. The present study was therefore carried out to determine the diagnostic value of preoperative inflammatory biomarkers and CA199, alone or in combination, in diagnosing pancreatic cancer (PCC).
Methods This retrospective study was comprised of 75 PCC patients and 83 healthy controls (HC). The participant's medical data was mined from the electronic records of the First Affiliated Hospital of Guangxi Medical University. The data included the preoperative circulating albumin/fibrinogen ratio (AFR), the platelet/lymphocyte ratio (PLR), the lymphocyte/monocyte ratio (LMR), the neutrophil/lymphocyte ratio (NLR), and the derived NLR (dNLR). The receiver operating characteristic (ROC) curve and the area under the ROC curve (AUROC) were used to evaluate the diagnostic efficacy of these candidate biomarkers for PCC.
Results A single AFR significantly distinguished PCC from the healthy controls (AUROC: 0.903, 95% CI: 0.846–0.945) and had a significantly higher sensitivity and larger AUROC than CA199 (AUROC: 0.814, 95% CI: 0.774–0.871). The combinations of AFR with CA199 (AUROC: 0.932, 95% CI: 0.881–0.966), RDW with CA199 (AUROC: 0.905, 95% CI: 0.849–0.946), Alb with

CA199 (AUROC: 0.869, 95% CI: 0.806–0.917), and Fib with CA199 (AUROC: 0.921, 95% CI: 0.868–0.958) also yielded higher sensitivities and larger AUROCs than CA199 alone.
Conclusions The present study is the first to comprehensively evaluate the diagnostic value of circulating inflammatory biomarkers alone and combined with CA199. Our results suggest that circulating AFR was an effective biomarker in distinguishing PCC patients from HCs, and combining AFR, RDW, Alb, and Fib with CA199 could significantly improve the diagnostic efficacy for PCC. However, as a retrospective single-center cohort with relatively small sample sizes, larger-scale and multi-center studies are warranted to confirm our findings.

PO-1356

48 例传染性单核细胞增多症患儿高荧光强度淋巴细胞比分比检测的临床意义

刘娟
吉林大学第一医院

目的 传染性单核细胞增多症患儿高荧光强度淋巴细胞百分比实验检查与临床特征的相关性
传染性单核细胞增多症(infectionmononucleosis,IM)是儿童常见病毒感染性疾病。诊断主要依据典型临床表现和外周血异型淋巴细胞比例增高和 EBV 或 CMV-lgM 抗体检测。尽管传染性单核细胞增多症外周血异型淋巴细胞增高很常见，但也常见于其他病毒感染性疾病，不具有特异性。本研究全自动血液细胞分析仪检测传染性单核细胞增多症患儿高荧光强度淋巴细胞百分比，探讨高荧光强度淋巴细胞百分比对 IMEB 病的诊断价值，同时分析高荧光强度淋巴细胞百分比与 EB 病毒感染程度的相关性，为传染性单核细胞增多症诊断提供快速有用价值。
材料与方法 研究对象：收集 48 例于本院儿科确诊的 IM 患者，其中男 23 例，女 25 例，男女比为 0.92：1。研究方法 ：对 IM 患儿进行血常规检测，检测血液中高荧光强度淋巴细胞百分比，同时进行外周血血细胞形态检查检查异型淋巴百分比，同时检测患儿 EB 和 CMV 病毒感染的核酸载量检测。统汁学处理：通过 SPSS18.0 统计软件，分析高荧光强度淋巴细胞百分比对 IM 的诊断效能，灵敏度和特异度，临界值；分析高荧光强度淋巴细胞百分比与 EB 和 CMV 病毒感染的相关性。
结果 48 位 IM 患儿，47 位患者高荧光高度淋巴细胞百分比明显升高；外周血细胞形态学检查，其中 36 位患者异型淋巴细胞比例大于 10%。相关性分析 IM 患儿高荧光强度淋巴百分比与 EB 病毒感染程度具有一致性。

PO-1357

糖尿病合并高血压患者血小板参数的变化及临床意义

孙婷、李艳
武汉大学人民医院

目的 研究血小板参数在糖尿病（DM）及 DM 合并高血压（HBP）患者中的变化及临床意义。
方法 收集 2018 年 10 月至 2019 年 8 月在武汉大学人民医院确诊为 2 型糖尿病（T2DM）的患者 113 例，将其作为 DM 组；T2DM 合并 HBP 患者 157 例，作为 DM 合并 HBP 组，并按照血压水平将其分为 HBPⅠ、Ⅱ、Ⅲ级三个亚组；检测并分析两组的空腹血糖（FPG）、糖化血红蛋白（HbAlc）、血小板计数（PLT）、血小板压积（PCT）、平均血小板容积（MPV）、血小板分布宽度（PDW）及大血小板比率（P-LCR），以及通过受试者工作特征（ROC）曲线比较 PLT、MPV、PDW、P-LCR、HbAlc 对 DM 合并 HBP 的诊断价值；并探究 DM 合并不同严重程度 HBP 患者以上指标的变化趋势。

结果 DM 合并 HBP 组的 HbAlc、PLT、MPV、PDW、P-LCR 的水平明显高于 DM 组，且差异有统计学意义（P < 0.05）。随着 HBP 严重程度的升高，FPG、MPV、PDW、P-LCR 的水平升高，呈明显的上升趋势。P-LCR 的 ROC 曲线下面积（AUC）为 0.812,大于 PLT(AUC 为 0.618)，MPV(AUC 为 0.805)、PDW(AUC 为 0.799)和 HbAlc（AUC 为 0.578），对 DM 合并 HBP 的诊断价值最大。
结论 血小板参数与 DM 合并 HBP 的发生关系密切，对于诊断评估 DM 合并 HBP 有一定的价值。

PO-1358

多发性骨髓瘤患者血清 TAT、TM、PIC 的变化及临床分析

王贝
东南大学附属中大医院

目的 探讨多发性骨髓瘤患者凝血酶-抗凝血酶复合物(TAT)、血栓调节蛋白(TM)、纤溶酶-α2 纤溶酶抑制剂复合物(PIC)水平变化在临床诊治中的价值。
方法 选择 2019 年 1 月至 2020 年 12 月我院收治的多发性骨髓瘤患者 82 例作为研究对象,设为 A 组;非多发性骨髓瘤患者 120 例,设为 B 组;选取同期体检健康者 86 例设为 C 组。多发性骨髓瘤患者按照诱导治疗危险度再分为低危组(n=31)、中危组(n=30)和高危组(n=21),检测各组受试者的血清 TAT、TM、PIC 水平变化情况,并应用受试者工作特征曲线(ROC 曲线)分析 TAT、TM、PIC 水平预测多发性骨髓瘤 患者早期死亡的诊断效能结果 A 组血清 TAT、TM、PIC 水平均明显高于 B 组组和 C 组(P 均<0.05),高危组患者的血清 TAT、TM、PIC 水平均高于中危组和低危组,差异均有统计学意义(,P 均 <0.05)。化疗后,早期死亡 8 例(9.76%),存活组患者的 TAT、TM、PIC 水平均低于死亡组,差异有统计学意义(P 均<0.05)。ROC 曲线分析显示,三者联合检测的曲线下面积均大于 TAT、TM、PIC 单独预测,可提高预测灵敏度和特异度,差异均有统计学意义(P 均<0.05)。
结论 多发性骨髓瘤患者血清 TAT、TM、PIC 水平异常升高提示患者预后不良,其在临床诊断及预后评估中均有较高价值

PO-1359

我国四川地区儿童患者蓝氏贾第鞭毛虫检出情况分析

胡正强、李节
四川大学华西第二医院

目的 了解我国四川地区儿童患者蓝氏贾第鞭毛虫（贾第虫）检出情况，分析易感人群及感染原因，提出防疫意见及建议。
方法 回顾四川大学华西第二医院 2019 年 9 月 1 日至 2020 年 8 月 31 日儿童患者大便常规检查数据及资料共 11575 例，检查方法均采用生理盐水直接涂片镜检法，可疑病例加做碘液染色。
结果 在 11575 例儿童患者粪便中查见贾第虫包囊或滋养体 4 例，其中 3 例为少数民族患者，1 例为汉族患者，电话追踪汉族患者有少数民族地区生活史。一年内汉族患者标本量为 10645 例，检出率为 0.009%，少数民族患者标本量为 930，检出率占 0.320%。少数民族患者检出率高于汉族患者，两者差异有统计学意义（P<0.05）。
结论 应重视四川地区低感染虫种和低致病性虫种如贾第虫的检出。贾第虫病易反复感染，建议基层医疗卫生单位定期对人群进行普查，发现确诊病例立即采取驱虫措施。相关部门加强人和动物宿主的粪便管理，搞好环境卫生，防止水源污染。建议加强对相关检验人员进行寄生虫专业培训和考核，以提高寄生虫检出率和寄生虫病诊断率。贾第虫病在少数民族患者检出率较高，主要与其个人卫生、生活习惯、饮食习惯等有关，建议加强少数民族地区防疫管理，培养儿童良好的卫生习惯，以减少贾第虫病的传播与流行。

PO-1360

不同尿液标记物检测对评价肾小管功能的临床意义

李帅[1]、马文静[2]、刘红[1]、王昌敏[1]
1. 新疆维吾尔自治区人民医院（新疆维吾尔自治区高血压诊疗研究中心、新疆维吾尔自治区临床皮肤性病研究所、新疆维吾尔自治区普外科微创研究所、新疆维吾尔自治区内分泌糖尿病研究所）
2. 新疆乌鲁木齐市中医医院检验科

目的 通过检测尿胱蛋白酶抑制剂 C（Cystatin C）、尿 α1-微量球蛋白（α1-MG）、尿 N-乙酰-β-D-氨基葡萄糖苷酶（NAG）和尿 β2-微球蛋白（β2-MG）的浓度水平，从而评价患者的肾小管功能。
方法 选择 2019 年 1 月～2020 年 10 月在我院肾病科住院的患者 90 例为观察组，另选健康体检者 50 例为对照组。尿 Cystatin C、α1-MG 和 β2-MG 测定采用酶联免疫法（ELISA）检测，尿 NAG 测定采用对硝基苯酚（PNP）比色法检测。并对检测结果进行比较及统计学分析，以受试者工作特征（ROC）曲线及曲线下面积（AUC）评价各项尿液标记物的敏感性。
结果 观察组尿 Cystatin C、α1-MG、NAG、β2-MG 的测定含量明显高于正常对照组，差异具有统计学意义（P＜0.001），通过 ROC 曲线、诊断试验结果显示：尿 NAG、Cystatin C 的曲线下面积分别为 0.862、0.902，95%可信区间分别为 0.805～0.921、0.895～0.963，较尿 α1-MG 和 β2-MG 更具有敏感性（P＜0.001）。
结论 联合各项尿液标记物检测对评价患者的肾小管功能具有重要的临床意义，可以作为肾小管损伤性疾病的早期诊断、疗效观察和预后判断的有效指标。

PO-1361

宿主免疫反应对华支睾吸虫感染诱发肝胆系统癌变机制的研究进展

张慧、许建成
吉林大学第一医院

目的 肝吸虫病早期一般无临床症状，容易产生误诊和漏诊。而在发现时往往已经有大量成虫寄生或阻塞胆总管出现黄疸，增加了发生胆管癌的可能性。深入了解其导致肝纤维化甚至肝癌的分子机制，有助于提出更有效的防治措施。
方法 综述 2000 年至今关于宿主免疫反应对华支睾吸虫感染诱发肝胆系统癌变机制的研究文献，针对两方面进行归纳总结：1.华支睾吸虫与肝胆病变的关系；2.宿主免疫反应在华支睾吸虫感染过程中诱发癌变的机制。提出宿主免疫反应在华支睾吸虫感染诱发肝胆系统癌变过程中发挥重要作用及具体作用机制。
结果 1.华支睾吸虫与肝胆病变的关系包括：（1）华支睾吸虫生活史及致病机制；（2）华支睾吸虫感染与肝胆系统癌的相关性。2.宿主免疫反应在华支睾吸虫感染过程中诱发癌变的机制包括：（1）细胞：巨噬细胞、树突状细胞、T 细胞；（2）细胞因子：TGF-β、TNF-α、IL；（3）其它：NO、Toll 样受体。
结论 长期的华支睾吸虫感染可诱发宿主发生一系列的病理生理及免疫反应，一方面通过促炎作用发展为慢性炎症，另一方面通过免疫抑制削弱机体抗肿瘤免疫。因此华支睾吸虫长期感染，因破坏宿主的免疫平衡导致肝胆管病变，甚至诱发胆管癌的发生。

PO-1362

地中海贫血继发血色病分析

项伶俐[1]、王 焱[2]、刘军权[1,2]、姬会春[2]
1. 杭州金域医学检验所有限公司
2. 宿迁市第一人民医院

血色病（hemochromatosis，HC）是一种铁代谢障碍性疾病，是指铁过量沉积在肝脏、心脏、胰腺及其他实质器官，对这些器官的功能和结构造成损害的疾病状态，多见于 40 岁以上男性，临床特征表现为：肝硬化，糖尿病，皮肤色素沉着等，可分为原发性和继发性血色病，本文报道的是一例不明原因长期贫血的女性患者查总铁结合力下降，铁饱和度明显增高，铁蛋白大于 1000μg/L，影像学、肝穿刺均提示肝血色病合并肝硬化，进一步查地中海贫血基因及血色病基因，排除原发性血色病，最终诊断为地中海贫血所致的继发性血色病。

PO-1363

D-dimer daily continuous tendency predicts the short-term prognosis for COVID-19 independently: a retrospective study from Northeast China

Yinting Xing、Wei Yang、Yingyu Jin、Chao Wang、Xiuru Guan
The First Affiliated Hospital of Harbin Medical University

BACKGROUND and OBJECTIVE To study whether D-dimer daily continuous tendency could predict the short-term prognosis of COVID-19.
PATIENTS and METHODES According to the short-term prognosis, 81 COVID-19 patients were divided into two groups, one of worse prognosis (Group W) and the other of better prognosis (Group B). The slope of D-dimer linear regression during hospitalization (SLOPE) was calculated as an indicator of D-dimer daily continuous tendency. The SLOPE difference between Group W and Group B was compared. The difference between the discharge results and the 3-month follow-up results was also compared. COX regression analysis was used to analyze the relationship between SLOPE and short-term prognosis of COVID-19.
RESULTS There were 16 patients in Group W and 65 patients in Group B. Group W had more critical proportion ($p<0.0001$), indicating that the symptoms of its patients were more severe during hospitalization. ARDS, the most visible cause of worse prognosis, accounted for up to 68.75%, and many symptoms merged and resulted in worse prognosis. The D-dimer levels of Group W not only were significantly higher ($p<0.0001$), but also showed an increasing trend. In addition, the D-dimer levels at discharge were significantly higher than those at follow-up ($p=0.0261$), and the mean difference was as high as 0.7474. SLOPE significantly correlated with the short-term prognosis of COVID-19 independently (RR: 1.687, 95%CI: 1.345-2.116, $P<0.0001$). The worst prognosis occurred most likely during the first month after COVID-19 diagnosis.
CONCLUSION Our study found that D-dimer daily continuous tendency independently correlates with worse prognosis and can be used as an independent predictor of the short-term prognosis for COVID-19.

PO-1364

471 例慢性淋巴细胞白血病的临床和实验室特征分析

杨莹、凌秋艳、金咏梅、曾婷婷、蒋能刚、廖红艳
四川大学华西医院

目的 本研究旨在探讨慢性淋巴白血病（CLL）的临床表现及主要实验室特征，深入了解不同分期 CLL 患者的实验室指标差异及其对 CLL 预后的指示作用，为临床诊断与治疗提供有效的参考信息。
方法 采用统计学方法对 2010 年 1 月-2015 年 1 月四川大学华西医院共 471 例慢性淋巴细胞白血病病人的临床信息及实验室检查资料包括血细胞计数、骨髓形态及免疫表型等结果进行回顾性分析。
结果 本组患者多发于老年，男性多见，中位年龄 64 岁，男女比例 1.89:1。大部分患者初诊时已有典型临床表现，就诊原因以发现白细胞增高或淋巴比例增高为主，占 47.34%。339 例（71.97%）初诊时 WBC>10×109/L 且淋巴细胞绝对值≥5×109/L。肝脾肿大 8 例（4.26%），发热 16 例（8.51%），乏力心累 8 例（4.26%）。56.21%的患者处于 BinetA-B 期，43.79%的患者处于 BinetC 期。49.42%的患者骨髓增生明显活跃至极度活跃。54.1%患者 β2-MG 升高。33.3%的患者出现 IgM 下降，不同 Binet 分期的 IgM 表达无差异(p>0.05)。外周血单核细胞绝对计数（AMC）与 IgG 存在显著相关性（p<0.05）。LDH 在 BinetA 期与 BinetC 期之间分布存在差异（X2=4.041，p=0.044），BinetC 期 LDH 水平较 BinetA 期高。
结论 本组 CLL 人群临床症状与免疫表型表达情况基本与典型 CLL 表型相符，一定程度上反应了我国 CLL 人群的发病情况。

PO-1365

Variable Ratio of Neutrophil-to-lymphocyte Ratio and C-reactive Protein Predict Prognosis of Acute Ischemic Stroke Treated with t-PA Thrombolysis

Bin Wang
Affiliated Hospital of Xuzhou Medical University
徐州医科大学

Background and purpose The mechanism linking systemic inflammatory changes and prognosis after tissue plasminogen activator (t-PA) thrombolysis for acute ischemic stroke(AIS) is not fully understood. We investigated whether peripheral inflammation after t-PA thrombolytic reperfusion therapy for AIS leads to disruption of the blood-brain barrier（BBB） and cerebral edema（CED） that hinders clinical recovery.
Methods We performed a study to investigate the correlation between systemic inflammatory changes and multiple factors of brain injury after t-PA thrombolysis for AIS in the Affiliated Hospital of Xuzhou Medical University between 2018 and 2020. The main inclusion criteria in brief: adults, with AIS, receiving t-PA thrombolytic reperfusion therapy. Neutrophil to lymphocyte ratio was collected from the patient's most recent health check-up prior to the stroke. In patients with AIS, 24h after t-PA thrombolytic therapy, neutrophil-to-lymphocyte ratio and C-reactive protein (CRP) concentrations were measured in peripheral blood, and the presence and grading of CED were assessed simultaneously by computed tomography. Calculate the variable ratio of neutrophil-to-lymphocyte ratio (variable ratio = (post-stroke ratio - healthy physical examination ratio)/healthy physical examination ratio). Clinical outcomes included early neurological function NIHSS (NIH Stroke Scale) and neurological function status at three months. Ordinal regression models and logistic regression models were obtained with adjusted odds ratios and 95% CI(confidence intervals). Receiver operating characteristics analysis in the training cohort was used to define the optimal cutoff values and validated on an independent dataset.

Results We included a grand total of 613 patients in this research. At 24 h after thrombolysis, CRP concentration were associated with brain injury (CED, adjusted odds ratio 1.53 [1.22–1.81], P<0.05), early neurological deterioration (NIHSS , adjusted odds ratio 1.65 [1.38 –1.84], P<0.05) and 90-d functional status (adjusted odds ratio 2.04 [1.51–2.72], P< 0.01).The variable ratio of neutrophil-to-lymphocyte ratio increased with higher degrees of brain injury(CED, adjusted odds ratio 1.34[1.10–1.69]，P<0.05), early neurological deterioration (NIHSS , adjusted odds ratio 1.35[1.08–1.67]，P<0.05) and 90-d functional status (adjusted odds ratio 1.82[1.31–2.52]，P<0.01). Systemic inflammatory response syndrome was related to CED due to altered white blood cell counts. The variable ratio of neutrophil-to-lymphocyte ratio and CRP concentration are ideal predictors of t-PA thrombolysis for AIS, with an area under the CRP curve of approximately 0.9 and an area under the variable ratio of neutrophil-to-lymphocyte ratio curve of approximately 0.8. The accuracy, sensitivity, and specificity of the variable ratio of neutrophil-to-lymphocyte ratio and CRP concentration ≥7 assay were around 60%.
Conclusions Increased early systemic inflammatory response after t-PA thrombolytic reperfusion therapy in patients with AIS is associated with the severity of brain injury. The variable ratio of neutrophil-to-lymphocyte ratio and CRP concentration in peripheral blood compared with patients before stroke can be used as valid markers of prognosis in AIS treated with t-PA thrombolysis-reperfusion.

PO-1366

UF-5000 全自动尿沉渣分析仪在快速筛查尿路感染中的应用

邓山鹰
四川大学华西医院

目的 利用 UF5000 全自动尿沉渣分析仪中细菌分型提示、细菌计数（BACT）及白细胞计数（WBC）检测结果，与尿细菌培养结果进行比较分析，探讨其在尿路感染快速筛查中的应用价值。
方法 收集 2019 年 7 至 2020 年 2 月怀疑尿路感染的门诊及住院病人的清洁中段尿共 2332 份，将标本分为两份，一份用于尿细菌培养，另一份用 UF-5000 进行定量分析，并对两种方法结果进行比较。同时应用受试者工作特征曲线（ROC 曲线）评价 UF-5000 的 BACT、WBC 计数的诊断效能并确定 Cut off 值。
结果 2332 例样本中病原学培养阳性标本 1092 例（46.8%），其中细菌培养阳性 916 例，真菌培养阳性 176 例。 在 2156 例非真菌感染样本中，尿细菌培养阳性率为 42.5%。UF-5000 细菌筛查分型提示阳性率为 39.7%，假阳性率为 5.2%，假阴性率为 13.5%，阳性预测值为 86.9%，阴性预测值为 90.5%；总符合率为 91.3%，其中革兰氏阴性菌符合率为 83.8 %，革兰氏阳性菌符合率为 72.5%。与尿培养阴性样本相比较，各尿培养阳性组 BACT 计数、WBC 计数均明显升高（P<0.001）。且在各类尿培养阳性病例中，不同水平菌落数分组其 BACT 计数均有明显差异（P<0.001），菌落数较多者 BACT 计数较高。UF-5000 的 WBC 与 BACT 计数相关性较弱（相关系数=0.134，P<0.01），且在不同水平尿培养阳性病例中，WBC 计数未见明显差异。ROC 曲线分析结果表明，UF-5000 的 WBC 计数、BACT 计数与各类尿细菌培养结果均具有相关性（P<0.001），其中 BACT 计数与革兰氏阴性菌培养结果的相关性最高（AUC 为 0.970），且 BACT 计数的诊断效能高于 WBC 计数。
结论 UF-5000 的 WBC、BACT 计数及分型提示可用于 UTI 快速筛查，且 BACT 计数诊断效能高于 WBC 计数。

PO-1367

血清 S100 蛋白在肺炎支原体感染合并脑炎患儿治疗中的意义

刘雅奇[1]、杨冰[2]
1. 郑州安图生物工程股份有限公司
2. 郑州大学附属儿童医院

目的 通过动态监测中枢神经系统特异性蛋白（S100 蛋白）在血清中含量的变化情况，为儿童肺炎支原体（MP）感染合并脑炎患儿的诊治和疗效监测提供辅助判断依据。
方法 选择 2019 年 10 月至 2020 年 4 月在郑州大学附属儿童医院收治的 229 例年龄在 5-8 岁之间的 MP 感染合并脑炎患儿进行血清 S100 蛋白动态监测，分析临床诊治效果与 S100 蛋白水平变化的关系。
结果 1、血清 S100 蛋白阴阳性与患儿中枢神经系统损伤的总符合率 87%，阴性符合率 85%，阳性符合率 95%；2、有 44 例患儿血清 S100 蛋白含量在 3-4 d 出现不同程度升高，多数患儿在 5d 后首发中枢神经系统损伤症状；介入脑炎方案治疗后 S100 蛋白含量的变化与患儿的治愈时间相关，治愈时间越短，血清 S100 蛋白含量降低至正常水平也越快，反之，治愈时间越长，血清 S100 蛋白含量下降速度越慢，最终下降至正常水平所需时间也就越长。
结论 血清 S100 蛋白的检测可以对 MP 感染合并脑炎患儿的提前判断提供依据，从而提前介入治疗以降低风险、提高预后质量，同时可以通过动态监测 S100 蛋白的含量变化对治疗方案的疗效提供辅助判断。

PO-1368

PLT-F 在低值血小板计数中的意义

毛志刚
四川大学华西医院

目的 探讨血小板荧光法（PLT-F）通道在低值血小板计数中的准确性与可行性。
方法 利用 Sysmex-XN 全自动血细胞分析仪分别经阻抗法、光学法、荧光法测定 100 例低值血小板标本，并将流式细胞仪方法作为参考方法，利用直线相关回归分析数据。
结果 低值血小板检测重复性 PLT-I 通道 CV 值为 5.5%—14.9%，PLT-O 通道 CV 值为 7.4—13.3，PLT-F 通道 CV 值为 1.9—11.1。以流式细胞仪计数为参考方法，PLT-I、PLT-O、PLT-F 通道相关系数（r）分别为 0.913、0.946、0.947，相关性均良好。其中低值血小板组（≤20×109/L）中，PLT-I、PLT-O、PLT-F 测定结果与参考标准 PLT-FCM 的相关系数（r）依次为 0.879、0.893、0.928。
结论 PLT-F 通道在低值血小板计数中准确性好，临床应用价值高。

PO-1369

早产儿凝血试验参考范围的研究与分析

赵树龙
徐州医科大学附属医院

目的 对于本院妊娠期小于 37 周早产儿 24 小时内凝血功能参考范围进行比较分析，同时对于已知参考范围适应性进行评价。

方法 回顾性分析 2017 年 9 月到 2017 年 12 月份之间的一个本院新生儿病 ICU 房内 108 例妊娠期＜37 周出生的早产儿 24h 内凝血功能的结果。分别计算均值与中位数，并与已知实验室凝血功能参考范围进行比较分析。
结果 108 例早产儿中有 2 例因 TT.APTT 结果过高无法测出而不进行分析。106 例早产儿中 PT、APTT、TT、FIB 的均值分别为 15.93、93.17、22.15、1.23。中位数分别为 15.25（15.30,15.20）、92.45（92.40,92.50）、21.3（21.3,21.3）、1.085（1.080,1.090）。
结论 早产儿凝血功能 PT、APTT、TT、FIB 与现已知的实验室参考标准相比较存在一定的差异性，PT、APTT、TT 存在明显的延长，FIB 明显降低。因此建立针对早产儿的凝血功能指标，对于知道临床早儿的治疗具有指导意义。

PO-1370

Prediction of morbidity in patients with acute pancreatitis: a retrospective study

Si Chen、Chaonan Liu、Jing Zhou
West China Hospital, Sichuan University

Background Acute pancreatitis (AP) is a common acute abdominal disease complicated by high incidence of severe complications. Mathematical models to predict them may help improve outcomes of AP.
Methods We retrospectively reviewed medical records of 1,297 patients with AP between January 2011 and March 2015. Records of 1,062 patients were used to derive models to predict morbidity as acute kidney injury (AKI), respiratory failure (RF) and infection, which were verified using records of the remaining 235 patients .
Results In the entire cohort, 66 patients suffered AKI, 131 suffered RF, and 152 experienced infection. After multivariable registration, higher level of glucose was an independent risk factor for all of the observed complications; endotracheal intubation and higher level of creatine were risks for AKI, calcium antagonists, higher urea and leukocyte levels, lower platelet number, as well as altered mental status were risks RF, and elder, higher urea and leukocyte levels, altered mental status, endotracheal intubation, noninvasive ventilation and surgery were factors for infection. Models for predicting morbidity were created using 2-7 simple indices. Risk model of AKI gave a high AUC of 0.94 based on data at admission. Risk models of RF and infection showed good predictive power using data at admission and better power after including in-hospital data. The performance was confirmed in the validation subset.
Conclusions We have developed simple risk models of morbidity to predict prognosis of AP patients. At admission, AKI can be predicted by risk model precisely. The other two complications predictive power are increased when in-hospital data were included in the models suggests that AP progression contributes substantially to morbidity and should be considered for accurate prediction of prognosis.

PO-1371

Evaluation of the Diagnostic Value of Peripheral Blood Parameters for Neonatal Pneumonia

Dan Liao
Daping Hospital, Army Medical University

Background To evaluate the diagnostic value of peripheral blood parameters including white blood cell (WBC), neutrophil, lymphocyte, monocyte, platelet, mean platelet volume (MPV), platelet distribution width (PDW), mean corpuscular volume (MCV), red cell distribution width

(RDW), neutrophil-to-lymphocyte ratio (NLR), monocyte-to-lymphocyte (MLR), platelet-to-lymphocyte ratio (PLR) and platelet-to-neutrophil ratio (PNR) for neonatal pneumonia.
Methods Two hundred and six full-term neonates in our hospital from January 2018 to December 2019 were en_x0002_rolled, including 73 pneumonic neonates and 133 health controls. Peripheral blood parameters were measured by an automatic blood cell analyzer. While C-reactive protein (CRP) and PCT concentrations were detected by electrochemical luminescence assay. Clinical signs, characteristic population, temperature, and chest radiograph findings were recorded. The receiver operating characteristic (ROC) curve was used to determine the cutoff values and analyze the diagnosis significances for neonatal pneumonia.
Results This study showed that WBC, neutrophil, RDW, NLR, and MLR levels in the pneumonic group were higher than that of the control group, whereas lymphocyte, monocyte, platelet, and PNR levels were lower ($p < 0.05$). The ROC curve result showed that NLR and PNR owned higher AUC values than the rest of peripheral blood variables. At a cutoff value 2.581, NLR exhibited 63.01% sensitivity, 90.98% specificity, and 0.847 area under ROC curve (AUC). In addition, at a cutoff value 52.77, PNR showed 84.93% sensitivity, 78.95% specificity, and 0.856 AUC.
Conclusions This study clarifies that peripheral blood parameter of NLR and PNR have good applied value in diagnosis neonatal pneumonia with high sensitivity and specificity.

PO-1372

探讨 7847 例液基细胞学联合普通涂片对甲状腺针吸细胞学的诊断价值

李琳
吉林大学第一医院

目的 探讨液基细胞学制片技术联合普通涂片在甲状腺针吸细胞学诊断的应用价值。
方法 对 7847 例门诊及住院甲状腺肿块患者进行回顾性分析，超声引导下细针抽吸穿刺，同时采用液基细胞学制片和普通制片两种制片和染色方法。由 2 名有经验的诊断医师同时对涂片进行诊断。分别评价液基制片和普通制片的制片效果和诊断结果。阳性病例进行病理追踪。
结果 液基细胞学制片和普通制片的效果分别从细胞数量、背景、密度、体积、核清楚程度及排列方式等方面评价，前者背景干净，细胞核结构清晰，可见核沟，核内包涵体。细胞排列和层次由于离心后受到破坏，单层平铺，成小团分布，少见乳头状排列。普通涂片背景血细胞干扰严重，胶质较多，细胞核结构欠清晰，可见核内包涵体，偶见核沟。细胞排列和层次保持完好，可见乳头团及平铺排列形式。液基细胞学涂片（例）检出率：34.8%；普通涂片（例）检出率：26.9%；两者联合（例）检出率：38.0%。两者联合与普通涂片比较（$P<0.05$）有统计学意义。两者联合与液基细胞学比较($P>0.05$)无统计学意义。阳性符合率两者联合与普通涂片之间有显著性差异（$P<0.05$）。两者联合与液基细胞学涂片之间无显著性差异。（$P>0.05$）。
结论 两种制片方法各有优缺点，两者联合应用可以互补优缺点，明显提高检出率及病理符合率，但由于针吸细胞学取材时受结节大小、位置因素等影响较大，故在临床诊断中，还应结合彩超及血清学结果综合考虑，避免出现假阳性及假阴性病例，做出最有利于患者诊治方案。

PO-1373

高荧光细胞和血清腹水白蛋白梯度在恶性腹水诊断中的价值

孙静芳、刘云、蒋清清、宋爽、李世宝、马萍、丁爽
徐州医科大学附属医院

目的 探讨高荧光细胞（HFC）和血清腹水白蛋白梯度（SAAG）在恶性腹水诊断中的应用价值。

方法 回顾性研究 2018 年 1 月至 2020 年 4 月收治的 202 例腹水患者，依据脱落细胞学检查结果分为恶性腹水（36 例）和良性腹水（166 例），分析 HF 和 SAAG 在良、恶性腹水中的分布差异，并计算单项及联合检测的敏感性、特异性和准确性。
结果 恶性腹水组 HF#和 HF%水平均显著高于良性组，SAAG 水平显著低于良性组。HF#、HF%和 SAAG 的曲线下面积分别为 0.797、0.704、0.770，单项指标分析时，HF#和 SAAG 的敏感性、特异性、准确度分别为 83.33、66.87、69.8 vs. 88.89、62.05、66.8，HF#和 SAAG 串联时敏感性、特异性、准确度分别为 77.78、80.12、79.7，HF#和 SAAG 并联时敏感性、特异性、准确度分别为 94.44、48.80、56.9。
结论 HF and SAAG 联合应用后虽灵敏度有所下降，但特异度和准确度均明显升高，更有利于恶性腹水的诊断。

PO-1374

活化部分凝血酶活时间纠正实验结果判读方法评价

刘超男、周静
四川大学华西医院

背景 活化部分凝血酶活时间(APTT)延长是凝血常规检测中最常见的异常结果之一，可能是由于因子缺乏，存在因子抑制剂或抗磷脂抗体(APL)导致。APTT 纠正实验可帮助快速筛选延长原因，明确诊疗方向。但是目前纠正实验结果判读的标准众多，如何解释纠正实验的结果是急需解决的问题。
目的 比较目前常用的判读纠正实验结果方法的实验室诊断效能，并探索一个最佳的标准更快、更准确的区分 APTT 延长的原因。
方法 纳入 2018 年 1 月 1 日至 2019 年 12 月 31 日在我院就诊的单独 APTT 延长的患者。所有样品均进行 1：1 混合比例的纠正实验，134 个样品加做了患者血浆和正常血浆 4：1 混合的纠正实验。评估现有 APTT 纠正实验判读标准的诊断效能和最佳分界值，并探讨何时以及如何将 1:1 和 4:1 混合实验有机结合。
结果 研究共纳入 251 例样本，其中因子缺乏 116 例，FVIII 抑制剂 75 例，APL60 例。Rosner 指数小于 11%，或孵育后延长时间小于 3s 是现有标准中区分因子缺陷和抑制剂、时间依赖性和非时间依赖性抑制剂的最佳方法，但是各个实验室设定自己的评价标准可获得更好的诊断效能。当 Rosner 指数在 5.0% ~ 9.1%之间时加做 4：1 混合的纠正实验，其余样本仅进行 1：1 纠正实验，结合 Rosner 指数和孵育后延长时间百分比可获得最佳的诊断效能。
结论 APTT 纠正实验对因子缺乏和抑制剂，甚至是时间和非时间依赖性抑制物都具有良好的诊断效能。与仅进行 1:1 混合相比，将 1:1 和 4:1 混合相结合，可以提高诊断效率。

PO-1375

Comprehensive application of nanopore direct RNA sequencing and short reads sequencing to evaluate nonsense-mediated RNA decay activity in prostate cancer patients

Ying Li
Beijing Hospital

Objective Nonsense-mediated mRNA decay (NMD) is a critical post-translational mechanism to guard cells against potential poisonous proteins. NMD plays an essential role in pathology and physiology. Inhibit NMD by small molecules can produce an abundance of truncated proteins that

can be prospective neoantigens. Therefore, therapies target NMD has the potential to be an adjuvant treatment of some cancers. However, methods to measure NMD activity in patients are rare. This study detects NMD activity and analyzes transcripts feature both at short reads sequencing and nanopore direct RNA sequencing. We chose several transcripts as potential candidates to reflect NMD activity by qPCR, further applied them to three cell lines and newly diagnosed prostate cancer patients.
Methods Native RNA sequencing was performed using Direct RNA Sequencing Kit (SQK-RNA002). The GridON Flow Cell (R9.4 chemistry) was run for 48hours on MinKNOW software. Guppy was used to base-calling and FLAIR software for further analysis. For short reads sequencing, the libraries were sequenced on an Illumina platform and 150 bp paired-end reads were generated. Data were analyzed use STAR, HTseq, StingTie, and DAVID. We chose several high-expression transcripts based on the relative transcriptional level as NMD indicators. qPCR validation was conducted use SYBR-green in BioRad5 system. Patients were enrolled at Beijing Hospital, prostate cancer and paracancerous tissues of patients were collected and stored in RNA-Later. Total RNA of tissue was isolated by TRIzol(Invitrogen) for further experiment.
Results We conducted parallel sequencing of DMSO and NMD inhibitor SMG1i both in short reads sequencing and Nanopore direct RNA sequencing. We found that NMD inhibition can significantly increase transcriptional isoforms and alternative splicing events. Approximately 40% of transcripts detected by Nanopore were unannotated. These NMD indicators we chose showed excellent performance in HEK293T, U2OS, and 22Rv1 cell lines under NMD inhibition. In clinical patients, NMD activity fluctuates widely among individuals.
Conclusions Combined with nanopore sequencing and short reads sequencing can reflect NMD activity and its' features. We have shown the ability and reliability of NMD indicators both in cell lines and clinical patients. These results provided a good foundation for future studies on the NMD activity measurement and NMD inhibition treatment for cancers.

PO-1376

A PCR-based detection and analysis system for personalized medicine in cardiovascular diseases

Zhaohui Liu[1]、Kai Cui[2]、Juan Zhao[2]、Kun Zhao[2]、Zhou Zhou[2]
1. Fuwai Yunnan Cardiovascular Hospital
2. 中国医学科学院阜外医院

Background Cardiovascular Diseases (CVDs) are the leading cause of death globally. According to the WHO reports, about 18 million people die from CVDs each year, accounting for about 1/3 of the total deaths in the world, and the prevalence and mortality of CVDs is continuously rising. Many factors contribute to this high prevalence of CVDs, such as hypertension, atherosclerosis, coronary heart disease, and stroke. Some commercialized drugs including β1-adrenergic receptors, statins, ACE Ⅰ, clopidogrel, warfarin, diuretics, and antiarrhythmics have been used commonly. However, the single nucleotide polymorphisms (SNPs) of key genes indrug metabolism is associated with the therapeutic responses and adverse reactions which shown the variation between different individuls. Commercially available genetic tests are mainly based on sequencing or real-time PCR platforms which only target a certain drug or a certain class of drugs. Guiding the selection and combination of drugs usually needs to test multiply, spending more time and increasing the financial burden for the patients.
OBJECTIVE In order to simultaneously test the related genes of multiple drugs, we established a geneticdetection method for 11 kinds of common cardiovascular drugs (clopidogrel, warfarin, statins, beta-receptor blockers, calcium antagonists, diuretics, ACE inhibitors, angiotensin II receptor antagonists, nitroglycerin, antiarrhythmic drugs and folic acid) in only one reaction. This method enables the direct amplification with blood sample and testing the SNPs,

eliminating the step of DNA extraction and simplifying the operation process. And we also developed an analysis software to assist in the interpretation of data.
Methods According to the Guidelines for Gene Detection of Drug Metabolizing Enzymes and Drug Targets by NHFPC as well as documents and guidelines by FDA and CPIC, DPWG and other authoritative organizations, we selected 25 SNPs related to the above 11 drugs. Based on allele-specific PCR (AS-PCR) and multiplex quantitative fluorescent PCR, the 25 SNPs can be amplified and detected in one tube with a capillary electrophoresis system.
RESULTS With this system, we tested 1500 clinical samples, detected the genotype of each gene we interested and analyzed the statistical data. Verified by Sanger sequencing, all the genes were accurately detected and the detection rate reached 99%, with the coincidence rate reached 100%. Except for the CYP2D6*10 100C>T site, the distribution of each genotype fit well with Hardy Weinberg Equilibrium and consistent with the frequency reported previously.
Conclusion In this research, we established a multiple SNPs detection system based on ThermoFisher genetic analysis CE platform. We detected 25 gene loci related to 11 common cardiovascular drugs with only one tube reaction, and the results shown high accuracy and reliability. With direct amplification of blood and automatic interpretation by software, this system can simplify the operation process, lower the risk of introducing experimental errors, reduce the cost of multiple gene testing. We expect that this system can be used to effectively guide the usage of drugs for morecardiovascular diseases and other kinds of diseases.

PO-1377

A predictive proteomic signature for he response to 5-FU based neoadjuvant chemoradiotherapy in Locally Advanced rectal cancer patients

Jianan Wang[1,2]、Chengbin Wang[1]
1. Department of Clinical Laboratory Medicine, The General Hospital of People's Liberation Army
2. 解放军医学院

Background Colorectal cancer is the third most common and the fourth most lethal cancer in the world. In the majority of cases, patients are diagnosed at an advanced stage or even metastatic, thus explaining the high mortality. The standard treatment for patients with locally advanced rectal cancer (LARC) is neoadjuvant chemoradiotherapy (nCRT) with 5-fuorouracil (5-FU) followed by surgery. Most patients with LARC present incomplete pathological response to nCRT, the resistance rate remains high with approximately 30% of non-responders. Despite the efforts to predict treatment response using tumor-molecular features, as differentially expressed genes, no molecule has proved to be a strong biomarker. The tumor proteomic analysis is a promising strategy for biomarkers identification, which can be used to identify a predictive model to forecast treatment response outcomes and figured out response relevant proteins in nCRT.
Methods We performed LC-MS/MS-based proteomic analysis to select potentially proteins and then used in silico approach to further validate the differential proteins screened out from our training cohort . 42 patients diagnosed with LARC and treated with 5-FU based nCRT between 2010-2018 at Chinese PLA General Hospital were enrolled in the study. All of these cases had available paired pre-treatment formalin-fixed paraffin-embedded (FFPE) biopsies and post-CRT FFPE surgical specimens from the same patients and histologically confirmed adenocarcinoma. According to Tumor Regression Grade (TRG), patients were divided into three treatment response groups: poor-responders (PR, AJCC TRG2+3), moderate responders (MR, AJCC TRG1) and total responders (TR, AJCC TRG0), and to compare the proteomes of these diferent groups. From 42 paired FFPE biopsies and surgical specimens, we extracted and analysed the tumor proteome of these patients.
Results Comparing TR and PR group, we have identified 91 differentially abundant proteins between biopsies, 165 between surgical specimens of two groups. Next, comparing biopsies and

surgical specimens of each group through paired t-test, we screened out 1467 and 771 proteins changed after nCRT in TR and PR group, respectively. 848 proteins with different change directions(from biopsies to surgical specimens) in TR and PR group were defined as response relevant proteins which might provide some indications to explain different response in TR and PR group. Then, 129 proteins were figured out in intersections between differentially expressed proteins and response relevant proteins, which might play a role in tumor resistant to nCRT and predict the patient response to the therapy. Among these proteins, we have identifed 43 genes expressed significantly different in rectal cancer tissue and normal tissue using GEPIA2 database(mainly involved in TFIID-class transcription factor complex binding, snoRNA binding, ATPase binding, RNA polymerase II transcription factor binding, etc), and there were 11 genes related to the overall survival of rectal cancer patients(favorable:SF3B6, NUP153, ARGLU1, GNL3, MTHFD1L, PTCD3, SLC27A2; unfavorable:SPTB, TMOD1, CD63, S100A13). , A set of 16 proteins(over-expressed in PR group: PLEKHA6, CHMP4B, VWA1, LMNA; over-expressed in TR group: PTPN6, SF3B3, HDAC2, NDUFA5, PHGDH, TIMM44, AHSA1, GNL3, POLR2A, MTHFD1L, PTP4A1, NUP35) was independently validated in a gene expression dataset for chemoradiosensitivity of colorectal cancer cells from GSE20298 to be related to nCRT resistance, enrichment analysis found that these 16 proteins were related to nuclear envelope reassembly, nucleus organization, processing of capped intron-containing pre-mRNA and generation of precursor metabolites and energy.

Conclusions From this retrospective study, protein differences between different response groups to nCRT in LARC patients were highlighted using FFPE proteomic analysis, they might be the novel biomarkers for diagnosis and guiding therapeutic strategies of rectal cancer. These results will pave the way for a larger cohort for better sensitivity and specificity of the signature to guide decisions in the choice of treatment.Furthermore, the findings will provide an insight about the proteins and molecular pathways involved in the response to treatment of LARC patients.

PO-1378

Epstein Barr virus encoded microRNA BART22 drives malignant transformation and predicts poor prognosis in patients with nasopharyngeal carcinoma

Ting Zhang[1]、Zui Chen[1]、Kaixiong Xu[1]、Xiaoqiong Gu[2]、Banglao Xu[1]
1. Guangzhou First People's Hospital
2. 广州市妇女儿童医疗中心

Purpose This study aims to clarify whether Epstein Barr virus encoded microRNA BART22（EBV-miR-BART22） was involved in the formation and metastasis of epithelial-mesenchymal transition (EMT) in nasopharyngeal carcinoma (NPC) cells，and explicate the signaling pathways and target gene by which EBV-miR-BART22 promotes EMT and metastasis in NPC cells, which provide clues for finding new effective intervention target as well as prognostic marker for nasopharyngeal carcinoma metastasis.

Methods The sequencing data of nasopharyngeal carcinoma tissues versus normal control tissues in the GEO database were analyzed to determine the target microRNAs. The expression of EBV-miR-BART22 in NPC tissues microarray and the relationship with patients prognosis were detected by the in situ hybridization(ISH) staining. After overexpression of EBV-miR-BART22 in EBV negative CNE-1, CNE-2, and SUNE-1 cell lines, or knockdown of EBV-miR-BART22 expression in EBV positive C666-1 cell line respectively, the detection of cell migration, invasion, and EMT related protein expression changes were performed. The effects of overexpression / knockdown of EBV-miR-BART22 on NPC cell metastasis were observed by in vivo animal experiments. Potential signaling pathways and target genes were selected by RNA sequencing and bioinformatic analysis. Plasmids or siRNAs were respectively used to overexpress or

interfere the β-Catenin or MOSPD2 expression in cell lines with lentiviral infection, and the changes in cell migration / invasion function and EMT indicators were observed.
Results Multiple GEO datasets showed that EBV-miR-BART22 expression was significantly higher and most variable in NPC tissues compared with normal tissues. The ISH results indicated that high expression of EBV-miR-BART22 was positively correlated with nasopharyngeal carcinoma distant metastasis, TNM stage as well as poor prognosis of patients, and EBV-miR-BART22 was an independent risk factor for poor prognosis of nasopharyngeal carcinoma patients. Overexpression of EBV-miR-BART22 could promote NPC cells migration and invasion, and downregulate EMT epithelial marker E-cadherin, upregulate mesenchymal markers N-cadherin and vimentin. EBV-miR-BART22 could promote nasopharyngeal carcinoma cells metastasis in nude mice in vivo. RNA sequencing, bioinformatic analysis, as well as in vitro cellular assays confirmed that EBV-miR-BART22 could directly target MOSPD2 and activate Wnt/β-Catenin pathway, thereby promoting EMT and metastasis of nasopharyngeal carcinoma cells.
Conclusions EBV-miR-BART22 activates Wnt/β-catenin pathway by targeting MOSPD2 to promote EMT and metastasis of NPC cells. EBV-miR-BART22 could serve as a potential biomarker for diagnosis and prognosis evaluation in nasopharyngeal carcinoma.

PO-1379

Potent RBD-specific neutralizing rabbit monoclonal antibodies recognize emerging SARS-CoV-2 variants elicited by DNA prime-protein boost vaccination

Yuxin Chen
Nanjing Drum Tower Hospital

Global concerns arose as the emerged and rapidly spreading SARS-CoV-2 variants might escape host immunity induced by vaccination. In this study, a heterologous prime-boost immunization strategy for COVID-19 was designed to prime with a DNA vaccine encoding wild type (WT) spike protein receptor-binding domain (RBD) followed by S1 protein-based vaccine in rabbits. Four vaccine-elicited rabbit monoclonal antibodies (RmAbs), including 1H1, 9H1, 7G5, and 5E1, were isolated for biophysical property, neutralization potency and sequence analysis. All RmAbs recognize RBD or S1 protein with KD in the low nM or sub nM range. 1H1 and 9H1, but neither 7G5 nor 5E1, can bind to all RBD protein variants derived from B.1.351. All four RmAbs were able to neutralize wild type (WT) SARS-CoV-2 strain in pseudovirus assay, and 1H1 and 9H1 could neutralize the SARS-CoV-2 WT authentic virus with IC50 values of 0.136 μg/mL and 0.026 μg/mL, respectively. Notably, 1H1 was able to neutralize all 6 emerging SARS-CoV-2 variants tested including D614G, B.1.1.7, B.1.429, P.1, B.1.526, and B.1.351 variants, and 5E1 could neutralize against the above 5 variants except P.1. Epitope binning analysis revealed that 9H1, 5E1 and 1H1 recognized distinct epitopes, while 9H1 and 7G5 may have overlapping but not identical epitope. In conclusion, DNA priming protein boost vaccination was an effective strategy to induce RmAbs with potent neutralization capability against not only SARS-CoV-2 WT strain but also emergent variants, which may provide a new avenue for effective therapeutics and point-of-care diagnostic measures.

PO-1380

3044 cases reveal important prognosis signatures of COVID-19 patients

Yang Yang、Xinyi Xia
Institute of Laboratory Medicine, Jinling Hospital, Nanjing University School of Medicine

Objective Critical patients and intensive care unit (ICU) patients are the main population of COVID-19 deaths. Therefore, establishing a reliable method is necessary for COVID-19 patients to determine the primary prognostic factors and distinguish patients who may have critical symptoms from other patients.

Methods Clinical characteristics, treatment efficacy,clinical outcome, demographics, basic diseases and laboratory test results of 3044 patients with COVID-19 in Wuhan Huoshenshan Hospitalwere analyzed. Then, logistic regression was used to explore the influence of various laboratory indicators on clinical critical illness and death, and random forest machine learning algorithm was used to find and verify the most importantlaboratory indicators leading to critical illness and death outcomes.

Results The study shows thatthe susceptible population was mainly between 61-70 years old (n=932, 30.62%). The elderly patients had poor clinical status and high mortality rate (P<0.0001).Logistic regression results after age and sex adjustment showed that hypertension (OR=1.4825, P =0.0141), diabetes (OR=1.5573, P =0.016) and tumor (OR=2.3150, P =0.0223) were the main risk factors. Next, 54 laboratory indicators were evaluated of the influence on critical illness and death, and the eight most important prognostic indicators (neutrophil percentage, procalcitonin, neutrophil absolute value, C-reactive protein, albumin, interleukin-6, lymphocyte absolute value and myoglobin) were identified by using the random forest algorithm, which present significantly distinct within differently clinical severities.Together with age and sex, these eightindicators can be used to construct a prognostic model that can accurately predictdisease severity and clinical outcome of the patients. The clinical reliability of the model was verified by 491 sample training sets, and the receiver operating characteristic curve (ROC) showed that the model had a good AUC of 0.875(95% CI：0.821-0.93), and also verified in a separate cohort of 170 patients with an AUC of 0.897 (95% CI: 0.78-1.00). Finally, by combining public lung single cells and bulk transcriptome data to analyze 15 cell populations from 8 normal lungs,we find that TMPRSS2 and FURIN genes promoting the binding of SARS-CoV-2 and ACE2 are mainly expressed in AT2 cells.The expression level and proportion of ACE2, TMPRSS2 and FERIN in males and the elderly were higher than those in females and the young, this may partly explain why older and male patients are more likely to develop critical illness and death.

Conclusion The eight most important prognostic indicators were neutrophil percentage, procalcitonin, neutrophil absolute value, C-reactive protein, albumin, interleukin-6, lymphocyte absolute value and myoglobin.Theprognosticmodel including these eight indicators, as well as sex and age was built to predict the outcome of disease progression and death of COVID-19patients, which has important clinical practical significance for the management and prediction of COVID-19patients.

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PO-1381

Bronchoalveolar Lavage Fluid Glycopatterns as Novel Potential Biomarkers for Early Diagnosis of Lung Cancer

Lina Liu[1,2]、Dan Li[2]、Jian Shu[3]、Li Wang[2]、Fan Zhang[3]、Chen Zhang[3]、Hanjie Yu[3]、Mingwei Chen[2]、Zheng Li[3]、Xuan Guo[2]
1. Xi'an No. 4 Hospital
2. 西安交通大学第一附属医院
3. 西北大学

Objectives Lung cancer (LC) is a prevalent and life-threatening neoplasia worldwide. Although aberrant glycosylation has been observed in human serum and tissue, little is known about the alterations in bronchoalveolar lavage fluid (BALF) that are associated with LC. Our aim was to systematically investigate and assess the alterations of protein glycopatterns in BALF and possibility as biomarkers for diagnosis of LC.
Methods In this study, lectin microarrays were utilized to detect and compare the differential expression of BALF glycoproteins from patients with 80 adenocarcinomas (ADC), 77 squamous cell carcinomas (SCC), 51 small cell lung cancer (SCLC), and 73 benign pulmonary diseases (BPD). Then, lectin blotting analysis was performed to verify the results of lectin microarrays. These 281 BALF specimens were then randomly divided into test group and validation group. First, five diagnostic models (Model LC, ModelADC, Model SCC, Model SCLC, and Model LC-ES (early stage of lung cancer)) were constructed to identify benign and malignant lung diseases, ADC, SCC, SCLC and LC-ES by binary stepwise logistic regression based on the lectin microarrays data from 163 BALF samples in the test group. Subsequently, the diagnostic models constructed in the test group were then applied to a validation group to assess the discriminatory efficiencies through ROC analysis. Moreover, an independent test was performed with 120 newly collected BALF samples enrolled in the double-blind cohort to further assess the clinical application potential of the diagnostic models.
Results According to the results, there were 15 (e.g., PHA-E, EEL, and BPL) and 14 lectins (e.g., PTL-II, LCA, and SJA) that individually showed significant variations in different types and stages of lung cancer compared to BPD. Notably, the diagnostic models achieved better discriminate power (Model LC (AUC: 0.61, sensitivity: 0.918 and specificity: 0.939), Model LC-ES (AUC: 0.856, sensitivity: 0.829 and specificity: 0.810), Model ADC (AUC: 0.619, sensitivity: 0.706 and specificity: 0.586), Model SCC (AUC: 0.693, sensitivity: 0.800 and specificity: 0.667), Model SCLC (AUC: 0.718, sensitivity: 0.721 and specificity: 0.684)) in the validation cohort and exhibited high accuracies of 0.917, 0.864, 0.712, 0.671 and 0.781 in the double-blind cohort for the diagnosis of LC, LC-ES, ADC, SCC, and SCLC, respectively.
Conclusions Taken together, the present study revealed that the abnormally altered protein glycopatterns in BALF are expected to be novel potential biomarkers for the identification and early diagnosis of lung cancer, which will contribute to explain the mechanism of the development of lung cancer from the perspective of glycobiology.

PO-1382

Ability of a machine learning algorithm to predict the need for perioperative red blood cells transfusion in pelvic fracture patients: A multicenter cohort study in China

Xueyuan Huang、Xinming Nie、Rong Gui
The Third Xiangya Hospital, Central South University

Background Predicting the perioperative requirement for perioperative red blood cells (RBCs) transfusion in patients with the pelvic fracture may be challenging. In this study, we constructed a

perioperative RBCs transfusion predictive model (ternary classifications) based on a machine learning algorithm.

Materials and Methods This study included perioperative adult patients with pelvic trauma hospitalized across six Chinese centers between September 2012 and June 2019. An extreme gradient boosting (XGBoost) algorithm was used to predict the need for perioperative RBCs transfusion, with data being split into training test (80%), which was subjected to 5-fold cross-validation, and test set (20%). The ability of the predictive transfusion model was compared with blood preparation based on surgeons' experience and other predictive models, including random forest, gradient boosting decision tree, K-nearest neighbor, logistic regression, and Gaussian naïve Bayes classifier models. Data of 33 patients from one of the hospitals were prospectively collected for model validation.

Results Among 510 patients, 192 (37.65%) have not received any perioperative RBCs transfusion, 127 (24.90%) received less-transfusion (RBCs <4U), and 191 (37.45%) received more-transfusion (RBCs ≥4U). Machine learning-based transfusion predictive model produced the best performance with the accuracy of 83.33%, and Kappa coefficient of 0.7967 compared with other methods (blood preparation based on surgeons' experience with the accuracy of 65.94%, and Kappa coefficient of 0.5704; the random forest method with an accuracy of 82.35%, and Kappa coefficient of 0.7858; the gradient boosting decision tree with an accuracy of 79.41%, and Kappa coefficient of 0.7742; the K-nearest neighbor with an accuracy of 53.92%, and Kappa coefficient of 0.3341). In the prospective dataset, it also had a food performance with accuracy 81.82%.

Conclusion This multicenter retrospective cohort study described the construction of an accurate model that could predict perioperative RBCs transfusion in patients with pelvic fractures.

PO-1383

Long non-coding RNA LINC02474 affects metastasis and apoptosis of colorectal cancer by inhibiting the expression of GZMB

Tiantian Du
The Second Hospital of Shandong University

Background Colorectal cancer (CRC) is one of the most frequently diagnosed malignancies. Metastasis is the main event that impedes the therapeutic effect on CRC, and its underlying mechanisms remain largely unclear. LINC02474 is a novel long noncoding RNA (lncRNA) associated with cancer metastasis, while little is known about how LINC02474 regulates these malignant characteristics.

Methods LINC02474 and GZMB expressions were assessed by quantitative real-time polymerase chain reaction (qRT-PCR) or Western blotting analysis. Cell metastasis was detected by transwell assay and metastatic nude mouse model, and apoptosis was determined by Western blotting analysis and flow cytometry. Besides, the interaction between LINC02474 and GZMB was detected by dual-luciferase reporter assays.

Results The expression of LINC02474 was significantly up-regulated in CRC tissues. Moreover, depletion of LINC02474 damaged the metastatic abilities of CRC cells while boosting apoptosis. Besides, up-regulation of LINC02474 could promote migration and invasion, while apoptosis was inhibited in CRC cells. Besides, down-regulation of LINC02474 promoted the expression of GZMB, and interference of GZMB could increase the metastatic abilities of CRC cells while reducing apoptosis. Furthermore, LINC02474 was related to the transcriptional repression of GZMB in CRC cells determined by the dual-luciferase reporter assay.

Conclusions The findings revealed that a novel lncRNA, LINC02474, as an oncogene, could promote metastasis but limit apoptosis partly by impeding GZMB expression in CRC. Besides, LINC02474 had the potential to be used as a biomarker in the prognosis of CRC.

PO-1384

Clinical prognostic value and contribution of m6A RNA methylation regulators and tumor microenvironment cell-infiltration characterization in Gastroesophageal Adenocarcinomas

duanrui liu
Jinan Central Hospital affiliated to Shandong University

Objective Gastroesophageal adenocarcinomas (GEA) is still a major cause of cancer-related mortality worldwide. Currently, development of effective targeted therapeutics for GEA patients lags behind other cancers. Tumor microenvironment (TME) is the complex cellular milieu consisting of immune cells, mesenchymal cells, endothelial cells, inflammatory mediators and extracellular matrix molecules adaptively or innately, which remarkable influence the immunotherapy. RNA N6-methyladenosine (m6A) modification plays nonnegligible role in shaping individual TME characterizations. However, potential roles of m6A modification in TME cell infiltration remain unknown in gastroesophageal adenocarcinomas (GEA).
Methods We examined the TME of GEA using assessments of the RNA-sequencing data focusing on the distinct m6A modification patterns from the public databases. Intrinsic patterns of m6A modification were evaluated for associations with clinicopathological characteristics, underlying biological pathways, tumor immune cell infiltration, oncological outcomes and treatment responses. We generated a single-cell transcriptome atlas of the GEA sample to validate the role of the m6A modification pattern on TME.
Results Most of 21 m6A RNA methylation regulators are higher expressed in GEA patients. The proportion of immune cells in GEA tumor tissues was significantly different from that in normal tissues. Therefore, changes in tumor-infiltrating immune cells (TIICs) proportions might be intrinsic to individual differences. Then, we identified two distinct m6A modification patterns of GEA (cluster1 and 2 subgroup) by applying consensus clustering to 21 m6A RNA methylation regulators, and correlated two subgroups with TME cell-infiltrating characteristics. Compared with the cluster1 subgroup, the cluster2 subgroup correlates with a poorer prognosis, and most of 21 m6A RNA methylation regulators are higher expressed in cluster2. Meanwhile, apart from Macrophages M0, the relative levels of three immune cell types (T cells CD8, Monocytes, Mast cells resting) in cluster 1 were higher than the cluster 2. Cox regression and Lasso regression were employed to identify three prognostic m6A methylation regulators (KIAA1429, HNRNPA2B1 and FMR1) and establish the risk signature. The risk signature was not only an independent prognostic marker for GEA patients but also a predictor of clinicopathological variables. GSEA analysis showed multiple signaling differences between high and low risk score group. Furthermore, through WGCNA analysis, COL4A1 and COL5A2 in the brown module were significantly correlated to the prognosis, PD-1/L1 and CTLA-4 expression of GEA patients. Interesting, low COL5A2 expression was linked to an enhanced response to anti-PD-1 immunotherapy. Finally, the single-cell transcriptome atlas of GEA samples validated the role of m6A modification pattern on TME and revealed that three m6A regulators are highly expressed in CD4+ T cells, CD8+ T cells, Treg cells and Macrophages.
Conclusions Our work revealed m6A RNA methylation regulators are a type of vital participant in the malignant progression and TME diversity of GEA. m6A modification patterns of COL5A2 may be the potential biomarker contributes to predicting the response to anti-PD-1 immunotherapy.

PO-1385

Dynamic serum biomarkers to predict the efficacy of PD-1 in patients with nasopharyngeal carcinoma

ao zhang、runkun han、luocan wang、rongzeng cai、shulin chen、peng sun、hao chen
Sun Yat-sen University Cancer Center

Background There is a lack of effective treatments for recurrent or metastatic nasopharyngeal carcinoma (RM-NPC) while the response rate of Programmed death 1 (PD-1) in NPC is about 20% to 30%. We aim to explore reliable and minimally invasive prognostic indicators for predicting the efficacy of PD-1 inhibitors combined therapy in RM-NPC.
Methods Serum markers of 160 RM-NPC patients were measured before and 3 weeks after the first anti-PD1 treatment. The least absolute shrinkage and selection operator (LASSO) logistic regression was performed to select dynamic serum indicators and construct prediction model. Univariate, multivariate, nomogram and survival analyses were conducted to identify independent prognostic factors associated with 1-year progression-free survival (PFS).
Results Based on 2 markers screened by Lasso logistic regression, we constructed a risk score prediction model for 8-12 weeks anti-PD1 efficacy prediction with the AUC of 0.737 in training cohort and 0.723 in validation cohort. Risk score and metastasis were included into nomogram, and the Kaplan–Meier survival curves showed that high risk group had a shorter PFS than the low risk group. The concordance index (C-index) of the nomogram for PFS was higher than that of TNM stage in the training cohort and validation cohort.
Conclusion We proposed a strategy for monitoring dynamic changes of biochemistry markers and emphasized their importance as potential prognostic biomarkers for advanced NPC treated with ICBs. Our risk score prediction model based on dynamic change of LDH and AST / ALT has predictive and prognostic value for NPC patients treated with PD-1 inhibitors.

PO-1386

Circulating tumor DNA methylation in hepatocellular carcinoma diagnosis using digital droplet PCR

Juan Wang [1]、liu yang[1]、jiayun liu[1]、yanjun diao[1]、lianghong zheng[2]、kang zhang[3]、yueyun ma[4]、xiaoke hao[1]
1. Department of Clinical Laboratory Medicine, Xijing Hospital, Air Force Medical University
2. 广州优泽生物技术有限公司
3. 澳门科技大学医学院
4. 解放军空军总医院检验科

BACKGROUND In recent years, several protein biomarkers, gene mutations, and epigenetic modifications were analyzed for the molecular diagnosis of hepatocellular carcinoma(HCC). As a non-invasive liquid biopsy analyte, circulating cell-free DNA (cfDNA) gained tremendous attention to diagnosevarious cancers, including HCC. The analysis of aberrant DNA methylation incfDNA is also used to diagnose early carcinogenesis. This study aimed to evaluate the performance of a DNA methylation-based digital droplet PCR (ddPCR) assay and its application to detect HCC patients.
METHODS Blood samples were obtained from 97 HCC patients, 80 healthy subjects, and 46 chronic hepatitis patients. cfDNA was extracted, bisulfite converted, and DNA methylation quantified using a ddPCR platform.
RESULTS Wequantitated cfDNAamount variation in different physical conditions.The level of cfDNA amount in the HCC group was significantly higher than that in the healthy control group. Subsequently, we validated the dynamic changes in the peripheral DNA methylation ratio that corresponds to the HCC progression. The higher level of DNA methylation status and ctDNA amount were also detected in advanced (BCLC C) and late (BCLC D) stages in the current

results. Furthermore, we explored the diagnostic value of methylation patterns for HCC diagnosis. The differential methylation status between HCC, chronic hepatitis, and healthy individuals was investigated using a cutoff value of 15.70% for DNA markers combined with the AFP level and cfDNA amount, the sensitivity was estimated to be 78.57%, and the specificity was 89.38% with the diagnostic accuracy of 89.27%. These results showed high diagnostic accuracy (ACC) of 85.27%, while positive predictive value (PPV) and negative predictive value (NPV) were 81.91% and 87.20%, respectively. However,DNA methylation markers could not be directly used in HCC diagnosis. We confirmed the potential application of tissue-specific methylation markers,combined with AFP and cfDNA analysis in the investigation of susceptible HCC patients differentiated from the asymptomatic population.The current data showed the AUC of AFP for asymptomatic population screening was 0.786 and could be improved to 0.958 if combined with specific DNA methylation patterns and cfDNA amount.We proved that ctDNA methylation analysis is a reliable and robust method for the early diagnosis of HCC.
CONCLUSION A sensitive methylation-based assay that might serve as a liquid biopsy test for diagnosing HCC. By using DNA methylation pattern in ddPCR platform, wedemonstrated that its efficiently detects trace amounts of DNA methylation. This relatively inexpensive approach is generalizable and could be popularized in personalized medicine, which would potentially open the pathway for health management.

PO-1387

A DNA Methylation-Based Epigenetic Signature for the Identification of Lymph Node Metastasis in T1 Colorectal Cancer

Yinghui Zhao、Chuanxin Wang
The Second Hospital of Shandong University

Background The T1 colorectal cancers (T1 CRC) are characterized as an early-stage, invasive cancers, that have infiltrated the sub-mucosal epithelial layer within the colonic lumen. Considering its invasiveness and risk of lymph node metastasis (LNM), the current guidelines recommend endoscopic resection for T1 CRC that are LNM-negative, and radical surgical resection in only those that are at high risk of LNM-positive. With the implementation of population-based CRC screening programs, the diagnostic rates for T1 CRC has increased considerably. However, the clinicopathological criteria for risk-stratification of T1 CRC are imperfect, which leads to erroneous diagnosis of as much as 70-80% of patients as high-risk, resulting in unnecessary and excessive radical surgeries and post-surgical complications. Given the importance of aberrant methylation in CRC, we conducted a genomewide methylation profiling analyses to develop methylated DNA (mDNA) biomarkers for the identification of LNM in patients with T1 CRC.
Methods For the biomarker discovery phase, we performed Infinium Methylation EPIC BeadChip microarrays in a cohort of 39 T1 CRC patients (17 LNM-positive and 22 LNM-negative). Following rigorous bioinformatic analysis and prioritization of aberrantly methylated biomarkers, we performed quantitative pyrosequencing analysis in 235 specimens from independent cohorts of patients, which included 195 resected tissues (training cohort: n = 128, validation cohort: n = 67) and 40 pre-treatment biopsies.
Results Through a systematic analysis based on the methylation profiles in LNM-negative and positive T1 CRC patients, we identified and trained a 9-methylated CpG signature (cg08463024, cg15246085, cg02558364, cg05928186, cg00353923, cg19929126, cg27136241, cg00450784, cg14044640), by performing logistic regression analysis in the training cohort patients. This resulted in a robust area under the curve (AUC) value of 0.88 (95% CI. 0.777 - 0.942) for distinguishing T1 CRC with vs. without LNM, which was subsequently validated in another independent patient cohort (AUC= 0.90; 95% CI. 0.797 - 0.958). However, for an easier

translation in the clinic, these mDNA biomarkers remarkably well even in pre-treatment biopsies (AUC=0.81; 95% CI. 0.723 - 0.906). Furthermore, a combination diagnostic model that combined mDNA and conventional clinicopathological features, further improved its diagnostic potential for the identification of LNM in T1 CRC.
Conclusions We have established a novel epigenetic signature that can robustly identify LNM status, even in pre-operative settings, in patients with T1 CRC; highlighting its potential clinical implication in more prudent selection of high-risk patients that require radical surgeries and spare the others from its complications and expense.

PO-1388

A 3-min UPLC-MS/MS method for the simultaneous determination of plasma catecholamines and their metabolites: Method verification and diagnostic efficiency

Meiling Jian[1]、Honglang Huang[2]、Kecheng Li[2]、Liangmin Chuan[3]、Lin Li[4]、Li Jiang[5]
1. Department of Laboratory Medicine, Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China.
2. School of Medicine, University of Electronic Science and Technology of China, Chengdu 610054, Sichuan, China
3. Department of Laboratory Medicine, Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China.
4. Department of Laboratory Medicine, Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China.
5. Department of Laboratory Medicine, Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China.

Objective To verify a rapid and sensitive ultraperformance liquid chromatography-tandem mass spectrometry (UPLC-MS/MS) method for the quantification of catecholamines and their metabolites, and to validate its efficiency for the diagnosis of phaeochromocytomas and paragangliomas (PPGLs).
Methods Plasma samples were pretreated with solid-phase extraction, followed by a 3-min UPLC-MS/MS analysis to quantify epinephrine (E), norepinephrine (NE), dopamine (DA), metanephrine (MN), normetanephrine (NMN) and 3-methoxytyramine (3-MT), simultaneously. The UPLC-MS/MS method was comprehensively verified and its diagnostic efficiency on PPGLs was tested using 7 PPGLs and 408 non-PPGLs patient plasma samples.
Results Using the developed method, the limit of detections (LODs) of the 6 analytes ranged from 0.0002 nmol/L (MN) to 0.0250 nmol/L (NE), while the lower limit of measuring intervals (LLMIs) ranged from 0.05 nmol/L (E, MN and NMN) to 0.10 nmol/L (NE and DA). The reportable ranges were 0.05-30.00 nmol/L for E, MN and NMN, 0.10-30.00 nmol/L for NE and DA, 1.00-300.00 pg/mL for 3-MT. No significant matrix effect was detected after correcting using internal standard. Besides, intra-day and inter-day precision were also within acceptance criteria with coefficient of variations (CVs) ≤15% and recoveries ranged from 95% to 115% for all the 6 analytes. The carryover effect was lower than 10%. Its diagnostic efficiency for PPGLs was significantly increased, the areas under the receiver operating characteristic (ROC) curves were increased from 68.7%-89.1% (using E, NE and DA) to 75.2%-99.9% (using MN, NMN and 3-MT).
Conclusion This study verified a rapid UPLC-MS/MS method for the determination of catecholamines and their metabolites in human plasma. It showed high diagnostic efficiency and will serve as an important tool to avoid the risk for missing patients with PPGLs.

PO-1389

Genetic diagnostic spectrum and exome-multigenic background study of childhood epilepsy

Ruen Yao、Jian Wang
Shanghai Children's Medicanl Center

Childhood epilepsy is a common but extremely heterogeneous neurological condition with a high incidence worldwide. Genetic diagnosis of childhood epilepsy patient provide the most accurate pathogenesis evidence, but still large proportion of highly suspected patients are undiagnosed. Multigenic factors in genetic background contribute to childhood epilepsy should be evaluated. In this study, exome-level sequencing was used to depict the mutation spectrum of childhood epilepsy cohort. Furthermore, variants information from sequencing data were analyzed besides monogenic diagnosis purpose to elucidate the possible multigenic factor related with epilepsy pathogenesis. Exome-sequencing reached a diagnostic rate of 30.6% and identified six genes not currently listed in epilepsy associated gene list. Multigenic study reveal that three-fold possibility of deleterious missense mutation occurrence in ion-channel and synaptic genes in those undiagnosed cohort may contribute to polygenic risk of childhood epilepsy.

PO-1390

The novel cytokine CSBF/C10orf99 plays a protective role in psoriasis

Xiulan Yang[1,2]、xixi Li[2]、wenling Han[2]
1. the affiliated hospital of guizhou medical university
2. 北京大学医学部

Cytokines are small secreted proteins usually produced upon activation of several types of cells. They are important molecules that regulate the function of the immune system. CSBF/C10orf99 is a novel cytokine identified by our group through Immunomics screening platform. It is highly expressed in the lesional skin of psoriasis patients and IMQ-induced psoriasis model. We have verified that CSBF/C10orf99 interacted with SUSD2 to inhibit colon cancer cell growth. Several studies show that CSBF/C10orf99 is upregulated in the lesion skin of psoriasis. Psoriasis, affecting approximately 2% of the global population, is a chronic autoimmune skin disease. It often occurs in the skin tissues of the back, abdomen, joints, etc. Psoriasis is characterized by epidermal hyperplasia, increased angiogenesis, and dermal infiltration of inflammatory cells including neutrophils and T cells. Psoriasis is an autoimmune disease caused by multiple genes, and its etiology and pathogenesis remain unclear. We also found that CSBF/C10orf99 was dramatically upregulated in human and mouse psoriatic tissues and it was mainly expressed in the epidermis of lesional skin. IL-17A and mCSBF/C10orf99 can significantly increased the expression of *Csbf/C10orf99* in primary keratinocytes. Administration of mCSBF/C10orf99 by intraperitoneal injection can significantly ameliorate IMQ-induced psoriasiform skin with milder redness and scaling, reduced cell infiltration especially neutrophils and γδ T cells. To know its physiological function, we prepared *Csbf/C10orf99* knockout mice and found that *Csbf/C10orf99* deficiency had no obvious influence on the development of main organs and immune cells. The redness and scaling induced by IMQ is increased in *Csbf/C10orf99*$^{-/-}$ mice, with more cell infiltration including neutrophils and γδ T cells. Bone marrow transfer assay indicates that CSBF regulates psoriasis largely through targeting non-hematopoietic cells, most likely keratinocytes. Our results suggest that the novel potential cytokine CSBF/C10orf99 is increased in psoriasis, keratinocytes is the major source of CSBF/C10orf99, CSBF/C10orf99 can ameliorate the IMQ-induced psoriasiform skin inflammation.

Multiple cytokines, including IL-17A, IL-23, TNF-α, have been observed to increase in lesional skin in IMQ-induced psoriasis-like mice. To examine which factor induces keratinocytes to express CSBF/C10orf99, we stimulated primary murine keratinocytes with a panel of cytokines that are involved in the pathogenesis of psoriasis. Cytokines such as IL-17A, IL-23, TNF-α significantly increased the expression of *Csbf/C10orf99*. IL-17A also upregulated the expression of *CSBF/C10orf99* in HaCaT cells.

In conclusion, our study found that IL-17A could upregulate the expression of CSBF/C10orf99. *Csbf/C10orf99*$^{-/-}$ mice showed significantly worse psoriasis-like symptoms. Our study reveals the protective role of CSBF/C10orf99 against IMQ induced psoriasis in Balb/c mice. CSBF/C10orf99 from non-hemopoietic cells plays a protective role in this disease. Our study is helpful to understand the pathogenesis of psoriasis and provide new ideas and methods for the development of targeted drugs for the treatment of psoriasis.

PO-1391

ZNF276 promotes malignant phenotype of breast carcinoma through upregulating CYP1B1-mediated Wnt/β-catenin pathway

Ting Lei[1]、Yongyin He[2]、Wenwu Zhang[1]、Yi Zhu[1]、Xiaoyu Song[1]、Zhenzhan Kuang[2]、Quan Zhou[2]、Zhaohui Sun[2]、Bin Xiao[1]、Linhai Li[1]

1. Department of Clinical Laboratory, The Sixth Affiliated Hospital of Guangzhou Medical University, Qingyuan People's Hospital

2. 中国人民解放军南部战区总医院

Background Breast cancer has replaced lung cancer as the most popular malignancy since 2020, largely due to the progression of a significant fraction of primary tumors to the metastatic stage. Zinc finger protein 276 (ZNF276) was first identified in a mouse model of Fanconi anemia, however, the expression and underlying role of ZNF276 in breast cancer is not fully understood.

Methods The mRNA and protein expression levels of ZNF276 in breast cancer tissues were detected by TCGA database analysis combined with tissue microarray, and the expression of ZNF276 in MCF-7, MDA-MB-231, SK-BR-3, BT-474 and UACC-812 breast cancer cell lines were analysed by RT-qPCR and Western blot. The effect of ZNF276 on the proliferation, invasion and migration was conducted by functional experiments both in vivo and in vitro. Transcriptome sequencing combined with CUT Tag to explore the potential downstream target genes of ZNF276, and the dual luciferase assay was used to verify the transcriptional regulatory relationship of ZNF276 to the target gene promoter. TOP/FOP Flash assay, immunofluorescence, RT-qPCR and Western blot were used to clarify the underlying role of ZNF326 on Wnt pathway activation. Screening of potential ZNF276 interacting proteins by immunoprecipitation and mass spectrometry (IP-MS), and identification of ZNF276 binding proteins by co-immunoprecipitation (co-IP).

Results ZNF276 is highly expressed in breast cancer tissues and cell lines. Mechanistically, ZNF276 interacted with MAGEB2 and transcriptionally promoted CYP1B1, leading to the activation of Wnt/β-catenin pathway, which gave rise to the proliferation, migration and invasion of breast cancer cells. Specifically, ZNF276 binds to the -1127 bp to -921 bp region of the CYP1B1 promoter through its C2H2 domain, thereby regulating the transcriptional activity of CYP1B1 promoter.

Conclusions Above all, ZNF276 promotes proliferation, migration and invasion of breast cancer cells by recruiting MAGEB2 to regulate CYP1B1, promoting β-catenin nuclear translocation and activating the Wnt/β-catenin pathway. Our findings shed light on the molecular mechanism of ZNF276 and offered a potential therapeutic strategy for breast cancer patients.

PO-1392

Circulating exosomal small RNAs are promising non-invasive diagnostic biomarkers for gastric cancer

Nan Zhang
Jinling Hoapital

Background Dysregulation of small non-coding RNA (ncRNA) is associated with various human diseases including cancer. Gastric cancer (GC) is the fifth most common cancer worldwide and the third leading cause of death from malignant tumours. The most commonly used GC tumour markers such as CEA, CA199, CA242 and CA724 are not diagnostically sensitive or specific enough to screen GC patients. Thus, there is an urgent need to develop new and simple diagnostic biomarkers for detection of GC.
Objectives This study aimed to evaluate the circulating exosomal small RNAs including microRNAs (miRNAs) and P-element-induced wimpy testis (PIWI)-interacting RNAs (piRNAs) as sensitive and specific non-invasive biomarkers for GC diagnosis.
Methods Serum exosomal small RNA transcriptome was examined using unique molecular identifiers (UMI) small RNA sequencing. Dysregulated miRNAs and piRNAs were verified in 70 GC patients and 60 healthy controls (HC) by reverse transcription quantitative PCR.
Results For the total samples in training cohorts and validation cohorts, both the expressions of miR-1307-3p, piR-018569, piR-004918 and piR-019308 were significantly increased ($P < 0.0001$) in GC patients ($n = 70$) as com-pared to those in HC ($n = 60$). Further, we analysed correlation between expression of miR-1307-3p/piR-018569/piR-004918/piR-019308 with clinical characteristics of GC patients. Our data showed that GC patients with metastasis had significantly higher ($P < .05$) expression levels of piR-004918 and piR-019308 in serum exosomes than GC patients without metastasis. However, no significant differences were detected for miR-1307-3p/piR-018569/piR-004918/piR-019308 in patients with other clinical characteristics such as sex, age or grade. Moreover, GC patients with metastasis had significantly higher expression levels of piR-004918 and piR-019308 than GC patients without metastasis. The area under the curve (AUC) for miR-1307-3p, piR-019308, piR-004918 and piR-018569 in the GC group was 0.845, 0.820, 0.754 and 0.732, and the results showed that the diagnostic values of miR-1307-3p, piR-019308, piR-004918 and piR-018569 were much better than that of CEA, CA199 and AFP, which had the AUCs of 0.689, 0.687 and 0.634, respectively. When miR-1307-3p/piR-019308/piR-004918/piR-018569 combined with CEA and CA199, the AUC of the biomarker panel reached 0.902 , 0.914, 0.859 and 0.868. The optimal cut-off values for miR-1307-3p/piR-019308/piR-004918/piR-018569 combined with CEA and CA199 were 5.5576, 8.5607 , 21.8673 and 7.8026, respectively. These data suggested that in addition to miR-1307-3p, serum exosomal piR-019308 combined with CEA and CA199 could provide excellent diagnostic capabilities for GC patients.
Conclusion Our study showed for the first time that in addition to miR-1307-3p, serum exosomal piR-019308, piR-004918 and piR-018569 are potential robust biomarkers for GC diagnosis. Serum exosomal piR-004918 and piR-019308 might be potential markers for monitoring metastasis of GC. The clinical values of piRNAs as biomarkers in other types of cancer need further investigation.

PO-1393

The effect of inflammatory cytokine neutralizing antibody therapy on TFH and TFR cells in collagen-induced arthritis and its significance

Chen Liu、Xingyue Zeng、Tianci Liu、Songsong Lu、Ying Song
Department of Clinical Laboratory, Peking University People's Hospital

Objective We aimed to illustrate the changes of follicular helper (TFH) and follicular regulatory (TFR) cells in rheumatoid arthritis using the collagen-induced arthritis (CIA) model and further clarity the impact of anti-inflammatory treatment on TFH and TFR cells.
Methods We established CIA model and used flow cytometry to analyze the changes of TFH and TFR cells in peripheral blood and spleen at different time points. The expression of TIGIT, CD226, ICOS and PD-1 that characterize the functions of TFH and TFR were also analyzed. The function of spleen TFH and TFR cells from CIA was further analyzed. The effects of anti-inflammatory antibody treatments on the subpopulation and function changes of TFH and TFR were also analyzed in CIA mice.
Results The levels of TFH and TFR were significantly increased in spleen and peripheral blood of CIA mice. After treatment, TFH and TFR cells decreased significantly. TIGIT+ and TIGIT+CD226-TFH cells in CIA mouse spleen were elevated and PD-1 and ICOS expression on TFH and TFR cells in the spleen were also significantly increased. The ability of TFH to secrete IL-21 and help B cells, and TFR to secrete IL-10 and inhibit TFH were both enhanced in CIA mouse spleen. After antibody treatment, cell subsets and functions were significantly recovered.
Conclusion In the pathogenesis of rheumatoid arthritis, TFH and TFR cells in the germinal center increases and their functions are enhanced. After the treatment by inflammatory factor antibodies, TFH and TFR subsets and their functions can be significantly recovered.

PO-1394

Long non-coding RNA RP11-490M8.1 inhibits lipopolysaccharide-induced pyroptosis of human umbilical vein endothelial cells via the TLR4/NF-κB pathway

Xuehui Liu[1]、Shaoguo Wu[1]、Yanwei Hu[2]
1. Guangzhou Twelfth People's Hospital，Guangzhou，Guangdong
2. 广州市妇女儿童医疗中心

Background and aims Pyroptosis is a relatively newly discovered form of programmed cell death that plays an important role in the development of atherosclerosis. Many evidence have reported that lncRNAs are participate in the regulation of atherosclerosis development. However, the regulatory mechanism of lncRNAs on pyroptosis must be further study.
Methods Here, In vitro assays were performed to study the role of lncRNA RP11-490M8.1 on pyroptosis. Moreover, the relative gene mRNA and lncRNA expression levels were tested by quantitative real-time PCR, and protein levels were evaluated by western blot analysis.
Results lncRNA RP11-490M8.1 was significantly downregulated in atherosclerotic plaques. LPS markedly reduced the expression of lncRNA RP11-490M8.1,while induced pyroptosis through increasing the levels of NLRP3, caspase-1, ASC, IL-1β, and IL-18 at both the mRNA and protein in HUVECs. The promotion effects of LPS on pyroptosis were markedly suppressed by overexpression of lncRNA RP11-490M8.1. In addition, LPS increased mRNA and protein of TLR4 and NF-κB, which was also markedly offset by overexpression of lncRNA RP11-490M8.1.

Conclusions These findings indicate that lncRNA RP11-490M8.1 inhibits LPS-induced pyroptosis via the TLR4/NF-κB pathway. Thus, lncRNA RP11-490M8.1 may provide a therapeutic target to ameliorate atherosclerosis.

PO-1395

Staphylococcus aureus Competition and Symbiosis with Nasal Microbiome through Sequestration of Environmental Iron

Yanfeng Zhao[1]、Simon Heilbronner[2]、Darya Belikova[2]
1. The Second Affiliated Hospital of Nanjing Medical University
2. 德国 Tubingen University

The human microbiome is critically associated with human health and disease. Antibiotic resistant bacterial pathogens such as methicillin resistant Staphylococcus aureus, reside within the microbiota, increasing the risk of infections. Epidemiological studies of the nasal microbiome showed positive and negative correlations of non-pathogenic species with S. aureus, but the underlying molecular mechanisms are poorly understood. The environment of the nasal cavities is iron limited and bacteria produces iron scavenging siderophores to overcome this limitation. Here we show that siderophore acquisition is crucial for S. aureus nasal colonization. We screened 80 nasal bacterial strains of seven genera for their capacity to produce siderophores as well as to consume siderophores produced by S. aureus and found that 80% of strains engaged in siderophore-mediated interactions with S. aureus. Especially non-pathogenic corynebacterial species consumed the staphylococcal siderophores staphyloferrin A, staphyloferrin B or both. In coculture experiments, corynebacteria species reduced S. aureus growth in an iron-dependent fashion while other members of the microbiome, producing siderophores accessible to S. aureus, did not. Our data show that consumption of S. aureus-derived siderophores by non-pathogenic species can reduce pathogen proliferation and gives first molecular explanation for the negative correlation of S. aureus and corynebacteria observed in previous studies.

书面交流

PU-0001

Evaluation of seven commercial SARS-CoV-2 RNA detection kits based on real-time polymerase chain reaction (PCR) in China

Bingqi Wang
The Second XiangYa Hospital of Central South University

Purpose SARS-CoV-2 is a new, rapidly spreading human beta coronavirus. It was first identified in Wuhan and caused a disease named COVID-19. SARS-CoV-2 real-time PCR assays represent one of the reference standards to make a definitive diagnosis of COVID-19. Various commercial kits were available for emergency use in China during the outbreak of disease. However, they lack validation for diagnostic use in the clinic. Here, we selected seven representative commercial kits to evaluate their performance in SARS-CoV-2 RNA detection.
Methods We collected 42 archived SARS-CoV-2-positive samples and 200 randomly selected SARS-CoV-2-negative samples. Total nucleic acid extractions were performed on the NP968-S Nucleic Acid Extraction System with paramagnetic particle method, using the Virus DNA/RNA Isolation Kit. Seven kits tested samples in parallel and according to the manufacturer's introductions. Sensitivity, specificity, positive predictive value, negative predictive value, andYouden index were calculated. Cohen's Kappa coefficient, chi-square values were carried out using SPSS software.
Results We selected seven domestic diagnosis kits: kit A (BGI BIOTECH CO., LTD), kit B (OUTDO BIOTECH CO., LTD), kit C (SANSURE BIOTECH INC.), kit D (PERKIN ELMER MEDICAL DIAGNOSTIC PRODUCTS, CO., LTD), kit E (DAAN GENE CO., LTD. OF SUN YAT-SEN UNIVERSITY), kit F (JIANGSU BIOPERFECTUS TECHNOLOGIES CO., LTD), and kit G (FOSUN LONG MARCH MEDICAL SCIENCE CO., LTD). The target genes by seven kits were not the same. All the kits were designed to target the virus ORF1ab gene. Still, kit F and kit G could simultaneously detect ORF1ab, N, and E. We discovered that all seven kits have excellent specificity, but there were differences in their clinical sensitivity. The concordance of kit A, kit B, kit D, and kit F and "reference result" was robust. Besides, the detection rate on different target genes of these assays are not the same; the detection ability of the ORF1ab gene for some kits was weak.
Conclusion To sum up, we summarized and compared the detailed information of seven SARS-CoV-2 RNA detection kits in this study. The overall sensitivity and specificity of all seven kits were sufficient for diagnosing COVID-19. However, there is some difference in their detection ability and clinical applications. At present, real-time PCR has become the "gold standard" of COVID-19 diagnosis. It's meaningful to select the most suitable detection kit to improve the detection rate of SARS-CoV-2 in clinical samples.

PU-0002

Exosomal long non-coding RNA 17A may serve as a novel plasma-based biomarker for diagnosis of Alzheimer's disease

Lina Wang
Laboratory Medical Center, The Second Hospital of Shandong University, Jinan, Shandong Province, China

Long non-coding RNA (lncRNA) and exosomes are involved in the pathological process of Alzheimer's disease (AD). Many lncRNAs, such as brain cytoplasmic 200 RNA (BC200), 17A and 51A were upregulated in the brains of patients with AD. The aim of the present study was to determine whether the expression levels of several lncRNAs derived from plasma exosomes

could be used as a biomarker of AD. A total of 59 patients with AD and 61 controls were recruited, and the expression levels of BC200, 17A and 51A were detected. Some other clinical characteristics were collected and analyzed simultaneously. The expression levels of 17A in patients with AD were significantly higher compared with the controls ($p < 0.05$). Receiver operating characteristic curve analysis showed that the area under the curve was 0.633, the sensitivity was 83.05%, the specificity was 45.90%, and the cutoff point was 0.595. Through subgroup analysis, we also found that 17A can distinguish moderate to severe AD from mild AD. In order to identify whether the diagnostic value of 17A was independent of some clinical data, such as age, sex, blood pressure, blood sugar, smoking and drinking status, blood levels of folic acid and et al , we did subgroup analysis and Spearman's rank correlation test. The results showed that there was no significant statistical difference. The present study showed that plasma exosomal 17A may be used as a potential novel biomarker for diagnosis of AD.

PU-0003

流式细胞技术在临床检验中的应用

黄薇、钱源
昆明医科大学第一附属医院

近年来医学研究发展越来越快，随之也加速发展的还有各种各样的医学技术。流式细胞技术（flow cytometry，FCM）是 20 世纪 70 年代初发展起来的一项高新技术，是一种综合应用光学、机械学、流体力学、电子计算机、细胞生物学、分子免疫学等学科技术，使被测溶液流经测量区域，并逐一检测其中每一个细胞的物理和化学特性，从而对高速流动的细胞或亚细胞进行快速定量测定和分析的方法。随着研究的日益深入，流式细胞技术已经不仅仅是在医学研究中有着重要的意义，而是进入临床应用阶段对于临床检验也有极大的影响。本文主要从流式细胞术在临床上的应用入手，分析其在临床检验中的应用。

PU-0004

二甲双胍通过 IGF-1/PI3K/Akt 信号通路对细胞衰老的影响

侯玉丽、付静轩、王培昌
首都医科大学宣武医院

目的 探讨二甲双胍（Met）通过 IGF-1/PI3K/Akt 信号通路对细胞衰老的影响。
方法 选取 2BS 细胞分成四组，即对照（NC）组、胰岛素样生长因子-1（IGF-1）组、Met 组、Met+IGF-1 组。加药处理后进行 SA-β-Gal 染色检测细胞衰老水平、CCK8 试验检测细胞增殖能力、EdU 试验检测 DNA 合成能力以及 Western blot 检测各组 PI3K、p-PI3K、Akt、p-Akt 蛋白表达。
结果 各组 SA-β-Gal 染色阳性率比较，差异有统计学意义（$P < 0.05$）。Met+IGF-1 组 SA-β-Gal 染色阳性率低于 IGF-1 组，差异有高度统计学意义（$P < 0.01$）。在相同时间点，Met+IGF-1 组 OD450 值高于 IGF-1 组，差异有统计学意义（$P < 0.05$）。EdU 染色后在 370 nm 处的染色结果显示，各组 OD370 值比较，差异有统计学意义（$P < 0.05$）；Met+IGF-1 组 OD370 值高于 IGF-1 组，差异有统计学意义（$P < 0.05$）。Met 组 p-PI3K、p-Akt 蛋白表达量低于其他组，差异有统计学意义（$P < 0.05$）。IGF-1 组 p-PI3K、p-Akt 蛋白表达量高于其他组，差异有统计学意义（$P < 0.05$）。Met+IGF-1 组 p-PI3K、p-Akt 蛋白表达量低于 IGF-1 组，差异有统计学意义（$P < 0.05$）。
结论 Met 可通过抑制 IGF-1/PI3K/Akt 信号通路来延缓细胞衰老。

PU-0005

线粒体 DNA（mtDNA）的可变拷贝数预测急性髓细胞白血病患者预后

黄松苓、赵滢
昆明医科大学第一附属医院

目的 线粒体 DNA（mtDNA）拷贝数的变化在包括急性髓细胞白血病在内的各种人类癌症中被广泛报道，并被认为是癌症的一个重要标志。然而，对于可变 mtDNA 含量在该癌症预后评估中的价值还尚未有相关报道。
方法 采用实时定量 PCR 方法，对一组急性髓细胞白血病患者和正常对照组进行 mtDNA 拷贝数检测，探讨不同 mtDNA 含量与急性髓细胞白血病患者临床结局的关系。
结果 与对照组相比，大多数急性髓细胞白血病患者的 mtDNA 含量较低，前者的相对平均 mtDNA 含量高于后者。值得注意的是，可变 mtDNA 含量并不影响急性髓细胞白血病患者的总生存率，但是我们发现，mtDNA 含量增加与晚期肿瘤患者的生存率低相关。
结论 在本研究中，我们发现 mtDNA 含量的增加与晚期肿瘤患者生存率的下降有着密切的联系。

PU-0006

Low expression of immune-related lnRNA HSPC324 is associated with poor prognosis in smoking-related luad

dajie zhou、Jing Wang
Yantai Yuhuangding Hospital

Background Smoking is one of the most dangerous factors associated with the growth of lung adenocarcinoma (LUAD). Through database mining, many survival- and prognosis-related biomarkers were collected. However, the accuracy of immune-related lncRNA predictions is not precise enough. Therefore, we pointed to found a new signature to boost the smoking-related LUAD prognosis estimation.
Methods Pearson correlation analysis were used to performed lncRNA expression and immune-related genes in the samples to distinguish immune-related lncRNAs. RNA high-throughput sequencing and clinicopathologic data of HSPC324 were downloaded from the TCGA. The relationship between the overall survival (OS) and HSPC324 expression was analyzed by the Kaplan-Meier method and the Cox regression analysis.
Results Based on a median expression of 0.343, we divided patients into high- and low-expression categories. Our results indicated that the HSPC324 expression was decreased in smoking-related LUAD (all tumor vs. adjacent tissues) (P= 9.573e−27). Also, Kaplan-Meier curves showed that low HSPC324 expression was associated with a better overall survival among the smoking-related LUAD patients (P=0.032). Univariate Cox regression analysis showed that reduced HSPC324 expression in smoking-related LUAD is associated with stage (HR =1.03, 95%CI [1.372-1.883], P =4.19E-09), T classification (HR = 1.545, 95%CI [1.233-1.936], P=0.000) and N classification (HR = 1.6749, 95%CI [1.378-2.035], P= 2.15E-07). MultiCox Cox regression analysis showed that stage (HR =1.3903, 95%CI [1.106-1.747], P =0.004), HSPC324 (HR =0.5767, 95%CI [0.349 -0.953], P =0.03) were independent prognostic biomarker for smoking-related LUAD.
Conclusions Low expression of HSPC324 may be a potential molecular marker for predicting poor prognosis of smoking-related LUAD. It also suggested that HSPC324 might potentially have biological functions in the development of smoking-related LUAD.

PU-0007

长链非编码 RNA Z38 在结直肠癌中低表达并作为一个肿瘤抑制因子

王晴美
郴州市第一人民医院

LncRNAs serve comprehensive roles in various diseases, including cancer. Z38 was up-regulated in breast cancer, which is a notable biomarker of prognosis;its potential biological roles and involvement in the progression of colorectal cancer (CRC) remains unclear. The present study aimed to investigate the expression of Z38 in patients with CRC and to investigate its effect on cells.Low expression levels of Z38 were associated with the old age of patients, large tumor size, poorly tumor differentiation (p <0.05).Up-regulation of Z38 could inhibit CRC cell proliferation in vitro.The results of the present study suggest that over-expression of Z38 inhibits proliferation and plays important roles in CRC, which may act as a novel candidate biomarker and therapeutic target in carcinomas.

PU-0008

47 例鹦鹉热衣原体阳性检出患者的临床特征分析

邓方芳、冯敏、谭筱醴、张玮佳
四川金域医学检验中心有限公司

目的 探讨宏基因二代测序技术检出鹦鹉热衣原体阳性患者的临床特征。
方法 回顾性分析 2020 年 8 月至 2021 年 5 月通过宏基因二代测序技术检出的 47 例鹦鹉热衣原体阳性患者的临床特征，包括性别、年龄、鸟禽接触史、实验室检查、影像学表现、临床症状等，为鹦鹉热衣原体的研究和临床诊疗提供依据。
结果 47 例阳性检出患者中男性居多，共 33 例，占 70.2%，女性 14 例，占 29.8%；年龄范围为 34 岁-82 岁，其中 60 岁-70 岁占 39.1%。6 例患者（12.8%）有明确鸟禽接触史，41 例患者（87.2%）接触史不详。阳性检出患者中 40%同时存在发热、咳嗽症状，15%仅表现为咳嗽，25%仅以发热为主要症状。阳性检出患者的 C 反应蛋白均高于正常值范围，占 100%。63.2%阳性者降钙素原升高。14.8%表现为白细胞计数升高，77.8%在正常值范围，7.4%低于正常值。中性粒细胞比率升高者占 77.8%，14.8%在正常范围内，7.4%低于正常值。影像学方面，5 例（25%）炎症部位为左肺，7 例（35%）炎症部位在右肺，8 例（40%）双侧同时存在，其中 6 例（30%）明确炎症部位以下叶为主，1 例（5%）上叶为主。
结论 鹦鹉热衣原体阳性检出患者主要表以男性为主，且老年人居多，临床表现为 C 反应蛋白普遍升高，中性粒细胞比率与降钙素原明显升高，白细胞计数基本正常。影像学多表现肺部炎症改变，分布无特异性。大部分存在发热、咳嗽症状。由于患者群体特征无明显特异性，因此宏基因二代测序技术对于及早发现鹦鹉热衣原体感染意义重大。

PU-0009

Serum metabolic profiling analysis of chronic gastritis and gastric cancer by untargeted metabolomics

Lin Yu[1]、Qinhuai Lai[2]、Qian Feng[1]、Yuanmeng Li[1]、Bei Xu[1]、Jiafu Feng[1]
1. Mianyang Central Hospital
2. 四川大学生物治疗国家重点实验室

Purpose Gastric cancer is a common tumor of the digestive system. Identification of potential molecules associated with gastric cancer progression and validation of potential biomarkers for gastric cancer diagnosis are very important. Thus, the aim of our study was to determine the serum metabolic characteristics of the serum of patients with chronic gastritis (CG) or gastric cancer (GC) and validate candidate biomarkers for disease diagnosis.
Experimental design: A total of 123 human serum samples from patients with CG or GC were for untargeted metabolomics analysis via UHPLC-Q-TOF/MS to determine characteristics of the serum. Principal component analysis (PCA), partial least squares discriminant analysis (PLS-DA) and heat map were used for multivariate analysis. In addition, commercial databases were used to identify the pathways of metabolites. Differential metabolites were identified based on a heat map with a t-test threshold ($p < 0.05$), fold-change threshold (FC > 1.5 or FC < 2/3) and variable importance in the projection (VIP >1). Then, differential metabolites were analyzed by receiver operating characteristic (ROC) curve to determined candidate biomarkers. All samples were analyzed for fasting lipid profiles.
Results Analysis of serum metabolomic profiles indicated that most of the altered metabolic pathways in the three groups were associated with lipid metabolism ($p < 0.05$) and lipids and lipid-like molecules were the predominating metabolites within the top 100 differential metabolites ($p < 0.05$, FC > 1.5 or FC < 2/3, and VIP >1). Moreover, differential metabolites, including hexadecasphinganine, linoleamide and N-Hydroxy arachidonoyl amine had high diagnostic performance according to PLS-DA. In addition, fasting lipid profile analysis showed the serum levels of total cholesterol (TC), high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C) and apolipoprotein A1 (Apo-A1) were decreased concomitant to the progression of the progression of the disease compared with those in the control group ($p < 0.05$).
Conclusions Thus, this study demonstrated that lipid metabolism may influence the development of CG to GC. Hexadecasphinganine, linoleamide and N-Hydroxy arachidonoyl amine were selected as candidate diagnostic markers for CG and GC.

PU-0010

Chinese Abnormal Compound Heterozygote Spinocerebellar Ataxia Type 8: A case report

Minjin Wang
West China Hospital

An elderly Chinese male patient was diagnosed with compound heterozygous spinocerebellar ataxia type 8, molecular diagnosis found that this patient with (CTA)n(CTG)n repeats unit of his ATXN8/ATXN8OS gene was 134/93. The patient has a 6-year medical history, mainly manifested by ataxia, dysarthria, abnormal eye movements, and pyramidal signs. Magnetic resonance imaging(MRI) showed no obvious abnormalities in the medulla oblongata and cervical spinal cord except for cerebellar atrophy and sulci enlargement. There are heterozygous SCA8 individuals among his family members, but there are significant differences in their onset-age and clinical manifestations. This case reminds us that (CTA)n(CTG)n repeats are very prone to dynamic mutations in intergenerational inheritance, and the ATXN8/ATXN8OS

gene penetrance is different in different SCA8 individuals, which suggests that genetic detection is of great importance.

PU-0011

Establishment of Real Time Allele Specific Locked Nucleic Acid Quantitative PCR for Detection of HBV YIDD (ATT) Mutation and Evaluation of Its Application

Yongbin Zeng 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

Background Long-term use of nucleos(t)ide analogues can increase risk of HBV drug-resistance mutations. The rtM204I (ATT coding for isoleucine) is one of the most important resistance mutation sites. Establishing a simple, rapid, reliable and highly sensitive assay to detect the resistant mutants as early as possible is of great clinical significance.
Methods Recombinant plasmids for HBV YMDD (tyrosine-methionine-aspartate-aspartate) and YIDD (tyrosine-isoleucine-aspartate-aspartate) were constructed by TA cloning. Real time allele specific locked nucleic acid quantitative PCR (RT-AS-LNA-qPCR) with SYBR Green I was established by LNA-modified primers and evaluated with standard recombinant plasmids, clinical templates (the clinical wild type and mutant HBV DNA mixture) and 102 serum samples from nucleos(t)ide analogues-experienced patients. The serum samples from a chronic hepatitis B (CHB) patient firstly received LMV mono therapy and then switched to LMV + ADV combined therapy were also dynamically analyzed for 10 times.
Results The linear range of the assay was between 1×10(9) copies/μl and 1 × 10(2) copies/μl. The low detection limit was 1 × 10(1) copies/μl. Sensitivity of the assay were 10(-6), 10(-4) and 10(-2) in the wild-type **Background** of 1 × 10(9) copies/μl, 1 × 10(7) copies/μl and 1 × 10(5) copies/μl, respectively. The sensitivity of the assay in detection of clinical samples was 0.03%. The complete coincidence rate between RT-AS-LNA-qPCR and direct sequencing was 91.2% (93/102), partial coincidence rate was 8.8% (9/102), and no complete discordance was observed. The two assays showed a high concordance (Kappa = 0.676, P = 0.000). Minor variants can be detected 18 weeks earlier than the rebound of HBV DNA load and alanine aminotransferase level.
Conclusions A rapid, cost-effective, high sensitive, specific and reliable method of RT-AS-LNA-qPCR with SYBR Green I for early and absolute quantification of HBV YIDD (ATT coding for isoleucine) variants was established, which can provide valuable information for clinical antiretroviral regimens.

PU-0012

外泌体 ABCA1 蛋白在阿尔茨海默病诊断价值的初步研究

刘辰庚、赵越、路尧、王培昌
首都医科大学宣武医院

目的 初步探索高 ABCA1 外泌体跨血脑屏障的现象及其作为阿尔茨海默病候选标志物的潜在价值。
方法 将 9 月龄 APP/PS1 模型小鼠脑脊液（CSF）高 ABCA1 外泌体注射至野生型（WT）小鼠脑室研究其转运过程，同时检测主 69 例观认知下降（SCD）、43 例轻度认知障碍（mild cognitive impairment，MCI）和 35 例痴呆期（dementia of Alzheimer's type，DAT）患者血清外泌体 ABCA1 水平。
结果 APP/PS1 双转基因小鼠 CSF 和血清中外泌体 ABCA1 水平随龄显著升高（$P < 0.05$）；注射 2 小时后 WT 小鼠血清外泌体 ABCA1 水平显著升高（$P < 0.05$）；MCI 和 DAT 患者血清外泌体 ABCA1 较对照组显著升高（$P < 0.05$），且 DAT 组高于 MCI 组（$P < 0.05$）。

结论 ABCA1 外泌体可经透过血脑屏障到达外周血而被有效检测，其可作为 AD 诊断的候选标志物，但在 SCD 的诊断中还需积累更多的研究数据。

PU-0013

A noval mutation analysis of the MMAA genes in Chinese boy with impaired health-related quality of life in children affected by methylmalonic acidemia

Dongling Tang[1]、Juan Le[1]、bo Wang[2]
1. Renmin Hospital of Wuhan University Wuhan,
2. 湖北省妇幼保健院（湖北省妇女儿童医院）

Background Isolated methylmalonic acidemia refers to a group of inborn errors of metabolism characerized by elevated methylmalonic acid concentrations in the blood and urine due to the failure of converting methylmalonyl-CoA into succinyl-CoA during propionyl-CoA metabolism.Mutations in the MMAA gene cause isolated methylmalonic acidemia. It occurs in approximately one to three out of every 100 thousand Chinese newborns.
METHODS A 13-month-old boy was diagnosed with isolated methylmalonic acidemia. Isolated methylmalonic acidemia was diagnosed by analyzing the organic acids in plasma and/or urine using gas-liquid chromatography and tandem mass spectrometry. The subtype of methylmalonic acidemia was established by cellular biochemical studies including 14¯C propionate incorporation, B12 responsiveness, complementation analysis, cobalamin distribution assays and molecular genetic testing. Identification of biallelic pathogenic variants in MUT, MMAA, MMAB, MCEE, and MMADHC genes and confirmation of carriers in parents can establish the diagnosis (2-4). In our case the MMAA mutations in the proband were detected by targeted sequencing. The mutations in the proband and his family members were validated by Sanger sequencing.
RESULT We identified two mutations in the MMAA gene in this case: c.491G>A and c.650T>A. The c.491G>A is a novel mutation in the MMAA gene. The boy is a heterozygous carrier of both mutations. The boy was treated with intravenous sodium benzoate and fluids. His sensorium gradually improved and he recovered from the acute illness. Other family members are heterozygous carriers of either mutations but with no symptoms.it is clear that a novel c.491G>A mutation was detected in the MMAA gene. Heterozygous carriers of both c.491G>A and c.650T>A mutations are associated with isolated methylmalonic acidemia.
Conclusion Mutations in the MMAA gene can affect either its GTPase activity or the interaction with MUT (10). In our case, the boy with symptoms is a heterozygous carrier of both mutations. On one allele, he has a Novel mutation in the MMAA gene previously reported nonsense p.Leu217* mutation. On the other allele, he has a novel p.Gly164Glu point mutation. His family members, who carry either mutations on one allele, have no symptoms. This novel mutation is likely to be pathogenic. However,the mechanisms of dysfunction of this mutant require further investigation. It is evident that the detection of novel mutations may be instrumental in the development of efficient non invasive genetic diagnosis and in the expansion of its application in other disorders.

PU-0014

血清外泌体 MT1-MMP 在胃癌中的表达及临床意义研究

董召刚
山东大学齐鲁医院

目的 检测血清外泌体 MT1-MMP 及 CEA、CA19-9、CA72-4 在胃癌、不典型增生、慢性萎缩性胃炎、健康对照中的表达，探讨对胃癌的早期诊断价值。
方法 收集 2016.12-2017.12 山东大学齐鲁医院住院的胃癌 119 例、不典型增生 33 例、慢性萎缩性胃炎 31 例，患者术前清晨空腹血清 3ml，收集 31 例健康对照血清。提取血清外泌体，并利用电镜、粒径、western blot 鉴定。试剂盒提取血清外泌体 RNA，实时荧光定量 PCR 检测血清外泌体 MT1-MMP 表达。电化学发光法检测 CEA、CA19-9、CA72-4 水平。MT1-MMP 表达采用 2-ΔΔCT 方法计算。数据用中位数表示，M-W 检验或 K-W 检验分析与胃癌临床参数的关系。绘制 ROC 曲线计算曲线下面积，计算胃癌 cut-off 及相应的敏感度、特异度、阳性预测值、阴性预测值。
结果 成功分离并鉴定血清外泌体，血清外泌体 MT1-MMP 在胃癌中表达高于不典型增生、慢性萎缩性胃炎及健康对照（P 均<0.05），不典型增生高于慢性萎缩性胃炎（P=0.022）及健康对照（P=0.001），慢性萎缩性胃炎高于健康对照（P=0.019）。胃癌 CEA 高于不典型增生、慢性萎缩性胃炎健康对照（P<0.05）。CA19-9 和 CA72-4 在三组表达无显著差异（P >0.05）。胃癌患者血清外泌体 MT1-MMP 表达与肿瘤大小、分化、分型、浸润深度、转移、TNM 分期密切相关（P 均<0.05）。ROC 曲线显示 MT1-MMP 与 CEA 联合可提高诊断效能，其灵敏度、特异度、阳性预测值、阴性预测值、曲线下面积为 75.6%、83.9%、94.7%、47.3%、0.821 (95% CI: 0.750-0.878)。
结论 血清外泌体 MT1-MMP 在胃癌表达升高，与分期转移密切相关，对胃癌早期诊断价值较高，有成为无创诊断标志物的潜能。

PU-0015

血清 lncRNA UCA1 在食管鳞癌的表达及临床意义

闫素真、杜鲁涛、王传新
山东大学第二医院

目的 探讨长链非编码 RNA(lncRNA) 尿路上皮癌胚抗原 1(UCA1) 在食管鳞癌患者血清中的表达及潜在 的临床意义。
方法 收集 96 例食管鳞癌患者血清样本，同时选取 96 例年龄、性别匹配的健康体检者作为健康对照组，其中 12 例食管鳞癌患者行术前、术后比较。采用实时荧光定量 PCR 的方法检测 lncRNA UCA1 在食管鳞癌 血清中的表达，并对食管鳞癌患者术前、术后进行比较。分析食管鳞癌患者血清 lncRNA UCA1 与其临床病理参 数的关系，采用受试者工作曲线(ROC) 对血清 lncRNA UCA1 的诊断效能进行评价。
结果 与健康对照组比较， 食管鳞癌患者血清中 lncRNA UCA1 的表达升高，且患者术后较术前表达下降，差异有统计学意义(P＜0．001) 。血 清 lncRNA UCA1 诊断食管鳞癌的 ROC 曲线下面积(AUC) 为 0．816，灵敏度和特异度分别为 77．1%和 76．0%。此 外，与传统肿瘤标志物鳞状细胞癌相关抗原(AUC = 0．679) 比较，lncRNA UCA1 对食管鳞癌诊断效能更高(P＜ 0．001) 。
结论 血清 lncRNA UCA1 可作为食管鳞癌早期诊断及术后监测潜在的新型肿瘤标志物。

PU-0016

前列腺癌骨转移相关基因学分析

李亚平
成都市第三人民医院

目的 通过对前列腺癌骨转移相关基因芯片数据的生物信息学分析，进一步了解前列腺癌骨转移发病的分子机理。
方法 从 Gene Expression Omnibus(GEO)网站下载前列腺癌骨转移相关芯片数据 GSE32269，选取其中的 51 个样本，包括 22 个原发性局限性前列腺癌样本，29 个前列腺癌骨转移组织样本。利用 BRB ArrayTools v 4.5.1 stable 对两组样本进行差异基因分析（DEGs）。所有差异基因根据其表达值的变化分为上调和下调组，导入 DAVID 进行 GO 富集分析以及 KEGG 信号通路分析。利用 string 在线分析差异基因的蛋白-蛋白相互作用（PPI）网络。
结果 两组基因表达谱比较，共筛选出 340 个差异基因。相对于原发性局限性前列腺癌样本，前列腺癌骨转移组织样本共 164 个基因表达上调，176 个基因表达下调。 GO 富集分析显示，上调基因富集主要与肌肉收缩、负调节生长、细胞对锌离子的反应、丝氨酸内肽酶活性等有关。而下调基因富集与细胞外基质、胶原蛋白分解代谢、胶原纤维组织、胶原结合、血小板衍生生长因子相关。KEGG 通路最重要的术式包括黏着斑、细胞外基质受体相互作用、细胞周期、嘌呤代谢、整合素信号通路等生物通路。 PPI 网络提示表达上调的 SPP1、HBB、AR、MMP9 及下调的 AZGP1 是重要的重要基因，被认为是中枢基因。
结论 SPP1、HBB、AR、MMP9、AZGP1、POSTN、FN1、VCAN 等基因与前列腺癌骨转移的生物学进程密切相关，其中 SPP1 基因上调表达明显，提示前列腺癌骨转移中可能存在 SPP1/MET 信号通路和 AR 失调现象。

PU-0017

Association between mitochondrial DNA copy number and non-small cell lung cancer risk

Songling Huang 、ying zhao
Department of Clinical Laboratory, the First Affiliated Hospital of Kunming Medical University, Kunming, 650032, China

BACKGROUND Alterations of mitochondrial DNA (mtDNA) copy number is widely reported in various human cancers, including lung cancer, and is considered to be an important hallmark of cancers. This study was undertaken to investigate the possibility of variable mtDNA copy number in peripheral blood lymphocytes (PBLs) as a risk predictor for non-small cell lung cancer (NSCLC).
METHODS Using real-time quantitative PCR approach, we examined mtDNA copy number in PBLs from 60 NSCLC patients and 60 matched controls.
RESULTS We found that the mitochondrial DNA copy number in NSCLC patients was significantly higher than that in the control group (median: 1.28 to 0.97; P < 001). We further assessed the association between mitochondrial DNA copy number and NSCLC risk using multivariate logistic regression. With the median of the control value as the cut-off point, it was found that the risk of NSCLC increased significantly in high mtDNA copy number compared with the low mtDNA copy number (the ratio of the adjusted ratio, 2.57; 95% confidence interval, 1.89-3.26).In trend analysis, we found that higher mitochondrial DNA copy number had a dose-response relationship with increased risk of NSCLC (P < 001).
CONCLUSIONS These findings provide the first epidemiological evidence that high mitochondrial DNA copy number in PBLs is associated with increased risk of NSCLC.

PU-0018

Expanding the Rules of Nucleic Acid Hybridization Using Junction Probes

Xuchu Wang、Zhihua Tao
the Second Affiliated Hospital of Zhejiang University School of Medicine

Nucleic acid hybridization is crucial in target recognition with respect to nucleic acid biosensing and gene regulation. Conventional linear probes or molecular beacon encounter challenges in multiplexing and specific recognition of intractable nucleic acids. Advances in nucleic acid nanotechnologies have gave birth to a set of novel structural probes: junction probes (JPs), which make full use of the advantages of specificity, stability, programmability and predictability of Watson–Crick base pairing. Recent years, junction probes have been regularly implemented in constructing systems related to biosensing synthetic biology and gene regulation. herein, we summarize the latest advances in JPs designs as potential nucleic acids biosensing systems and expansive applications, and provided some general guidelines for developing JPs based sensing strategies for implement of such systems.

PU-0019

Loading of "cocktail siRNAs"into extracellular vesicles via TAT-DRBDfor the treatment of castration-resistant prostate cancer

Yanjun Diao 、liu yang、mingquan su、rui li、yue zhang、lei zhou、weixiao fan、xiaoke hao、jiayun liu
Department of Clinical Laboratory Medicine, Xijing Hospital, Fourth Military Medical University, Xi'an, China

Extracellular vesicles (EVs) are cell-derived, membranous nanoparticles that mediate intercellular communication by transferring biomolecules between cells. As natural delivery vehicles, EVs may exhibit higher delivery efficiency, lower immunogenicity, and better compatibility than existing therapeutic RNA carriers. One major limitation for their therapeutic use is the lack of an efficient, robust, and scalable method to load EVs with therapeutic siRNA molecules of interest. Here, we report a novel strategy using polycationic membrane-penetrating peptide TAT to encapsulate siRNAs into EVs. **METHODS** Three TAT peptides were expressed with DRBD as 3TD fusion protein in a in E. coli prokaryotic expression system. DRBD binding with siRNAs in a sequence-independent manner facilitates multiplex genes（FLOH1, NKX3 and DHRS7） targeting, which is particularly important in complex multi-genic CRPC.**RESULTS** EVs were isolated using differential centrifugation from WPMY-1 cell culture medium. The increase of mergered yellow fluorescence in the engineered EVs showed by TIRFM and the decrease of zeta potential absolute valuescertificatedthe co-localization of siRNA with EVs, which indicated that siRNA has been successfully delivered into WPMY-1 EVs. qRT-PCR analysis revealed that the mRNA level of FLOH1, NKX3 and DHRS7 wasdramatically decreased when cells treated with engineered EVs loaded of siRNAs mixtures relative to thelevel of untreated cells. Western and flow cytometryresults indicate that delivery of siRNA mixtures by engineered EVs can effectively downregulate AR expression and induce LNCaP-AI cellapoptosis.**CONCLUSION**The uptake efficiency of the EVs and the significant downregulated expression of three genes suggested the potential of TAT as efficient siRNAs carriers by keeping the function of the cargoes.

PU-0020

SOD 和 8-OHdG 子痫前期患者胎盘组织的表达及临床意义

景丽萍、庄学伟
山东省立第三医院

目的 测定子痫前期患者胎盘组织超氧化物歧化酶（Superoxide dismutase,SOD）及 DNA 氧化损伤产物 8-羟基脱氧鸟苷(8-hydroxy-2-deoxyguanosine,8-OHdG)的表达，探讨其在子痫前期发病机制中的作用。
方法 采用实时定量 PCR 检测 SOD1 和 SOD2 mRNA,免疫组化法检测 SOD1，SOD2 和 8-OHdG 在正常第三期和子痫前期胎盘组织的表达水平。
结果 与正常胎盘组织相比，子痫前期胎盘组织中 SOD1 和 SOD2 mRNA 和蛋白表达降低（P<0.05），而 DNA 氧化损伤产物 8-OHdG 升高。
结论 子痫前期患者抗氧化应激能力下降，氧化损伤产物增加，氧化应激是子痫前期病因之一。

PU-0021

Exosomal LncRNA RP5-977B1 as a novel minimally-invasive biomarker for early diagnosis and prognostic prediction in non-small cell lung cancer

Ling Min
Cancer Center of Guangzhou Medical University

Lung cancer is the leading cause of cancer-related deaths in the world. Non-small cell lung cancer (NSCLC) accounts for 85% of all lung cancer cases. For lack of conveniently sensitive and specific biomarkers, the majority of patients are in the late stage at initial diagnosis. Long non-coding RNAs (LncRNAs), a novel type of non-coding RNA, have recently been recognized as critical factors in tumor initiation and progression, but the role of exosomal LncRNAs has not been thoroughly excavated yet. In the present study, we isolated exosomes from the serum of NSCLC patients and healthy controls. RNA deep sequencing was subsequently performed to detect differentially expressed exosomal LncRNAs. On the basis of analysis, we find that exosomal LncRNA RP5-977B1 exhibited higher levels in NSCLC than that in the healthy controls, this result was also verified by qRT-PCR assay. Furthermore, RP5-977B1 is validated to be mainly encapsulated by exosomes that are protected from RNase digestion. ROC curve, with AUC values of 0.8899 in distinguishing of NSCLC patients and controls, was performed to evaluate the diagnostic values of RP5-977B1, the diagnostic efficiency was superior to conventional biomarker serum CEA and CYFRA21-1, especially in early stage patients. Kaplan-Meier analysis revealed that high expression of exosomal RP5-977B1was closely related with worse prognosis in NSCLC (P=0.036). Together, our results suggest that exosomal RP5-977B1 serve as a novel “liquid biopsy” diagnostic and prognostic biomarker to monitor NSCLC and improve possible therapy.

PU-0022

孕妇年龄风险与胎儿染色体异常发生率的相关性分析

李辉斌
南方医科大学珠江医院

目的 探讨高龄孕妇各年龄段与胎儿染色体异常的相关性。

方法 回顾性分析 925 例高龄孕妇(≥35 岁)，行绒毛膜穿刺、羊膜腔穿刺和脐带穿刺收集绒毛、羊水和脐血进行培养及染色体 G 显带核型分析，分析高龄孕妇与胎儿染色体异常率及类型的分布情况，按年龄分组(35-37 岁组、38-40 岁组、40 岁以上组)，用 χ2 检验各年龄组的异常率的差异。
结果 在 925 例高龄孕妇的羊水染色体核型分析中，共检出异常核型 66 例(7.13%)，其中染色体数目异常 53 例(6.93%)，占异常构成比 80.3%，其中 21 三体比例最高 29 例(3.14%)，占异常构成比 43.93%，18 三体/13 三体/性染色体数目异常比例分别为 11 例（1.19%)/4 例(0.43%)/9 例(0.97%)。结构异常 13 例(1.05%)，占异常构成比 19.7%，其中易位 8 例(0.86%)，倒位 5 例(0.54%)。从 35 到 37 岁、38 到 40 岁、40 岁以上 3 个年龄组的染色体核型异常率依次为 5.49%、6.02%和 10.38%，孕妇年龄递增胎儿染色体异常率逐年上升。各年龄组间总体异常率差异有统计学意义(χ2＝6.436，P＝0.04)。
结论 胎儿染色体异常的风险随孕妇年龄的增长而增加，结构异常的分布与母亲年龄因素相关性，40 岁以上胎儿染色体总体异常率显著上升。对高龄孕妇进行产前诊断染色体核型分析是避免染色体异常儿出生的重要手段。

PU-0023

Overexpression of LINC00673 promotes the proliferation of cervical cancer cells

Shengkai Huang 、Ruo-Xuan Ni、Wen-Jie Wang、Di Wang、Mei Zhao、Cheng-Zhi Lei、Chang-Zhi Huang、Ping Bai、Yi-Qun Che、Jian-Ping Xu
National Cancer Center/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, 100021, China

Objective To study the expression of LINC00673 in cervical cancer and cervical intraepithelial neoplasia (CIN) and to explore the role of LINC00673 in the development of cervical cancer.
Methods The expression of LINC00673 in serum from cervical cancer patients, CIN patients, and healthy participants was detected by RT-qPCR. The function of LINC00673 in cervical cancer cells was analyzed using in vitro and in vivo experiments.
Results Our results revealed that serum LINC00673 levels were highest in cervical cancer patients, followed by patients with CIN and healthy controls. In vitro experiments demonstrated that overexpression of LINC00673 enhanced the proliferation and cell cycle progression of HeLa and SiHa cells. In vivo experiments showed that the tumor weight and volume of nude mice subcutaneously injected with LINC00673-overexpressing HeLa cells were larger than those of nude mice injected with control cells ($P < 0.05$). Western blotting showed that cell cycle-related proteins cyclin A2 and cyclin E and interstitial-associated proteins Snail and N-cadherin were upregulated and p53 signaling pathway-related proteins were downregulated in LINC00673-overexpressing HeLa and SiHa cells.
Conclusion LINC00673 plays an important role in the development of cervical cancer and may serve as a new therapeutic target for cervical cancer.

PU-0024

无创产前筛查对胎儿染色体非整倍体检出的临床价值

周慕平、刘娜、文君、黄艳
邵阳市妇幼保健院

目的 探究无创产前筛查对胎儿染色体非整倍体检出的临床价值。
方法 选取 2017 年 6 月至 2019 年 6 月某院产科收治的产前检查孕妇 102 例作为研究对象，统一应用无创产前 DNA 检测技术采集母体外周血进行无创产前筛查，系统评估胎儿染色体非整倍体疾病

患病风险率。针对高风险筛查结果孕妇采取分析染色体核型方式，研究无创产前筛查对胎儿染色体非整倍体疾病的诊断价值。
结果 对纳入研究 102 例孕妇进行外周血检测，共 102 份标本，NIPT 检测显示性染色体非整倍异常 16 例。经咨询发现，16 例孕妇均自愿接受检测，其中 NIPT 与染色体核型分析结果一致 6 例，包括（45，X）3 例；（46，XXX）1 例；（46，XX）1 例；（47，XXY）1 例。检测显示高风险 8 例，检出阳性率 7.84%。染色体核型分析结果等同于无创产前筛查检测结果。
结论 针对胎儿染色体非整倍体疾病产前筛查应用无创产前 DNA 检测具有重要临床价值，由于该检测技术敏感性较高。
因此，具有较高的准确性，且为无创操作，对孕妇及胎儿的伤害较小，是提高生育质量的重要技术。

PU-0025

Isocitrate dehydrogenase 3A, a rate-limiting enzyme of the TCA cycle, promotes hepatocellular carcinoma and functions as a prognostic marker

Wenzhe Si、Liyan Cui
Peking University Third Hosiptal

Background The precise molecular mechanism of hepatocellular carcinoma (HCC) remains ambiguous. Isocitrate dehydrogenase 3A (IDH3A) is known as a subunit of the IDH3 heterotetramer. To the best of our knowledge, the biological effect of IDH3A in malignant tumors is unclear.
Methods Cell transfection was used to upregulate and downregulate the expression of IDH3A in HCC cells. Wound scratch assays were assessed using the migration activity. While transwell assays were carried out to detect the invasion of HCC cells. RNA-seq, RT-qPCR and western blot were used to validate MTA1 as a potential target gene.
Results Here, we report that IDH3A is significantly upregulated in HCC tissues; moreover, high expression of IDH3A is strongly associated with tumor size and the clinicopathologic stage of HCC. RNA-seq revealed that depletion of IDH3A affects the expression of metastasis associated 1 (MTA1), an oncogene which is related to the progression of numerous cancer types to the metastasis stage. The present study suggested that IDH3A can upregulate MTA1 expression and promote epithelial-mesenchymal transition (EMT) in HCC by inducing MTA1 expression, thereby facilitating cell migration and invasion of HCC cells.
Conclusions In the present study, we demonstrated the importance of IDH3A in HCC progression. The identification of the IDH3A axis provides novel insight into the pathogenesis of HCC, and the IDH3A axis might represent a novel target for the treatment of HCC.

PU-0026

HPV 基因分型联合 TCT 筛查宫颈病变的价值分析

吴颖、彭荣、谢艳、李思、张莉、廖丹
长沙迪安医学检验所有限公司

目的 了解湖南地区人乳头瘤病毒(HPV)的感染情况和各亚型分布特征，探讨 HPV 检测联合液基细胞学（TCT）检查在宫颈癌筛查中的价值。
方法 采用荧光 PCR 熔解曲线法对 2020 年 1 月-2020 年 12 月湖南地区送检的 71212 例女性宫颈脱落细胞进行 HPV23 种基因亚型检测，HPV 阳性感染者进行液基细胞学（TCT）检查，TCT 结果为高度鳞状上皮内病变（HSIL）的病例进行组织病理诊断。

结果 送检的 71212 例女性两癌筛查标本，HPV 感染率为 10.99%，其中单一型别感染率为 9.27%（6600 例），多重型别感染率为 1.72%（1223 例）；高危型感染为 9.51%（6775 例），低危型感染为 1.48%（1048 例），高危型以 52 型、58 型和 16 型为主，低危型以 81 型和 70 型为主。年龄中以 51-60 岁感染率最高，为 45.35%，不同年龄段感染率差异有统计学意义（x2=397.537，p<0.001）。HPV 阳性感染者宫颈脱落细胞进行 TCT 检查，阳性符合率为 40.02%（3131 例）；HPV 联合 TCT 检查与组织病理诊断符合率为 83.33%。
结论 湖南地区 HPV 感染以高危型 HPV52 型、HPV58 型和 HPV16 型为主，具有地域性特征, HPV 联合 TCT 筛查，有助于提高宫颈上皮内瘤变（CIN）、宫颈癌检出率，以尽早发现和治疗宫颈癌。

PU-0027

胰腺癌患者外周血清 microRNA-25 水平的定量评估

许笑、关明
复旦大学附属华山医院

目的 胰腺癌是常见的消化道恶性肿瘤之一，由于其隐匿性强却病势凶险，导致了高死亡率、低治愈率的特点。当前，主流检测胰腺癌的肿瘤标志物是血清癌抗原 19-9（Ca19-9），但是在诸多消化道肿瘤中会升高，甚至有的急性胰腺炎患者也会升高，所以在还没有出现显著的临床症状时，Ca19-9 无法为胰腺癌患者提供及时的鉴别提示。近年，一种新的核酸标志物已经引起了广泛的注意，这就是 microRNA-25。miR-25 唯有微染色体维持蛋白（MCM7），miR-25 的过度成熟，会抑制 PHLPP2 的表达，进而激活 AKT 通路，诱发胰腺癌。本研究旨在通过绝对定量检测血清 miR-25，揭示其在胰腺癌治疗过程中的定量改变及与其他肿瘤，尤其是胃肠道肿瘤中的血清定量差异，为该 microRNA 在胰腺癌鉴别检测和辅助预后中提供进一步依据。
方法 本研究收集来自复旦大学附属华山医院胰腺癌患者 50 例，包含 20 对术前术后配对样本，健康人对照 50 例和胰腺炎患者 50 例的血清样本。此外，还收集了卵巢癌、肺癌、食管癌、胃癌、肝癌和结直肠癌，各 20 例病例血清。使用江苏命码 miR-25 检测试剂盒检测并比较各组间的差异。
结果 性能验证显示本方法线性良好，R2>0.99，批间和批内精密度均小于 10%，检测阈值为 3300copies/μl。50 例胰腺癌患者的 miR-25 检测结果均为阳性，手术治疗后，14（70%）例病例出现了显著下降。此外，健康人对照组、胰腺炎患者组和其他肿瘤患者组，均未测出 miR-25 升高。miR-25 的特异性和灵敏度都达到 100%，同比组内胰腺癌样本的 Ca19-9 结果只有 70%的灵敏度和 80%特异性。
结论 miR-25 比起常规的 Ca19-9 有着显著提升的特异性和灵敏度。同时，在血清中的定量检测 miR-25 不但能有有效鉴别胰腺癌和良性胰腺疾病患者，也能鉴别有关的消化道及其他肿瘤。从手术前后的定量结果，更显示了该项目不但有助于胰腺癌的监测，还对手术疗效的评估有着积极的意义。

PU-0028

2019 新型冠状病毒感染患者血标本病毒核酸的检测与分析

高勇[1,2]、刘赟蕾[1]
1. 阜阳市第二人民医院
2. 安徽医科大学附属阜阳传染病医院

目的 探讨 2019 新型冠状病毒感染患者血标本中病毒核酸阳性情况，以及血标本病毒核酸阳性与临床表现重症化的关系。
方法 采用实时荧光 RT-PCR 方法，对 15 例确诊新型冠状感染患者 67 份血标本进行 2019-nCoV 核酸检测。

结果 67 份血标本中，有 3 份 2019-nCoV 核酸阳性，且均来自 2 例危重型患者。
结论 确诊 COVID-19 患者血液中可能存在病毒颗粒，并与临床表现重症化或危重症化有关，在临床诊疗的过程中，应加强医务人员的生物安全防护及确诊患者标本的管理。

PU-0029

新型冠状病毒肺炎患者痰液与咽拭子标本核酸检测阳性率比较及 时间差分析

高勇[1,2]、韩明锋[1]
1. 阜阳市第二人民医院
2. 安徽医科大学附属阜阳传染病医院

目的 比较新型冠状病毒肺炎（COVID-19）患者痰液与咽拭子标本核酸检测阳性率，并分析不同标本阳性率时间差，为临床诊断提供参考。
方法 本研究收集 2020 年 1 月 22 日至 2020 年 2 月 28 日确诊的 COVID-19 患者 166 例，回顾性分析上述患者 1192 份痰液与咽拭子标本核酸检测数据。
结果 在第 0-7 天采样时间段，痰标本与咽拭子标本对重症患者 SARS-CoV-2 感染的临床灵敏度分别为 94.1%、33.3%（P<0.001），对轻症患者 SARS-CoV-2 感染的临床灵敏度分别为 66.5%、29.8%（P<0.001）；在第 8-14 天及≥15 天采样时间段，由于病人在持续治疗过程中其体内病毒逐渐清除，两类标本的临床灵敏度均有所降低，但对于轻症患者痰液标本诊断 SARS-CoV-2 感染的阳性率仍显著高于咽拭子标本组。在各采集时段，痰标本组病毒基因（ORF1ab/N）核酸检测 Ct 值均有低于咽拭子标本组趋势，提示痰标本中病毒载量高于咽拭子标本。部分 COVID-19 患者痰标本检出 SARS-CoV-2 的持续时间比咽拭子标本长，其咽拭子标本的阳性检出时间晚于痰液标本。
结论 痰液标本诊断 SARS-CoV-2 感染的阳性率在感染早期与轻症患者组显著高于咽拭子标本。为提高核酸检测灵敏度，建议尽可能留存痰液标本，同时对疑似患者多点采样或同一部位反复核酸检测，结合血清抗体、CT 影像学等联合评估，以提高疑似病例的诊断灵敏度。

PU-0030

血清可溶性甘露糖受体在肝癌患者中的表达水平及其临床意义

黄程荣、王琴
安徽医科大学第二附属医院

目的 探讨肝癌（HCC）患者体内可溶性甘露糖受体（sMR）的表达水平及其临床意义。
方法 采用酶联免疫吸附实验分别检测肝癌患者、慢性乙型肝炎（CHB）患者及健康对照（HC）血清 sMR 水平，统计分析一般资料，比较不同分期及病理特征患者血清 sMR 水平，并通过绘制 ROC 曲线评价 sMR 及 AFP 对肝癌的诊断效能。
结果 肝癌患者血清 sMR 水平高于慢性乙型肝炎及健康对照者，根据巴塞罗那临床肝癌分期分类标准将 HCC 患者的疾病严重程度分为巴塞罗那 A、B、C、D 期（早、中、晚、终末期），其中 A 期 27 例，B 期 39 例，C 期 42 例，D 期 21 例。结果提示随着疾病进展，肝癌患者体内 sMR 水平升高，同时发现 HCC 患者血清中 sMR 水平在肝癌组肿瘤直径＞5 cm 及多发结节组中均升高但 AFP 水平与肿瘤数目及肿瘤大小差异无显著性。进一步以不同研究对象作为对照组绘制 ROC 曲线评估 sMR 及 AFP 对 HCC 患者的诊断效能，研究发现以 HC 组或非肝癌患者为对照组 sMR 曲线下面积（0.992 和 0.864）均高于 AFP（0.848 和 0.761），且当 AFP 与 sMR 联合检测时，ROC 曲线下面积（0.996 和 0.909）均高于单个指标。说明 AFP+sMR 是 HCC 患者诊断的良好预测指标。以非肝癌组为对照组，AFP 阴性 HCC 患者（49 例）作为病例组，ROC 曲线下面积为 0.854

（0.783~0.909），当 sMR 截断值为 110pg/ml 时，敏感性和特异性分别为 79.59%、80.0%，表明 sMR 对于 AFP 阴性的 HCC 患者也有一定的补充诊断价值。
结论 血清 sMR 水平在肝癌患者中升高，其表达水平与肿瘤分期、大小及数目有关，同时发现血清 sMR 及 AFP 联合检测对于肝癌的诊断水平高于单个指标对肝癌诊断具有重要临床意义和应用价值。

PU-0031

Decreased serum vitamin D levels and low liver vitamin D receptor expression in patients with chronic hepatitis B are related to liver fibrosis

张浩、王琴、汪玲妹、周强
安徽医科大学第二附属医院

Background To investigate whether any association existed between serum 25(OH)D level and liver histology in chronic hepatitis B (CHB) patients.
Methods Serum 25(OH)D levels were examined and associations between serum 25(OH)D concentration and clinical parameters were analysed. The expression levels of hepatic VDR protein were determined using immunohistochemical staining (IHS).
Results The 25(OH)D serum levels decreased significantly compared with healthy controls. The decrease in 25(OH)D was concomitant with an increase in viral load, as well as levels of total bile acid（TBA）in CHB patients. Moreover, serum 25(OH)D levels in patients with fibrosis stage 2 or 3/4 were significantly decreased compared with that of in patients fibrosis stage 1. VDR expression was less strongly present on the cytosol of hepatocytes in CHB patients compared with those of healthy controls, and negatively correlated with fibrosis stage.
Conclusions These results may suggest that declined in 25(OH)D levels and low expression of hepatic VDR are related to the severity of liver damage in CHB patients.

PU-0032

CRISPR/Cas13a 检测肿瘤驱动基因 TP53 R248W 的研究

邝振展、孙朝晖
中国人民解放军南部战区总医院

成簇的规律间隔的短回文重复序列(clustered regularly interspaced short palindromic repeats,CRISPR)及其相关蛋白是近年来火爆的研究热点，它们组成的系统在分子诊断，RNA 干扰和基因编辑上有着巨大的潜力。CRISPR/Cas13a 是一种 RNA 引导的 RNA 酶，它的活性由高等真核生物和原核生物核苷酸结合(higher eukaryotes and prokaryotes nucleotide-binding ，HEPN)结构域决定。Cas13a 可以与 CRISPR RNA (crRNA)结合形成 Cas13a/crRNA 复合物，通过 crRNA 间隔序列的引导下识别靶 RNA。Cas13a/crRNA/靶 RNA 复合物可以激活 HEPN 结构域，使 Cas13a 蛋白获得 RNA 酶活性。因此，CRISPR/Cas13a 在分子诊断中具有广泛的应用价值，例如可对肿瘤病人组织和血浆样本中的突变基因进行检测。
目的 建立一种 TP53 R248W 变异体分子检测技术。
方法 根据 TP53 基因 R248W 变异体设计合成特异性扩增引物，通过优化扩增引物和扩增技术，寻找 TP53R248W 变异体最合适的扩增条件；设计特异性 crRNA，通过使用特异性高的 crRNA 来引导 Cas13a 蛋白检测扩增产物；评价不同浓度 crRNA 对 CRISPR/Cas13 方法检测效能的影响；通过不同突变率 TP53 R248W 变异体及模拟血浆 ctDNA 评价 CRISPR/Cas13a 方法的检测灵敏度。
结果 CRISPR/Cas13a 检测产物大小适宜在 300bp 左右，CRISPR/Cas13a 检测强度受 crRNA 浓

度的影响，crRNA 浓度越高，CRISPR/Cas13a 检测强度越高。CRISPR/Cas13a 检测 TP53 R248W 变异体的灵敏度为 104 copies / μl，最低可以检测出突变率为 0.01%的变异体。
结论 建立的 CRISPR/Cas13a 方法具有快速、简便、灵敏、特异等优点，为组织和血浆中的 TP53 R248W 变异体的检测提供了新的技术手段。

PU-0033

通过生信分析法推测多发性骨髓瘤中潜在的抑癌基因

阎赟梦
郑州大学第一附属医院

Multiple myeloma (MM) is characterized by aberrant accumulation of monoclonal plasma cells within the bone marrow compartment. In this study, we performed an integrated bioinformatic analysis of DNA methylation and gene expression profile from the gene expression omnibus to identify potential molecular mechanisms and functional genes in MM. In this study, Gene expression profiles (GSE16558 and GSE21304) were analyzed utilizing the R software and GEO2R to obtain aberrantly methylated differentially expressed genes (DEGs). Functional and pathway enrichment analysis of candidate genes were conducted utilizing the cluster profiler package. Twenty-seven upregulated hypomethylated genes and fourteen downregulated hypermethylated genes were identified. As for biological pathways, up-hypomethylated genes were significantly enriched in iron ion homeostasis, B cell differentiation, lymphocyte proliferation. The down-hypermethylated genes were significantly enriched in B cell activation.

PU-0034

2018-2020 年上海北部 45296 例流感样病例病原监测分析

刘晴晴、杨振华
上海市宝山区中西医结合医院

目的 对 2018-2020 年冬春季就诊于上海某三甲医院发热门诊的流感样病例进行病原检测分析，追踪上海北部流感流行的特点。
方法 采用免疫胶体金法和逆转录定量 PCR 方法(reverse transcription-polymerase chain reaction, RT-PCR)对 45296 例流感样病例(influenza-like illness, ILI)的鼻咽拭子标本进行甲型流感(简称甲流)和乙型流感(简称乙流)病毒抗原快速检和核酸检测。采用全自动五分类血球仪 XN-1000 分析患者的外周血全血细胞分析，并对结果进行统计学分析。
结果 胶体金法快速检测出流感病例 7518 例，阳性率 16.60%。其中甲型流感阳性 5180 例，占 68.90%，乙型流感阳性 2193 例，占 29.17%，甲、乙型流感混合感染 145 例，占 1.93%。0-20 岁儿童和青少年流感的发病率很高，阳性率为 20.14%。0-10 岁男童的甲、乙流的阳性率均高于女童（差异均有统计学意义，P<0.5）。随机抽取流感样病例 500 例鼻咽拭子标本，通过 RT-PCR 进行核酸检测，共检出流感阳性 122 例，检出率 24.4%，甲流 74 例，占 60.7%，乙流 48 例，占 39.3%，与临床一致率较高。甲流的 WBC、N%、NLR、CRP 均高于乙流，甲流的 LY%、M%均低于乙流，差异均有统计学意义（P<0.5）。比较八项血细胞指标的受试者特征曲线(receiver operator chamcteristic curve，ROC)的曲线下面积(area under the curve，AUC)，发现中性粒细胞/淋巴细胞比值(neutrophil-to-1ymphocyte ratio, NLR)高于其他指标。
结论 上海北部地区冬春季仍以甲流为主，乙流也在冬春季暴发流行，应引起重视。年龄、性别因素是影响冬春季节甲流和乙流感染的主要因子。NLR 对于鉴别甲流与乙流有一定的意义。

PU-0035

Investigation of the association between ten pathogens causing sexually transmitted diseases and high-risk human papilloma virus infection in Shanghai

Li Xie
Shanghai First People's Hospital Baoshan Branch, Shanghai, P.R.China

Cervical cancer, one of the high-incidence female malignant tumors, has predominated in recent years. Persistent infection with high-risk human papillomavirus (HR-HPV) is the main cause of cervical cancer. Studies have shown that infection with certain sexually transmitted disease (STD) pathogens increases the risk of persistent infection with HR-HPV and is a high-risk factor for cervical cancer. In the present study, cervical specimens were collected for Thinprep cytology test detection, while DNA of cervical cells was extracted for HPV genotyping and detection of 10 STD pathogens, including Neisseria gonorrhoeae, Chlamydia trachomatis (CT), Ureaplasma urealyticum, Ureaplasma urealyticum parvum (Uup)1, Uup3, Uup6, Uup14, Mycoplasma hominis (Mh), Mycoplasma genitalium (Mg) and herpes simplex virus II. Significant differences were observed between CT, Mh and Mg infections and HR-HPV infection ($P<0.05$). In addition, CT, Uup3, Uup6 and Mh infections were associated with HR-HPV infection (odds ratio >1; $P<0.05$). In the comparison of Uup3, Uup6 and Mg infections between the cervical intraepithelial neoplasia (CIN) group and the control group, statistically significant differences were observed ($P<0.05$). In conclusion, the incidences of CT, Mh and Mg infections were similar with HR-HPV infection. CT, Uup6, Mh and Mg infections were risk factors for HR-HPV infection. Finally, Uup3, Uup6 and Mg were risk factors of CIN.

PU-0036

血清胎盘来源外泌体和外泌体中 miR-210 与子痫前期的相关性

段玉萍、谢骊、蔡雷鸣、吴晶晶、洪茂、厉倩
复旦大学附属中山医院吴淞医院

目的 探讨孕妇血清中胎盘来源外泌体和外泌体内 miR-210 在子痫前期孕期中的变化规律及临床意义。
方法 收集 2018 年 1 月-2019 年 12 月在我院收治的子痫前期（preeclampsia， PE）孕妇 30 例和正常孕妇 30 例孕早中晚期血清标本。通过 ExoQuick 提取试剂盒分离正常孕妇和 PE 孕妇孕早中晚期血清中外泌体，利用 CD63 ELISA 试剂盒检测 CD63 表达水平计算外泌体总量；通过胎盘碱性磷酸酶（(placental alkaline phosphatase，PLAP）ELISA 试剂盒检测胎盘来源外泌体的水平；通过实时荧光定量 PCR 方法检测正常孕妇和 PE 孕妇不同孕期血清中外泌体内 miR-210 的表达；并对血清外泌体 PLAP 水平和 miR-210 相对表达水平进行相关性分析。
结果 血清外泌体总量，外泌体 PLAP 浓度和外泌体内 miR-210 随着孕期的进展均逐步增加。与正常孕妇相比，在孕中期和孕晚期，PE 血清中外泌体的总量升高（$P<0.05$）；PE 孕妇血清外泌体中 PLAP 水平在孕早期，孕中期和孕晚期中均较正常孕妇组高（$P<0.05$）；从孕早期开始，PE 孕妇血清外泌体中 miR-210 水平即比正常孕妇组高（$P<0.05$）；孕妇血清外泌体 PLAP 表达量和 miR-210 相对表达水平具有正相关关系（r/P =0.691/0.001）。
结论 孕妇胎盘来源外泌体和外泌体内 miR-210 的水平可能在早期预测和诊断子痫前期中发挥一定的作用。

PU-0037

C1QBP regulates apoptosis of renal cell carcinoma via modulating xanthine dehydrogenase (XDH) mediated ROS generation

Dan Yue
天津医科大学医学检验学院

Complement component 1 Q subcomponent binding protein (C1QBP) is a multifunctional protein and plays a vital role in the progression and metabolism of cancer. Our previous study has revealed that the low expression of C1QBP in renal cell carcinoma (RCC) and knockdown of C1QBP promotes the adhesion and invasion of RCC cells. However, its functions in metabolism, oxidative stress, and apoptosis of RCC cells have not yet been explored. Metabolomics assay was applied to investigate the role of C1QBP in RCC metabolism. C1QBP knockdown and overexpression cells were established via lentiviral infection and subjected to apoptosis and ROS assay in vitro. RNA stability assay was applied to characterize the mechanism of C1QBP regulating XDH transcription. In vivo, orthotopic tumor xenografts assay was performed to investigate the role of C1QBP progression. Metabolomics investigations revealed that C1QBP dramatically diminished the hypoxanthine content in RCC cells. C1QBP promoted the mRNA and protein expression of hypoxanthine catabolic enzyme xanthine dehydrogenase (XDH). Meanwhile, C1QBP regulated the XDH gene expression at the pre-transcriptional level by regulating XDH transcriptional stimulators IL-6, TNF-α, and IFN-γ. Moreover, the expression of C1QBP and XDH was lower in RCC tumors compared with the para-tumor normal tissues, and their down-regulation was associated with higher levels of Fuhrman grade. In RCC cells, C1QBP significantly increased reactive oxygen species (ROS) levels, apoptosis, and the expression of apoptotic proteins such as cleaved caspase-3 and bax/bcl2 via regulating XDH. In conclusion, C1QBP promotes the catabolism of hypoxanthine and elevates the apoptosis of RCC cells by modulating XDH-mediated ROS generation.

PU-0038

Crybb2 基因敲除小鼠晶状体环状 RNA 测序分析

高谦、厉倩
上海市宝山区吴淞中心医院

目前，关于晶状体中 circRNAs 表达谱的信息很少。 βB2-晶状体蛋白 (CRYBB2) 是哺乳动物晶状体中含量丰富的蛋白质，其异常表达可导致白内障的产生。本研究旨在探索 Crybb2 敲除小鼠晶状体中 circRNA 的表达谱。

方法和结果 我们从野生型 (WT) 和 Crybb2-/- 小鼠的晶状体中提取总 RNA，将 RNA 逆转录为 cDNA 并对其进行测序。此外，我们进行了生物信息学来识别和分析差异表达的 circRNA 并预测它们的潜在功能。我们通过定量 RT-PCR 验证了一些差异表达的 circRNA。我们使用 RNA-seq 鉴定 49,494 个 circRNA，与 WT 晶状体相比，在 Crybb2-/-小鼠晶状体中，149 个 circRNA 上调，172 个下调。利用前 300 个 miRNA-circRNA 相互作用对，我们构建了一个 circRNA-miRNA 相互作用网络。此外，那些差异表达的 circRNAs 参与了各种生物过程，如晶状体纤维细胞发育、钙通道复合体、晶状体结构成分。它们参与了几个重要的通路，例如经典的 Wnt 信号通路。定量 RT-PCR 验证了 Crybb2-/- 小鼠晶状体中一些不同表达的 circRNA。

结论 Crybb2 敲除显著调节了小鼠晶状体中 circRNA 的表达谱，这可能有助于阐明 circRNA 在年龄相关性白内障中的作用。

PU-0039

The direct interaction between Rab5a and Rab4a enhanced EGF-stimulated proliferation of gastric cancer cells

Di Wang[1]、Ming Guan[2]
1. Department of Laboratory Medicine, Huashan Hospital North, Shanghai Medical College, Fudan University
2. 复旦大学附属华山医院

Background Gastric cancer is one of the leading causes of cancer-related death worldwide. Although targeted therapies such as antibodies against HER2 or VEGFR-2 have been widely used in the treatment of metastatic cancer, the overall outcomes are poor. Therefore, elucidation of the mechanism underlying cancer progression is important to improve prognosis. Overexpression of the Rab5a gene has been confirmed to correlate with tumorigenesis of many cancers, but the mechanism underling, especiallly of gastric cancer, is still unclear.
Aim To investigate the effects of Rab5a overexpression on the tumorigenesis of gastric cancer.
Methods First, the expression levels of Rab5a and Rab4a in primary tumorous tissues of gastric cancer patients diagnosed between 2015 and 2018 were analyzed. Then we constructed HGC-27 cell lines overexpressing GFP-Rab5a or RFP-Rab4a and investigated the interaction between Rab5a or Rab4a using Western blotting, co-immunoprecipitation, confocal microscopy and colocalization analysis. Finally, EGF-stimulated proliferation of these cell lines was analyzed using CCK-8 cell viability assay.
Results Compared with normal gastric tissues, the expression levels of Rab5a and Rab4a increased progressively both in paracancerous tissues and in advanced cancerous tissues. EGF could promote the proliferation of HGC-27 cells, especially Rab5a-overexpressing HGC-27 cells. Notably, Rab5a and Rab4a co-overexpression promoted the proliferation of HGC-27 cells to the greatest extent. Further analysis identified a direct interaction between Rab5a and Rab4a in HGC-27 cells.
Conclusion Co-overexpression of Rab5a and Rab4a in gastric cancer may promote the endosomal recycling of EGFR, which in turn contributes to poor prognosis and tumor progression in gastric cancer patients. Inhibit Rab5a or Rab4a expression might be a promising therapy for refractory gastric cancer.

PU-0040

硫辛酸对改善 PFOS 所致雄性大鼠生殖能力影响机制的研究

张智燕
内蒙古科技大学包头医学院第一附属医院

目的 探讨全氟辛酸（Perfluorooctane sulfonate, PFOS）对雄性大鼠生殖毒性作用，并分析硫辛酸（Lipoic acid, LA）对 PFOS 致雄性大鼠生殖毒性的改善作用。
方法 6 周龄雄性 SD 大鼠 40 只，随机分为 5 组（每组 8 只）：正常对照组；LA 对照组：100 mg/(kg•bw•d)；PFOS 染毒组：10 mg/(kg•bw•d)；低剂量 LA 组：PFOS 10 mg/(kg•bw•d)+LA 50 mg/(kg•bw•d)；高剂量 LA 组：PFOS 10 mg/(kg•bw•d)+LA 100 mg/(kg•bw•d)。干预 7 周后，腹主动脉取血，留取睾丸、附睾，计算脏器系数；采用计算机辅助精子分析系统进行精子数量的检测；HE 染色进行睾丸组织的病理学检查；分光光度法检测睾丸内琥珀酸脱氢酶（SDH）、乳酸脱氢酶（LDH）活性；ELISA 法检测大鼠血清中睾酮（T）和卵泡刺激素（FSH）含量；Western Blotting 法检测各组大鼠睾丸组织中 FSHR 蛋白表达水平。
结果 与正常对照组和 LA 对照组相比，PFOS 染毒组大鼠附睾和睾丸系数均增高($P<0.05$)，附睾精子数量降低($P<0.05$)；睾丸组织病理学观察显示，PFOS 染毒组较正常对照组大鼠生精小管内生精细胞层次减少，生精细胞排列紊乱，生精上皮出现较多的空泡化改变，而各剂量 LA 干预组病变明显减轻。与正常组大鼠相比，PFOS 染毒组大鼠血浆 SDH、LDH 酶活力均下降($P<0.05$)，而经 LA

干预后可以明显逆转这种变化，且差异有统计学意义(P<0.05)。此外，PFOS 染毒组大鼠与正常对照组相比，睾丸内 T 水平降低，FSH 水平升高，睾丸组织 FSHR 蛋白表达量显著降低(P<0.05)，而 LA 干预后可明显看到紊乱的激素水平得到改善，同时也抑制了睾丸组织 FSHR 蛋白的这种变化。**结论** PFOS 对雄性大鼠具有生殖毒性效应，而适量的 LA 补充可以改善 PFOS 所致的生殖损伤。

PU-0041

Characterisation of the novel clinical isolate X-4 containing a new tp0548 sequence-type

Dan Liu
Center of Clinical Laboratory, Zhongshan Hospital, School of Medical, Xiamen University, Xiamen, China,

Objectives To precisely define and characterise a new clinical isolate,we performed further genome-scale molecular analysis.
Methods The pooled segment genome sequencing method followed by Illumina sequencing was performed.
Results This novel sequence-type contained a unique nucleotide substitution 'T' at position 167 and belonged to the SS14-like clade of TPA strains, as determined by phylogenetic analysis. Multi-locus sequence analysis of nine chromosomal loci demonstr ated that the X-4 isolate was clustered within a monophyletic group of TPA strains.
Conclusion The novel tp0548 sequence-type was determined to belong to a new TPA isolate, X-4. The identification of variable length in homopolymetic tracts (G/C and A/T) could provide a snapshot of the genes that potentially involved in genotype–phenotype variations. These findings provide an unequivocal characterisation for better understand.

PU-0042

厦门市医疗机构开展基因检测服务现况

刘莉莉
厦门大学附属中山医院

目的 对厦门市医疗机构开展"基因检测"服务情况进行调查，为今后基因检测工作提供依据。
方法 厦门市临床检验质量控制中心设计调查表对医疗机构进行调研。
结果 厦门市医疗行业基因检测工作主要由非营利性医疗机构承担，开展项目较全面，可检测标本种类较广；大部分参研实验室参加各级室间质评，遵守法律法规和行业准则，但目前福建省没有适用于医疗机构基因检测实验室的监管办法；厦门市基因检测行业存在从业人员培训渠道有限、技术与人才分布不均、机构间发展不均衡等问题。
结论 福建省基因检测工作急需出台专业监管办法，同时增加培训渠道，重视多层次人才培养，加大对基层、非公立医疗机构实验室的扶持。

PU-0043

流感病毒两种检测方法结果一致性的比较

邢志芳、刘瑞来、关明
复旦大学附属华山医院

目的 胶体金法和 PCR 荧光探针法同时用于流感病毒的检测，比较两种检测方法结果的一致性。

方法 选择 2019 年 11 月 1 日至 12 月 31 日来复旦大学附属华山医院北院儿科就诊的 300 例流感疑似患者，均采集双份鼻拭子样本，分别用胶体金法和 PCR 荧光探针法同步检测，对于检测结果不一致的样本采样测序发进行验证，并分析外周血中性粒细胞、淋巴细胞和血清淀粉样蛋白 A（SAA）等感染性指标变化对于甲、乙型流感病毒感染临床诊断的价值。
结果 胶体金法检测出 18 例甲型流感病毒阳性患者，42 例乙型流感病毒阳性患者，PCR 荧光探针法检出 45 例甲型流感病毒阳性患者，乙型 124 例流感病毒阳性患者。胶体金法检测甲型流感病毒的灵敏度为 40%，特异度为 100%，胶体金法检测乙型流感病毒灵敏度为 33.87%，特异度为 98.3%。
结论 抗原检测法灵敏度低于 PCR 荧光探针法，甲型流感病毒胶体金法与 PCR 荧光探针法检测结果有一致性，乙型流感抗原检测法与 PCR 荧光探针法结果一致性差。甲、乙型流感在性别、CRP、SAA 数值差异无统计学意义。甲、乙型阳性患儿和阴性患儿的白细胞计数差异有统计学意义、中性粒细胞计数和淋巴细胞计数中位数均低于流感阴性组的患儿。两两结果比较显示：乙流的中性粒细胞计数与流感阴性组的差异有统计学意义，但是在甲流差异无统计学意义。

PU-0044

UCHL1 表达对结肠癌细胞系 HCT8 蛋白表达的影响

钟佳伶
四川省医学科学院·四川省人民医院

目的 UCHL1(ubiquitin C-terminal hydrolase-L1)是去泛素化酶家族的成员之一。实验前期结果显示，具有泛素水解酶活性的 UCHL1 表达对结肠癌细胞系 HCT8 的成瘤能力、转移和迁移能力均产生明显影响。本研究利用 pcDNA3.1 真核表达系统和双相电泳技术探讨具有泛素水解酶活性的 UCHL1 表达对 HCT8 细胞蛋白表达的影响。
方法 构建 pcDNA3.1-UCHL1 质粒，再通过 Overlap PCR 构建了泛素水解酶活性缺失的 pcDNA3.1-UCHL1-C90S 突变体质粒。分别转染空载质粒 pcDNA3.1、pcDNA3.1-UCHL1、pcDNA3.1-UCHL1-C90S 到 HCT8 细胞中，经 G418 筛选后获得稳定转染细胞系 HCT8/pcDNA3.1、HCT8/UCHL1 和 HCT8/UCHL1-C90S。采用强还原剂裂解液提取细胞蛋白并进行醋酸铵沉淀纯化，得到蛋白样品。用双向电泳方法对样品中的蛋白进行分离，采用 Imagemaster-v501-trial-2D 分析软件对图像进行分析，寻找差异表达的蛋白，再用 MALDI-TOF-MS 法对蛋白质进行鉴定。
结果 分析筛选出在 HCT8/pcDNA3.1 与 HCT8/UCHL1 之间，以及 HCT8/UCHL1、HCT8/UCHL1-C90S 之间均存在差异的蛋白共 11 个。最后质谱鉴定成功 9 个，其中 7 个蛋白表达上调，2 个蛋白表达下调。
结论 通过该方法，能够得到具有泛素水解酶活性的 UCHL1 在 HCT8 细胞中表达后所带来的蛋白质水平的表达差异，建立了双向电泳分析蛋白质组学研究的平台，为研究 UCHL1 在结肠癌细胞系 HCT8 中参与的细胞通路打开了局面。

PU-0045

抗 CCP 抗体、RF、CRP 和 ESR 在 RA 诊断中的应用价值

张萌
郑州大学第一附属医院

目的 检测抗环瓜氨酸肽抗体(抗 CCP 抗体)、类风湿因子(RF)、C 反应蛋白(CRP)和红细胞沉降率(ESR)的水平，并探讨其联合检测在类风湿关节炎(RA)诊断中的临床应用价值。
方法 收集 100 例 RA 患者（RA 组）、50 例体检健康者（对照组）的抗 CCP 抗体、RF、CRP、ESR 四项血清学指标检测结果。分析四项指标在 RA 诊断过程中的临床价值。

结果 与对照组相比，RA 组中抗 CCP 抗体、RF、CRP 和 ESR 检测结果及阳性率均明显升高，且有统计学差异（P<0.05）；抗 CCP 抗体诊断 RA 的特异度高于 RF，RF 诊断 RA 的灵敏度高于抗 CCP 抗体，抗 CCP 抗体、RF、CRP 和 ESR 联合检测具有较高的特异度，达到 99.92%。
结论 抗 CCP 抗体、CRP、RF 及 ESR 联合检测对 RA 的诊断具有较高特异度，有助于 RA 的临床诊断，有较高的应用价值，值得临床推广应用。

PU-0046

基于生物信息学分析氮杂胞苷调控食管腺癌的关键基因

李美美、张楠楠
郑州大学第一附属医院

目的 用生物信息学的方法分析抗肿瘤药物氮杂胞苷(Azacytidine)对食管腺癌起调控作用的关键基因。
方法 从 GEO 数据库中下载数据 GSE57130，获得氮杂胞苷处理食管腺癌细胞系 OE33 的数据集，通过 GEO2R 对差异表达基因进行分析，通过 NetworkAnalyst 分析获得调控关键基因差异表达的转录因子和 miRNA。
结果 从数据集 GSE57130 中获得 13 个差异表达基因 ASS1，GDF15，ANXA10，UCA1，NT5E，HOPX，ABCA1，LINC00704， PYGB，UBD，GSDMB，C15orf48，CD55。获得调控关键基因的转录因子 214 个，包括转录因子 ATF1,BCL6，EGR1，KLF1，STAT3 等，调控关键基因的 miRNA 204 个，例如 hsa-mir-5692a，hsa-mir-8069，hsa-mir-202-5p 等。
结论 进一步从分子水平理解抗肿瘤药物氮杂胞苷对食管腺癌的调控作用。

PU-0047

原发性胆汁性胆管炎患者血浆中环状 Rnas 的微阵列表达谱分析

王永峰、明亮
郑州大学第一附属医院

目的 环状 RNA (circRNAs) 在几种疾病的发生中起着至关重要的作用。疾病，然而，它们在原发性胆汁性胆管炎中的作用 仍不清楚。在这里，我们旨在确定血浆中的 circRNA 表达谱来自 PBC 患者并进一步探讨 circRNA 在诊断 PBC 中的价值。
方法 circRNA 微阵列用于确定血浆样本中的 circRNA 表达谱来自 6 名 PBC 患者和 6 名健康对照者。统计分析发现差异表达 circRNA，并且这些 circRNA 在 29 名 PBC 患者和 30 名健康人中通过 qRT-PCR 验证。 MicroRNA (miRNA) 目标预测软件确定了推定的 miRNA 反应元件（MRE），用于构建 circRNA-miRNA 相互作用图差异表达的 circRNA。
结果 我们的结果表明有 18 个上调与 PBC 患者血浆中的 4 个下调的环状 RNA 相比，健康的个体。在差异表达的 circRNA 中， hsa_circ_402458 （ P=0.0033 ）， hsa_circ_087631 和 hsa_circ_406329 (P=0.0185) 上调，hsa_circ_407176(P=0.0066) 和 hsa_circ_082319 在 PBC 组与健康组相比下调。特别是 hsa_circ_402458 在未接受 UDCA 治疗的 PBC 患者比接受 UDCA 治疗的 PBC 患者(P=0.0338)。 hsa_circ_402458 的受试者工作特征曲线下面积诊断 PBC 为 0.710（P=0.005）。对于 hsa_circ_402458，两个推定的 miRNA 靶标 hsa-预测了 miR-522-3p 和 hsa-miR-943。
结论 circRNA 失调可能发挥作用在 PBC 发病机制中的作用，并且 hsa_circ_402458 显示出作为候选生物标志物的前景。

PU-0048

Molecular Characterization Based on MLST and ECDC Typing Schemes and Antibiotic Resistance Analyses of Treponema pallidum subsp. pallidum in Xiamen, China

shumin He
厦门大学附属中山医院

Objective In total, 49 clinical samples were analyzed using two typing schemes, Enhanced Centers for Disease Control and Prevention (ECDC) and multilocus sequence typing (MLST), to describe the molecular characteristics of circulating Treponema pallidum isolates in Xiamen between 2016 and 2017.
Methods Forty fifive samples were fully typed by ECDC, and 14 different subtypes were detected.
Results Interestingly, the allelic profifile 1.3.1 widespread in Europe and North America was not detected in this region. Additionally, A2058G mutation in 23S rRNA was found in all detectable samples (38/38), and no mutation in 16S rRNA was observed (36/36).
Conclusion This study showed that the genotypes of T. pallidum isolates in Xiamen between 2016 and 2017 were different from those in other geographic areas. The resistance-related variants of T. pallidum isolates identifified in this study could provide awareness for clinicians in the treatment of syphilis.

PU-0049

不同提取系统提取病毒核酸的比较研究

阴晟、王敏、崔扬飞、王敏
中南大学湘雅二医院

目的 通过对天隆，中元和硕世三种全自动核酸提取系统对全血和尿液两种类型的临床样本提取出的核酸的质量进行分析比较，分析三种提取系统的临床适用性。
方法 首先用 16 个全血标本和 16 个尿液标本对三种提取系统提取效果进行评估，按照三种提取系统和试剂盒的说明书进行加样和提取，用 ThermoNanoDrop 2000 核酸蛋白分析仪检测所提取的核酸的浓度与纯度，再比较天隆和硕世提取系统提取 EBV,CMV 和 BKV 三种临床标本的 Ct 值的差异，结果用 SPSS25.0 进行处理。
结果 全血标本和尿液标本，天隆，中元和硕世所提取的核酸浓度范围在 16.8-356.1ng/ul， 6.1-146.8ng/ul， 17.2-75.5ng/ul，1.8-5.0 ng/ul，0-22.3 ng/ul，1.3-4.8 ng/ul，差异具有统计学意义（P<0.05）；全血和尿液标本平均核酸纯度天隆，中元和硕世分别为 1.88±0.01，1.87±0.02 和 1.91±0.01，1.32±0.02，1.19±0.10 和 4.04±0.87，差异具有统计学意义（P<0.05）；天隆和硕世所测得 EBV，CMV 和 BKV Ct 值之间平均差异分别为 0.020-0.064 和 0.38。
结论 三种核酸提取系统对于全血标本和尿液标本所提取出的核酸纯度和浓度之间是有差异的，但都满足临床要求，而其中天隆对于核酸提取能力较其他两个系统更强。

PU-0050

胰腺癌患者风险预测评分的研发和验证

贾苗苗、许青霞
河南省肿瘤医院

目的 本研究旨在研究和验证胰腺癌 (PC) 患者总生存期 (OS) 的有效预测模型。
方法 本研究对 600 名患者进行了回顾性分析。我们使用随机森林图来确定胰腺癌患者总生存期的重要预后因素。然后使用校准图和一致性指数（C-index）来评估列线图模型的预测准确性。
结果 我们使用随机森林图选择三个最重要的特征，它们与胰腺癌患者的总生存期显着相关。我们的 OS 模型的 C 指数在两个队列中分别为 0.733（95% CI：0.673~0.793）和 0.772（95% CI：0.691~0.853）。根据模型风险评分，将患者分为低危组和高危组两组。 Kaplan-Meier 曲线显示，两个亚组与主要队列和验证队列中的 OS 显著相关。随后，我们建立了 OS 的列线图，包括两个队列中的风险评分、TNM 分期。它在初级中实现了比风险评分模型 0.733（95% CI：0.673~0.793）更高的 C 指数 0.783（95% CI：0.730~0.836）（P = 0.005）。
结论 建立的风险评分模型和列线图可以对胰腺癌个体患者进行更准确的预后预测。

PU-0051

Long noncoding RNA NORAD function in tumor progression of colorectal cancer

Lili Wang
Qilu Hospital of Shandong University

Purpose To elucidate the role and clinical significance of long noncoding RNA-activated by DNA damage (NORAD) in colorectal cancer (CRC).
Methods Sixty pairs of tumorous and adjacent nontumorous tissues derived from CRC patients were subjected to quantitative real-time polymerase chain reaction to determine the expression level of NORAD. The serum levels of NORAD expression were also measured in an independent cohort of CRC patients as well as patients with benign diseases and healthy controls. Comparative analyses were performed to investigate the relationships between NORAD levels in tissues and clinicopathological features of CRC. Receiver operating characteristic (ROC) curve analysis was used to assess the diagnostic value of NORAD in patients with CRC. Furthermore, the potential functions of NORAD in the development of CRC were explored in vitro, using the HCT116 and SW1116 CRC cell lines.
Result NORAD expression was significantly up-regulated in the tumorous tissues of CRC patients ($P < 0.001$) compared to the adjacent nontumorous tissues. Higher NORAD expression was associated with advanced CRC. Moreover, serum levels supported that NORAD could distinguish CRC patients from healthy controls and patients with benign diseases, indicating a potential diagnostic role in CRC. The ROC curve analysis showed a diagnostic efficacy with area under the curve of 0.800 (95% confidence interval: 0.737-0.853). Mechanistic investigations indicated that NORAD silencing reduced CRC cell proliferation, migration and invasion.
Conclusion NORAD may serve as a novel predictor in CRC and may be a potential target for future therapy.

PU-0052

β-catenin phosphorylation regulated by APC in colorectal cancer

Lili Wang
Qilu Hospital of Shandong University

AIM To study the role of mutated adenomatous polyposis coli (APC) with first direct analysis of the endogenous β-catenin phosphorylation activity in colorectal cancer.
METHODS By comparing parental SW480 cells that harbor a typical truncated adenomatous polyposis coli (APC) form, cells expressing full-length APC and APC-depleted cells, we provide the formal demonstration that APC is necessary for β-catenin phosphorylation, both for priming of the protein at residue serine 45 and for the subsequent phosphorylation of residues 33, 37 and 41.
METHODS Truncated APC still sustains a surprisingly high phosphorylation activity, which requires the protein to bind to β-catenin through the APC 20-amino-acid (20AA) repeats, thus providing a biochemical explanation for the precise truncations found in cancer cells. We also show that most of the β-catenin phosphorylation activity is associated with a dense insoluble fraction. We finally examine the impact of full-length and truncated APC on β-catenin nuclear transport. We observe that β-catenin is transported much faster than previously thought.
CONCLUSION APC plays an important role in β-catenin cellular transport as a nuclear shuttle protein, which might have an effects on he nuclear function of β-catenin in tumor cells.

PU-0053

Clinical Value and underlying mechanisms of upregulated LINC00485 in hepatocellular carcinoma

Xinyu Zhu、Yanlin Feng、Dingdong He、Zi Wang、Fangfang Huang、Jiancheng Tu
ZHONGNAN HOSPITAL OF WUHAN UNIVERSITY

Aims This study aimed to reveal the functional role of LINC00485 in hepatocellular carcinoma (HCC).
Methods 210 serum samples from Zhongnan Hospital of Wuhan University were employed to evaluate clinical value of LINC00485. Bioinformatics analysis was adopted to explore its potential mechanisms.
Results LINC00485 was confirmed to be upregulated in HCC tissues and serum samples. Survival analysis and receiver operating characteristic curve revealed its prognostic and diagnostic roles. The combination of serum LINC00485 with AFP can remarkably improve diagnostic ability of HCC. Exploration of the underlying mechanism demonstrated that LINC00485 might exert pro-oncogenic activity by LINC00485—three miRNAs—four mRNAs network.
Conclusions our study unveiled that upregulated LINC00485 could act as a potential diagnostic and prognostic biomarker and provide a novel insight into the molecular mechanisms of LINC00485 in HCC pathogenesis.

PU-0054

HOXC11 作为结直肠癌潜在预后标志物的研究

陈涌泉[1]、林宇宁[2]
1. 厦门弘爱医院
2. 福建医科大学附属厦门弘爱医院

目的 同源异型盒（HOX）基因家族参与了肿瘤的发生，HOXC11 属于同源框 C（HOXC）基因簇，在多种癌症的发生发展中起着重要作用。然而，其在结直肠癌中的表达及临床价值尚不清楚。本研究拟初步探讨 HOXC11 作为结直肠癌潜在预后标志物的临床应用价值。
方法 下载 TCGA 数据库结直肠癌数据（肿瘤组 480 例、癌旁 41 例），采用 Kruskal-Wallis 检验、Wilcoxon 符号秩次检验和 logistic 回归分析 HOXC11 表达与临床病理特征的关系；采用受试者特性曲线（ROC）曲线，用面积曲线下（AUC）评分描述 HOXC11 的诊断效能，采用 Kaplan-Meier 法和 Cox 回归分析法评价影响预后的因素；基因集富集分析（GSEA）分析鉴定 HOXC11 的重要功能。
结果 结直肠癌组织中 HOXC11 表达增加与 N 分期（P<0.001）、M 分期（P<0.001）、主要治疗结果（P<0.001）、淋巴侵犯（P<0.001）和癌胚抗原（CEA）有关（P<0.001）。ROC 曲线显示 HOXC11 具有显著的诊断和预后能力（AUC=0.734）。
结论 HOXC11 的表达与结直肠癌的生存率显著相关，可能是结直肠癌的一个有前途的预后生物标志物。

PU-0055

结直肠癌细胞中解螺旋酶 DHX32 分泌途径的初步研究

陈涌泉、张忠英
厦门弘爱医院

目的 RNA 解螺旋酶是一类参与核糖体的合成、转录、剪切、翻译等与 RNA 多项功能相关的水解酶，其在肿瘤组织中异常表达与肿瘤的发生、发展相关。2009 年，本课题组在筛选结直肠癌特异性标志物时，首次发现解螺旋酶 DHX32 在结直肠癌组织中表达水平高于癌旁，并且能促进癌细胞的增殖、迁移及侵袭，以及通过 Wnt/β-catenin 通路促进结血管生成，有望作为潜在的肿瘤标志物，但是其在血液中的表达情况未知，分泌途径亦未见报道。因此，本研究的目的是在结直肠细胞中对 DHX32 胞外分泌现象进行确定并对其分泌途径进行初步探索。
方法 通过对 SW480 细胞株上清进行免疫共沉淀，再对产物进行鉴定以确定 DHX32 的分泌现象。用经典分泌途径的抑制剂对 SW480 细胞进行处理，以及通过免疫荧光共聚焦分析 DHX32 与高尔基体标志物和内质网的标志物是否有共定位，以确定 DHX32 能否通过经典分泌途径进行分泌。用 ABC 转运蛋白分泌途径的抑制剂对细胞进行处理，以确定 DHX32 是否通过非经典分泌途径-ABC 转运蛋白分泌途径进行分泌；通过 ELISA 检测裂解后的外泌体是否有反应性，以确定 DHX32 是否也可以通过外泌体途径进行分泌。
结果 免疫沉淀结果表明，实验组中能够鉴定到目的条带，但是对照组中没有，验证了 DHX32 存在于细胞上清中。经典分泌途径抑制剂阻断实验结果表明，与对照组相比，实验组中，DHX32 在上清中表达量下降，说明抑制剂能够阻断 DHX32 的分泌，并且对照组与实验组中 LDH 浓度无差异，表明抑制剂能够阻断 DHX32 的分泌。在免疫荧光共聚焦中，DHX32 与高尔基体和内质网的标志物有共定位，进一步说明了 DHX32 通过通过经典分泌途径进行分泌。在 ABC 转运蛋白分泌途径抑制剂阻断实验中，与对照组的相比，细胞上清中 DHX32 的表达量没有差异，同时实验组和对照组中 LDH 的浓度没有差异，说明不能阻断 DHX32 的分泌，即 DHX32 不通过 ABC 转运蛋白非经典分泌途径分泌。外泌体实验中，ELISA 能够鉴定到反应性，说明 DHX32 有可能通过外泌体途径进行分泌。

结论 本研究表明，DHX32 虽然没有预测到经典的信号肽序列，但是其也可以通过经典分泌途径进行分泌，具体的分泌机制有待进一步探明；在非经典分泌途径的研究中，DHX32 不通过 ABC 转运蛋白分泌途径分泌，但是有可能通过外泌体途径进行分泌。

PU-0056

济南地区 2705 例耳聋相关基因变异检测及分析

赵敬杰、刘玲、刘军莉、袁超
山东大学第二医院

目的 分析济南地区人群耳聋相关基因位点变异的频率、分布及其与听力损失间的关系，明确区域人群中的基因变异情况。
方法 应用微阵列芯片法检测 2705 名受检者 GJB2 基因、GJB3 基因、SLC26A4 基因和 MT-RNR1 基因上的热点变异，利用 Mutation Surveyor 软件检测 386 名 Sanger 测序结果中的其他位点变异，根据听力诊断结果将受检者划分为听力损失组和正常听力组，对携带热点变异与听力损失间的关系、各位点变异频率、基因型分布及其在两组间的差异进行分析。
结果 听力损失组的热点变异携带率高于正常听力组，热点变异携带者的听力受损率高于未携带者（P<0.001）。热点变异中 c.235del 的变异率最高，其次是 c.919-2A>G。c.176_191del 和 c.235del 的组间基因型分布差异有统计学意义（P<0.05、P<0.001）。GJB2 基因变异的发生率最高。c.79G>A 和 c.341A>G 属于常见多态，两者存在较弱的连锁不平衡，但其单体型未见统计学差异。c.109G>A 的 MAF 高于 5%，纯合型都致病，其组间基因型分布差异有统计学意义（P<0.001）。c.357C＞T 同义变异是 GJB3 基因上的常见多态。MT-RNR1 以均质和良性变异多见。多个少见变异仅在听力损失组中检出。
结论 基因变异是听力受损的重要因素，听力损失人群中易检出致病的热点变异。GJB2 基因位点易发生变异。常见多态在人群中广泛存在，而少见变异和致病变异易分布在听力损失人群中。

PU-0057

Non-invasive prenatal testing for trisomies 21, 18 and 13: clinical experience from 5341 pregnancies in Kunming area

Qiuyue Xu、yong duan、yang su
Department of Clinical Laboratory,the Frist Affiliated Hospital of Kunming Medical University

Objectives Cell-free fetal DNA has been widely used in prenatal genetic testing during recent years. We explored the feasibility of non-invasive prenatal testing (NIPT) for analysis of common fetal aneuploidies among pregnancies in Kunming area.
Methods 5341 pregnant women who underwent NIPT screening in the First Affiliated Hospital of Kunming Medical University from January 2017 to December 2020 were selected.21/18/13 trisomy,sex chromosome aneuploidy (SCA),copy number variations (CNV) and other autosomal aneuploidywere compared.The correlation of fetal free DNA concentration (cffDNA) with age,gestational age,body weight and BMI was analyzed.
Results Among 5341 NIPT screening cases, 4813 cases were followed up, with a follow-up rate of 90.11% ,The average gestational age of pregnant women was (31.02 ± 4.69) years, and the average gestational age of NIPT was (18.46 ± 4.35) weeks.Among 4813 pregnant women,94 cases had high risk of NIPT,78 cases had prenatal diagnosis (amniocentesis karyotype analysis),and 26 cases had positive diagnosis.Among them,3 cases of NIPT showed high risk of XO,which was inconsistent with karyotype analysis,so the detection rate was 29.49% (23 / 78).Among the 23 confirmed karyotypes,9 cases were T21,2 cases were T18,2 cases were T13,4 cases were SCA,5 cases were CNV,and 1 case was other autosomal aneuploidy (T7).The

sensitivity and specificity of trisomy 21/18/13,T21,T18,T13,SCA,CNV and other autosomal aneuploidy Were 100%,99.92%;100%,99.98%;100%,99.98%;100%,99.96%;100%,99.52%;100%,99.83%;100%,99.58% respectively.The positive predictive value and false positive rate of trisomy 21/18/13,T21,T18,T13,SCA,CNV and other autosomal aneuploidy were 76.47%,0.08%;90.00%,0.02%;66.67%,0.02%;50.00%,0.04%;14.81%,0.48%;38.46%,0.17% and 4.76%,0.42% respectively.CffDNA was positively correlated with gestational age,negatively correlated with age and body weight,but not correlated with BMI.

Conclusion The accuracy of NIPT in screening T21,T18 and T13 is higher than that of SCA,CNV and other autosomes. At the same time,the risk of fetal trisomy 21 is higher in fetuses of elderly pregnant women.

PU-0058

高敏乙肝病毒 DNA 定量检测在低病毒载量肝病患者中的应用

金郑宝
中国人民解放军联勤保障部队第九〇〇医院

目的 评价基于 Smart32 自动核酸提取仪和 ABI ViiA7 荧光定量 PCR 仪的高敏乙肝病毒 DNA 定量检测体系的检测性能是否符合临床的检测要求，探究在低病毒载量肝病患者中高敏乙肝病毒 DNA 定量检测是否更具应用价值。

方法 采取 Smart32 全自动核酸提取仪提取乙肝病毒核酸以及 ABI ViiA7 荧光定量 PCR 仪进行高敏乙肝病毒 DNA 检测，评估该高敏乙肝病毒核酸检测体系的性能，评价项目包含精密度、最低检测限和准确度。将 154 例低病毒载量肝病患者的血清进行高敏乙肝病毒 DNA 定量检测，ALT 定量检测，HBeAg 定量检测及乙肝两对半定性检测。根据高敏乙肝病毒 DNA 检测结果将 154 例患者分为 HBV DNA<30 IU/ml 与 HBV DNA30～500IU/ml 两组，分析低载量乙肝病毒 DNA 与丙氨酸氨基转移酶（ALT）异常率及乙肝两对半血清学检出模式的关联。

结果 精密度：四种浓度分别为 5x107、5x106、5x105、5x104IU/mL 的参考品分别检测 20 次的 Ct 值的 CV 值均<10% 。最低检测限：该高敏乙肝病毒核酸检测系统的最低检测限为 10IU/ml。准确度：使用福建省室间质评的 5 份标本进行检测,检测值与靶值的对数值之间的偏差≤±0.4 lg。154 例患者的高敏乙肝病毒 DNA 检测值在 30～500 IU/ml 有 55 例，占 35.71%，检测值<30 IU/ml 有 99 例，占 64.29 %。乙肝病毒 DNA 在 30～500 IU/mL 的患者与<30 IU/mL 的患者相比，ALT 异常率更高，差异具有统计学意义（$\chi2=5.580$，$P=0.026$）。乙肝病毒 DNA 载量<30 IU/ml 和 30～500 IU/ml 两组患者之间的各乙肝两对半血清学模式分布差异无统计学意义（$\chi2=6.028$，$P=0.110$）

结论 高敏乙肝病毒 DNA 定量检测系统精密度高、最低检测灵敏度好、准确度高，适合临床 PCR 实验室开展。高敏乙肝病毒 DNA 定量检测对低病毒载量乙肝患者更适用，可以为临床医生在为低病毒载量肝病患者进行病情诊断、指导用药和病情监测时提供值得信赖的依据。

PU-0059

HPV 各种方法学检测的比较

杨清翔、陈鸣
陆军军医大学第一附属医院（西南医院）

比较并分析阴道镜检查,液基薄层细胞检测技术，第二代杂交捕获法(Hybrid Capture Ⅱ assay，HC-Ⅱ)，生物芯片，PRC 一膜杂交，的检测结果， 探讨其不同的应用价值。

PU-0060

艾滋病核酸检测方法的特点及应用

林蝶
大理大学第一附属医院（云南省第四人民医院）

现今艾滋病仍是威胁人类健康一大传染性疾病。随着艾滋病感染患者的不断增多，艾滋病检测技术的发展也在不断地进步，并向着高灵敏度、高特异性、简便快速及检测方法的多样性发展，在防止艾滋病的大规模流行以及在艾滋病早期诊断和治疗方面发挥着重要作用。与 HIV 抗体检测相比较，艾滋病核酸检测在提高艾滋病检测的特异性、降低假阳性的概率、缩短艾滋病病毒的检测窗口期、提高艾滋病诊断和治愈率方面占相对优势。本文主要就实验室几种常见艾滋核酸检测方法作一综述。

PU-0061

IL-5、Snail 和 E-cadherin 蛋白与胃窦癌相关性的研究

符自清、向波、易平、王永杰
吉首大学第一附属医院（湘西土家族苗族自治州人民医院）

目的 研究胃窦癌中 IL-5、转录因子 Snail 和黏附因子 E-cadherin 的表达水平，并进一步探讨三者与胃窦癌的浸润、转移及分化程度等因素之间的相关性。
方法 收集某三甲医院 122 例手术切除的胃窦癌组织和 32 例癌旁组织标本。采用免疫组化技术分别检测胃窦癌组织和癌旁组织中 IL-5、Snail 与 E-cadherin 的表达情况。分析三者在不同分化程度的胃窦癌组织中的表达，以及与相关临床病理因素及预后间的关系。
结果 胃窦癌组织中 IL-5 表达水平较癌旁组织上调，阳性表达率分别为 61.5%和 27.8%，差异有统计学意义（P<0.05）；胃窦癌组织 IL-5 表达上调与 TNM 分期（P<0.05）、分化程度（P<0.05）密切相关；而 IL-5 表达与性别、年龄、肿瘤体积、是否远处转移、吸烟史及饮酒史均无关（P 均>0.05）；胃窦癌组织 Snail 阳性率 60.2%，显著高于癌旁组织 31.3%（P<0.05）；Snail 的表达与胃窦癌不同分化程度、淋巴结转移有关（P<0.05）。胃窦癌组织 E-cadherin 的阳性率为 32.3%低于癌旁组织 65.2%（P<0.05），其表达与胃窦癌不同分化程度、淋巴结转移、分期有关性（P<0.05）。Snail 与 E-cadhrin 的表达在胃窦癌组织中体现出负相关性（P<0.05）。
结论 我们推测 IL-5、Snail 蛋白表达上调与 E-cadherin 蛋白表达抑制可能与胃窦癌浸润和转移的事件相关，三者均可作为其重要生物学标志，联合检测可利于胃窦癌早期诊断以及预后评估。

PU-0062

Predictive Protein Biomarkers for Response to Neoadjuvant Chemoradiation in Locally Advanced Rectal Cancer

Jianan Wang、Chengbin Wang
Department of Clinical Laboratory Medicine, The General Hospital of People’s Liberation Army

Background Colorectal cancer is the third most common and the fourth most lethal cancer in the world. In the majority of cases, patients are diagnosed at an advanced stage or even metastatic, thus explaining the high mortality. The standard treatment for patients with locally advanced rectal cancer (LARC) is neoadjuvant chemoradiotherapy (nCRT) with 5-fuorouracil (5-FU) followed by surgery. Most patients with LARC present incomplete pathological response to nCRT, the

resistance rate to this treatment remains high with approximately 30% of non-responders. Despite the efforts to predict treatment response using tumor-molecular features, as differentially expressed genes, no molecule has proved to be a strong biomarker. The tumor proteomic analysis is a promising strategy for biomarkers identification, which can be used to identify a predictive model to forecast treatment response outcomes and figured out response relevant proteins in nCRT.
Methods We performed LC-MS/MS-based proteomic analysis to select potentially proteins and then used in silico approach to further validate the differential proteins screened out from our training cohort . 42 patients diagnosed with LARC and treated with 5-FU based nCRT between 2010-2018 at Chinese PLA General Hospital were enrolled in the study. All of these cases had available paired pre-treatment formalin-fixed paraffin-embedded (FFPE) biopsies and post-CRT FFPE surgical specimens from the same patients and histologically confirmed adenocarcinoma. According to Tumor Regression Grade (TRG), patients were divided into three treatment response groups: poor-responders (PR, AJCC TRG2+3), moderate responders (MR, AJCC TRG1) and total responders (TR, AJCC TRG0), and to compare the proteomes of these diferent groups. From 42 paired FFPE biopsies and surgical specimens, we extracted and analysed the tumor proteome of these patients.
Results Comparing TR and PR group, we have identified 91 differentially abundant proteins between biopsies, 165 between surgical specimens of two groups. Next, comparing biopsies and surgical specimens of each group through paired t-test, we screened out 1467 and 771 proteins changed after nCRT in TR and PR group, respectively. 848 proteins with different change directions(from biopsies to surgical specimens) in TR and PR group were defined as response relevant proteins which might provide some indications to explain different response in TR and PR group. Then, 129 proteins were figured out in intersections between differentially expressed proteins and response relevant proteins, which might play a role in tumor resistant to nCRT and predict the patient response to the therapy. Among these proteins, we have identifed 43 genes expressed significantly different in rectal cancer tissue and normal tissue using GEPIA2 database(mainly involved in TFIID-class transcription factor complex binding, ATPase binding, RNA polymerase II transcription factor binding, etc), and there were 11 genes related to the overall survival of rectal cancer patients(favorable: SF3B6, NUP153, ARGLU1, GNL3, MTHFD1L, PTCD3, SLC27A2; unfavorable: SPTB, TMOD1, CD63, S100A13). A set of 16 proteins(over-expressed in PR group: PLEKHA6, CHMP4B, VWA1, LMNA; over-expressed in TR group: PTPN6, SF3B3, HDAC2, NDUFA5, PHGDH, TIMM44, AHSA1, GNL3, POLR2A, MTHFD1L, PTP4A1, NUP35) was independently validated in a gene expression dataset for chemoradiosensitivity of colorectal cancer cells from GSE20298 to be related to nCRT resistance, enrichment analysis found that these 16 proteins were related to nuclear envelope (NE) reassembly, nucleus organization, and generation of precursor metabolites and energy.
Conclusions From this retrospective study, protein differences between different response groups to nCRT in LARC patients were highlighted using FFPE proteomic analysis, they might be the novel biomarkers for diagnosis and guiding therapeutic strategies of rectal cancer. These results will pave the way for a larger cohort for better sensitivity and specificity of the signature to guide decisions in the choice of treatment.Furthermore, the findings will provide an insight about the proteins and molecular pathways involved in the response to treatment of LARC patients.

PU-0063

分子诊断技术在结核病诊疗中的应用进展

彭瑾
大理大学第一附属医院（云南省第四人民医院）
无

结核是由结核分枝杆菌引起的一种世界性慢性传染病，通常对肺及淋巴系统造成感染破坏，其它多器官，多系统亦可受累，主要经呼吸道传染，起病隐匿、进展缓慢、传染性强。灵敏、准确及

快速的诊断方法是有效控制结核病传播的重要手段。对于结核病的诊断，主要通过临床表现、免疫学、微生物学及影像学检测结果进行综合分析，随着分子诊断的快速发展，为结核病的诊治提供了新思路，目前，多种新的分子诊断技术已经或即将应用于临床，获得了 WHO 的认证推荐，应用前景广，基于核酸分子杂交、基因测序的分子诊断技术取得了巨大的进展 ，而很多新的分子诊断技术也处于快速发展中，有些成熟的技术已取得了较为广泛的应用，分子诊断技术的发展及应用进一步增强了结核病的诊疗，对于及早发现、及早治疗结核病起了积极的推进作用。

PU-0064

一种高灵敏检测 miRNA 的荧光生物传感方法

孙玉洁、张玉林、张国军
湖北中医药大学

目的 构建一种新型基于双链特异性核酸酶（DSN）放大和磁吸减少内滤光效应（IFE）的聚多巴胺磁纳米颗粒(MNPs@PDA)的荧光共振能量转移（FRET）生物传感器用于 miRNA 的检测。
方法 在碱性缓冲液中，加入盐酸多巴胺和磁性纳米颗粒避光混悬制备 MNPs@PDA，并采用拉曼光谱仪、红外光谱仪、透射电镜进行表征。FAM 标记的 DNA 探针在无靶标 miRNA 存在的情况下，因 π-π 堆积作用吸附在 MNPs@PDA 表面，发生 FRET 导致荧光淬灭。在靶标 miRNA-141 存在的情况下，标记探针与 miRNA 互补杂交形成 DNA-RNA 杂合双链，因构象改变，便从 MNPs@PDA 表面发生解吸附。DSN 选择性地消化 DNA-RNA 杂交链中的 DNA，使探针被酶切成短小的片段，同时靶 miRNA 被释放出来。探针碎片因为长度短，与 MNPs@PDA 亲和力弱，于是荧光信号恢复。而释放的靶 miRNA 再次与下一个标记探针杂交，上述过程循环发生，从而导致荧光信号成几何级数放大。此外，由于 IFE 的存在，分散在溶液中的 MNPs@PDA 会减弱荧光信号。而将 MNPs@PDA 通过磁力吸引到比色皿的底部，进一步增大了荧光信号。通过检测荧光信号，实现对 miRNA 的定量检测。
结果 优化后的体系检测条件为 MNPs@PDA 浓度为 10 μg/mL、DSN 酶的工作温度为 50℃、DSN 酶的浓度 0.2 U/mL，酶反应时间为 90 分钟。在优化条件下，miR-141 在 5 pM~ 5 nM 范围内，其浓度的对数与体系荧光信号呈线性关系，检测限低至 0.42 pM。将非互补核酸序列 miR-21、RS ssDNA、SM RNA 与 miR-141 分别加入反应体系进行检测，能成功区分出靶标 miR-141，说明了该传感器良好的选择性。此外，分别检测前列腺癌细胞株 PC-3 细胞和前列腺上皮细胞株 RWPE-1 细胞来源的 RNA，癌细胞来源的 miRNA-141 表达上调，表明该平台对生物样本的适用性。
结论 基于 DSN 放大和 MNPs@PDA 的荧光生物传感器用于 miRNA 的检测，具有操作简单、稳定性好、特异性强、灵敏度高等优点，可以实现对生物复杂样品中 miRNA 的检测，未来采用多种荧光标记的探针有望应用于多种 miRNA 的同时检测。

PU-0065

荧光定量聚合酶链反应技术在结核病诊断中的应用

李若兰
石河子大学医学院第一附属医院

结核病是临床常见的一种传染性疾病。实验室检测结果的准确性直接影响到结核病的临床诊断与治疗转归，并且是临床治疗的主要依据之一 。因此，尽可能提升实验室检出准确率与有效率，改进检测技术的应用价值，促使患者早期诊断、早期治疗，有效控制患者疾病，预防患者病情蔓延是非常有必要的。但传统检验方法需要较长时间才能得出结果，且结核分枝杆菌的临床检出率比较低，无法满足临床的诊断、治疗需求。近年来，结核病诊断中应用荧光定量聚合酶链反应（PCR）技术，可通过 PCR 体外扩增法准确检出结核分枝杆菌 DNA，且检测时间比较短。

PU-0066

Aberrant methylation of PAX5 in human prostate cancer and its relation to clinicopathologic features

Shibao Li
The Affiliated Hospital of Xuzhou Medical University

Backgrounds PAX5, a number to the PAX gene family, is frequently silenced in various carcinomas and linked to tumor progression. However, the expression profile of PAX5 and its regulatory mechanism in human prostate cancer (PCa) remains unknown. Here, we explored the expression and an epigenetic change of PAX5 in PCa and determined whether these findings were correlated with clinicopathologic characteristics of PCa.
Methods The expression profile of PAX5 in both mRNA level and protein content was investigated via qRT-PCR, Western blotting, and immunohistochemistry in 3 PCa cell lines (LNCaP, PC-3 and DU145), a cohort of frozen prostate tissues including 47 primary PCa, 9 paired noncancerous and cancerous prostate tissues and a tissue microarray sets including 100 paraffin-embedded prostate samples (3 normal tissues, 36 cases of adjacent tissues and 61 cases of tumor). Subsequently, the methylation status of PAX5 gene promoter was analyzed using bisulfite sequencing(BSP) and methylation-specific PCR(MSP) . Finally，the response of PCa cell lines, differing in the initial PAX5 mRNA content, to epigenetic modifier, 5-aza-2-deoxycytidine, was detected by qRT-PCR.
Results Down-regulation of PAX5 mRNA expression was observed in 30 of 47 (63.8%) PCa compared with normal adjacent tissues. Meanwhile, the methylation of PAX5 gene promoter was detected in 25 of 47 (53.2%) PCa. Immunostaining analysis showed that PAX5 protein was negative or weakly positive in 39 of 61 (63.9%) prostate cancer samples. PCa patients with high Gleason scores have a higher frequency of PAX5 methylation than those with low Gleason scores. Furthermore, expression of PAX5 mRNA can be restored by the demethylated drug 5-aza-2'-deoxycytidine in DU145 cells.
Conclusions Our study provides evidence that the epigenetic inactivation of PAX5 may be a novel candidate biomarker of PCa and play an important tumor-suppressor role in PCa progression.

PU-0067

基于回文 DNA 的纳米机器人用于复杂分子突变的识别及诊断

袁睿[1]、辇伟奇[2]、丁世家[3]、罗阳[1]
1. 重庆大学
2. 重庆大学附属肿瘤医院
3. 重庆医科大学

表皮生长因子受体 (EGFR) 基因突变的可靠鉴别和诊断在肺癌治疗中具有关键作用。然而，目前对 EGFR 外显子的特定缺失方式的快速和准确识别仍然具有挑战性。在此，我们提出了一种基于回文结构辅助自退火转录扩增（PASTA）策略，用于可靠地检测循环 DNA 中 EGFR 外显子突变。首先，我们设计了一个回文 DNA 发夹纳米机器人，其由回文序列、 T7 启动子区域、目标识别区域和转录模板组成；当靶标单链 DNA 存在时，纳米机器人可以迅速自组装形成靶标-发夹/发夹-靶标的二聚体结构；随后在引入 DNA 聚合酶和 T7 RNA 聚合酶后，将发生回文结构介导的延伸和体外转录，同时产生大量 RNA 产物。最后，这些产物可以使用亚甲蓝染料辅助电化学生物传感器准确读出。以循环 15n-del EGFR 突变为模型验证该策略，在 1 fM 至 100 pM 范围内具有较好的线性关系，最低检测限可低至 0.78 fM 。该方法的有效应用也可作为分子亚型检测的通用平台。

PU-0068

SEMA3B-AS1 在食管鳞癌中的鉴别诊断价值

李世宝
徐州医科大学附属医院

目的 探讨 SEMA3B-AS1 在食管鳞癌(esophageal squamous cell carcinoma，ESCC)鉴别诊断中的价值及其临床意义。
方法 本研究共纳入 41 例食管鳞癌患者与 31 例食管良性疾病患者，收集患者外周血，使用实时荧光定量聚合酶链反应(quantitative polymerase chain reaction，qRT-PCR)检测患者血清中 SEMA3B-AS1 表达水平，分析其与患者临床病理特征的关系。受试者工作曲线(receiver operator characteristic curve, ROC 曲线)评估 SEMA3B-AS1 在食管鳞癌的鉴别价值。
结果 食管鳞癌患者的血清 SEMA3B-AS1 表达水平明显高于食管良性疾病组，差异具有统计学意义（P < 0.01）；SEMA3B-AS1 的表达水平与患者的肿瘤直径大小和淋巴结转移有关(P<0.05），而与患者年龄、性别、TNM 分期、神经侵犯、分化程度均无显著相关性(P>0.05）；ROC 曲线结果显示：SEMA3B-AS1 鉴别食管癌和食管良性肿瘤的曲线下面积（AUC）为 0.886（95%CI：0.8144~0.9579，P 值＜0.0001），敏感度为 76.47%，特异度为 90.32%。。
结论 食管鳞癌患者的血清 SEMA3B-AS1 表达水平明显高于食管良性疾病患者，且其表达水平与患者肿瘤直径大小与淋巴结转移正相关，提示 SEMA3B-AS1 是一个潜在地鉴别食管鳞癌与食管良性疾病患者的标志物。

PU-0069

Regulation of estrogen signaling and breast cancer proliferation by PSMD14

Xiao Yang
Xinxiang Medical University

Breast cancer is the number one malignant tumor in women, among which estrogen receptor positive accounts for 65%-70%. Clinically, patients with estrogen receptor positive breast cancer can receive endocrine therapy. However, resistance to endocrine therapy has become a clinically urgent problem. A large number of previous studies have proved that the post-translational modification of the estrogen receptor is significantly related to endocrine therapy resistance. The preliminary screening of the deubiquitinating enzyme siRNA library suggested that the PSMD14 protein is a key deubiquitinating enzyme that regulates the stability of the estrogen receptor protein and the activity of the estrogen signaling pathway. PSMD14 silence can significantly inhibit breast cancer estrogen receptor protein levels and breast cancer cells proliferation. PSMD14 can interact with estrogen receptors and regulate the stability of estrogen receptors. Therefore, we hypothesized that PSMD14 is a key deubiquitinating enzyme that regulates the estrogen signaling pathway and breast cancer cells proliferation. This project uses molecular biology experiments, cytology experiments, animal experiments, and clinical samples to explore the mechanisms of PSMD14 regulating breast cancer progression and endocrine therapy resistance via regulating the estrogen pathway, with a view to helping to provide new ideas for the treatment of breast cancer and the reversal of endocrine therapy resistance.

PU-0070

microRNA-4458 regulates insulin resistance in hepatic cells by targeting the insulin-like growth factor 1 receptor

周敬敬
芜湖市第一人民医院

Background The objective of the research was to investigate the roles of miR-4458 in the regulation of insulin resistance in hepatic cells and to explore the underlying molecular mechanisms.
Methods The blood samples were collected from the T2D patients and the health controls, and the liver tissues were collected from the DM and control rats. The relationship between IGF1R and miR-4458 was predicted by TargetScan and verified by the dual luciferase reporter gene system. qRT-PCR was used to measure the mRNA expression of miR-4458, IGF1R, G6Pase and PEPCK. The protein expression of IGF1R, p-AKT and AKT were measured by Western blot analysis.
Results miR-4458 was high expressed in T2D patients. We predicted and verified that IGF1R was a direct target of miR-4458, and the mRNA expression of IGF1R was reduced in type 2 diabetes patients.
Conclusion miR-4458 regulated the insulin resistance in hepatic cells by regulating the IGF1R/PI3K/AKT signal pathway, which will be a potential target for the treatment of diabetes.

PU-0071

血清 Linc01503 在食管鳞状细胞癌中的表达及鉴别诊断价值

李世宝
徐州医科大学附属医院

目的 研究长链非编码 RNA Linc05103 在食管鳞状细胞癌（esophageal squamous cell carcinoma，ESCC）患者血清中的相对表达水平，探讨其对 ESCC 鉴别诊断的价值。
方法 收集 34 例食管良性病变样本、47 例未放化疗的食管鳞癌样本及 126 例已放化疗的 ESCC 的血清样本。运用实时荧光定量聚合酶链反应(quantitative polymerase chain reaction，qRT-PCR)技术检测各组血清中 Linc01503 的表达水平，并分析其与临床病理参数的相关系，同时 ROC 曲线分析血清中 Linc01503 对食管鳞状细胞癌的鉴别诊断价值。
结果 Linc01503 在 ESCC 组表达水平明显高于食管良性病变组(P<0.05)，Linc01503 在 ESCC 放化疗前后的表达差异无统计学意义(P>0.05)。ROC 曲线分析结果显示：区分 ESCC 和食管良性炎症的曲线下面积为 0.875(95%CI 0.798~0.953，P<0.001)，敏感度 91.5%，特异度 73.5%。
结论 Linc05103 在 ESCC 患者外周血中的表达较食管良性病变显著提高，提示 Linc05103 具有鉴别 ESCC 和食管良性炎症的价值。

PU-0072

Identification of Type I Interferon-stimulated Genes and Their Clinical Significance in Pancreatic Adenocarcinoma.

Duo Zuo 、Ren Li
Tianjin Medical University Cancer Institute and Hospital

Objective The main reasons for the poor prognosis of pancreatic adenocarcinoma (PA) are rapid early-stage progression, late-stage metastasis and chemotherapy resistance. Identification of

novel diagnostic and prognostic biomarkers of PA is urgently needed. Furthermore, many studies have been done on identifying potential diagnostic and prognostic biomarkers for pancreatic adenocarcinoma (PA) via bioinformatics analyses but few have noticed some genes enriched in the defense response to virus and the type I interferon (IFN) signaling pathway. Oncolytic viruses (OVs) are emerging immunotherapeutics for the majority of cancers. However, researchers have found that some PA patients develop drug resistance due to the type I IFN responses of the host that restrict viral replication. Therefore, there is an urgent need to identify specific defects in genes involved in IFN signaling pathways as potential biomarkers to classify candidate patients for oncolytic therapy to make the strategy effective.

Methods Three mRNA microarray datasets were obtained from the GEO database to select differentially expressed genes (DEGs). Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analyses for hub genes were performed using DAVID. Correlations between expression levels of hub genes and cancer-infiltrating immune cells were investigated by TIMER. Cox proportional hazard regression analyses were also performed. Serum hub genes were screened by the HPA platform and verified for diagnostic value by enzyme-linked immunosorbent assay (ELISA). For immunohistochemistry (IHC)analysis, categorical variables were analyzed using the chi-square test. The Kaplan–Meier method and log-rank test were used to estimate the survival time of PA patients. For ELISA analysis, differences between the PA group and the healthy control group were assessed by the Mann–Whitney U test. Receiver operating characteristic curve (ROC) were established to assess sensitivity, specificity, and AUCs with 95% confidence intervals (CI).

Results We identified 59 hub genes among 752 DEGs and found 24 hub genes enriched in the type I IFN signaling pathway and 19 hub genes enriched in the defense response to virus by GO enrichment analysis, such as radical S-adenosyl methionine domain containing 2 (RSAD2), IFN-stimulated gene 15 (ISG15), 2'-5'-oligoadenylate synthetase 2 (OAS2), and IFN gamma inducible protein 16 (IFI16). We also found that these hub genes were associated with immune cells infiltration in the microenvironment of PA. Furthermore, alteration of RSAD2 was associated with poor overall survival (OS), progression-free survival (PFS), and disease-specific survival (DSS) of PA patients. Additionally, the ISG15 protein levels were evaluated to differentiate cancerous tissues from adjacent noncancerous tissues using ROC curve analysis (AUC = 0.729, 95% CI: 0.594-0.838). The protein encoded by ISG15, which exists in peripheral blood, was validated as a potential diagnostic biomarker that distinguishes PA patients from healthy controls (AUC=0.902, 95% CI: 0.819-0.961).

Conclusion Our study suggested that RSAD2 was associated with immune cell infiltration in the PA microenvironment, which provides new insight for OV therapy. ELISA indicated that serum ISG15 could be a potential novel diagnostic biomarker for PA.

PU-0073

2018-2020 年丽水地区不同年龄人群甲型流感病毒检测结果与分布特征分析

张强
丽水市人民医院

目的 分析丽水地区疑似病例甲型流感病毒检测结果，了解丽水地区甲型流感流行特征，为后续流感早期诊治及防控工作方案制定提供依据。

方法 对 2018 年-2020 年到丽水市人民医院就诊的 3204 例流感疑似病例，采集病人咽拭子标本，采用 Real-time RT-PCR 进行甲型流感病毒核酸检测，根据不同性别和年龄等进行统计分析。

结果 在 3204 例疑似病例中，阳性病例 907 例，甲型流感的总的阳性率是 28.3%（907/3204），男性阳性率为 26.95%（482/1788），女性阳性率为 30.01%（425/1416）；不同性别之间阳性率比较差异无统计学意义（P>0.05）。在不同年龄组中，儿童组甲流阳性率最高为 45.79%，其次是

老人组为 27.8%，最低是青年组为 23.23%，不同年龄组阳性率比较差异有统计学意义（P<0.05）。甲型流感高发时间为每年的 1 月、2 月和 12 月，确诊患者分布科室以呼吸内科、EICU、儿科居多，依次为 24.14%、12.45%、11.79%。
结论 对于呼吸内科、EICU、儿科甲流患者比较集中科室需要设置隔离屏障，防止院内感染，丽水地区婴幼儿和学龄儿童属于甲型流感易感人群，需重点防护。

PU-0074

新型冠状病毒（2019-nCoV）社区核酸筛查假阴性结果分析及对策

陈逸平[1]、刘敏[2]
1. 湖南省人民医院
2. 湖南师范大学医学院

目的 总结分析 2020 年国务院应对新型冠状病毒肺炎疫情联防联控机制（医疗救治组）在北京和新疆已开展的单管单采样与单管混采共 513336 例新型冠状病毒核酸筛查的结果，深入分析可能导致假阴性结果的原因并提出应对策略。
方法 从社区核酸筛查数据中筛选出核酸检测结果为阳性的病例进行回顾性分析，通过比较多轮筛查的结果，并找出具有代表性意义的病例进行讨论。结合实际情况从样本取材、样本质量、样本保存、检测方法等多个方面进行分析。
结果 共检出阳性病例 27 例（一轮：0、二轮：19、三轮：7、四轮：1）。
结论 规范操作流程、实行严格的质量控制、联合检测均可以有效的提高阳性检出率。

PU-0075

高危型 HPV 与 TCT 联合检测对宫颈癌的价值评估

葸静、赵重阳、杨宝珍
宁夏金域医学检验所

目的 研究 HPV 分型与 TCT 联合检测对宫颈癌的价值评估。
方法 选取 2021 年 1 月至 2021 年 4 月送检至宁夏某第三方 920 例样本，同时进行人乳头瘤病毒（HPV）和宫颈液基薄层细胞学检测（TCT）检测，以病理活检为金标准。
结果 HPV 及 TCT 检测阳性率分别是 35.9%、8.5%，其中两者联合的阳性率为 5.5% ；两者联合检测敏感度、特异度、准确性分别为 99.6%、86.2%、90.1%；
结论 研究表明，HPV 及 TCT 联合检测相对于单一检测具有高的灵敏度，对宫颈癌及癌前病变的筛查具有一定的诊断价值。

PU-0076

miR-30-5p 及 SOCS1 在食管癌组织中的表达及临床意义

黄义、黄友军、颜彦
郴州市第一人民医院

目的 研究微小 RNA （microRNA,miR）-30-5P 和细胞因子信号传导抑制因子(suppressor of cytokinesignaling1, SOCS1)在食管癌组织中的表达及临床意义。

方法 应用实时定量 PCR 及免疫印迹检测我院 2018 年 6 月至 2020 年 6 月期间诊治的 85 例食管癌患者癌及癌旁组织中 miR-30-5p 及 SOCS1 的表达。统计学分析癌组织中 miR-30-5p 及 SOCS1 表达与临床病理参数关系。Pearson 线性相关分析癌组织中 miR-30-5p 与 SOCS1 表达的相关性，生物信息学预测两者之间相互作用位点。Kaplan-Meier 生存分析（Log-rank 检验）miR-30-5p、SOCS1 表达与患者预后的关系。
结果 与癌旁组织相比，食管癌癌组织中 miR-30-5p 表达较高，而 SOCS1 表达较低（P<0.05）。miR-30-5p 与 SOCS1 的表达与肿瘤分期、病理分级及淋巴结转移有关（P＜0.05），与性别、年龄、肿瘤大小及肿瘤位置无关（P 均>0.05）。癌组织中 miR-30-5p 与 SOCS1 的表达呈明显负相关（r=0.547,P=0.000），生物信息学预测 SOCS1 mRNA 的 3'UTR 区存在与 miR-30-5p 相互结合的位点。miR-30-5p 高表达、SOCS1 低表达患者的 3 年总体生存率分别显著低于 miR-30-5p 低表达、SOCS1 高表达患者（P 均＜0.05）。
结论 食管癌组织中 miR-30-5p 表达升高，而 SOCS1 表达降低，两者与肿瘤分期、病理分级及淋巴结转移及患者的生存预后有关，共同促进食管癌的恶性进展。

PU-0077

实验室诊断中的人工智能

董程[1]、段勇[2]
1. 凉山彝族自治州第二人民医院
2. 昆明医科大学第一附属医院

通过机器学习分析大数据为同化和评估大量复杂的医疗数据提供了相当大的优势。然而，为了在医疗保健中有效地使用机器学习工具，必须解决几个限制，并考虑一些关键问题，如其临床实施和医疗保健服务中的伦理。与传统生物统计学方法相比，机器学习的优点包括灵活性和可扩展性，这使得机器学习可用于许多任务，如风险分层、诊断和分类，以及生存预测。机器学习算法的另一个优势是能够分析不同的数据类型(如人口数据、实验室发现、成像数据和医生的自由文本笔记)，并将它们纳入疾病风险、诊断、预后和适当治疗的预测中。尽管有这些优势，机器学习在医疗保健服务中的应用也提出了独特的挑战，需要数据预处理、模型训练和针对实际临床问题的系统改进。同样重要的还有伦理方面的考虑，包括医学法律方面的影响、医生对机器学习工具的理解以及数据隐私和安全。在这篇综述中，我们讨论了医疗保健领域的大数据和机器学习的一些好处和挑战。

PU-0078

Harnessing CRISPR/Cas System for Nucleic Acid Fluorescence Labeling

Lang Yi
xiangya hospital central south university

The CRISPR/Cas system is widely used in gene editing and gene regulation by simultaneously delivering the Cas9 protein and guide RNA (sgRNA) into the cell. The recent studies showed that the dead Cas9 (dCas9) protein, which lacking endonuclease activity, can conjugate fluorescent protein or tag protein as a universal nucleic-acid labeling tool for specific DNA or RNA sequences labeling in living cells or fixed cells. Furthermore, by assembling RNA aptamers MS2 or PP7, different fluorescent proteins can be recruited to the dCas9/sgRNA complex for monochromatic of polychromatic DNA fluorescence labeling. CRISPR system based platform for gene imaging is simple, flexible, and having good application prospect. Thus, here we summarize the applications of the CRISPR/Cas system in DNA or RNA imaging.

PU-0079

基于 LC-MS/MS 法检测的妊娠中期血清 25(OH)D2、25(OH)D3 水平与不良妊娠结局的相关性

冯跃
绵阳市中心医院

目的 有研究表明，25(OH)D2 可能会影响 25(OH)D3 的生物效能。目前妊娠中期 25(OH)D2 水平与不良妊娠结局的相关性的尚未见报道，且 25(OH)D3 与不良妊娠结局的研究有限。故本研究旨在研究妊娠中期血清 25(OH)D2、25(OH)D3 水平与主要不良妊娠结局的相关性。
方法 纳入 2018 年 6 月至 2021 年 5 月，本院接受妊娠监督并分娩的，无产前的基础性疾病的自然受孕者。采用液相色谱-串联质谱(LC-MS/MS)的方法检测其血清 25(OH)D2 与 25(OH)D3 水平。25(OH)D=25(OH)D2+25(OH)D3。维生素 D 状态根据 25(OH)D 水平分为两组(充足与不足组: 25(OH)D≥20ng/ml; 缺乏组:25(OH)D<20ng/ml)。不良妊娠结局患者设为观察组，非该不良妊娠结局者为对照组。
结果 共纳入受试者 2966 例。受试人群妊娠中期 25(OH)D2 水平为 1.52(0.87-3.07) ng/ml，25(OH)D3 水平为 24.16±9.72 ng/ml，维生素 D 缺乏的比例为 27.6%。高危妊娠患者 25(OH)D3 (p=0.009)、25(OH)D (p=0.017)水平显著高于对照组。轻度贫血患者 25(OH)D 2(p=0.001)、25(OH)D3 (p=0.012)、25(OH)D (p=0.001)水平组显著低于对照组，中度贫血患者 25(OH)D3 (p=0.004)、25(OH)D (p=0.003)水平组也显著低于对照组。高尿酸血症患者 25(OH)D3 水平显著高于对照组(p=0.032)，D2/D3 水平则显著低于对照组(p=0.012)。脐带扭转患者 25(OH)D2 (p=0.023)、D2/D3(p=0.012)水平则显著低于对照组。此外，维生素 D 缺乏组的高危妊娠(p=0.001)、妊娠期糖尿病(p=0.002)发生的比例显著低于对照组。而轻度贫血发生的比例显著高于对照组(p=0.014)。此外，logistic 回归结果显示，相比于维生素 D 不足或充足，维生素 D 缺乏是高危妊娠的保护因子(OR=0.702, p=0.002),却是轻度贫血的危险因子(OR=1.259, p=0.014)。
结论 妊娠中期血清 25(OH)D、25(OH)D3、D2/D3 水平可能与部分不良妊娠结局相关。妊娠中期血清低 25(OH)D3、25(OH)D 水平可能增加轻度与中度贫血风险，却也可能增加高危妊娠的风险。低 25(OH)D2、D2/D3 水平可能增加脐带扭转风险。而高 25(OH)D3，低 D2/D3 水平则可能增加高尿酸血症风险。

PU-0080

miR-200 家族对卵巢癌的诊断价值

王丽雯
云南省肿瘤医院

目的 卵巢癌是第二常见的妇科恶性肿瘤（仅次于宫颈癌），其潜伏期长，在潜伏内很少甚至没有表现出临床症状，直到当疾病进展到转移，表现出不同的组织学亚型和相应的临床症状，因此对于诊断和治疗具有巨大的挑战。越来越多的证据表明 miR-200 家族与卵巢癌之间存在联系，影响其诊断、治疗及预后。针对 miR-200 家族与卵巢癌的关联性研究，本研究我们进行卵巢癌循环中血清 miR-200 家族（miR-200a/b/c，miR-141/429）进行定量检测，同时采用卵巢巧克力囊肿和正常体检健康大于 40 岁的女性作为对照组，分析 miR-200 家族对卵巢癌的诊断价值。
方法 采用 QRT-PCR 的方法，实验组为卵巢癌，良性对照组为卵巢巧克力囊肿，正常对照组为正常体检健康大于 40 岁的女性，进行循环中血清 miR-200 家族（miR-200a/b/c，miR-141/429）进行定量检测。运用 SPSS 22.0 统计软件，两两比较对实验组和对照组进行统计学分析，分析 miR-200 家族与卵巢癌的相关性，运用 ROC 曲线分析诊断价值。

结果 本次研究中量化了卵巢癌血清中 miR-200a、miR-200b、miR-200c、miR-141 和 miR-429 的表达水平，结果显示 miR-200 家族的所有亚型均可区分了健康女性中卵巢癌患者，卵巢巧克力囊肿中卵巢癌患者，其中 miR-200a 与 miR-200b 的血清水平的诊断价值最高。
结论 循环血清中 miR-200 家族（miR-200a/b/c，miR-141/429）的所有亚型对卵巢癌，与卵巢巧克力囊肿和正常女性有很好的区分度，是良好的诊断调控基因，可能涉及与上皮-间质转化、肿瘤干细胞转化、细胞的增殖与凋亡有关。miR-200 家族在卵巢癌中的诊断、治疗及预后价值还需要大样本的临床数据进一步挖掘，其更具体的分子机制和调控网络也迫切需要更多的研究成果加以完善。

PU-0081

炎症微环境中 JAK2/STAT3 通过上调 Sirtuin1 抑制滑膜细胞的焦亡

蒋大勇
电子科技大学附属医院.四川省人民医院临床医学检验中心

目的 探究滑膜炎组织中的炎症微环境是否可以激活 JAK2/STAT3 信号通路，以及是否可以调控 Sirtuin1 的表达，并进一步揭示滑膜细胞凋亡的机制。
方法 通过常规病理染色，免疫荧光以及实时定量 PCR 观察患者滑膜组织的病理结构，中性粒细胞和巨噬细胞的招募以及多种炎症因子 IL-1β，IL-6, TNF-α，IL-4 的 mRNA 水平。通过提取滑膜组织中的原代滑膜细胞进行 JAK2/STAT3 信号通路活化的验证以及细胞活力的检测；通过 TNF-α 刺激 MH7A 细胞模拟构建滑膜炎的炎症微环境，借助抑制剂对各自信号通路的的干扰，western blot 实验探究 JAK2/STAT3 与 Sirtuin1 信号通路的上下游关系以及对滑膜细胞凋亡的影响以及 CCK8 检测细胞活力；通过 TNF-α 刺激 MH7A 细胞模拟构建滑膜炎的炎症微环境，实时定量 PCR 实验探究细胞焦亡特征因子 IL-18 和 IL-1β 的 mRNA 水平变化；通过 TNF-α 刺激 MH7A 细胞模拟构建滑膜炎的炎症微环境，western blot 实验探究细胞焦亡特征蛋白 caspase1/4/5，Gastdermin 和 NLRP3 的水平变化。
结果 HE 染色结果发现炎症滑膜组织病理结构紊乱；实时荧光定量 PCR 检测发现炎症因子 IL-1β，IL-6, TNF-α，IL-4 的 mRNA 水平在炎症滑膜组织中显著升高；免疫荧光可见中性粒细胞和巨噬细胞的大量招募，western blot 检测发现炎症微环境可以激活 JAK2/STAT3 信号通路，并上调 Sirtuin1 表达，继而促进滑膜细胞的增殖；在 MH7A 细胞实验中，JAK2 被抑制后，我们发现 STAT3 表达下降，同时 Sirtuin1 与 Ki67 也被下调；并且抑制 Sirtuin1 可以抑制滑膜细胞增殖并促进滑膜细胞焦亡，表征细胞焦亡的主要细胞因子 IL-18、IL-1β、caspase1/4/5，Gastdermin 和 NLRP3 蛋白均下调。
结论 我们的研究发现 JAK2/STAT3 信号通路在滑膜炎中活化，并上调 Sirtuin1 通路来促进滑膜细胞增殖并抑制滑膜细胞焦亡，而下调 Sirtuin1 可以抑制滑膜细胞的增殖并促进焦亡，因此，调节 Sirtuin1 的表达可能成为治疗滑膜炎的新靶点。

PU-0082

Analysis of the Serum Metabolome Variations for Identification of Potential Biomarkers for Anti-tumor Effect of Imatinib by Untargeted Metabolomics

Bei Xu
Mianyang Central Hospital

Background Gastrointestinal stromal tumors (GISTs) are the most common mesenchymal tumors of the gastrointestinal tract. Imatinib, a tyrosine kinase inhibitor, is a small molecule

protein kinase inhibitor, which can block one or more protein kinases. It is used in the treatment of chronic myeloid leukemia and malignant gastrointestinal stromal tumors. Although Imatinib displays bright prospects in tumor treatment, including GISTs, its molecular mechanism has not been well-explored.Metabolomic technologies, especially untargeted metabolomic approaches, often provide additional information about the global profiling of the metabolome and are used to explore new mechanisms of carcinogenesis. Metabolomic technology is also a powerful tool for the discovery of key differential metabolites that can be used as biomarkers in various tumors, such as breast cancer, epithelial ovarian cancer, and lung cancer, et al.
This study was designed to assess the possible mechanisms of Imatinib against GISTs by untargeted metabolomics.
Methods 41 patients were divided into four groups: high concentration Imatinib group (H), medium concentration Imatinib group (M), low Imatinib concentration group (L) and healthy subjects (C). All subjects were analyzed for serum metabolites using non-targeted metabolomics based on ultra-performance liquid chromatography-tandem mass spectrometry (UPLC-MS/MS). The original data file obtained was firstly converted into mzML format by ProteoWizard software. Peak extraction, alignment and retention time correction were performed by XCMS program. The "SVR" method was used to correct the peak area. Filter the peaks with deletion rate > 50% in each group of samples. After that, metabolic identification information was obtained by searching the databases of Metlin, MoNA, and HMDB. Finally, statistical analysis was carried out by R program. Statistical analysis includes univariate analysis and multivariate analysis. Univariate statistical analysis includes Student's t-test and variance multiple analysis. Multivariate statistical analysis includes principal component analysis (PCA), partial least squares discriminant analysis (PLS-DA) and orthogonal partial least squares discriminant analysis (OPLS-DA).
Results In recent years, the methodology for LC-MS technology is deeply developed. More details have been revealed about the target metabolite. For example, quantitative LC-tandem MS (LC-MS/MS) analysis has been used for the study of comprehensive structural glycomic characterization. LC-MS might be more widely used in clinic work in the future to observe the specific molecular changes in liquid biopsy. The serum metabolomic profiles between the Imatinib H, M, L groups and healthy control group were significantly different, and 150 different metabolites were identified among the four groups. Metabolic pathway analysis of these differential metabolites found that the top three significantly changed metabolic pathways were drug metabolism-cytochrome P450, ascorbate and aldarate metabolism, and vitamin digestion and absorption metabolism.There are 6 metabolites enriched in these three metabolic pathways. In detail, compared with those in thehealthy groups, the levels of citalopram and (2R,3S)-2,3-Dihydroxy-5-oxohexanedioate in the Imatinib group were increased markedly, while the levels of rac-Didemethylcitalopram, Pyruvic acid, Threonic acid and Nicotinamide were reduced significantly.
Conclusion The serum metabolomic profiles between the Imatinib group and the HC group are significantly different. Imatinib has indicated favorable pharmacological effect on serum biochemical indexes. Metabolomics is a promising approach to unraveling anti-tumor effect by partially regulating the perturbed pathways, which provide insights into anti-tumor mechanisms of Imatinib.

PU-0083

Dickkopf 家族蛋白在非小细胞肺癌中的作用机制研究进展

董程[1]、段勇[2,3]
1. 凉山彝族自治州第二人民医院
2. 昆明医科大学第一附属医院
3. 云南省重点实验室

非小细胞肺癌(Non-small cell lung cancer,NSCLC)占所有肺癌的 80%～85%,是全世界发病率和致死率极高的恶性肿瘤。最初 NSCLC 对现有治疗的反应良好,但最终还是产生了耐药性。因此,

有必要探索有效且新颖的治疗方法。随着对 NSCLC 研究的深入,发现 Dickkopf 家族蛋白(DKKs)的信号传导在 NSCLC 发展中扮演重要角色,DKKs 是 Wnt/β-catenin 信号通路的重要调节因子,并与 NSCLC 细胞增殖、转移和侵袭密切相关。本文主要介绍了 DKKs 家族成员在 NSCLC 中的作用机制,讨论了 DKKs 在 NSCLC 治疗中的潜力,为进一步防治 NSCLC 提供了新思路。

PU-0084

Vitamin D deficiency in children with short stature: Accurate evaluation of serum vitamin D components using high performance liquid chromatography-tandem mass spectrometry

Bei Xu
Mianyang Central Hospital

Objective Vitamin D is one of essential nutrient for short stature children. However, levels of vitamin D status of these patients are sparsely reported. In this study, we tested various vitamin D components, and used different **Methods** to evaluate the true vitamin D storage of short stature children in vivo.
Methods A case-control study including 99 short stature children and 186 healthy controls was performed. Serum levels of 25-hydroxyvitamin D2 [25(OH)D2], 25-hydroxyvitamin D3 [25(OH)D3], 3-epi-25-hydroxyvitamin D3[3-epi-25(OH)D3, C3-epi] and free 25(OH)D [f-25(OH)D] were accurately measured. Total 25(OH)D [t-25(OH)D], 25(OH)D2/25(OH)D3 ratio, as well as C3-epi/25(OH)D3 ratio were then respectively calculated.
Results Serum levels of 25(OH)D3and f-25(OH)D in short stature subgroups 2 (school age: 7~12 years old) and 3 (adolescence: 13~18 years old) were significantly lower than those of healthy controls (all $P<0.05$), whilst C3-epi levels and C3-epi/25(OH)D3 ratios were all markedly higher in three short stature subgroups (all $P<0.05$) compared to healthy cohorts. The true sufficient storage capacities of vitamin D in short stature subgroup 1, subgroup 2 and subgroup 3 were only 42.8%, 23.8%, and 9.0% by Method 3 [25(OH)D2/3+25(OH)D3], which was lower than those of 57.1%, 28.6%, and 18.2% by Method 1 [25(OH)D2+25(OH)D3+C3-epi] and 45.7%, 28.5%, and 13.6% by Method 2 [25(OH)D2/3+25(OH)D3+C3-epi]. In both short stature and healthy control cohorts, 25(OH)D2 levels were found to be weak negatively correlated with 25(OH)D3, and higher 25(OH)D3 levels were strong positively associated with higher levels of C3-epi. Furthermore, f-25(OH)D levels were also found positive association with 25(OH)D3 and C3-epi in both cohorts.
Conclusion Short stature children had more severe vitamin D deficiency than healthy subjects. Though the results of vitamin D storage in short stature children evaluated by various **Methods** are different, simultaneous detection of 25(OH)D2, 25(OH)D3, C3-epi and f-25(OH)D levels could accurately evaluate the vitamin D storage in vivo.

PU-0085

miR-338-3p 调控肺癌生长和转移的作用及在宣威肺癌患者血浆中的表达研究

陶清元[1]、段勇[2]、熊秋霞[2]
1. 云南大学附属医院
2. 昆明医科大学第一附属医院

目的 课题组前期研究发现 miR-338-3p 在宣威非小细胞肺癌组织中表达显著下调并在人群中做了初步验证，本研究聚焦 miR-338-3p 影响 A549 细胞和宣威肺癌细胞增殖、凋亡以及迁移侵袭的能力，探究 miR-338-3p 过表达调控肺癌细胞生长和转移的作用。检测宣威地区非小细胞肺癌患者以及非肿瘤患者血浆标本中 miR-338-3p 的表达情况，探索 miR-338-3p 作为非小细胞肺癌早期诊断指标的可能性。

方法 将 miR-338-3p mimics 转染到 A549 细胞和宣威肺癌细胞中，创建 miR-338-3p 过表达的细胞模型。MTT 检测肺癌细胞的活力；PI 实验检测肺癌细胞的细胞周期；AnnexinV/PI 实验肺癌细胞发生凋亡的情况；Transwell 实验检测肺癌细胞的迁移能力。收集宣威非小细胞肺癌患者血浆标本 30 例、非肿瘤患者血浆标本 20 例， RT-qPCR 对标本中 miR-338-3p 的相对表达量进行测定， F 检验分析外周血中 miR-338-3p 的表达差异。收集患者的相关临床资料，Mann Whitney 检验分析 miR-338-3p 表达量与相关临床资料的相关性。

结果 miR-338-3p mimics 转染两种肺癌细胞后，细胞的活力都明显下降，A549 细胞的活力下降为 77.79%，宣威肺癌细胞下降为 69.24%。A549 细胞周期阻滞在 S 期，而宣威肺癌细胞周期阻滞在 G2/M 期。都明显诱导了细胞凋亡的发生，A549 细胞早期凋亡细胞的比例是 6.52%，宣威肺癌细胞早期凋亡细胞的比例是 2.66%（P <0.001）。miR-338-3p 过表达对肺癌细胞迁移有明显的抑制作用，都可以明显抑制肺癌细胞的迁移能力（ P <0.001 与 P <0.01）。肺癌患者组血浆标本中 miR-338-3p 的表达量显著降低，而且 miR-338-3p 的表达量与肺癌分期显著相关，与 I/II 期肺癌组相比，III/IV 期肺癌组 miR-338-3p 表达量显著降低(P< 0.05)。miR-338-3p 表达量与淋巴结转移显著相关，淋巴结转移组 miR-338-3p 表达量显著低于无淋巴结转移组(P < 0.05)，但与年龄、性别以及是否吸烟无关。

结论 1、MiR-338-3p 过表达能不同程度的抑制 A549 肺癌细胞与宣威肺癌细胞的增殖、迁移，且都能促进两种肺癌细胞的凋亡。但也导致 A549 肺癌细胞周期停滞在细胞周期的 S 期，而宣威肺癌细胞周期停滞在细胞周期的 G2/M 期。2、相对于非肿瘤患者，宣威非小细胞肺癌患者血浆中 miR-338-3p 的表达量显著降低，且相对表达水平与肿瘤分期、是否有淋巴结转移显著相关。

PU-0086

临床结核病患者中利福平表型药敏和分子药敏结果不一致的回顾性分析

胡培磊[1,2]、王珏[1,2]、陈振华[1,2]、刘彬彬[1,2]、陈忠南[1,2]、龚道方[1,2]、余艳艳[1,2]、郭婧玮[1,2]、谭云洪[1,2]
1. 湖南省胸科医院
2. 湖南省结核病防治所

目的 分析导致临床结核病患者的利福平表型药敏和分子药敏结果不一致（即分子药敏为利福平敏感而表型药敏为利福平耐药）的影响因素，以提高临床结核病利福平耐药实验室诊断的准确性。

方法 基于湖南省胸科医院结核病实验室信息系统，回顾性分析 2014 年-2019 年 Bactec MGIT 960 和 Xpert MTB/RIF 的检测数据，找出 Xpert MTB/RIF 检测结果为利福平敏感而 Bactec MGIT 960 检测结果为利福平耐药的病例，并对已保藏的患者的分离菌株进行复苏和菌种鉴定；然后分别采用

Bactec MGIT 960 和分子线性探针对鉴定为结核分枝杆菌复合群的菌株进行表型和分子药敏检测；最后，对两种药敏结果经确认存在差异的菌株进一步进行 rpoB 基因全长测序、最低抑菌浓度（MIC）及固体比例法药敏试验测定。

结果 在 31038 例同时进行 Bactec MGIT 960 和 Xpert MTB/RIF 检测的患者中，共得到 58 例 Bactec MGIT 960 为利福平耐药而 Xpert MTB/RI 为利福平敏感患者的患者。经菌株复苏，最终成功获得 43 例患者的分离菌株，包括 37 株结核分枝杆菌复合群菌株（MTBC）、5 株非结核分枝杆菌菌株（NTM）和 1 株为结核分枝杆菌复合群和非结核分枝杆菌混合菌株（MTBC/NTM）。在 37 株 MTBC 菌株中，11 株（29.7%）再次经 Bactec MGIT 960 测试为利福平敏感，且 rpoB 测序显示 RRDR 区无突变，支持以往 Xpert MTB/RIF 的检测结果，提示以往 Bactec MGIT 960 检测存在失误；另外的 26 株经 Bactec MGIT 960 检测为利福平耐药，且其中有 18 株的 RRDR 区存在利福平耐药相关突变，提示以往 Xpert MTB/RIF 的检测存在失误。在剩余的 8 株 MTBC 中，仅有 2 株存在敏感菌株和耐药菌株的混合现象，而在最终剩余 6 株 MTBC 中，3 株在 rpoB RRDR 区域之外存在 V170F 突变，1 株存在 I491F 突变，2 株菌株 rpoB 未检测到任何突变，有待全基因组测序进一步揭示。

结论 导致分子药敏为利福平敏感而表型药敏为利福平耐药的影响因素较为复杂，基于菌株的回顾性研究而提供的参考价值有限。尽管如此，实验室检测相关失误应为主要因素。在排除实验室检测相关失误的基础上，进一步基于菌株的实验验证分析可揭示与利福平耐药相关的罕见的突变位点，从而帮助我们理解利福平表型药敏和分子药敏结果不一致的分子机制。

PU-0087

miRNA 与宿主基因（综述）

刘华、贾正仙
昆明医科大学第一附属医院

MicroRNA(miRNA)是一组长度介于 20 到 24bps 的内源性非编码 RNA，有人使用 TCGA 数据集研究了这些 miRNAs 与宿主基因之间的共表达关系，不仅发现了常见的共表达模式，还揭示了肿瘤特异性甚至亚型特异性的关系，这对于理解 miRNA 的转录调控和转录后调控以及进一步发展 miRNA 在癌症中的治疗是非常有帮助的，miRNA 的定位是 miRNA 研究的热点之一，因为它是决定 miRNA 如何被调控的主要因素，基因内 miRNA 及其宿主基因的定义，基因内 miRNA 与宿主基因之间的相互作用，基因内 miRNA 与宿主基因之间的相互作用

结论 miRNA 表达失调在人类疾病中尤其是在癌症中起着重要作用。miRNA 与宿主基因之间存在密切的功能联系和复杂的相互作用;因此，有必要研究其同源宿主基因背景下的 miRNA 调控。由于大多数 onco/ts-miRs 是基因内 miRNA，我们研究了基于 TCGA 的这些 miRNA 与宿主基因的共表达关系数据集。常见的和特定于癌症的共表达关系将会促进治疗方法的设计，以沉默/激活 onco/ts-miRs 有效的表观遗传同源宿主基因的改变。

PU-0088

Correlation between multi-type human papillomavirus infections and viral loads and the cervical pathological grade

Yanfang Li[1]、HaiRu Wang[2]、YaBin Hou[3]、ChongHua Hao[1]、Xuan Jing[1]、YanJun Zhang[1]
1. Shanxi Provincial People's Hospital
2. 山西白求恩医院
3. 山西医科大学

Objective To investigate the relationship between single/multiple HPV infections and cervical lesions, and the correlation between viral load and the degree of cervical lesions.
Methods A total of 27 284 patients who underwent testing for HPV were retrospectively screened and 3728 women were enrolled who tested positive for HPV when examined by liquid-based ThinPrep cervical smear cytology test and diagnosed by histopathology at the Shanxi Provincial People's Hospital between May 2017 and March 2019. The genotype and viral load of HPV were determined by fluorescence quantitative polymerase chain reaction. Based on the pathological grade, the cervical lesions were stratified into three groups: chronic cervicitis/cervical intraepithelial neoplasia (CIN) I; CIN II/CIN III; and cervical cancer.
Results There were significant intergroup differences in the distribution of single and multiple HPV infections. There was a positive correlation between the viral load and cervical pathological grade when the infections were caused by HPV 16, 18, 31, 33, 51,52, 53, and 58.
Conclusion Multi-type HPV infections are more likely to aggravate the degree of cervical lesions than single-type infections. The HPV type-dependent viral load is associated with the cervical pathological grade.

PU-0089

二维 PCR 检测 1、2、3 类整合子

朱雯雯、朱玉、王童、魏取好
上海市奉贤区中心医院

目的 整合子是细菌基因组中常见的通用基因获取系统，能捕获并表达外源基因，同时，整合子可位于质粒、转座子或染色体上，造成耐药基因的广泛传播。根据整合酶氨基酸序列，将整合子分为 5 类，临床常见的是 1、2、3 类。本研究旨在开发了一种基于碱基淬灭探针技术的二维 PCR 技术，是一种结合 PCR 和熔融曲线分析的多重 PCR 检测方法，可以同时检测 3 种主要整合子。
方法 通过检测 104 拷贝/μl 的 3 种整合子质粒样品及其混合物来评估特异性，检测 10-108 拷贝/μl 的 3 种整合子质粒样本检测最低检出限和评估灵敏度，每个样本做 3 个复孔，去离子水做阴性对照，为了评估二维 PCR 应用于临床检测的价值与潜力，运用二维 PCR 检测 105 株临床变形杆菌样本，检测结果阳性标本进行测序验证，测序结果经 NCBI 的 BLAST 验证，评估二维 PCR 结果的准确性，同时采用临床常用的筛查整合子的普通 PCR 方法筛查 105 株变形杆菌的 1、2、3 类整合子，对两种方法的检测结果做一致性比较，评估二维 PCR 的特异性。
结果 结果显示二维 PCR 各型引物只能检测出对应的型别的质粒，各型之间无交叉反应，1、2、3 类整合子对应的溶解温度在 46。C、55。C、66。C 附近，结果非常容易区分，最低检出限实验显示 1、2、3 类整合子质粒的最低检出限分别为 10、102、102 拷贝/反应,测序结果表明二维 PCR 的特异性为 100%。

结论 通过质粒水平方法学实验以及临床样本检测评估，证明二维 PCR 能同时检测 3 种主要的整合子，具有特异性好、灵敏度高、成本低 、检测通量高、反应时间短等优点，可用于临床进行大规模整合子筛查及整合子分型。

PU-0090

FBXO22 对急性髓系白血病发病机制的研究

李玉云[1]、马丽[1]、王珏[2]、耿建[1]、张英杰[1]、曹蕴[1]
1. 蚌埠医学院
2. 蚌埠医学院第一附属医院

急性髓系白血病(AML)是一种以不成熟髓细胞异常增殖为特点的血液学恶性肿瘤，分化和成熟功能受损。因其发病机制复杂，极大程度的阻碍了临床的治疗。FBXO22 作为 FBXO 蛋白家族的一员， 参与多种癌症的发生发展，但是在 AML 中作用报道甚少。本文主要利用急性髓系白血病 FBXO22 基因过表达稳转株来探讨 FBXO22 在 AML 的作用研究。

目的 本研究以 FBXO22 过表达稳转株为研究对象，探讨 FBXO22 对 AML 细胞的增殖和凋亡以及分化等能力的影响，旨在为 AML 治疗提供新的治疗靶点改善病人预后。

方法 本实验我们利用急性髓系白血病常用的细胞株 U937、K562 进行实验。1.将 HBLV-ZsGreen-PURO 过表达对照、HBLV-h-FBXO22-3xflag-ZsGreen-PURO 慢病毒稳转入 U937、K562 细胞，qRT-PCR、W B 分别检测 FBXO22 相对表达量。2.细胞株稳转 FBXO22 后采用 CCK-8、细胞周期实验检测细胞增殖情况。3.采用 W B 检测细胞 bcl-2、Caspase-9 蛋白表达情况。4.采用流式细胞仪、瑞士吉姆萨染色、硝基四氮唑蓝（NBT）还原实验、W B 实验探究 FBXO22 对白血病细胞分化的影响。5.动物实验。将免疫缺陷鼠进行 X 光射线辐照，第二天将稳转株注射到小鼠尾静脉观察白血病症状，当小鼠出现驼背或后肢瘫痪时处死，观察小鼠脾脏和小鼠转移灶情况。

结果 qRT-PCR、W B 实验结果均表明 FBXO22 过表达细胞株构建成功（P<0.05）。CCK-8 实验证明 FBXO22 过表达后细胞增殖能力减弱（P<0.05）；细胞周期实验结果显示 FBXO22 过表达后细胞聚集在 G0/G1 期，S 期减少，上述结果表明，FBXO22 通过阻滞细胞周期至 G0/G1 期来抑制 AML 细胞的增殖（P<0.05）。过表达 FBXO22 后凋亡蛋白 Caspase-9 表达水平增强，BCL2 则相反;（P<0.05）。FBXO22 诱导 AML 细胞分化。与对照组相比，流式细胞术显示 FBXO22 过表达后 CD11b 的表达水平增高；瑞士吉姆萨染色结果显示，FBXO22 过表达后细胞核变成肾型、蚕豆型； NBT 阳性细胞增多；PU.I 蛋白水平也显著升高。注射经 FBXO22 过表达转导的 U937 细胞的小鼠脾脏肿大和转移灶大小明显小于对照组（P<0.01）。

结论 FBXO22 抑制 AML 细胞增殖，且通过阻滞细胞周期至 G0/G1 期来抑制细胞增殖。FBXO22 促进 AML 细胞凋亡。FBXO22 诱导 AML 细胞分化。

PU-0091

Current progress in metabolomics of gestational diabetes mellitus

Yu Zeng
Nanjing Maternity and Child Health Care Hospital Affiliatedto Nanjing Medical University

Gestational diabetes mellitus (GDM) is one of the most common metabolic disorders of pregnancy and can cause short- and long-term adverse effects in both pregnant women and their offspring. However, the etiology and pathogenesis of GDM are still unclear. As a metabolic disease, GDM is well suited to metabolomics study, which can real-time monitor the changes in small molecular metabolites induced by maternal stimuli or perturbations. The application of metabolomics in GDM can be used to discover diagnostic biomarkers, evaluate the prognosis of

the disease, guide the application of diet or drugs, evaluate the curative effect and explore the mechanism. This review provids comprehensive documentation of metabolomics research **Methods** and techniques as well as the current progress in GDM research. We anticipate that the review will contribute to identifying gaps in the current knowledge or metabolomics technology, provide evidence-based information and inform future research directions in GDM.

PU-0092

Preparation and verification of a monoclonal antibody Cal26B11 against CALR mutations in MPN

Jingjing Tian、Ming Guan
Huashan Hospital,Fudan University

Purpose Calreticulin (CALR) mutations are recognized as driver mutations in myeloproliferative neoplasms (MPNs) with no JAK2 or MPL mutations and could be served as a putative therapeutic target. The purpose of this study is to obtain a high specificity and high titer of monoclonal antibody by hybridoma technique, and to establish a method based on immunohistochemistry and flow cytometry to detect CALR mutations in MPN patients.
Method A polypeptide sequence that targets the common carboxyl terminus of the mutated CALR protein was designed and synthesized. The mass spectrometry (MS) was used to determine the correctness of the polypeptide sequence. The BALB/c mice were immunized three times after the polypeptide coupled with keyhole limpet hemocyanin (KLH). Mouse spleen cells and myeloma cells (sp2/0 cells) were taken for cell fusion and positive clones were selected for cloning and strain establishment. 293T cell lines overexpressing wild type CALR, CALR type I and type II mutations verified the specificity of the monoclonal antibodies. 5 cases of bone marrow biopsy carrying CALR type I mutations, 4 cases carrying CALR type II mutations, 1 case carrying CALR type V mutations, and 18 cases carrying JAK2V617F MPN was collected for immune histochemistry. Cal26B11 was used as immunohistochemical antibody for CALR mutations in bone marrow biopsies of MPN patients. Peripheral blood from 7 cases carrying CALR type 1 and 2 cases carrying CALR type 2 were collected for flow cytometry. 12 cases from other hematological diseases or healthy people were collected as negative control. Approximately 1×10^7 Cells were added into each tube , 0.2μL CD15-FITC (Becton, Dickinson and Company, USA) ,0.2μL CD64-PE (Becton, Dickinson and Company, USA) and 1:1500 diluted Cal26B11- CFTM647 was added to each tube for flow cytometry analysis. The suspension was detected using BD FACS Canto (Becton, Dickinson and Company, USA) and analyzed with FlowJo2.
Result A 100% positive hybridoma cell secreting an anti-CALR mutant protein was obtained. The monoclonal antibody (clone No. Cal26B11) had a titer of 1:1500. It had no cross reaction with the wild-type CALR and specifically identifies the mutated CALR proteins. Cal26B11 antibody used in immunohistochemistry to detect the CALR mutations in the bone marrow biopsies of MPN patients reacted with the CALR mutations specifically. No positive signal in bone marrow tissue in other blood diseases was observed. The results are completely consistent with the Sanger sequencing, and the specificity of detection is equivalent to the commercial antibody CAL2. The average rate of CALR215+ cells were 0.57%±0.48% by flow cytometry in patients with CALR mutations and there was a significant difference between CALR mutation group and control group(p=0.0024**). The results indicated that home-made Cal26B11-CFTM647 could qualitatively distinguish CALR mutations in patients from wildtype using flow cytometry.
Conclusion A monoclonal antibody (Cal26B11) was obtained which can specifically recognizes the CALR mutations in MPN patients. The self-made Cal26B11 antibody can be used to screen CALR mutant proteins by immunohistochemistry and flow cytometry in MPN patients as the effective supplements for molecular detection.

PU-0093

基于 MPA 技术检测呼吸道 18 种病原体

胡雪姣、廖建枫、顾兵
广东省人民医院

目的 常见呼吸道致病病原体的广谱准确检测是下呼吸道感染早期准确诊断和流行病学调查的关键。本研究旨在建立一种基于多重探针扩增技术（Multiple Probe Amplification Technique, MPA）的快速分子检测方法，并评估 MPA 方法对临床标本呼吸道病原体的检测性能。
方法 建立一种单次聚合酶链反应(PCR)同时检测和鉴别 18 种呼吸道病原体的 MPA 方法，涵盖的病原体包括新型冠状病毒（SARS-CoV-2）、甲型流感病毒（IFA）、乙型流感病毒（IFB）、副流感病毒 1（PIV1）、副流感病毒 2（PIV2）、副流感病毒 3（PIV3）、副流感病毒 4（PIV4）、腺病毒（HADV）、肺炎支原体（MP）、肺炎衣原体（CP）、鼻病毒（HRV）、呼吸道合胞病毒（RSV）、博卡病毒（HBOV）、偏肺病毒（HMPV）、冠状病毒 229E、冠状病毒 HKU1、冠状病毒 NL63、冠状病毒 OC43。分析 MPA 检测方法的重复性、交叉反应性和最低检测限度。纳入 2019 年 1 月-2021 年 2 月就诊于广东省人民医院和广东省第二人民医院的疑似呼吸道病原体感染患者 1200 例，收集患者的呼吸道标本（鼻咽拭子、肺泡灌洗液、痰等）进行 MPA 检测，以测序为参考方法评价 MPA 技术对呼吸道常见病原体检测的诊断效能。
结果 MPA 技术可在一次 2 个封闭 PCR 管反应中同时检测和识别 18 种呼吸道病原体，可区分出临床混合感染以及单一感染的样本。MPA 方法对常见呼吸道病原体检测有良好的重复性（CV＜5.0%）、检测限为 103copies/mL，对分析谱以外的病原体标本无交叉反应。进一步检测 1200 例临床呼吸道样本，以测序为参考方法，MPA 的灵敏度为 92.94%，特异性为 99.91%，阳性预测值为 98.75%，阴性预测值为 99.46%，结果表明 MPA 方法具有简便、稳定、灵敏和特异等特点。
结论 MPA 方法可实现对 18 种常见呼吸道病原体的检测，有利于临床对疑似呼吸道病原体感染患者的早期诊断与及时治疗。

PU-0094

特异性核酸内切酶辅助的荧光传感器用于 miRNAs 的检测研究

张思琦
吉林金域医学检验技术所有限公司

目的 MicroRNAs 作为一类内源性非编码小分子 RNA，是一种重要的细胞调控因子，具有转录后调控基因表达的重要意义。本文的目的是制备一种具有较强荧光信号的 SiO_2-ssDNA-FS 探针，实现对 miRNAs 的定量检测。
方法 本文通过液相生物芯片技术，使用 SiO_2 微球作为检测平台，偶联 DNA 分子及荧光纳米球来制备探针，结合 DSN 酶的信号放大功能，将其应用于流式细胞术中，用于高灵敏的、多通道的 miRNAs 检测分析。单链 DNA 作为连接分子，将 FS 固定在 SiO_2 微球表面，通过酰胺键反应制备了 SiO_2 -ssDNA-FS 探针，此时 SiO_2 微球上附着了大量的 FS。当目标 miRNAs 存在时，SiO_2 -ssDNA-FS 探针与目标结合后，DSN 酶开始剪切双链中的 DNA，使得 FS 从 SiO_2 微球表面脱落，荧光减弱。之后通过流式细胞仪检测每一个 SiO_2 微球上的荧光强度，根据平均荧光强度（MFI）对目标分子进行定量检测。
结果 TEM 表征显示探针微球表面粗糙，附着了一层 FS 颗粒，流式细胞仪检测表明，SiO_2-ssDNA-FS 探针具有较强的荧光信号，SiO_2 微球上的荧光强度明显下降，检测灵敏度为 39.73 fM。同时，通过设计不同的探针序列及标记不同的荧光分子，基于流式细胞仪的多通道检测，实现了对 miRNA-21 及 Let-7d 共存条件下的检测。最后使用此方法对乳腺癌病人全血中的 miRNA-21 进行了检测，检测结果与实时荧光定量 PCR 基本一致。

结论 DNA 的扩增或易位可能引发基因的异常表达，而基因的异常表达与人类肿瘤和癌症的发生密切相关，实现对 miRNAs 生物标志物的准确、高灵敏检测对癌症的早期诊断和癌症治疗效果的监测具有重要作用。SiO_2-ssDNA-FS 探针的检测灵敏度为 39.73 fM，不仅实现了对 miRNA-21 及 Let-7d 共存条件下的检测，且具有较高的准确性及可行性。

PU-0095

新型冠状病毒 RT-PCR 核酸检测系统的性能验证

骆贞红、张彦懿、梁树梅、李亚平、刘华伟
成都市第三人民医院

目的 对由圣湘生物核酸提取试剂、圣湘生物新型冠状病毒核酸检测试剂（荧光 PCR 法）、圣湘 Natch 96 核酸提取仪和雅睿 MA 6000 扩增仪组成的 RT-PCR 核酸检测系统进行性能验证。
方法 阳性样本采用新型冠状病毒（SARS-CoV-2）假病毒核酸标准物质进行稀释，阴性样本采用阴性患者标本，对该核酸检测系统检测 SARS-CoV-2 阴性和阳性准确度、精密度和检出限进行验证。
结果 10 例阳性和 5 例阴性样本的 ORF1ab 基因和 N 基因准确性和重复性的符合率为 100%。 2 个不同浓度阳性样本 ORF1ab 基因重复性 CV 分别为 0.64%、1.05%；N 基因重复性 CV 分别为 0.62%、1.03%，均小于允许变异系数。最低检测限为 1.0 × 102 copies/mL。
结论 该 RT-PCR 新冠核酸检测系统重复性好，灵敏度高，最低检出限符合要求，适用于临床进行 SARS-CoV-2 核酸检测。

PU-0096

探究 CRISPR RNA 引导的 FokI 核酸酶对 bcr-abl 的靶向破坏作用及其对慢性粒细胞白血病细胞凋亡的影响

骆贞红
成都市第三人民医院

目的 通过构建 CRISPR RNA 引导的 FokI 核酸酶/gRNA 体系，并利用 CRISPR RNA 引导的 FokI 核酸酶（RFNs）转染 bcr-abl+的慢性粒细胞白血病（CML）细胞，探究 RFNs 对 bcr-abl 基因的破坏作用及对 CML 细胞凋亡的影响。
方法 利用分子克隆的方法构建靶向 bcr-abl 特异的 gRNA 表达质粒，与 FokI-dCas9 表达质粒构成 RFNs 系统，同时构建 Donor 质粒作为模板 DNA。用核转染的方式在 K562 细胞中分别导入 gRNA+Donor，RFNs-half+Donor 和 RFNs+Donor 质粒，同时设置 wild type 组作为对照。在核转染 60 小时后提取细胞基因组 DNA，通过免疫荧光、T7E1 酶切和 NotI 酶切以及 Sanger 测序分析 RFNs 对 bcr-abl 的破坏作用。通过 western blot 检测 RFNs 作用于 bcr-abl 基因后 BCR-ABL 蛋白的表达情况，以及凋亡相关分子 PARP 和 Caspase-3 的激活情况。通过 DAPI 染色和 FCM 检测 RFNs 对 CML 细胞凋亡的作用。
结果 Sanger 测序结果显示成功构建靶向 bcr-abl 的 gRNA 表达质粒。DAPI 染色显示 RFNs+donor 转染的 K562 细胞核高表达 γH2AX,证明该细胞基因发生明显双链断裂；T7E1 酶切，NotI 酶切以及 Sanger 测序结果显示将 RFNs+donor 电转入 K562 细胞能够有效插入 NotI 酶切位点，使 bcr-abl 基因发生框移突变，在下游提前遇到终止密码子，从而终止 BCR-ABL 蛋白的翻译。Western blot 证实 RFNs 作用于 bcr-abl 基因使 BCR-ABL 蛋白表达显著下调，PARP 和 Caspase-3 发生激活。DAPI 染色和 FCM 检测显示 RFNs+donor 作用于 K562 细胞后，凋亡细胞数量显著增加。
结论 构建靶向 bcr-abl 特异的 RFNs 能够有效切割 bcr-abl 融合基因，通过 HDR 的方式将外源模板中的 NotI 酶切位点成功插入 bcr-abl 基因，使其发生框移突变，提前终止 BCR-ABL 的翻译。RFNs 破坏 bcr-abl 基因后能显著降低 BCR-ABL 蛋白的表达并促进其凋亡。

PU-0097

High PD-L1 expression associates with low T-cadherin expression and poor prognosis in HPV-negative head and neck squamous cell carcinoma

Qiuju Wang
Sichuan Cancer Hospital & Institute

Aim T-cadherin is an immunoglobulin-like adhesion molecule which acts as a tumor suppressor gene, programmed cell death ligand 1 (PD-L1) is a cell surface protein that involves in the suppression of the immune system. This study aimed at exploring the correlation between T-cadherin and PD-L1, as well as their prognostic value in patients with HPV-negative head and neck squamous cell carcinoma (HNSCC).
Methods In this study, immunohistochemical staining was used to determine the protein expression of T-cadherin and PD-L1 in 104 tissue specimens of HPV-negative HNSCC. Spearman linear correlation analysis was used to determine the association between protein expression of T-cadherin and PD-L1. Kaplan-Meier analysis was used to plot overall survival (OS) and disease-free survival (DFS) curves. Cox proportional hazards regression analysis was used to conduct univariate and multivariate analysis.
Results The results showed a negative association between protein expression of T-cadherin and PD-L1 ($r=-0.775$, $P<0.01$), expression of T-cadherin and PD-L1 were associated with OS ($P=0.021$ and 0.034, respectively) and DFS ($P=0.012$ and 0.016, respectively) in patients with HPV-negative HNSCC. Cox proportional hazards regression analysis revealed that expression of T-cadherin and PD-L1 were independent prognostic predictors for OS and DFS in patients with HPV-negative HNSCC. The worst prognosis was observed in patients with T-cadherin negative/PD-L1 positive.
Conclusion In conclusion, expression of T-cadherin and PD-L1 were inversely correlated and were independent prognostic factors for patients with HPV-negative HNSCC. Expression of PD-L1 may be involved in T-cadherin-mediated poor prognosis in patients with HPV-negative HNSCC.

PU-0098

AKR1B10 promotes breast cancer cell proliferation and migration via the PI3K/AKT/NF-κB signaling pathway

jiayao qu[1]、dixian luo[2]
1. 深圳市第三人民医院检验科
2. 华中科技大学协和深圳医院（南山医院）检验科

Background Aberrant expression of Aldo-Keto reductase family 1 member B10 (AKR1B10) was associated with tumor size and metastasis of breast cancer in our published preliminary studies. However, little is known about the detailed function and underlying molecular mechanism of AKR1B10 in the pathological process of breast cancer.
Methods The relationship between elevated AKR1B10 expression and the overall prognosis and disease-free survival of breast cancer patients was analyzed by Kaplan-Meier Plotter database. Breast cancer cell lines overexpressing AKR1B10 (MCF-7/AKR1B10) and breast cancer cell lines that knock down AKR1B10 (BT-20/shAKR1B10) were constructed to analyze the impact of AKR1B10 expression on cell proliferation and migration of breast cancer. The expression levels of AKR1B10 were detected and compared in the breast cancer cell lines and tissues by RT-qPCR, western blot and immunohistochemistry. The proliferation of breast cancer cells was monitored by CCK8 cell proliferation assay, and the migration and invasion of breast cancer cells were

observed by cell scratch test and transwell assay. The proliferation- and EMT-related proteins including cyclin D1, c-myc, survivin, wist, snail, slug, ZEB1, E-cadherin, PI3K, p-PI3K, AKT, p-AKT, IKBα, p-IKBα, NF-κB p65, p-NF-κB p65 were detected by western blot in breast cancer cells. MCF-7/AKR1B10 cells were treated with LY94002, a PI3K inhibitor, to consider the impact of AKR1B10 overexpression on the PI3K/AKT/NF-κB signal cascade and the presence of NF-κB p65 in nuclear. In vivo tumor xenograft experiments were used to observe the role of AKR1B10 in breast cancer grwoth in mice.

Results AKR1B10 expression was significantly greater in breast cancer tissue compared to paired non-cancerous tissue. The expression of AKR1B10 positively correlated with lymph node metastasis, tumor size, Ki67 expression, and p53 expression, but inversely correlated with overall and disease-free survival rates. Gene Ontology analysis showed that AKR1B10 activity contributes to cell proliferation. Overexpression of AKR1B10 facilitated the proliferation of MCF-7 cells, and induced the migration and invasion of MCF-7 cells in vitro in association with induction of epithelial-mesenchymal transition (EMT). Conversely, knockdown of AKR1B10 inhibited these effects in BT-20 cells. Mechanistically, AKR1B10 activated PI3K, AKT, and NF-κB p65, and induced nuclear translocation of NF-κB p65, and expression of proliferation-related proteins including c-myc, cyclinD1, surviving, and EMT-related proteins including ZEB1, Slug, twist, but downregulated E-cadherin expression in MCF-7 cells. AKR1B10 silencing reduced the phosphorylation of PI3K, AKT, and NF-κB p65, the nuclear translocation of NF-κB p65, and the expression of proliferation- and migration-related proteins in BT-20 cells. LY94002, a PI3K inhibitor, attenuated the phosphorylation of PI3K, AKT, and NF-κB p65, and the nuclear translocation of NF-κB p65. In vivo tumor xenograft experiments confirmed that AKR1B10 promoted breast cancer growth in mice.

Conclusions AKR1B10 promotes proliferation and migration of breast cancer cells via the PI3K/AKT/NF-κB signaling pathway and represents a novel prognostic indicator as well as a potential therapeutic target in breast cancer.

PU-0099

Improving Detection Efficiency of SARS-CoV-2 Nucleic Acid Testing

Jie Zhang、Li Jiang
Sichuan Academy of Medical Sciences & Sichuan Provincial People's Hospital

BACKGROUND SARS-CoV-2 nucleic acid testing (NAT) has been routinely used for COVID-19 diagnosis during this pandemic, however, there have been concerns about its high false negative rate. We dissected its detection efficiency with a large COVID-19 cohort study.

METHODS We analyzed SARS-CoV-2 NAT positive rates of 4275 specimens from 532 COVID-19 patients in Sichuan Province with different disease severities, statuses, and stages, as well as different types and numbers of specimens.

RESULTS The total positive rate of the 4275 specimens was 37.5%. Among seven specimen types, BALF generated a 77.8% positive rate, followed by URT specimens (38.5%), sputum (39.8%), and feces/rectal swabs (34.1%). Specimens from critical cases generated a 43.4% positive rate, which was significantly higher than that of other severities. With specimens from patients at stable status, the SARS-CoV-2 positive rate was 40.6%, which was significantly higher than that of improved status (17.1%), but lower than that of aggravated status (61.5%). Notably, the positive rate of specimens from COVID-19 patients varied significantly from 85%-95% during 3 days before and after symptom onset, to 20% at around 18 days after symptom onset. In addition, the detection rate increased from 72.1% after testing one throat swab, to 93.2% after testing three consecutive respiratory specimens from each patient.

CONCLUSIONS SARS-CoV-2 NAT detection rates vary with patient disease severity and status, specimen type, number of specimens, and especially disease progression. Sampling as close to

symptom onset as possible, and consecutively collecting more than one respiratory specimen could effectively improve SARS-CoV-2 NAT detection efficiency.

PU-0100

Circulating Tumor Cell Clusters from Gastric Cancer Patients Co-Cultured in Label-free Microfluid System Predicts Cancer Metastasis and Monitors Treatment Strategies.

Yunlan Zhou、Yanhui Ma、Yi Liu、Hui Chen、Guohua Xie、Lisong Shen
Xinhua Hospital, Shanghai Jiaotong University School of Medicine

Circulating tumor cells (CTC) has been proposed to be used as non-invasive cancer liquid biopsy, but the low sensitivity of capture and detection of CTCs limits its clinical use. There are various techniques reported for the detection of CTCs, but none of them has been widely used for clinical diagnostics. We developed a microfluidic-based approach for the culture of CTC clusters using minimal preprocessing and no need for prior enrichment of CTCs. The microfluidic model had the unique advantage of recapitulating the tumor microenvironment in a comparatively easier way.

We tested microwell-based assay in gastric cancer (GC) patients and generated CTC clusters from liquid blood biopsy of patients. Clusters were maintained under tumor-like conditions and are multi-component structures comprising CTCs and tumor-associated immune cells. We found the presence of CTC clusters correlated with survival outcomes of GC patients.

Then we profiled genome wide expression of CTC clusters co-cultured with immune cells using RNA sequencing. Compared to single CTCs, CTC clusters from GC patients had differential expression of Sox2, Survivin9 and Notum, which were the stemness and proliferation-associated characteristics of CTC clusters.

CTC phenotyping revealed subpopulation of tumorigenic cells, which may present heightened tolerance of or resistance to specific chemotherapeutic drugs for GC. These subpopulations of cancer cells with favorable survival traits are valuable drug targets for novel therapies. Genome wide expression of CTC clusters also showed intra-patient heterogeneity of cancer cells upon selection pressures of therapeutic drugs.

Our data demonstrate the ability of CTCs and immune cells to form clusters has been linked to increased metastatic potential. Our work will gain insights into the biology of CTC clusters of GC, and provide potential markers for CTC clusters of GC patients. These results will lead to high resolution analyses of GC and improve personalized therapy for patients.

PU-0101

云南地区肾移植受者 BK 病毒感染 HLA-A 抗原分布频率及相关性分析

汪佳婕
昆明市第一人民医院

目的 研究云南地区肾移植受者 BK 病毒（BKV）感染人类白细胞抗原（human leukocyte antigen，HLA）A 抗原分布频率，探讨肾移植受者 BK 病毒感染与 HLA-A 抗原之间的相关性。
方法 以云南地区 384 例肾移植受者 BKV 感染尿液阳性（>2000 拷贝/ml）患者为研究对象，应用聚合酶链反应一序列特异性引物（PCR-SSO）技术对患者 HLA-A 抗原进行检测，用 SPSS 软件分

析肾移植受者 BKV 感染尿液阳性 HLA-A 抗原分布频率，并运用病例对照研究设计及 SPSS 软件分析比较 HLA-A 抗原与 BK 感染不同结局的关系。
结果 对照组检出的 HLA-A 等位基因有 16 种，其中占比大于 5%的基因型有 5 种，分别为 HLA-A*2（22.32%）， HLA-A*11（30.25%）， HLA-A*24（19.42%），HLA-A*33（5.28%），HLA-A*203（5.28%）；BK 病毒感染组中检出的 HLA-A 等位基因有 13 种，其中占比大于 5%的基因型有 3 种，分别为 HLA-A*2（23.33%）， HLA-A*11（32.96%）， HLA-A*24（19.26%）。
结论 云南地区人群感染 BK 病毒 HLA-A*2，-A*11，-A*24,可能与较低的 BKV 风险相关。

PU-0102

MassARRAY 在高尿酸血症和痛风风险预测中的应用研究

高媛[2]、张心菊[1]、关明[1]
1. 上海市华山医院中心实验室
2. 江苏省苏州市苏州高新区人民医院检验科

目的 痛风是炎症性关节炎最常见的形式之一，是一种多因素疾病，典型特征是高尿酸血症和关节等部位尿酸钠晶体的沉积。多个基因 SNPs 已确定与血清尿酸和痛风易感性相关。群体在血清尿酸浓度和痛风的遗传贡献方面表现出共同的异质性，因而需要进行跨祖先研究以确定影响痛风发病的群体特异性位点。痛风诊断标准缺乏相关的分子生物学指标，为了探讨血清尿酸与痛风的基因关系，以期根据患者的遗传特征建立疾病风险早期预测模型，探讨 MassARRAY 芯片检测技术在临床实践中应用的可行性。
方法 本课题组根据预先确定的标准，筛选全基因组关联研究(GWAS)明确的 20 个候选基因中与血清尿酸浓度和个体化用药相关的 63 个 SNPs 位点，并应用 MassARRAY 技术在 579 名中国个体(233 名痛风患者、141 名高尿酸血症患者和 205 名健康受试者)中进行基因分型。对不同组合血清尿酸（痛风与对照、痛风与 HUA、HUA 与对照)的遗传效应进行了分析，以显示遗传变异对痛风的影响。
结果 采用 Plink 软件完成哈迪-温伯格遗传平衡（Hardy-Weinberg equilibrium，HEW）检验、等位基因、基因型和不同遗传模型与痛风易感性的关联分析。采用 GMDR 软件进行基因交互作用分析。在表达量性状位点(eQTL)数据库预测痛风易感 SNPs 位点的生物信息学功能。
结论 本课题系统地研究了 63 个 SNPs 与 HUA 和痛风的遗传效应关系，并明确了尿酸相关基因特异性 SNPs 在痛风的发病风险预测中的作用。初步建立了痛风和 HUA 的疾病风险预测模型,基因检测可以作为诊断的补充方法为临床诊断提供咨询建议。

PU-0103

A Novel Variant Analysis of CHD3 Gene from a Family with Snijders Blok-Campeau syndrome by Whole Exome Sequencing: Expanding the Genotypic and Phenotypic Spectrum of CHD3 disease

Yuan Tian 、Linlin Zhang、Erfeng Yuan、Jinshuang Gao、Yaqing Guo、Liying Song、Haiyang Yu
The Third Affliated Hospital of Zhengzhou University

Background Snijders Blok-Campeau syndrome (SNIBCPS) is an autosomal dominant neurodevelopmental disorder characterized by global developmental delay with impaired intellectual development and delayed speech acquisition, and Snijders Blok-Campeau syndrome is caused by heterozygous mutation in the CHD3 gene on chromosome 17p13.

Methodology/Laboratory Examination DNA of the family was extracted and sequenced by whole exome sequencing.The results were validated with Sanger sequencing analyzed with Bioinformatics software.
Results Sequencing result showed that the patient has carried a heterozygous variant of c.3709T>C of the CHD3 gene. The patient's father and mother has not carried the variant of c.3709T>C of the CHD3 gene.
Discussion and Conclusion The heterozygous variant of c.3709T>C of the CHD3 gene probably underlie the disease in this child and the case related to Snijders Blok-Campeau syndrome is the first reported in China.

PU-0104

Bioinformatics analysis identifies biomarkers related to immune infiltration in white adipose tissue of obese patients with type 2 diabetes

Xuewei Tong
Hospital of Xinjiang Production and Construction Corps

OBJECTIVE To identify potential immune infiltration-related biomarkers in the white adipose tissue (WAT) from obese people with type 2 diabetes mellitus (T2DM).
METHODS Gene expression datasets (GSE16415 and GSE71416) of the WAT from the abdomen of obese patients with T2DM and those with simple obesity were downloaded from the Gene Expression Omnibus database. R was used to screen differentially expressed genes (DEGs), and Gene Ontology and Kyoto Encyclopedia of Genomes pathway analyses were performed. Candidate biomarkers were identified and their discriminative ability was evaluated. Additionally, the GSE29231 dataset was used to verify the expression levels of biomarkers as well as their diagnostic value in obese patients with T2DM. Gene set variation analysis and GeneMANIA were used. The correlation between biomarkers and infiltrating immune cells was also evaluated.
RESULTS A total of 130 DEGs were screened. Six key genes were obtained after verification, including cidea and fscn1. Immune cell infiltration analysis showed that cidea was related to tumor-infiltrating lymphocytes (TILs) and human lymphocyte antigen, while fscn1 was related to TILs and helper T cells.
CONCLUSIONS cidea and fscn1 may be biomarkers of obesity-related T2DM; further research is needed to explore their role in the molecular mechanisms of T2DM.

PU-0105

Screening and verification of differentially expressed genes in adipose tissue of obese patients with type 2 diabetes

Xuewei Tong
Hospital of Xinjiang Production and Construction Corps

Object White adipose tissue (WAT) plays an important role in the occurrence and development of type 2 diabetes mellitus (T2DM) combined with obesity, but its exact mechanism is not yet clear. In this study, based on bioinformatics technology, we screened the differentially expressed genes (DEGs) of the greater omentum WAT in T2DM patients with obesity and simple obesity, verified the tissue mRNA and protein levels of key DEGs, and analyzed the tissues of key DEGs The correlation between the expression level and the corresponding biochemical indicators aims to explore the pathophysiological mechanism of WAT in T2DM with obesity, and provide a

theoretical basis for the prediction of the risk of T2DM and the discovery of new targets for drug therapy.

Methods Download the gene expression data set (GSE16415 and GSE71416) of the intra-abdominal greater omentum WAT in T2DM patients with obesity and simple obesity through the gene expression database Use R software to screen DEGs, and perform functional enrichment analysis on DEGs through Metascape database. Combine Lasso regression and Boruta feature selection algorithm to identify key DEGs, and use the GSE29231 data set to further identify the expression levels of key DEGs in obese patients with T2DM. Gene set variation analysis (GSVA) was used to evaluate the main signaling pathways that key DEGs participate in the disease. According to the body mass index (BMI), 8 cases of normal control group (NC), 12 cases of simple obesity group (Obese, OB), and 4 cases of T2DM combined with obesity group (T2DM+OB) were selected for the study. General information of the subject, testing fasting plasma glucose (FPG), Hemoglobin A1c (HbA1c), total cholesterol (TC), triglyceride (TG), low density lipoprotein-cholesterol (LDL-C), high density lipoprotein-cholesterol (HDL-C) biochemical indicators. Use qRT-PCR and Western Blot technology to verify the mRNA and protein expression levels of key DEGs in intra-abdominal omentum WAT samples, and analyze the correlation between tissue key DEGs mRNA expression levels and biochemical indicators.

Results Bioinformatics analysis screened out 130 DEGs between obese patients with T2DM and simple obesity. Among them, 40 genes were up-regulated and 90 genes were down-regulated in T2DM patients with obesity. GO function annotations show that DEGs are mainly involved in biological processes such as the production of metabolites and energy, neutrophil-mediated immunity, cofactor biosynthesis, positive regulation of exercise, and monocarboxylic acid metabolism. KEGG signaling pathway analysis showed that DEGs are mainly involved in the tricarboxylic acid cycle, glycolysis/gluconeogenesis, pertussis, tryptophan metabolism, PPAR signaling pathway and other pathways. After combining Lasso regression and Boruta feature selection algorithms, and verifying the GSE29231 data set, CIDEA and FSCN1 genes were identified as key DEGs. GSVA results show that CIDEA gene is mainly involved in oxidative phosphorylation, lipogenesis, fatty acid metabolism and other pathways; while FSCN1 gene is mainly involved in Wnt/β-catenin signaling pathway, C3 signaling pathway, interleukin-2 signal transduction and transcription activator 5 signaling Transduction and other pathways. The general data of the study subjects showed that the body weight and BMI of the OB group and T2DM+OB group were significantly higher than those of the NC group ($P<0.05$). The results of biochemical indicators showed that the FPG, HbA1c and TG in the T2DM+OB group were significantly higher than those in the OB and NC groups ($P<0.05$), and the HDL-C in the T2DM+OB group was significantly lower than that in the OB and NC groups ($P<0.05$). The validation results of human intra-abdominal omentum WAT samples showed that the mRNA and protein expression levels of CIDEA in the T2DM+OB group were significantly lower than those in the NC and OB groups ($P<0.05$), and the OB group was significantly higher than the NC group ($P<0.05$). The mRNA and protein expression levels of FSCN1 in the T2DM+OB group were significantly higher than the NC and OB groups ($P<0.05$), and the OB group was significantly higher than the NC group ($P<0.05$). The mRNA and protein expression levels of CIDEA and FSCN1 in each group The results are consistent. Correlation analysis between the mRNA expression levels of CIDEA and FSCN1 and biochemical indicators showed that high mRNA expression of CIDEA was positively correlated with HDL-C levels and negatively correlated with TG levels ($P<0.05$); high mRNA expression of FSCN1 was correlated with FPG and HbA1c There was a significant positive correlation with TG ($P<0.05$).

Conclusion (1) This study used bioinformatics technology to determine the CIDEA and FSCN1 genes in WAT as the key differentially expressed genes between obese patients with T2DM and simple obesity. (2) CIDEA was down-regulated in the intra-abdominal greater omentum WAT in the T2DM+OB group, and up-regulated in the intra-abdominal greater omentum WAT in the OB and NC groups, suggesting that CIDEA may play a protective role in the development of T2DM and obesity. (3) FSCN1 was up-regulated in the intra-abdominal greater omentum WAT in the T2DM+OB group, and down-regulated in the intra-abdominal greater omentum WAT in the OB and NC groups, suggesting that FSCN1 may play a role in the development of T2DM and obesity.(4) The high expression of CIDEA was positively correlated with HDL-C levels and

negatively correlated with TG levels; the high expression of FSCN1 was positively correlated with FPG, HbA1c and TG levels. It is speculated that CIDEA and FSCN1 may be involved in the pathophysiological mechanism of glucose and lipid metabolism disorders in obese patients with T2DM.

PU-0106

siBCL-2 联合维生素 K2 抑制肝癌细胞 smmc-7721 机制的初步研究

姚玉亭
上海交通大学医学院附属第九人民医院检验科

目的 siBCL-2 联合维生素 K2 能够协同抑制肝癌细胞 smmc-7721。siBCL-2 的作用机理主要在于通过抑制 BCL-2 基因过表达来增强细胞凋亡，VK2 能够通过调节细胞内 p53 的表达来抑制细胞增殖。本研究拟通过对 BCL-2 和 p53 基因介导的细胞凋亡及细胞周期的检测初步探索联合治疗导致细胞生长抑制的机制。
方法 用 FCM 和 Annexin-V 观察分析 siBCL-2 联合 VK2 作用 smmc-7721 细胞后细胞周期的变化以及早期凋亡情况；用 Western blot 检测细胞株中 p53，p21，BAX 蛋白的表达；用 Real time PT-PCR 检测细胞株中自噬相关基因 Map1lc3b 的表达；以期初步探讨 siBCL-2 联合 VK2 对 smmc-7721 细胞增殖抑制的分子机制。
结果 siBCL-2 转染 36 小时和 VK2 加药 24 小时后，联合治疗组导致 smmc-7721 细胞 G2 期阻滞，但不引起早期凋亡。Western blot 检测，联合治疗组显著提高细胞内 p53 和 p21 蛋白的表达，对 BAX 的表达没影响。Real time PT-PCR 分析，联合治疗组能够显著提高自噬相关基因 Map1lc3b 在基因水平的表达。
结论 化学合成的 siBCL-2 能够抑制细胞中 BCL-2 的表达并使 p53 表达上调。同时联合化疗药物 VK2 的作用，可进一步使 p53 下游激活产物 p21 蛋白的上调更加迅速和明显，从而导致细胞周期的 G2 期阻滞，抑制肿瘤生长。siBCL-2 联合 VK2 并不引起细胞凋亡，但能够显著提高自噬相关基因 Map1lc3b 在基因水平的表达。

PU-0107

EphA7 基因高甲基化和宫颈癌发生发展相关性的研究

王蓉、张文帆、陆婷婷、郑佳琪、周霖
天津医科大学

目的 EphA7 基因在肿瘤的发生、发展及预后中有着重要意义。因此，本研究拟鉴定并验证 EphA7 在宫颈癌发生中的 DNA 甲基化水平及互作的转录调控因子。
方法 首先，采用甲基化特异性聚合酶链反应(MSP)方法检测宫颈癌细胞系及组织的基因启动子的甲基化水平；进而，采用荧光定量甲基化特异性聚合酶链反应(QMSP)检测了正常，癌前及癌症共 111 例的宫颈液基细胞样本(TCT)，并分析其基因甲基化检测对宫颈癌筛查的临床价值；然后，采用特异性的 CRISPR 甲基化干扰系统(dCas9-Tet1/Dnmt3a)对 EphA7 基因的甲基化进行了双向调控，并通过 RT-PCR 及 pyrosequencing 证实了 DNA 甲基化对 EphA7 基因的转录表达具有直接调控作用；此外，基于在线数据平台对 EphA7 基因启动子的转录因子进行筛选，并采用特异性的原位捕获技术，鉴定其基因启动子区域的转录因子。
结果 EphA7 在宫颈癌细胞系及组织呈现高甲基化，且其甲基化水平与 mRNA 表达负相关；在 TCT 样本中 EphA7 基因甲基化水平随着癌症进展逐渐升高($P<0.05$)，其 ROCAUC 为 0.816。CRISPR 甲基化干扰系统可以有效调控 EphA7 基因的转录表达，在宫颈癌细胞系中可提高其 mRNA 表达水

平达 6.20，7.51 倍等(p<0.05)，同样在正常 EphA7 非甲基化细胞系，其转录水平可下调 72.75%。另外，在 Siha 细胞系中也初步鉴定 SP1 和 MAZ 与 EphA7 基因结合，调控其表达。
结论 EphA7 基因甲基化是宫颈癌诊断和治疗的新型潜在生物标志物。CRISPR 甲基化干扰系统可以特异性的作用于 EphA7 基因甲基化的调控，原位捕获技术可特异性的捕获结合与靶位点的调控元件，为下一步机制的深入研究及后续的宫颈癌治疗及预后的监测奠定了良好的基础。

PU-0108

The study of mechanism of interaction between NLRP3 and PKR in the activation of inflammasome

Qian Feng[1,2,3]、yuling chen[4]、yuanjian song [2,3,4]
1. Affiliated Hospital of Xuzhou Medical University
2. 徐州医科大学遗传学教研室
3. 徐州市医学遗传与转化工程中心
4. 徐州医科大学

Objective Protein kinase PKR can directly bind to NLRP3 and phosphorylate NLRP3, to promote the activation of NLRP3 inflammasome. PRKRA (PKR activator A)activates PKR, through binding to DRBM domain of PKR, and their DRBMI and DRBM2 domain sequences are very similar, so it is possible that PRKRA directly interacts with NLRP3 and activates NLRP3 inflammasome. The purpose of this study is to find the domain of the interaction between PRKRA and NLRP3. and to design interfering peptides to interfere with the interaction between PRKRA and NLRP3.inhibit the activation of NLRP3 inflammasome, and relieve LPS-induced neuroinflammation .
Methods Part I: Finding the domain of the interaction between PRKRA and NLRP3 with the help of His pull down experiment Search the cDNA sequences corresponding to PRKRA and NLRP3 in the Uniprot database and order them. molecular cloning experiment. The full-length and domains of PRKRA and NLRP3 were cloned into pET-30a(+) or a modified T4 lysozyme (T4L)vector to construct recombinant plasmids, then transformed into BL21(DE3) competent cells. The recombinant protein fragments containing 6 x His tags were induced by IPTG and purified by Ni-NTA. The protein expression was detected by SDS-PAGE. The recombinant plasmid corresponding to the domain of clonal expression of NLRP3.protein was reacted with PCR, and the recombinant plasmid with FLAG tag and without6 x His tag was constructed. The PRKRA protein containing 6 x His tag and the fragment containing FLAG tag were incubated with Ni-NTA magnetic beads to detect the existence of FLAG tag in magnetic beads, and the fragment directly binding PRKRA to NLRP3 was obtained.
Part II: Interference peptides were designed by homologous modeling and molecular docking, and the interaction sites between PRKRA and NLRP3 were verified by co-crystallization.The fragment structure of direct interaction between PRKRA and NLRP3 is found by PDB (Protein Data Bank) database, and the non-existing structure is obtained by Swiss Model homologous modeling. The first 15 structures with the highest score were docked by ZDOCK software, and the amino acid distribution of the interface between PRKRA fragment and NLRP3 fragment was analyzed. According to these amino acid distribution, the interfering peptide TAT-pLRR, was obtained and the disordered peptide TAT-pLRR-Scr was obtained by disrupting the amino acid sequence. The recombinant plasmid obtained in the first part was transformed into BL21 (DE3) competent cells, and the protein expression was induced by IPTG. The protein was purified by Ni-NTAand molecular sieve, and the ultrafilter tube was condensed to 5mg/mL. Hampton kit was used to screen the crystal conditions on the sitting drop crystal plate.
Part III: to verify the function of interfering peptides in LPS-induced BV2 cells BV2 cells were divided into Control group , LPS (10 ug/mL) induced for 24 h, small peptide TAT-pLRR (40mg/mL) pretreated with 3h then LPS for 24 h, and small peptide TAT-pLRR-Scr (40mg/mL) pretreated with 3h then LPS for 24 h. The total RNA, was extracted from the adherent cells of the four groups. The mRNA levels of inflammatory cytokines IL-1 B. IL-6. IL-18, TNFa and PKR in the four

groups were detected by RT-qPCR method to evaluate the effect of interfering peptides on the transcription of inflammatory factors. The models of experimental peptides and disordered peptides were established by molecular dynamics simulation. The conformational changes of experimental peptides and disordered peptides in NaCI aqueous solution were simulated at 25 ℃ and latm. and their stability. residue flexibility and relative movement coordination ability between residues were compared, and the direction of further improvement of interferon peptides was put forward.

Results 1. The recombinant plasmids constructed with full-length PRKRA. MI+M2domain and pET-30a (+) plasmids were highly cloned and expressed in E. coli, while the recombinant plasmids constructed with LRR domain and T4 lysozyme were cloned and expressed in small quantities in E. coli. His Pull-down experiment showed that both the full length of purified PRKRA and the MI+M2 domain could bind to the LRR domain in the buffer. Gel filtration chromatography results show that the stability of MI+M2 was poor, and the full-length PRKRA exists in a form of polymer. After condensed to 5mg/mL, the crystallization conditions were screened out. Small broken crystals were observed in 0.2mL HEPES pH7.5,24% polyethylene glycol 1500condition. 2. Through homologous modeling and molecular docking, we found that(WRLPEYTLSQE) at position 140 and 150 in M1+M2 domain, and R772. W774, D802,K829. W831. R857 and Y859 of NLRP3 is the main part of the interaction between MI+M2 domain (belonging to PRKRA) and LRR (belonging to NLRP3). The designed interfering peptide sequence is WRLPEYTLSOE. which disrupted sequences toOLELYPTSEWR, which is called disordered peptide sequence. The experimental peptide and disordered peptide are added with the TAT sequence and ordered. 3. TheRT-APCR results of BV2 cells in each group showed that there was no significant change in the expression of mRNA of PKR and IL-6 among different groups, but the mRNA expression levels of IL-1 B and IL-18 in the LPS group were significantly lower than those in the Control group. The mRNA expression of IL-1 B, IL-18 and TNF a in TAT-pLRR and TAT-pLRR-Scr small peptide pretreatment group was significantly lower than that in LPS stimulation group.

Conclusion 1. The interaction between PRKRA and NLRP3 is through the MI+M2domain of PRKRA and the LRR domain of NLRP3. 2. The interfering peptide designed based on the 140150 residues of PRKRA can inhibit the transcription of IL-1B IL-18,IL-6 and TNFa at the cellular level, and has the ability to relieve inflammation.

PU-0109

Development and validation of an N6-methyladenosine regulation and mRNAsi related prognostic index for lower-grade glioma

Guihua Tang[1]、Wen Yin[2]
1. Hunan Provincial People's Hospital
2. 中南大学湘雅医院

Background N6-methyladenosine (m6A) modification is involved in tumorigenesis and progression as well as closely correlated with stem cell differentiation and pluripotency. Moreover, tumor progression includes the acquisition of stemness characteristics and accumulating loss of differentiation phenotype. Therefore, we integrated m6A modification and stemness indicator mRNAsi to classify patients and predict prognosis for LGG.

Methods We performed consensus clustering, weighted gene co-expression network analysis (WGCNA), and least absolute shrinkage and selection operator (LASSO) Cox regression analysis to identify an m6A regulation and mRNAsi related prognostic index (MRMRPI). We also explored the differences in immune microenvironment between high and low-risk populations based on this prognostic index.

Results Ten genes (DGCR10, CYP2E1, CSMD3, HOXB3, CABP4, AVIL, PTCRA, TIMP1, CLEC18A, and SAMD9) were identified to construct the MRMRPI, which was able to successfully

classify patients into high- and low-risk group. Significant differences in prognosis and immune microenvironment were found between distinct groups. A nomogram integrating the MRMRPI and other prognostic factors was also developed to accurately predict prognosis.
Conclusion These findings provide novel insights into understanding the interactions of m6A methylation regulation and tumor stemness on LGG development and contribute to guiding more precise immunotherapy strategies.

PU-0110

846 例孕晚期妇女 B 族链球菌感染检测及妊娠结局分析

肇玉博[1]、李然[2]、马艳侠[1]
1. 陕西中医药大学附属医院
2. 陕西中医药大学医学技术学院

目的 了解咸阳地区孕妇感染 B 族链球菌（GBS）与年龄、妊娠情况及妊娠结局等因素的相关性,为孕晚期妇女防治 B 族链球菌感染提供建议。
方法 选取 2019 年 9 月至 2021 年 3 月在陕西中医药大学附属医院产科进行 B 族链球菌检测的 846 名孕妇作为研究对象，采用实时荧光定量聚合酶链反应（PCR）的方法检测 B 族链球菌,按照患者年龄、妊娠情况及妊娠结局对检测结果进行分析。
结果 846 例妊娠孕妇 GBS 阳性率为 7.40%。其中 82.54%（52/63）GBS 阳性孕妇伴随有不良妊娠症状，脐带绕颈症状占比 66.67%（42/63）有统计学意义。21～25 岁孕妇感染 GBS 的阳性率为 12.12%、26～30 岁孕妇感染 GBS 的阳性率为 6.97%、31～35 岁孕妇感染 GBS 的阳性率为 7.86%、<20 岁和≥36 岁孕妇的 GBS 阳性率为 0%。
结论 年龄在 21～25 岁的孕妇易感染 B 族链球菌,感染 GBS 阳性孕妇的胎儿易发生脐带绕颈现象。

PU-0111

实时 PCR 扩增检测 SARS-CoV 及 SARS-CoV-2 的方法学建立及性能评价

韩琦[1,3]、陈天垠[3]、沈建如[1]、吴秋保[2]、冼汉福[1]、杨创慧[1]
1. 广州金域医学检验中心
2. 广州医科大学附属第一医院广州呼吸健康研究院呼吸疾病国家重点实验室
3. 海南金域医学检验中心

目的 开发一种实时聚合酶链反应方法用于对新型冠状病毒及 SARS 病毒感染的核酸诊断，并进行该方法学的性能评价。
方法 本研究使用单步实时 PCR 检测方法，采用同源 IC，该 IC 是由来自小鼠肌肉的 190bpRAB3A 癌基因片段，在该片段两端连接 SARS-CoV 与 SARS-CoV-2 同源的基因组成的重组 DNA。本方法使用四套探针三套引物。为了防止插入序列被过量同源 IC 竞争，将同源 IC 工作浓度优化为每反应 10 拷贝，使阴性对照同源 IC 的 ct 值在一个稳定范围内。从临床收集的七例阴性三例阳性新型冠状病毒核酸及一例含有 SARS 的基因片段质粒进行所建立方法学性能评价，并与圣湘新型冠状病毒核酸检测方法相比较。
结果 此方法在 SARS-CoV 及 SARS-CoV-2 诊断方面具有优越性。单次检测敏感性（100%）和特异性（100%）。与圣湘新型冠状病毒核酸检测方法相比较单项检测敏感性及特异性为 100% 。此检测和同源 IC 在一个单一的反应中，PCR 抑制可以很容易的区别于真阴性结果，
本方法不需要人工操作 PCR 扩增产物，从而大大减少交叉污染的机会。

结论 该方法作为一种实时 PCR 检测方法，可为检测临床 SARS-CoV 及 SARS-CoV-2 标本提供阳性存在的依据。该方法检测具有良好的诊断性能，准确性高可应用于临床检测，但由于样本量少无法做更详细的验证故后续需继续补充数据。

PU-0112

通过 SALP-seq 和机器学习分析血浆游离 DNA 遗传和表观遗传信息初探

张晓雪、夏欣一
中国人民解放军东部战区总医院

目的 血浆中的游离 DNA (cfDNA) 携带着丰富的遗传和表观遗传信息。基于 cfDNA 的液体活检目前仍限于 ctDNA 突变、甲基化修饰、外泌体等，开发新的建库和分析方法可拓展其在液体活检中的应用。
方法 首先采集 11 例食管癌患者术前、5 例食管癌患者术后和 4 例健康者的 cfDNA 样本，并采用 SALP-seq 技术构建 cfDNA 样本的 NGS 文库后进行测序，使用机器学习算法分析 cfDNA NGS 数据，利用生物信息学方法分析食管癌患者与健康人在遗传和表观遗传上的差异，以寻找新型食管癌标志物，并通过分析另外 10 例食管癌患者术前的 cfDNA 样本来验证这些标志物。
结果 本研究中开发的 SALP-seq 成功的制备了多个 cfDNA 样本的 NGS 文库，可用于有效分析大量临床血液样本。分析结果显示，不同样品中 cfDNA 的分布差异很大，EC 患者的 cfDNA 的平均 reads 密度高于术后患者和正常人的 reads 密度，表明 EC 患者比正常人具有更高的染色质开放状态；转录起始位点(TSS) 5 kb 区域的 reads 密度主成分分析(PCA)结果显示正常 cfDNA 样本与 ESCA cfDNA 样本的 reads 密度差异较大；有 49 个在所有癌症样本中显示出极低的读码密度的启动子 reads，术后这些基因的启动子 reads 密度明显增加；使用 MDA 筛选出 88 个食管癌相关区域，36.36%的区域位于远端基因间区域，25%位于近端调控区。cfDNA 在全基因组水平上的大小的计算结果显示，术前 EC 患者 cfDNA 最短，正常人 cfDNA 最长。不同 cfDNA 的 GC 含量计算结果显示术前 EC 患者的 cfDNA 的 GC 含量最低，正常人的 cfDNA 的 GC 含量最高。cfDNA 样本 SALP-seq 读数分析 ESCA 相关突变，结果显示大多数单核苷酸变异 (SNV) 位于远端基因间和内含子区域，且术前患者中存在 37 个独特的突变基因。
结论 本研究通过 SALP 技术与机器学习相结合，分析了来自食管癌患者和正常人的 cfDNA 样本，不仅发现了食管癌患者的染色质开放状态发生显著改变的基因以及染色质开放性区域的基因突变情况, 为调控食管癌发生的分子机制提供了重要见解，还探讨了应用 cfDNA 监测肿瘤发生发展的潜在价值，为新型肿瘤标志物的发现及其在液体活检中的应用提供参考，也为 cfDNA 的临床价值提供了重要的新见解。（本研究部分内容已发表于 Comput Struct Biotechnol J，IF=6.018）

PU-0113

53 株耐碳青酶烯药物粘质沙雷菌耐药表型分析

张燕
南京大学医学院附属鼓楼医院

目的 研究耐碳青酶烯药物粘质沙雷菌耐药机制。
方法 收集南京大学医学院附属鼓楼医院 2018 年 6 月至 2019 年 9 月临床分离 235 株非重复粘质沙雷菌，采用 Vitek 2 Compact 配套 GN13 药敏板卡和纸片扩散法进行药物敏感性检测；采用改良碳青霉烯酶灭活试验（mCIM）和 EDTA-改良碳青霉烯酶灭活试验（eCIM）对碳青霉烯酶表型筛选；采用 PCR 及测序分析检测碳青霉烯酶基因携带情况。

结果 235 株粘质沙雷菌中检出同时对美罗培南和亚胺培南耐药菌株 53 株（22.6%）。53 株碳青霉烯类耐药菌株中对头孢他啶敏感和中介分别为 23 株（43.4%）和 21 株（39.6%），对头孢曲松、氨曲南、环丙沙星、左氧氟沙星的耐药率均大于 98%，对阿米卡星、复方新诺明的耐药率分别为 1.7%和 1.6%。mCIM 均阳性，eCIM 阳性 3 株。53 株菌中检出 blaKPC-2 基因 50 株，检出 blaNDM-1 基因 1 株, 同时携带 blaKPC-2 和 blaNDM-1 基因 1 株，未检出 blaIMI、blaOXA48、blaFOX、blaIMP 和 blaVIM 基因。
结论 本院耐碳青霉烯粘质沙雷菌检出率较高，blaKPC-2 基因是介导本院粘质沙雷菌碳青霉烯类药物耐药的主要流行基因型。

PU-0114

A literature review on function and regulation mechanism of DKK4

Xiaoli Lou 、Yuchen Meng、Yanqiang Hou
Songjiang Hospital Affiliated to Shanghai Jiaotong University School of Medicine

Dickkopf-related protein 4 (DKK4) is a member of the dickkopf family and an inhibitor of the Wnt/β-catenin signalling pathway. This review surveyed the single nucleotide polymorphisms (SNPs), copy number variations (CNVs), hypermethylation, regulation mechanism, correlation with clinicopathological parameters and chemotherapeutic resistance of DKK4. The signal pathways involved in DKK4 mainly include Wnt/β-catenin pathway and Wnt-JNK pathway independent β-catenin. DKK4 expression was upregulated in Renal Cell Carcinoma (RCC), Colorectal Cancer, Gastric Cancer (GC), Non-small Cell Lung Cancer (NSCLC) and Epithelial Ovarian Cancer (EOC), while downregulated in Hepatocellular Carcinoma (HCC). DKK4 is not only involved in tumour growth, invasion, migration and chemotherapy resistance, but also in osteoblastogenesis and secondary hair or meibomian gland formation. DKK4 has also been linked to schizophrenia.

PU-0115

博乐市人乳头瘤病毒感染流行病学分析及病毒载量与宫颈癌的关系研究

彭燕
新疆生产建设兵团第五师医院

目的 探讨液基细胞学技术（TCT）、人乳头瘤病毒（HPV）感染以及 HPV 病毒载量在临床诊断宫颈疾病中的应用价值。
方法 选取新疆生产建设兵团第五师医院在 2018 年 1 月至 2021 年 4 月住院及门诊的 356 例成年女性患者进行 TCT 及 HPV-DNA 联合检测。
结果（1）HPV 检测**结果** 博乐地区 HPV 好发的高危亚型分别为 HPV16、HPV52、HPV58，好发年龄段为 41~45 岁；（2）TCT 检测**结果** 56~60 岁组 TCT 诊断结果阳性率最高，而 41~45 岁组阳性率最低；（3）TCT 与 HPV 病毒载量联合诊断**结果** 高危型 HPV DNA 载量与 TCT 阳性结果大致呈正相关关系。
结论 博乐市 HPV 感染率相对较高，并以单一感染为主，而 HPV 持续感染的人数却相对较少，提示早诊断早治疗在预防宫颈癌方面有至关重要的作用。

PU-0116

Protein Glycopatterns in Bronchoalveolar Lavage Fluid as Novel Potential Biomarkers for Diagnosis of Lung Cancer

Lina Liu[1,2]、Dan Li[2]、Jian Shu[3]、Li Wang[2]、Fan Zhang[3]、Chen Zhang[3]、Hanjie Yu[3]、Mingwei Chen[2]、Zheng Li[3]、Xuan Guo[2]
1. Xi'an No. 4 Hospital
2. 西安交通大学医学院第一附属医院
3. 西北大学

Objectives Lung cancer (LC) is a prevalent and life-threatening neoplasia worldwide. Although aberrant glycosylation has been observed in human serum and tissue, little is known about the alterations in bronchoalveolar lavage fluid (BALF) that are associated with LC. Our aim was to systematically investigate and assess the alterations of protein glycopatterns in BALF and possibility as biomarkers for diagnosis of LC.
Methods In this study, lectin microarrays were utilized to detect and compare the differential expression of BALF glycoproteins from patients with 80 adenocarcinomas (ADC), 77 squamous cell carcinomas (SCC), 51 small cell lung cancer (SCLC), and 73 benign pulmonary diseases (BPD). Then, lectin blotting analysis was performed to verify the results of lectin microarrays. These 281 BALF specimens were then randomly divided into test group and validation group. First, five diagnostic models (Model LC, ModelADC, Model SCC, Model SCLC, and Model LC-ES (early stage of lung cancer)) were constructed to identify benign and malignant lung diseases, ADC, SCC, SCLC and LC-ES by binary stepwise logistic regression based on the lectin microarrays data from 163 BALF samples in the test group. Subsequently, the diagnostic models constructed in the test group were then applied to a validation group to assess the discriminatory efficiencies through ROC analysis. Moreover, an independent test was performed with 120 newly collected BALF samples enrolled in the double-blind cohort to further assess the clinical application potential of the diagnostic models.
Results According to the results, there were 15 (e.g., PHA-E, EEL, and BPL) and 14 lectins (e.g., PTL-II, LCA, and SJA) that individually showed significant variations in different types and stages of lung cancer compared to BPD. Notably, the diagnostic models achieved better discriminate power (Model LC (AUC: 0.61, sensitivity: 0.918 and specificity: 0.939), Model LC-ES (AUC: 0.856, sensitivity: 0.829 and specificity: 0.810), Model ADC (AUC: 0.619, sensitivity: 0.706 and specificity: 0.586), Model SCC (AUC: 0.693, sensitivity: 0.800 and specificity: 0.667), Model SCLC (AUC: 0.718, sensitivity: 0.721 and specificity: 0.684)) in the validation cohort and exhibited high accuracies of 0.917, 0.864, 0.712, 0.671 and 0.781 in the double-blind cohort for the diagnosis of LC, LC-ES, ADC, SCC, and SCLC, respectively.
Conclusions Taken together, the present study revealed that the abnormally altered protein glycopatterns in BALF are expected to be novel potential biomarkers for the identification and early diagnosis of lung cancer, which will contribute to explain the mechanism of the development of lung cancer from the perspective of glycobiology.

PU-0117

9850 例女性人乳头瘤病毒筛查情况及感染特征分析

郭霞、陈艳芝、段培增、李巧清、刘璐、翟秀伟、张思荣、张学林
保山市人民医院

目的 分析保山市 9850 例女性人乳头瘤病毒（HPV）感染情况，为宫颈癌的预防和治疗提供实验室参考依据。

方法 以 2019 年 1 月 1 日至 2020 年 12 月 31 日前往保山市人民医院就诊并自愿接受 HPV-DNA 检测的女性为研究对象，用专用的宫颈脱落细胞采集器采集宫颈分泌物，采用反向点杂交法进行 HPV-DNA 分型检测，分析 HPV-DNA 亚型感染情况。
结果 本次研究共收集 9850 例样本（排除同一受检者的重复样本）。小于 20 岁女性筛查人数为 41 例，阳性率高达 43.90%（18/41）；20-29 岁女性筛查人数为 1770 例，阳性率为 17.51%（485/1770）；30-39 岁女性筛查人数最多为 3192 例，阳性率为 15.19%（485/3192）；40-49 岁女性筛查人数为 3106，阳性率为 14.20%（441/3106）；50-59 岁女性筛查人数为 1390，阳性率为 17.84（248/1390）；60 岁以上女性筛查人数为 351，阳性率为 17.66%（62/351）。不同年龄段女性 HPV 阳性率进行比较，差异具有统计学意义（P<0.05）。共检出 1564 例阳性样本，占比 15.89%（1564/9850），其中单一亚型感染者 1219 例，占比 77.94%（1219/1564），非单一亚型感染者 345 例，占比 22.06%（345/1564）；高危型感染者 1063 例，占比 67.97%（1063/1564），低危型感染者 297 例，占比 18.89%（297/1564），高低危混合感染者 204 例，占比 13.04%（204/1564）。18 种高危亚型中检出率最高的是 HPV52,占比 19.43%（304/1564）、其次是 HPV16，占比 15.47%（242/1564）及 HPV58，占比 11.13%（174/1564）。6 种低危亚型中，检出率最高的是 HPV81，占比 9.09%（142/1564）
结论 该院女性 HPV 感染率较高，以单一亚型、高危亚型感染为主，常见亚型为 HPV52、HPV16、HPV58 及 HPV81。

PU-0118

C/EBPα 高表达的肝细胞肝癌关联分子的筛选和机制研究

娄晓丽、侯彦强、杨丽媛、陈洪卫
上海市松江区中心医院

目的 研究和筛选 C/EBPα 高表达的肝细胞肝癌患者关联分子及相关机制。
方法 采用 Western-blot 检测 C/EBPα 在肝癌细胞株中的表达水平，通过 shRNA 干扰技术和 RNA-sequencing 技术筛选 C/EBPα 相关分子，通过差异分析和聚类分析得出差异分子和关联信号通路。采用 Western-blot、免疫组化检测二者的关联表达情况，应用荧光素酶实验验证 C/EBPα 对关联分子的调控机制。
结果 C/EBPα 在 HepG2 和 Huh7 高表达，C/EBPα 降低表达后，细胞增殖能力显著减弱。通过差异分析共发现上调 mRNA 1257 个和下调 mRNA 1055 个，其中差异最明显的是 DKK4 和 IGFBP1。免疫组化发现 C/EBPα 与 IGFBP1 负相关（p<0.05），C/EBPα 负调控 IGFBP1 的表达。
结论 C/EBPα 高表达的肝细胞肝癌通过下调 IGFBP1 促进肿瘤增殖。

PU-0119

男性特发性低促性腺激素性性腺功能减退症的分子遗传学研究

齐晨阳、夏欣一
中国人民解放军东部战区总医院

目的 男性特发性低促性腺激素性性腺功能减退症（IHH）是一种罕见的临床异质性遗传疾病，分为卡尔曼综合征（KS）和嗅觉正常的 IHH（nIHH）两种形式。以往文献报道的致病基因仅占其致病原因的 50%左右，仍有未知的致病基因和相关致病机制有待探索。本文旨在进一步扩大 IHH 基因型突变谱并为该病症的临床治疗和产前诊断提供依据。
方法 本研究纳入 40 例 IHH 患者，其中 nIHH 患者 18 例，KS 患者 22 例。检查记录患者的性腺功能相关临床数据，提取患者及部分患者家族成员的外周血基因组 DNA，进行全外显子测序

（WES），测序数据经生物信息学分析，Sanger 测序验证，突变位点致病性预测，突变位点在不同物种中的保守性比对，以确定疾病的原因，并且分析各个突变基因在总样本中的突变率。
结果 在 2 个 KS 家族中发现了 SEMA3E 错义突变(p.P323S)和 SOX10 移码突变(p.S431Rfs*69)；2 个 nIHH 家族中发现 FGFR1 无义突变(p.R661X)和 KISS1R 已知无义突变(p.R331X)。在 8 例散发无相关 IHH 患者中发现 2 个 ANOS1 移码突变(p.R282Vfs*26，p.R631Sfs*36)，2 个 FGFR1 移码突变(p.E705Gfs*16，p.F745Rfs*45)，1 个 CHD7 复合杂合突变(p.G1899R，Q1900_W1903del)，1 个 CHD7 错义突变(p.W1785C)，1 个 PROKR2 复合杂合突变(p.Y223D 和 p.R298C)和 1 个 KISS1R 已知纯合突变(p.Y103X)；经生物信息学分析，突变位点氨基酸高度保守且会影响到蛋白质的结构，预测具有导致 IHH 发生的可能性。并且分析验证了 40 例患者的总阳性检出率为 30% (nIHH 8/18 + KS 4/22)，其中 FGFR1 突变率占 7.5%(3/40)；ANOS1、CHD7 和 KISS1R 突变率分别占 5%(2/40)；SEMA3E、PROKR2 和 SOX10 突变率分别占 2.5% (1/40)。
结论 本研究鉴定出 10 种新的与 IHH 相关的基因突变位点，扩大了 IHH 基因型突变谱，为 IHH 相关基因的功能，致病机制等深入研究奠定了基础；确定了患者的致病基因，为患者的后续临床治疗和辅助生殖过程中的遗传咨询提供重要依据和有效帮助。

PU-0120

肝细胞癌预后相关 miRNA 的功能及其调节异常机制研究

秦士杰、夏欣一
中国人民解放军东部战区总医院

目的 许多 miRNAs 已被报道与肝细胞癌（Hepatocellular Carcinoma，HCC）的进展密切相关，异常调控的 miRNA 也被证明是 HCC 患者的诊断和预后因素之一，然而，miRNA 在 HCC 发生发展中的失调机制尚不清楚。
方法 TCGA 数据库中下载 HCC 样本 mRNA 及 pre-miRNA 表达数据以临床信息。对配对癌和癌旁 mRNA 进行差异表达分析，最终保留了 344 个癌症样本，其中 48 个匹配的癌旁样本。将这些样本随机分为独立的训练集（240 个样本）和测试集（104 个样本），训练集用于筛选生存相关 miRNA 并建立预后模型，测试集用于验证预后模型的可靠性和准确性。根据筛选出的相关 miRNAs 构建多基因预测模型来预测 HCC 患者的风险值，绘制不同风险分层的生存曲线来检验模型是否能够预测肝癌患者的预后。绘制 ROC 曲线，根据 AUC 曲线评价预测模型的可靠性。同时计算这些组织中差异表达 miRNA 启动子区域的甲基化程度及鉴定转录因子对 miRNA 的调控。
结果 首先发现了 7 个上调的 miRNAs（miR-9-5p miR-452-5p, miR-452-3p, miR-1180-3p, miR-4746-5p, miR-3677-3 和 miR-4661-5p）可以作为癌基因，通过抑制多个参与代谢的肿瘤抑制基因来促进肿瘤的发生，而下调的 miRNAs（miR-99-5p, miR-5589-5p, miR-5589-3p, miR-139-5p, miR-139-3p, miR-101-3p 和 miR-125b-5p）可通过抑制多个参与肿瘤相关通路的致癌基因来抑制细胞的异常增殖。其次，发现了异常调节的转录因子（如 E2F1、EBF1、FOXM1、ESR1、FOXO1、EGR1）是导致上述 14 个肝癌预后 miRNA 表达紊乱的主要原因，而不是这些 miRNA 启动子区域的 DNA 甲基化。最后，我们的发现揭示了转录因子和 miRNA 相互作用可以形成多种调控回路，协同控制 HCC 的发生和发展的机制。特别是 FOXO1 这一关键转录因子能够激活一定数量的肿瘤抑制 miRNAs，从而提高肝癌患者的生存率，提示 FOXO1 可能是肝癌患者有效的治疗靶点。
结论 本研究发现 14 个 HCC 预后相关 miRNAs 并揭示了它们在 HCC 中的异常调节机制，为 HCC 患者提供新的预后生物标志物和 FOXO1 等潜在治疗靶点。

PU-0121

快速的含内参的重组酶介导的扩增技术对 EB 病毒和巨细胞病毒的检测

高源
河北省人民医院

目的 EB 病毒(Epstein-Barr virus，EBV)和巨细胞病毒(Cytomeg-alovirus, CMV)是临床上两种常见的人类疱疹病毒，能够引起呼吸道疾病、神经系统疾病和传染性单核细胞增多症等多种疾病。重组酶介导的扩增技术(Recombinase-aided amplification，RAA)是一项具有我国自主知识产权的等温核酸扩增技术，被广泛应用于病原体核酸检测中。本研究利用人源性内参联合 RAA 技术分别建立两种人类疱疹病毒的双重非竞争性内参控制的(Non-Competitive Internal Controlled, NCIC)重组酶介导的扩增技术检测方法(NCIC-RAA)。
方法 根据 RAA 引物探针设计原理，在 EBV、CMV、管家基因 RNaseP 和 human β-globin(HHB)四种靶基因的保守区设计 RAA 引物探针。分别利用系列稀释的含有靶基因片段的标准质粒筛选最优的引物探针组合并分别建立四种靶基因的单重实时荧光 RAA 反应。随后，在已建立好的 EBV 和 CMV 单重 RAA 反应体系中引入 NCIC 的引物探针，优化和建立双重实时荧光 EBV 和 CMV NCIC-RAA 法,并对其灵敏度和特异性进行评价分析。应用本实验室收集的 250 份临床样本进行临床标本检测效能评价，并与商业化的(quantitative polymerase chain reaction，qPCR)试剂盒进行比较。
结果 EBV NCIC-RAA(RNaseP)和 CMV NCIC-RAA(HHB)方法的灵敏度分别为 2 拷贝/反应和 10 拷贝/反应，与其他病原体(人类疱疹病毒 1 型、2 型、3 型、6 型、人类乙肝病毒、人类丙肝病毒和西尼罗病毒)无交叉反应。在临床效能评价中，与商业化的 qPCR 相比，提取的 DNA 用于 EBV 和 CMV NCIC-RAA 方法的敏感性分别为 100.00%和 96.97%，特异性分别为 98.75%和 100.00%，Kappa 值分别为 0.983 和 0.979(p<0.001)。
结论 本研究所建立的两种双重实时荧光 EBV 和 CMV NCIC-RAA 检测方法灵敏度和特异性均较高,且方法操作简单,在 40 分钟内即可完成检测，适合于 EBV 和 CMV 的快速检测，为临床实验室提供了一个快速可靠的检测方法。

PU-0122

ApoE 及 SLCO1B1 基因多态性与血脂水平的相关性分析

张旭
四川绵阳四 0 四医院

目的 探究 ApoE、SLCO1B1 基因多态性与血脂水平是否存在相关性，为科学预防、控制血脂，合理使用降脂药提供科学依据。
方法 收集四川绵阳四 0 四医院 2019 年 1 月到 2020 年 12 月期间的住院患者 650 例，筛选同时期 ApoE、SLCO1B1 基因检查和血脂结果，分析基因型和基因表型分布特征，采用统计学方法比较各表型组血脂指标浓度水平的差异。
结果 ApoE 基因在 526C>T 位点和 388T>C 位点上都主要为野生型，两位点突变差异无统计学意义（P>0.05）；SLCO1B1 基因在 388A>G 位点主要为杂合突变型（AG）和纯合突变型（GG），在 521T>C 位点主要为纯合野生型（TT），两位点突变差异有统计学意义（P<0.05）；ApoE 基因表型以 ApoE3 型为主，ApoE4 型次之，E3/E3 基因型检出率最高；SLCO1B1 基因低风险型占 79.38%、中风险型占 19.39%和高风险型占 1.23%，*1a/*1b、 *1b/*1b 基因型为两种主要基因型；ApoE 三种基因表型在 TG、ApoB、LDL-C 浓度水平差异有统计学意义（P<0.05），但在 TCH、ApoA、HDL-C、HCY 浓度水平差异无统计学意义（P>0.05）；SLCO1B1 三组基因表型在 TCH、TG、ApoA、ApoB、HDL-C、LDL-C、HCY 浓度水平差异无统计学意义（P>0.05）。

结论 ApoE 和 SLCO1B1 基因型及基因表型频率分布不均，可针对不同人群进行基因筛查，为科学指导高血脂的预防提供理论依据。

PU-0123

Low CFB expression is independently associated with poor overall and disease-free survival in patients with lung adenocarcinoma

Chenglu He 、Yong Duan
The First Affiliated Hospital Of Kunming Medical University

Background The present study aimed to investigate the association between low expres-sion levels of CFB and the clinical features and survival status of patients with lung adenocarcinoma (LUAD).
Methods Patient data were based on RNA-sequencing and clinical data from The Cancer Genome Atlas database. All patients were divided into two groups based on the median expression of CFB. Kaplan-Meier curve and univariate Cox regression analyses were used to investigate the association between CFB and survival status. Gene set enrichment analysis was used to examine the effects of CFB expression on signaling pathway impairment. Furthermore, reverse transcription-quantitative PCR (RT-qPCR) and western blotting were used to verify the relative expression levels of CFB in LUAD tissues.
Results The data revealed that residual tumor classification, Karnofsky performance score and cancer stage were associated with overall survival, and that Karnofsky performance score and stage were associated with disease-free survival. The results demonstrated that high expression levels of CFB were associated with increased patient overall and disease-free survival according to both continuous and categorical models. The results of multivariate analysis identified that high expression levels of CFB were associated with increased overall and disease-free survival according to both the continuous model [hazard ratio (HR), 0.48; 95% confidence interval (95% CI), 0.25-0.93; P=0.029 for overall survival; HR, 0.29; 95% CI, 0.15-0.59; P=0.001 for disease-free survival] and the categorical model (HR, 0.46; 95% CI, 0.22-0.93; P=0.031 for overall survival; HR, 0.25; 95% CI, 0.12-0.55; P=0.001 for disease-free survival) after adjusting for corresponding covariates (residual tumour classification, Karnofsky performance score and stage).Furthermore, the results of both RT-qPCR and western blotting indicated that the relative mRNA and protein expression levels of CFB in lung tumor tissues were downregulated compared with those in adjacent non-tumor tissues.
Conlusion the present results suggested that CFB expression was an independent predictor of overall and disease-free survival in patients with LUAD.

PU-0124

乙肝大三阳患者 HBV-DNA 病毒载量与 HBeAg、PreS1、AST/ALT 水平之间的关系研究

刘君君、张炳杨
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 探讨乙肝大三阳患者血清中 HBV-DNA 病毒载量与血清中 HBeAg 水平、PreS1 抗原水平、肝功能指标(AST/ALT 比值)之间的关系；
方法 回顾性分析 2017 年 7 月至 2018 年 4 月在山东省千佛山医院就诊的乙肝大三阳患者 692 例，统计其 HBV-DNA 病毒载量检测结果，同时统计其乙肝五项(HBeAg 水平)、PreS1 抗原水平、肝功

能(AST/ALT 比值)结果。将纳入研究的患者按照 HBV-DNA 病毒载量结果分为三组，病毒高复制组（HBV-DNA≥106 IU/mL, 305 例）,中低复制组（106>HBV-DNA≥102 IU/mL，375 例）, 无复制组（HBV-DNA<102 IU/mL, 即低于检测下限，12 例），借助 SPSS 16.0 统计分析软件分析三组中 HBeAg 水平、PreS1 抗原水平、AST/ALT 比值的变化以及其与 HBV-DNA 病毒载量的相关性。
结果 HBV-DNA 病毒高复制组 HBeAg>1000 COI 者占 61.97% (189/305)，HBV-DNA 病毒中低复制组 HBeAg>1000 COI 者占 12.80% (48/375)，相关性分析发现乙肝大三阳患者 HBV-DNA 病毒载量与 HBeAg 水平呈正相关(相关系数 r=0.482)；乙肝大三阳患者 HB-DNA 病毒载量与 PreS1 抗原水平相关系数 r 为-0.095，提示 PreS1 抗原水平与 HBV-DNA 病毒复制水平相关性不大；HBV-DNA 低复制组 AST/ALT 为 1.05±0.92，HBV-DNA 高复制组 AST/ALT 为 0.91±0.57，AST/ALT 比值在 HBV-DNA 高复制组下降差异有统计学意义（P<0.05）。
结论 乙肝大三阳患者 HBV-DNA 病毒载量与血清中 HBeAg 水平呈正相关，与 PreS1 抗原水平相关性差，且 HBV-DNA 高复制状态下常伴随 AST/ALT 下降的现象。

PU-0125

山东省 4833 例乙肝病毒定量与乙肝两对半检测结果分析

徐健、张守都、王青、彭德志、王佳佳
济南金域医学检验中心有限公司

目的 针对乙肝病毒乙肝五项指标检测不同模式与乙肝 DNA 定量的相关性进行分析。
方法 将近三年本实验室检测的 4833 份血清标本作为研究对象，对来源病例进行回顾性分析.所有受检对象均采集空腹血液样本 3.0ml 两管,分别进行乙肝五项指标检测以及乙肝病毒 DNA 定量检测，对乙肝五项指标不同模式与乙肝病毒 DNA 检测阳性对照结果以及 HbeAg 与乙肝病毒 DNA 拷贝数的对应关系进行分析。
结果 本组 4540 例 HbsAg 阳性血清样本中,乙肝病毒 DNA 阳性检出率为 36.28%(1647/4540)."大三阳"模式下乙肝病毒 DNA 阳性检出率为 54.08% (1047/1936),HbsAg HbeAg(+)模式下乙肝病毒 DNA 阳性检出率为 54.48% (1203/2208)，显著高于乙肝五项的其他模式,对比检验存在显著差异(P<0.05),有统计学意义."大三阳"模式下 HbeAg 与乙肝病毒 DNA 拷贝数呈显著正相关关系,与其他乙肝五项模式对比检验存在显著差异(P<0.05),有统计学意义.
结论 ①乙肝患者血液循环系统中乙肝病毒 DNA 与 HbeAg 以及 HbsAg 有相关性关系,"大三阳"模式下 HbeAg 与乙肝病毒 DNA 拷贝数呈显著正相关关系，值得临床重视。②乙肝病毒 DNA 检测较乙肝五项指标作为反映病毒复制的指标更敏感。

PU-0126

NCAM and ABCA1 Dual-labeled Exosome Contain Higher Aβ42 and MicroRNA-135a in Peripheral Blood of Alzheimer's Disease

sihai ling
Beijing Anding Hospital, Capital Medical University

Objective We aimed to establish a method to determine whether microRNA-135a (miR-135a) levels in NCAM and ABCA1 Dual-labeled serum exosomes might be serve as a marker for the diagnosis of Alzheimer’s disease.
Methods We used immunocapture **Methods** to determine the levels of NCAM and ABCA1 Dual-labeled exosomal miR-135a in cultures of white blood cells (WBCs), red blood cells (RBCs), mouse hippocampal neuron HT-22 cells, and primary mouse neuronal cells. NCAM and ABCA1

Dual-labeled exosomal miR-135a levels were also evaluated in the CSF (CSF) and serum of APP/PS1 double transgenic mice, as well as control subjects (n = 60) and study participants with subjective cognitive decline (SCD, n = 89), stage and mild cognitive impairment (MCI, n = 92), and dementia of the Alzheimer type (DAT, n = 92).
Results ABCA1 levels of exosomes harvested from the medium of HT-22 cells and neurons were significantly higher than those of RBCs and WBCs (P < 0.05). Exosomal ABCA1 from the CSF of APP/PS1 mice were transmitted to the serum of wild-type mice after injection, and high miR-193b levels were observed in both serum and CSF after injection. The NCAM and ABCA1 Dual-labeled exosomal miR-135a levels were higher in the CSF of MCI and DAT patients compared with the CSF of the control group (P < 0.05). The NCAM and ABCA1 Dual-labeled exosomal miR-135a were also slightly higher (P > 0.05) in the serum of SCD patients and significantly higher in the serum of MCI and DAT patients compared with the serum of the control group (P < 0.05).
Conclusion This study provides a method to capture specific exosomes. Detection of serum exosomes labeled with ABCA1 may facilitate the early diagnosis of AD.

PU-0127

基于电化学传感器检测的人乳头瘤病毒 DNA 检测及其应用进展

魏雪菊[1,2]、洪国斋[1,2]
1. 厦门大学附属第一医院检验科
2. 厦门市基因检测重点实验室

宫颈癌是世界第二大最常见的女性癌症类型，因目前缺乏足够廉价的 HPV 疫苗和 HPV 筛查方法，导致宫颈癌发病率在发展中国家地区的发病率居高不下。电化学生物传感器因其快速响应，简便和低成本而成为 HPV 的理想诊断工具，以及电化学作为检测方法对人乳头瘤病毒 DNA 进行检测，提高检出灵敏性，使得更多的患者获益，从而有助于临床早期筛查和干预。

PU-0128

HIV/HCV 合并感染者 microRNA 表达谱分析

闫新丽[1]、李晓非[1]、杨瑾[1]、朱永玉[1]、保凌[1]、王玉明[2]
1. 昆明市第三人民医院
2. 昆明医科大学第二附属医院

目的 人类免疫缺陷病毒 (Human immunodeficiencyvirus, HIV) 感染和丙型肝炎病毒 (Hepatitis C virus, HCV) 感染是世界公认的严重的公共卫生问题，两者有相似的感染途径（血液及血制品传播、性接触传播和母婴传播）容易并发感染。文章通过对 1 型艾滋病病毒（HIV-1）与丙型肝炎病毒合并感染者血浆中 miRNA 表达谱的分析，评估 miRNA 作为 HIV/HCV 合并感染者早期诊断、病情监测辅助指标的可行性, 并为阐明共感染者的发病机制提供依据。
方法 实时定量 PCR（RT-qPCR）分别检测 40 例健康对照组（对照组），40 例 HIV-1 感染未经抗病毒治疗 HCV 阴性组（HIV+组）,40 例 HIV-1 阴性 HCV 阳性组（HCV+组）及 40 例 HIV-1 感染未经抗病毒治疗 HCV 阳性组（HIV+/HCV+组）血浆 miR-29a、miR-122、miR-155、miR-200a 相对表达量的差异。
结果 与健康对照组相比 HIV+组血浆 miR-29a、miR-122、miR-155 表达升高，且差异具有统计学意义(p<0.05)；HCV+组血浆 miR-122 和 miR-155 表达均升高，且差异具有统计学意义（p<0.05）；HIV+/HCV+组血浆 miR-29a、miR-122 和 miR-155 表达均升高，且差异具有统计学意义（p<0.05）；HIV+/HCV+组较 HIV+及 HCV+组血浆 miR-122 和 miR-155 表达均升高，且差异具有统计学意义（p<0.05）；HCV+组中血浆 miR-122、miR-155 与 HCVRNA 呈正相关(p<0.05)，

与 CD4+ T 细胞计数无显著相关性（p>0.05）；HIV+/HCV+组中血浆 miR-122，miR-155 与 HIV-1RNA/HCVRNA 呈正相关(p<0.05)，与 CD4+ T 细胞计数呈负相关(p<0.05)。
结论 血浆中 miR-122、miR-155 可能参与了 HIV 和 HCV 感染的临床进展和发病机制；HIV/HCV 混合感染很可能加速了 HIV RNA 的复制, 进而因 HIV RNA 复制的增长加速了对 T 淋巴细胞亚群的损害。

PU-0129

不同检测试剂对人乳头瘤病毒检测结果一致性及对临床诊断的影响

朱亚荣
西安金域医学检验所有限公司

目的 分析不同检测试剂对人乳头瘤病毒检测结果一致性及对临床诊断的影响。
方法 1.收集 2021 年 4 月 1 日我单位基因室使用深圳亚能人乳头瘤病毒基因分型（23 型）检测试剂盒（PCR-反向点杂交法）200 例样本的检测结果,其中包括阴性结果 50 例，16 型 12 例，18 型 22 例，16 型与 18 型混合感染 16 例，非 16 型与 18 型其他型检测结果为阳性样本 100 例。2.当日对该 200 例样本使用湖南圣湘人乳头瘤病毒（16，18 型）核酸检测试剂盒（PCR-荧光探针法）进行复测。
结果 该 200 例样本使用湖南圣湘人乳头瘤病毒（16，18 型）核酸检测试剂盒（PCR-荧光探针法）检测结果为:1.50 例阴性检测结果均为阴性，符合率 100%。2.16 型 12 例，18 型 22 例，16 型与 18 型混合感染 16 例，共计 50 例样本检测结果均为阳性，符合率 100%。3.非 16 型与 18 型其他型别检测结果为阳性 100 例样本中检测为阳性样本 38 例（该 38 例阳性样本 CT 值偏大，荧光信号强度较低），符合率 62%。
结论 该 200 例样本中阴性结果、16 型、18 型、16 型与 18 型混合感染两种试剂检测结果一致，符合率 100%，使用深圳亚能人乳头瘤病毒基因分型（23 型）检测试剂盒（PCR-反向点杂交法）检测非 16 型与 18 型但其他型检测结果为阳性的 100 例样本中，使用湖南圣湘人乳头瘤病毒（16，18 型）核酸检测试剂盒（PCR-荧光探针法）检测为阳性样本 38 例，但该 38 例阳性样本 CT 值偏大，荧光信号强度较低，符合率 62%。因此对于临床样本中使用湖南圣湘人乳头瘤病毒（16，18 型）核酸检测试剂盒（PCR-荧光探针法）检测人乳头瘤病毒（16，18 型）时发现 CT 值偏大，荧光信号强度较低的临床样本应该使用其他厂家检测试剂对该临床样本进行复测，保证检测结果的准确性，从而保证临床对该患者正确的诊断与治疗。

PU-0130

肺癌患者 ACE2 和 TMPRSS2 高表达致其 COVID-19 高易感性与不良预后

韩莹、夏欣一
中国人民解放军东部战区总医院

目的 COVID-19 已在全球迅速蔓延，从分子和临床水平上对肺癌患者进行系统分析，以了解疾病的病理和临床特征。
方法 对武汉火神山医院 65 例 COVID-19 患者进行单中心回顾性队列研究（其中 13 例诊断为肺癌），并对公共数据库中肺癌手术切缘组织和正常肺组织的单细胞 RNA 测序数据进行分析。
结果 1. 肺癌手术切缘组织中，表达 ACE2 和 TMPRSS2 的上皮细胞比例高于正常组织，ACE2 的 mRNA 表达亦高于正常 (P = 0.013)，辅助因子 TMPRSS2 的表达（P < 0.001)也显著高于正常组

织，均提示肺癌组织更易受 COVID-19 侵袭；2.治疗过程中，肺癌患者更易发生重症感染（P = 0.064）。肺癌患者感染新冠肺炎后的潜伏期为 10.5（10.0-17.5）天，明显短于其他患者[30.0（14.0-35.0）；P = 0.016]。此外，肺癌患者治疗后症状缓解时间为 12 (11.0-18.0) 天，比非癌症患者 (5.8-14.0) 长 4 天 （P = 0.020），但在中/短期肺癌生存者之间，上述指标间没有观察到明显差异。可见，1.在本队列研究中，肺癌患者的死亡率 (7.7%, 1/13) 高于其他患者 (2.3%)，并且肺癌患者感染 SARS-COV-2 后的潜伏期短，缓解时间长，病情进展较快；2. ACE2 和 TMPRSS2 基因在肺癌不同病理类型（鳞癌/腺癌）以及不同分期中的表达一致，与研究队列中不同病理分型、分期的肺癌患者对 SARS-CoV-2 的易感性相同是一致的；3.肺癌患者手术切缘组织的 ACE2 和 TMPRSS2 水平高于正常组织，癌症中期患者尽管进行了癌症切除，剩余的组织仍然保留了癌细胞的特征，如基因组不稳定性和强大的局部浸润和外渗能力。

结论 本文从 ACE2 和 TMPRSS2 高表达特点和临床特征层面解释肺癌患者对 COVID-19 高易感性以及较差预后的原因，为 COVID-19 大流行背景下肺癌患者的管理提供依据。（本文部分内容已发表于 Front Oncol，IF=4.848）

PU-0131

结核病分子诊断技术研究进展

樊茹[1]、李晓非[1,2]
1. 大理大学
2. 昆明市第三人民医院

结核病是由结核分枝杆菌感染引起的病死率最高的且是人类发展史最长的一种慢性传染性疾病。早期有效的筛查、诊断和治疗对于全球结核病疫情防控和预防耐药菌株的出现至关重要。从目前来看，细菌学检测是诊断结核病最基本的检测技术，免疫学检测技术可作为有效辅助诊断，适用于各级实验室开展。传统诊断技术如涂片镜检、培养技术、药敏试验等，由于培养时间长、阳性率仍有待提高等局限性已无法满足早期准确、快速诊断结核病的需求，从而造成大量结核病患者漏诊和延迟诊断；特别是涂阴结核、肺外结核的临床表现和影像学特征均不是很典型且诊断技术较少，导致结核病的防控形势更加复杂、困难。全球结核病的发病率虽然正在缓慢下降，但速度仍达不到 2020 年的疫情防控战略目标，更无法实现 2035 年终止结核病的计划。基于人类基因组学、核酸扩增试验和基因测序技术的发展及多学科融合，一系列新兴的分子诊断技术不断涌现并凭借其准确、高效、高通量等优点为结核病的诊治带来了新曙光。2017 年国家卫计委重新修订的《肺结核诊断标准》中，已把 MTB 核酸检测阳性列为确诊结核病的标准之一,这大大提升了结核病诊断的准确率。国内外学者针对结核病的分子诊断技术不断探索研究，期望可以为临床制定治疗方案提供有力帮助，让患者得到及时规范的治疗。本文简要概述了近年来出现的结核病新型分子诊断技术各自的优点与局限，对临床选择合适的分子检测技术具有一定参考意义。

PU-0132

血浆 microRNA 与 HIV 感染及治疗关系的研究

闫新丽[1]、李晓非[1]、杨瑾[1]、吕松琴[1]、王玉明[2]
1. 昆明市第三人民医院
2. 昆明医科大学第二附属医院

目的 miRNAs 是在真核生物中发现的一类内源性的具有调控功能的非编码 RNA，在转录后水平对基因表达调控有重要影响。miRNA 在 HIV 的感染及疾病进展中发挥着重要作用，被认为是预测 HIV 感染、治疗评估及 HIV 相关疾病的新型生物学标志物，文章分析了 1 型艾滋病病毒（HIV-1）

感染者血浆中 miRNA 的表达特点 ，探讨血浆 miRNA 作为 HIV-1 感染及治疗监测生物学标志物的潜在可行性。
方法 应用 qPCR 技术检测 50 例健康对照组，50 例 HIV-1 感染未经抗病毒治疗组及 50 例 HIV-1 感染抗病毒治疗组血浆 miR-29a、miR-122，miR-155 相对表达量的差异。结合患者 HIV-1 病毒载量及 CD4+T 淋巴细胞计数指标，分析这两项指标与 miRNA 表达量的相关性。
结果 与正常对照组相比 HIV-1 感染未经抗病毒治疗组血浆 miR-29a、miR-155、miR-122 表达均升高，差异有统计学意义（$p<0.05$）；未治疗与治疗组相比较血浆 miR-29a、miR-155 和 miR-122 表达均升高，差异有统计学意义（$p<0.05$）。未治疗组血浆 miR-29a、miR-155 表达水平与 HIV-1RNA 病毒载量呈正相关（$p<0.05$），miR-122 与 HIV-1RNA 病毒载量无显著相关($p>0.05$)。miR-29a、miR-155 表达水平与 CD4+ T 细胞计数呈负相关($p<0.05$)。
结论 血浆 miR-29a、miR-155、miR-122 在 HIV-1 感染后显著升高，血浆 miR-29a、miR-122，miR-155 与 HIV-1 感染相关，可能具有成为 HIV-1 感染后新型生物学标志物的潜在意义。而抗病毒治疗可以诱导 miR-29a、miR-155 和 miR-122 表达降低，这些 miRNA 可能具有成为监测 HIV-1 感染抗病毒治疗效果观察指标的潜在价值。未治疗组血浆 miR-29a、miR-155 与 HIV-1RNA 呈正相关，表明其与 HIV-1 病毒复制相关。在未来，miRNA 可能被用作生物标志物来估计或预测受感染患者的疾病进展率 ，并为开发新的治疗策略提供依据。

PU-0133

生殖道病原体感染 STD-DNA 与女性不孕症及胎膜早破的相关性

李颖
东南大学附属中大医院

目的 调查育龄期女性 STD-DNA 感染现状,探讨 STD-DNA 感染与女性不孕症及胎膜早破的相关性,为不孕症的预防和诊治提供参考。
方法 收集 2016 年 10 月至 2019 年 1 月在东南大学附属中大医院进行 STD-DNA 检测的 153 例不孕症妇女，剔除多囊，卵巢功能异常、子宫因素、机械因素、免疫因素、输卵管阻塞等外部因素的影响，记录 STD-DNA 检测的结果，作为实验组。选取正常育龄女性作为对照组，进行分析。另外收集 131 例胎膜早破的产妇，排除产妇有流产史、宫内压（巨大儿、多胎等） ，排除妊娠高血压、糖尿病、贫血等，以及其他宫腔外力的影响，记录 STD-DNA 检测的结果为实验组，选取正常产妇为对照组。不孕症的诊断标准以最新的美国生殖医学学会（ASRM）[1]2015 年制订的指南为准。计量资料采用均数±标准差（x±s）描述其集中和离散程度,在满足方差齐性的条件下,计量资料采用 t 检验;计数资料中采用率和 95%置信区间（95%CI）描述分布,二分类资料采用卡方检验;不孕症的多因素分析采用二元 logistic 逐步回归进行分析。以 $P<0.05$ 认为差异具有统计学意义。
结果 (1)本次调查最终获得有效数据不孕症妇女 153 人中 STD-DNA 感染率为 64%（98/153），其中解脲支原体（UU）感染率最高，占感染人数的 84.69%（83/98），沙眼衣原体（CT）占感染人数的 17.34%（17/98）。(2)在 131 例胎膜早破产妇中，STD-DNA 感染率为 38.17%（50/131），其中 UU 感染率最高，占感染人数的 78%（39/50）。相关分析显示：不孕症实验组 $P<0.05$ 认为差异具有统计学意义,胎膜早破组 $P<0.05$ 认为差异具有统计学意义。
结论 (1)生殖道病原体 STD-DNA 感染是是女性不孕症和产妇胎膜早破的高危因素，应早期筛查，并建议患者需要定期进行检查，主动排除该因素对女性不孕症及胎膜早破的影响。（2）生殖系是外界致病菌较容易侵犯导致病变的部位。生殖道病原体感染是引起泌尿道感染的常见病因，其危害性大，传染性较强，因及时给予相应的正确治疗。

PU-0134

TNF-α、IL10 基因多态性与肝癌易感性的相关分析

周蓉
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 分析 TNF、IL 10 基因多态性与肝细胞癌（HCC）易感性之间的相关性。
方法 以 241 例肝细胞癌患者及 286 例健康对照者作为研究对象。抽提全血基因组 DNA，PCR 结合直接测序法测定 TNF（-238 G/A，-308 G/A）和 IL10（-592 C/A，-819 C/T）基因多态性的分布。ELISA 法检测血清中 TNF-α、IL-10、IL-2、IL-4 和 TGF-β 的水平。
结果 TNF-238 AA 基因型、等位基因 A 的频率与 HCC 的发病风险呈负相关关系（P<0.05）。IL10-592 CA、-819 CT/TT 基因型和 IL10 -819 T 等位基因与 HCC 的发病风险呈正相关关系（P<0.05）。对于 TNF -238 G/A，AA 基因型与血清 IL-2、IL-4 水平升高相关（P<0.05），而 IL10 -819 CC 基因型与 TGF-β、IL-10 水平降低密切相关（P<0.05）。我们还发现，IL10 -819 T/C 与 HCC 的严重程度有关（P<0.05）。
结论 IL10 -819 CT/TT 与 HCC 的发生发展密切相关，可能与 Th1/Th2 型细胞因子的下调、Th3 型细胞因子的上调有关。

PU-0135

D- 二聚体在胰腺癌转移中的临床意义

李建华
天津医科大学肿瘤医院

目的 探讨 D 一二聚体在胰腺癌淋巴结转移和远处转移的意义。
方法 采用全自动免疫分析系统酶联分析法检测 100 例恶性肿瘤患者及 50 例健康对照受试者血浆 D-二聚体水平并进行比较。
结果 显示各组胰腺癌肿瘤患者 D 一二聚体检测数值均较正常对照组高，有淋巴结转移，或者有远处转移的患者血浆中的 D-二聚体数值明显高于无转移组，差异有统计学意义(P<O．05)。
结论 D 一二聚体 可作为恶性肿瘤患者纤溶状态、及淋巴结转移，远处转移的重要指标。

PU-0136

基于 CRISPR-Cas9 的核酸快速检测方法建立与应用

夏欣一
中国人民解放军东部战区总医院

目的 核酸检测技术一直是分子诊断的关键，特别是在当前 COVID-19 大流行的背景下。目前核酸检测技术仍受到传统扩增和杂交技术的限制，迫切需要一种简便、快速、灵敏度高、特异性强的方法。本研究开发了一种新的基于 CRISPR-Cas9 的 DNA 检测方法，称为 CRISPR-Cas9-assisted DNA 检测（CADD）。
方法 首先针对目标 DNA 设计一对捕获 sgRNA (sgRNAa 和 sgRNAb)。SgRNAa 和 sgRNAb 有不同的 3’末端捕获序列。目标 DNA 被一对 dCas9 -sgRNA 复合物结合时，dCas9 -sgRNA-DNA 复合物可通过偶联在固体载体上的寡核苷酸和 sgRNAa 的捕获序列之间的退火而被捕获到珠粒或微孔板表面，然后通过与 sgRNAb 互补的序列偶联一种荧光或比色信号进行报告。最后，通过检测细菌、肿瘤细胞和病毒的 DNA，验证了该方法的有效性，同时设计一套针对 15 种高危 HPV 的 sgRNAs 检测临床宫颈刷标本。

结果 设计 15 种高危型 HPV 对应的 sgRNAs，发现使用特异的 sgRNAsp（sgRNA special）或混合的 sgRNAct（sgRNA cocktail）均可特异性检出靶标 HPV，证明 dCas9-sgRNA 可特异性捕获靶序列。以 HPV16 质粒为靶标进行检测证明采用磁珠荧光报告体系，靶标浓度在 100pM~10fM 范围内时 DNA 浓度与荧光强度呈线性相关。利用不同的 sgRNAsp 和 sgRNAct 检测临床样本，结果显示所有样本都可检出，与临床采用的 PCR-反向点杂交测试结果相比，使用 CADD 可 100%的检测出感染的基因型，具有良好的敏感性和特异性。此外，偶联 ELISA-CADD 检测还在这些临床样本中发现了更多的多重感染。所有检测可在室温下 30min 内完成。
结论 我们开发的这种新的基于 CRISPR-Cas9 的 DNA 检测方法 CADD，与现有的方法相比，具有简单、快速、不需预扩增等优点，该方法有望实现快速现场检测。（本文部分内容已发表于基因编辑专业期刊 CRISPR J，IF=5.343）

PU-0137

STAG2 的基因突变及蛋白异常表达与浸润性膀胱癌患者术后生存期的相关性研究

乔艳、王国良、贺慧颖、张文静、崔丽艳
北京大学第三医院

目的 骨髓基质细胞抗原 2（stromal antigen 2, STAG2）是维持姐妹染色单体结合的黏连蛋白中重要的成员。编码 STAG2 的 stag2 基因是高通量测序中新发现的膀胱癌高频突变基因，突变频率高达 20%。我们的前期研究发现，膀胱癌组织中 STAG2 蛋白的缺失与患者的预后良好显著相关，但在浸润性膀胱癌中，这一相关性还需要更大的样本量进行证明。
方法 通过 TCGA 高通量数据库，我们用 Log-rank 方法分析了 429 例浸润性膀胱癌患者的临床信息与 stag2 基因突变的相关性。另外，我们用免疫组化的方法检测了 STAG2 蛋白在 101 例浸润性膀胱癌患者肿瘤组织中的表达情况，用 Log-rank 方法分析了 STAG2 蛋白与患者临床特征及患者预后生存时间的相关性。
结果 对 429 例 TCGA 数据库的患者信息分析显示，与 stag2 基因野生型相比，在肿瘤组织中存在 stag2 基因突变的患者具有更长的生存时间（Log-rank, P=0.044）。免疫组化结果显示，57.4%的肿瘤组织中检测出 STAG2 蛋白在细胞核的正常表达，20.8%的肿瘤组织中 STAG2 在细胞核内低表达或在细胞浆中表达，此外 21.8%的肿瘤组织中 STAG2 蛋白缺失表达。Log-rank 分析显示与 STAG2 的正常表达组相比，STAG2 低表达组和 STAG2 缺失表达组具有较长的生存时间（P = 0.025）。
结论 通过 TCGA 数据库的分析和较大样本量的回顾性研究，stag2 基因突变和蛋白异常表达与浸润性膀胱癌患者手术后较好的预后相关，提示 STAG2 可以作为预后的潜在标志物。

PU-0138

52 型 58 型 53 型 HPV 在川南地区分布及其临床特征

张驰
西南医科大学附属医院

目的 了解 52 型 58 型 53 型高危人乳头瘤病毒(High risk Human papillomavirus,hr- HPV)在川南地区女性基因型的分布特点及其易感因素，为 HPV 感染的防治提供依据。
方法 采用 PCR-反向点杂交法对患者进行 HPV 基因分型并探讨影响 HPV 感染的因素。
结果 (1).2379 例川南女性就诊者中，共发现 617 例 HPV 感染者，阳性率为 25.93％；基因分型结果显示，有 23 种共 891 例 HPV 亚型被检出高危型 18 种共 750 例（占 84.18％），主要型别为：

52 型、16 型、58 型；(2).检出 52 型 58 型 53 型单一感染 431 例（占 69.85%）;多重感染 186 例（占 30.15%),包括双重—六重 5 种感染类型；(3).1290 例宫颈病变患者中，炎症组、宫颈上皮内瘤变组、宫颈癌组在 52 型 58 型 53 型 HPV 阳性率差异均有统计学意义（P <0.05）；(4).患者的年龄、阴道酸碱度、清洁度明显影响 52 型 58 型 53 型 HPV 的感染率（P <0.05），但季节、霉菌及滴虫感染对其感染率无显著影响（P >0.05）。

结论 52 型 58 型 53 型在川南地区女性 HPV 高危感染位居第 1 位、第 3 位第 4 位，占到了高危型的 50%以上，显示出与周边及全国其它地区迥异的分布特点，患者年龄、阴道酸碱度、清洁度则是其感染的重要影响因素。

PU-0139

c-Met and PD-L1 on Circulating Exosomes as Diagnostic and Prognostic Markers for Colorectal Cancer

Chenzheng Gu
Department of Laboratory Medicine, Shanghai Tongji Hospital, Tongji University School of Medicine

Background Exosomes are membrane vesicles that offer potential as blood-derived biomarkers for malign tumors in the clinical study. Colorectal cancer (CRC) ranks as the third most common cancer with a high risk of metastasis and recurrence worldwide. The present work aims to assess whether colorectal cancers release exosomes which express c-Met (Cellular-mesenchymal to epithelial transition factor) and PD-L1 (programmed cell death 1 ligand 1) and whether the detection of such expression in plasma has diagnostic or prognostic meaning for the suffering patients.

Methods By the way of ultracentrifugation, exosome isolation was performed on plasma samples from 32 patients who were primarily diagnosed with colorectal cancer and 20 healthy donors. Western blot was used to analyze the expression of c-Met and PD-L1 of exosomes which were derived from the plasma samples. Soluble PD-L1 and c-Met in plasma were measured by enzyme-linked immunosorbent assay(ELISA）, and PD-L1 and c-Met in exosome levels were measured by using Exocounter. ROC curve was used to assess the sensitivity and specificity of the model of Exo-c-Met and Exo-PD-L1.

Results The results of western blot demonstrated that the expression of Exo-c-Met and Exo-PD-L1 in CRC patients was significantly higher than in healthy donors. In terms of c-Met, The levels of Exo-c-Met were significantly higher compared with soluble c-Met in the plasma which was barely detectable. Exo-c-Met levels were higher in CRC patients with advanced tumor stage, larger tumor size (>2.5 cm) ($p<0.001$), and distant metastasis ($p<0.05$). On the contrary, soluble c-Met levels had no significant difference between CRC patients and healthy donors, and it was not correlated with any clinic-pathologic characteristics except for tumor size (>2.5 cm) ($p<0.05$). Exo-c-Met was defined, yielding a 98% sensitivity, a 70% specificity, a 91% positive predictive value, and 54% negative predictive values for disease progression. In terms of PD-L1, Exo-PD-L1 was detected in all patients whereas only 75% of tumor biopsies were PD-L1 positive. The levels of Exo-PD-L1 were also significantly higher compared with soluble PD-L1. There was the same correlation between Exosome-PD-L1 levels and the clinic-pathologic features. Exo-PD-L1 was defined, yielding an 84% sensitivity, a 79% specificity, an 87% positive predictive value, and 50% negative predictive values for disease progression.

Conclusions In conclusion, c-Met and PD-L1 in exosomes, but not in soluble, were correlated with CRC disease progression, including tumor size, metastasis, and TNM stage. As a result, c-Met and PD-L1 levels in circulating exosomes seem to be more reliable markers. Monitoring of circulating Exo-c-Met and Exo-PD-L1 may be useful for diagnosis and prognosis of Colorectal Cancer.

PU-0140

Combined detection of Sialic Acid and Hydroxyproline in diagnosis of ovarian cancer and its comparison with Human Epididymis Protein 4 and Carbohydrate Antigen 125

Peilong Li
The Second Hospital of Shandong University

Background Elevated serum sialic acid (SA) and hydroxyproline (Hyp) levels have been found in a variety of malignant cancers. The aim of this study was to simultaneously detect serum levels of SA and Hyp (SA&Hyp) in ovarian cancer, and compare its diagnostic value with classic tumor markers—human epididymis protein 4 (HE4) and carbohydrate antigen 125 (CA125).
Materials and Methods Serum levels of SA&Hyp, HE4 and CA125A were detected in a total of 767 serum samples collected from 484 patients with gynecologic diseases, 180 healthy individuals, 45 pregnant women and 58 patients with renal failure using chemical colorimetry and electrochemiluminescence immunoassay (ECLIA), respectively. Risk of ovarian malignancy algorithm (ROMA) was calculated based on HE4 and CA125 values.
Results Serum SA&Hyp levels were influenced significantly by renal failure and pregnancy but not age and menopausal status. The median concentrations of SA&Hyp, HE4 and CA125 in patients with ovarian cancer were 119.0 U/mL, 190.2 pmol/L and 366.0 pmol/L, which were significantly higher than levels in patients with benign gynecologic diseases ($P<0.001$). SA&Hyp showed a significant higher AUC than HE4 and CA125 in the diagnosis of gynecologic malignancies ($P<0.001$), while no significance was found when compared with ROMA. Specially, SA&Hyp in 48.3% subjects (29/60) diagnosed as positive before primary surgery showed negative after surgery.
Conclusions Renal failure and pregnancy are the main source for increased false positive of SA&Hyp. Compared with HE4 and CA125, SA&Hyp shows a better diagnosis value and can be used in the diagnosis and dynamic monitoring of gynecologic pelvic malignancies, while no statistical significance was found compared with ROMA.

PU-0141

LncRNA HOTAIR Contributes to 5-fluorouracil Resistance through Suppressing MiR-218 and Activating NF-κB/TS Signaling in Colorectal Cancer

Peilong Li
The Second Hospital of Shandong University

Purpose In clinical situations, acquired drug resistance and enhanced metastasis frequently follow chemotherapeutic regimens, leading to treatment failure in tumor patients. Despite the extensive research on chemoresistance, the detailed mechanism underlying this phenomenon remains unclear. Long non-coding RNA HOTAIR has been considered as a pro-oncogene in multiple cancers. However, the precise functional mechanism of HOTAIR in chemoresistance is not well known. To further explore the possible mechanisms and promote chemosensitivity of CRC treatment, we evaluated the prognostic effect of HOTAIR in patients received 5-FU-based treatment and investigated the underlying regulatory mechanism of HOTAIR in 5FU resistance.
Methods The small interfering RNAs (siRNAs) that specifically target human HOTAIR, EZH2, and VOPP1 mRNA were designated. The coding sequence of VOPP1 was amplified, cloned into PCDNA3.1 vector. The lentivirus vector containing HOTAIR short-hairpin RNA (Lv-ShHOTAIR) was amplified and cloned. Human CRC cells lines were transfected with small interfering RNAs or overexpressing precursor followed by assays to investigate the influence of HOTAIR and VOPP1

on cell proliferation, cell-cylce phase and pathways involved in molecular mechanisms of chemoresistance to 5-FU. RNA immunoprecipitation (RIP) and Chromatin immunoprecipitation (ChIP) experiments were performed to investigate the potential interaction. Western blot and immunofluorescence analysis were performed to detect the protein expression of NF-κB/TS signaling pathway. Primary tumor specimens and adjacent non-tumor sites were used to determine the HOTAIR expression distribution and explore the potential prognostic value of HOTAIR on the chemoresponse to 5-FU-based treatment in CRC patients.

Results HOTAIR negatively regulated miR-218 expression in CRC cells. RIP and ChIP assay showed that HOTAIR interacted with EZH2, and this interaction subsequently silenced miR-218-2. Both HOTAIR and miR-218 suppressed cell proliferation, and HOTAIR knockdown dramatically inhibited cell viability and induced G1-phase arrest by promoting miR-218 expression. Luciferase activity assay showed that VOPP1 was a functional target of miR-218. More importantly, the main downstream targets signaling of NF-κB, including the pathway involved in cell survival (p65-NF-κB, pAkt, pERK), cell cycle (E2F-1) and 5FU-targeted protein (thymidylate synthase, TS), were inactivated by HOTAIR through the suppression of miR-218 expression. Additionally, HOTAIR knockdown partially reversed 5FU resistance through promoting miR-218 and inactivating NF-κB signaling. Furthermore, HOTAIR restrained 5FU-induced cytotoxicity on CRC cells through promotion of TS expression.

Clinical exploration of HOTAIR indicated that the HOTAIR expression level was much higher in CRC tissues from patients who did not respond to 5FU treatment than those from patients who experienced response to chemotherapy. ROC curve analysis was performed, and these patients were stratified into a low (n=56) and a high (n=96) HOTAIR expression group with an established cut-off value (4.01). The area under the curve (AUC) and diagnostic sensitivity and specificity reached 0.716, 81.58%, and 55.26% with the established cut-off value, respectively. Furthermore, the proportion of patients not responding to chemotherapy was significantly higher in the high HOTAIR expression group than in the low expression group. Kaplan–Meier survival analysis indicated that high HOTAIR expression was associated with poor overall survival (OS) and recurrence-free survival (RFS) in CRC patients, and Cox regression univariate/multivariate analysis showed that HOTAIR expression level maintained its significance as independent prognostic factors for OS of CRC patients receiving 5FU treatment.

Conclusion Our integrated approach demonstrated for the first time that HOTAIR contributes to CRC tumorigenesis and 5FU resistance through downregulation of miR-218 and activation of NF-κB signaling. This lncRNA directly recruits EZH2 and suppresses miR-218 by binding to its promoter, which provides a mechanistic foundation for the aberrant VOPP1 activation in CRC. This pro-resistant role of HOTAIR was further validated in an independent set of CRC patients who received standard 5FU treatment. Thus, HOTAIR may be a novel prognostic biomarker and therapeutic target in CRC patients. Suppression of HOTAIR could be a future direction for enhancing chemosensitivity to 5FU-based chemotherapy regimens.

PU-0142

MicroRNA-218 is a prognostic indicator in colorectal cancer and enhances 5-fluorouracil-induced cytotoxicity through suppressing BIRC5

Peilong Li、Wang Chuanxin
The Second Hospital of Shandong University

Objective One major reason for the failure of advanced colorectal cancer (CRC) treatment is the resistance to fluoropyrimidine(FU)-based chemotherapy. The enhanced ability of tumor cells to undergo anti-apoptosis process is the main contributor to drug resistance. Various reports showed that ectopic expression and function of miRNAs play key roles to mediate apoptosis by primarily down-regulating protein expression at the post-transcriptional level. To further explore

the possible mechanisms and promote chemosensitivity of CRC treatment, we evaluated the prognostic effect of miR-218 in patients received 5-FU-based treatment and investigated the pro-apoptotic role of miR-218.
Methods Primary tumor specimens and adjacent non-tumor sites were used to determine the miR-218 expression distribution and explore the potential prognostic value of miR-218 on the chemoresponse to 5-FU-based treatment in CRC patients. Human CRC cells (HCT116 and HT29) were transfected with precursor miR-218 or negative control followed by assays to investigate the influence of miR-218 on cell apoptosis, cell proliferation and pathways involved in molecular mechanisms of chemoresistance to 5-FU.
Results The expression of miR-218 was significantly decreased in tumour tissues compared with paired normal tissues. Moreover, the CRC tissues in 68.3% (43 of 63) of cases had at least two-fold lower expression of miR-218. In addition, miR-218 expression level was much lower in patients who did not respond to 5FU treatment than those who experienced response to chemotherapy. ROC curve analysis was performed to establish the optimal cut-off value of miR-218 (6×10-3) for distinguishing the responding and non-responding patients. Under these stratification criteria, patients were stratified into high (n = 34) and low (n = 29) miR-218 expression groups. The proportion of patients that responded to chemotherapy was significantly higher in the high miR-218 expression group than in the low miR-218 expression group. Kaplan-Meier survival analysis was performed to further investigate the effect of miR-218 on 5-FU treatment for CRC. The results indicated that high miR-218 expression was associated with long overall survival and progressive-free survival rate.
Up-expression of miR-218 promoted apoptosis, inhibited cell proliferation in CRC cells. The anti-apoptotic gene-BIRC5, was identified as a direct target of miR-218 and the intrinsic apoptotic pathway triggered by miR-218 was through the silence of BIRC5. Gain and loss function assay indicated that miR-218 enhanced 5-FU-induced cytotoxcity and it has a strong synergistic effect with 5-FU on CRC cell growth. More importantly, western blotting showed that miR-218 silenced the 5-FU targeted enzyme, thymidylate synthase (TS).
Conclusion In this study, we demonstrated that high miR-218 predicted positive response to 5-FU-based treatments in CRC patients and discovered a novel mechanism mediated by miR-218 to promote apoptosis and to function synergically with 5-FU to promote chemosensitivity by suppressing TS in CRC. These suggests a unique potential of miR-218 as a tumor suppressor and a novel candidate for developing miR-218-based therapeutic strategies in CRC.

PU-0143

Patients with acephalic spermatozoa syndrome linked to novel TSGA10/PMFBP1 variants have favorable pregnancy outcomes from ICSI

Weina Li [1,2]、Xiaowei Xing[3]、Gang Liu[2,4]
1. Hunan Guangxiu Hi-tech Life Technology Co., Ltd
2. Reproductive and Genetic Hospital of CITIC-Xiangya
3. Center for Medical Experiments, The Third Xiangya Hospital, Central South University
4. The Institute of Reproduction and Stem Cell Engineering,Central South University

Objectives Acephalic spermatozoa syndrome is a rare form of teratozoospermia characterized by headless spermatozoa.Previous studies have found that variants in *SUN5, PMFBP1, TSGA10, BRDT*, and *SPATC1L* are associated with this phenotype.Many researchers have suggested that variants in *TSGA10* without a proximal centriole might influence early embryonic development. Do novel variants in *PMFBP1/TSGA10* influence early embryonic development and pregnancy outcomes?
Methods This retrospective cohort study included twelve infertile men with severe acephalic spermatozoa in China. We performed Computer-assisted sperm analyzer, semen leukocyte detection, Papanicolaou staining, scanning electron microscopy, transmission electron

microscopy, whole-exome sequencing, Sanger sequencing, RT-PCR, immunoblotting, immunofluorescence staining,and analyzed the various phenotypes and ICSI outcomes for each type of variant.
Results We identified 6 heterozygous variants and 4 homozygous variants in *TSGA10/PMFBP1* in 7 patients by whole-exome sequencing. Acephalic spermatozoa defects due to different genetic variations may affect only spermatozoa morphology but do not reduce the chances of fertilization, affect embryo quality at early stages or impair ICSI outcomes.
Conclusion We expanded the mutation spectrum, and patients with *TSGA10/PMFBP1* variations were all expected to have good prognoses with ICSI.

PU-0144

液滴数字 PCR 技术临床应用探讨

陈登奕、崔曦
襄阳市第一人民医院

目的 探讨液滴数字 PCR 技术的研究现状，发掘其临床应用前景。
方法 通过与临床常用基因检测技术比较、讨论 dd-PCR 技术检测的优劣。
结果 Dd-PCR 检测技术极大缩短了时间检测，提高了检测灵敏度，减少交叉污染，机动性更高，摆脱了传统方法对 Ct 值和标准品的依赖。
结论 Dd-PCR 在技术上的优势明显，但缺乏技术人员和临床转化，限制了其应用。

PU-0145

MALAT1 is Associated with Poor Response to Oxaliplatin-Based Chemotherapy in Colorectal Cancer Patients and Promotes Chemoresistance through EZH2/miR-218 pathway

Peilong Li、chuanxin wang
The Second Hospital of Shandong University

Purpose Chemoresistance to oxaliplatin-based therapy has been a key barrier to the efficacy of colorectal cancer (CRC) treatment. One major reason for oxaliplatin chemoresistance in CRC is the acquisition of epithelial-mesenchymal transition (EMT) in cancer cells. The long non-coding RNA MALAT1, is a highly conserved nuclear ncRNA and a key regulator for metastasis development in several cancers. However its role in oxaliplatin-induced metastasis and chemo-resistance is rarely known. In our study, we aim to investigate the prognostic role of MALAT1 in CRC patients receiving oxaliplatin-based therapy, and further explore the potential transcriptional regulation through interaction with EZH2 and miR-218 based on the established HT29 oxaliplatin-resistant cells.
Methods For chemo-response study, 221 serum samples and 48 primary tissues were collected from the patients who received standard Oxaliplatin-based chemotherapy, and 46 serum samples from patients who received standard FOLFOX chemotherapy were collected at Qilu Hospital of Shandong University between 2011 and 2015. RT-qPCR and RT-qPCR-D method previously established by ourselves were used to determine the expression of mRNA expression in primary tissues and serum, respectively. Cell migration and invasion were assessed with Boyden chambers or modified Boyden chambers according to the protocol of the manufacturer. RNA immunoprecipitation (RIP) and Chromatin immunoprecipitation (ChIP) experiments were performed to investigate the potential interaction. Finally, the survival curves of CRC patients

were estimated via the Kaplan–Meier method and the difference in survival curves was estimated using log-rank testing.
Results MALAT1 expression level was much higher in patients who did not respond to treatment than those who experienced response to chemotherapy. We then stratified patients into a low (n=37) and a high (n=16) MALAT1 expressing group with an established cut-off value (0.432) by using a ROC curve analysis. In the validation group containing 168 serum samples of CRC patients, proportion of patients not responding to chemotherapy was significantly higher in the high MALAT1 expressing group than in the low group. The diagnostic sensitivity and specificity were 75.0% (72/96) and 61.1% (44/72). Further more, the Kaplan–Meier survival analysis indicated that high MALAT1 expression was associated with shorter OS and DFS in CRC patients. CRC cell line HT29 that had acquired resistance to oxaliplatin at the clinically relevant concentration of 2 μmol/L (HT29 OxR cells) were built. MALAT1 was significantly increased in HT29 OxR cells and MALAT1 silencing reversed oxaliplatin-induced EMT. Moreover, EZH2 directly interacts with 3'end of MALAT1, which subsequently suppressed the expression of E-cadherin. CRC cells attained increased migration and invasion ability after being treated with oxaliplatin, and this increased migration and invasion ability was partially suppressed by MALAT1 or EZH2 knockdown. Importantly, our results suggest that the interaction between MALAT1 and miRNA-218 has reciprocal effects. The Kaplan-Meier survival analysis showed that patients with low MALAT1 and high miR-218 expression had the longest OS, while the high MALAT1 and low miR-218 group showed the shortest for patients who received standard FOLFOX treatment.
Conclusions In conclusion, the present work has identified that lncRNA MALAT1 was correlated with tumor metastasis and associated with poor response to oxaliplatin-based chemotherapy in CRC patients. MALAT1 mediates oxaliplatin-induced EMT and chemoresistance through EZH2 and interacting with miR-218. Thus, MALAT1 may be a novel functional biomarker and therapeutic target in CRC patients. Suppression of MALAT1 combining with miR-218 over-expression could be a future direction to develop a novel therapeutic strategy to enhance chemosensitivity to FOLFOX chemotherapy regimen.

PU-0146

血浆 EBV DNA 在非高发区人群中对鼻咽癌筛查及其临床应用价值的相关研究

贺巧[1]、李贤兵[1]、李罗娜[1]、黄叶才[2]、周杰[2]、王秋菊[1]、兰美[2]、吴立春[1]、罗皓[1]、张莉[1]、宋晓玉[1]、杨牧[3]、王东生[1]
1. 四川省肿瘤医院检验科
2. 四川省肿瘤医院放疗科
3. 四川省肿瘤医院基础研究部

目的 研究血浆 EBV DNA 检测在非高发区人群中对鼻咽癌筛查及其临床应用价值。
方法 采用荧光定量 PCR 法检测 2015-2020 年就诊于四川省肿瘤医院的 1153 例初治鼻咽癌患者治疗前血浆 EBV DNA 及 244 例性别年龄相匹配的健康正常人 EBV DNA，用 ROC 曲线分析 EBV DNA 对鼻咽癌诊断敏感性及特异性，再进一步比较不同临床分期和地域患者血浆中 EBV DNA 拷贝数分布特征。
结果 以试剂盒推荐 400copies/ml 作为临界值，初治鼻咽癌与正常健康对照相比较，血浆 EBV DNA 明显增高，诊断的敏感度是 40.85%,特异性是 100%，曲线下面积：0.704。将检测结果低于 400copies/ml 伴有 S 型扩增者根据实际扩增值作为病毒载量，重新计算敏感性及特异性分别为 82.0%和 99.2%，曲线下面积为 0.909。TNM 及临床分期越靠后，血浆 EBV DNA 阳性检出率逐渐升高。
结论 在鼻咽癌非高发区，血浆 EBV DNA 以试剂盒推荐 400copies/ml 为临界值，对鼻咽癌诊断的敏感性仅为 40.85%，临床应用价值受限，应进一步优化检出限，在保证诊断特异性的基础上提高诊断敏感性，提高临床应用价值。

PU-0147

不同新冠核酸检测试剂的结果比对分析

朱艳
西安金域医学检验所有限公司

目的 分析不同品牌新冠核酸检测试剂的检测性能，以评估其新冠核酸检测的应用价值。
方法 本实验室将 8 例广州邦德盛新冠定值质控物 S2（批号 2021004，浓度均值为 1.93E+04 copies/ml）稀释 10 倍至 1.93E+03copies/ml，使用深圳亚能新冠磁珠提取试剂（MNP202101036 批）提取核酸，之后分别使用圣湘生物科技股份有限公司（2021015 批）、中山大学达安基因股份有限公司（2020099 批）、上海伯杰医疗科技有限公司（20210102A 批）、北京卓诚惠生生物科技股份有限公司（C20210143 批）、中山大学达安基因股份有限公司（2021018 批-快检试剂）进行扩增，对 5 套扩增结果进行统计分析。
结果 湖南圣湘新冠核酸检测试剂 ORF 基因 Ct 值均值、SD、CV 分别为 32.04、0.44、1.37%，N 基因 Ct 值均值、SD、CV 分别为 32.04、0.35、1.08%；
中山大学达安新冠核酸检测试剂 ORF 基因 Ct 值均值、SD、CV 分别为 32.07 、0.42 、1.30%，N 基因 Ct 值均值、SD、CV 分别为 35.32 、0.56、1.58%；
上海伯杰新冠核酸检测试剂 ORF 基因 Ct 值均值、SD、CV 分别为 33.56 、0.49 、1.45%，N 基因 Ct 值均值、SD、CV 分别为 34.27 、0.44、1.29%；
北京卓诚惠生新冠核酸检测试剂 ORF 基因 Ct 值均值、SD、CV 分别为 33.39、0.46、1.39%，N 基因 Ct 值均值、SD、CV 分别为 33.41、0.37、1.12%；
中山大学达安新冠核酸快检试剂 ORF 基因 Ct 值均值、SD、CV 分别为 25.54、0.42、1.64%，N 基因 Ct 值均值、SD、CV 分别为 24.52、0.39、1.60%。
结论 5 种新冠核酸检测试剂品牌——湖南圣湘、中山大学达安、上海伯杰、北京卓诚惠生、中山大学达安快检，检测结果 CV 相近，且均≤5%，提示该试剂性能均较为稳定，可同时用于临床新冠核酸的检测。

PU-0148

siRNA 靶向抑制 STAT 对人胃癌细胞增殖的影响

童书青
山东第一医科大学附属省立医院

目的 胃癌是我国最常见的恶性肿瘤之一，其发生是由多基因共同作用的多步骤、多阶段的复杂过程，其中信号转导子和转录激活子(Signal transducers and- activators-of transcription，STATs)信号通路在胃癌的发生中发挥着重要作用。
本研究构建针对 STAT 的小干扰 RNA（small interfering RNA,siRNA）表达载体 STAT-siRNA，研究 siRNA 干扰 STAT 基因表达后对人胃癌细胞株细胞增殖的影响。
方法 1. 设计并合成两个 STAT-siRNA 片段，经脂质体介导分别转染胃癌细胞株。
2. RT-PCR 和 Western blot 检测转染后胃癌细胞株 STAT mRNA 和蛋白的表达。
3. MTT 法检测 STAT-siRNA 对细胞增殖作用的影响。
结果 1. 酶切鉴定、紫外分光光度计检测及测序鉴定均证实 STAT-siRNA1 和 STAT-siRNA2 表达载体构建成功。
2. RT-PCR 和 Western blot 结果显示，转染后细胞中 STAT mRNA 和蛋白的表达量均下降，与空白对照组及 si-NC 转染对照组相比，差异均具有统计学意义（P<0.05）。
3. MTT 结果显示，与 si-NC 转染对照组相比，转染 STAT-siRNA 后，细胞的增殖能力明显下降。
结论 1. 本研究构建的 STAT-siRNA 表达载体可有效抑制 STAT 在胃癌细胞株中的表达。
2. siRNA 干扰沉默 STAT 在胃癌细胞中的表达后可抑制胃癌细胞的增殖。

PU-0149

粪便 SDC2 甲基化检测在大肠癌的临床筛查中的应用价值

刘艳枚、彭蕾、陈晨、周鹏
清远市人民医院

目的 检测肠癌高危人群的粪便脱落细胞中 SDC2 的甲基化表达，为大肠癌早期诊断寻找一种非侵入性、检测性能良好的新型筛查方法。
方法 收集受检者粪便样本，用磁珠捕获法提取 DNA 片段，亚硫酸盐转化未被甲基化的基因片段，采用荧光定量甲基化特异性聚合酶链反应（qMSP）分析 SDC2 基因甲基化水平，根据 Ct 值判定 SDC2 基因甲基化程度，随访并结合结肠镜或 Ct 影像检查，有肠道病变者取组织病理活检。
结果 11283 例受检者中 SDC2 基因甲基化阳性 860 例（7.62%），阴性 10423 例（92.38%）。分析年龄≥50 岁的高危人群，最终获得 667 例阳性、1146 例阴性病例的完整随访资料，阳性受检者中肠癌 160 例，进展期腺瘤 51 例，SDC2 甲基化筛查肠癌和进展期腺瘤的阳性预测值达到 44.23%。阳性受检者的肠道病变检出率远高于阴性受检者。按照肠道病变情况分组，肠癌组的 SDC2 甲基化水平显著高于腺瘤组、息肉组和正常组，且有统计学意义。192 例诊断肠癌的阳性受检者中，不同性别、肿瘤大小、生长部位及分化程度的肠癌患者的 SDC2 甲基化水平皆有统计学显著差异，其中不同年龄段结直肠癌患者有显著差异；根据年龄分组，<68 年龄段和≥68 年龄段的男性肠癌患者的检出率均高于女性，其中≥68 岁年龄组中男性肠癌检出率高出女性将近一倍。
结论 SDC2 基因甲基化检测诊断大肠癌有高的准确性，该检测手段有望在肠癌筛查中发挥重要作用。随着病程延长，病变组织的病理性质逐渐向肿瘤进展，治疗难度逐步加大，因此，筛查有助于降低大肠癌的发病率，同时通过提高大肠癌早期发现比例而降低大肠癌死亡率。

PU-0150

炎性巨噬细胞介导的细胞互作加剧新冠肺炎 T 细胞耗竭、抑制细胞免疫的潜在机制研究

张泉
湖北省中西医结合医院

2.2 单细胞 RNA 转录组测序数据收集及分析
2020 年 6 月 Liao et al. (深圳市第三人民医院)等研究人员收集了 6 例新冠肺炎患者肺泡灌洗液，通过单细胞 RNA 测序在国际顶级医学杂志《Nature Medicine》上发表了题为“Single-cell landscape of bronchoalveolar immune cells in patients with COVID-19”的论文[1]，并公开了测序数据。我们下载，整理，清洗的该单细胞测序数据，通过下游分析探索重症新冠肺炎患者机体抗病毒免疫失衡的潜在因素。
结果 3.1 本研究纳入病例的重症组外周血 WBC、BUN、AST、D-dimer 等指标明显高于轻症组，提示新冠肺炎重症患者存在不同程度的多器官功能损伤。值得注意的是，依据上述指标建立的 logistic 回归模型，其诊断效能与 CD4+T、CD8+T 流式细胞计数呈正相关，提示新冠肺炎重症病例效应 T 细胞计数下降是疾病急性进展的重要因素。上述结果与同行已发表论文的结论一致[2]。
3.2 通过预处理单细胞测序数据，我们获得 16681 细胞，19231 个基因的转录组表达谱，其中正常对照组、轻症及重症组分别为 5723，3875 和 3733 个细胞。
3.3 细胞异质性、拟时序及细胞通讯分析。重症组巨噬细胞，单核（DC 细胞）的丰度明显高于轻症及正常对照组，而 T 细胞丰度则正好相反。此外巨噬细胞亚群的代谢活性也呈现出明显差异，TREM 基因高表达的一群巨噬细胞在时序分析的过度期占比很高，特别是在缺氧环境下该细胞亚群代谢活性也随之波动，提示该群细胞有可能是轻症患者向重症或者好转期过度的重要节点。最后，

构建细胞互作网络，我们发现 TREM 高表达的巨噬细胞释放 TGFβ，激活 CD8+T 细胞免疫抑制信号，诱导 CD8+T 细胞耗竭，抑制了该群细胞的抗病毒功能。
结论 T 细胞耗竭是新冠肺炎重症患者的重要临床特征，其背后的免疫调控机制极其复杂。高表达 TREM 的炎性巨噬细胞通过释放 TGFβ, 激活 T 细胞抑制信号，诱导 T 细胞耗竭、抑制细胞免疫是本研究主要亮点，为临床管理新冠肺炎提供了新的靶点。

PU-0151

重组酶聚合酶扩增技术用于新型冠状病毒的检测

尚美云、李若煦、苏宁、孙献歌、李博文、鲁卫平、黄庆
陆军特色医学中心（大坪医院）

目的 新型冠状病毒（severe acute respiratory syndrome coronavirus 2，SARS-CoV-2）的爆发给全球经济和健康造成了巨大损失。尽管近几个月来我国疫情防控一直处于一个平稳阶段，但仍有多起城市小规模爆发的事件发生，因此早期诊断对控制疫情发展意义重大。
方法 为了更好地监控采样过程的有效性，本研究应用重组酶聚合酶扩增技术（recombinase polymerase amplification，RPA）同时检测 SARS-CoV-2 的 ORF1ab 基因和人 ACTB 基因，然后使用假病毒对建立的双重检测体系进行确认以及灵敏度评估；使用一系列冠状病毒对其进行特异性评价；为进一步减少测试费用，低至 10μL 的单靶标反应体系被进一步测试。检测结果同时与荧光定量 PCR 比较。
结果 建立了双重 RPA 反应体系，其检测限为 100 拷贝/反应，特异性实验结果表明其他冠状病毒检测结果均为阴性。42℃条件下，扩增所需时间仅为 20 分钟。对于中高浓度的待测样本，10μL 反应体积的单靶标反应体系在 5 分钟内即可获得阳性信号。
结论 相比与荧光定量 PCR, RPA 实验检测速度更快，且实验操作过程简单，且内参基因的并入可确保检测结果的准确性。此外，小体积 RPA 反应体系的成功扩增可以进一步减少实验所需成本，若进一步结合微流控芯片能实现“单一样本进-多个结果出”的目标，可应用于偏远地区的检测。总之，该反应体系有望用于 SARS-CoV-2 确诊病例的进一步优化以及评估。

PU-0152

Prostate cancer classification using supervised machine learning techniques

Khan Adeel[1]、Tariq Irfan[2]、Li zhiyang[1]
1. Department of Clinical Laboratory, the Affiliated Drum Tower Hospital of Nanjing University Medical School, Nanjing 210008, China
2. Southeast University, Nanjing, China

Background Prostate cancer (PC) is a highly spread cancer among men. Early detection of PC is vital for deciding whether a patient should receive costly and invasive biopsy, that can also lead to many other complications associated with it. It is a very interesting area of research to be able to classify between benign and malignant PC using machine learning techniques, that will be helpful for clinicians in the decision making. Machine learning has revolutionized the avenue of clinical diagnosis of cancer and many other diseases. Currently most research efforts are dedicated to data mining for accuracy of the diagnosis models, with less focus on F-score. F-score is the geometric mean of precision and recall and highly valuable for judging the diagnosis model.
Methods The data was acquired from a public resource Kaggle.com (https://www.kaggle.com/sajidsaifi/prostate-cancer/version/1). Data set include 100 observations and 10 variables (8 numerical variables and 1 categorical variable). The feature selected for

differentiating between benign and malignant PC are Radius, Texture, Perimeter, Area, Smoothness, Compactness, Symmetry and Frontal Dimensions. To take both precision and recall into consideration, we proposed supervised machine learning algorithms; Random Forest (RF), Support vector machine (SVM) and K-nearest neighbor (KNN). To balance the imbalance data, we used Synthetic Minority Oversampling Technique (SMOTE). Then applied RF, SVM and KNN to the balanced data.
Results From the results we observed that the KNN algorithm outperform other algorithm in precision and recall, having a high F-score than the competing algorithms using the same dataset. The F1-score obtained for the KNN (B 0.88 M. 0.93) was higher than that of the SVM (B. 0.88 M. 0.83) and RF (B. 0.83 M. 0.88). KNN is the best suitable classifier for differentiating between benign and malignant PC.
Conclusion From our work it can be concluded that KNN showed superlative abilities for the classification between the benign and malignant PC. We also recommend the application of the KNN classifier on a large dataset, so that ultimate decision about its successful application in clinical setup is being made.

PU-0153

KIF3A 介导 N-cadherin 转运调节非小细胞肺癌侵袭转移的机制研究

杨宜娥
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 本研究旨在运用全基因表达谱技术初步筛选 NSCLC 转移差异表达基因，寻找与 Wnt/Twist 通路相关的转移基因并分析其基因功能，采用 RT-qPCR 技术对目的基因进行相对定量检测与分析，并研究靶基因在 NSCLC 中的功能和作用机制，为非小细胞肺癌的浸润转移机制研究及治疗位点提供新思路。
方法 1、收集 2014 年 4 月至 10 月山东大学齐鲁医院胸外科手术切取的肺癌组织，且经病理证实为原发性非小细胞肺癌。从中选取淋巴结转移组 6 例为实验组，无淋巴结转移组 6 例为对照组。采用 Agilent 人类 4 × 44K 基因表达微阵列 v2，进行全基因组表达谱实验，并进行基因本体论（GO）分析和 Pathway 分析，筛选与 Wnt/Twist 通路相关的转移差异基因并分析其可能参与的生物学过程。2、从上述筛选出的差异基因中挑选出与肿瘤发生发展有密切关系的基因 KIF3A 作为目的基因，采用配对 t 检验检测实时定量 PCR 结果与基因芯片结果是否具有一致性。3、通过实时定量 PCR 检测四株常用肺癌细胞中 KIF3A 的表达丰度，选取 KIF3A 表达丰度高的细胞株，通过划痕实验及 Transwell 迁移实验检测敲减 KIF3A 后细胞增殖、凋亡、侵袭和转移能力的变化。
结果 1、差异基因及 GO 分析、Pathway 分析：根据倍数法筛选出差异基因 11975 个，转移上调基因 5812 个，下调基因 6163 个。2、筛选 Wnt/Twist 通路差异基因：筛选出与 Wnt/Twist 通路相关的 NSCLC 转移差异基因共 34 个，其中上调基因 18 个，下调基因 16 个，涉及细胞周期素基因、蛋白激酶 C 基因、卷曲家族受体基因、转录因子基因等。3、KIF3A 的验证：所选取的差异基因 KIF3A 在淋巴结转移组中较无淋巴结转移组均呈表达上调，且实时定量 PCR 与表达谱芯片的上调倍数对比，二者差别无统计学意义（t=0.4539, P>0.05）。4、Transwell 侵袭、迁移实验显示，KIF3A 的敲除显著抑制了肺癌 H1975 及 H520 细胞的侵袭转移能力（$p < 0.05$）。且 KIF3A 敲除后显著抑制了 H1975 及 H520 细胞的增殖，促进细胞的凋亡。
结论 1、KIF3A 实时定量 PCR 结果与表达谱芯片结果一致，全基因表达谱芯片技术能够高通量筛选出具有研究意义的差异表达基因，与人类肿瘤发生发展密切相关，在肺癌转移中表达水平上调，表明其在肺癌侵袭转移中具有重要研究价值。
2. KIF3A 的敲除抑制肺癌细胞的增殖、侵袭和转移，并促进细胞的凋亡，KIF3A 可被视为非小细胞肺癌新的致癌基因。

PU-0154

子宫内膜癌患者的血清脂质组学分析

程峰
Women's Hospital of Nanjing Medical University, Nanjing Maternity and Child Health Care Hospital

目的 子宫内膜癌（Endometrial carcinoma, EC）是全球女性最常见的恶性肿瘤之一。近年来随着人口老龄化、肥胖以及激素替代疗法的广泛推广，子宫内膜癌发病率逐年上升。然而相对于诊断为子宫内膜癌晚期或分化程度低的患者 20%的死亡率，诊断为早期子宫内膜癌患者的 5 年生存率可高达 95%。因此，早发现、早诊断对于降低子宫内膜癌死亡率具有重要的意义。本研究拟通过对 EC 患者血清进行非靶向脂质组学分析，以期找到早期 EC 的脂质标志物。
方法 收集 EC 患者及健康志愿者血清标本，经脂质提取后通过液相色谱串联质谱技术进行非靶向脂质组学分析，质谱检测数据经归一化、尺度化及数据转换等一系列数据前处理后，采用单变量及多变量相结合的模式选出 VIP(Variable Importance) > 1，FC(Fold Change) > 1.5，P < 0.05 的脂质作为候选的生物标志物。
结果 经质谱检测共得到 600 多种脂质分子，包括胆固醇脂、甘油酯、溶血磷脂酰胆碱、溶血磷脂酰乙醇胺、磷脂酰胆碱、磷脂酰乙醇胺（Phosphatidylethanolamines, PE）、磷脂酰肌醇、鞘磷脂、游离脂肪酸，胆汁酸、氧化脂质等多种脂质。VIP > 1，FC > 1.5，P < 0.05 的脂质有 63 种，而其中 PE 的变化最为显著，占差异脂质总数的 29%，包括 PE(22:6_18:0)，PE(22:6_16:0)，PE(20:5_18:1) ， PE(20:3_18:0) ， PE(20:2_16:0) ， PE(18:2_16:0) ， PE(18:2_14:0) ，PE(18:1_18:1) ， PE(18:1_16:1) ， PE(18:0_22:4) ， PE(18:0_18:2) ， PE(16:1_18:2) ，PE(16:1_16:0)，PE(16:0_22:5)，PE(16:0_22:4)，PE(16:0_20:4)，PE(16:0_20:3)等脂质，这些脂质有望作为 EC 的早期诊断标志物。
结论 EC 患者和健康人血清中脂质谱存在显著差异，而其中变化差异较大的 PE 类脂质有作为 EC 早期诊断标志物的潜力。

PU-0155

胃肠道肿瘤患者的中医体质辨识及 MLH1 基因多态性研究

郭建巍、陈亮、顾景辉、林楠、廖强华、苏霄翔、兰小琴、孙雪平、王琳
北京市第一中西医结合医院

目的 寻找胃肠道肿瘤高危人群的分子靶标及辨识胃肠道肿瘤患者的中医体质类型，为胃肠道肿瘤的中医防控提供理论依据。
方法 分别对 100 例胃肠道肿瘤患者（胃肠道肿瘤组）和 80 例健康人群（健康人群组）通过发放标准化中医体质量表问卷，采用被调查者自填问卷方式，对两组患者进行中医体质辨识，用 Sanger 测序进行错配修复基因 MLH1 SNP 检测。
结果 胃肠道肿瘤的发病率与性别无关，60 岁以上人群罹患胃肠道肿瘤的概率高于 60 岁以下人群。胃肠道肿瘤患者的体质类型与健康人群有明显区别，所有胃肠道肿瘤患者均表现为气虚质（P＜0.000），其他主要的体质类型分别为阳虚质（P＜0.000）、痰湿质（P＜0.000）和湿热质（P＜0.000）。MLH1 基因检测胃癌患者和肠癌患者等位基因 A 的携带率明显高于健康人群（P＜0.01），MLH1-1151T＞A(rs63750447)突变与胃肠道肿瘤的发生具有相关性。
结论 胃肠道肿瘤患者主要表现为气虚为主的混合偏颇体质，大多数患者具有阳虚质、痰湿质和湿热质。MLH1 基因检测胃肠道肿瘤人群中等位基因 A 的携带率显著高于健康人群，MLH1 1151T＞A 突变者为胃肠道肿瘤高危人群。以气虚为主线索，通过中医药调整胃肠道肿瘤高危人群的气、血、痰平衡，是中医防控胃肠道肿瘤发生、发展的一条途径。

PU-0156

载脂蛋白 E（ApoE）基因型检测试剂盒（基因芯片法） 性能验证

李汉华、陈学飞、闵向阳、赵旭鸿、翁文浩
同济大学附属杨浦医院

目的 对载脂蛋白 E（ApoE）基因型检测试剂盒（基因芯片法）进行性能验证。
方法 参照产品行业标准和相关文献，设计实验方法对珠海赛乐奇生物技术股份有限公司《载脂蛋白 E（ApoE）基因型检测试剂盒（基因芯片法）》的特异性、准确性、精密度、重复性等四个方面进行性能验证。
结果 本实验共测序比对 20 例样本。对于特异性符合验证 ε2ε2 型 2 例，符合率 100%。ε2ε3 型 4 例，符合率 100%。ε3ε3 型 6 例，符合率 100%。ε3ε4 型 4 例，符合率 100%。ε4ε4 型 2 例，符合率 100%。ε2ε4 型 2 例，符合率 100%。总符合率 100%。对于精密度重复性验证，对于 6 个基因型别的样本,随机选取 1 个样本,重复 20 次,20 次的实验结果一致,型别正确。对于重复性验证，随机将 1 例已知型别的样本分别重复检测，再重复检测 5 天，每天 3 次，实验结果一致,型别正确。
结论 本次实验检测结果表明，该产品的特异性、重复性符合要求，该方法具有高特异性和准确度，在临床应用中的安全性和有效性均能保证。

PU-0157

Development and Application of Cas13a-based Diagnostic Assay for Neisseria Gonorrhoeae Detection and Identification of Azithromycin Resistance

Hao Luo、Wentao Chen、Heping Zheng
Dermatology Hospital of Southern Medical University

Background Gonorrhea is a common bacterial sexually transmitted infection (STI) in the world, caused by *Neisseria gonorrhoeae*. The prevalence of N. gonorrhoeae has increased rapidly and remains a public health concern. Due to the use and abuse of antibiotics, antimicrobial resistance (AMR) of *N. gonorrhoeae* has emerged to all first-line therapeutic drugs used to date, including to the ceftriaxone-azithromycin combination, currently recommended as first-line therapy. Therefore, there is a need for clinicians to rapidly acquire resistance data for antibiotics, which could help manage rational drug use and further slow the development of drug resistance.
Methods We developed a Cas13a-based assay combained recombinase polymerase amplification (RPA) and CRISPR/Cas13a for *N. gonorrhoeae* detection assay (porA target) and azithromycin resistance identification assay (A2059G and C2611T point mutation in 23S rRNA gene). Firstly, we evaluated the sensitivity and specificity of this method through serial dilutions of dsDNA and a panel of urogenital tract pathogenic bacteria (n=12) and *Neisseria meningitides*. 23 urine samples were performed to validate *N. gonorrhoeae* detection in porA target and compare its capability with Roche Cobas 4800 assay. 24 isolated *N. gonorrhoeae* strains (A2059G, C2611T, wild-type strains) were used to validate this assay in identification of A2059G and C2611T point mutation of azithromycin resistance, besides, the sequencing results were used to confirm our assay. Moreover, we adopted lateral flow for SHERLOCK readout. 27 urethral swabs from patients with urethritis were used for *N. gonorrhoeae* detection and azithromycin-resistance identification to evaluate the capability.
Results In our study, 10 copies per reaction can be achieved in porA detection and C2611T identification, and 100 copies per reaction in A2059G assay, with no cross-reactions. Comparison of Cas13a-based assay (porA target) with Roche Cobas 4800 assay revealed 100% concordance in all urine samples. All tested mutant strains (8 A2059G strains and 8 C2611T strains) were

successfully distinguished by our assay and verified by testing MIC for azithromycin and sequencing the 23S rRNA gene. Lateral flow showed a visible difference between test group and NC group **Results** Finally, 62.96% (17/27) strains of swab samples were detected with no mutant strains and confirmed by sequencing.
Conclusion We successfully developed and applied this Cas13a-based assay in *N. gonorrhoeae* which exhibit excellent capability in detection and point mutation identification and we tested a panel of clinical samples and clinical isolates. The novel Cas13a-based assay for rapid *N. gonorrhoeae* detection combined with azithromycin drug resistance testing is a promising assay for application in clinical practice.

PU-0158

Resistance trends of Klebsiella pneumoniae causing Urinary Tract Infections in Chongqing, 2011-2019

Yanhui Dingyanhui
the First Affiliated Hospital of Chongqing Medical University, Chongqing, China

Purpose To analyze the characteristics and trends of drug resistance for Klebsiella pneumoniae (K. pneumoniae), isolated from urinary tract infections (UTIs), to common antibiotics used in clinics.
Methods This retrospective study was conducted at a teaching hospital in Chongqing from 2011 to 2019. Laboratory data of isolated bacteria were collected and analyzed statistically.
Results Among the 17966 non-repetitive strains isolated from the urine sample, a total of 1543 K. pneumoniae isolates were identified, with an isolation frequency secondary only to Escherichia coli (E. coli) and there was a peak in the K. pneumoniae isolates in 2013. During the period, the rate of extended-spectrum beta-lactamase (ESBL)-producing K. pneumoniae fell from 48.4% in 2011 to 32.9% in 2019，but a marked jump of resistance was seen in carbapenems from 2.2% to 18.0%. The peak of carbapenem resistance rate (22.6%) to K. pneumoniae was observed in 2017 along with a low ESBL-producing rate (30.9%). Piperacillin/tazobactam and cefepime resistance levels went up from 4.4% to 25.7% and from 18.2% to 30.5%, respectively. Its resistance rate to carbapenems and amikacin gradually grew up, showing their peaks in 2017, and then dropped year by year. Ceftazidime and Aztreonam resistance levels were relatively stable, fluctuating between 21.8% and 35.6%, 32.2% and 39.4% respectively.
Conclusion There is a significant upward trendency in carbapenem resistance rate and a downward trendency in ESBL-production rate in K. pneumoniae isolates from UTIs, but the resistance rate has gradually increased year by year and continuous surveillance is necessary in the future.

PU-0159

HLA-B27 基因亚型在葡萄膜炎患者中的分布情况

丁艳辉
重庆医科大学附属第一医院

目的 探讨葡萄膜炎患者 HLA-B27 基因亚型的分布情况。
方法 收集并分析 265 例葡萄膜炎患者 HLA-B27 基因的检查结果及发病年龄、性别等相关临床资料。
结果 265 例葡萄膜炎患者中 HLA-B27 阳性者 148 例（55.8%），其中 HLA-B*2704 亚型 92 例（62.2%），HLA-B*2705/07 亚型 54 例（36.4%）；葡萄膜炎患者 HLA-B27 基因阳性者达半数以上，其中 HLA-B*2704 占比约为 HLA-B*2705/07 的 1.7 倍，且在各年龄段均表现为优势亚型；不同亚型的葡萄膜炎患者在性别构成及发病年龄方面未表现出差异。

结论 葡萄膜炎患者的 HLA-B27 基因阳性率达 50%以上，且 HLA-B*2704 亚型在各年龄段均表现为优势亚型。

PU-0160

环状 RNA circMVP 通过 miR-136-5p 靶向 CBX4 促进胃癌恶性进展

沈蕾
南通大学附属医院

目的 检测 circMVP 在胃癌细胞及胃癌（GC）患者组织、血清中的相对表达水平；体内、体外研究 circMVP 对 GC 细胞增殖、凋亡以及迁移、侵袭能力的影响；探讨 circMVP 调控 GC 发生发展的具体机制。
方法 构建实时荧光定量 PCR（qRT-PCR）法以检测 circMVP 在胃癌细胞及胃癌（GC）患者组织、血清中的相对表达水平；核浆分离试验及荧光原位杂交（FISH）检测 circMVP 在 GC 细胞中的定位；通过 CCK-8 法、克隆形成、EDU 实验检测 circMVP 对 GC 细胞增殖的影响；通过 transwell、划痕等试验检测 circMVP 对 GC 细胞迁移和侵袭的影响；通过流式细胞术检测 circMVP 对 GC 细胞周期和凋亡的影响；慢病毒干扰载体转染 MKN-45 细胞建立稳转株，构建裸鼠移植瘤模型，生长曲线、免疫组化等验证 circMVP 在体内对肿瘤组织生长的影响；在线数据库预测与 circMVP 结合的 miRNA 及其靶基因，双荧光素酶报告实验验证其结合。
结果 qRT-PCR 检测发现 circMVP 在 GC 细胞中的表达高于正常胃黏膜上皮细胞，在 GC 组织中的表达高于癌旁组织，在 GC 患者血清中的表达高于健康体检者。
FISH 和核浆分离实验显示 circMVP 多数定位于 GC 细胞浆中。细胞功能学实验证实，在 AGS 和 MKN-45 细胞中干扰 circMVP 后，GC 细胞增殖速度减慢（P<0.05），迁移和侵袭能力下降（P<0.05），凋亡细胞增加（P<0.05），S 期细胞减少，但差异无统计学意义（P<0.05）。在 BGC-823 细胞中过表达 circMVP 后，GC 细胞增殖速度增强（P<0.05），迁移和侵袭能力增强（P<0.05），凋亡细胞减少（P<0.05）。体内裸鼠移植瘤模型证实，circMVP 敲除后，细胞成瘤能力显著下降，肿瘤生长速率减慢。双荧光素酶报告实验证实 circMVP 与 miR-136-5p 相结合，miR-136-5p 与 CBX4 有结合。
结论 circMVP 在 GC 细胞、组织和血清中均高表达，主要定位于胞浆。干扰 circMVP 表达后，抑制细胞的增殖、迁移和侵袭，促进肿瘤细胞凋亡。过表达 circMVP 表达后，促进肿瘤细胞的增殖、迁移和侵袭，抑制细胞凋亡发生。机制研究表明 circMVP 可能通过海绵 miR-136-5p 靶向 CBX4 促进 GC 的恶性进展。

PU-0161

基于 PCR-RDB 方法对湖北地区地中海贫血基因类型分析

邓鹏、申建维、商震、李幸幸、胡庆
武汉千麦医学检验实验室有限公司

目的 了解湖北地区地中海贫血基因类型及分布特征。
方法 对 2020 年 10 月至 2021 年 5 月武汉千麦医学检验室收集的 941 例临床标本，采用反向杂交法（PCR-RDB）进行常规的 α、β-地中海贫血检测与分析。
结果 941 例临床中确定有 114 例携带地中海贫血基因，阳性率为 12.11%（114 例/941 例）。其中，携带 α-地中海贫血基因型 60 例（缺失型 55 例、突变型 5 例），占比 6.38%；携带 β-地中海贫血基因型 55 例，占比 5.74%；α-地中海贫血复合 β-地中海贫血基因型 3 例，占比 0.32%。在 114 例地中海贫血基因型中，最常见的为-α 3.7 基因型，占比为 22.81%（26 例/114 例），其次分别为--

SEA 基因型（19.30%，22 例/114 例）、IVS-Ⅱ-654 基因型（18.42%，21 例/114 例）、CD41-42 基因型（14.04%，16 例/114 例），最低为复合型地中海贫血基因型（2.63%，3 例/114 例）。
结论 湖北地区地中海贫血基因突变类型特点为缺失型 α-地中海贫血＞突变型 β-地中海贫血＞突变型 α-地中海贫血＞α-、β-复合型，其中缺失型 α-地中海贫血主要为-α 3.7 基因型，其次为东南亚缺失型（--SEA）基因型；β-地中海贫血等位基因以最常见的为 IVS-Ⅱ-654 型，其次为 CD41-42 型，突变型 α-地中海贫血主要为 αQS；α -地中海贫血检出率较高于 β-地中海贫血检出率。

PU-0162

Hydrogen sulfide contributes to uterine quiescence through inhibition of NLRP3 inflammasome activation by suppressing the TLR4/NF-κB signalling pathway

Zixi Chen
Putuo Hospital, Shanghai University of Traditional Chinese Medicine

Background The NLRP3 inflammasome plays a critical role in inflammatory responses in various diseases. Our previous study showed that NLRP3 expression was significantly increased in human pregnancy tissue during term labour. Therefore, we explored whether NLRP3 participated in inflammatory responses of preterm and term labour and whether this process could be relieved by H2S, one anti-inflammatory gasotransmitter.
Methods Human myometrium was obtained from non-labouring and labouring women. Mouse myometrium was obtained from LPS-induced infectious preterm labour. Uterine smooth muscle cells were isolated from non-labouring women's myometrial tissues, transfected with siRNA, and treated cells with IL-1β, H2S donor NaHS, NF-κB inhibitor BAY 11-7082 and TLR4 inhibitorTAK-242. The NLRP3 inflammasome, CSE, CBS, TLR4, uterine contraction-associated proteins (CAPs), NF-κB activation and inflammatory cytokine expression were assessed by western blotting and RT-PCR.
Results The NLRP3 inflammasome, TLR4 and activated NF-κB expression were upregulated in human term labour, mouse preterm labour and human uterine smooth muscle cells treated with IL-1β. NLRP3 levels were negatively correlated with CSE and CBS expression. Treatment with the H2S donor NaHS delayed LPS-induced preterm birth in mice and inhibited NLRP3 inflammasome activation. In siNLRP3-transfected cells, there was a significant decrease in the expression of CAPs and inflammatory cytokines compared with IL-1β stimulation. In addition, treatment with the H2S donor NaHS inhibited NLRP3 inflammasome activation, reduced the expression of uterine contraction-associated proteins and inflammatory cytokines and reduced the activation of TLR4 and NF-κB compared with stimulation with IL-1β in human uterine smooth muscle cells. Furthermore, treatment of uterine smooth muscle cells with BAY 11-7082 and TAK-242 found that NLRP3 activation was regulated by the TLR4 and NF-κB pathways.
Conclusions H2S suppresses CAP expression and the inflammatory response and contributes to uterine quiescence by inhibiting the TLR4/NF-κB signalling pathway and downstream NLRP3 inflammasome activation. Thus, H2S contributes to uterine quiescence through inhibition of NLRP3 inflammasome activation by suppressing the TLR4/NF-κB signalling pathway.

PU-0163

Overexpression of small nucleolar RNA SNORD1C is associated with unfavorable outcome in colorectal cancer

Yonghui Liu[1]、Jing Sun[1]、Chengwen Zhao[1]、Minqi Gu[1]、Guihua Wang[1,2]、Shaoqing Ju[1]、Cheng Qian[1]、Xudong Wang[1,2]
1. Affiliated Hospital of Nantong University
2. 南通大学公共卫生学院

Aim This research aims to identify serum SNORD1C as a new biomarker for the diagnosis of colorectal cancer (CRC) and evaluate its clinical value.
Methods We detected the expression of small nucleolar RNA SNORD1C in the serum of CRC patients by quantitative real-time polymerase chain reaction (qRT-PCR). The receiver operating characteristic (ROC) curves were estimated, and the area under the ROC curves (AUCs) was calculated. GO and KEGG analysis of co-expressed genes was performed by DAVID, and visualized by R language.
Results The results showed that the expression level of SNORD1C in patients with CRC was significantly higher than that in normal people and patients with benign colorectal diseases ($P < 0.05$). The over-expression of serum SNORD1C was related to poor tissue differentiation and high CEA level ($P < 0.05$). Under ROC curves analysis, SNORD1C serum expression combined with CEA in blood had better prediction and judgment for the diagnosis of CRC (AUC = 0.838) compared with SNORD1C (AUC = 0.748) or CEA (AUC = 0.796) alone.
Conclusion Serum SNORD1C may be a novel and feasible biomarker for the diagnosis of CRC. High expression of SNORD1C was closely related to the patients' prognosis, especially unfavorable outcome in CRC.

PU-0164

基于 HIV-1 CRF01_AE 毒株进化规律的分子传播网络分析技术优化

柳明辰、赵彬、安明晖、韩晓旭
中国医科大学附属第一医院

目的 近年来我国 HIV 疫情仍未得到有效控制，分子传播网络分析是新兴的分子流行病研究方法，其应用广泛有助于精准干预提高成本效益。基因距离阈值是构建分子传播网络的关键，以往研究均沿用国外对 B 亚型进化规律的研究结果。与欧美地区广泛流行单一 B 亚型不同，我国多 HIV 亚型并存，CRF01_AE 为本地主要流行株，目前研究主要针对 B 亚型 HIV，缺乏对 CRF01_AE 的 HIV-1 进化规律的系统研究。
方法 收集 2000-2017 年间于中国医科大学附属第一医院艾滋病研究所的 HIV 急性期队列 CRF01_AE 单毒株感染者和"传播对"队列中 CRF01_AE 受者为单毒株感染者的真实传播对。应用深度测序方法获得 pol 的 RT 区部分序列，应用 TN93 模型计算个体内及个体间基因距离，计算进化速率。
结果 所有 CRF01_AE 亚型单毒株感染者个体内平均进化不超过 0.015s/s；所有"传播对"供受者间基因距离均小于 0.3s/s。感染≤1 年、1-2 年、2-3 年和 3-6 年的基因分化程度分别为 0.003±0.003s/s、0.004±0.002s/s、0.007±0.002s/s 和 0.009±0.004s/s；受者感染 1 年内、1-2 年、2-3 年和 3 年以上平均的基因距离为 0.008±0.006 s/s、0.012±0.007 s/s、0.009±0.003 s/s、0.015±0.009 s/s。所有 CRF01_AE 单毒株感染者平均的进化速率为 0.0024±0.001s/s/y。基于最高网络分辨率原则和个体内进化及"传播对"供受者间基因距离分布曲线显示最佳阈值范围为 0.005-0.007，最终我们设定阈值为 0.005。

结论 基于 CRF01_AE 毒株在个体内及个体间进化规律，为了解病毒在人群中的传播规律以及构建分子传播网络的阈值的设定提供了理论依据。为我国开展 HIV 分子传播网络以及基于网络干预等地区性研究提供理论基础和实践范例。

PU-0165

重庆地区冠心病患者 cyp2c19 基因多态性研究

唐翌姝
重庆医科大学附属第一医院

目的 探讨重庆地区冠心病患者药物代谢酶 cyp2c19 基因多态性的分布情况。
方法 采用基因芯片方法对 179 例服用氯吡格雷的冠心病患者进行基因分型，分析基因型和代谢表型的分布。
结果 共检测到 6 种 cyp2c19 基因型和 3 种代谢型。广泛代谢物纯合表型频率为 32.96% (59/179)，广泛代谢物杂合表型频率为 53.07% (95/179)，低代谢物表型频率为 13.96% (25/179)。
结论 重庆地区冠心病患者 cyp2c9 基因存在遗传多态性，等位基因频率和代谢表型频率的分布与国内其他地区相似。

PU-0166

噬菌体随机肽库淘选幽门螺杆菌 ArsS 酸信号感应区拮抗短肽和活性评价

向瑜
重庆医科大学附属第一医院

目的 幽门螺杆菌(Helicobacter pylori, H.pylori)是慢性胃炎，胃溃疡，胃癌等疾病的重要病因，目前尚无理想的防治措施。H.pylori 通过感知并适应高酸性环境在胃内存活，它的双组分信号传导系统(TCSTs)中的 ArsRS 是已知的主要的酸感受器。本研究的目的是获得 H.pylori ArsS 酸感应区的拮抗短肽，通过短肽与感应区结合，封闭 H.pylori 的酸感应信号，阻碍 H.pylori 的酸适应调节反应，使其在胃内高酸性环境中不能存活。
方法 通过 proSite 预测 H.pylori J99 ArsS N 端的酸感应区结构域，以纯化的酸感应区重组蛋白 P-ArsS-A 为诱饵，用 Ph.D7 噬菌体随机肽库淘选能与 P-ArsS-A 特异性结合的短肽。
结果 获得 8 个能与 P-ArsS-A 结合的阳性噬菌体克隆，展示了 5 条短肽序列。经体外 MIC 检测和菌落计数试验验证，P03（MMSYPKH）和 P06（LTPMPNW）均能明显抑制 H.pylori J99 生长（P＜0.050)，P03 对 H.pylori J99 的 MIC 为 8μM，P06 的 MIC＞16μM，P03 的抑菌作用强于 P06。
结论 通过分子对接将 P03 和 P06 与 ArsS- N 端结合，两条短肽共有 TYR25，ASN39,ARG73,GLU74 四个相同的结合位点，而 P03 与 ArsS 还额外形成了较强的氢键连接。

PU-0167

新冠患者病情预测新工具——血浆 DNA 内标法定量技术应用

穆原[1]、陈其告[2]、徐建[1]、林勇平[2]、潘世扬[1]
1. 江苏省人民医院（南京医科大学第一附属医院）
2. 广州医科大学附属第一医院

目的 探讨血浆 DNA 定量能否在新冠患者监测中用于病情进展的预测。
方法 前瞻性纳入广州医科大学附属第一医院 2020 年 3 月收治入院的 COVID-19 确诊患者，按 WHO 新冠指南进行疾病的诊疗管理，并随访至治愈出院，将 6h 时段与其 72h 后的临床资料进行比较，以评估 72h 病情是否进展作为结局变量。偏态资料以中位数（四分位间距）[M (P25，P75)]表示，率的比较采用卡方检验，等级相关采用 Spearman 秩相关分析，多元 logistic 回归用于预测模型的建立，并以 Nomogram 作模型可视化，模型预测性能评价采用非参数 ROC 分析。
结果 17 名患者中，男性 11 例，女性 6 例，年龄 27~83 岁[57 (50-72)岁]，在纳入研究时 10 例入住 ICU，7 例行气管插管，2 例行 ECMO 治疗。重型/危重型患者 APACHE II 评分、SOFA 评分及血浆 DNA 均显著高于轻型/普通型患者。血浆 DNA 水平与临床评分间相关性低（APACHE II：ρ=0.441；SOFA：ρ=0.512）。共收集到 174 个病情进展结局事件，按结局有无恶化，随机分为建模组与验证组，全部建模变量在两组间差异均无统计学意义。经多元 logistic 回归分析，血浆 DNA 与 D-二聚体与 72h 病情恶化相关。ROC 分析显示血浆 DNA 预测性能（AUC=0.883）优于 APACHE II（AUC=0.715）、SOFA（AUC=0.708）及 D-二聚体（AUC=0.684）。
结论 血浆 DNA 定量在新冠患者监测中，可于病情恶化前 72h 进行预警。

PU-0168

Highly reproducible and sensitive electrochemiluminescence biosensor for HPV detection based on bovine serum albumin carrier platform and hyperbranched rolling circle amplification

Yinghao He[1]、Yinhuan Liu[2]、Lingjun Cheng[1]、Yuanyuan Yang[1]、Bin Qiu[3]、Longhua Guo[3]、Yan Wang[4]、Zhenyu Lin[3]、Guolin Hong[1]
1. The First Affiliated Hospital of Xiamen University
2. 厦门大学附属福州第二医院
3. 福州大学
4. 厦门大学附属心血管病医院

Most DNA-based electrochemiluminescence (ECL) biosensors are established through the self-assembly of thiolated single-stranded DNA (ssDNA) probes on the Au electrode surface. Due to this random assembly process, a significant discrepancy among the distribution of modified DNA film on different electrodes, which greatly affects the reproducibility of biosensor. In this study, a porous bovine serum albumin (BSA) layer was first modified on the electrode surface, which can improve the position distribution and spatial orientation of the self-assembly ssDNA probe. It was then coupled with hyperbranched rolling circle amplification (HRCA) to develop the high-reproducibility-and-sensitivity ECL biosensor for human papillomavirus 16 (HPV16) E6 and E7 oncogenes detection. In the presence of the target DNA, the surface of the electrode accumulates abundant amplified products through reaction, which contain double-stranded DNA (dsDNA) fragments of different lengths, followed by plentiful dichlorotris (1,10-phenanthroline) ruthenium (II) hydrate (Ru(phen)3 2+, acting as an ECL indicator) insertion into grooves of dsDNA fragments, and a strong signal can be detected. There is a linear relationship between the signal and the target concentration range from 10 fM to 15 pM, and the detection limit is 7.6 fM

(S/N= 3). After the BSA modification step, the relative standard deviation was reduced from 9.20% to 3.96%, thereby achieving good reproducibility. The proposed ECL strategy provides a new method for constructing high-reproducibility-and-sensitivity ECL biosensors.

PU-0169

FISH 技术在乳腺癌 HER-2 基因扩增检测中的应用

魏琦、王永超、刘秀生、许雪
合肥金域医学检验实验室有限公司

目的 乳腺癌在女性恶性肿瘤发病率居第一位，人表皮生长因子受体 2（HER-2）基因是乳腺癌的重要分子标志物和治疗靶点。本研究主要探讨荧光原位杂交技术（FISH）在乳腺癌 HER-2 基因检测中的应用及临床意义。
方法 选取近半年合作医院送到本实验室进行乳腺癌 HER-2 基因扩增检测的 427 个标本为研究对象，这些标本原单位 HER-2 免疫组化结果均为 2+。与病理室合作，分别采用免疫组化技术（IHC）和 FISH 对蜡块标本中的 HER-2 蛋白表达以及 HER-2 基因扩增状态进行分析，由同一个病理医生判读 FISH、IHC 结果。
结果 FISH 检测 HER-2 基因扩增阳性病例共 141 例（33%）；IHC 检测 HER-2 蛋白表达（0-1+）共 37 例、（2+）共 303 例、（3+）共 87 例，对应的 FISH 结果中 HER-2 基因扩增阳性病例分别为 0 例、54 例、87 例，两者检测结果的阳性符合率分别为 100%、17.8%、100%；结果显示，除 IHC（2+）外，IHC 检测与 FISH 检测有较好的一致性。IHC 检测中 HER-2（0-1+）、（3+）的结果判断与原单位存在不一致，可能与标本固定不及时、抗体浓度不同有关。
结论 采用 FISH 法对乳腺癌患者进行 HER-2 基因扩增检测具有较高价值，临床实践中可以根据实际情况，结果 IHC 综合使用，以便指导临床治疗。

PU-0170

非小细胞肺癌 EGFR 基因突变状态分析及临床意义

魏琦、李志强
合肥金域医学检验实验室有限公司

目的 肺癌是严重危害人类健康的恶性肿瘤之一，其中非小细胞肺癌（NSCLC）占 80%-85%，近年来表皮生长因子受体（EGFR）为靶点的分子靶向治疗已成为 NSCLC 的一种新的治疗方案。本文旨在回顾性分析 NSCLC EGFR 基因外显子突变，探讨 EGFR 突变与 NSCLC 临床病理特征及其临床意义。
方法 收集近期本实验室 NSCLC 病理标本 98 例，利用突变扩增阻滞系统（ARMS-PCR）方法检测 EGFR 基因外显子突变状态，回顾性分析其临床病理特征及临床意义。
结果 受检 98 例标本中，EGFR 基因总突变率为 40.81%（40/98）。其中 18 号外显子突变率 9.52%（4/42），19 号外显子突变率占 42.85%（18/42），20 号外显子突变率占 2.38%（1/42），21 号外显子突变率 38.09%（16/42）,1 例患者为 EGFR 基因 19、21 外显子双突变。肺腺癌患者突变率为 51.19%，明显高于非腺癌 NSCLC 突变率 8.08%，差异有统计学意义（P＜0.05）；女性患者中的突变率为 55.38%，高于男性患者 30.18%；无吸烟患者突变率 50.07% ，高于有吸烟史患者突变率 24.59%，差异有统计学意义（P＜0.05）。
结论 NSCLC 患者中 EGFR 突变以 19 号外显子缺失突变和 21 号外显子 L858R 突变为主；EGFR 突变常见于女性、肺腺癌、无吸烟使的患者。

PU-0171

甲状腺乳头状癌差异表达 lnc RNA 的筛选与分析

杨敏、黄国虹、王昌敏
新疆维吾尔自治区人民医院

目的 探讨 lnc RNA 在甲状腺乳头状癌发生过程中的潜在功能，为甲状腺乳头状癌的发病机制研究、诊断及治疗提供新的理论依据。
方法 按照纳入标准及排除标准收集 5 例甲状腺乳头状癌患者癌组织及癌旁组织标本，通过高通量测序技术完成 lnc RNA 表达谱的检测，并对表达差异大于 5 倍以上的 lnc RNAs 进行靶基因预测，GO 富集分析及 KEGG 通路分析。
结果 在甲状腺乳头状癌组织及癌旁组织中存在大量差异表达的 lnc RNAs 及 mRNAs，本研究共筛选出差异表达 5 倍以上的 lnc RNAs 2444 个，其中上调 1707 个，下调 737 个；共筛选出差异表达 5 倍以上的 mRNAs 3983 个，其中上调 2228 个，下调 1755 个。对这些差异表达的 lnc RNAs 进行靶基因预测，发现有 195 个差异表达上调的 lnc RNAs 及 100 个差异表达下调的 lnc RNAs 具有靶基因。GO 富集分析结果显示与差异上调 lnc RNAs 相关性最强的功能为 protein serine/threonine kinase activity（蛋白质丝氨酸/苏氨酸激酶活性）；与差异下调 lnc RNAs 相关性最强的功能为 DNA-binding transcription activator activity，RNA polymerase II-specific（DNA 结合转录激活因子活性，RNA 聚合酶 II 特异性）。KEGG 通路分析显示上调信号通路最明显的为 pentose phosphate pathway（磷酸戊糖途径），下调信号通路最明显的为 glycerophospholipid metabolism（甘油磷脂代谢）。
结论 在甲状腺乳头状癌中存在大量差异表达的 lnc RNAs，可能通过某些信号通路参与甲状腺乳头状癌的发生、发展过程，基于上述信号通路可作进一步深入研究。

PU-0172

葡萄糖-6-磷酸脱氢酶基因突变检测试剂的性能验证

杨建林
昆明医科大学第一附属医院

目的 对本实验室应用于临床检测的葡萄糖-6-酸脱氢酶基因突变检测试剂的性能进行验证。
方法 采用 12 个 G6PD 突变型质粒、野生型全血样本，磁珠法提取核酸，多重荧光定量 PCR 标准溶解曲线法扩增，对试剂的符合率、检测限、抗干扰能力、交叉反应进行试验验证。
结果 突变型样本的 Tm 值≥±2，野生型样本的 Tm 值≤±1，Tm 的 CV 均小于≤±10%，试剂符合率达 100%，提取的核酸 DNA 浓度稀释到最低检测限于 1ng/μL，扩增突变型和野生型符合率达 100%。血红蛋白、胆红素、胆固醇、甘油三脂对试剂的检测无干扰；地中海贫血和个 G6PD 的交叉反应相互不影响。
结论 由厦门至善生物公司生产的葡萄糖-6-酸脱氢酶基因突变检测试剂的性能参数符合厂家声明，可以应用于临床检测工作。

PU-0173

Systematic review the prevalence of HIV-1 drug resistance in antiretroviral-naïve and -experienced individuals in Yunnan

Mi Zhang 、cuixian yang
Yunnan Infectious Diseases Hospital

Background Since 2007, the HIV-1 genotypic drug resistance was performed in HAART-failed patients in Yunnan, and the difference of drug resistance rate among different time points is not clear.
Methods We reviewed the HIV-1 drug resistance reports systematically in Yunnan province from the data information management system for the prevention and control of AIDS in CDC information system of China between 2010 and 2012.
Results According to the CDC information system in China, HIV-infected individuals of treated naïve, treated in one year and treated in two years enrolled 88, 448 and 336, respectively. HIV-1 drug resistance was found in five individuals (5.7%, 5/88) in treated naïve individuals. The prevalence of acquired HIV-1 drug resistance in one year and two years were 42.4% (190/448) and 48.5% (163/336) in HAART failure patients (P<0.001). In treat-naive group, V179D (9.1%), K103N (4.5%), M184V (1.1%) and Y181C (1.1%) were most common mutations in RT regions, and in the protease region only L33F (1.1%) was found. In the two HAART failure groups, we found highly significant increases in percentages of patients carrying HIV-1 variants with M184V, T69Ins, K103N or V108I mutations, but no significant increases in percentages of patients carrying HIV-1 with D67N, K70R, K65R, A62V, K101E, V106M, V179D/E, Y181C, G190A, P225H or M230L mutations.
Conclusions The HIV-1 drug resistance occurred when the treatment time extension and the strategies of monitoring HIV treatment and resistance should be enhanced. In addition, the transmitted drug resistance should be given rise to our attention and reinforced to monitor in the further.

PU-0174

布尼亚病毒 RNA 提取方法的优化及临床应用

李雷
南京大学医学院附属鼓楼医院

发热伴血小板减少综合征（severe fever with thrombocytopenia syndrome, SFTS）是由发热伴血小板减少综合征病毒（SFTS virus, SFTSV）引起的新发传染性疾病，2009 年，在中国的中部和东北部最早被报道。截止 2015 年，SFTS 病例在中国 23 个省、日本和韩国被报道。SFTS 主要表现为急性发热、血小板减少及白细胞减少、胃肠道和中枢神经系统症状，重症者可出现多器官功能障碍综合征（Multiple Organ Dysfunction syndrome, MODS）甚至死亡。SFTS 病死率达 12.7%-32.6%，而且目前尚无有效的治疗方法，仅有对症支持治疗。由于在全球范围广泛存在、高病死率以及缺乏有效的治疗手段，SFTS 已严重威胁人类健康。

PU-0175

Analysis of Serum Hepatitis B Virus RNA Levels Among HBsAg and HBsAb Co-positive Patients and its correlation with HBV DNA

yu xiang
Department of Laboratory Medicine, the First Affiliated Hospital of Chongqing Medical University

Background To analyze the levels of HBV RNA in serum of HBsAg and HBsAb co-positive patients and the correlation with HBV DNA, HBsAg, ALT and AST.
Methods A total of 149 HBsAg and HBsAb co-positive patients were screened out from 66, 617 outpatients who had undergone HBV serological marker test. The levels of HBV RNA and HBV DNA were determined by real-time fluorescence quantitative PCR, and HBV genotyping was performed on those patients by PCR-fluorescent probe method. The natural course of co-positive patients was divided into four phases in accordance with the natural history of HBV infection, the levels of HBV RNA, HBV DNA, HBsAg, ALT and AST in different phases were compared. Meanwhile, the correlation between HBV RNA and HBV DNA, HBsAg, ALT, AST levels were analyzed as well as the influence of HBeAg expressions on HBV RNA levels.
Results Among the 149 HBsAg and HBsAb co-positive patients, 141 patients (94.63%) were genotype B and 8 (5.37%) were genotype C. According to the status of HBeAg, the 149 HBsAg and HBsAb co-positive patients could be divided into HBeAg positive group (66 patients, 44.30%) and HBeAg negative group (83 patients, 55.70%).The serum levels of HBV RNA and HBV DNA were higher in HBeAg positive group than in HBeAg negative group, with statistically significant difference ($P < 0.01$).The serum levels of HBV RNA, HBV DNA, HBsAg, ALT and AST were significantly different in different natural phases of HBV infection (immune tolerance phase, immune clearance phase, low replication phase and reactivation phase), with statistical significance ($P < 0.01$). HBV RNA levels were positively correlated with HBV DNA ($r=0.667$, $P=0.000$), HBsAg ($r= 0.330$, $P = 0.000$), ALT ($r = 0.263$, $P = 0.001$), and AST levels ($r=0.218$, $P = 0.007$) in serum. In HBeAg positive group, HBV RNA levels were positively correlated with HBV DNA ($r=0.595$, $P=0.000$) and HBsAg levels ($r=0.508$, $P=0.000$). In HBeAg negative group, HBV RNA levels were positively correlated with HBV DNA ($r=0.530$, $P=0.000$).
Conclusion B is the dominant genotype in HBsAg and HBsAb co-positive patients; as the advancement of disease into different phases (immune tolerance phase, immune clearance phase, low replication phase), the HBV RNA levels decreased gradually with the decrease of HBV DNA levels. The HBV RNA levels in serum were positively correlated with HBV DNA, HBsAg, ALT and AST levels. HBV RNA could be used as virological indicators for antiviral therapy in HBsAg and HBsAb co-positive patients with hepatitis B; the expressions of HBeAg had an impact on the expressions of HBV RNA.

PU-0176

云南省 HIV-1 感染儿童一线抗病毒治疗后病毒学反弹分析

杨壁珲
云南省传染病医院云南省艾滋病关爱中心云南省心理卫生中心

目的 云南省 HIV-1 感染儿童一线抗病毒治疗后病毒学出现反弹 85 例，分析该类患儿更换和没有更换二线药物在后期治疗中的病毒学抑制和耐药情况。
结果 85 例病毒学反弹儿童(VL>400 拷贝/ml)反弹时间中位数为 2.25 年（1.63-3.26）。48 例（56.5%）患儿在病毒学反弹后转为二线药物继续治疗，28 例（32.9%）患儿在病毒学反弹后没有更换二线药物病毒学再次得到抑制，9 例（10.6%）患儿在病毒学反弹后没有更换二线药物病毒学也没有再次得到抑制。

结论 云南省 HIV-1 感染儿童经过一线抗病毒治疗后有 85 例发生病毒学反弹，其中有 1/2 的患儿更换二线药物，有 1/3 患儿没有更换二线药物病毒学再次得到抑制，其余 1/10 患儿仍在接受治疗失败的一线治疗方案。更换二线抗病毒治疗药物前，应考虑病毒学再抑制的可能性，通过服药依从性咨询、耐药检测结果和药代动力学等来评估治疗效果，以最大限度的提高一线药物的持久性和对二线药物治疗的反应性。

PU-0177

A novel PCR-Cas13a assay for syphilis: diagnosis, genotyping, and macrolide-resistance-associated mutation identification.

Wentao Chen、Hao Luo、Heping Zheng
Dermatology Hospital， Southern Medical University

Nucleic acid amplification test (NAAT) possesses highly sensitive and specific capabilities, which has been largely utilized for pathogen detection in clinical practice. However, the sensitivity of molecular diagnosis for syphilis is insufficient sensitivity and depends on the type of collected biological sample. Herein, we develop a novel syphilis molecular diagnosis by paring the PCR and CRISPR-Cas13a. The PCR-Cas13a assay exhibits robust sensitivity and specificity in detecting TPA from different clinical specimen sources. We also applied this assay for TPA genotyping and macrolide resistance-associated mutations detection in real-time, providing a powerful tool for syphilis molecule surveillance and antibiotic selection suggestion. Additionally, we adapted the lateral flow test strip for visualizing the result of the PCR-Cas13a assay. In summary, we provide a PCR-Cas13a assay, which exhibits robust capabilities and prospects in syphilis diagnosis.

PU-0178

微阵列芯片法和流式细胞术检测 HLA-B27 的结果分析

刘义庆[1,2]、白晓卉[1,2]、渠滕[1,2]、卢志明[1,2]
1. 山东省立医院
2. 山东第一医科大学附属省立医院

目的 比较欧盟微阵列芯片法和流式细胞术两种方法检测人类白细胞抗原 B27（HLA-B27）的临床应用价值。
方法 分别采用欧盟微阵列芯片法和流式细胞术两种方法检测 238 例疑似强直性脊柱炎患者血中 HLA-B27，比较和分析两种方法的检测**结果** 。
结果 90.76%样本检测结果相同，差异不具有统计学意义（P＞ 0.05），将存在差异的标本进行基因测序后，结果与微阵列芯片法的检测结果一致。
结论 两种方法检测 HLA-B27 均具有较高的灵敏度和特异度，微阵列芯片法在结果的准确性上更优于流式细胞术。

PU-0179

EB-DNA 阳性患者的疾病分布及对临床建议

许红攀
南京大学医学院附属鼓楼医院

非洲淋巴细胞瘤病毒，简称ＥＢ病毒（Epstein-Barr，EBV），是一种 DNA 病毒，属疱疹病毒科，广泛存在于自然界。在人群中的感染极其普遍，主要通过唾液传播，感染后可以终身携带病毒。EB 病毒主要感染 B 淋巴细胞、上皮细胞,故主要损伤人的免疫系统和上皮组织而导致相应的疾病，如淋巴瘤、传染性单核细胞增多症及类风湿关节炎等。

PU-0180

分析 HBsAg 和 HBsAb 共同阳性的特殊血清学模式患者血清中 HBV RNA 的表达水平及与 HBV DNA 的相关性

向瑜
重庆医科大学附属第一医院

目的 检测 HBV 感染者中 HBsAg 和 HBsAb 共同阳性的特殊血清学模式患者血清中 HBV RNA 的表达水平，并分析其与 HBV DNA， HBsAg， ALT，AST 的相关性。
方法 从 66617 例检测 HBV 血清学标志物的门诊患者中筛选出 149 例 HBsAg 和 HBsAb 共同阳性的特殊血清学模式患者，采用实时荧光定量 PCR 法检测 HBV RNA 和 HBV DNA 的表达水平，用 PCR-荧光探针法对上述特殊模式患者进行 HBV 基因分型。按照 HBV 感染的自然史分为四期，比较不同自然病程时期的 HBV RNA，HBV DNA，HBsAg，ALT，AST 的表达差异，同时分析 HBV RNA 与 HBV DNA，HBsAg，ALT，AST 的相关性及 HBeAg 表达对 HBV RNA 水平的影响。
结果 在 149 例 HBsAg 和 HBsAb 共同阳性的特殊血清学模式患者中，B 基因型 141 例，C 基因型 8 例；在 HBV 感染的不同自然病程期，HBV RNA，HBV DNA， HBsAg，ALT 和 AST 的表达水平有差异，具有统计学意义。血清 HBV RNA 与 HBV DNA 呈正相关，与 HBsAg 呈正相关，与 AST 呈正相关；上述 149 例特殊模式患者根据 HBeAg 的状态可分为： HBeAg+阳性组和 HBeAg -阴性组。 在 HBeAg+组中 HBV RNA 和 HBV DNA 的表达水平高于 HBeAg-组，差异有统计学意义。在 HBeAg+组，HBV RNA 与 HBV DNA 呈正相关，与 HBsAg 呈正相关。在 HBeAg-组，HBV RNA 与 HBV DNA 呈正相关。
结论 HBsAg 和 HBsAb 共同阳性的特殊血清学模式患者中，HBV 基因型以 B 型为优势基因；随着不同自然病程分期进程，HBV RNA 水平随着 HBV DNA 水平降低而逐渐降低；血清中 HBV RNA 水平与 HBV DNA，HBsAg，ALT，AST 水平呈正相关，HBV RNA 可作为乙型肝炎抗病毒治疗的病毒学指标；HBeAg 的表达对 HBV RNA 表达水平有影响。

PU-0181

基于传播途径改变基础上的新疆 HIV-1 亚型分子流行特征分析

黄国虹、马晶、杨敏、王昌敏
新疆维吾尔自治区人民医院

目的 基于新疆地区艾滋病传播呈现传播途径由性途径取代共用注射器吸毒，男男性接触人群感染人数快速上升的新特点基础上，了解该地区 HIV-1 亚型分子流行特征。
方法 采用横断面调查方式对 2015 年-2019 年就诊于新疆某传染病医院 500 例 HIV 阳性患者全血进行分子流行特征研究。采集研究对象抗凝全血及临床资料，分离血浆，提取 RNA 并进行 RT-PCR

和 Nest-PCR 扩增 gag、pol 和 env 基因序列片段并测序，使用 Sequencher4.1.4 软件进行序列拼接和处理后经 MEGA7.0 软件 Neighbor-joining 法进行 gag、env 系统进化树构建。
结果 500 例 HIV-1 阳性患者中，以男性居多 61.00%（305/500），40～59 岁年龄段所占比重最大 47.00%（235/500），已婚者为主 81.20%（406/500），维吾尔族占 67.00%（335/500），63.00%为中学文化程度（315/500），以异性传播为主 54.60%（273/500）。HIV-1 基因分析以 CRF_07BC 型所占比例最高，其次为 CRF_01AE 型。HIV-1 基因亚型在不同性别、不同民族、不同感染途径中均以 CRF07_BC 型为主，而在不同族别的分布的差异有统计学意义。
结论 虽然传播途径发生改变，但该地区 HIV-1 分流流行特征仍以 CRF_07BC 型为主，该研究结果为掌握本地区 HIV-1 流行最新动态及 HIV-1 防控、治疗、疫苗的研制开发提供有力的分子流行病学依据。

PU-0182

BOP1 as a novel prognostic marker and correlates with tumor microenvironment in Pan-cancers

Wei Li[1,2]、Ke Shi[2]、Chongge You[1]、Peipei Song[1]
1. Laboratory Medicine Center, Lanzhou University Second Hospital
2. Department of Geriatrics, Clinical Laboratory, Xiangya Hospital of Central South University

Objective Cancer is one of the main causes of death all over the world. Previous studies have indicated the important role of Block of proliferation 1 (BOP1) in the tumorigenesis and progression of several cancers, no systematic pan-cancer analysis of BOP1 is available. In present study, we aim to systematically identify the prevalence and prognostic value of BOP1 expression in 33 cancer types.
Methods The gene expression profiles, somatic mutation data, and related clinical data in TCGA, Genotype Tissue-Expression (GTEx) and Cancer Cell Line Encyclopedia (CCLE) were downloaded from the UCSC XENA website. The R software packages were used to evaluate the expression of BOP1 mRNA in 31 normal tissues, 33 cancer tissues and 21 tumor cell lines. The UALCAN and the Human Protein Atlas (HPA) database were utilized to verify the expression of BOP1 protein in tumors. The univariate Cox analysis and the Kaplan-Meier curves performed by R packages were used to investigate the prognostic value of BOP1 expression. Then we used a series of bioinformatics **Methods** implemented by R software packages to explore the potential oncogenic roles of BOP1, including analyzing the relationship between BOP1 and microsatellite instability (MSI), tumor mutational burden (TMB), DNA methylation, tumor microenvironment, immune checkpoints, and immune cell infiltration of different tumors. We also explored the potential signaling pathway mechanism through gene set enrichment analysis (GSEA). Finally, the reverse transcription-quantitative polymerase chain reaction (RT-qPCR), Western blotting(WB), and Transwell Assay were performed to verify related findings in lung cancer cell lines.
Results BOP1 expression was higher in 25 types of cancer tissues compared with adjacent normal tissues, but present at low levels in acute myeloid leukemia (LAML) and thyroid carcinoma (THCA). High BOP1 expression was related to worse prognosis and a higher clinicopathologic stage in most tumors. Moreover, BOP1 expression was strongly correlated with the TMB, MSI, tumor microenvironment, immune checkpoints, and immune cell infiltration in most tumors. The GSEA showed that a variety of tumor- and immune-related pathways were differentially enriched in the phenotypes of high or low BOP1 expression. The RT-qPCR analysis indicated that BOP1 was significantly augmented in lung cancer cells compared to HBE cell. Transwell Assay showed that enhanced of expression of BOP1 significantly facilitated cell migration, while its down-regulation displayed the opposite effect. Additionally, BOP1 silencing diminished snail and N-cadherin expression, and further up-regulated E-cadherin.

Conclusion BOP1 can be used as a potential prognostic molecular biomarker for predicting poor survival in various malignant tumors and may function as an oncogene with a strong role in tumorigenesis and tumor immunity.

PU-0183

肿瘤饥饿环境对肺癌细胞中 HMGB1 表达的调控及其 HMGB1 在肺癌筛查中的应用价值

郑齐锶
南京大学医学院附属鼓楼医院

目的 探讨 Hank′s 平衡盐溶液（Hank′s balanced salt solution,HBSS）诱导的饥饿环境对肺癌细胞凋亡相关分子高迁移率组蛋白 B1（HMGB1）表达的调控作用,并分析肺癌患者血清 HMGB1 水平在肺癌筛查中的应用价值。
方法 设置 HBSS 处理组（使用 HBSS 更换完全培养基后继续培养）与对照组（使用完全培养基进行培养）。利用 HBSS 处理 Lewis 肺癌细胞 12 h 后,采用分光光度法检测肺癌细胞中含半胱氨酸的天冬氨酸蛋白水解酶-3（Caspase-3）活性。利用 HBSS 处理 Lewis 肺癌细胞 0.5 h 后,采用流式细胞术检测饥饿条件下肺癌细胞中氧化应激效应分子——活性氧（ROS）的表达水平。利用 HBSS 处理 Lewis 肺癌细胞 0、4、8 和 12 h 后,使用 western blot 检测细胞内 HMGB1 蛋白的表达水平。采用 ELISA 法检测肺癌患者（n=50）血清中 HMGB1 的表达水平,并分析其与血清肿瘤标志物水平间的相关性。
结果 与对照组（0.14±0.01 U/L）相比,HBSS 刺激 12 h 后,Lewis 肺癌细胞中 Caspase-3 活性（0.24±0.01 U/L）明显升高（P<0.01）。流式细胞术检测结果表明,与对照组（MFI:63.00±4.58）相比,HBSS 刺激 0.5 h 后,Lewis 肺癌细胞中 ROS 水平（MFI:293.00±9.54）上调（P<0.01）。western blot 结果显示,HBSS 刺激 0、4、8 和 12 h 后,Lewis 肺癌细胞中 HMGB1 蛋白的表达水平明显升高（P 均<0.01）。ELISA 法结果显示,与健康人对照（3.36±0.20 ng/mL）相比,肺癌患者血清中 HMGB1 的水平（12.76±0.74 ng/mL）明显升高（P<0.05）,且与血清 CEA 水平呈正相关（r=0.44,P<0.01）。
结论 肿瘤饥饿环境能够促进肺癌细胞中凋亡相关分子 HMGB1 的表达,肺癌患者血清 HMGB1 水平与肺癌发展密切相关。

PU-0184

HCY 与 2 型糖尿病和视网膜病变关系的研究

何川疆、许爱敏
喀什地区第一人民医院

目的 探讨同型半胱氨酸（HCY）与 2 型糖尿病和视网膜病变的关系。
方法 选择喀什地区第一人民医院 2018 年 4 月-2019 年 11 月入院的 2 型糖尿病患者 200 例，设为病例组。所有患者入院后均进行眼底情况检查，根据是否诊断为视网膜病变分为视网膜病变组和非病变组；选择同期健康体检者 200 例，设为对照组；采用循环酶法试验测定各组 Hcy 水平；采用 PCR-芯片杂交法检测叶酸基因 MTHFR C677T 位点的基因型；采用化学发光免疫法检测血清叶酸、血清 VB12 水平；数据采用 SPSS Statistics 25 软件进行处理，分析血清 Hyc、叶酸、VB12 水平与 2 型糖尿病及视网膜病变关系。
结果 病例组 Hcy 水平高于对照组（P<0.05）；血清叶酸及血浆 VB12 水平低于对照组（P<0.05）；病例组叶酸基因 MTHFR C677T 位点中 CC 及等位基因频次 C 病例数均低于对照组（P<0.05）；CT、TT 病例数高于对照组（P<0.05）；Pearson 相关分析结果表明：Hcy 水平与糖尿病与视网膜

病变发生率呈正相关性（P<0.05）；血清叶酸及血浆 VB12 水平低与视网膜病变发生率呈负相关性（P<0.05）。

结论 2 型糖尿病患者 HCY 水平显著高于对照组，且 HCY 水平与视网膜病变存在强正相关性。这些发现提示：加强患者 Hcy 水平测定可为预防视网膜病变提供理论依据。

PU-0185

Long non-coding RNA RUNXOR accelerates MDSC-mediated immunosuppression in lung cancer

Xinyu Tian
Nanjing Drum Tower Hospital

Background RUNX1 overlapping RNA (RUNXOR) is a long non-coding RNA that has been indicated as a key regulator in the development of myeloid cells by targeting runt-related transcription factor 1 (RUNX1). Myeloid-derived suppressor cells (MDSCs) are a heterogeneous population of cells consisting of immature granulocytes and monocytes with immunosuppression. However, the impact of lncRNA RUNXOR on the development of MDSCs remains unknown.
Methods Both the expressions of RUNXOR and RUNX1 in the peripheral blood were measured by qRT-PCR. Human MDSCs used in this study were isolated from tumor tissue of patients with lung cancer by FCM or induced from PBMCs of healthy donors with IL-1β + GM-CSF. Specific siRNA was used to knockdown the expression of RUNXOR in MDSCs.
Results In this study, we found that the lncRNA RUNXOR was upregulated in the peripheral blood of lung cancer patients. In addition, as a target gene of RUNXOR, the expression of RUNX1 was downregulated in lung cancer patients. Finally, the expression of RUNXOR was higher in MDSCs isolated from the tumor tissues of lung cancer patients compared with cells from adjacent tissue. In addition, RUNXOR knockdown decreased Arg1 expression in MDSCs.
Conclusions Based on our findings, it is illustrated that RUNXOR is significantly associated with the immunosuppression induced by MDSCs in lung cancer patients and may be a target of anti-tumor therapy.

PU-0186

血清 miRNA-223 在非小细胞肺癌化疗疗效监测中应用

苏光建、陈燕
福建肿瘤医院

目的 探讨 microRNA-223（miRNA-223,miR-223）作为非小细胞肺癌（NSCLC）晚期（Ⅲ-Ⅳ期）患者化疗疗效评价指标的可行性。
方法 收集 14 例非小细胞肺癌晚期患者化疗前及化疗第一周期后血清，提取总 RNA 后采用实时荧光定量 PCR 方法检测血清 miRNA-223 水平变化，计算各个患者化疗第一周期后相对化疗前的变化量，并依据临床对患者疗效进行的化疗疗效评估（RECIST），将 14 例样本分为疾病进展（PD, progressive disease）组、疾病稳定(SD, stable disease) 组、部分缓解(PR, partial response)组，比较三组患者化疗第一周期后血清 miR-223 变化量，探讨不同组别血清 miR-223 作为 NSCLC 患者化疗疗效评估指标的可行性。
结果 数据统计显示，miRNA-223 在 PR 组中化疗后表达水平低于化疗前的水平，其相对表达含量为 0.70±0.32，在 SD 组中化疗后相对表达含量为 1.18±0.34，在 PD 组中化疗前后相对表达含量最高，为 2.84±0.87。化疗后 miR-223 相对化疗前的表达水平与患者年龄(u=23.00,P=0.848)、性别(u=10.00,P=0.157)、TNM 分期（u=20.00,P=1.000）差异无统计学意义。PR、SD、PD 组间 miR-223 化疗后水平呈趋势性变化，差异具有统计学意义（χ2=8.9,P=0.012）。

结论 血清 miR-223 在化疗一个周期后的变化水平能较好预示 NSCLC 患者的化疗疗效，提示血清 miR-223 可作为 NSCLC 患者化疗疗效评价指标之一，对于实现肺癌个性化治疗有着重要的临床意义。

PU-0187

血浆热休克蛋白 90α 和 EBV DNA 定量检测对鼻咽癌的诊断和预后评价

叶倩、陈燕
福建肿瘤医院

目的 检测鼻咽癌患者血浆中 HSP90α 和 EBV DNA 治疗前、后及健康人中的表达情况，探讨其在鼻咽癌诊断与临床病理特征关系以及疗效评价和预后评估中的作用。
方法 应用定量酶联免疫吸附法和实时定量 PCR 方法检测 92 例初治鼻咽癌患者治疗前后、放化疗后转移或复发以及持续缓解鼻咽癌患者血浆中 HSP90α 和 EBV DNA 的表达情况，并以 30 名健康体检者为对照。
结果 血浆中 HSP90α 水平为 87.28ng/ml 诊断鼻咽癌的敏感度为 92.1%，特异度为 86.0%。血浆 EB DNA 中位拷贝数为 4900/ml 对初诊鼻咽癌患者的诊断敏感性为 89.0%，特异性为 92.0%。92 例鼻咽癌患者经过治疗后均达到完全缓解或者部分缓解。鼻咽癌患者治疗前血浆中 HSP90α 和 EBV DNA 水平显著高于治疗后和健康对照者。血浆中 HSP90α 与鼻咽癌临床分期相关，与性别、年龄、病理分型（T、N）无关(P>0.05)，治疗后完全缓解患者降至健康对照者水平。部分缓解患者仍高于健康对照者水平，而完全缓解与部分缓解患者的治疗后血浆 HSP90α 降至健康对照者水平。在半年内远处转移的患者治疗后血浆中 HSP90α 和 EBV DNA 水平均明显高于未发生远处转移患者和健康对照者。血浆中 HSP90α 和 EBV-DNA 表达之间存在相关性。
结论 血浆 HSP90α 水平作为辅助诊断鼻咽癌的指标有一定的临床意义。血浆中 HSP90α 与 EBV-DNA 检测有助于判断鼻咽癌的诊断、病情监测和预后评估具有重要价值。

PU-0188

Association between genetic variation of Hippo pathway genes and clinical outcome of EGFR-TKI treated NSCLC patients

Yu Jiang[1]、WenJing Xie[1]、RongWei Chen[1]、WenXu Chen[1]、JianPing Xu[2]
1. Fuzhou Second Hospital Affiliated to Xiamen University, Fuzhou, Fujian, China
2. 福建医科大学

Background Hippo pathway play an important role in cell differentiation, organ size and carcinogenesis. However, the association between genetic variation of Hippo pathway and survival of EGFR-TKI treated NSCLC patients remains unclear.
Materials and Methods A retrospective study including 300 advanced EGFR-mutated NSCLC patients were included in this study. We selected and detected genotypes of 31 candidate functional genetic polymorphisms within Hippo pathway using MassARRAY time-of-flight mass spectrometer. We also follow-up these included patients to obtain three-years survival. Kaplan-Meier curve with log-rank test, univariate and multivariate COX regression were selected to analysize the association between them.
Results In this study, we found in clinical samples that LATS1 Rs2297928, MOB1B Rs147762156, SKT3 Rs3019295, RASSF1A Rs1989839, and YAP1 Rs1820453 were related to the clinical efficacy of EGFR-TKI in patients with stage IIIb-V NSCLC patient with mutated-EGFR.

LATS2 Rs141692953, FAT4 Rs7676612, YAP1 Rs1820453, TEAD2 Rs2288480 were significantly related to the three-year progression-free survival or overall survival of these patients. It also verified that only YAP1 rs1820453 site was significantly related to the clinical efficacy of EGFR-TKI and the survival prognosis of NSCLC patients. Among them, 62.00% of patients with TT genotype had a complete or partial response after EGFR-TKI treatment, 27.60% of patients showed stable disease, and only 10.40% of patients showed disease progression; while the percentages of patients with complete/partial response, stable disease and disease progression in TG/GG carriers were 38.10%, 42.85%, and 19.05%, respectively, and the clinical efficacy was significantly lower than that of carriers of the TT genotype ($p<0.05$). Further analysis with the patient's three-year progression-free survival and overall survival revealed that the median progression-free survival of patients with TT and TG/GG genotypes were 14.3 and 6.2 months, respectively, and the difference between the two was statistically significant (Plog-rank<0.001). After multivariate adjustment, the progression-free survival of patients with TT genotype was significantly better than that of patients with TG/GG genotype (adjusted HR=0.56, 95%CI=0.23-0.89). K-M curve, univariate and multivariate COX regression analysis also found that YAP1 rs1820453 locus TT and G allele carriers harbored significantly longer overall survival than G allele (adjusted HR=0.42, 95%CI=0.12-0.69). Also, the TT genotype at the rs1820453 locus was significantly negatively correlated with tumor invasion and lymph node metastasis.
Conclusion The findings indicated that YAP1 rs1820453 was significantly associated with clinical efficacy and survival of EGFR-TKI treated NSCLC patients, and the locus could be used as a molecular biomarker to predict the outcome of these patients.

PU-0189

标准曲线法定量检测人类和模式生物全基因组 DNA 双链断裂数目

戴寒莹、徐克前
中南大学

目的 建立标准曲线法，用于简单、快速地检测人类和模式生物全基因组 DNA 双链断裂数目(number of DNA double-strand breaks, N_{DSBs})。采用不同限制性内切酶完全酶切人类和模式生物全基因组 DNA 获得标准品，再联合生物信息学和连接介导实时荧光定量 PCR (ligation-mediated real-time quantitative PCR，LM-qPCR)技术，建立标准曲线法。同时对该方法进行条件优化，并评价其可靠性、重复性与敏感性，从而建立一种简便、可靠、可对任何已知核苷酸序列样本的 N_{DSBs} 进行定量分析的方法。
方法（1）以人类和模式生物（小鼠、拟南芥、酿酒酵母、大肠杆菌）基因组 DNA 为研究对象；（2）采用不同平端限制性内切酶（AluI、BsuRI、DraI、SspI、StuI、EcoRV、EheI）酶切基因组 DNA 模拟自然界 DSBs 损伤，获取系列标准品；（3）设计自制软件识别基因组 DNA 上特定核酸序列数，计算标准品 DSBs 数目的理论值（N_{DSBs} 的理论值）；（4）LM-qPCR 检测标准品的 Ct 值，以标准品的 lgN_{DSBs} 值为横坐标，Ct 值为纵坐标建立标准曲线，对反应条件进行优化，并研究其重复性、敏感性及特异性；（5）采用 DNA 平端化技术将待测样本中 DNA 黏性末端补平及评价；（6）采用不同剂量 X 射线、不同浓度 H_2O_2 处理标本后，使用标准曲线法检测标本的 DNA 双链断裂；（7）将建立的标准曲线法与经典的中性单细胞凝胶电泳和 γ-H2AX 流式细胞法进行比较，从而评价标准曲线法的可靠性，通过批间和批内变异系数（CV）评价其重复性。
结果（1）自制软件可在 30s 内得出限制性内切酶酶切后 DSBs 的理论值（N_{DSBs}）；（2）通过平端限制性内切酶可以完全酶切人类和模式生物基因组 DNA，得到标准品；（3）LM-qPCR 法可检测不同生物标准品的 Ct 值，计算出 5 种生物的标准曲线的拟合方程，其 $R^2>0.9$。LM-qPCR 效率为 87.9%至 115.4%，检测限 $10<N_{DSBs}<10^8$，重复性实验的平均批内 CV 为 1.101%，平均批间 CV 为 2.528%；（4）通过 Klenow 片段可以有效地对 DNA 进行补平；（5）不同处理后的标本，

随着处理水平增加，N_{DSBs} 值增加，Ct 值显著降低（P<0.001）。三种方法的结果存在显著相关关系，Pearson 相关系数 r 的绝对值均大于 0.9。
结论 标准曲线法可以定量检测人类和模式生物的全基因组 DNA 双链断裂数目，其操作简单、结果可靠、重复性好、可标准化，为检测不同标本的 DNA 双链断裂数目提供了一个全新的方法与思路。

PU-0190

山东地区 913 例丙肝患者 HCV 基因分型研究

刘义庆[1,2]、白晓卉[1,2]、渠滕[1,2]、卢志明[1,2]
1. 山东省立医院
2. 山东第一医科大学附属省立医院

目的 了解近年来山东地区丙型肝炎病毒（HCV）感染者基因型的分布特点及其与 HCV-RNA 病毒载量的相关性。
方法 抽取山东省立医院门诊及住院丙肝患者实时荧光定量 PCR 检测 RNA 阳性标本 913 例，用焦磷酸测序法进行基因分型。
结果 共检出 7 种基因亚型，1a、1b、2a、2b、3a、3b、6a 比例依次为 1.53%、59.91%、37.68%、0.11%、0.44%、0.11%、0.22%。1b 亚型病毒载量高于 2a，其他亚型病毒载量之间无显著差异。
结论 山东地区丙型肝炎病毒基因型以 1b 为主，其次为 2a，且 1b 亚型病毒载量高于 2a。

PU-0191

基于 CRISPR/Cas9 系统靶向敲减 miR-21 对鼻咽癌放疗抵抗的影响

肖振州、陈燕
福建省肿瘤医院

目的 本研究拟通过 CRISPR/Cas9 系统靶向敲减 CNE2 细胞中的 miR-21，评估对 CNE2 细胞生物学特性的影响并探讨分子机制。
方法 通过 CRISPR/Cas9 系统对放疗抗拒的 CNE2-R 和正常 CNE2 鼻咽癌细胞株进行内源性 miR-21 基因敲除，通过 T7EN1 酶切和 Real-time PCR 验证敲除效果。通过设置体外相关实验，探讨 miR-21 基因敲除对 CNE2-R 和正常 CNE2 细胞增殖状态、克隆形成、凋亡状态等生物学特性的影响，进行放疗敏感性及侵袭能力的比较。通过生物信息学分析预测 miR-21 在鼻咽癌中参与调控的信号通路，免疫印迹进一步验证。
结果 CRISPR/Cas9 载体系统可有效敲减对 CNE2-R 和 CNE2 细胞系中内源性 miR-21 基因，编辑效率接近 50%。miR-21 靶向敲减可明显抑制 CNE2-R 和 CNE2 细胞的生长增殖，克隆形成及侵袭转移等能力，并诱导细胞凋亡。生物信息学分析共找到 28 个 KEGG，并筛选出共同交集的通路。免疫印迹显示，miR-21 敲减组 PI3K/AKT/mTOR 通路相关蛋白及其磷酸化水平发生明显改变。Meta 分析结果显示，miR-21 联合其他 miRNA 分子表达谱在诊断鼻咽癌中的灵敏度、特异度、及曲线下面积（AUC）分别为 0.78、0.79 和 0.85。本项目研究结果证实，内源性 miR-21 与 CNE2-R 细胞的放疗抗拒有关，靶向敲减 miR-21 可通过阻断 PI3K/AKT/mTOR 信号通路来抑制 CNE2-R 和 CNE2 细胞的生长增殖，诱导细胞凋亡，从而增加放疗的敏感性。
结论 靶向敲减 miR-21 可通过抑制 PI3K/AKT/mTOR 信号通路抑制 CNE2-R 和 CNE2 细胞的生长增殖，诱导细胞凋亡，增加放疗的敏感性。

PU-0192

鼻咽癌患者血浆外泌体 miR-BART 水平与临床转移之间的关系

郑瑜宏、陈燕
福建省肿瘤医院

目的 检测鼻咽癌患者血浆外泌体中 miR-BART 的含量，分析和鼻咽癌 miR-BART 的表达和患者临床病理参数之间的相关性，探讨它在 NPC 侵袭转移过程中的作用。
方法 收集 24 对鼻咽癌患者的配对血浆（治疗前和发生转移时总共 48 份血浆）和 12 名健康人的血浆，通过 exoRNeasy 血清/血浆 Maxi 试剂盒对鼻咽癌患者血浆中外泌体和外泌体中总 RNA 的提取。再通过 TaqMan MicroRNA 逆转录试剂盒进行多重 RT-PCR 完成 60 份标本的 miR-BART3、miR-BART7 和 miR-BART13 的检测。用 SPASS13.0 进行数据分析，探讨鼻咽癌患者血浆外泌体中 miR-BART 的表达水平与鼻咽癌临床病理参数(年龄、远处转移和临床分期)之间和复发转移的关系。
结果 血浆外泌体中的 miR-BART3 和 miR-BART7 对鼻咽癌有诊断意义，诊断的准确率为 0.794 和 0.817（95%置信区间分别为：0.641-0.946 和 0.671-0.964）；血浆外泌体中的 miR-BART13 在 NPC 组合健康对照组间不存在相关性。不同性别血浆外泌体中的 miR-BART3、miR-BART7、miR-BART13 表达量无差别；血浆外泌体中的 BART7、BART13 表达水平与年龄不存在相关性，但年龄大于 50 岁患者血浆外泌体中的 BART3 呈现高表达；BART7 与 T 分期、N 分期、临床分期均无相关性；而 BART13 与 T 分期、N 分期及临床分期都存在相关性，但由于其表达量很低，因此无意义；BART3 则与 N 分期存在较强相关性，但是随着 N 分期越晚，miR-BART3 表达量增加。
结论 miR-BART3 和 miR-BART7 对鼻咽癌有诊断意义，诊断的准确率分别为 0.794 和 0.817；转移前后的 miR-BART3 表达量有较大差别，但二者在统计学上的差异并不十分显著；miR-BART3 在 50 岁以上的鼻咽癌患者中高表达，且二者存在相关性；miR-BART3 则与 N 分期存在较强相关性，随着 N 分期越晚，miR-BART3 表达量增加。

PU-0193

鼻咽癌不同患者血浆 EB 病毒 DNA 与肿瘤疗效关系探讨

林莺莺、陈燕
福建省肿瘤医院

目的 评价血浆 EBVDNA 在鼻咽癌筛查和早期诊断价值，探讨不同患者血浆 EBVDNA 含量与肿瘤疗效的关系。
方法 以 2017 年 1 月至 2017 年 12 月来福建省肿瘤医院就诊的鼻咽癌首诊患者为研究对象，按入组标准分为鼻咽癌首诊组 485 例和治疗组 238 例。用磁珠提取法结合实时荧光定量 PCR 测定研究对象的 EBVDNA 含量。建立 EBVDNA 检测数据库并分析首诊组患者治疗前血浆 EBVDNA 的诊断效能以及与 TNM 分期、临床分期的关系，治疗组患者在治疗过程中不同首诊血浆 EBVDNA 的下降速率和治疗后不同血浆 EBVDNA 与疗效的关系以及复发时的患者血浆 EBVDNA 变化趋势。
结果 485 例首诊患者的 ENDNA 扩增检出率为 93.6%，与健康体检者相比（5.2%），差异有统计学意义。EBDNA 诊断鼻咽癌的 ROC 曲线下面积为 0.964（0.951-0.977），敏感性为 93.6% ，特异性为 94.8% ，准确性为 88.4% ，阳性预测值 94.8%，阴性预测值为 93.6% 。患者治疗前血浆 EBVDNA 含量与 TNM 分期和临床分期正相关，TNM 及临床分期早期的患者 EBDNA 含量显著低于中晚期，首诊血浆 EBVDNA 含量>10000copies/ml 的患者通过三次放化疗的下降为 0 的病例百分比显著低于血浆 EBVDNA≤10000copies/ml 患者，差异有统计学意义。复发患者血浆 EBVDNA 呈上涨趋势。EBDNA 的复发检出率为 90%。首诊 EBVDNA 含量为 0~200copies/ml 的复发患者甚至在治疗过程中可持续检测到低含量的 EBDNA。

结论 血浆 EBVDNA 含量检测有助于鼻咽癌的筛查和早期诊断，首诊患者血浆 EBVDNA 含量越高，分期越晚。治疗过程中 EBVDNA 含量变化可反映治疗效果，治疗后 EBVDNA 含量持续复制或上升患者有较高的复发风险。

PU-0194

Tumor-educated platelets for non-small cell lung cancer (NSCLC): an update on recent developments

Erfu Xie
the First Affiliated Hospital of Nanjing Medical University

Recently, liquid biopsies are considered as an emerging tool for the early detection of cancer. In contrast to tumor tissue biopsies, liquid biopsies are easier to manipulation and faster to get **Results** Tumor-educated platelets (TEPs) as one of detection targets for liquid biopsies have attracted widespread attention. In this review, the following will be reviewed. Firstly, the basic knowledge, which include characteristic, formation and detection of TEPs, are described. Secondly, the application of TEPs in non-small cell lung cancer (NSCLC) are reviewed. In conclusion, TEPs could serve as an ideal means of liquid biopsy for NSCLC. However, more research on TEPs is needed before it could be widely used in clinic.

PU-0195

Islet-1 诱导 C3H10T1/2 心肌样分化过程 Akt 参与干性维持的作用研究

黄月
成都市第三人民医院

目的 探究在 Islet-1 诱导的 C3H10T1/2 心肌样细胞分化过程中 Akt 与干性因子的表达调控是否相关。
方法 在 C3 细胞中转染过表达 Islet-1 的慢病毒，构建心肌样细胞分化模型，通过反转录定量 PCR（RT-qPCR）检测蛋白激酶（Akt）及干性因子 Sox2、Nanog 的基因表达；western blotting 检测 Akt 及干性因子的蛋白表达；免疫荧光检测干性因子及 Akt 的定位改变。采用 Akt 激活剂 SC79 与抑制剂 MK2206 分别作用于 C3 细胞，western blotting 检测 p-Akt 表达情况以摸索出药物最佳浓度；以两种药物的最佳浓度分别作用于 C3 细胞后，RT-qPCR 检测干性因子基因表达，western blotting 检测干性因子蛋白表达，免疫荧光检测干性因子定位改变。
结果 转入 Islet-1 后 C3 发生了心肌样细胞分化，分化过程中 Akt 活性及入核量降低，但干性因子的基因表达、蛋白表达、细胞定位均未发生改变；摸索出的 SC79 最佳作用浓度为 4ug/ml，MK2206 最佳作用浓度为 1umol/L。激活及抑制 Akt 后，干性因子的 mRNA 表达、蛋白表达及核定位均未产生改变。
结论 在 Islet-1 诱导的 C3 心肌样细胞分化模型中，未发现 Akt 直接参与干性因子表达调控的证据，其间的发生机制有待进一步探究。

PU-0196

液体活检在肺癌诊疗中的应用进展

谢而付
江苏省人民医院（南京医科大学第一附属医院）

肺癌是最常见的恶性肿瘤之一，近年来发病率有上升趋势。液体活检是一种新兴的分子检测技术，其主要通过对患者血液或体液中循环肿瘤细胞、循环肿瘤 DNA、DNA 甲基化、微小 RNA、外泌体及肿瘤血小板等项目的检测，来进行早期肿瘤的辅助诊断和治疗决策。它不同于常规的生物标志物检测，它具有侵入性小和取样风险低的优点。越来越多的深入研究发现，液体活检在肺癌的早期诊断、精准治疗和疗效监测上有广泛的应用，但也存在许多问题丞待解决。

PU-0197

喀什地区结核分枝杆菌谱系及亚谱系的构成及分布

何川疆、许爱敏
喀什地区第一人民医院

喀什地区地处欧亚大陆中部，同时该地区与巴基斯坦、印度等结核病高负担国家接壤，因此了解本地区结核分枝杆菌（Mtb）谱系组成，可为本地区结核病的防控工作提供基础依据。本研究对 159 例 Mtb 临床株进行全基因组测序，基于单核苷酸变异（SNV）通过最大似然法（Maximum Likelihood，ML）构建系统进化树，并利用主成分分析（PCA）进行验证，结合地理信息分析不同区域 Mtb 种群结构。结果显示：喀什地区（一市六县）Mtb 临床株由 Lineage 2（46.54%, 74/159）、Lineage 3（33.96%, 54/159）和 Lineage 4（19.50%, 31/159）构成；根据谱系特异性 SNV 将 3 个谱系细分为 9 个亚系，其中 Lineage 2 包括 Lineage 2.2.2/Asia Ancestral 1（9/74）、Lineage 2.2.1-Asia Ancestral 2（10/74）、Lineage 2.2.1-Asia Ancestral 3（16/74）及 Lineage 2.2.1-Modern 型北京亚系（39/74），Lineage 3 包括 Lineage 3.2（15/54）与 Lineage 3.3（39/54），Lineage 4 包括 Lineage 4.4（1/31）、Lineage 4.5（28/31）及 Lineage 4.8（2/31），PCA 结果与其一致；筛选获得 Lineage 2 特异性 SNV 共 150 个，Lineage 3 特异性 SNV 共 54 个，Lineage 4.5 与 Lineage 4.8 特异性 SNV 各 3 个。综上所述，喀什地区 Mtb 临床株由 Lineage 2、Lineage 3 和 Lineage 4 组成，其中 Lineage 3 在巴基斯坦为主要流行菌株，但在我国仅新疆地区流行，推测可能由于彼此地区人员流动频繁，导致该谱系菌株的传入，进而有向内陆传入的趋势；基于 Mtb 谱系特异性 SNV，将上述 3 个谱系进一步分为 9 个亚系；通过筛选并获得了喀什地区 Mtb 谱系及亚系标签。本研究为喀什地区结核病的防控工作提供了理论研究。

PU-0198

基于数字 PCR 的新型冠状病毒超敏检测策略

胡孝林[1,2]、张洪[1,2]、陈恒屹[1,2]、刘睿宁[1,2]、罗阳[1,2]
1. 重庆大学医学院智慧检验与分子医学中心
2. 重庆大学医学院公共实验中心

An ultra-sensitive, high-throughput and fast diagnostic system for novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is essential for controlling the source of infection and monitoring the progression of the disease. At present, reverse transcription polymerase chain reaction (RT-PCR) is regarded as the gold standard for COVID-19 diagnosis. However, the sensitivity and reliability of RT-PCR were questioned due to the limitation of the technology. Herein, we developed a high-throughput, multi-target one-step digital PCR assay for

COVID-19 diagnosis. This assay reduced the possibility of contamination by one-step amplification, and improved the accuracy by detecting SARS-CoV-2 specific sites (ORF, N, E gene) and human reference genes (RNP gene) synchronously. The detection limit could be up to 3 copies per reaction, which is hundreds of times higher than RT-PCR. Besides, this assay could realize the detection of 960 samples in a single reaction. This strategy provides a new opportunity for establishing an ultra-sensitive nucleic acid detection platform.

PU-0199

EB 病毒感染与 XRCC1- Arg399Gln 基因多态性在鼻咽癌发生中的交互作用研究

郭俊英、陈燕
福建省肿瘤医院

目的 探讨 VCA-IgA、EA-IgA、Rta-IgG 三种抗体在鼻咽癌中的临床应用价值，评估 XRCCl-Arg399 Gln 单核苷酸多态性在鼻咽癌发病中的风险；研究 XRCCl-Arg399 Gln 单核苷酸多态性与 EB 病毒感染的交互作用。

方法 采用 ELISA 检测 2155 例未经治疗的鼻咽癌患者及 6957 例健康体检者血清中 VCA-IgA、EA-IgA、Rta-IgG 水平；采用病例对照研究，并按照性别和年龄 1：1 配对，抽取全血基因组 DNA 进行 PCR 扩增，对扩增产物再进行酶连接检测反应扩增，最后测序分析得出 XRCC1 Arg399Gln 的基因型。

结果 VCA-IgA、EA-IgA、Rta-IgG 在鼻咽癌组中阳性率分别达 89.88%、46.59%和 63.25%；ROC 曲线分析显示，曲线下的面积 VCA-IgA>Rta-IgG >EA-IgA；危险度分析显示，VCA-IgA、EA-IgA 和 Rta-IgG 三项检测均阳性者危险度最高，其次为 VCA-IgA 和 Rta-IgG 两项阳性，三项抗体均阴性者危险度最低；VCA-IgA 抗体检测在鼻咽癌中以 41~60 岁阳性率最高（P<0.01），而 Rta-IgG 阳性率随着年龄增加而增高，另外 VCA-IgA 以非角化未分化性鳞癌阳性率最高（P<0.01）；EA-IgA 阳性率与 T 分期具呈线性相关（P<0.01），三种抗体检测阳性率分别与 N 分期、临床分期均呈线性关系（P<0.01）；EB 病毒感染能增加鼻咽癌发病风险：VCA-IgA、EA-IgA 和 Rta-IgG 抗体三项阳性时可以增加鼻咽癌风险因素，但单项 VCA-IgA 阳性是鼻咽癌发病的最强危险因素，单因素分析显示与携带 XRCC-1 Arg399Gln 的 AA 基因型相比，携带 XRCC-1 Arg399Gln 的 GG 基因型可以增鼻咽癌发病风险；XRCC-1 Arg399Gln 的 GA 基因型与 VCA-IgA 存在交互作用（OR=20.755）。

结论 三种抗体诊断价值以 VCA-IgA 最优，其次是 Rta-IgG，EA-IgA 相对较弱。鼻咽癌筛查中，以 VCA-IgA、EA-IgA 和 Rta-IgG 三项阳性危险度最高，VCA-IgA 和 Rta-IgG 两项阳性危险度次之，而三项抗体均阴性者危险度最低；XRCC-1 基因的 Arg399Gln 基因多态性能够增加患鼻咽癌的风险，且 Arg399Gln 的 GA 基因型与 EB 病毒感染具有一定的交互作用。

PU-0200

Serum miR-27a is a biomarker for the prognosis of non-small cell lung cancer patients receiving chemotherapy

Erfu Xie、shiyang pan
the First Affiliated Hospital of Nanjing Medical University

Background Lung cancer has a high incidence and a 5-year survival rate of less than 15%. Non-small cell lung cancer (NSCLC) accounts for approximately 85% of lung cancer cases. Chemotherapy and immunotherapy are the most frequently used alternative treatments for

patients with advanced-stage NSCLC in whom surgery failed. Previous studies have suggested that miR-27a is involved in cancer development and progression. The purpose of this study was to investigate the clinical value of miR-27a in the prognosis of NSCLC patients after chemotherapy.

Methods Flow cytometry was used to detect the apoptosis rate of SPC-A1 cells treated with optical cisplatin at different times. Simultaneously, the expression of miR-27a in supernatants and cells was detected. Fifty-two newly diagnosed NSCLC patients were recruited. All patients received gemcitabine and cisplatin as first-line chemotherapy and docetaxel as second-line chemotherapy. At the end of every chemotherapy cycle, a therapeutic evaluation was performed according to the RECIST criteria. The expression of serum miR-27a was detected in each cycle.

Results After treatment with 2.5 μg/mL cisplatin, the apoptosis rates of SPC-A1 cells were significantly greater than those of the paired untreated control groups at 12, 24, 48 and 72 h. The expression of miR-27a in supernatants and cells was also consistent with the apoptosis rate and changed a time-dependent manner. The chi-square test showed that an increase in miR-27a after chemotherapy was more common in patients who achieved partial response (PR) than in those who achieved no response (NR) (61.5% vs 30.8%, P=0.026). Kaplan–Meier survival analysis indicated that patients with decreased miR-27a levels had poorer outcomes than those with increased miR-27a levels (P<0.05). Furthermore, dynamic changes in serum miR-27a with a gradual increasing trend during chemotherapy predicted a good prognosis.

Conclusions Collectively, our results suggest that miR-27a is involved in the apoptosis of lung cancer cells and that serum miR-27a levels are related to the prognosis of NSCLC patients. The expression levels of miR-27a in the serum may be an independent predictor for the prognosis of NSCLC.

PU-0201

抑癌基因 ARID1A 在急性髓系白血病中的诊疗价值及抑癌机制

任天莹、陈东亮、王爽、李阳、杨大伟
聊城市人民医院

急性髓系白血病(简称急性髓系白血病，AML)是一种造血系统恶性肿瘤，由造血干细胞过度增殖引起。急性髓系白血病的发病率很高，尤其是在儿童和青少年中。近年来，随着治疗水平的不断提高，AML 存活率大幅提高，患者病情得到有效控制甚至完全缓解。然而，仍有一半以上的 AML 患者因复发或耐药而预后不良。寻找新的分子靶点，包括癌基因、抑癌基因、表观遗传学和免疫治疗靶点等，是 AML 治疗的研究热点之一。

本实验通过收集临床急性髓系白血病病人骨髓标本，根据病程进展分组，利用实时荧光定量 PCR 法分析 ARID1A 的 mRNA 表达水平，分析病程进展与 ARID1A 表达水平的相关性。利用慢病毒载体，构建 ARID1A 敲低表达白血病细胞株，作为后续细胞分析模型。MTT 法分析 ARID1A 敲低表达对细胞凋亡的影响，并利用流式细胞术分析细胞凋亡和细胞周期。体外分析 ARID1A 敲低表达后细胞对化疗药物柔红霉素和阿糖胞苷耐药性的改变。最后通过分析信号通路探究 ARID1A 参与调控白血病细胞的相关分子机制。

结果 发现 ARID1A mRNA 的低表达与急性髓系白血病的复发显著相关(P<0.001)。ARID1A 的低表达可能成为 AML 复发的一个新的生物标志物。ROC 曲线测定 ARID1A 表达对急性髓系白血病复发的诊断价值(曲线下面积为 0.978)。ARID1A 低表达导致细胞凋亡抑制，细胞周期阻滞。并发现 ARID1A 低表达可激活 TGF-β1/Smad3 信号通路并抑制凋亡分子 Caspase3。

结论 ARID1A 低表达或可能成为 AML 复发的一个新的生物标志物。在急性髓系白血病中 ARID1A 通过激活 TGF-β1/Smad3 信号通路同时抑制 Caspase3 调控白血病细胞凋亡。

PU-0202

Construction of a circRNA-miRNA-mRNA Network to Unveil the Mechanism of Hepatocellular Carcinoma Occurrence and Prognosis

Yingying Lin、 Jing Wu、Zhaolei Cui、Yan Chen
Fujian Cancer Hospital

Background This study aimed at understanding the mechanisms of pathogenesis and providing novel biomarkers involved in the occurrence and prognosis of hepatocellular carcinoma (HCC) by constructing a circular (circ)RNA-micro (mi)RNA-mRNA network ceRNA network.
Methods High-throughput sequencing data covering circRNA, miRNA, and mRNA expression profiling in HCC were downloaded from the Gene Expression Omnibus (GEO) database. Differentially expressed circRNAs, miRNAs, and mRNAs were identified with the cutoff adj. $P < 0.05$ and $|Log2FC| > 2$ and screened by Limma package in R language. Based on circRNA-miRNA pairs and miRNA-mRNA pairs, a ceRNA network was constructed. The possible functions of these differentially expressed circRNAs were analyzed using gene ontology (GO) and Kyoto encyclopedia of genes and genomes (KEGG) enrichment analysis.
Results Forty-nine down-regulated circRNAs, 7 up-regulated miRNAs, and 702 down-regulated mRNAs were identified differentially expressed in HCC. A ceRNA network composed of target genes was constructed, incorporating 10 circRNAs, 5 miRNAs, and 13 differently expressed genes (mRNAs). Among the target mRNAs, 6 mRNAs (CPD, ESR1, HAT1, MAPK1, PPARGC1A, SRD5A3) could be associated with HCC prognosis. The network enrichment analysis showed that sex steroid hormone regulation and MAPK activation could be key processes associated with the target mRNAs in hepatocarcinogenesis.
Conclusions Our study provides a vision for the circRNA-miRNA-mRNA regulatory network as a promising tool for the mechanism research and biomarker identification of HCC occurrence and prognosis. The selected 6 prognostic differently expressed genes are expected to uncover new targets for clinical treatments.

PU-0203

Polymorphic variants of CCL2, IL-10 in recipients were associated with cytomegalovirus infection after hematopoietic stem cell transplantation

Ziyao Yang、Xiaotao Zhao
Peking University People's Hospital

OBJECTIVE Cytomegalovirus (CMV) infection is an important cause of non-recurrence death in hematopoietic stem cell transplantation (HSCT) patients. Host genetics of CMV pathogenesis has recently attracted increasing interest, however, there are few reports on CMV in HSCT population. To investigate the correlation between SNPs of CCL2, IL-10 and CMV infection, which would assist in predicting the infection incidence and managing CMV infection.
METHODS This was a retrospective observational study. CMV surveillance was performed on 128 HSCT recipients by real-time polymerase chain reaction (PCR) twice a week till +100d. Then, we analyzed their SNPs of CCL2 (rs1024611, rs13900) and IL-10 (rs1800871) by PCR and Sanger sequencing. The correlation between cytokine SNPs and CMV infection was further evaluated based on virological and clinical parameters.
RESULTS Among the 128 recipients, CMV infection was found in 73 recipients till +100d. As for rs1024611, GA genotype ($p=0.003$, HR=0.109, 95% CI: 0.026-0.463) and AA genotype ($p<0.001$, HR=0.019, 95% CI: 0.003-0.133) showed significantly lower risk of CMV infection than GG

genotype. In addition, TC genotype (p=0.032, HR=4.702, 95% CI: 1.141-19.381) and CC genotype (p<0.001, HR=32.593, 95% CI: 5.290-200.806) of CCL2 rs13900 increased risk of CMV infection when compared with TT genotype. Besides, as for rs1800871, TC genotype (p=0.028, HR=1.824, 95% CI: 1.066-3.121) and CC genotype (p=0.035, HR=2.099, 95% CI: 1.054-4.181) showed significantly higher risk of CMV infection than TT genotype respectively, either. In CMV infected recipients, the highest CMV DNA load during continuous surveillance was associated with the number of high-risk genotypes the recipient carried (H=6.267, p=0.044).
CONCLUSION SNPs of CCL2 (rs1024611, rs13900) and IL-10 (rs1800871) in recipients were associated with CMV infection after HSCT.

PU-0204

Expression and Clinical Implications of Basic Leucine Zipper ATF-Like Transcription Factor 2 in Breast Cancer

Yingying Lin、Zhaolei Cui、Yan Chen
Fujian Cancer Hospital

Objective Basic leucine zipper ATF-like transcription factor 2 (BATF2) has been reported to participate in the occurrence and development of some malignancies. But little is known about its roles in breast cancer (BC). In this work, we aimed to explore the expression pattern and clinical implications of BATF2 in BC.
Methods We assessed the differences in BATF2 mRNA expression between cancerous and noncancerous tissues in BC using online databases. In external validations, BATF2 protein expression in BC tissues was quantitated using a tissue microarray and immunohistochemical (IHC) analysis, and BATF2 mRNA expression in serum and serum-derived exosomes of BC patients using qRT-PCR.
Results There were low-to-moderate levels of increases in BATF2 protein expressions in BC cases. BATF2 mRNA expression was negatively correlated with androgen receptor (AR) and positively correlated with BRCA2, Mki67, and TP53 expressions. Subgroup analyses showed that triple-negative breast cancer (TNBC) patients with high BATF2 mRNA expressions had a longer overall survival (OS). Our IHC analysis revealed a positive rate of BATF2 protein expression of 46.90%. The positive rates of BATF2 mRNA expressions in the serum and exosomes were 45.00% and 41.67%, respectively. Besides, the AUCs of serum and exosomal BATF2 mRNA for BC diagnosis were 0.8929 and 0.8869, respectively.
Conclusions BC patients exhibit low-to-moderate increases in BATF2 mRNA expression levels in cancerous tissues, of which low BATF2 mRNA expression serves as an indicator of a poor TNBC prognosis. The high BATF2 protein expression can be a potential indicator of a better BC prognosis. Serum and exosomal BATF2 mRNA levels also serve as promising noninvasive biomarkers for BC diagnosis.

PU-0205

Diagnostic and Prognostic Potential of Circulating and Tissue BATF2 in Nasopharyngeal Carcinoma

Yingying Lin、Zhaolei Cui、Yan Chen
Fujian Cancer Hospital

Objective At present, there is still a lack of effective markers for early diagnosis and prognostic monitoring of nasopharyngeal carcinoma (NPC). A large number of studies have shown that the basic leucine zipper ATF-like transcription factor 2 (BATF2) gene is closely related to the

occurrence and development of a variety of malignant tumors. However, the expression of BATF2 in NPC and its clinical significance is still unclear.
Methods A high-throughput tissue microarray combined with immunohistochemistry (IHC) was used to detect the expression of BATF2 proteins in NPC tissues, and to explore its relationship with clinicopathological characteristics and the prognosis of NPC. Meanwhile, a quantitative reverse transcription-polymerase chain reaction (qRT-PCR) was used to detect the expression of BATF2 mRNA in serum and serum-derived exosomes of NPC patients.
Results The IHC showed that BATF2 was mainly localized to the nucleus of NPC tissue cells. Survival analysis showed that the NPC patients with a positive BATF2 expression enjoyed a longer duration of overall survival than those with a negative BATF2 expression. The positive expression rates of BATF2 mRNA in serum and serum exosomes of NPC patients were 51.47% and 48.52%, respectively. The AUCs of NPC patients diagnosed by serum and exosomal BATF2 and healthy control groups were 0.9409 and 0.8983, respectively. The BATF2 levels of serum and exosomes of NPC patients in the treatment group were higher than those in the initial group, but lower than those in the recurrence group.
Conclusion BATF2 is expected to be a promising prognostic marker for NPC. BATF2 in serum and serum exosomes can be used as an important biomarker for diagnosis, efficacy evaluation, and recurrence monitoring of NPC.

PU-0206

The Novel Key Genes of Non-obstructive Azoospermia Affect Spermatogenesis: Transcriptomic Analysis Based on RNA-Seq and scRNA-Seq Data

Haihong He[1]、Fan Yu[1]、Wang Shen[2]、Yiwen Zhou[1]
1. Clinical Laboratory Medical Center, Shenzhen Hospital, Southern Medical University,
2. 江门市五邑中医院

Non-obstructive azoospermia (NOA) is one of the most important causes of male infertility. It is mainly characterized by the absence of sperm in semen repeatedly or the number of sperm is small and not fully developed. At present, its pathogenesis remains largely unknown. The goal of this study is to identify hub genes that might affect biomarkers related to spermatogenesis. Using the clinically significant transcriptome and single-cell sequencing data sets on the Gene Expression Omnibus (GEO) database, we identified candidate hub genes related to spermatogenesis. Based on them, we performed Gene Ontology (GO) functional enrichment analysis, Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment pathway analyses, protein-protein interaction (PPI) network analysis, principal component analysis (PCA), cell cluster analysis, and pseudo-chronological analysis. We identified a total of 430 differentially expressed genes, of which three have not been reported related to spermatogenesis (C22orf23, TSACC, and TTC25), and the expression of these three hub genes was different in each type of sperm cells. The results of the pseudo-chronological analysis of the three hub genes indicated that TTC25 was in a low expression state during the whole process of sperm development, while the expression of C22orf23 had two fluctuations in the differentiating spermatogonia and late primary spermatocyte stages, and TSACC showed an upward trend from the spermatogonial stem cell stage to the spermatogenesis stage. Our research found that the three hub genes were different in the trajectory of sperm development, indicating that they might play important roles in different sperm cells. This result is of great significance for revealing the pathogenic mechanism of NOA and further research.

PU-0207

RPA 技术快速检测 SARS-CoV-2

陈斌、梁广铁、吴斌、徐邦牢
广州市第一人民医院

目的 2019 年 12 月发现的新型冠状病毒（SARS-CoV-2）肺炎已经蔓延全球，截止目前全球累计近 1 亿人确诊，250 多万人死亡，疫情对全球公共卫生体系造成了极大的威胁。因此，需要研制出新的技术方法快速检测 SARS-CoV-2，有效控制疫情和阻断病毒的传播。
方法 本研究应用重组酶聚合酶恒温扩增技术（Recombinase Polymerase Amplification， RPA），根据 GenBank 查找 SARS-CoV-2 病毒的 N 基因，以其为靶序列设计生成出一套合适的引物和荧光探针，建议 RT-RPA 快速检测 SARS-CoV-2 的方法；使用标准质粒 RNA 模板考察该方法的灵敏度；同时，使用其他 5 种常见呼吸道冠状病毒的 RNA 模板考察该方法的特异性；最后使用临床样本比较该方法与荧光定量 RT-PCR 检测方法的结果。
结果 RT-RPA 检测 SARS-CoV-2 仅需 15 分钟；该方法的检测灵敏度为 101 拷贝/μL；该方法对其他常见呼吸道冠状病毒无交叉反应；与 RT-qPCR 结果符合率为 100%。
结论 RT-RPA 检测 SARS-CoV-2 方法具有操作简便快捷、成本低、灵敏度低和特异性高等优点，可应用于临床检测和大规模人群筛查。

PU-0208

外周血单个核细胞的 DNA 甲基化测序对鉴别良恶性肺结节的初步分析

刘士标
山东大学第二医院

目的 现阶段，肺癌在中国的发病率和死亡率均居第一位。相对于中晚期患者，早期肺癌的五年生存率较高。提高早期肺癌的诊断率已成为改善患者预后的较好方法。目前，低剂量螺旋 CT 是筛查早期肺癌最普遍的方法，但假阳性率较高，尤其是对于直径小于 3cm 的肺部结节，难以区分其良恶性。而穿刺活检具有侵入性，且对于微小结节的穿刺操作，难度较大。如何鉴别诊断良恶性肺结节已成为临床上亟待解决的一大难题。作为表观修饰的一种形式，DNA 甲基化被证实与肿瘤的发生发展密切相关。而外周血单个核细胞（单核细胞、T 细胞、B 细胞、NK 细胞）在肿瘤免疫中发挥着重要作用。因此，外周血单个核细胞的 DNA 甲基化测序极有可能成为鉴别良恶性肺结节的一种新型无创诊断工具。
方法 在我们的研究当中，共有 25 例经病理学诊断为恶性肺结节病人的外周血样本和 30 例年龄、性别相匹配的经病理学诊断为良性肺结节病人的外周血样本。其中，25 例恶性肺结节病人包括 15 例原位癌和 10 例Ⅰ期肺癌病人，30 例良性肺结节病人的病理类型包括错构瘤、肺泡细胞瘤、肺细支气管腺瘤、结核坏死灶、肉芽肿性炎、肺纤维结缔组织结节状增生伴碳沫沉积、非典型腺瘤样增生等，且所有病人在抽取外周血前未经手术、放疗、化疗等任何治疗。我们利用 Ficoll 分离液，根据密度梯度离心的原理，从外周血中分离出单个核细胞，于-80℃保存。我们通过 850K 芯片对以上病人的外周血单个核细胞进行 DNA 甲基化测序分析，以了解良恶性肺结节甲基化位点的差异情况，从而为良恶性肺结节的鉴别提供一种新型无创诊断工具。
结果 850K 芯片测序结果显示，以|deltaBate|≥0.06 且 adj.P.Val＜0.01 为参考界限，共筛选出 166 个差异甲基化位点。我们对 166 个差异甲基化位点的分布情况进行了分析，发现其中 42.6%分布在 Island，29.4%分布在 N-Shore，20.6%分布在 S-Shore，5.9%分布在 S-Shelf，1.5%分布在 N-Shelf。进一步，我们发现这些差异甲基化位点位于基因的不同调控区，其中 60.8%位于 Body，

20.5%位于 TSS1500，9.1%位于 5'UTR，4%位于 TS200，2.8%位于 3'UTR，2.8%位于 1stExon，可以看出绝大多数位于 Body 和 TSS1500。

结论 良恶性肺结节病人的外周血单个核细胞中存在显著差异甲基化位点，进而会影响与之对应的基因表达情况。下一步，经多中心、大样本验证，外周血单个核细胞的 DNA 甲基化测序有望成为鉴别良恶性肺结节的一种新型无创诊断工具。

PU-0209

The effects of miR-139-5p in heart injury

Ziyao Yang、Ming Su、Xiaotao Zhao
Peking University People's Hospital

Objective Heart failure is a serious end-stage syndrome of many cardiac diseases. Previously, we reported that miR-139-5p is an anti-hypertrophic molecular in hypertrophic cardiomyopathy. However, whether miR-139-5p is correlated with cardiac injury and heart failure remains unclear. In the present study, we investigated the role of miR-139-5p in cardiac injury and observed the changes of circulatory miR-139-5p in heart failure patients.

Methods Neonatal rat cardiac myocytes (NRCM) were transfected with miR-139-5p and co-treated with isoproterenol (ISO) or adriamycin (ADR). The expression of MYH6 and MYH7 and potential targeting genes (TCF4 and PPP2R2A) was determined using Western blot. The morphology of NRCM was observed by fluorescence microscopy, and NRCM viability was detected using CCK-8 assay. The ADR-induced heart injury mice model was established and the circulatory miR-139-5p in mice was determined using real-time qPCR. We recruited 35 cases of heart failure patients and 27 cases of healthy controls. The plasma miR-139-5p was detected using real-time quantitative PCR detecting system.

Results In ISO-treated NRCM, we observed that both MHY7 and MYH6 were up-regulated. In the presence of miR-139-5p overexpression, MYH7 was partially recovered, whereas MYH6 remained unchanged. We found that the expression of potential targeting genes: TCF4 and PPP2R2A were both downregulated by overexpression of miR-139-5p. We observed that overexpression of miR-139-5p partially rescued ADR-induced cardiomyocyte injury. However, the expression of miR-139-5p in the serum of ADR-treated mice showed no significant changes compared with the control mice. Consistently, we found that the circulatory miR-139-5p levels in heart failure patients' plasma and healthy controls were comparable.

Conclusion miR-139-5p may participate in ISO- and ADR-induced cardiac injury in heart tissues, but circulatory miR-139-5p might not be served as a biomarker for heart failure.

PU-0210

肺腺癌患者外周血单个核细胞的 DNA 甲基化测序初步分析

刘士标
山东大学第二医院

目的 当今，肺癌在全球范围内的发病率和死亡率逐年升高，预后较差。从病理学分型角度来看，腺癌占肺癌绝大部分，所以我们把目标集中在肺腺癌。目前，低剂量螺旋 CT 是筛查肺癌最普遍的方法，但有时会出现假阳性，而穿刺活检具有侵入性。作为表观修饰的一种形式，DNA 甲基化被证实与肿瘤的发生发展密切相关。而外周血单个核细胞（单核细胞、T 细胞、B 细胞、NK 细胞）在肿瘤免疫中发挥着重要作用。因此，外周血单个核细胞的 DNA 甲基化测序极有可能成为肺腺癌的一种新型无创诊断工具。

方法 在我们的研究当中，共有 35 例经病理学诊断为肺腺癌病人的外周血样本和 50 例年龄、性别相匹配的健康人外周血样本，其中 35 例肺腺癌病人具有不同的 TNM 分期（原位癌：15 例；Ⅰ期：

10 例；Ⅱ期+Ⅲ期+Ⅳ期：10 例），且抽取外周血前未经手术、放疗、化疗等任何治疗。我们利用 Ficoll 分离液，根据密度梯度离心的原理，从外周血中分离出单个核细胞，于-80℃保存。我们通过 850K 芯片对肺腺癌和健康人的外周血单个核细胞进行 DNA 甲基化测序分析，以了解肺腺癌的发生发展过程中甲基化位点的改变情况，从而为肺腺癌提供一种新型无创诊断工具。

结果 850K 芯片测序结果显示，以|deltaBate|≥0.06 且 adj.P.Val＜0.05 为参考界限，共筛选出 1415 个差异甲基化位点。我们对 1415 个差异甲基化位点的分布情况进行了分析，发现其中 27.2%分布在 N-Shore，26.3%分布在 S-Shore，22.5%分布在 Island，13%分布在 S-Shelf，11%分布在 N-Shelf。进一步，我们发现这些差异甲基化位点位于基因的不同调控区，其中 67.5%位于 Body，15%位于 5'UTR，10.3%位于 TSS1500，3.5%位于 TS200，1.9%位于 3'UTR，1.8%位于 1stExon。基于 TSS 对基因表达的重要调控，我们又针对 TSS 附近位点的甲基化水平进行了分析比较，发现：在 TSS 的相同距离处的位点，肺腺癌病人的甲基化水平显著高于健康人（P≤0.01）。

结论 在肺腺癌的发生发展过程中，外周血单个核细胞的 DNA 甲基化水平发生了明显改变，进而会影响与之对应的基因表达情况。下一步，经多中心、大样本验证，外周血单个核细胞的 DNA 甲基化测序有望成为肺腺癌的一种新型无创诊断工具。

PU-0211

昆明医科大学第一附属医院 260 例 HBV 耐药基因突变检测及统计分析

张艳亮[1,2]、段勇[1,2]
1. 昆明医科大学第一附属医院
2. 云南省检验医学重点实验室

目的 乙肝病毒（HBV）复制过程中存在较高的核苷酸错配率，导致 HBV 对核苷（酸）类似物药物耐药率。本文旨在对云南省昆明地区 HBV 进行耐药基因突变检测及统计分析，了解本地区 HBV 耐药基因突变的变化趋势，为临床合理用药提供理论依据。

方法 收集 2013 年 12 月~2018 年 5 月期间到昆明医科大学第一附属医院就诊并被确诊为乙肝的 260 例患者，各抽取 3mL EDTA-K2 抗凝外周血，3000 rpm 离心 10min，取血浆-80°C 冻存备用。提取 HBV DNA，针对 HBV 聚合酶逆转录酶区，采用 AB3500Dx 测序仪进行 Sanger 测序，测序结果采用 Celloud 数据库进行比对分析，确定 HBV 基因型以及是否存在位点突变，并进行统计分析。

结果 260 例 HBV 中，C 型 171 例（65.77%），B 型 89 例（34.23%），未检出其他基因型（图 1）。检测到临床意义明确的耐药位点突变的 HBV 64 例（24.62%），无临床意义明确的耐药位点突变但有临床意义尚不明确的位点突变的 HBV 186 例（71.54%），既有临床意义明确的耐药位点突变又有临床意义尚不明确的位点突变的 HBV 62 例（23.85%），有临床意义明确的耐药位点突变但无临床意义尚不明确的位点突变的 HBV 有 2 例（0.76%），无任何位点突变的 HBV 有 10 例（3.85%）（图 2）。临床意义明确的耐药位点突变数共 99 个，其中 rtM204I 28 个（28.28%）、rtL180M 28 个（28.28%）、rtM204V 20 个（20.20%）、rtA181V 6 个（6.06%）、rtV173L 6 个（5.05%）、rtA181T 5 个（5.05%）、rtN236T 4 个（4.04%）、 rtM250L 3 个（3.03%）（图 3）；临床意义不明确的位点突变共 715 个，其中 rtL169I 163 个（22.79%）、rtS223A 154 个（21.54%）、rtI224V 116 个（16.22%）、rtF221Y 87 个（12.18%）、rtT222A 67 个（9.37%）、rtQ267L 46 个（6.43%）、rtV278I 39 个（5.46%）、rtQ267H 21 个（2.93%）、rtE263D 12 个（1.68%）、rtV191I 10 个（1.40%）（图 4）。

结论 云南昆明地区 HBV 以 C、B 型为主，存在较高的耐药突变率，204 位点和 180 位点是已知耐药突变位点中突变频率最高的两个位点。大部分 HBV 的聚合酶逆转录酶基因存在临床意义尚不明确的位点突变，这些位点的统计分析为 HBV 耐药机制的阐明及新耐药位点的揭示奠定了良好基础。

PU-0212

恒温扩增技术及临床应用进展

王琪、刘春林
云南大学附属医院

随着分子生物学技术的迅猛发展，基于核酸检测的诊断方法已大量建立并广泛应用于各种实验室检测中。恒温扩增技术是近年新发展起来的一门新型的能够在体外进行的核酸扩增技术。基于 PCR 的基本原理和对 PCR 技术进行研究和改进，与其他的核酸扩增技术相比，无论是在实际操作还是仪器要求方面，恒温扩增技术有快速、高效、特异的优点且无需专用设备，在临床和现场快速诊断中显示了良好的应用前景，已经成为了生物分析研究领域的重点，并被广泛应用在科学研究、病原物诊断、人类基因组工程研究、法医、组织和群体生物学等各个领域。在众多的恒温扩增技术中，环介导恒温扩增、滚环扩增等技术在目前比较熟知，也已经在一定范围内得到了很好的应用，而其他一些新派生出来的恒温扩增技术，如依赖核酸序列的扩增、转录介导的扩增、链替代恒温扩增和单引物恒温扩增等技术，也在不断发展和完善中。为了更好地对这些技术的原理、特点以及临床应用进行研究和改进，使其得到完善，现对这些技术进行综述。

PU-0213

Study on the proportion of asymptomatic or mildly ill COVICD-19 patients and their immunological responses in Fangcang shelter hospital

ying li
Department of Laboratory Medicine, the First Affiliated Hospital of Chongqing Medical University

Background Asymptomatic or mildly ill COVID-19 patients who had no obvious symptoms were considered to be a great source of infection, whereas their proportion and immunological responses were still unknown.
Objective To Study the proportion and immunological responses of asymptomatic or mildly ill patients.
Methods Retrospectively collected clinical manifestations, IgM and IgG antibodies responses, and nucleic acid test results of 92 consecutive COVID-19 patients, in Wuhan Dongxihu Fangcang Shelter Hospital, to calculate proportions of patients with different manifestations and evaluate their respective seroconversion rates of antibodies.
Results A total of 368 nasopharyngeal swab samples were collected from 92 patients and the accumulated positive cases and rates of the first to fifth time of nucleic acid tests were 23(25.0%), 40(43.5%), 51(55.4%), 55(59.8%) and 57(62.0%), respectively (Table 1). Of 92 patients, 89(96.7%) were tested positive for both IgM and IgG on admission, and 3 were negative for both IgM and IgG but developed into both positive before discharge. Of 92 patients, 7(7.6%) patients had fever before or after admission, 27(29.4%) patients had respiratory symptoms but no fever, and 58(63.0%) had no obvious symptoms, and their positive rates of both IgM and IgG were 100%, 92.6% and 98.3%, respectively (Table 2).
Conclusion Among patients admitted to the Fangcang shelter hospital, there were a high proportion of asymptomatic or mildly ill patients. Those patients have a higher seroconversion rate of IgM and IgG on admission, which have important diagnostic value for COVID-19.

PU-0214

蝙蝠葛碱对肝癌细胞 Huh7 增殖和凋亡的作用及机制研究

朱鹏飞、明亮
郑州大学第一附属医院

目的 研究蝙蝠葛碱对肝癌细胞 Huh7 的增殖和凋亡的作用，探索其抗肿瘤的作用机制和与 Hedgehog 信号通路的关系。
方法 给予不同浓度的蝙蝠葛碱，采用四甲基偶氮唑蓝（MTT）法检测 Huh7 细胞增殖能力的变化；流式细胞术分析 Huh7 细胞凋亡变化；Real-time PCR、Western blot 法检测 Hedgehog 信号通路相关基因及蛋白表达水平。
结果 随着蝙蝠葛碱浓度及作用时间的增加，Huh7 细胞增殖的抑制率升高。其中 8 μg/mL 蝙蝠葛碱作用 48 h 对细胞抑制率最高（48.8%）。蝙蝠葛碱可明显诱导 Huh7 细胞发生凋亡。随着蝙蝠葛碱作用浓度的增大，细胞的凋亡率显著升高。Hedgehog 信号通路中 PTCH1、GLi1、SMO、SHH 基因的 mRNA 表达水平明显降低，并与蝙蝠葛碱的浓度呈负相关。Western blot 分析结果显示，Hedgehog 信号通路中 PTCH1、GLi1、SMO、SHH 蛋白水平明显降低，同时 cleaved Caspase 3 蛋白水平显著升高，而 Bcl-2 表达水平降低，并与蝙蝠葛碱呈浓度依赖性。
结论 蝙蝠葛碱可明显抑制肝癌细胞 Huh7 的增殖，促进其凋亡，其机制可能通过抑制 Hedgehog 信号通路发挥作用。

PU-0215

Comprehensive analysis of aberrantly expressed circRNAs, mRNAs, and lncRNAs in patients with non-keratinizing undifferentiated nasopharyngeal carcinoma

Dayang Chen、Dan Xiong、Wei Wu、Xiaowen Dou、Xiang Ji、Xiuming Zhang
Medical Laboratory of Shenzhen Luohu Hospital Group

Purpose Nasopharyngeal carcinoma (NPC) is one of the most common types of human cancers in east and southeast Asia. Dysregulation of long non-coding RNA (ncRNA)have huge impacts on the occurrence and development of NPC. In this study, we aim to investigate expression profiles of circRNAs, mRNAs and lncRNAs and to provide some basis for further study.Materials & **Methods** The expression profiles of circRNAs, mRNAs and lncRNAs were analyzed by microarray technology. The differentially expressed ncRNA was calculated by bioinformatics. Gene ontology and Kyoto Encyclopedia of Genes and Genomes were used to predict the functions of differentially circRNAs, mRNAs and lncRNAs. In addition, we constructed circRNA-miRNA, circRNA-mRNA and lncRNA-mRNA networks to determine functional interactions among ncRNA. Cis- and trans-acting lncRNAs involved in NPC were predicted by bioinformatics. With the implementation of the R package of “glmnet” methods, we applied Least Absolute Shrinkage and Selection Operator (LASSO) for building a diagnostic model on the training dataset. The tuning parameter was determined according to the binomial devicance estimated from 10-fold cross-validation, and we adopted the lowest binomial deviance, known as "lambda.min". The difference of RiskScore distribution was examined by Wilcoxon Rank Sum test.
Results A total of 3,048 circRNAs, 2,179 lncRNAs and 2,015 mRNAs were detected to be significant differentially expressed in NPC. The differentially expressed (DE) non-coding RNA were assessed through bioinformatics. Notably, 3,048 circRNAs, 2,179 lncRNAs, and 2,015 mRNAs were found to be significantly differentially expressed in NPC. The number of upregulated DE lncRNAs was twice more than those downregulated. Based on our data, 80.44% lncRNAs and cis-mRNAs pairs demonstrated a positive correlation. For lncRNAs and trans-mRNAs pairs, 53.7% of pairs were positively correlated. We revealed lncRNA-mediated cis-regulation as a

prevalent regulatory mode in the development of NPC. CR1, LRMP, and SORBS2 were predicted to be mediated by cis-acting lncRNA modes of action and via trans-acting lncRNA mechanisms. Additionally, A four-gene diagnostic risk model was built: 0.7889 *FERMT1 -1.4967 *STOML3 -1.0247 *MROH2A -0.5226 *AMY1C. The RiskScore has 94.4% sensitivity and 100% specificity as compared with clinical diagnosis.
Conclusion Our study provides a theoretical basis for using ncRNA as new biomarkers for predicting the tumorigenesis of NPC.

PU-0216

一步法巢式 PCR 方法的研究现状及在病原体高通量测序中的应用

杨传坤
东南大学附属中大医院

一步法巢式 PCR(onestepnested-PCR,OSN-PCR)把内外引物同时配置在反应管内，使得传统的两轮扩增反应中途无需再次打开管盖。在整个 OSN-PCR 中，两阶段的扩增反应是连续进行的，反应管不需要为添加新试剂而打开或更换。这种策略使得 OSN-PCR 比 N-PCR 的操作过程更简便，降低了交叉污染的风险，并减少了反应试剂的用量。

本文综述了国内外多个团队针对微生物检测的各种 OSN-PCR 方法，包括甲型肝炎病毒，人类免疫缺陷病毒Ⅰ型，结核分枝杆菌和鼠疫耶尔森氏菌等检测中比较流行的 OSN-PCR 设计策略是把内引物预先固定在管盖内壁，通常是将内引物和溴酚蓝溶液固定于管盖内壁。也有一些研究人员利用结构特殊的反应管实现内外引物的分离，这种 PCR 管的内部另有一个预制的细管，用于存放内引物溶液。还有一些 OSN-PCR 方法利用内外引物不同的 Tm 值，通常外引物被设计得比内引物更长，使其 Tm 值提高，通过改变首轮和次轮的退火温度，不用开盖即可做到两轮 PCR 的独立反应。为了保证外引物在第二轮 PCR 中完全失效，有人利用反义寡聚核苷酸来减少非特异性扩增，这种寡聚核苷酸的一部分序列与外引物匹配，可以在低退火温度条件下给外引物的 3 ’末端引入错配，彻底封闭其延伸能力，进一步保证了第二轮扩增的独立性。一步法巢式 PCR 以其操作简单和有效避免开盖污染等特点，已被广泛应用于二代测序等技术流程中，对于 PCR 技术发展具有深刻意义与广泛用前景。

PU-0217

克罗恩病(CD)患者对抗肿瘤坏死因子 α（anti-TNF-α）治疗无应答的分子机制分析

郑静、张铁、王萍、王立伟、韩呈武、曹永彤
中日友好医院

目的 临床疗效表明抗肿瘤坏死因子 α (anti-TNF-α)治疗能有效诱导和维持克罗恩病(CD)的缓解。然而，多达 40%的患者不能对 anti-TNF-α 药物产生应答。在本研究中，我们旨在通过生信分析，探索 CD 患者对 anti-TNF-α 治疗无应答的分子机制。
方法 从 GEO (Gene Expression Omnibus)数据库获得一系列 CD 患者接受 anti-TNF-α 治疗前后肠道活检的转录组测序数据集，分析 anti-TNF-α 治疗应答组和无应答组治疗前后的差异表达基因。采用基因集变异分析(GSVA)、基因集富集分析(GSEA)、KEGG 通路分析和蛋白互作网络分析(PPI)等方法，分析 anti-TNF-α 治疗应答相关信号通路和特征基因。
结果 分析表明，anti-TNF-α 的应答伴随着大量基因的显著调控，包括 REG1A、IL8、S100A8、S100A9、IL1B、MMP1 和 MMP3 等，它们的下调与黏膜愈合相关。而对 anti-TNF-α 的无应答的

患者 IL1B、IL17A 和 S100A8 持续高表达。值得注意的是，不管患者对 anti-TNF-α 的有无应答，anti-TNF-α 都下调 IL6、IL23p19、MMP9、CD69、CD83 和 VCAM1 等炎症介质的表达。
结论 IL1B、IL17A 可能是 anti-TNF-α 治疗无应答的关键分子，是潜在的治疗靶点。而 anti-TNF-α 药物对 IL6 和 IL23p19 的下调与治疗效果无关，提示靶向后者的治疗可能得不到治疗 CD 的效果。

PU-0218

富集技术在宏基因组测序技术中应用的研究进展

杨传坤
东南大学附属中大医院

高通量测序与计算机分析流程共同组成的宏基因组技术在微生物研究领域引起重大变革，影响深远。但是用以解决基于组装或编排的宏基因组，尤其是高度复杂样品或环境中与已知基因组相似度有限的物种，现有的测序与分析流程均存在一定的局限性，因此需要对于宏微生物组实施更加有效的富集技术及方法。本文中对于现有的富集微生物组细胞及基因组片段的方法进行了梳理与总结。这其中包括：超速离心技术、多核酶处理技术、全基因组扩增、单细胞测序、流式分选技术、原位富集技术、培养及微培养、序列捕获技术、免疫磁珠分离技术、背景（人原宿主及真核细菌）去除技术等。这些技术及方法极大的提高了宏微生物组序列信息的富集效率，以及随之而来的测序数据的利用率。但是，这些方法也都不同程度的存在各种各样的问题及局限性。本文针对宏病毒组鸟枪法测序（Virome shotgun sequencing,VSS），宏病毒组富集技术的发展趋势是需要能够覆盖更宽广的病毒种类，取得特异性与病毒种类覆盖度的平衡。因此，开发针对病毒基因组序列，而又不依赖于其序列信息的病毒基因组富集技术，并将之应用于二代测序技术流程，提高病毒序列检出灵敏度，对于未知病原检测及宏病毒组研究具有深刻意义与实用前景。

PU-0219

新型冠状病毒核酸混样检测模式的评估

杨传坤
东南大学附属中大医院

目的 对新型冠状病毒核酸混样检测样本混采模式和稀释混样模式进行评估。
方法 样本混采模式：分别把 2、4、7 个阴性咽拭子同一个阳性拭子放在一个采样容器中，然后加 3 mL 洗脱液充分洗脱样本；稀释混样模式：先把样本充分洗脱混匀，再分别把 2、4、7 个阴性咽拭子同一个阳性拭子从各自容器取 100 μL 保存液进行混合。取 200 μL 混合样本在全自动核酸提取仪进行核酸提取，然后进行实时荧光 RT-PCR 反应。
结果 不论混样模式及混样数量下，浓度越高的标本越容易被检出；样本混采模式较稀释混样模式更易检出阳性标本；样本混采模式下，混样数量对强阳性标本的检出没有影响；稀释混样模式下，混合标本数量越多，越不利于其检出。对于弱阳性标本，5 管合并及 8 管合并时出现 O 基因漏检情况。
结论 合理选择混样模式及混样数量，提高集中筛查的检测效率且不放过一个阳性标本，将有助于发现社区传播及时进行防控。

PU-0220

SNHG3 promotes migration, invasion, and epithelial-mesenchymal transition of breast cancer cells through the miR-186-5p/ZEB1 axis

Qun Wan
The Fifth Affiliated Hospital of Sun Yat-sen University

Objectives Breast cancer is the most common malignant tumor among women in the world. Currently, a variety of drugs have been used for treatment of breast cancer in clinic. However, due to its highly heterogenous morphology and complex molecular phenotype, the recurrence and metastasis of breast cancer cannot be solved, which seriously endangers the health of women. Therefore, it is of great clinical significance to search for the key molecules and pathways in the development of breast cancer.
Methods Clinical samples of breast cancer were analyzed by bioinformatics, and the correlation between SNHG3 and breast cancer was observed and verified in cell experiments. The localization of SNHG3 was observed by fluorescence in situ hybridization. The proliferation ability of breast cancer cells was measured by colony formation assay. Scratch healing assay and Transwell assay were used to detect the migration and invasion ability of breast cancer cells. The direct binding sites of SNHG3 and miR-186-5p were predicted by StarbaseV2.0 database. Combined with literature and database analysis, it was found that miR-186-5p could directly regulate the expression of target gene ZEB1. The regulatory effects of SNHG3 on miR-186-5p and ZEB1 were verified by dual luciferase reporter gene assay and Western blot. The related markers of EMT pathway were detected by qRT-PCR and Western blot. Finally, the subcutaneous tumor-forming model of nude mice was used to investigate the effect of SNHG3 on breast cancer in mice and observe tumor growth. The expression of SNHG3 was detected by qRT-PCR, and the expression of ZEB1, MMP2 and Snail was performed by Western blot. The expressions of PCNA, E-cadherin and Vimentin in the tumor were detected by immunohistochemistry.
Results Our investigation has demonstrated that SNHG3 presented abnormally high expression in breast cancer tissues and cells, and transgenic expression of SNHG3 promoted the proliferation, migration, and invasion of breast cancer cell lines. The mean volume of xenografts from SNHG3-knockdown MCF-7 cells was smaller than that of control tumor cells. Moreover, the expression of ZEB1 increased after SNHG3 overexpression and vice versa. The overexpression of ZEB1 subsequently triggered cellular migration and invasion behaviors. Analysis of the mechanism underlying these effects revealed that SNHG3 may be an effective sink for miR-186-5p and modulate ZEB1 repression, conferring an additional level to its post-transcriptional regulation.
Conclusions SNHG3 promoted the migration and invasion of breast cancer cells through miR-186-5p/ZEB1 regulation and induction of epithelial to mesenchymal transition, which shed light of SNHG3 on being a potential treatment target for breast cancer.

PU-0221

湖南地区 MTHFR C667T 基因多态性的分布研究

王泽友、董贤
中南大学湘雅二医院检验医学科

目的 研究湖南长沙地区亚甲基四氢叶酸还原酶（MTHFR）C677T 基因多态性分布特征，比较不同种族，不同地区及与国内外 MTHFR C677T 基因的频率的分布特点。

方法 收集 2017 年 11 月至 2020 年 12 月在湖南省长沙市中南大学湘雅二医院进行 MTHFR C677T 基因多态性检测汉族患者的基因检测结果，共计 1932 例，分析 MTHFR C677T 基因频率分布特点，分析比较不同地区，不同种族及国外 MTHFR C677T 等位基因和基因频率的分布。
结果 湖南长沙地区人群 MTHFR C677T 基因型 CC、CT 和 TT 实际例数分别为 829、815 和 288，其频率分别为 42.9%、42.2% 和 14,9%，等位基因 C 和 T 频率分别为 64% 和 36%；在国外，非洲地区 T 等位基因的频率最低为 10.3%，在欧洲最高为 34.1%；在亚洲各国的研究中，东亚国家 T 等位基因频率（中国为 44.7%，韩国为 40.3%，日本为 39.9%）高于南亚国家（印度为 11.4%，巴基斯坦为 16%，斯里兰卡为 4.5%）；对于中国各地区 MTHFR C677T 基因型分布整体来看，MTHFR C677T 基因存在明显地域分布差异， TT 基因型呈现北高南低的趋势；各地区少数民族中布依族，白族，穿青族，哈萨克族与当地汉族 MTHFR C677T 等位基因和基因型存在统计学差异（$P < 0.05$），而布依族，蒙古族与当地汉族基因频率不存在统计学差异（$P > 0.05$）。
结论 MTHFR C677T 基因多态性分布全球不同国家，国内不同地区，不同种族间具有统计学意义。

PU-0222

SNHG3 通过 miR-186-5p/ZEB1 轴促进乳腺癌细胞的迁移，侵袭和 EMT

万群
中山大学附属第五医院

目的 乳腺癌是全球女性最常见的恶性肿瘤，目前临床上有多种药物用于乳腺癌的治疗，但由于形态学上的高度异质和复杂的分子表型，仍无法解决其复发和转移问题，严重危害广大女性的健康。因此，寻找针对乳腺癌发生发展过程中的关键分子及其通路的研究具有重要的临床意义。
方法 采用生物信息学分析乳腺癌临床样本，分析 SNHG3 与乳腺癌的相关性，并在细胞实验中验证；使用荧光原位杂交技术观察 SNHG3 的细胞定位；通过克隆形成试验检测乳腺癌细胞的增殖能力；划痕愈合试验，Transwell 试验检测乳腺癌细胞迁移与侵袭能力。通过 StarBasev2.0 数据库预测 SNHG3 与 miR-186-5p 有直接结合位点，结合文献和数据库分析发现 miR-186-5p 能直接调控靶基因 ZEB1 的表达，采用双荧光素酶报告基因试验及 Western blot 验证 SNHG3 对 miR-186-5p 和 ZEB1 的调控作用；qRT-PCR、Western blot 检测 EMT 通路相关标志物的变化。最后采用裸鼠皮下成瘤模型在小鼠体内探究 SNHG3 对乳腺癌的作用，观察瘤体生长情况。通过 qRT-PCR 检测 SNHG3 的表达，Western blot 检测 ZEB1、MMP2、Snail 的表达；免疫组化检测 PCNA、E-cadherin、Vimentin 等在瘤体中的表达情况。
结果 在乳腺癌组织和细胞中 SNHG3 表达显著增高。体外实验中证实，过表达 SNHG3 促进了乳腺癌细胞的增殖、迁移和侵袭；相反，敲低 SNHG3 抑制乳腺癌细胞的迁移和侵袭。同时体内实验也证实，敲低 SNHG3 的 MCF-7 细胞成瘤体积明显减少。此外，过表达 SNHG3 后，ZEB1 表达增加，反之亦然；ZEB1 的过表达能够促进乳腺癌细胞迁移和侵袭。机制分析表明，SNHG3 通过 miR-186-5p/ZEB1 轴促进乳腺癌细胞的迁移，侵袭和 EMT。
结论 SNHG3 通过 miR-186-5p/ZEB1 调控上皮细胞向间充质转化促进乳腺癌细胞的迁移和侵袭，提示 SNHG3 可能是乳腺癌治疗的一个潜在靶点。

PU-0223

Association of soluble epoxide hydrolase (sEH) with diabetic nephropathy: mechanisms and potenial application

Peng Gao、Liang Ma、Meimei Zhao、Yi Liu、Xiaomu Kong、Yongwei Jiang、Xiao Cong、Yongtong Cao
China-Japan Friendship Hospital

Diabetic nephropathy (DN), one of the microvascular complications of diabetes mellitus (DM), is the primary single driver of end-stage kidney disease, which is a problem with serious consequences for society's health. A soluble epoxide hydrolase (sEH) encoded by EPHX2 gene, a member of epoxide hydrolases (EH) family, presents in almost all living organisms, including kidney. The expression and activity were reported upregulated in many kidney diseases for human and animals and it was found that the inhibition of sEH had a reno-protective effect in many experimental studies. The attention to the relationship between sEH and DN has been consistently rising in the last years. So, in this review, we aim to clearly demonstrate the potential molecular mechanisms of sEH in DN and the important role of sEH inhibitors as a potential target in the treatment in DN. We first enumerate the some typical EPHX2 single nucleotide polymorphisms (SNPs) related to DN and figure out the sEH regulated potential mechanisms in mRNA and protein level. Subsequently, we introduce the sEH inhibitors clinical researches in DN within three aspects, respectively, which includes the results of the sEH inhibitors in vivo, sEH inhibitors in DN animal models and the recent sEH inhibitors clinical trials, aiming to prove the potential role of sEH inhibitors in the treatment of DN. Furthermore, we summarize and present an overview diagram to clearly illustrate the application of sEH inhibitor as potential target in DN.

PU-0224

Intrahepatic gene expressions and immune cell infiltration characteristics of hepatitis B virus-related liver diseases

Shu Feng 、Jialing Zhong、Yongchang Yang
Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China

Objective The purpose of this study is to clarify the intrahepatic gene expressions and immunological changes of healthy control population (HC), patients with HBV-associated acute liver failure (HBV-ALF), patients with chronic hepatitis B virus infection (Chronic hepatitis B, CHB), and hepatitis B virus-associated hepatocellular carcinoma (HBV-associated hepatocellular carcinoma, HBV-HCC) patients at both molecular and cellular levels. We also tried to understand the gene expressions and immune cell infiltration characteristics in different disease progress after HBV infection.
Methods By using bioinformatics, we analyzed the original microarray data of HC, HBV-ALF, CHB and HBV-HCC liver tissues. We compared each diseased group with HC, and analyzed the differentially expressed genes and KEGG pathways. The relative immune cell infiltration percentages of the four groups were calculated and compared by using CIBERSORT deconvolution. Furthermore, the immune cell types related to HBV-HCC survival were explored via single-factor Cox regression and Kaplan-Meier survival analysis.
Results The sample sizes of each group included in this study were HC (n=34), HBV-ALF (n=38), CHB (n=340) and HBV-HC (n=134). Compared with HC, the significantly changed genes in HBV-ALF were KRT19, MMP7, C9, CFHR4, etc., and the pathways were metabolic pathways related to substances such as amino acids. SKI, FETUB, SPINK1, CRP, etc. were abnormally expressed in CHB, and infectious diseases and their related immune response signaling pathways were significantly changed. AKR1B10, GPC3, HAMP, OIT3, etc. were abnormally expressed in HBV-

HCC, and tumor-related signaling pathways were notably changed. The cell components of HBV-ALF with their unique tendencies were plasma cells, macrophages, and NK cells. The immune cell components of CHB and HBV-HCC liver tissues were similar, like T cells, plasma cells, monocytes, and macrophages. However, dendritic cells were only abnormally increased in HBV-HCC liver tissues. Compared with HC, the innate immune cells with the same changing tendency in the three groups of HBV-ALF, CHB and HBV-HCC were mast cells, neutrophils and eosinophils. Kaplan-Meier survival curve suggested that abnormally increased M0 macrophages and resting dendritic cells in liver cancer tissues of HBV-HCC patients may be risk factors for reducing overall survival (HR=1.0360, P=0.0013; HR=1.0584, P=0.0175).
Conclusions This study explored the differential gene expression profiles of three HBV-related liver diseases, namely HBV-ALF, CHB, and HBV-HCC. It was found that each disease has a unique gene expression profile. The immune cell characteristics were similar in patients with CHB and HBV-HCC. However, the immune cells in the liver tissue of HBV-ALF were relatively specific. This study offered the theoretical basis for understanding the important genes and immune cells in HBV-related diseases.

PU-0225

固相吸附法与氯仿-异丙醇提取法提取丙型肝炎病毒的方法学比较

渠滕
山东第一医科大学附属省立医院临床医学检验部

目的 比较氯仿-异丙醇法和核酸提取柱法在丙型肝炎病毒(HCV)RNA 荧光定量检测中的灵敏度、重复性和抗干扰性。
方法 选取 50 例丙型肝炎患者，采集所有患者血液，分离血清。分别用两种方法提取核酸后，采用荧光定量 PCR 技术检测 HCV RNA 含量，比较两种方法对检测灵敏度、重复性和抗干扰性的影响。
结果 经研究比较发现：①血清采用氯仿-异丙醇法提取核酸，稀释 1×104 倍后，荧光定量 PCR 可以检测，继续稀释则无法检测。按照固相吸附法提取核酸，稀释 1×105 倍后，荧光定量 PCR 可以检测，继续稀释则低于检测限。②氯仿-异丙醇法提取核酸荧光定量 PCR 检测后，阳性 32 例，阳性率 64%。核酸提取柱法提取核酸荧光定量 PCR 检测后阳性 36 例，阳性率 72%。两组结果比较 P＜0.05，有显著性差异。③当血红蛋白浓度为 5g/L 时，两组抗干扰能力差别不大，P＞0.05。当血红蛋白浓度为 50g/L 时，两组结果比较 P＜0.05。
结论 与氯仿-异丙醇核酸提取方法相比，固相吸附法提取的丙型肝炎病毒-RNA 灵敏度、阳性率更高，抗溶血干扰能力更好，具有一定优势。

PU-0226

泰山紫草提取物-乙酰紫草素诱导 前列腺癌 PC3 细胞凋亡机制的研究

杨宏
泰安市中心医院

目的 泰山紫草为传统中药，是泰山四大名药之一，属硬紫草，其有效成分为多种萘醌类物质。现代药学研究证明紫草具有治疗烧伤、强心、抗炎、抗菌、抗病毒及抗肿瘤等作用。为了进一步研究泰山紫草抗肿瘤机制，本课题组的前期研究从泰山紫草中分离纯化得到了三种主要成分：乙酰紫草素、β-羟基异戊酰紫草素和异丁酰紫草素；发现乙酰紫草素能抑制多种肿瘤细胞系的生长，并可诱

导肿瘤细胞凋亡。有关紫草素（软紫草中含量较多的一种萘醌类物质）抗肿瘤的研究近几年已有文献报道，但乙酰紫草素抗肿瘤作用的研究报道较少，其分子机制尚不清楚，值得研究探讨。本研究以乙酰紫草素为诱导剂，通过 MTT 法已经筛选出前列腺癌 PC3 细胞株为乙酰紫草素细胞毒性敏感的细胞株，并从形态学和部分生化指标观察到明显的凋亡特征。进一步研究乙酰紫草素诱导前列腺癌 PC3 细胞株凋亡的分子机制，为天然新型抗肿瘤药物的开发奠定基础。
方法 MTT 法检测乙酰紫草素对前列腺癌 PC3 细胞增殖的影响；流式细胞术检测细胞周期和线粒体膜电位的变化；Annexin-V/PI 双染分析凋亡率；实时荧光定量 PCR 检测凋亡相关基因表达水平；Western blotting 检测相关蛋白的表达和激活。
结果 乙酰紫草素显著抑制 PC3 细胞的生长，其半数抑制浓度（IC50）为 8.59 ± 0.42μM，并使细胞周期阻滞在 S 期。乙酰紫草素抑制 Bcl-2 蛋白的表达，促进 Bax 的表达，引起线粒体膜电位下降，导致细胞色素 c 释放，进而通过激活内源性凋亡途径诱导 PC3 细胞死亡。
结论 乙酰紫草素能抑制 PC3 细胞增殖，且改变了 PC3 细胞的周期分布，诱导其凋亡。

PU-0227

lncRNA SNHG11 promotes colorectal cancer growth and metastasis by targeting has-miR-184/AKT2.

Xueni Xu
Nanjing First Hospital, Nanjing Medical University

Background Mounting evidence demonstrates that the dysregulation of long non-coding RNAs (lncRNAs) have profoundly been associated to the initiation and progression of colorectal cancer (CRC). Yet the further investigations regarding the regulatory mechanism of lncRNAs is elusive. In this study, we report a highly conserved lncRNA, the small nucleolar RNA host gene 11 (SNHG11), which is specially expressed in colorectal tissues and is significantly overexpressed in CRC. Here, we systematically elucidated its functions and the underlying molecular mechanisms in CRC.
Methods RNA sequencing data from the TCGA database was employed to screen the differential expression profile of lncRNAs in colorectal cancer. Starbase v3.0 dataset was used to analyze the SNHG11 expression between CRC and the corresponding normal tissues. The expression level of SNHG11 in tissues and cells was determined by quantitative reverse transcription polymerase chain reaction (qRT-PCR) and the subcellular location of SNHG11 in CRC cells was indicated by fluorescence in situ hybridization (FISH). Kaplan–Meier survival analysis and receiver operating characteristic (ROC) curve, including its area under the ROC curve (AUC) were respectively utilized to assess the prognosis and diagnostic value of lncRNA SNHG11 for CRC. Then, the biological functions of SNHG11 on CRC in vitro and vivo assay like cell proliferation, migration, invasion and apoptosis were detected by colony assay, CCK-8 assay, EdU assay, transwell assay, flow cytometry, xenograft model, immunohistochemistry, and western blot. Subsequently, The potential mechanisms of SNHG11 were explored by dual luciferase reporter assay, RNA pull-down assay, RNA immunoprecipitation (RIP).
Results Our study revealed that SNHG11 was significantly upregulated in CRC tissues and cells. FISH and subcellular fractionation observed that the vast majority of SNHG11 expressed in the cytoplasm. High SNHG11 was obviously associated with advanced TNM stage, tumor invasion depth and distant metastasis. Besides, survival analysis and ROC curve analysis indicated that SNHG11 expression was negatively correlated with overall survival of CRC patients and its potent diagnosis value for CRC. Functional experiments and bioinformatics analysis revealed that SNHG11 promoted CRC cells proliferation, migration, invasion and inhibits apoptosis in vitro and vivo. Mechanistic investigations demonstrated that SNHG11 served as a sponge for miR-184, decreasing its ability to repress AKT2 expression. Moreover, functional experiments and Western blot displayed SNHG11/miR-184/AKT2 regulatory loop was critical for CRC cell proliferation, migration, invasion and apoptosis.

Conclusions Taken together, our study demonstrated that how SNHG11 formed a regulatory network to contribute to CRC growth and metastasis and suggested that SNHG11 may act as a potential target for CRC prognosis and diagnosis.

PU-0228

生物信息学筛选活动性肺结核潜在生物标志物

冶学燕、刘春燕、张新
新疆生产建设兵团医院

目的 利用生物信息学技术筛选活动性肺结核（PTB）诊断和治疗监测的潜在生物标志物。
方法 通过 GEO 数据库下载 GSE19444 和 GSE19435 基因芯片数据集。利用 GEO2R 工具筛选活动性 PTB 患者与健康对照间的差异表达基因（DEG），使用 CentiScape 插件确定中枢基因（Hub 基因），并通过 GSE56153 数据集验证 Hub 基因在活动性 PTB 治疗期间的变化。
结果 两个数据集中共筛选 505 个 DEG，上调 251 个，下调 254 个。DEG 网络的 9 个子模块中模块 1 评分最高，包含的 25 个基因主要参与病毒防御、干扰素信号通路等反应。在 25 个基因中筛选了 13 个 Hub 基因，通过验证，提示上调的 IFIT3、IFI35、STAT1 和 GBP1 在初诊活动性 PTB、治疗 8 周、治疗 28 周和对照组的不同治疗阶段表达水平有显著降低趋势。
结论 筛选出的 IFIT3、IFI35、STAT1 和 GBP1 与活动性 PTB 的发生和治疗密切相关，有望成为 PTB 诊断和治疗监测的潜在生物标志物。

PU-0229

血浆血栓球蛋白 β 联合抗血小板因子 4/肝素抗体在血小板相关疾病中的临床意义

邱旸、崔朝杰、张庆、渠滕
山东第一医科大学附属省立医院

目的 骨髓增生性肿瘤(MPN)遇到血栓是由于多种已知的危险因素引起的。肝素诱导血小板减少症(HIT)是一种由抗血小板因子 4 (PF4)/肝素抗体介导的血栓综合征，对 MPN 血栓形成的意义尚不明确。我们推测血浆血栓球蛋白 β 联合抗 pf4 /肝素抗体可能出现在 MPN 中并促进血栓形成。
方法 对 27 例 MPN 患者(包括 76 例 PV 和 51 例 ET)的血浆血栓球蛋白 β 和抗 pf4 /肝素抗体进行分析。
结果 19.7%的 PV 和 11.4%的 ET 检测到血浆血栓球蛋白 β 和抗 pf4 /肝素抗体同时存在，而肝素暴露患者检测到的单一抗体为 0.3-3%。阳性和阴性患者在性别,年龄,血红蛋白水平,血小板计数方面的差异均无统计学意义(P 均>0.05)。总体而言，45%的 PV 患者发生血栓，13%的血浆血栓球蛋白 β 和抗 pf4 /肝素同时存在阳性，而无血栓的 PV 患者为 7.4%。观察血浆血栓球蛋白 β 和抗 pf4 /肝素抗体联合应用在不同 mpn 分类中的意义，发现其在 PV 和 ET 中联合阳性率明显高于其他组别。
结论 血浆血栓球蛋白 β 和抗 pf4 /肝素抗体是内源性的，在 MPN 中比肝素暴露时更频繁。血浆血栓球蛋白 β 和抗 pf4 /肝素 IgG 阳性 PV 的血栓风险增加，这反映了潜在的影响，需要更大的确证队列。PV 血栓形成时应评估血浆血栓球蛋白 β 和抗 pf4 /肝素 IgG，以避免抗 pf4 /肝素 IgG 阳性的 PV 使用肝素。

PU-0230

地中海贫血血液学表型和基因型相关性分析

熊君
南方医科大学珠江医院

目的 了解人群地中海贫血基因携带率，探讨地中海贫血不同基因型对血液学表型的影响以及 HbA2 的界值筛查地中海贫血的价值。
方法 收集 2016～2017 年期间来本院做地中海贫血诊断的患者或正常人的相关数据。采用回顾性分析方法，整理的数据资料包括基因诊断结果、血常规结果（MCV、MCH、HGB）以及电泳结果，计算地中海贫血基因人群总携带率以及各突变携带率，比较地中海贫血的常见基因型对血液学表型的影响程度，分析本院 HbA2 界值对诊断地中海贫血的影响。数据分析使用 Graphpad prism 6.0 。
结果 共收集本院 2234 例样本，实查正常人 1237 例以及地中海贫血携带者或患者 997 例。地中海贫血基因携带率 44.6%，人群突变携带率较高的前六种基因型依次为：(--SEA/)，24.5%；CD41-42(-CTTT)，7.7%；(-α3.7/)，7.1%；IVS-Ⅱ-654(C>T)，4.6%；CD17(AAG>TAG)，2.9%；(-α4.2/)，2.7%；-28(A>G)，1.7%。MCV、MCH 在 α-地中海贫血与 β-地中海贫血男女人群中没有差异，但是 HGB 男性比女性高；--SEA 血液学表型比(-α3.7/)和(-α4.2/)严重，(-α3.7/)和(-α4.2/)之间血液学表型没有差异；在 β- 地中海贫血中， -28(A>G) 突变影响表型较轻， CD41-42(-CTTT) 、IVS-Ⅱ-654(C>T)、CD17(AAG>TAG)之间没有血液学表型差异；(--SEA/)合并 CD41-42(-CTTT)突变血液学表型变轻。本院把 HbA2 界值提高至 2.8%降低了 α-地贫漏检率。
结论 本次调查分析真实地反映了本院地中海贫血检测的基本情况，为临床诊断地中海贫血提供可靠的参考资料。

PU-0231

基于 DIA 技术筛选结核性胸腔积液诊断标志物的研究

冶学燕、刘春燕、张新
新疆生产建设兵团医院

目的 采用数据非依赖采集（DIA）蛋白组学技术分析结核性胸腔积液（TPE）与其他性质胸腔积液间差异表达蛋白，旨在为 TPE 的诊断与鉴别诊断寻找潜在标志物。
方法 收集 2019 年 10 月至 2020 年 8 月于新疆生产建设兵团医院住院患者胸腔积液 102 例。采用 DIA 技术对 8 例 TPE、7 例恶性胸腔积液（MPE）和 5 例类肺炎胸腔积液（PPE）样本进行差异表达蛋白的比较分析，通过生物信息学研究手段筛选 TPE 潜在标志物并在 29 例 TPE、31 例 MPE 和 22 例 PPE 应用酶联免疫吸附试验（ELISA）验证，并评估潜在标志物在 TPE 中的诊断价值。
结果 初步筛选出 118 个 TPE 差异表达蛋白，通过蛋白-蛋白交互网络、蛋白通路和 TPE 组单独表达蛋白分析，最终筛选出了 7 个 TPE 潜在标志物（CORO1A、TUBB、SAA1、AGT、ICAM-1、HSPG2 和 IGF-2）。ELISA 结果显示，TPE 组的 CORO1A、TUBB、SAA1 和 AGT 浓度均高于 MPE 组和 PPE 组（P＜0.05），MPE 组与 PPE 组间差异无统计学意义（P＞0.05）；TPE 组中 ICAM-1 和 HSPG2 浓度均高于 MPE 组（P＜0.05），TPE 组与 PPE 组、MPE 组与 PPE 组间差异无统计学意义（P＞0.05）；IGF-2 浓度在三组间差异均无统计学意义（P＞0.05）。CORO1A、TUBB、SAA1 和 AGT 的受试者操作特征曲线（ROC）面积分别为 0.857、0.935、0.833 和 0.875，灵敏度分别为 0.724、0.862、0.724 和 1，特异度分别为 0.962、0.981、0.962 和 0.774。
结论 初步验证的 CORO1A、TUBB、SAA1 和 AGT 在 TPE 的诊断中具有较高的灵敏度和特异度，为 TPE 的诊断与鉴别诊断提供了新的方向。

PU-0232

METTL3 suppresses neuropathic pain via modulating N6-methyladenosine-dependent primary miR-150 processing

Le Zhang 、 Chuanxin Wang
The Second Hospital, Cheeloo College of Medicine, Shandong University

Purpose Neuropathic pain (NP) is a complicated, chronic pain state that is generally caused by tissue damage that affects the somatosensory nervous system. However, the therapeutic approaches for NP are not satisfactory mainly due to the lack of effective molecular targets. Therefore, finding novel predictive markers and new targets to cure NP are urgently needed. Recently, an increasing number of findings demonstrated that m6A methylation played essential roles in RNA biogenesis at post-transcriptional level. However, the potential role of m6A methylation in NP progression remains unknown. In this study, we sought to define the functional role of METTL3 in NP progression and elucidate the mechanism by which METTL3 regulates miRNA maturation to participate in NP.

Methods A spare nerve injury (SNI) was done in rats to imitate NP model. Paw withdrawal threshold (PWT) and paw withdrawal latency (PWL) were used for evaluation of hypersensitivity in NP. qRT-PCR, western blot and immune-histochemistry were performed to determine the quantity of involved genes. RNA immunoprecipitation and pulldown assays were employed for reveal the regulatory mechanism of miR-150 in NP.

Results To determine the expression of METTL3, we established NP rat model by using a SNI method. In response to the operation, PWL and PWT were significantly decreased and the concentrations of inflammatory cytokines including IL-6, TNF-α and IL-1β were significantly upregulated in SNI -NP rats while no significant change was identified in sham rats. Moreover, we found that METTL3 was significantly downregulated in NP rats compared to controls at both transcript and protein levels. Overexpressed METTL3 in rats by intrathecal administration of Lv-METTL3 significantly inhibited NP behaviors as evidenced by the elevated PWL and PWT and downregulated the concentrations of IL-6, TNF-α and IL-1β. While silencing METTL3 by constructing respective lentivirus could restore NP with decreased PWL, PWT and upregulated IL-6, IL-1β and TNF-α levels. Thereafter, we suppose that METTL3 may regulate NP progression via participating in the maturation of miRNAs by DGCR8. m6A methylation level was significantly increased in RN-SC cells by transfection of Lv-METTL3, whereas downregulated by deletion of METTL3. Consistently, m6A level in spinal cord was also regulated by METTL3 in SNI-NP rats. By performing co-immunoprecipitation, we observed a direct interaction between METTL3 and DGCR8, and this interaction could be reduced by Rnase in RN-sc cells (Fig. 3C), indicating that their binding might be modulated by miRNAs. We found that only miR-150 was significantly elevated upon upregulation of METTL3 and decreased by METTL3 deletion in spinal cord tissues. our results suggested that METTL3 induced miR-150 processing by mediating DGCR8 recognition in an m6A-dependent manner. m6A methylation is a characterized process which needs the involvement of m6A reader proteins, including YTHDFs. Thus, we revealed that YTHDF2, along with METTL3, mediated m6A methylation and regulate the processing of miR-150. As expected, inhibition of miR-150 in RN-sc cells dramatically reversed the METTL3-mediated suppression of IL-6, TNF-α and IL-1β. While miR-150 mimics could restore the shMETTL3-caused upregulation of neuroinflammation markers. Collectively, we revealed that miR-150 was essential for METTL3-modulated NP in vitro and in vivo. As METTL3 and miR-150 was tightly interacted, we sought to define whether BDNF was also regulated by METTL3. We found that overexpression of METTL3 reduced while deletion of METTL3 increased BDNF expression in RN-SC cells and SNI -NP rats. Our results verified BDNF was a direct target of miR-150 and regulated by METTL3. overexpression of BDNF in SNI rats could partly reverse METTL3-regulated suppression of NP progression, whereas deletion of BDNF interfered sh-METTL3-induced promotion of NP. Meanwhile, dysregulated BDNF also reversed the METTL3-mediated regulation on neuroinflammation. Taken together, we proved that METTL3 influence NP progression via regulating miR-150/BDNF signaling pathway. We then defined the expression

level of METTL3 in NP patients in remission after treatment, and found that METTL3 was dramatically downregulated in contrast to the level before treatment. Correlation analysis revealed a negative association between METTL3 and BDNF, miR-150 and BDNF.
Conclusion our study revealed that METTL3/YTHDF2-mediated m6A modification regulates NP progression via modulation of miR-150 processing and further suppressing BDNF expression. Moreover, serum METTL3 was upregulated in NP patients and may serve as promising diagnostic biomarker. Our study uncovers a strong evidence of METTL3-mediated m6A methylation in NP inhibition, which provides potential diagnostic and therapeutic target for NP treatment.

PU-0233

Performance verification of Ustar UC0102 rapid nucleic acid amplification detection analyzer for Sars-CoV-2 qualitative detection

Fan Chang
Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China

Objection To verify the analytical performance of Ustar UC0102 rapid nucleic acid amplification detection analyzerfor Sars-CoV-2qualitativedetection.
Methods The accuracy, limitof detection and repeatability were validated according toChina National Accreditation Service for Conformity Assessment (CNAS) documents (CL02-A009 and GL039) and People's Republic of China Health Industry Standards document (WS/T 505-2017). In the meantime,the results obtained would be compared with the manufacturer statement.
Results Compared with the traditional fluorescent PCR method, the method compliance rate of Ustar UC0102 rapid nucleic acid amplification detection analyzer was 100%. The LoD of Sars-CoV-2 qualitativedetection was 200 copies/mL. The compliance rates of repeatability within and between batches, within and between days, within and between operators were all 100%.
Conclusion Performance verification of Ustar UC0102 rapid nucleic acid amplification detection analyzer for Sars-CoV-2 qualitativedetection was consistent with the manufacturer statement also in accordance with《Sars-CoV-2Nucleic Acid Testing Manual for Medical Institutions (Trial Version, Second Edition)》related standards, which could meet the expectant use of prevention and control to COVID-19.

PU-0234

干扰肽 TAT-T407 通过抑制 TRPV1-CDK5 的相互作用减轻缺血性脑卒中后神经凋亡的分子机制

冯潜[1,2,3]、李颖[1]、张震[3]、刘丹[3]、梁佳[3]、朱延东[3]、宋远见[2,3]
1. 徐州医科大学附属医院
2. 徐州医科大学遗传学教研室
3. 徐州市医学遗传与转化工程中心

目的 1. 探明干扰肽 TAT-T407 对缺血性脑卒中后运动和记忆的作用；2. 阐明干扰肽 TAT-T407 对缺血性脑卒中后运动和记忆起保护作用的可能分子机制。
方法 以雄性 C57BL/6J 小鼠为研究对象，以经典的 MCAO 模型模拟人缺血性脑卒中的疾病过程。通过旷场实验评估小鼠的自发活动，水迷宫实验评估小鼠的认知功能。采用 mNSS 评分评价小鼠神经功能缺失程度。通过 TTC 染色观测小鼠脑梗死体积，HE 染色观察杏仁核病理变，TUNEL 染色法检测细胞凋亡，IF 染色观察 CDK5 与 TRPV1 二者共定位。通过 Western blotting 检测 TRPV1、

Bcl-2，Bax，Caspase-3，Cleaved Caspase-3，Cytochrome c 以及 NOX2 的表达。采用 Co-IP 法检测 CDK5 与 TRPV1 的结合。
结果 与 sham 组相比，I/R 后小鼠同侧大脑半球有广泛梗死区。CPZ 或 TAT-T407 预处理可以明显减少 I/R 同侧大脑半球小鼠梗死体积，减小 mNSS 评分。进一步的研究表明，给予 CPZ 或 TAT-T407 肽导致梗死体积显著减少，并且这与再灌注后神经功能的改善平行相关。与 I/R 组相比，CPZ 或 TAT-T407 预处理可以明显改善在旷场实验中小鼠在运动总距离，穿格次数以及在中央区域的时间方面均表现出明显的运动行为学缺陷，改善在水迷宫实验中小鼠表现出明显的学习记忆行为学缺陷。I/R 与 sham 组相比 TRPV1 膜转位增强，Bcl-2/Bax 比值显著降低，凋亡效应分子 Cytochrome c 与 Cleaved Caspase-3 表达显著增强，氧化应激蛋白 NOX2 的表达显著增高。与 I/R 组、I/R+T407A 组相比，I/R+T407 组 TRPV1 膜转位减少，Bcl-2/Bax 比例提高，凋亡效应分子 Cytochrome c 与 Cleaved Caspase-3 表达显著减少，氧化应激蛋白 NOX2 的表达显著减低。紧接着，免疫共沉淀实验发现 TRPV1 与 CDK5 在小鼠 I/R 中结合增加，TAT-T407 预处理后 TRPV1 与 CDK5 在小鼠 MCAO 缺血模型再灌注中存在结合降低。进一步免疫荧光显示与 I/R 组、I/R+T407A 组相比，I/R+T407 组 TRPV1 与 CDK5 共定位减少，凋亡率明显下降。有趣的是，TAT-T407 效应是损伤特异性的，对假手术治疗的非缺血动物的细胞凋亡或认知功能几乎没有影响。
结论 小肽 TAT-T407 能够有效改善小鼠脑的缺血再灌注损伤，改善运动行为和认知功能，其机制是通过干扰 TRPV1 和 CDK5 的结合从而减少 TRPV1 向膜上的转移，抑制了凋亡通路的激活进而减轻了凋亡。

PU-0235

基于链置换反应的 RNA 检测新技术的建立

童尧、杜鲁涛、王传新
山东大学第二医院

目的 建立一种基于链置换反应的新型 RNA 检测新技术用于 mRNA 和 miRNA 检测。
方法 依据 SPHK1 mRNA 和 miR-19a 的序列设计特异性用于链置换的双链探针，对该检测方法的反应条件进行优化，合成序列单链 mimics 进行梯度稀释对该检测技术的灵敏性和特异性进行验证并绘制标准曲线。
结果 通过可行性分析发现 A2T2 可以对实验体系的荧光信号实现扩增效应，与目的分子不相关的 miRNA 单链 mimics 对实验组信号几乎没有影响。通过比较信噪比，发现 100nM A1T1、5nM A2T2 反应时间 20min 为最佳反应条件。为验证探针的性能，采用 RNA 模拟物进行梯度稀释，探究目的 RNA 浓度与荧光强度的线性关系。最佳实验条件下孵育后进行荧光强度测量发现该监测体系的线性范围在 1fM-100pM 之间。
结论 链置换反应是一种低成本反应快速、不依赖于热循环的新型 RNA 检测技术，在检测 1fM-100pM 浓度目的分子时拥有较好的稳定性与特异性，有望实施临床转化。

PU-0236

Hsa-piR-28395 促进结直肠癌细胞增殖与迁移侵袭

童尧、杜鲁涛、王传新
山东大学第二医院

目的 探讨 Hsa-piR-28395 在结直肠癌中的表达及其对结直肠癌细胞生物学行为的影响。
方法 采用 qRT-PCR 方法验证组织中 Has-piR-28395 在结直肠癌组织以及癌旁正常组织中的表达，同时检测正常结肠上皮细胞 CCDK841 和各结直肠癌细胞系 Hsa-piR-28395 的表达。利用 piRNA 单链 mimics 和 inhibitor 分别转染 Hsa-piR-28395 低表达和高表达细胞系，通过 RTCA、EdU 细胞

增殖实验、Transwell 和 invasion 实验检测过表达和敲减 Hsa-piR-28395 对结直肠癌细胞增殖、迁移、侵袭等生物学行为的影响。
结果 我们通过对结直肠癌组织和癌旁正常组织进行组织小 RNA 测序发现，结直肠癌组织中 Hsa-piR-28395 表达显著高于癌旁正常组织（P<0.05），同时对组织样本库中 50 对癌组织与癌旁正常组织进行 qRT-PCR 验证发现 Hsa-piR-28395 表达差异具有统计学意义。通过对不同细胞系进行 qRT-PCR 发现，相对于结直肠正常上皮细胞系 CCDK841，HCT116 和 SW1116 细胞系 Hsa-piR-28395 表达较低，SW480 和 SW620 细胞系表达高于 CCDK841。通过瞬时转染 Hsa-piR-28395 单链 mimics 和 inhibitor 进行细胞功能实验我们发现，相对于 control 组、HCT116 和 SW1116 过表达组细胞增殖、迁移能力及侵袭能力增强，差异有统计学意义（P<0.05）；SW480 和 SW620 敲减组细胞增殖速度、迁移能力及侵袭能力减弱（P<0.05）。
结论 Hsa-piR-28395 在结直肠癌中呈高表达，且过表达 Hsa-piR-28395 可促进结直肠癌细胞迁移、增殖、侵袭能力，可为结直肠癌治疗提供新的治疗靶点。

PU-0237

基于 DNA 水凝胶的沙眼衣原体 16S 核糖体 RNA 电化学生物传感器的开发

程玲军
厦门大学附属第一医院
厦门大学医学院

目前，临床迫切需要一种简单，定量的生物传感器来检测沙眼衣原体。本研究开发了一种快速、灵敏的沙眼衣原体 16S rRNA 电化学生物传感器，结合了 DNA 水凝胶的优异识别能力和较快的反应速率以及电化学传感技术的高特异性和高灵敏度。在没有靶标的情况下，电化学指示剂 HRP 嵌入 DNA 水凝胶中，因此无法生成信号。相反，靶标 rRNA 可以触发 DSN 反复水解 DNA 水凝胶并释放 HRP。然后，通过 BSA 载体平台捕获释放的 HRP。 HRP 催化 TMB 和 H2O2 之间的氧化还原反应，该反应由电化学工作站记录。电化学响应与沙眼衣原体的 16S rRNA 量成正比，在 10 fM 至 25 pM 范围内具有线性关系。检出限为 5.77 fM（S / N = 3），符合临床测试要求。此外，这种 DNA 水凝胶易于存储，检测时间仅需 90 分钟。因此，有望为广泛筛查生殖道病原体提供一种快速准确的定量检测方法。

PU-0238

miR-324-3p reverses cisplatin resistance by inducing GPX4-mediated ferroptosis in lung adenocarcinoma cell line A549

Shihua Deng
The First Affiliated Hospital of Chengdu Medical College

Purpose MicroRNAs act as crucial regulators of a diverse range of biological processes, including chemoresistance. Our study aimed to investigate the effect of miR-324-3p on lung adenocarcinoma cell line A549 resistant to cis-diamminedichloroplatinum II (DDP, aka cisplatin).
Methods The miR-324-3p expression levels in cisplatin-sensitive A549（A549） and cisplatin-resistantA549 (A549/DDP) cells were determined by qRT-PCR assay. Cell proliferation was determined with thecommercial kit CCK-8 and colony formation assay, whereas cell death was analyzed using flow cytometry. The target gene of miR-324-3p was identified and validated with

the luciferase reporter andwestern blot assays. The role of miR-324-3p in modulating cisplatin resistance was evaluated in vitro.
Results The expression of miR-324-3p was found to be significantly downregulated in the A549/DDPcells. Conversely, miR-324-3p overexpression reversed cisplatin resistance in the cells. With regard to the possible mechanism underlying this phenomenon, we identified the glutathione peroxidase 4 (GPX4)gene as the direct target of miR-324-3p, where overexpression of the gene reversed the miR-324-3p effect of sensitizing the A549/DDP cells to cisplatin. Furthermore, the GPX4 inhibitor RSL3 couldmimic the effect of miR-324-3p upregulation in increasing the sensitivity of the cisplatin-resistant cells to the drug. Significantly, miR-324-3p enhanced cisplatin-induced ferroptosis in the A549/DDP cells.
Conclusion Our findings revealed the role of the miR-324-3peGPX4 signaling axis in A549/DDP cells and how the targeting of this axis could be a potential strategy for reversing cisplatin resistance in human non small cell lung cancer (NSCLC).

PU-0239

TRPV1 调控缺血性脑卒中小鼠抑郁样行为和 PI3K-AKT-mTOR 通路的机制

冯潜[1,2,3]、李颖[1]、张震[3]、刘丹[3]、付燕燕[2]、周晓燕[2,3]、温相如[3]、宋远见[2,3]
1. 徐州医科大学附属医院
2. 徐州医科大学遗传学教研室
3. 徐州市医学遗传与转化工程中心

目的 探讨辣椒素受体（TRPV1）对小鼠神经元自噬和抑郁样行为的影响及分子机制。
方法 小鼠随机分为 Sham 组（假手术组），I/R 组（脑缺血/再灌注组），I/R+CPZ 组（CPZ 预处理的脑缺血/再灌注组）。采用线栓法建立小鼠 MCAO 脑缺血/再灌注模型，通过 mNSS 评分评价神经功能缺失程度，用悬尾实验检测小鼠的抑郁样行为，用 TTC 染色观测梗死体积，用 HE 染色观察杏仁核病理变化，用 Western blot 检测 Beclin-1、LC3、p62 及 p-mTOR 蛋白表达。使用 SPSS23.0 软件进行统计分析，两组间比较采用 t 检验，多组均数的比较采用单因素方差分析。
结果 与 I/R 组相比，TRPV1 抑制剂辣椒平（Capsazepine，CPZ）可明显改善小鼠神经功能缺损评分（t=3.097，P<0.01），并且明显改善小鼠焦虑和抑郁样行为（t=2.941，P<0.01），减少脑梗死体积（t=6.595，P<0.001），减轻小鼠杏仁核病理，下调自噬相关蛋白 Beclin-1（t=2.937，P<0.05）和 LC3（t=3.158，P<0.05）的表达水平，显著上调 p62（t=3.601，P<0.05），p-PI3K（t=7.789，P<0.01），p-AKT（t=4.152，P<0.01）和 p-mTOR（t=6.145，P<0.001）表达水平。
结论 脑缺血/再灌注激活神经元自噬，而 CPZ 可能调控 PI3K-AKT-mTOR 通路，进而抑制自噬的过度激活，从而起到神经保护和改善卒中后抑郁样行为的作用。

PU-0240

A Review on the Role of Micro-ribonucleic Acid in Gastric Cancer

Xinlin Li
Affiliated Hospital of Xuzhou Medical University

MicroRNAs(miRNA)are a class of endogenously-initiated non-coding RNAs that negatively regulate the expression of genes at the post-transcriptional level. MiRNA are responsible for many physiological processes，including cell growth and differentiation，maintenance of internal environmental stabilization and immune response. MiRNA exists stably in human serum and participates in many important regulation of the life process, but also confirmed that the

occurrence and development of tumors play an important role in the process. Tumor-specific circulating miRNAs have been recognized as a potential non-invasive cancer biomarker. It plays a carcinogenic or tumor suppressor role in Gastric cancer. Gastric Cancer is one of the most common digestive system tumors. Researches have demonstrated that miRNAs act as potential oncogenes in Gastric Cancer. This articleintroduces the expression and roles of miRNA in Gastric Cancer and the latest progress of their therapeutic effects.

PU-0241

基于电化学生物传感器检测环状 RNA 在肿瘤中的应用

魏雪菊[1,2]、洪国斋[1,2]
1. 厦门大学附属第一医院
2. 厦门市基因检测重点实验室

环状 RNA（circRNA）是最新确认的一类特殊的非编码 RNA，主要由外显子经非线性反向剪接形成。研究发现，circRNA 在人体细胞中广泛表达，在转录、转录后水平均具有调控基因表达的重要功能。有些 circRNA 具有天然微小 RNA（microRNA,miRNA）海绵作用，可通过与 miRNA 结合抑制其活性，从而调控 miRNA 靶标发挥作用。circRNA 在动脉粥样硬化，神经系统紊乱，糖尿病和肿瘤等疾病发生过程中起着较为重要的作用。因此，circRNA 的检测技术引起了人们的关注。电化学生物传感器属于化学传感器的一种，其将电化学换能器的高灵敏度与生物识别过程的高特异性结合在一起。由于电化学检测方法具有高灵敏度、高特异性、低成本等优点,因而在生化研究和临床分析等领域具有较大的应用价值。本文将对电化学生物传感器在环 RNA 检测的研究进行系统阐述。

PU-0242

遗传性肿瘤高通量测序结果的致病性分类与临床意义分级同步解读建议

邹秋艳[1]、喻长顺[1,2]
1. 天津金域医学检验实验室有限公司
2. 广州医科大学金域检验学院

随着高通量测序技术尤其是全外显子组测序技术的迅猛发展，肿瘤患者在辅助诊断、用药治疗和预后监测的及时性、精准性不断提高；精准的基因检测更是病种多、发病率低的遗传病患者查询病因、产前预防不可替代的诊断方法。因而，从患者个体的基因组数据库中鉴定出致病性突变，精准解读并出具有临床辅助价值的基因检测报告愈加重要且更具挑战。事实上，目前基因检测报告中基因变异的致病性分类不能与临床医生所关注的病例因果关系、临床诊断意义划等号，也不能很清晰的服务临床。此外，随着实验室数据分析人员与临床医生的频繁接触与沟通，本实验室发现依据 ACMG 指南出具的基因检测报告还存在一定的不足，该指南缺少基于病例水平的临床指导意义的分级标准，且没有功能多态性的概念描述。

为了进一步完善数据解读指南，将 NGS 检测报告更便于临床医生理解与使用，本实验室建议，在基于 ACMG 指南基因变异的致病性分类法的基础上增加“功能多态性变异”用于描述那些已知与特定的非疾病性的表型相关的变异；并且在临床意义的分级办法中增加“意外发现的具有重要临床意义的变异”，将与病例主诉无关的“意外发现”的致病性变异或与病例主诉无关的外显率较高、可引起严重损害、提前诊断可以使病例获益的致病性变异的临床意义均划分为此类。本实验室参考肿瘤体细胞变异的临床意义分级标准，提议遗传病胚系基因检测报告中补充临床意义分级，并自创 5 级分类标准。本文结合一例林奇综合征病例基因检测报告分析过程，阐述了基因检测报告中应当同时描

述基因变异的致病性分类和临床意义的分级，以提高基因检测报告的严谨性，降低基因检测报告被误读的风险。本方案的实施将进一步促进实验室分析人员与临床医生之间的相互理解，为临床遗传性肿瘤的数据解读提供新的范式，更有利于基因检测报告的解读和遗传咨询。

PU-0243

A preliminary study of risk factors for hematoma expansion and its predictive value in patients with spontaneous cerebral hemorrhage

Er Huang、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Objective By analyzing the imaging and clinical laboratory findings of our patients with spontaneous cerebral hemorrhage. We explore the factors associated with early hematoma enlargement in patients with sICH and its predictive value for hematoma enlargement, so as to provide guidance for the occurrence and prognostic assessment of clinical sICH patients.
Methods The clinical data of 116 patients with sICH admitted to the First Hospital of Fujian Medical University were retrospectively analyzed, and the 116 patients were divided into hematoma enlargement group and hematoma non-enlargement group according to the head CT imaging findings, and the general clinical information and laboratory examination data of the patients were collected to analyze the value of factors affecting early hematoma enlargement and independent influencing factors of hematoma enlargement on the occurrence of hematoma enlargement.
Results There were significant differences in cerebrospinal fluid chlorine, hematoma shape, initial hematoma volume, admission GCS score, hematoma clearance, blood glucose, lipoprotein a, cystatin C, homocysteine, bicarbonate and procalcitonin between the two groups ($P<0.05$).Multifactorial regression analysis identified hematoma shape, hematoma removal, initial hematoma volume, admission GCS score, cerebrospinal fluid Cl, bicarbonate, and calcitoninogen as independent risk factors. Predictive effect evaluation analysis of admission GCS score ≤6.5 had the highest sensitivity for predicting the occurrence of hematoma enlargement in patients with sICH, and hematoma debridement had the highest specificity for predicting hematoma enlargement. Combining the above seven independent influencing factors had the highest predictive value for the development of hematoma enlargement in patients with sICH, with a combined diagnostic ROC curve area (AUC) of 0.801, $P<0.001$
Conclusion Cerebrospinal fluid chlorine, hematoma shape, initial hematoma volume, admission GCS score, hematoma clearance, blood glucose, lipoprotein a, cystatin C, homocysteine, bisarbonate and calcitonin were the original factors affecting hematoma enlargement in sICH patients.Cerebrospinal fluid chlorine, hematoma shape, initial hematoma volume, admission GCS score, hematoma clearance, bicarbonate and calcitonin were independent risk factors for hematoma enlargement in patients with sICH.

PU-0244

PAI-1、MTHFR、APOE 基因多态性与静脉血栓栓塞症的相关性研究

方笑涵、徐永艳、赵晓涛
北京大学人民医院

目的 探究纤溶酶原抑制物激活物（PAI-1）、亚甲基四氢叶酸还原酶（MTHFR）和载脂蛋白 E（APOE）的基因多态性与静脉血栓栓塞症的相关性。
方法 选择 2019 年 10 月到 2021 年 02 月中就诊于本院血管外科的住院患者或门诊已确诊的静脉血栓栓塞症患者，平均年龄为 57.7±6.4 岁，排除易栓症诊断的患者与有明显诱发因素的患者，共 215 人作为实验病例组。同时选择本院体检中心健康志愿者共 200 名作为对照组。两组患者均使用 PCR-Sanger 测序技术进行 PAI-1 rs1799762 位点、MTHFR C677T rs1801133 位点、APOE rs429358 位点和 rs7412 位点的基因多态性检测。
结果 PAI-1 三种基因型 4G4G、4G5G、5G5G 在病例组中的出现频率分别为：40.5%、49.8%、9.7%，而在对照组中三种基因型的分布为：19.5%、34.5%、46%; MTHFR 三种基因型 CC、CT、TT 在病例组中的出现频率分别为：15.8%、40.9%、43.3%，而在对照组中这三种基因型的分布分别为：43.5%、35.5%、21%; APOE 三种亚型 APOE2、APOE3、APOE4，在病例组中这三种亚型的分布频率为 14.9%、62.8%、22.3%，而在对照组中这三种亚型的分布分别为 38.0%、54.0%、8.0%，其中 PAI-1 4G 等位基因在病例组中的出现频率 65.3%，在对照组中为 36.7%; MTHFR T 等位基因在病例组中的出现频率 63.7%，在对照组中为 38.7%; APOE4 亚型在病例组中的出现频率 22.3%，在对照组为 8.0%，三组基因的病例组均明显高于对照组（P<0.01），结果具有统计学意义。
结论 PAI-1 基因 4G 基因型、MTHRF T 基因型以及 APOE4 亚型基因多态性均与静脉血栓栓塞症相关，可作为临床参考依据辅助临床医生对患者进行静脉血栓栓塞症的相关风险预测。

PU-0245

Comprehensive analysis of TPX2 in Head and neck squamous cell carcinoma with prognostic values

miaomiao chen、wenjun Cao
Eye & ENT Hospital, Fudan University

Objective Targeting protein for Xenopus kinesin-like protein 2 (TPX2) is a microtubule-associated protein required for mitosis and spindle assembly. It has been revealed that TPX2 is overexpressed in various human cancers and promotes cancer progression, while its role in head and neck squamous cell carcinoma is unknown. We aimed to demonstrate the relationship between TPX2 and head and neck squamous cell carcinoma.
Methods This study investigated the expression and roles of TPX2 in HNSC using Oncomine, The Cancer Genome Atlas, UALCAN, Human Protein Atlas, Clinical Proteomics Tumor Analysis Consortium, GeneMANIA, Tumor IMmune Estimation Resource, GEPIA databases.
Results High mRNA and protein expression of TPX2 members were found to be significantly associated with clinical cancer stages, nodal metastasis status, and patient’s gender in HNSC patients.
Conclusion Taken together, these results indicated that TPX2 could be a potential target in the development of anti-HNSC therapeutics and an efficient marker of the prognostic value of HNSC.

PU-0246

Long noncoding RNA LINC01119 promotes neuropathic pain by stabilizing BDNF transcript

Le Zhang 、 Chuanxin Wang
The Second Hospital, Cheeloo College of Medicine, Shandong University

Purpose Neuropathic pain (NP) is a complicated, chronic pain state that is generally caused by tissue damage that affects the somatosensory nervous system. NP is linked with multiple diseases, commonly caused by Shingles (postherpetic neuralgia, PHN), diabetes (painful diabetic neuropathy, PDN) and others including trauma, stroke or cancer. In recent years, lncRNAs were reported to play essential roles in various diseases, including cancer, cardiovascular, diabetes and neuropathy-related affaires. However, the expression pattern, biological function, and underlying mechanism of lncRNAs in NP remains unclear. Previously, we identified the essential role of BDNF in NP progression. However, how BDNF was regulated and the functional link between lncRNA and BDNF was not defined. Therefore, our study aims to uncover the essential role of LINC01119 in NP progression and further clarify the underlying regulatory mechanism at post-transcriptional level.

Methods A spare nerve injury (SNI) was done in rats to imitate NP model. Paw withdrawal threshold (PWT) and paw withdrawal latency (PWL) were used for evaluation of hypersensitivity in NP. qRT-PCR, western blot and Immunofluorescence staining were performed to determine the quantity of involved genes. RNA immunoprecipitation and pulldown assays were employed for reveal the regulatory mechanism of LINC01119 in NP.

Results LINC01119 expression was significantly upregulated in the spinal cord tissues of SNI group compared to controls, and PWL and PWT were significantly decreased in SNI rats while no significant change was identified in sham rats. Functionally, silence of LINC01119 significantly suppressed NP behaviors and downregulated the concentrations of IL-6, IL-1β and TNF-α. Mechanistically, BDNF was downregulated in spinal cord tissues after injection of sh-LINC01119, suggesting that LINC01119 may influence NP via regulating BDNF expression in spinal cord areas. In addition, BDNF was also suppressed by silence of LINC01119 in rat microglia cells. Analysis with ELISA showed that BDNF overexpression by intrathecal injection of Lv-BDNF could partially attenuate the suppressive effect of sh-LINC01119 on the expressions of IL-6, TNF-α and IL-1β in SNI rats. Consistently, the effects on NP-like behaviors caused by knockdown of LINC01119 were also abrogated by overexpression of BDNF. Besides, an RNA binding protein, ELAVL1 could directly interact with LINC01119, and this formed LINC01119- ELAVL1 complex binds to BDNF mRNA, strengthening its RNA stability and increasing the expression level of BDNF at both transcript and protein levels. Downregulation of ELAVL1 by intrathecally injection of sh-ELAVL1 induced decreased expression of BDNF in spinal cord at both transcript and protein levels, suggesting that ELAVL1 may function synchronously with the interaction of LINC01119. To demonstrate whether silenced ELAVL1 reverses LINC01119-mediated NP production, Lv-LINC01119 and sh-ELAVL1 vectors were injected intrathecally into SNI rats. The results showed that silencing ELAVL1 abrogated the LINC01119-mediated NP behaviors. Taken together, the above data suggests that LINC01119-ELAVL1 complex may directly bind to BDNF mRNA and regulate its stability, thereby causing NP progression. Clinically, By detecting the expression level of LINC01119 in serum samples, we verified that LINC01119 was significantly upregulated in NP patients compared to healthy individuals. ROC analysis indicated a high diagnostic potential of serum LINC01119 in differentiating NP and healthy population. By stratifying all populations into a high and a low LINC01119-level group based on the stratification criterion of 1.32 according to the ROC curve, we revealed that the proportion of NP patients was much higher in high LINC01119-level group when compared to that of low LINC01119 group, which further indicates LINC01119 is a promising diagnostic marker.

Conclusions To conclude, our study revealed the novel contribution of LINC01119/ELALV1/BDNF axis in NP progression. LINC01119 induces NP progression via

binding with ELAVL1 and increasing BDNF mRNA stability and expression level. Our discovery not only help us get a better understanding on the regulatory potential of LINC01119 in NP, but also useful for finding promising drug targets and developing novel therapeutic strategies to overcome NP.

PU-0247

单细胞测序技术在恶性肿瘤研究中的应用进展

朱俊梅
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 简要综述单细胞测序技术在恶性肿瘤研究中的应用进展。
方法 查阅国内外近年来单细胞测序技术在肿瘤异质性研究的相关文献进行总结。
结果 随着单细胞分离技术以及基因测序技术的快速发展，单细胞测序技术已在微生物学、神经科学及肿瘤学等生物医学领域中展示出广泛的应用前景，对于癌症早期的诊断、追踪以及个体化治疗具有重要意义。相比于传统的群体多细胞测序技术，单细胞测序技术能够对单个细胞的性质和功能进行分析，揭示其异质性，解析细胞谱系及其之间的关系，且能够对数量稀少的特殊细胞的特性进行探索。作为恶性肿瘤的主要特征之一，肿瘤异质性影响肿瘤的生长、侵袭、转移和耐药性等。
目前，单细胞测序主要可分为基因组、转录组、表观基因组和蛋白质组测序。相比于单一组学技术，单细胞多组学技术可以在同一细胞中获得多个层面的组学信息，能够更全面地反应细胞特性，有利于更系统地了解肿瘤细胞异质性、多样性及生物学机制，推动肿瘤精准医学发展。
单细胞测序的关键步骤包括：单细胞分离、扩增及建库、高通量测序、数据分析。其中，单细胞的分离和扩增对测序结果的准确性具有关键性作用，也是单细胞测序的技术难点。随着技术的不断发展，扩增的覆盖度和灵敏度都在不断提高，单细胞测序技术将展现出更强的应用价值，有望开发新的单细胞测序产品，推进肿瘤的精准诊疗。
结论 单细胞测序技术能够在单个细胞的不同组学水平上反映细胞的异质性，展现肿瘤异质性以及肿瘤演化，有利于研究肿瘤的发展机制和转移机制，也为恶性肿瘤的临床诊治提供了新视角和新思路。

PU-0248

CircHN1 affects cell proliferation and migration in gastric cancer

张宇
南京鼓楼医院

Background Increasing evidence indicates that circular RNAs (circRNAs) are dysregulated in human cancers. The biological roles of circRNAs in gastric cancer (GC) have not been well-characterized.
Methods The GEO database was used to analyze circRNA expression profile in GC. The biological roles of circRNAs in cell proliferation, migration, and invasion were determined by cell counting, colony formation, transwell migration, Matrigel invasion. The interactions between circRNAs and miRNAs were verified by RNA immunoprecipitation and luciferase reporter assays.
Results We found that circHN1 was upregulated in GC tissues and cell lines compared to adjacent non-tumor tissues and normal gastric epithelial cells. circHN1 silencing significantly promoted GC cell growth, colony formation, migration, and invasion. MiR-1248 and miR-375 were predicted to interact with circHN1 by bioinformatic analyses and experimental verification.
Conclusion CircHN1 is aberrantly expressed in GC and affects the proliferation and migration of gastric cancer cells by acting as miRNA sponge.

PU-0249

PIWI-interacting RNAs serve as promising diagnostic biomarkers of lung adenocarcinoma

Juan Li、Lutao Du、Chuanxin Wang
The Second Hospital of Shandong University

Purpose Lung cancer is the malignant tumor with the highest morbidity and mortality, and lung adenocarcinoma (LUAD) is the main subtype of primary lung cancer. Recent studies have shown that piwi-interacting RNAs (piRNAs), as a type of small non-coding RNAs, may play crucial roles in the progression of cancer and serve as biomarker for tumor detection This study aimed to explore the profiles and diagnostic value of piRNAs in LUAD.
Methods Small RNAs sequencing was analyzed to investigate the tissue piRNA profiles from 5 LUAD patients. The top 10 upregulated piRNAs were selected and evaluated by reverse transcription quantitative real-time PCR (qRT-PCR) in 14 LUAD tissues and paired non-tumor tissues, as well as serum exosome samples of 70 LUAD patients and 57 healthy people. Exosomes were extracted from serum samples by ExoQuickTM kit and identified by transmission electron microscope (TEM), nanoparticle tracking analysis (NTA) and western blotting assays. Receiver operating characteristic (ROC) curve was performed to quantify the diagnostic potentials of piRNAs in LUAD. Finally, piRNAs-panel was developed by multivariate logistic regression model.
Results We found that 85 differentially expressed piRNAs by the critecia of fold change ＞2 and p ＜0.05, of which 76 piRNAs were highly expressed and 9 piRNAs were lowly expressed in LUAD tissues compared to adjacent non-tumor tissues. Among the top 10 overexpressed piRNAs, 4 piRNAs levels were verified to be significantly upregulated in LUAD tissues. Then, piR-hsa-26925 and piR-hsa-5444 were found to be obviously higher levels in serum exosomal samples of LUAD patients than health controls, and the area under the ROC curve (AUC) were 0.751 and 0.713. Furthermore, we established the 2 piRNAs-panel combined piR-hsa-26925 with piR-hsa-5444 by multivariate logistic regression analysis, which showed higher diagnostic performance with the AUC of 0.833 for LUAD.
Conclusion Our finding suggested that piRNAs were abnormally expressed in LAUD, and serum exosomal piR-hsa-26925 and piR-hsa-5444 could serve as potential biomarkers for LAUD diagnosis.

PU-0250

VN1R5 基因调控头颈部鳞状细胞癌顺铂耐药的机制

郭海艳
上海交通大学医学院附属第九人民医院

目的 本研究的目的在于深入阐明头颈部鳞状细胞癌（HNSCC）顺铂化疗耐药的分子机制，为临床逆转顺铂化疗耐药提供数据支持。
方法 通过蛋白质谱法分析顺铂敏感和顺铂耐药癌细胞中异常表达的蛋白质，qPCR 和蛋白质免疫印迹验证顺铂相关蛋白；使用 CRISPR/cas9 技术在 HNSCC 细胞中敲除 VN1R5 基因；为了探索 VN1R5 调控的下游靶点，对 VN1R5 敲除或过表达的 HNSCC 细胞进行基因微阵列分析；通过使用 Smart Silencer 沉默细胞中 lnc-POP1-1 的表达；反义寡核苷酸 (ASO)用于沉默动物实验中的 lnc-POP1-1。相反，通过慢病毒表达载体在细胞中过表达 lnc-POP1-1。
结果（1）蛋白质谱的结果显示，与顺铂敏感细胞株（HN4 和 HN30）相比，顺铂耐药细胞 HN4/DDP 和 HN30/DDP 中 VN1R5 蛋白表达水平显著升高。（2）在 HNSCC 临床样本中，与 TPF 方案敏感组织相比，VN1R5 在 TPF 方案耐药组织中高度表达。并且 VN1R5 高表达组患者 5

年生存率明显低于 VN1R5 低表达组。（3）体外实验结果显示，VN1R5 敲除导致顺铂的 IC50 值显著降低。相反，VN1R5 过表达显著增加顺铂的 IC50 值。（4）在动物实验中，VN1R5 敲除组的肿瘤体积和重量显著低于对照组。（5）基因芯片的结果证实，lncRNA lnc-POP1-1 是 VN1R5 的下游靶标。在临床样本中，Lnc-POP1-1 表达与 VN1R5 表达呈正相关。（6）lnc-POP1-1 沉默导致 HN4/DDP 和 HN30/DDP 细胞中顺铂的 IC50 显著降低。lnc-POP1-1 的过表达增加了顺铂的 IC50。（7）在动物实验中， lnc-POP1-1 敲低组的肿瘤体积和重量显著低于对照组。此外，lnc-POP1-1 过表达组的肿瘤体积和重量显著高于对照组。
结论 在这项研究中，我们鉴定了一个关键的顺铂耐药相关蛋白—VN1R5。VN1R5 通过 cAMP 途径促进 lnc-POP1-1 的转录，导致 HNSCC 细胞发生顺铂的获得性耐药。

PU-0251

涉及三条常染色体复杂易位病例分享

尹燕军、柯江维
江西省儿童医院

患者　女，1 天，以新生儿心肺复苏 1 小时为主诉入院。系第 1 胎第一产，胎龄 38+6 周，剖宫产，宫内窘迫史，羊水污染，出生时有窒息史，行气管插管及心肺复苏等治疗。查体发现双瞳孔欠清，角膜模糊、浑浊。完善检查心超提示房间隔缺损（II），动脉导管未闭肺动脉高压。B 超提示双肾下极于脊柱前方融合（马蹄肾？）；腹腔局部肠管干瘪，未及明显内容物。肺部 X 片提示新生儿肺炎。患者多发畸形首先考虑先天遗传病，行外周血染色体检查及全外显基因检测。

患者染色体核型为：46，XX，t(3；7；12)(3pter→3p13::7p21→7q36::3q22→3qter；7pter→7p22::12p11→12pter；3q21→3p12::12q11→12qter)见图 1。全外显子测序检测**结论** 检测与患者表型部分相关的临床意义未明变异，高通量测序数据提示 9 号染色体短臂有片段重复可能。

PU-0252

不同乙型肝炎患者体内 HBV-DNA 载量对血小板参数变化的影响分析

谢铠何
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 血小板生成素（thrombopoietin，TPO）其产生部位至今无明确的结论，肝脏有可能是 TPO 产生部位之一，因此乙型肝炎患者有可能影响血小板的产生。本研究分析乙型肝炎患者体内 HBV-DNA（乙肝病毒 DNA）载量对血小板相关参数变化的影响，为临床乙型肝炎患者的治疗提供参考。
方法 随机抽取 2020 年 3 月到 2020 年 10 月徐州市中医院的门诊及住院患者禁食 12h 后的 274 份乙肝表面抗原（HBsAg）阳性血标本，检测患者血清中的乙肝病毒基因 HBV-DNA 载量，同时检测患者血小板的 6 项参数，包括血小板的计数、血小板比率、血小板的比容、平均血小板的体积、血小板分布宽度和血小板生成素。使用多功能酶标仪（奥地利 Anthos，Anthos2010）检测 TPO 的含量。将健康体检 HBsAg 阴性无基础疾病的 274 人作为正常对照组比较不同。HBV-DNA 载量组血小板参数的变化，分析不同乙型肝炎患者 HBV-DNA 载量和乙肝相关的肝硬化 Child-Pugh 分级对血清 TPO 和血小板相关参数的影响。
结果 不同乙型肝炎患者随着体内 HBV-DNA 载量的不同，血小板参数也存在着明显的差异，并且随着载量的增大，PLT（血小板）、PCT（血小板压积） 和 TPO 减少，而 P-LCR（大血小板比例）、 MPV（平均血小板体积） 和 PDW（血小板分布宽度） 增大；Child-Pugh A 级、B 级、C

级血清 TPO 均低于正常对照组；随着肝损伤的严重程度的加深，MPV、PDW 和 P-LCR 升高；慢性肝衰竭组和肝硬化组 PLT、PCT 和 TPO 低于慢加急肝衰竭组。
结论 血小板参数的变化能够在临床上更好的判断 HBV 复制的严重性，对于乙型肝炎患者的血小板参数出现严重异常者可以判断是否为病毒复制严重，及时采取抗病毒治疗，以减轻 HBV 对骨髓的抑制作用。

PU-0253

Weighted gene co-expression network analysis of hub genes in lung adenocarcinoma

Xuan Luo 、Lei Feng、Wenbo Xu、Xuejing Bai、Mengna Wu
Department of Laboratory, People's Hospital of Yuxi City （Department of Laboratory, The Sixth Affiliated Hospital of Kunming Medical University）

Lung adenocarcinoma (LUAD) is a tumor with high incidence. This study aimed to identify the central genes of LUAD. LUAD were analyzed by weighted gene co-expression network (WGCNA), and differentially expressed genes (DEGs) were identified. Samples were obtained from The Cancer Genome Atlas (TCGA) and Genotype Tissue Expression (GTEx) databases and included 515 LUAD samples and 347 normal samples. The WGCNA algorithm generated a total of 10 modules. The top 2 modules (MEturquoise and MEblue) with the highest correla_x0002_tion to LUAD were selected. Ten Hub genes (IL6, CDH1, PECAM1, SPP1, THBS1, HGF, SNCA, CDH5, CAV1, and DLC1) were screened in the intersecting genes of DEGs and WGCNA (MEturquoise and MEblue). Only SPP1 was correlated with LUAD poor survival, indicating that SPP1 may be a key Hub gene for LUAD. The competing endogenous RNA (ceRNA) network was constructed to analyze the regulatory relationship of Hub genes, and SPP1 may be directly regulated by 4 microRNAs (miRNAs) and indirectly regulated by 49 long noncoding RNAs (lncRNAs).

PU-0254

HPV 整合引起的宿主靶基因功能异常参与宫颈癌的发生

张瑞阳
上海交通大学医学院附属第九人民医院

本研究通过综合分析 HPV 病毒宿主整合序列，探究 HPV 在人类基因组上的整合特点，并通过对 HPV 整合影响的宿主靶基因的功能注释分析，探明 HPV 整合靶基因在宫颈癌发生中所起的作用。文献检索收集 HPV 整合位点。通过 GO 及 KEGGpathway 数据库对整合靶基因进行功能注释分析。Real-timePCR 检测整合靶基因在宫颈癌组织及细胞系中的表达，流式细胞术检测细胞周期分布，EdU 掺入实验检测细胞增殖。通过文献检索收集到 499 个 HPV 整合位点。通过对这些整合位点分析，我们发现 HPV 整合在人类基因组中染色体上的分布有热点区域，并且整合易发生在基因内部尤其是外显子区、基因密集区域和转录活跃区等与基因功能密切相关的区域，这样的整合特点为 HPV 整合影响宿主基因的表达和功能提供了前提条件。随后通过对整合靶基因进行功能条目和信号通路聚类分析发现，这些基因显著富集于肿瘤相关功能条目和信号通路，如“血管生成”、“细胞分化”、“转录调控”、“细胞增殖”、“基因表达”、“细胞死亡调控”、“细胞粘附”、“ErbB 信号通路”、“mTOR 信号通路”、“癌症信号通路”等与肿瘤发生发展相关的条目。可见，受 HPV 整合影响的整合靶基因与宫颈癌密切相关。进一步对 HPV 整合片段与整合靶基因的互作机制研究发现，HeLa 细胞中整合的 HPV 片段与下游靶基因 MYC 存在远程调控作用，且通过 CRISPR-Cas9 技术敲除整合的 HPV 片段可以下调 MYC 基因的表达，引起 HeLa 细胞发生凋亡，进一步证明了整合靶基因在宫颈癌中的重要作用。最后，为了从整合靶基因中筛选出更多的宫颈癌相关基因，通过对整合靶基因进

行定量分析发现，部分整合靶基因在宫颈癌组织中异常表达。对异常低表达的整合靶基因 MPPED2 进行功能研究发现，其可作为抑癌基因抑制宫颈癌细胞的细胞周期转换及细胞增殖。HPV 整合可通过影响整合位点周围宿主靶基因功能参与宫颈癌的发生。

PU-0255

靶向 PFKFB3 调控 CD4+T 细胞分化缓解实验性自身免疫性脑脊髓炎的机制研究

王清泰
福建省第二人民医院

多发性硬化症（multiple sclerosis，MS）病人会发生间断的或持续的髓鞘损伤，炎症病灶和脱髓鞘病变使其主要的病理指征。尽管人们对 MS 进行了多年研究，但其病因及病理机制尚未完全明了，目前亦无能彻底治疗 MS 的药物。PFKFB3 被证明参与多种免疫性疾病的发生。在本研究中，我们发现，在 MS 动物模型实验性自身免疫性脑脊髓炎（experimental autoimmne encephalomyelitis，EAE）小鼠中 PFKFB3 高表达，采用 PFK15 干预 PFKFB3 作用能够显著降低 EAE 小鼠疾病的严重程度，促进 EAE 小鼠的生存并改善其临床评分，但对脾脏和 CNS（central nervous system）中炎症细胞的比例并没有显著影响。进一步通过体内外研究发现，PFK15 可抑制 Th1、Th17 细胞分化而促进 Treg 细胞的分化，从而重建 EAE 疾病小鼠体内 Th1/Th17/Treg 细胞平衡，缓解 EAE 疾病进展。我们还发现，PFK15 对 Th1/Th17/Treg 细胞分化平衡的调控可能依赖于其对 mTOR 表达的调控。这些研究结果表明，靶向抑制 PFKFB3 能够在体内和体外调控 Th1/Th17/Treg 细胞分化平衡，有望成为治疗 MS 的新靶标。

PU-0256

肝细胞癌组织和癌旁组织中乙肝病毒前 S 基因分析

朱平安
深圳市盐田区人民医院

目的 分析肝细胞癌组织和癌旁组织中乙肝病毒前 S 基因，了解其变异情况。
方法 采用巢式 PCR 和琼脂糖凝胶电泳的方法对 100 份肝细胞癌组织和癌旁组织中乙肝病毒前 S 基因进行扩增和分析。选择第二轮前 S 基因目的片段,正反链测序，并与 HBV 参考序列（AY518556）进行比对。
结果 肝癌组织及癌旁组织乙肝病毒前 S 基因检出率分别为 44%、43%。10 份肝癌组织乙肝病毒前 S 基因缺失片段，其中 pre-S1 突变体占 50.00%（5/10），pre-S2 突变体占 10.00%（1/10），pre-S1+pre-S2 突变体占 40.00%（4/10）。6 份标本肝细胞癌组织和癌旁组织 HBV 前 S 基因同时阳性，HCC14、HCC64 缺失位置和片段不一致，包含 pre-S1、pre-S1+pre-S2 突变体，其它肝癌组织及癌旁组织存在点突变。癌旁组织 2 份标本 HBV 前 S 基因缺失，HCCP76、HCCP85 存在 pre-S1+pre-S2 突变体，15 个标本前 S 基因存在点突变。肝细胞癌组织 HBV pre-S73、HBV pre-S82 和癌旁组织 HBV pre-S8 存在插入突变。肝癌组织 HBV pre-S35、HBV pre-S60、HBV pre-S64、HBV pre-S73 序列内含终止密码子，提前终止翻译，导致截短前 S 蛋白和改变蛋白质结构。另外，肝癌组织测序阳性 22 份，其中 C 基因型 5 份，B 基因型 17 份，分别为 22.73%（5/22）、77.27%（17/22）；癌旁组织测序阳性 17 份，其中 C 基因型 2 份，B 基因型 15 份，分别占 11.76%(2/17)、88.24%（15/17）。
结论 肝细胞癌组织和癌旁组织乙肝病毒前 S 基因出现缺失突变和插入突变，导致截短乙肝病毒前 S 蛋白或蛋白改变，可能与肝细胞癌发生相关。

PU-0257

组蛋白去甲基化酶 JMJD3 调控辅助型 CD4+T 细胞增殖和分化在类风湿性关节炎中的作用

王清泰
福建省第二人民医院

目的 类风湿性关节炎（rheumatoid arthritis，RA）是一种慢性、全身性的自身免疫性疾病，以滑膜关节病变为主，在全世界的发病率为 1%，其主要病理改变为关节滑膜炎症，随着病情进展可出现软骨和骨破坏以及关节重构，其确切的病因和发病机制尚未完全明了，可能与遗传、感染、自身抗体和环境因素相关。近年表观遗传调控对 RA 的作用机制已引起了人们的极大关注，而组蛋白去甲基化酶 JMJD3 作为重要的表观遗传分子，可使发生双甲基化和三甲基化的组蛋白 H3K27 去甲基化，调控细胞发育分化等生命活动。本研究探讨组蛋白去甲基化酶 JMJD3 调控 RA 患者外周血 $CD4^+$ T 细胞亚群变化，以期为 RA 的临床诊治和新药靶点的开发提供思路。
方法 选择入住福建省第二人民医院（三甲医院）内分泌科 30 例确诊类风湿关节炎患者的外周血(从 2016 年 6 月至 2017 年 12 月住院期间病例)，所有入组的 RA 患者均符合 1987 年美国风湿病学会类风湿关节炎分类标准。采用欧洲抗风湿病联盟颁布的 DAS28 评定患者的病情活动度，所有 RA 的 DAS28 均大于 2.6。同时采集同期门诊 30 例健康体检者外周血作为健康对照组。
分离了 RA 病人和健康人外周血 $CD4^+$ T 细胞，用免疫印迹和 Real-time PCR 检测 JMJD3 的蛋白表达和 mRNA 表达以及其表达与 $CD4^+$ T 细胞亚群比例的相关性。建立了 T 细胞的活化和分化体系，在此体系中加入 JMJD3 的抑制剂，分析 JMJD3 对 $CD4^+$ T 细胞的影响并分析在 RA 疾病中的调控作用。4. 流式细胞术检测 $CD4^+$ T 细胞亚群活化、分化和凋亡水平。
结果 与健康人相比，RA 病人外周血 $CD4^+$ T 细胞中 JMJD3 的表达显著升高，并与 RA 疾病状态呈正相关。 在 $CD4^+$ T 细胞的活化体系中，JMJD3 的表达呈现先升后降的趋势。抑制 $CD4^+$ T 细胞中 JMJD3 后，T 细胞的活化、增殖下降，并且抑制 Th1 和 Th17 细胞亚群的分化，促进 Treg 的分化。JMJD3 的表达与 RA 中 Th1 和 Th17 细胞比例呈正相关，与 Treg 细胞比例呈负相关。
结论 JMJD3 通过表观调控 $CD4^+$ T 细胞的活化、增殖和分化，进而参与 RA 的疾病进程，我们的发现为 JMJD3 的新功能拓展了思路，为临床 RA 疾病的治疗提供了新策略和潜在靶点。

PU-0258

TARGETING SALL4 BY JQ1 IN SEROUS EPITHELIAL OVARIAN CANCER

Yue Wu、Wei Cui
Department of Clinical Laboratory, National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Background SALL4 is a stem cell factor that is involved in maintaining self-renewal and pluripotency in embryonic stem cells. Numerous studies have shown that SALL4 is abnormally highly expressed in many malignant tumors. However, in epithelial ovarian cancer, the role of SALL4 is rarely reported. Therefore, we aimed to explore the role of stem cell factor SALL4 in the development and treatment of epithelial OC.
Methods Lentiviral expression vector was constructed to establish SALL4 stable knockdown and overexpressing OC cell lines; Western blot, real-time qPCR was used to detectprotein and RNA levels, CCK-8 kit was used to detect the cell proliferation ability and the toxic effect of JQ1, flow cytometric analysis was used to assess cell cyle with propidium iodide DNA staining.
Results Comparision of normal ovarian tissues revealed elevated SALL4 mRNA levels that were greater than two-fold in 94% epithelial serous OC tissues (65/69, $P<0.001$). After knocking down SALL4 in A2780, cells showed decreased proliferation and colony formation ability. The cell cycle

analysis showed that the proportion of cells in GO/G1 phase was significantly increased, and the proportion of cells in S phase and G2/M phase was significantly decreased (P<0.05). SALL4 overexpression increased cell proliferative and colony formation ability. The cell cycle analysis showed that the proportion of cells in the GO/G1 phase was significantly decreased, and the proportion of cells in the S phase and G2/M phase was significantly increased (P<0.05).
Further, we explored the role of JQ1 on SALL4. This is the first study to investigate the role of JQ1 on SALL4. We found that treatment of A2780 with 0.05 μM JQ1 reduced 70% SALL4 RNA in only 6 h and SALL4 protein were almost gone after treatment with 2.5 μM JQ1 for 24 h. Meanwhile, low concentration of JQ1 can significantly inhibit the colony formation ability (0.05 μM) and proliferation (0.5 μM) of A2780, and A2780 can be blocked in G0/G1 phase after treatment with 0.05 μM JQ1 for 24 h. In addition, we compared the drug sensitivity to JQ1 between endogenously high SALL4 expression cell A2780 and low/no SALL4 expression cell lines (SKOV3, CAOV3, OVCAR3) . We found A2780 showed much higher inhibition rate after 0.5 μM, 2.5 μM and 5 μM JQ1 treatment for 96 h than SKOV3, CAOV3, and OVCAR3. Cell cycle results showed that no G0/G1 phase block effects were found after 0.5 μM JQ1 treatment with SKOV3, CAOV3, and HO8910 for 24 h and 48 h.
Conclusion SALL4 acts as an oncology gene role in OC. JQ1 treatment of endogenously high SALL4 cells showed similar effects as knockdown, suggesting SALL4 may beone of the targets of JQ1. Also, endogenously high SALL4 cells are more sensitive to JQ1. Overall, our studies suggest that targeting SALL4 by JQ1 may be a novel approach for ovarian cancer treatment.

PU-0259

Spy1 介导喉鳞癌原发性放射抗拒的作用研究

柯青[1]、龚倩[1]、邓鑫州[2]、柴晶晶[2]
1. 复旦大学附属中山医院青浦分院（上海市青浦区中心医院）
2. 湖北医药学院附属太和医院

目的 细胞周期调节蛋白 Spy1（speedy/RINGO cell cycle regulator family member A）与肿瘤的发生发展密切相关。本研究主要探讨 Spy1 的表达改变对人喉鳞癌细胞原发性放射抗拒的影响。
方法 采用 Western blot 检测喉鳞癌原发性放射抗拒细胞 Hep-2max 及敏感细胞 Hep-2min 中 Spy1 的表达；将 Spy1 的干扰质粒转染 Hep-2max 细胞，Spy1 过表达慢病毒感染 Hep-2min 细胞，然后运用荧光定量 PCR 及 Western blot 检测干扰及过表达效果；采用克隆形成实验检测不同剂量 X 线照射后细胞存活率的变化；采用流式细胞术检测经 4GyX 线照射后细胞凋亡与周期的变化。
结果 Western blot 实验表明，Spy1 在 Hep-2max 中的表达显著高于 Hep-2min；荧光定量 PCR 及 Western blot 结果显示，Hep-2max 细胞中 Spy1 shRNA-4 干扰效果最佳，感染慢病毒的 Hep-2min 细胞中 Spy1 的表达显著升高；克隆形成实验显示，Spy1 干扰组细胞存活分数（0.476±0.038）较阴性对照组（0.819±0.013）明显降低, 而 Spy1 过表达组细胞存活分数（0.967±0.021）较阴性对照组（0.753±0.012）明显升高；流式细胞术检测结果显示：Spy1 干扰组细胞凋亡率(21.70±2.35)%较阴性对照组(7.09±1.05)%显著增加；而 Spy1 过表达组细胞凋亡率(2.20±1.98) %较阴性对照组(7.27±1.65)%则明显降低； Spy1 干扰组 G2/M 期细胞比例(33.91±1.39) %较阴性对照组(17.52±1.26)%明显增加，而 Spy1 过表达组 G2/M 期细胞比例(11.22±1.07)%较阴性对照组(18.16±1.75)%则明显降低，差异均具有统计学意义（P<0.05）。
结论 干扰 Spy1 表达增强了喉鳞癌原发性放射抗拒细胞 Hep-2max 的放射敏感性，而过表达 Spy1 则使敏感细胞 Hep-2min 的放射抗拒性增强，表明 Spy1 参与调控了喉鳞癌的原发性放射抗拒，为喉鳞癌放射增敏研究提供了新的靶点。

PU-0260

肺腺癌顺铂耐药基因 UCA1 相关下游通路和分子分析

周慧新
温州医科大学附属第一医院

目的 分析肺腺癌中长链非编码 RNA UCA1 相关顺铂耐药的下游通路和分子。
方法 构建针对 UCA1 和 TXNIP 的过表达和 siRNA 载体，并使用下一代测序比较 A549 细胞的 UCA1 过表达和阴性对照细胞株。Q-PCR 检测肺腺癌组织与癌旁组织中 mRNA 的差异表达水平，以及人支气管上皮细胞 BEAS-2B 与肺癌细胞（A549、A549/DDP）中 TXNIP 表达水平。收集对数期的 A549 细胞,分为两组：NC 和 UCAI 过表达组；收集对数期的 A549/DDP 细胞，分为两组：NC 和 UCA1 敲低组，并通过 Q-PCR 检测下游 TXNIP 表达水平，CCK8 检测细胞增殖能力，并计算顺铂的半数抑制浓度(half inhibitory concentration, IC50)。GO（Gene Ontology）分析下调的 mRNAs 相对应的基因生物学过程和分子功能，最后通过蛋白互作网络（protein protein interaction network, PPI network）分析蛋白质之间的相互作用。
结果 测序结果显示有 647 个上调的和 633 个下调的差异表达的 mRNA，前 10 个上调的是 CPD、AC007192.1、TGOLN2、LGR4、TFPI、CYP1B1、TOMM6、HLA-B、SLC35F6 和 TOP2A，前 10 个下调的是 TXNIP、SESN2、STC2、HSPA1A、MMP10、CHAC1、DNAJB1、AC004922.1、ATF3 和 GABARAPL1。我们发现 TXNIP 基因表达水平是最显著下调的基因。肺腺癌组织中 TXNIP 表达水平明显低于癌旁组织。顺铂不敏感组中 UCA1 表达水平明显高于顺铂敏感组，而顺铂不敏感组中 TXNIP 基因表达水平明显低于顺铂敏感组。与 BEAS-2B 相比，A549 和 A549/DDP 细胞中 TXNIP 基因表达水平降低，并且在 A549/DDP 细胞的表达水平低于 A549 细胞。UCA1 过表达后，TXNIP 基因表达明显降低，而 A549 细胞增殖能力和 IC50 升高。敲除 UCA1 后，TXNIP 基因表达显著增加，而 A549/DDP 的增殖能力和 IC50 降低。PPI 分析结果表明，TXNIP 可与 TXN、DDIT4、NLRP3 等多种蛋白质相互作用。
结论 UCA1 通过下调肺腺癌中 TXNIP 的表达促进顺铂耐药，TXNIP 可与多种蛋白相互作用。因此，UCA1/TXNIP 轴可能影响肺腺癌对顺铂的耐药性。

PU-0261

两种 RNA 恒温扩增检测技术在儿童肺炎支原体肺炎中诊断价值的比较

李毅、周良琼、刘萍、张立群
陆军军医大学第二附属医院检验科

目的 新型荧光定量 NASBA -CRISPR 技术与实时荧光核酸恒温扩增检测技术(SAT)在肺炎支原体肺炎早期诊断中的应用比较。
方法 选取自 2020 年 5 月至 2021 年 2 月于本院初诊的肺炎支原体肺炎患儿 40 例作为观察组，另设正常对照儿童 10 例。对两组人群咽部分泌物标本分别采用量 NASBA -CRISPR 技术和 SAT 技术进行检测，使用临床评价血清比较两种测定方法的重复性、线性和临床样本符合情况。
结果 两项技术的性能参数显示：NASBA-CRISPR 的检测灵敏度和线性范围都优于 SAT 技术。且 NASBA-CRISPR 技术的样本批内变异系数 (Log10)均比 SAT 技术低。两种方法的对肺炎支原体识别特异性相同。对于临床样本的检测, NASBA-CRISPR 和 SAT 技术的相关系数为 0.893($P<0.05$)。
结论 在肺炎支原体肺炎患儿的临床检测中,采取 NASBA-CRISPR 技术和 SAT 技术均能提高临床诊断的特异性,但由于 NASBA-CRISPR 技术具有较高灵敏度，对疾病的早期诊断更有优势。但在检测方式的选择上，应注意患儿的患病时间以及院外药物服用情况,择取最合适的检测方法。

PU-0262

The Effect of Spy1 on inherent radioresistance of laryngeal squamous cell carcinoma

Qing Ke[1]、Qian Gong[1]、Xinzhou Deng[2]、Jingjing Chai[2]
1. Qingpu Branch of Zhongshan Hospital, Fudan University
2. 湖北医药学院

Objective Spy1 (speedy/RINGO cell cycle regulator family member A) is closely related to the occurrence and development of tumors. The purpose of this study was to investigate the effect of Spy1 expression on inherent radioresistance in human laryngeal squamous cell carcinoma.
Methods Western blot was used to detect the expression of Spy1 in radioresistant cell hep-2max and radiosensitive cell hep-2min. Spy1 interfering plasmid was transfected into Hep-2max cells, and Spy1 overexpressing lentivirus infected Hep-2min cells, then the interfering and overexpressing effects were detected by Real-time PCR and Western blot. The changes of cell viability after different doses of X-ray irradiation were detected by clonogenic assay, and the changes of cell apoptosis and cell cycle were detected by flow cytometry after 4 Gy X-ray irradiation.
Results Western blot showed that the expression of Spy1 in hep-2max was significantly higher than that in hep-2min. Real-time PCR and Western blot showed that the effect of Spy1 shRNA-4 interference was the best in Hep-2max, and Spy1 expression was significantly increased in Hep-2min cells by infected with lentivirus. The colony forming assay showed that the cell survival fraction of Spy1 interference group (0.476±0.038) was significantly lower than that of negative control group (0.819±0.013), while the cell survival fraction of Spy1 overexpression group (0.967±0.021) was higher than that of negative control group (0.753±0.012). The flow cytometry assay showed that the apoptotic rate of Spy1 interference group (21.70 +2.35)% was significantly higher than that of negative control group (7.09 +1.05)%, while the apoptotic rate of Spy1 overexpression group (2.20 +1.98)% was significantly lower than that of negative control group (7.27 +1.65)%. The proportion of G2/M phase cells in Spy1 interference group (33.91 +1.39) was significantly higher than that of negative control group (17.52 +1.26)%, while the proportion of G2/M phase cells of Spy1 overexpression group (11.22±1.07)% was significantly lower than that of negative control group (18.16 +1.75)%. The difference has statistically significant ($P < 0.05$).
Conclusions Interference with Spy1 expression enhances the radiosensitivity of Hep-2max, while overexpression of Spy1 enhances the radioresistance of Hep-2min, suggesting that Spy1 participates in regulating the inherent radioresistance of laryngeal squamous cell carcinoma and provides a new target for radiosensitization of laryngeal squamous cell carcinoma.

PU-0263

miR-146a 在尿路感染病原菌耐药性中指示作用的研究

崔金鹏
烟台市烟台山医院

目的 探究 miR-146a 在尿路感染病原菌耐药性中指示作用。
方法 选取自 2018 年 12 月至 2020 年 4 月间来我院收治的首次确诊的仅由一种细菌感染的尿路感染患者 125 例作为研究对象，于来诊时取静脉血 2mL 进行实时荧光定量 PCR 检测 miR-146a 含量。取其清晨空腹中段尿进行尿液培养并进行药敏试验。
结果 本研究中未发现耐药的菌株共 18 株，耐药菌株 107 株，MDR 95 株、XDR 12 株。其中金黄色葡萄球菌对红霉素、环丙沙星、四环素、克林霉素、左氧氟沙星的耐药率，屎肠球菌对红霉素、环丙沙星、克林霉素、左氧氟沙星的耐药率，粪肠球菌对红霉素、环丙沙星、四环素、克林霉素、左氧氟沙星、莫西沙星的耐药率，大肠埃希菌对头孢曲松、环丙沙星、哌拉西林、庆大霉素、氨曲

南、左氧氟沙星的耐药率，铜绿假单胞菌对环丙沙星、亚胺培南、庆大霉素、氨曲南的耐药率，肺炎克雷伯菌对头孢曲松、哌拉西林、左氧氟沙星的耐药率均高于 40%。 耐药的革兰氏阳性菌及革兰氏阴性菌尿路感染的患者血 miR-146a 表达量均显著高于不耐该药的患者，差异具有统计学意义（P<0.05）。耐药菌株标本所属患者血 miR-146a 表达量显著高于不耐药菌株，且随着耐药性的增强，血 miR-146a 的表达量逐渐增加，差异具有统计学意义（P<0.05）。

结论 miR-146a 对尿路感染病原菌耐药性具有一定指示作用，但成熟的应用于临床仍需较多研究验证与探索。

PU-0264

提出一种在共分离分析中 Bayes 因子的个性化估算方法

孙思哲[1]、喻长顺[2]
1. 天津金域医学检验实验室有限公司
2. 天津金域医学检验实验室有限公司；广州医科大学金域检验学院

目前，在基因变异致病性分类中，对共分离证据的使用通常使用 ACMG 发表的相关文献中贝叶斯因子（Bayes factor）的估算方法。但该方法对于年龄相关的外显率和拟表型率等参数的计算极为苛刻，同时也未将家系中不符合共分离的个体对结果的影响纳入考虑。ACMG-AMP 指南文件提出，增加共分离证据的数量可能会导致证据升级，因而在应用上需要相对统一的认定标准。在此基础上，本工作组设计了一种适用范围更宽松、对已知信息利用更充分的计算方法。根据变异与表型在个体中的组合，四种情况均可以被纳入计算范围：（1）有变异有表型。变异-表型相关的概率为变异和表型关联、不存在拟表型两个独立事件相乘，即 1/2（1-φ）（φ=拟表型率），不相关的概率为 $N_{Affected}$=1-[1/2(1-φ)]=1/2+φ/2。（2）无变异无表型。变异-表型不相关的概率为不相关且表型未外显、单纯不相关两种情况相加，即 $N_{Unaffected}$=1/2（1-β）+1/2=1-β/2。（β=外显率）（3）有表型无变异。表型-变异相关的概率为变异和表型关联、存在拟表型两个独立事件相乘，即 1/2φ，表型-变异不相关的概率为 $N_{Affected'}$=1-φ/2。（4）有变异无表型。表型-变异相关的概率为变异和表型关联、表型此刻未外显两个独立事件相乘，即 1/2（1-β），表型-变异不相关的概率为 $N_{Unaffected'}$=1-1/2（1-β）=1/2+β/2。最终，总体 BF 值被定义为：BF 值反映变异-表型相关的概率大小，BF 值越大，变异-表型相关的可能性越大。对于存在不满足完全共分离的家系，本方法开创性地将不符合共分离证据的个体一并纳入证据认定中，同时将延迟外显、拟表型等特殊证据纳入一般分析当中，充分平衡了证据准确性和方法简便性之间的关系，也扩展了共分离证据的应用范围。

PU-0265

Identification of prognostic signature based on the copy number variation and expression in acute myeloid leukemia

牛长春、廖璞
重庆市人民医院

Acute myeloid leukemia (AML) can be caused by multiple genetic alteration in the hematopoietic progenitors, and molecular analysis has provided large amounts of useful information for AML diagnosis and prognosis. However, integrative understanding the prognosis value of specific Copy number variance (CNV) and CNV-modulating gene expression was limited. In this study, we integrative analyzed the CNV profiling and gene expression using data from TARGET and TCGA AML cohort. CNV was observed in distinct patterns in the AML risk groups, and the expressions of 251 genes were significantly modulated by CNV overlapped in both cohorts. A total of CNV genes that associated with worse outcomes in AML were identified. This

study identified CNVs and CNV-modulating gene expression alterations, which are crucial for new modes of prognosis evaluation and target therapy.

PU-0266

Whole-exome sequencing identifies a novel nonsense mutation in EXT1 in a Chinese family with hereditary multiple exostoses

Ruirui Ren[1]、Yongan Zhou[3]、Jianping Cheng[2]
1. Affiliated Hospital of Yunnan University
2. 山西医科大学第二附属医院
3. 山西医科大学第二附属医院

Hereditary multiple exostoses (HME; OMIM: 133700) is a rare autosomal dominant skeletal disorder characterized by the formation of multiple benign cartilage-capped tumors on the bone surface. HME is generally thought to be associated with mutations in the EXT gene family. The pathogenic mutations of the EXT gene result in insufficient heparan sulfate biosynthesis, which leads to an imbalance in the proliferation and differentiation of chondrocytes in the extracellular matrix, boosts abnormal bone growth of the neighboring regions, causes multiple exostoses, and ultimately leads to possible malignant transformation. In the present study, a family who displayed typical features of HME was screened for mutations using whole-exome sequencing, Sanger sequencing, and bioinformatics analysis. We identified a novel heterozygous nonsense mutation, c.1258G>T (p.Glu420X), in exon 4 of the EXT1 gene in the proband. The mutation introduced the termination codon, resulting in the truncation of 326 amino acids at the C-terminus of the wild-type EXT1 protein consisting of 746 amino acids. The lost portion includes a glycosyltransferase domain. The mutation was also found in other affected members of the family, but not in normal family members, which is consistent with cosegregated genotypes and phenotypes. Therefore, the present study identified a novel pathogenic EXT1 mutation in a family with HME, which provides additional evidence for developing quick and accurate genetic diagnosis of HME and further enriches the mutation spectrum of HME.

PU-0267

Lmo4 对胃癌细胞转移增殖能力的作用及机制探究

陈璐
南京市浦口区中心医院

目的 探讨在胃癌、癌旁组织和胃癌细胞株中，Lmo4 的表达差异，及其对于胃癌细胞的影响。
方法 应用 qRT-PCR 和免疫组织化学技术，检测 90 例胃癌患者的癌组织及对应癌旁组织中 Lmo4mRNA 的表达差异，分析 Lmo4 表达与胃癌发展各个阶段的相关性。采用 Western blot 方法比较不同人胃癌细胞株中 Lmo4 的表达，通过 RNA 干扰技术抑制 BGC-823 胃癌细胞中 Lmo4 的表达，应用平板克隆形成实验、Transwell 迁移实验、CCK-8 实验、划痕试验及 Western blot 等方法检测 Lmo4 被沉默后对胃癌细胞的生长迁移能力的影响，以及其对细胞通路产生的影响。构建 Lmo4 过表达质粒 Lmo4-pcDNA，检测其对胃癌细胞的增殖、迁移情况及 EMT 相关蛋白的影响，并运用细胞周期试验评价 Lmo4 过表达后细胞增殖情况的变化。
结果 qRT-PCR 和免疫组织化学结果均显示胃癌组织中 Lmo4 相对表达量明显高于对应的癌旁组织（$p<0.001$），且 Lmo4 在胃癌组织中的表达与肿瘤的分型有关（$p<0.001$）、浸润程度有关（$p<0.001$），但是与肿瘤大小、年龄、性别无关。沉默 Lmo4 后的胃癌细胞的迁移能力显著减弱，

细胞克隆形成数量减少，抑制了 EMT 发生；过表达的 Lmo4 在体外可以促进胃癌细胞生长和胃癌细胞迁移，促进 EMT 的发生，并通过 TGF-β 信号通路调节。
结论 Lmo4 可能通过诱导胃癌细胞发生 EMT 而促进胃癌的转移，在胃癌的发生、发展进程中起着非常重要作用。

PU-0268

Detection of mosaic mutations through deep next-generation sequencing in thoracic aortic aneurysm/dissection

Guoyan Zhu 、Hang Yang、Mingyao Luo、Weizhen Zhou、Yinhui Zhang、Chang Shu、Zhou Zhou

Background Thoracic aortic aneurysm/dissection (TAAD) is an insidious and rapid onset disease with high mortality rate when it is undiagnosed or untreated in time. Marfan syndrome (MFS) is the most commonly seen syndromic thoracic aortic aneurysm/dissection (TAAD), which is caused by mutations in FBN1 gene. It was reported that about 25% of MFS patients had a de novo mutation. However, parental mosaicism was not easily distinguished from these sporadic cases, which should not be neglected. Otherwise, if the mosaic mutation spreads from asymptomatic carriers to their children, it will lead to an accidental disease. Mosaicism was also reported in symptomatic MFS patients and in other TAAD conditions. Unfortunately, the mosaic prevalence of TAAD was still unknown, which made genetic counseling and clinical diagnosis difficult. Therefore, more sensitive and special genetic tests for mosaicism in TAAD were highly required.
Methods 1085 patients affected with MFS or TAAD who had been performed a targeted genetic testing were included in our study. We reanalyzed all these panel sequencing data and retrieved those low allele frequency variants (AF<30%) which were filtered in the routine bioanalysis pipeline. Deep sequencing of single amplicon (approximately 5000×) was conducted to confirm whether they were mosaic mutations in the Life PGM Dx platform. Besides, there were 64 probands with a causative mutation and both parental blood samples. In these families, parental mosaicism was detected with the same method for them.
Results A total of four symptomatic affected patients were identified with a mosaic mutation, c.2607_2608insGAGCC, c.3284G>A, c.6509G>A in *FBN1* gene and c.631C>A in *TGFB2* gene. Notably, the low-level mosaic mutation in *TGFB2* was detected combined with a causative *FBN1* truncating mutation in patient AD2001, which should be paid close attention in the genetic counseling. Besides, there were two parental mosaic mutations (2/64) detected in the trio-families, c.2167+1G>A and c.3914G>T in *FBN1* gene. Neither of the two parental carriers with mosaic mutations had significant clinical manifestations.
Conclusions Mosaic mutation could be a more common phenomenon in TAAD than it had been realized so far. Hence, whenever children are identified with harmful mutations, the parents should be detected by genetic testing, which will provide more accurate guidance for genetic counseling. We also can't ignore the uncommon fact that mosaic mutations may be present in patients with clinically significant signs. TAAD patients for whom the significant mutations are not detected should be recommended for the panel with an adaptive parameter of the bioinformatics analysis, which can improve the detection rate of mosaicism.

PU-0269

基于 RNA 测序研究过表达 Ajuba 对 T47D 细胞基因表达谱的影响

徐北惠[1]、邹秀群[2]、徐洪[2]、王家敏[2]、侯照远[2]、倪培华[3]
1. 上海交通大学医学院附属第九人民医院
2. 上海交通大学医学院生物化学与分子细胞生物学系
3. 上海交通大学医学院附属瑞金医院检验系

目的 探究 AJUBA 基因对于雌激素受体阳性乳腺癌细胞 T47D 基因表达的影响。
方法 构建 AJUBA 稳定过表达的 T47D 细胞系。载体对照和实验组分别提取 RNA 进行 RNA-SEQ 测序，将所得序列映射到人类基因组并进行转录组重建，样品标准化后寻找实验组和对照组之间的差异基因，利用生物信息学方法进一步对所得的差异基因进行基因本体论分析（即 GO 分析）和 KEGG 通路富集性分析，同时挑选部分基因用 QRCR 技术进行基因表达验证。
结果 实验组与对照组细胞相比共找到 568 个差异基因，其中上调基因 239 个，下调基因 329 个。GO 分析中，注释到分子功能、生物学过程和细胞组成的上调差异基因分别有 3 个，23 个，8 个；下调差异基因分别有 21 个，35 个，9 个。KEGG 分析中上调基因显著富集通路有 2 个，下调基因显著富集通路有 4 个。
结论 Ajuba 过表达可以影响 T47D 细胞的一系列生物学过程和多条信号通路，可能在乳腺癌发生发展中起重要作用。

PU-0270

miR-29a sensitizes the response of glioma cells to temozolomide by modulating the P53/ MDM2 feedback loop

Qiudan Chen[1]、Weifeng Wang[2]、Shuying Chen[3]、Xiaotong Chen[3]、Yong Lin[3]
1. The Department of Central Laboratory, Clinical Laboratory, Jing'an District Center Hospital of Shanghai, Fudan University, Shanghai 200040, China.
2. 上海市第十人民医院
3. 复旦大学附属华山医院

Recently, pivotal functions of miRNAs in regulating common tumorigenic processes and manipulating signaling pathways in brain tumors have been recognized; notably, miR‐29a is closely associated with p53 signaling, contributing to the development of glioma. However, the molecular mechanism of the interaction between miR-29a and p53 signaling is still to be revealed. Herein, a total of 30 glioma tissues and 10 noncancerous tissues were used to investigate the expression of miR‐29a. CCK-8 assay and Transwell assay were applied to identify the effects of miR-29a altered expression on the malignant biological behaviors of glioma cells in vitro, including proliferation, apoptosis, migration and invasion. A dual-luciferase reporter assay was used to further validate the regulatory effect of p53 or miR-29a on miR-29a or MDM2, respectively,at the transcriptional level. The results showed that miR‐29a expression negatively correlated with tumor grade of human gliomas; at the same time it inhibited cell proliferation, migration, and invasion and promoted apoptosis of glioma cells in vitro. Mechanistically, miR‐29a expression was induced by p53, leading to aberrant expression of MDM2 targeted by miR‐29a, and finally imbalanced the activity of the p53-miR-29a-MDM2 feedback loop. Moreover, miR-29a regulating p53/MDM2 signaling sensitized the response of glioma cells to temozolomide treatment. Altogether, the study demonstrated a potential molecular mechanism in the tumorigenesis of glioma, while offering a possible target for treating human glioma in the future.

PU-0271

Poly-Gene Fusion Transcripts and Chromothripsis in Prostate Cancer

jian zhang
Shandong Provincial Hospital Affiliated to Shandong First Medical University

Complex genome rearrangements are frequently observed in cancer but their impact on tumor molecular biology is largely unknown. Recent studies have identified a new phenomenon involving the simultaneous generation of tens to hundreds of genomic rearrangements, called chromothripsis. To understand the molecular consequences of these events, we sequenced the genomes and transcriptomes of two prostate tumors exhibiting evidence of chromothripsis. We identified several complex fusion transcripts, each containing sequence from three different genes, originating from different parts of the genome. One such poly-gene fusion transcript appeared to be expressed from a chain of small genomic fragments. Furthermore, we detected poly-gene fusion transcripts in the prostate cancer cell line LNCaP, suggesting they may represent a common phenomenon.Finally in one tumor with chromothripsis, we identified multiple mutations in the p53 signaling pathway, expanding on recent work associating aberrant DNA damage response mechanisms with chromothripsis. Overall, our data show that chromothripsis can manifest as massively rearranged transcriptomes. The implication that multigenic changes can give rise to poly-gene fusion transcripts is potentially of great significance to cancer genetics.

PU-0272

宏基因组二代测序和 PCR 杂交技术检测新生儿血液巨细胞病毒的结果对比

刘勇
吉林大学第一医院

新生儿感染是造成新生儿发病率和死亡率增高的原因之一，能否快速确认感染病原体，成为后续对症治疗的关键，基于宏基因组新一代测序技术（mNGS）为解决这一问题提供了一个可能的突破方向。

本研究运用 mNGS、PCR 杂交技术对 21 例新生儿的血液样本进行巨细胞病毒检测，并利用荧光定量 PCR 技术进行验证。mNGS 和 PCR 杂交技术同时检出巨细胞病毒阳性的样本 7 例，mNGS 检出阳性而 PCR 杂交技术检出阴性的样本有 4 例， 利用荧光定量 PCR 技术进行验证结果全为阳性。PCR 杂交技术检出阳性而 mNGS 检出阴性的样本有 1 例，利用荧光定量 PCR 技术进行验证结果为阳性。另外， mNGS 还检出 EB 病毒阳性 2 例，B 族链球菌阳性 1 例。 本次研究中，mNGS 对新生儿血液中巨细胞病毒检出敏感性为 52%，显著高于 PCR 杂交技术 38%的敏感性。

mNGS 技术可以无目标、无差异地检测样本微生物，与传统的 PCR 检测相比，mNGS 技术的优势在于不仅可以针对特定的微生物，而且可以在单次测序中同时检测不同的病原体，发现已知和未知的病原体序列。mNGS 因其不需要分离培养病原体、可同时分析多种病原体、检测灵敏度高、周期短、应用范围广等优点而受到广泛关注。

PU-0273

PHF1 is an oncogene for pancreatic cancer

Yujiao Xie
the Second Hospital of Shandong University

Pancreatic cancer is one of the leading causes for cancer death worldwide. Though several vital genes were found in pancreatic cancer progressing, the epigenetics change in pancreases tumorigenesis is poorly understood. Here, we test the expression of PHD finger protein 1 (PHF1) using immunohistochemical（IHC）, qRT-PCR, and western blot. Lentiviral transduction was used to induce PHF1 overexpression or silencing in vitro, followed by monitoring cell proliferation, colony formation, and metastasis. Xenografts was employed for in vivo experiment. Finally, we found that PHF1 could promote pancreatic cell growth and migrationin vitro and vivo. In conclusion, our data indicate PHF1 is an oncogene for pancreatic cancer.

PU-0274

Serum Long Noncoding RNAs Act as Potential Novel Diagnosis and Prognosis Biomarkers in Non-small Cell Lung Cancer

Yujiao Xie
the Second Hospital of Shandong University

Objective NSCLC is the most prevalent type of lung cancer and the first cause of cancer death. Increasing evidences hint lncRNAs have close bond with tumor. We aimed to evaluate underlying lncRNAs as the biomarker for NSCLC diagnosis and prognosis prediction.
Methods 14 lncRNAs expression profiles were validated in paired NSCLC and normal samples by RT-qPCR. ROC analysis was utilized to estimate the diagnosis proficiency of the candidate lncRNAs. Moreover, Kaplan-Meier survival analysis was performed within validation set.
Results SOX2OT and ANRIL were shown to be obviously upregulated in NSCLC samples. A panel composed of two lncRNAs (SOX2OT, ANRIL) and three traditional tumor markers (CEA, CYFRA21-1, SCC) was built in training set. The AUC of this panel was superior to any biomarker alone. This result appeared in validation set yet. Intriguingly, the low expression of SOX2OT and ANRIL correlated with high survival rate. SOX2OT could be the independent prediction factor.
Conclusion Our study showed that the panel could be the valuable biomarker for NSCLC diagnosis and two lncRNAs SOX2OT and ANRIL may be ideal biomarkers for predicting NSCLC prognosis.

PU-0275

Hsa_circRNA_103092/ miR-224/ PRLR axis participates in unexplained recurrent miscarriage by inhibiting proliferation and promoting apoptosis

Yan Su[1]、Rufei Gao[2]、Chunli Li[1]
1. Chongqing Health Center for Women and Children
2. 重庆医科大学

Background Recurrent miscarriage (RM) refers to 3 or more consecutive miscarriages occurred before 24 weeks. It is a type of disease with complex etiology and unclear pathogenesis. Infectious diseases, abnormal uterine structure, endocrine dysfunction etc. are reported being

related to RM. However, there are still nearly 50% of RM patients with unclear etiology. And the specific regulation mechanism has not been identified clearly. It has been revealed that molecules such as hormones, miRNAs and transcription factors, participate in the regulation of RM. Circular RNAs (circRNAs), a class of endogenous non-coding RNAs, are stable and conserved among species, and they often exhibit developmental stage and disease-specific expression patterns. Recent studies have demonstrated that circRNAs serve as sponges for miRNAs or binding proteins to participate in biological processes. In our previous study, circRNAs microarray analysis was used to identify the differentially expressed circRNAs and mRNA in the decidua of patients with unexplained RM and unintended pregnancy control group. And 78 up-regulated and 45 down-regulated circRNAs, and 109 up-regulated and 97 down-regulated mRNAs were screened out in the decidua of patients with early RM (fold change≥1.5 and P-value <0.05). Expression of hsa_circRNA_103092 was significantly higher in the decidua of patients with unexplained recurrent miscarriage. However, the specific roles of hsa_circRNA_103092 in RM remain unclear.
Methods Bioinformatics analysis was performed to establish circRNA-miRNA-mRNA interaction network. Luciferase reporter assay was used to validate the interaction among hsa_circRNA_103092, miR-224 and PRLR in HKE293T cells. RT-PCR, immunohistochemistry and in situ hybridization were used to detect the expression of hsa_circRNA_103092, miR-224 and PRLR in the decidua tissue of patients with unexplained recurrent miscarriage. RT-PCR and western-blot was preformed to detect expression of PRLR, CyclinD3, PCNA, Bax and Bcl-2 protein in Ishikawa cell after hsa_circRNA_103092 silencing or miR-224 activation.
Results RT-PCR verified the high expression of hsa_circRNA_103092 in the decidua of patients with unexplained recurrent miscarriage. TargetScan and miRanda bioinformatics method analysis and Luciferase reporter assay showed the competing endogenous function of hsa_circRNA_103092 regulating PRLR via sponging miR-224. RT-PCR, immunohistochemistry, and in situ hybridization showed that the expression of hsa_circRNA_103092 and PRLR in the decidua of patients with unexplained recurrent miscarriage was significantly increased, while the expression of miR-224 was significantly decreased. After hsa_circRNA_103092 silencing, the expression of miR-224 in Ishikawa cells was significantly increased, while the expression of PRLR was significantly decreased. And the expression of PRLR in Ishikawa cells was significantly decreased after miR-224 activation. Moreover, after hsa_circRNA_103092 silencing, the expression level of cell proliferation-related proteins CyclinD3 and PCNA decreased significantly, which indicated low proliferation, and the expression level of apoptosis-related protein Bax increased significantly, the expression of Bcl-2 decreased significantly. After PRLR expression was down-regulated, the expression of PCNA and cyclinD3 in Ishikawa cells decreased significantly, the expression level of Bax increased, and the expression of Bcl-2 decreased significantly.
Conclusion Hsa_circRNA_103092 / miR-224 / PRLR axis participates in the regulation of recurrent miscarriage through inhibiting proliferation and promoting apoptosis.

PU-0276

长链非编码 RNA NNT-AS1 在乳腺癌中的生物信息学分析

盖婵婵[2]、曹源[1]
1. 解放军第九六〇医院
2. 解放军第九六〇医院

目的 本研究采用生物信息学方法结合公共数据库集探讨长链非编码 RNA（lncRNA）烟酰胺核苷酸反义转氢酶 RNA1（NNT-AS1）在乳腺癌中的表达及意义，并对 NNT-AS1 进行靶基因预测，为乳腺癌的相关研究提供思路。
方法 通过 UALCAN 数据库分析 NNT-AS1 在乳腺癌和正常乳腺组织中的表达情况，并通过 K-M plotter 数据库对 NNT-AS1 进行生存分析。利用 ENCORI、LncBase Predicted v.2、LncRNASNP

筛选与 NNT-AS1 相互作用 microRNAs 并取其交集，通过 TargetScan、microT-CDS 进行 NNT-AS1 的靶基因预测，构建 lncRNA NNT-AS1-microRNAs-mRNAs 调控网络，并运用 FunRich 平台对预测的靶基因进行 GO 分析和 KEGG 信号转导通路富集分析。
结果 lncRNA NNT-AS1 在乳腺癌中表达明显降低，且低表达患者的无进展生存期比高表达患者短。通过数据库筛选出 4 个可能与 NNT-AS1 结合的 microRNAs，包括 hsa-miR-320a、hsa-miR-320b、hsa-miR-320c、hsa-miR-1271-5p。microRNAs 的靶基因预测结果显示共有 387 个靶基因可能受这 4 个 microRNAs 的调控。通过整合 lncRNA NNT-AS1-microRNAs 和 microRNAs-mRNAs 网络构建 lncRNA NNT-AS1 -microRNAs-mRNAs 调控网络。通过 GO 分析以及 KEGG 信号转导通路富集分析发现这些靶基因高度富集在碱基、核苷、核苷酸、核酸代谢调节、转录因子活性等过程以及 PI3K-Akt、FoxO、Hippo 等信号转导通路。
结论 NNT-AS1 在乳腺癌中表达降低，并且其表达水平的降低与乳腺癌预后不良相关，参与多种生物过程，有望成为乳腺癌潜在的诊断标志物。

PU-0277

趋化因子 CXCL16 对脓毒症小鼠生存率、组织损伤及炎症反应的影响

李佳熹
重庆医科大学附属第一医院

目的 探讨趋化因子 CXCL16 在脓毒症小鼠中的表达，组织损伤及炎症反应过程。
方法 CLP 诱导 C57BL/6 小鼠形成脓毒症模型。收集血清，腹腔灌洗液及肝、肺、肾脏组织样本。记录小鼠生存情况;Elisa 检测趋化因子 CXCL16 及 IL-6、IL-8、IL-1O、TNF-α 和 IFN-γ 分泌量；血液分析仪及流式细胞术分析炎症细胞；病理切片观察组织损伤；Anti-CXCL16 抗体蛋白治疗脓毒症并观察效果。
结果 CXCL16 在脓毒症小鼠血清、腹腔灌洗液、组织蛋白中水平显著升高(P＜0.05)。与 CLP+PBS 组相比，CLP+CXCL16 组小鼠生存率明显降低 (P＜0.05)，中性粒细胞、巨噬细胞和淋巴细胞数量增加且促进炎症因子释放 (P＜0.05)，肝、肺、肾组织损伤加重，肝肾功能血清指标 ALT、AST、Urea 和 Creatinine 升高(P＜0.05)。与 CLP +IgG 组相比，Anti-CXCL6 组死亡率降低，组织损伤减轻，肝肾功能血清指标降低(P＜0.05)，抗体治疗具有一定效果。
结论 CXCL16 在脓毒症小鼠中表达上调，其高浓度与脓毒症免疫病理过程有关，CXCL16 能够通过加重炎症反应促进脓毒症发生发展。

PU-0278

细胞外囊泡肿瘤标志物及膜表面表面标志物筛选方法的研究进展

徐东杰、李智洋
南京鼓楼医院

肿瘤的快速诊断有助于疾病的早发现，早治疗，但是由于高特异性，高灵敏度的临床诊断标志物的缺乏，使得肿瘤的早期诊断成为难题。肿瘤来源细胞外囊泡（EVs）近年来在生物医学领域大放异彩，EVs 由多种细胞分泌，其所含的标志物信息丰富，在细胞间通信中发挥相关的作用，同时参与不同的病理过程。使其成为诊断和治疗疾病的极具潜力的生物标志物。目前的筛选方法由于在 EVs 的提取、蛋白的分离纯化技术方面的各种原因，导致重现性差、步骤耗时繁琐，严重阻碍了 EVs 表面标志物的发掘。此外，绝大多数针对肿瘤标志物的检测都只能连同正常细胞 EV 一起分析，导致肿瘤来源蛋白表达信号受到干扰。核酸适配在发现蛋白天然三维构象以及标准化制备方面有着很大的优势，以肿瘤来源的 EVs 进行筛选，结合指数富集（SELEX）获得高特异性的核酸适配体，

对肿瘤进行诊断，预后监测以及区分不同肿瘤亚型具有重要价值。本文主要综述了 EVs 与肿瘤的关系以及 EVs 膜表面蛋白标志物的筛选策略。

PU-0279

早产儿解脲脲原体感染的实验室检查及临床特点分析

刘应红
资阳市第一人民医院

目的 探讨早产儿解脲脲原体(UU)感染的临床特点。
方法 选取 2018 年 7 月-2021 年 3 月资阳市第一人民医院收治的早产儿为研究对象，出生后入院 24h 内进行下呼吸道分泌物 UU 的采集和测定，并比较分析 UU 阳性组和 UU 阴性组的实验室检查及临床差异。
结果 共纳入 453 例早产儿，其中 UU 阳性组 83 例，UU 阴性组 370 例。UU 阳性组出生平均胎龄(33.34±2.58)周、平均体质量(2.085±0.545)克，UU 阴性组出生平均胎龄(35.10±1.82)周、出生平均体质量(2.417±0.482)克，UU 阳性组胎龄和出生体质量均低于 UU 阴性组，差异有统计学意义(P＜0.01)。两组间的出生窒息发生率和 Apgar 评分比较，差异均无统计学意义(P＜0.05)。UU 阳性组母亲绒毛膜羊膜炎、胎膜早破的发生率均高于 UU 阴性组，差异有统计学意义(P＜0.05)；UU 阳性组生后 24h、72h、7d 的白细胞计数、中性粒细胞计数均高于阴性组，差异均有统计学意义(P＜0.05)。UU 阳性组的新生儿呼吸窘迫综合征(NRDS)比率、支气管肺发育不良(BPD)发生率高于 UU 阴性组，差异均有统计学意义(P＜0.05)。
结论 早产儿呼吸道 UU 阳性可能与小出生胎龄、低出生体质量相关、NRDS、BPD 相关。

PU-0280

眉山地区 7052 名育龄女性叶酸基因多态性与不孕、流产及不良妊娠结局的相关性分析

罗艳
眉山市妇女儿童医院

目的 对眉山地区育龄女性叶酸代谢基因多态性进行检测，分析 MTHFR *A1298C*、 *C677T* 和 MTRR *A66G* 基因变异与不孕、流产及不良妊娠结局的相关性。
方法 选择 2013 年 1 月 1 日～ 2020 年 12 月 30 日在眉山市妇幼保健院进行产前检查的育龄女性 7052 例，采集研究对象口腔黏膜上皮细胞，用荧光定量 PCR 检测亚甲基四氢叶酸还原酶(MTHFR) 基因 *A1298C*、 *C677T* 和甲硫氨酸合酶还原酶(MTRR) *A66G* 的基因型，分析基因多态性的分布特征与不孕、流产及不良妊娠结局的关系。
结果 统计全部标本中的 MTHFR *A1298C* 基因野生型（AA）、杂合突变型（AC）及纯合突变型（CC）基因型频率分别为 65.5%、31%和 3.5%; MTHFR*C677T*，其中野生型（CC）、杂合突变型（TT）及纯合突变型（CT）基因型频率分别占 35.8%、47.5%和 16.7%； MTRR *A66G* 野生型（AA）、杂合突变型（AG）及纯合突变型（GG）基因型频率分别为 55.6%、38.39%和 6%。MTHFR *C677T* 基因型分布与中国人群差异具有统计学意义（P<0.01）。MTHFR *A1298C*、和 MTRR *A66G* 基因型分布与中国人群差异均无统计学意义（P>0.05）。同时，对 7052 名育龄妇女进行追踪，其中不孕患者 117 名，流产患者为 68 名，畸形儿（21-三联体、唇裂、胎儿心脏畸形、无脑儿、唐氏儿、死胎）患者 14 名，不孕患者中 MTRR *A66G* 杂合突变型（AG）达 100%。流产患者中 MTHFR *A1298C* 位点野生型（AA）达 100%。畸形儿患者中，MTRR *A66G* 位点野生型（AA）达 71.4%。

结论 叶酸代谢障碍与不孕、流产及不良妊娠结局有相关性。根据叶酸代谢基因检测结果，对育龄妇女给予补充相应剂量的叶酸，对防止不孕、流产及畸形胎儿具有重要的指导意义。

PU-0281

基于杂交链式反应无清洗外泌体检测技术

徐东杰、李智洋
南京鼓楼医院

外泌体是由细胞分泌的直径为 30nm-150nm 的小泡，大量存在有各种体液环境中，如血液，尿液，唾液以及泪液。外泌体通过将亲代细胞来源的蛋白质、核酸和脂质，运送到受体细胞参与细胞间的信息交流。肿瘤来源的外泌体与肿瘤细胞具有相似性，在癌症的发展和进程中起着至关重要的作用。目前，由于外泌体粒径较小，检测困难，外泌体的识别和定量具有一定的挑战性。在本研究中，我们开发了一种荧光传感器，通过设计特异性适配体 MUC1，对肿瘤来源的外泌体进行特异性识别，暴露出杂交链式反应触发序列，结合杂交链式反应，进行信号放大。通过设计的适配体的特异结构，进行肿瘤来源的外泌体的无清洗的特异性检测。本研究为液体活检提供了一种新的方法，促进了液体活检的发展。

PU-0282

肺腺癌患者血清 TSLP 和 Bcl-2 与 IL-1α 表达水平及其临床意义

崔鲂
重庆医科大学附属第一医院

目的 探讨胸腺基质淋巴淋巴细胞生成素（thymic stromal lymphopoietin，TSLP）、白细胞介素-1α（Interleukin-1α，IL-1α）、B 淋巴细胞瘤-2（B-cell lymphoma-2，Bcl-2）在肺腺癌患者血清的表达水平及其临床意义。
方法 采用酶联免疫吸附实验（Enzyme-linked immunosorbent assay, ELISA）检测 69 例肺腺癌患者和 30 例健康人血清 TSLP、IL-1α、Bcl-2 浓度,分析血清 TSLP、IL-1α、Bcl-2 血清浓度与 TNM 分期、淋巴结转移、远处转移、肿瘤大小、肺癌肿瘤标志物的相关性。
结果 肺腺癌患者血清 TSLP、Bcl-2 浓度显著高于正常对照组（$p<0.05$）,在中晚期（II 期+III 期、IV 期）、肿瘤直径≥3cm、有淋巴结转移的肺腺癌患者中血清 TSLP 浓度增高（$p<0.05$）；肺腺癌组血清 IL-1α 浓度与对照组相比无统计学差异（$p>0.05$）；肺腺癌患者血清 TSLP、IL-1α、Bcl-2 浓度无相关性（$P>0.05$）；血清 TSLP 水平与肺腺癌患者的 TNM 分期、淋巴转移、肿瘤直径、CYFRA21-1、CEA 正相关（$P<0.05$），血清 Bcl-2 浓度与与血清 CEA 水平正相关（$P<0.05$）。
结论 TSLP、Bcl-2 在肺腺癌患者的血清中升高，均与血清 CEA 相关， TSLP、Bcl-2 在肺腺癌辅助诊断中具有一定价值。血清 TSLP 与肺腺癌患者病情发展存在相关性，检测肺腺癌患者血清 TSLP 浓度可用于评估肿瘤进展。

PU-0283

慢性乙型肝炎和肝硬化患者血清 HBV 基因型分析

何奇瑶
资阳市第一人民医院

目的 分析慢性乙型肝炎和肝硬化患者血清乙型肝炎病毒(HBV)分型分布情况。

方法 2020 年 5 月～2021 年 4 月资阳市第一人民医院就诊的慢性乙型肝炎患者 150 例，乙型肝炎肝硬化患者 25 例，肝细胞癌 15 例，采用上海之江试剂盒（qPCR 法）检测血清 HBV 基因型。
结果 在 190 例 HBV 感染者中，有 91 例(47.89％)为 B 型感染，98 例(51.57％)为 C 型感染，1 例(0.53％)为 D 型感染；慢性乙型肝炎患者与肝硬化患者血清 TBIL、ALT 和 AST 水平比较差异均无统计学意义(P>0.05)；乙型肝炎肝硬化患者和肝细胞癌患者 C 型感染比例均显著高于慢性乙型肝炎患者，差异具有统计学意义(P<0.05)。
结论 慢性乙型肝炎和肝硬化患者 HBV 感染以 B 基因型和 C 基因型为主，而肝硬化患者以 C 型感染居多，提示 C 型感染患者可能比 B 型患者更容易出现严重的肝损伤，并产生严重的临床结局。

PU-0284

AKR1A1/C4 as oncogene biomarkers and AKR1B1/B10/B15/C1/C2 as Tumor suppressor gene for the colorectal cancer

HUI LI[1]、Lei Zheng[2]、Dixian Luo[1]
1. Chenzhou first people`s hospital
2. 南方医科大学南方医院

Objective To investigate the significance of AKR1 expression level in 10 family members in clinical diagnosis of colorectal cancer.
Methods The transcriptional and survival data of AKR1s in patients with colorectal cancer(CRC) were investigated from ONCOMINE, Gene Expression Profiling Interactive Analysis(GEPIA), Kaplan–Meier Plotter, and cBioPortal databases. The mRNA and protein expression levels in normal and tumor tissues were detected by QPCR and Western-blot individually.
Results AKR1A1/C4 expression levels were found higher in colorectal cancer tissues than in normal colorectal tissues, whereas AKR1B1/B10/B15/C1/C2 expression level were lower in the former than in the latter. The expression levels of AKR1A1/C1/C2/C4 were correlated with advanced tumor stage. ROC curve analysis of AKR1B10/C4 level has high specificity（59.1%，70.7%） and sensitivity（92.1% ，73.2%） for the diagnosis of CRC(p=0.000). The correlation analysis between high and low AKR1s expression and clinicopathology showed that AKR1B15 expression level is related to Invasion depth，Akr1c2 expression level was significantly related to Invasion depth and distant metastasis. Survival analysis using GEPIA showed that AKR1 expression levels were not significantly associated with overall survival or disease-free survival in CRC patients. AKR1s functions and genes significantly related to AKR1s alterations .GO enrichment analysis predicted the function of target host genes in terms of biological process, cell composition and molecular function.AKR1s participated in Tumor-associated metabolic pathways, such as Metabolism of xenobiotics by cytochrome P450,Steroid hormone biosynthesis,Pentose and glucuronate interconversions, Glycerolipid metabolism, and Metabolic pathways.
Conclusion AKR1A1/C4 may be an oncogene marker for colorectal cancer, while AKR1B1/B10/B15/C1/C2 may be involved in the occurrence of colorectal cancer as a tumor suppressor gene.

PU-0285

4887 例患者人疱疹病毒 6 型感染情况分析

刘义庆[1,2]、张庆[1,2]、邱旸[1,2]、刘春梅[1,2]、鞠瑛[1,2]、卢志明[1,2]
1. 山东第一医科大学附属省立医院
2. 山东省立医院

目的 了解山东地区人疱疹病毒 6 型(HHV-6)的感染情况。
方法 采用整体抽样的方法收集 2016 年 12 月~2021 年 5 月来山东省立医院就诊的 4887 例可疑感染患者，用 PCR 方法进行人疱疹病毒 6 型核酸检测。并对不同年龄、性别的患者人疱疹病毒感染情况进行分析。
结果 4887 例检测的患者中，人疱疹病毒 6 型核酸检测阳性数为 956 例，总阳性率为 19.56%，女性阳性率为 19.90%，男性阳性率为 19.33%，差异无统计学意义(P ＞0.05);0 岁～3 岁感染率最高，阳性率为 36.15%，其次为 4 岁～6 岁，阳性率为 30.52%，≥16 岁者人疱疹病毒 6 型核酸阳性率最低，为 6.52%。
结论 人疱疹病毒 6 型的感染率无性别差异；各年龄段均可感染，但以儿童为主。

PU-0286

Long non-coding RNA LINC01296 as a potential prognostic biomarker in human cancers: a meta-analysis

Lijuan Rong
The First Affiliated Hospital of Zhengzhou

Purpose Long intergenic non-protein coding RNA 1296 (LINC01296) is a novel lncRNA that is reported to be abnormally expressed in various cancers and is related with poor clinical outcomes. The purpose of this meta-analysis was to evaluate the potential role of LINC01296 in predicting human cancer prognosis.
Materials and Methods The databases we searched for literature included Pubmed, Embase, Web of science, Cochrane library, and China National Knowledge Infrastructure (CNKI) up to July 2019, with no language restrictions. Ultimately, a total of 13 studies with 913 patients were included in the present meta-analysis.
Results This meta-analysis showed that high LINC01296 expression level was related to poor overall survival (OS) (HR=2.29, 95%CI: 1.76-2.96, P<0.001). We also confirmed the results using online database TCGA (HR=1.3, P<0.001). Further analysis revealed that high expression of LINC01296 was associated with the clinicopathological characteristics of the tumor, including lymph node metastasis, advanced TNM stage, higher histologic grade, larger tumor size, and older patient age.
Conclusions Our meta-analysis suggested that LINC01296 can be expected to serve as a new marker for tumor prognosis.

PU-0287

血管内皮功能损伤及修复与动脉粥样硬化的相关研究

魏红霞、张葵
南京大学医学院附属鼓楼医院

在发达国家，动脉粥样硬化性心血管疾病被称为威胁人类健康的“头号杀手”，随着经济的迅速发展，我国动脉粥样硬化性心血管疾病的发病与死亡率均呈上升趋势，已接近发达国家水平。过去

对动脉粥样硬化（AS）的研究大多集中在动脉管腔的狭窄或堵塞，而导致管腔狭窄或堵塞的主要原因是管壁出现了病变。血管壁是心血管多重危险因素作用的靶点，血管壁损害是心血管疾病发生和发展的共同病理基础。面对世界范围内与日俱增的心血管疾病患者，人们已经认识到对血管病变的干预不应该局限于通过解除管腔的局部机械阻塞而达到治疗目的，早期发现和及时干预才是延缓和控制心血管事件的根本措施。多年研究发现，以前认为的危险因素如吸烟、高血压、高血脂等已不足以解释 AS 的发生发展，而有关 AS 的内皮功能障碍和自身免疫因素越来越受到关注。因此，简便而准确的评估血管内皮损伤状态及修复对于预防 AS 性血管病变的发生发展无疑具有重要意义。

PU-0288

The MIR137HG/miR-2467/Twist1 regulatory network fosters malignant phenotypes in hepatocellular carcinoma

haoming shen[1]、di zhang[2]
1. Hunan Cancer Hospital & The Affiliated Cancer Hospital of Xiangya School of Medicine, Central South University
2. The Third Xiangya Hospital of Central South University

Background Hepatocellular carcinoma (HCC) is seemed as the second common cancer of cancer-related mortality worldwide. Increasing evidences have identified the malfunctioning roles of long non-coding RNAs (lncRNAs) in various human cancers. Herein, we aim to investigate the functional role and underlying regulatory mechanism of lncRNA MIR137 host gene (MIR137HG) in HCC.
Methods A cohort of 50 paired HCC tumor tissues and adjacent normal tissues were collected for measuring the expression pattern of MIR137HG by qRT-PCR assay, as well as evaluating its relationship with tumor grade or stage, and prognosis. Stable HCC cell lines with MIR137HG knockdown was established for the functional experiments, including CCK-8, immunofluorescence staining, wound healing and transwell assays, to assess cell proliferation, migration and invasion, respectively. Luciferase reporter assay was employed to validate the MIR137HG/miR-2467/Twist1 axis. Levels of epithelial-mesenchymal transition (EMT)-related biomarkers and Wnt/β-catenin signals were further detected using western blot analysis.
Results MIR137HG was significantly elevated in patients with HCC, as well as positively associated with high tumor grade, advanced tumor stage, and low survival rate. Silencing of MIR137HG exerted the suppressive effects on cell proliferation, migration and invasion. Mechanistically, MIR137HG induced up-regulation of Twist1 via sponging miR-2467, thereby activating Wnt/β-catenin pathway in HCC cells. Depletion of β-catenin blocked the biological effects of MIR137HG overexpression on HCC cells.
Conclusion Our findings identified that MIR137HG promoted malignant phenotypes of HCC cells via targeting miR2467/Twist1 axis, indicating a potential prognostic biomarker for HCC therapy.

PU-0289

血清淀粉样蛋白 A 在儿童 EB 病毒感染早期诊断中的价值

刘志强、成秀妹、柯江维
江西省儿童医院

目的 研究血清淀粉样蛋白 A(SAA)在儿童 EB 病毒感染早期诊断中的价值。
方法 2018 年 7 月至 2018 年 10 月期间本院收治的 100 例外周血 EBV-DNA 阳性患儿为病例组，同期来院健康体检的 50 例外周血 EBV-DNA 阴性儿童为对照组，进行 SAA、C 反应蛋白(CRP)和外周血白细胞计数(WBC)检测，并采用 ROC 曲线进行统计与分析。

结果 病例组 SAA、CRP、WBC、SAA/CRP 水平均高于健康对照组，差异有统计学意义（P<0.05）；病例组的 SAA、CRP、WBC 及 SAA/CRP 曲线下的面积分别为 0.911、0.803、0.766 及 0.928，三项指标联合检测曲线下面积为 0.961。
结论 SAA 对 EB 病毒感染均有较高的诊断价值，SAA、CRP、WBC 三项联合检测意义更大。

PU-0290

基于糖基化修饰组学的结肠癌组织早期特异性生物标志物的筛选

王金金、王瑾、王芳、柯青、袁梦娇、龚倩
上海市青浦区中心医院

目的 结直肠癌（CRC ）是常见的恶性肿瘤之一，早期症状隐匿，一经发现常为中晚期且五年生存率极低。目前，组织活检是诊断 CRC 的金标准，但具有创伤性和危险性；血清学标志物检测是 CRC 诊断、治疗监控和判断预后较为理想的方法。其中 CEA、CA199，CA242 是临床常见的用于诊断结肠癌的血清标志物，但这些标志物的敏感性、特异性均不佳，难以满足当前精准诊疗的要求。因此，寻找和鉴定特异性的生物标志物用于 CRC 的早期诊断、治疗监测和预后判断,是目前临床亟待解决的重要科学问题。
方法 采用串联质谱标记、N-糖基化修饰富集和高效液相色谱-质谱定量蛋白质组学技术筛选和鉴定 CRC 的生物标志物，并在组织水平进行分析。
结果 筛选特异性糖基化蛋白（ITGB、COX-2）。
结论 糖基化 ITGB 和 COX-2 可作为 CRC 潜在早期免疫诊断标志物，同时为建立一种新的 CRC 诊断技术奠定理论依据和实践基础。

PU-0291

探讨两种方法提取人宫颈脱落细胞中的 HPV 阳性率及主要型别的差异性

郭俊英
德州市人民医院

目的 人乳头瘤病毒是引起人体皮肤黏膜鳞状上皮增殖的一种病毒，是宫颈上皮增生和宫颈癌的主要致病因素。此文是探讨两种方法提取人宫颈脱落细胞中的 HPV 阳性率及主要型别的差异性。
方法 对本院 200 例病人的 HPV 标本分别用两种**方法** 一种是采用氧化硅纳米磁珠微球和缓冲液，通过外加磁场对磁珠吸附转移从而提取纯化；另一种是利用聚苯乙烯螯合离子交换树脂吸附金属元素离子，对悬浮液加热使 DNA 裂解释放并纯化检测。比较两种提取方法下，HPV 的感染型别以及阳性率的差异，并对其比较进行统计学分析。
结果 在本次 200 例病例中，磁珠提取法得到的结果 HPV 感染率为 18.50%（37/200），其中 HPV16、52、58 分别占比 27.02%（10/37）、18.91%（7/37）、16.21%（6/37）。加热裂解法提取法得到的结果 HPV 感染率为 20.00%（40/200），其中 HPV16、52、58 分别占比 27.50%（11/40）、20.00%（8/40）、17.50%（7/40）。Kappa 一致性分析总符合率为 96.08%，总符合率的 95%置信区间（0.95,0.97）。
结论 磁珠吸附法和加热裂解法提取的 HPV 阳性率及主要型别并无显著性差异。

PU-0292

转录因子 E2F 家族蛋白在肝癌组织中的表达特征及其与预后的相关性

沈浩明[1]、章迪[2]
1. 湖南省肿瘤医院
2. 中南大学湘雅三医院

目的 分析肝癌组织中 E2F 家族蛋白的表达特征,并探讨 E2F 家族蛋白与肝癌患者预后的关系。
方法 从癌症基因组图谱数据库查询公开的肝癌组织与癌旁组织表达量数据,样本共 424 例,其中癌旁组织样本 50 例。应用 R 软件对肝癌组织中 E2F 家族蛋白表达量与癌旁组织的差异进行统计学分析各组间两两比较差异均显著（P<0.05）。肝癌患者 E2F 表达与肿瘤分期的相关性研究中, E2F1、E2F2、E2F3、E2F4、E2F6、E2F7、E2F8 mRNA 表达的分布与肿瘤分期相关;生存分析中除 E2F4 外，其余蛋白表达量与患者生存预后呈明显相关性（P<0.05）,各蛋白的表达量越高,则患者的预后越差,生存率越低；ROC 曲线分析 E2F 家族蛋白与肝癌生存预后的相关性,E2F2、E2F7 对肝癌的预测有一定的准确性,E2F1、E2F8 对肝癌的预测有较高准确性；GO 和 KEGG 分析提示 E2F 家族关键基因主要集中在细胞周期、DNA 复制、细胞分裂相关通路中。
结论 E2F 家族蛋白中的 E2F1、E2F2、E2F3、E2F5、E2F7 和 E2F8 蛋白在肝癌组织中呈高表达,其表达水平与肝癌患者的发生发展及生存预后密切相关, E2F1、E2F2、E2F7 和 E2F8 分子可以为肝癌分子诊断与靶向治疗提供参考。

PU-0293

环状 RNA 与肿瘤

张宇
南京鼓楼医院

环状 RNA（circular RNAs，circRNAs）是一类具有闭合环状结构的 RNA 分子，大量存在于真核转录组中，具有一定的组织、时序和疾病特异性。circRNAs 可作为竞争性内源 RNA（competing endogenous RNAs，ceRNAs）竞争性结合 microRNA，可调控亲本基因的表达和调控可变剪切等。越来越多的研究显示 circRNAs 在多种疾病特别是肿瘤的发生发展中发挥重要作用，在肿瘤诊断、治疗和预后等方面具有巨大的潜能。本文将对目前 circRNAs 在肿瘤中的研究情况作一综述。

PU-0294

自噬分子 ATG14 与甲状腺乳头状癌细胞恶性行为的相关性研究

朱莹、乔焱源、陈穆群、吴惠玲、高晓玲
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨自噬分子 ATG14 与甲状腺乳头状癌细胞恶性行为的相关性。
方法 采用瞬时转染 ATG14-siRNA 下调甲状腺乳头状癌细胞的 ATG14 表达水平，用 MTT 法、划痕实验及流式细胞分析等检测甲状腺乳头状癌细胞的增殖能力、侵袭能力及凋亡情况。
结果 RT-qPCR 结果显示，ATG14 在甲状腺乳头状癌细胞中高表达。MTT 结果显示，敲降 ATG14 后甲状腺乳头状癌细胞活力明显下降；流式细胞术检测结果显示，敲降了 ATG14 后甲状腺乳头状癌细胞 PTC-1 的凋亡率明显降低；细胞划痕实验结果显示，敲降 ATG14 细胞迁移能力明显增强，

细胞侵袭实验也得到相似的结果；此外，ATG14 过表达后，发现甲状腺乳头状癌细胞 PTC-1 对抗癌药物顺铂敏感性降低；而敲降 ATG14 后，甲状腺癌细胞对抗癌药物顺铂敏感性增加。
结论 ATG14 促进甲状腺乳头状癌细胞恶性行为，并且增加其对顺铂的耐药性。

PU-0295

采用自上而下的方法评定 HBV-DNA 测量不确定度

徐秋月、段勇
昆明医科大学第一附属医院

目的 对乙肝 DNA 的测量不确定度进行评价。
方法 参照 CNAS-TRL-001：2012《医学实验室-测量不确定度的评定与表达》,采用“自上而下”的方法，评定偏移和实验室内测量复现性两部分分量引入的不确定度并合成，计算相对扩展不确定度。
结果 低浓度及高浓度合成标准不确定度(对数值)分别为 0.21、0.22， 相对合成标准不确定度分别为 6.45%、3.82%。扩展不确定度分别为 0.42、0.44，相对扩展不确定度（k=2）分别为 12.9%，7.64%。PT 引入的实验室相对合成标准测量不确定度 5.58%。相对扩展不确定度为 11.16%(k = 2)。
结论 医学实验室应定期对乙肝 DNA 的测量不确定度进行评定。

PU-0296

资阳地区妇科门诊患者高危型人乳头瘤病毒感染情况分析

郭琴
资阳市第一人民医院

目的 探讨资阳地区女性高危型人乳头瘤病毒（high-risk human papilloma virus, HR-HPV）的感染情况及其与宫颈病变的相关性，为本地区宫颈癌的早期筛查及 HPV 疫苗选择提供理论依据。
方法 收集 2017 年 3 月-2021 年 4 月期间在资阳市第一人民医院妇科门诊进行宫颈癌筛查患者的 HR-HPV 检测结果，分析计算 HR-HPV 总体感染率、HR-HPV 亚型分布、不同年龄段 HR-HPV 感染特征、HR-HPV 感染与宫颈病变的相关性。
结果（1）资阳地区妇科门诊患者 HR-HPV 感染率为 17.54%（3177/18117），感染率居前 5 位的 HR-HPV 亚型依次为 HPV52、HPV58、HPV16、HPV51 和 HPV39。（2）HR-HPV 感染者以单一感染为主，占 78.06%（2480/3177），混合感染以双重感染最多见，占比 16.81%（534/3177）。（3）各年龄段分组中，小于 20 岁年龄组的 HR-HPV 感染阳性率最高（34.75%），30～39 岁年龄组的 HR-HPV 感染阳性率最低（16.28%），感染率随年龄呈"U"形分布。（4）在同时接受 TCT 检查的 1183 例 HR-HPV 感染者中，962 例未查见上皮内病变细胞或恶性细胞 （NILM），135 例查见非典型鳞状上皮细胞（ASC），86 例存在鳞状上皮内病变（SIL），NILM、ASC、SIL 患者排名前五的 HR-HPV 亚型略有差异。
结论 资阳地区女性 HR-HPV 感染率较高，HPV52、HPV58、HPV16 在总人群及伴宫颈细胞学异常的人群中的感染率均排名前三，建议至少选择可覆盖 HPV52、HPV58、HPV16 等型别的多价疫苗。

PU-0297

无创 DNA 检测技术在胎儿染色体非整倍体疾病产前筛查中的应用

万彦谷
南方医科大学珠江医院

目的 通过对无创 DNA 产前筛查（NIPT）结果进行回顾性分析，探讨 NIPT 在胎儿染色体非整倍数疾病（21 三体综合征、18 三体综合征、13 三体综合症、以及性染色体非整倍数疾病）的临床应用价值。
方法 对本院近两年报告的 NIPT 样本进行回顾性分析。采用 BGI500 平台测序，结合生物信息学分析，对 21 三体、18 三体、13 三体以及性染色体非整倍数疾病进行产前筛查。NIPT 高风险的孕妇充分知情选择后，进行羊水/脐血穿刺的染色体核型分析并随访。
结果 NIPT 结果提示高风险的为 17 例，阳性率为 0.084%。其中 11 例进行染色体核型分析，结果为 21-三体 4 例、18-三体 2 例、13-三体 1 例、性染色体异常 1 例，阳性预测值分别为 100%、100%、100%和 25%。比较 NIPT 筛查与染色体核型分析两种方法，结果无统计学差异（P＝0.810>0.05）。
结论 NIPT 对 2l 三体综合征、18-三体综合征和 13-三体综合征的检测的符合率较高，但是对性染色体异常疾病检测的符合率偏低。迄今为止，NIPT 仍只能作为产前筛查技术，其高风险的孕妇仍需进行产前诊断，以确保产前检测的准确性。

PU-0298

八基因联合检测在非小细胞肺癌中的突变分析

谭茜
岳阳市一人民医院

目的 探讨运用基于二代测序（NGS）的杂交捕获富集法检测 ALK、BRAF、EGFR、 ERBB2、KRAS、 MET、 RET 和 ROS1 八基因在非小细胞肺癌（NSCLC）的突变情况，分析其与临床病理的关系，探索八基因突变联合检测的临床应用价值。
方法 收集 2020 年 5 月至 2021 年 6 月在岳阳市一人民医院病理确诊为非小细胞肺癌患者 130 例（肺腺癌 120 例，肺鳞癌 10 例）。采取磁珠法提取 DNA，突变检测采用杂交捕获富集法，在 illumina Miseq^{DX} 测序仪上进行测序分析。
结果 非小细胞肺癌八基因联合检测的总突变频率为 80.8%（105 /130），各驱动基因突变分布为: EGFR：56.2% (73 /130) 、KRAS：9.2%（12 /130）、ALK 融合：7.7%（10 /130）、BRAF：2.3%（3/130）、MET 14 号外显子跳读突变：1.5%（2/130）、ROS1 融合：1.5%（2 /130）、ERBB2：1.5%（2 /130)、RET 重排（融合）:0.8% (1 /130)。肺腺癌突变频率（90.8%，101/120）高于肺鳞癌（40%，4/10）；男性患者中 KRAS 突变率和 ALK 融合率明显高于女性患者；而 EGFR 突变频率低于女性患者；KRAS 突变在吸烟患者的发生率显著高于无吸烟史患者。EGFR 突变率在年龄低于 60 岁和年龄高于 60 岁的患者之间无差异。另外在 2 例样本中检出双突变，突变率达到 1.5%。
结论 在 8 个驱动基因突变中，EGFR 突变和 ALK 融合与患者性别以及组织学类型密切相关；KRAS 突变与患者吸烟史密切相关，其它较为罕见驱动基因突变并未发现与组织学类型、患者性别及吸烟与否相关。杂交捕获法八基因联合检测可一次获得更多基因突变信息，可作为 NSCLC 理想的基因检测方法，为分子靶向用药提供更加全面的指导信息，从而精准指导临床治疗。

PU-0299

H7 亚型流感疫苗交叉反应的系统评价

苟晓琴
资阳市第一人民医院

目的 接种疫苗是目前用于干预流感的主要措施，但当新型的高致病性流感病毒大规模流行时，生产新型疫苗并尽快应用于临床却是一大挑战。H7 亚型流感病毒的血凝素（HA）具有相似的抗原表位，可以诱导产生交叉反应性抗体。该研究中，对一种 H7 亚型流感疫苗针对其他 H7 亚型病毒诱导的交叉反应性抗体进行系统评价。
方法 计算机在 PubMed，Cochrane Library，EMBASE，MEDLINE，中国生物医学数据库（CBM）和万方数据库中检索有关 H7 亚型流感疫苗交叉反应的随机对照试验及临床试验，检索时间截止到 2020 年 12 月。
结果 共检索到 9 篇文章，共计 811 名受试者。结果显示 H7 流感疫苗诱导的特异性保护性抗体[血清转化率（SCR）= 0.74，95％CI（0.65，0.82）; 血清保护率（SPR）= 0.81，95％CI（0.78，0.83）]。在血凝素抑制试验（HI），微量中和试验（MN）和免疫吸附试验（ELISA）中，所有 H7 流感病毒单价疫苗均与其他 H7 亚型病毒存在交叉反应。 H7N1，H7N3，H7N7 和 H7N9 疫苗可对其他 H7 亚型流感病毒产生交叉反应抗体[SCR = 0.66，95％CI（0.50，0.82）; SPR = 0.79，95％CI（0.67，0.91）]。其中 H7N1 和 H7N3 疫苗交叉反应抗体 SCR（95％CI）分别为 0.88（0.85，0.91）和 0.40（0.26，0.54）；H7N1 和 H7N7 疫苗交叉反应抗体 SPR（95％CI）分别为 0.89（0.86，0.92）和 0.93（0.81，1.06）。 所有 H7 疫苗均可诱导针对 H7N9 病毒的交叉反应抗体[SCR = 0.69，95％CI（0.52，0.86）； SPR = 0.85，95％CI（0.76，0.94）。
结论 当出现新型高致病性 H7 病毒时，可接种 H7 其它亚型疫苗进行初步防预。

PU-0300

资阳市宫颈人乳头瘤病毒感染型别分布

付英
资阳市第一人民医院

目的 了解资阳市人乳头瘤病毒(HPV)感染情况和基因类型分布，为本地区的宫颈癌防治提供依据。
方法 采用荧光 PCR 的方法对来院的 8620 例 HPV 检测者进行 HPV15 种基因分型检测。
结果 8620 例检测者中，感染 HPV 者 1852 例，阳性率为 21.48%，其中 52、58 和 16 型比例最高；总感染率和多重感染率的高峰年龄段均在＜20 岁和≥60 岁；HPV 感染模式以单一感染为主，占 77.24%，多重感染以两重感染为主。
结论 资阳市 HPV 常见基因型符合亚洲人群感染规律，感染率随年龄呈现 U 型分布。

PU-0301

Integrating serum microRNAs and electronic health records improved the diagnosis of tuberculosis

Junwei Zhao
Department of Clinical Laboratory, The First Affiliated Hospital of Zhengzhou University

Background To verify the differential expression of miR-30c and miR-142-3p between tuberculosis patients and healthy controls and to investigate the performance of microRNA (miRNA) and subsequently models for the diagnosis of tuberculosis (TB).

Methods We followed up 460 subjects suspected of TB, and finally enrolled 132 patients, including 60 TB patients, 24 non-TB disease controls (TB-DCs) and 48 healthy controls (HCs). The differential expression of miR-30c and miR-142-3p in serum samples of the TB patients, TB-DCs and HCs were identified by reverse transcription-quantitative real-time PCR. Diagnostic models were developed by analyzing the characteristics of miRNA and electronic health records (EHRs). These models evaluated by the area under the curves (AUC) and calibration curves were presented as nomograms.
Results There were differential expression of miR-30c and miR-142-3p between TB patients and HCs ($p < 0.05$). Individual miRNA has a limited diagnostic value for TB. However, when we integrated miR-142-3p and ordinary EHRs to develop two models for the diagnosis of tuberculosis, diagnostic performance has been both significantly improved. The AUC of the model for distinguishing tuberculosis patients from healthy controls has increased from 0.75 (95%CI: 0.66-0.84) to 0.96 (95%CI: 0.92-0.99) and the model for distinguishing tuberculosis patients from non-TB disease controls has increased from 0.67 (95%CI: 0.55-0.79) to 0.94 (95%CI: 0.89-0.99).
Conclusions Integrating serum miR-142-3p and EHRs is a good strategy for improving the TB diagnosis.

PU-0302

资阳地区地中海贫血基因突变类型分析

刁雪
资阳市第一人民医院

目的 分析资阳地区疑似地中海贫血患者的地中海贫血基因检测结果，了解资阳地区地中海贫血基因突变类型。
方法 选取 2020 年 5 月至 2021 年 4 月于资阳市第一人民医院收治的疑似地中海贫血患者 323 例，采用 PCR 结合溶解曲线分析法进行非缺失型 α、缺失型 α 和 β 地中海贫血基因检测。
结果 323 例受检者存在地中海贫血基因的有 98 例，阳性率为 30.34%。98 例中携带 α 地中海贫血基因 45 例，β 地中海贫血基因 51 例，α 合并 β 地中海贫血基因 2 例。45 例 α 地中海贫血基因中共检测出 4 种常见 α 地中海贫血等位基因，以东南亚缺失型 αα/--SEA 基因最多共 31 例，占比为 68.89%。51 例 β 地中海贫血基因携带者共检测出 11 种常见地中海贫血等位基因，排名前三的基因型分别是 CD17（15 例，占比 29.41%），IVS-II-654（14 例，占比 27.45%），CD41-42（12 例，占比 23.53%）。
结论 资阳地区地中海贫血基因突变类型中 α 地中海贫血等位基因以东南亚缺失型 αα/--SEA 基因最多，β 地中海贫血等位基因以 CD17 基因最多；β 地中海贫血基因检出率稍高于 α 地中海贫血基因。

PU-0303

Association between lncRNA MALAT1 polymorphisms and cancer susceptibility: a meta-analysis

Lei Zheng
The First Affiliated Hospital of Zhengzhou University

Background LncRNA metastasis associated with lung adenocarcinoma transcript-1 (MALAT1) was involved in pathogenesis and progress of diverse cancers. To investigate the association of MALAT1 and cancer susceptibility, this meta-analysis was appraised.
Methods 12 studies including 7007 cancer patients and 8791 controls were selected for this meta-analysis. Ratio radiation (ORS) and 95% confidence interval (CIS) were used to assess cancer susceptibility.

Results There was no significant association between rs3200401 polymorphism and the risk of cancer. However, rs3200401 was correlated with an increased risk of digestive cancer in allelic model (OR=1.15, 95%CI=1.04-1.28, P=0.009) and dominant model (OR=1.16, 95%CI=1.02-1.31, P=0.02). There was a borderline association between rs664589 and cancer susceptibility under the dominant model (OR=1.17, 95%CI=1.00-1.38, P=0.05). Rs619586 was associated with decreased cancer risk in all populations under four models (G vs A: OR=0.86, 95%CI=0.78-0.94, P=0.001; GG vs AA: OR=0.60, 95%CI=0.42-0.84, P=0.003; GG+AG vs AA: OR=0.87, 95%CI=0.78-0.97, P=0.009; GG vs AG+AA: OR=0.61, 95%CI=0.44-0.84, P=0.003). Moreover, rs1194338 was decreased associated with cancer susceptibility (A vs C: OR=0.89, 95%CI=0.80-0.98, P=0.01; AA vs CC: OR=0.77, 95%CI=0.62-0.96, P=0.02; AA+AC vs CC: OR=0.87, 95%CI=0.77-1.00, P=0.04; AA vs AC+CC: OR=0.82, 95%CI=0.67-1.00, P=0.05).
Conclusion Our results suggest that rs619586 and rs1194338 are associated with decreased cancer risk, while rs3200401 and rs664589 correlated with increased digestive cancer risk.

PU-0304

TCP1α 对胰腺癌细胞株的生物学影响

王乐乐
山东大学第二医院

胰腺癌目前的五年生存率为 6%，手术治疗使其比较好的治疗方法，但胰腺癌一旦被发现就已经处于晚期，因此分子靶向治疗等新的治疗方法以迫在眉睫。理想的分子靶向治疗药物能够特异地选择肿瘤细胞内某个致癌靶位点与之相结合发生作用，从而特异地抑制肿瘤细 胞的生长增殖，进而导致肿瘤细胞的死亡。癌基因成癮概念的提出为肿瘤的分子 靶向治疗研究提供了良好的生物学基础，已经成为当前抗癌药物研发及癌症治疗 的重要研究热点。在前期研究中，我们已经鉴定出多种短寿命蛋白的快速降解可 、能与癌细胞中成癮癌基因急性抑制后发生的急性凋亡有关，T 复合蛋白 1 亚基 α(T-complex protein 1 subunitalpha，TCP-1-alpha，简称 TCP1α、CCT1)就是其中的蛋白之一。TCP1α 是构成分子伴侣复合物 TRiC（也称 TCP-1、CCT）的一种亚基，当前已有多项研究显示 TRiC 亚基在多种肿瘤标本中过表达，包括肝癌、肺癌、乳腺癌、胃癌、结肠癌等，并且发现多种亚基对于肿瘤的发生发展起着至关重要的作用。但是，目前关于 TCP1α 在胰腺癌中的相关研究还知之甚少。因此，本课题将重点研究 TCP1α 在胰腺癌发生发展中的作用，为胰腺癌的发病机制及靶向治疗提供理论和实验依据。

PU-0305

裂殖酵母 Clr1 蛋白在 DNA 损伤应答中的机制探究

谷璐婷
南华大学附属第一医院

DNA 损伤应答是机体应对损伤作出的一系列反应。DNA 损伤应答有效的协调，在机体适应环境、细胞的分裂、分化过程中发挥了重要作用。研究 DNA 损伤应答相关的分子机制，将会加深对人类许多疾病发生发展机制的理解，为疾病的预防和治疗提供新的思路和方法。

以裂殖酵母（Fission yeast, S.pombe）为模式生物， 研究真核生物中 DNA 损伤应答相关机制，通过遗传筛选方法寻找参与 DNA 损伤应答新的蛋白。ATR/Rad3 蛋白是目前已知 DNA 损伤应答中至关重要的一个上游蛋白激酶，它参与了 DNA 损伤应答多方面的调控。在 *Rad3* 基因缺失的背景下，筛选出对 DNA 损伤药物敏感表型产生回补的突变株，再通过对突变株深度测序确定相关突变基因，其中一个可能参与 DNA 损伤应答反应的新基因为 *Clr1*。Clr1 蛋白是一个转录负调控蛋白，已报导的主要功能是参与异染色质的组装。

本研究通过遗传实验，初步证明了 Clr1 蛋白与 DNA 损伤应答具有相关性，且 *Clr1* 缺失可以回补 *Rad3* 基因缺失对 DNA 损伤药物的敏感性。通过生化实验，证明在损伤应答反应时，Clr1 蛋白会受到 Rad3 蛋白的调控，再通过泛素化途径降解。但 Clr1 作为 Rad3 的下游蛋白，在损伤应答中并不直接受到 Rad3 蛋白磷酸化调控。通过质谱鉴定，发现在进行 DNA 损伤药物处理后 Clr1 蛋白存在多个位点的磷酸化修饰。

PU-0306

巨噬细胞炎性蛋白 3α（MIP-3α/CCL20）结构功能及其与肿瘤关系的探讨

宋志纯
丽水市人民医院

趋化因子巨噬细胞炎性蛋白 3α（MIP-3α/CCL20）是 CC 亚家族中的一员，其在体内与其受体 CCR6 结合之后诱导 T 细胞和树突状细胞定向迁移，能够在肿瘤免疫及自身免疫性疾病中发挥重要的作用。本文旨在深入研究来增强对其病理生理学意义的认识，为相关疾病的预防及治疗提供新的方法。

PU-0307

香烟烟雾提取物改变原代人支气管上皮细胞中 lncRNA 和 mRNA 全基因组图谱

王楠
山东第一医科大学
山东大学第二医院

目的 研究香烟烟雾提取物(CSE)刺激下原代人支气管上皮细胞(HPMECs)中的 lncRNAs 的表达模式，以探究慢性阻塞性肺病（COPD）的发病机制。
方法 利用香烟烟雾提取物处理的原代人支气管上皮细胞，构建 COPD 发病模式下的的细胞凋亡模型，用 Annexin V-FITC/PI 双染细胞凋亡检测试剂盒进行染色(贝博公司；BB-4101-1)检测 HPMECs 凋亡模型构建成功。随后提取 RNA 后进行转录组测序，通过 RNA 测序和生物信息学分析并预测差异 lncRNA 调控的 mRNA，并进行 GO 功能与 KEGG 信号通路聚类。
结果 首先用 0.1%、1%和 10%CSE 刺激 HPMECs 24h，观察 CSE 对 HPMECs 的影响。流式细胞仪分析显示早期凋亡率随 CSE 浓度从 0.1%增加到 10%而增加，提示在 CSE 诱导的 HPMECs 的凋亡有剂量依赖性。经 1.0%CSE 处理后，HPMEC 凋亡率显著升高(流式细胞仪检测为 36.23±4.20%)。与 0.0%CSE 组(7.33±1.36%)和 0.1%CSE 组(19.50±2.03%)相比，差异均有统计学意义(P<0.05)。10%CSE 组细胞凋亡率(41.19±5.61%)持续升高，差异仍有显著性(P<0.05)。在随后的实验中，我们决定将细胞暴露在 1.0%的 CSE 中 24 小时。
经 1%CSE 刺激 24h 后，提取 HPMECs 总 RNA，采用基因芯片技术进行基因表达谱分析。我们以 P value< 0.05 且|log2FC|>2 为筛选标准，其中上调的 lncRNAs 有 54 个(P<0.05)，下调的 lncRNAs 有 29 个(P<0.05)，我们从生物过程(BP)、细胞成分(CC)和分子功能(MF)三个方面对差异表达的 lncRNA 预测到 mRNA 靶基因，以探讨其可能的功能作用。
结论 CSE 诱导的 HPMECs 存在一组独特的 lncRNAs 和 mRNAs 表达模式，这些异常的 lncRNAs 可能通过转录后调节 ceRNA 网络参与血管内皮细胞对香烟烟雾应激的反应，可能有助于阐明 COPD 的潜在机制。

PU-0308

BRCA 基因突变和血清肿瘤标志物在 HBOC 卵巢癌患者中的临床意义研究

邓红玉、刘牧奇、李瑛花、李佶刚、衡建福、沈浩明、屈斌、黄宏君、熊海玉、包莹、唐发清
湖南省肿瘤医院

目的 调查 HBOC 卵巢癌患者与其他癌症家族史卵巢癌患者 BRCA1/2 特定位点突变情况，分析临床数据及手术前后血清肿瘤标记物浓度变化，探讨其临床意义。
方法 1. 通过 Sanger 测序分析 HBOC 卵巢癌患者与患有其他肿瘤家族史患者 BRCA1 基因 c.220C>T、c.3770-3771delAG、c.4712delT、BRCA2 基因 c.3109C>T 突变情况。2. 统计分析 HBOC 卵巢癌患者与患有其他肿瘤家族史患者病例及手术前后血清肿瘤标记物浓度变化。
结果 40 例 HBOC 卵巢癌患者 4 个特定位点总体的突变率为 7.5%（3/40），其中 BRCA1 c.3770-3771delAG 的突变率为 2.5%（1/40），BRCA1c.4712delT 的突变率为 5%（2/40）。40 例其他癌症家族史卵巢癌患者无突变。术前 CA125、术后 CA125、术前 HE4、术后 HE4 血清学水平在研究组和对照组之间差异无统计学意义（*P*>0.05）；术后铁蛋白浓度变化情况与对照组有显著差异（*P*<0.05）。HBOC 卵巢癌患者 CA125、HE4 血清学水平术后均低于术前，差异具有统计学意义（*P*<0.05）。其他癌症家族史患者 CA125、HE4 血清学水平术后均低于术前，差异具有统计学意义（*P*<0.05）。HBOC 卵巢癌患者单项检验 C A125 灵敏度 87.50%最高，HE4 和 FERRITIN 特异性 94.12%最高。联合检验中 CA125+HE4+Ferritin 的联合检验诊断能力最强。
结论 1. BRCA1c.3770-3771delAG 与 BRCA1 c.4712delT 可能是中国湖南省地区 HBOC 卵巢癌患者 BRCA1/2 基因高频有害胚系突变位点。2. 肿瘤标志物 CA125、HE4 血清学水平变化可作为卵巢癌患者治疗监测及预后判断的指标，CA125+HE4+Ferritin 的联合检验诊断能力最强。3. 铁稳态调节及 FERITIN 浓度变化可能对 HBOC 卵巢癌患者诊断及治疗具有指导意义。

PU-0309

乙肝患者的血清标志物联合乙肝病毒 DNA 检测用于乙肝病毒感染诊断的价值

文琪
资阳市乐至县人民医院

目的 探究乙肝病毒（HBV）感染应用血清标志物联合乙肝病毒 DNA 检测的临床诊断价值。
方法 遴选时段 2018 年 6 月-2019 年 6 月内 120 例乙型肝炎患者，以血清 HBV 检测结果为参考设置分组，大三阳组（36 例）、小三阳组（50 例）、其他模型组（34 例），纳入对象均开展 HBV DNA 检测、血清标志物检测，检测结果分析对比。
结果 大三阳组 HBV DNA 定量检测结果明显高于小三阳组、其他模型组，且经 HBV DNA 检测大三阳组阳性率为 86.11%高于小三阳组 44.00%、其他模型 8.33%，组间对比均存在统计学差异（P＜0.05）；同时检测阳性患者共计 56 例，经血清标志标志物检测，其中 HBeAg 阳性率 4.64%、HBsAg 阳性阳性率 91.07%。
结论 对乙型肝炎患者开展 HBV DNA +血清标志物检测对乙肝病毒感染情况进行诊断，为疾病早期诊断及病情评估提供有效数据支持，以便于后期临床诊疗工作的开展。

PU-0310

低氧微环境对胰腺癌细胞转录水平的影响

刘小艳
山东大学第二医院

目的 胰腺癌(Pancreatic cancer, PC)是消化道肿瘤中死亡率最高的恶性肿瘤, 其特点是初期症状不明显、恶化快、手术切除率低、整体预后差。目前主要治疗方法是根治 性切除后加以辅助治疗，但大部分病人在诊断时已是晚期，只有 15%-25%的患者适 合手术切除。由于早期复发转移和多化疗药物耐药，即使接受了切除手术，患者的 5 年生存率只有 8%。 癌细胞恶性转移是胰腺癌发展的早期过程，是导致预后较差的 独立影响因素。因此探索导致胰腺癌发生发展的遗传或表观遗传因素，发现新的治 疗靶点和生物标志物，是提高患者生存率的关键。与其他肿瘤相比，胰腺癌是含氧量最低的实体肿瘤，低氧微环境对肿瘤的发生进展的影响非常复杂，需深入探究。
方法 体外模拟低氧微环境，寻找低氧微环境影响的特异调控基因。分别在正常氧和低氧（2% 02）条件下培养胰腺癌细胞 PANC-1 48h，qRT-PCR 和 Western blot 验证 HIF-1a 的表达水平。正常氧和低氧组分别 3 个重复，进行 RNA-seq，即转录组测序。提取细胞中总 RNA，用 RiboMinus 方法建库、采用 Hiseq 2000 平台测序；采用 DESeq2、Wilcoxon rank sum test 等分析方法，以 $p<0.05$ 且$|\log2\text{Fold Change}|>2$ 为筛选标准， 筛选出差异基因。 对差异基因分别进行 GO 功能富集和 KEGG 通路分析。
结果 RNA-seq 结果表明，与正常氧相比，在低氧条件下表达上调的基因有 1286 个，表达下调的基因有 1669 个。差异基因富集分析发现，这些差异基因主要集中在有氧应激反应，Pathway 分析表明 HIF-1 信号途径、果糖和甘露糖代谢、淀粉和蔗糖等糖代谢途径。

PU-0311

miR-1204 促进乳腺癌细胞上皮-间充质转化及侵袭转移的作用机制研究

刘小艳
山东大学第二医院

目的 全球范围内乳腺癌每年新诊断出的病例都高居不下，严重威胁女性健康和生活质量。 肿瘤转移是乳腺癌死亡的根本原因， 据统计，约 6%的患者在诊断时已经出现转移，约 20%-50%的早期乳腺癌患者最终将发展成转移性乳腺癌。 肿瘤转移是乳腺癌治疗的主要障碍，因此，寻找更多调控肿瘤细胞转移的关键分子对于乳腺癌的预后以及新治疗策略的开发十分重要。miR-1204 位于染色体 8q24 位点长链非编码 RNA PVT1 区 的 miRNA 基 因 簇 ，我们研究发现 miR-1204 在乳腺癌中过表达并促进乳腺细胞上皮-间充质转化，最终促进乳腺癌转移。
方法 首先利用公共数据库 METABRIC 和 TCGA 统计分析染色体 8q24 位点基因扩增情况。利用实验室收集的新鲜乳腺癌组织和恶性程度不同的乳腺癌细胞系验证生物信息分析的结果。结合患者病历和随访结果分析 miR-1204 表达水平与乳腺癌临床病理分期和生存期的关系。通过 qRT-PCR 和 WB 检测 miR-1204 对 EMT 标志分子 E-cadherin、N-cadherin 的表达影响，通过构建小鼠远端转移瘤模型，体内验证 miR-1204 促进乳腺癌细胞转移。
结果 生物信息统计分析和乳腺癌组织验证发现 miR-1204 位点在乳腺癌中高表达；体外分子实验表明 miR-1204 促进 EMT 标志分子 N-cadherin 的表达，抑制上皮标志分子 E-cadherin 的表达；小鼠远端转移瘤模型验证了 miR-1204 促进乳腺癌细胞体内远端转移，转移瘤主要集中在肺部。
结论 我们的研究发现，miR-1204 在乳腺癌中高表达，通过促进细胞上皮-间充质转化促进乳腺癌细胞远端转移。本研究丰富了 PVT1 区域的基因功能，为乳腺癌的防治提供理论基础。

PU-0312

LAMP 在肺炎及呼吸道相关病原体基因检测中的应用

王云娟
昆明医科大学第一附属医院

目的 应用环介导恒温扩增芯片法（ＬＡＭＰ）对肺炎及呼吸道感染患者的痰液或肺泡灌洗液标本，进行 13 种常见致病菌的基因检测。探讨其临床应用价值，以便临床及时、准确的诊断和治疗。
方法 采用 LAMP 技术、病原体分离与培养技术，对 2020 年 9 月至 12 月收集到的 1900 例昆明医科大学第一附属医院疑似肺炎及呼吸道感染患者的痰液或肺泡灌洗液样本，对样本进行检测。然后按标本类别、性别、年龄、科室及检测方法的不同进行分析。
结果 在 1900 例样本中，LAMP 法检出了 51.63%的病原菌检出率，传统细菌培养法检出 33.95%的病原菌检出率，LAMP 法病原体检出率明显比细菌培养法检出率高。其主要病原菌为 HIB（17.58%）、MSSA（12.74%）、Kpn（11.53%）、CSAB（9.05%）、S.p（7.63%）、PA(6.63%)和 E.coli（5.47%)。男性和女性的 MP、S.a 和 CP 感染阳性率具有显著性差异(P<0.05)。小于 20 岁组患者的 S.a 和 CP 感染阳性率高于 20-60 岁组和大于 60 岁感染阳性率，差 异具有统计学意义（P<0.05）。将病原体检出最多科室老年呼吸科、儿科和 ICU 做病原菌检出情况分析，其主要病原菌为 HIB（19.02%）、MSSA（10.83%）、Kpn（10.46%）、S.p（8.13%）和 CSAB（7.16%）。
结论 LAMP 法能快速、高效、灵敏和准确地检测常见呼吸道病原体。有助于临床在快速和可靠的实验室依据下对患者进行呼吸道感染病原体的快速诊断。

PU-0313

Y 染色体上与衰老相关的 DNA 甲基化

李谷亚男[1]、郭欢[2]、林勇[3]
1. 复旦大学附属上海市第五人民医院检验科
2. 华中科技大学同济医学院公共卫生学院
3. 复旦大学附属华山医院检验科

目的 已有研究发现常染色体上存在大量与衰老相关的 DNA 甲基化位点（CpG 位点）。衰老相关疾病的发病率和死亡率存在性别差异，提示性染色体可能在衰老的进程中起着重要作用。本研究旨在探讨男性外周血细胞 Y 染色体上与衰老相关的 CpG 位点。
方法 采用发现-验证两阶段人群研究设计。发现阶段为 419 名来自武汉-珠海队列、武汉焦炉工职业人群和十堰健康体检的男性，验证阶段为 564 名来自 3 个 GEO 数据集以及 587 名来自东风-同济队列的男性研究人群。采用 Illumina 甲基化芯片检测上述研究对象外周血细胞全基因组 DNA 甲基化水平。在数据分析过程中，采用多元线性回归模型，校正吸烟状态、饮酒状态、BMI 和外周血白细胞计数，分析实足年龄与 Y 染色体 CpG 位点甲基化水平的关联。发现阶段显著性水平定义为假阳性发现率 *FDR*<0.05，验证阶段显著性水平为 *P*<0.05。为探讨 Y 染色体上衰老相关的 DNA 甲基化对相应基因表达水平的影响，通过 Illumina 表达谱芯片检测上述十堰健康体检人群外周血的基因表达谱。为探讨 Y 染色体上衰老相关 DNA 甲基化与死亡风险的关联，采用 Cox 风险比例回归模型评估 DNA 甲基化对总体死亡风险的影响，计算相应风险比。
结果 在发现阶段，41 个 Y 染色体 CpG 位点的甲基化与实足年龄之间的关联达到显著性水平（*FDR*<0.05）。其中，18 个 CpG 位点的甲基化在验证人群中与实足年龄存在显著关联（*P*<0.05）。位于 *TTTY14* 和 *EIF1AY* 上的 CpG 位点甲基化水平分别与其相应基因表达水平之间呈显著的负向关联 [cg13845521-TTTY14: β=-0.24；cg11816202-TTTY14: β=-0.21; cg01988452-EIF1AY: β=-0.28; cg13308744-EIF1AY: β=-0.36]。cg03441493 高甲基化和 cg17816615 低甲基

化的研究对象总体死亡的风险更高 [cg03441493: HR(95%CI)=1.37 (1.04, 1.79); cg17816615: HR(95%CI)=0.70 (0.54, 0.93)]。
结论 本研究首次在中国男性人群 Y 染色体上发现与衰老相关的 DNA 甲基化。Y 染色体上年龄相关的 CpG 位点（cg03441493 和 cg17816615）与死亡风险相关。

PU-0314

tsRNA 在肿瘤中研究进展及检测方法现状

范柏月、李智洋
南京大学医学院附属鼓楼医院

目的 非编码 RNA 是生命活动重要的调控因子，tsRNA（tRNA-derived small RNAs）是近年来通过高通量测序发现的一类新的非编码小 RNA，是由成熟 tRNA 或其前体在特定的核酸酶，如血管生成素 (ANG)、Dicer、核糖核酸酶 Z(RNase Z)和核糖核酸酶 Z(RNase P)作用下，产生的长度 18~40nt 的小片段，根据初始 RNAA 和酶作用位置的不同主要分为以下亚型：①tRNA 半分子 (tRNA halves,tRH），是成熟的 tRNA 分子在多种应激条件下反密码环处被特定切割产生的半分子，长度约 30-40nt ,具有 5′-tRH 和 3′-tRH 两个亚型;②tRNA 衍生片段(tRNA-derived RNA fragment,tRF)，来源于成熟 tRNA,根据匹配区域不同主要分为 tRF-5、tRF-3、tRF-1 和 i-tRF 四亚类,分别对应 5’端至 D 环或反密码子茎环区切割处；T 环切割出至 3’端；pre-tRNA 的 3’端尾部；反密码子环和茎。现有研究表明，tsRNA 并非随机裂解的产物，而是在压力条件下特性裂解生成的，在正常生理条件下很少发生，且越来越多证据表明 tsRNA 与肿瘤的发生发展密切相关，预示其作为新型肿瘤生物标志物的巨大潜力。由于 tsRNA 上具有丰富的碱基修饰保护其躲避核酸酶的切割，在使 tsRNA 拥有更高的稳定性的同时，也增加了检测的难度，此外其较短的长度、ANG 切割产生的 5’羟基（5’-OH）末端与 3’环磷酸（3’-cP）末端、天然的二级结构均对研究造成了阻碍。本文主要对 tsRNA 的分类、特点、在肿瘤中作用研究进展及现有检测方式进行综述。
方法 对近五年的 tsRNA 相关文章进行调研总结
结果 tsRNA 与肿瘤进展密切相关
结论 tsRNA 具有作为生物标志物的潜力

PU-0315

基于滚环扩增结合分子信标检测胰腺癌小分子 RNA 的新方法

范柏月、李智洋
南京大学医学院附属鼓楼医院

目的 胰腺癌是一种常见消化道恶性肿瘤，恶性程度高，缺乏准确灵敏的早期诊断方法。tsRNA(tRNA derived small RNA)是一类由 tRNA（细胞中数量最多的非编码 RNA 之一）衍生的小 RNA，近年来大量研究表明 tsRNA 在多种癌症中异常表达，具有作为疾病诊断的标志物的潜力。定量逆转录 PCR(quantitative reverse transcription PCR, RT-qPCR)是目前最常用于检测小 RNA 的方法，灵敏度高,特异性好，但步骤繁琐、试剂昂贵、依赖能加热循环的精密仪器限制了其在临床的应用。滚环扩增（rolling circle amplification，RCA）作为恒温扩增技术反应的一种，全程在同一温度下进行,对仪器要求大大简化,反应时间短,无需逆转录,操作简单,更能满足现代分子检测技术“快速简便”的要求。综上，本研究旨在筛选特异性 tsRNA 作为胰腺癌早期诊断标志物，并建立相应的基于滚环扩增的信号放大检测方法，实现快捷、简便的检测。
方法 通过测序筛选出在胰腺癌患者血清中高表达的 tsRNA，通过 RT-qPCR 评估其临床价值；建立 Toehold 介导的滚环扩增技术结合分子信标的快速检测方法，并对其特异性和灵敏度进行研究，应用该技术对 20 对胰腺癌患者和健康人血清中 tsRNA 进行定量检测。

结果 此方法可有效地对胰腺癌高表达 tsRNA 进行扩增和检测，且特异性高，耗时短。与普通 RCA 相比，能显著区分目标分子与单碱基突变的近似序列；无需逆转录和反复热变性，2h 即可完成检测。
结论 Toehold 介导的滚环扩增技术结合分子信标能够作为检测胰腺癌 tsRNA 的快速特异的方法。

PU-0316

全外显子组测序技术寻找圆头精子症家系的致病基因

任会均
郑州大学第一附属医院

目的 寻找一圆头精子症家系的致病基因。
方法 对一个圆头精子症家系两患者进行精液常规分析及形态观察，利用全外显子组捕获测序及生物信息学技术对该家系基因组进行分析，采用 Sanger 测序及 qPCR 技术对致病基因的变异进行验证。
结果 该家系两患者圆头精子率分别为 97%、98%，头核深染，顶体缺乏，除顶体酶活性明显降低外，精液常规分析其余指标均正常。经全外显子组测序分析、Sanger 测序及 qPCR 验证显示兄弟两患者及其母亲均存在 DPY19L2 基因杂合点突变 c.384dup（p.Glu129*），两患者及其父亲存在覆盖 DPY19L2 基因全长的约 164.5kb 的大片段杂合缺失。
结论 该家系两患者遗传于母亲的 DPY19L2 基因点突变 c.384dup（p.Glu129*）以及父亲的 DPY19L2 基因缺失，从而表现出圆头精子症的纯合表型，符合常染色体隐性遗传规律。本研究发现一个 DPY19L2 基因的新突变位点 c.384dup（p.Glu129*），为圆头精子症发病机制的研究提供新线索。

PU-0317

Improved EGFR mutation detection sensitivity after enrichment by Cas9/sgRNA digestion and PCR amplification

DIXIAN LUO
HUAZHONG UNIVERSITY OF SCIENCE AND TECHNOLOGY UNION SHENZHEN HOSPITAL

The detection of circulating tumor DNA is important in cancer research and clinical practice. In the present study, we aimed to improve the sensitivity of downstream mutation detection of next-generation sequencing using the clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 (Cas9) system to selectively target wild-type fragments but with low or no cleavage activity to mutant fragments, followed by amplification using polymerase chain reaction. We selected different mutant sites of epidermal growth factor receptor gene (EGFR)-exon19 deletions in patients with lung cancer and constructed mixed templates of mutant and wild-type DNA comprising ratios of 10% to 0.01% to test the effectiveness of the enrichment method. The results showed that after CRISPR/Cas9 enrichment, a low concentration of mutant DNA fragments (0.01%) could be detected by Sanger sequencing, which represented a 1000-fold increase compared with the untreated samples. We further verified the feasibility of the introduced method and obtained similar results in clinical samples from patients with non-small cell lung cancer, indicating that this method has the potential to detect low copy number mutations at the early stage.

PU-0318

The construction of circRNA-miRNA-mRNA network and prognostic evaluation model in Bladder Cancer

Qi Mi、Peilong Li、Juan Li、Chuanxin Wang、Lutao Du
The second hospital of Shang Dong University

Objective To identify the dysregulated circRNAs in bladder cancer (BC) and construct a ceRNA regulatory network. Further to establish and evaluate a prognostic model of BC.
Methods Sequencing data of BC were obtained from Gene Expression Omnibus (GEO) and The Cancer Genome Atlas (TCGA) database. By using "|log2FC|>1, *P*-value<0.05" as the standard, the sequencing data were analyzed and the RNA differential expression profiles were drawn. Multiple databases, such as CircInteractome and TargetScan, were used to construct a ceRNA regulatory network mediated by circRNAs. GO and KEGG were applied to predict the function of ceRNA network; Subsequently, the online database String was used to explore the interaction relationship between molecules in ceRNA network; The molecules related to prognosis were screened by the univariate Cox regression and *Kaplan-Meier* analysis, and were used to construct a prognostic risk assessment model. A ROC curve was drawn with "time ROC" package to evaluate the effectiveness of the model.
Result 4 circRNAs were screened through two GEO data sets (GSE147985 and GSE92675) , namely hsa_circ_0102787, hsa_circ_0103114, hsa_circ_0102402 and hsa_circ_0104387. A ceRNA network was constructed which contains 4 circRNAs, 23 miRNAs and 86 mRNAs. Functional analysis showed that the network has tumor regulation potential, and there were closely interaction relationship between mRNAs in the network. Survival analysis found that 6 mRNAs (ABRACL, CDK1, MAP3K8, POU5F1, XAF1 and ZNF525) were related to prognosis of BC. Then, a prognostic risk assessment model was established accoriding to "the risk score=(-0.3569)*ABRACL+(-0.2644)*MAP3K8", *Kaplan Meier* analysis showed patients with high risks had a poor prognosis(*P*<0.001), the AUC of the five-years overall survival rate was 0.744.
Conclusion 4 circRNAs were screened in this study, then a ceRNAs network mediated by circRNAs was constructed. By further screened prognostic related molecules in this network, a prognostic model was established and evaluated, which provided theoretical support for the molecular mechanism research, diagnosis and prognosis evaluation of BC.

PU-0319

High concentrations of hypochlorous acid-based disinfectant in the environment reduced the load of SARS-CoV-2 in nucleic acid amplification testing

Xiuzhi Duan、Xuchu Wang、Yiyi Xie、Zhihua Tao
The Second Affiliated Hospital of Zhejiang University School of Medicine

During the severe acute respiratory syndrome coronavirus type 2 (SARS-CoV-2) pandemic, chlorine-containing disinfectants have been widely used in nucleic acid amplification testing laboratories. Whether the use of disinfectants affect the results of viral nucleic acid amplification is unknown. We examined the impact of different hypochlorous acid (HOCl) concentrations on the quantitative results of SARS-CoV-2 by reverse transcription polymerase chain reaction (RT-PCR). We also explored the mechanisms and models of action of chlorine-containing disinfectants that affected the detection of SARS-CoV-2. The results showed that different HOCl concentrations and different action times had an impact on the SARS-CoV-2 **Results** High concentrations of ambient HOCl have a greater impact than low concentrations, and this effect will increase with the extension of the action time and with the increase in ambient humidity. The impact of HOCl on

the detection of SARS-CoV-2 is more likely to be caused by the destruction of the primers and probes in the PCR system rather than the destruction of the enzymes or the extracted RNA required for RT-PCR. The false negative result still existed after changing the ambient disinfectant to ethanol but not peracetic acid. The use of hypochlorous acid in the environment will have an unpredictable impact on the nucleic acid test results of SARS-CoV-2. In order to reduce the possibility of false negative of SARS-CoV-2 nucleic acid test and prevent the spread of epidemic disease, environmental disinfectants should be used at the beginning and end of the experiment rather than during the experimental operation.

PU-0320

ARMS TaqMan real-time PCR for genotyping factor V Leiden mutation in Han Chinese

Pan Yu、Yibei Dai、Jiantao Dong、Zhihua Tao
The Second Affiliated Hospital of Zhejiang University School of Medicine

Factor V Leiden (FVLeiden) is a missense mutation of 1691 position (G1691A) in exon 10 of FV gene, and being a genetic risk for venous thrombosis. Currently, there are several PCR-based **Methods** for detecting FVLeiden mutation; however, these **Methods** have disad_x0002_vantages such as time-consuming, cumbersome steps and potentially hazardous gels. The aims of present study were to develop a simple, time-saving, accurate, and gel-free method, called amplification refractory mutation system (ARMS) TaqMan real-time PCR, for detect_x0002_ing FVLeiden mutation. We severally designed two specific reverse primers for mutant and wild-type through intentional introduction of mismatched nucleotide at the penultimate 3_x0002_ position. Although target amplicon amplification efficiency is reduced, but another cor_x0002_responding amplicon is almost completely inhibited. Then, specific TaqMan-probe was designed to detect target amplicon. Established method was used to detect 500 unselected samples in Han Chinese, the results showed 499 cases of wild-type and one heterozygote. Afterward, 50 randomly picked wild-type cases and one heterozygote were reexamined by bidirectional DNA sequencing, which is considered as “Gold standard method.” Exhilarat_x0002_ingly, the results detected by the two **Methods** were completely consistent. At last, allelic frequency of FVLeiden was calculated the in Han Chinese. Given the above results, A FVLeiden heterozygote has been found in 500 random samples in Han Chinese, and the allelic fre_x0002_quency was 0.1%. In conclusion, the ARMS TaqMan real-time PCR is an ideal detecting system for genotyping FVLeiden mutation in clinical application, and FVLeiden mutation ex_x0002_ists in Han Chinese despite extremely low prevalence

PU-0321

HDAC11 Regulates Glycolysis Through the LKB1/AMPK Signaling Pathway to Maintain Hepatocellular Carcinoma Stemness

Yidan Ren、Yunshan Wang
The Second Hospital of Shandong University

Hepatocellular carcinoma (HCC) contains a subset of cancer stem cells (CSC) that cause tumor recurrence, metastasis, and chemical resistance. Histone deacetylase 11 (HDAC11) mediates diverse immune functions and metabolism, yet little is known about its role in HCC CSCs. In this study, we report that HDAC11 is highly expressed in HCC and is closely related to disease prognosis. Depletion of HDAC11 in a conditional knockout mouse model reduced hepatocellular tumorigenesis and prolonged survival. Loss of HDAC11 increased transcription of

LKB1 by promoting histone acetylation in its promoter region, thereby activating the AMPK signaling pathway and inhibiting the glycolysis pathway, which in turn leads to the suppression of cancer stemness and HCC pro- gression. Furthermore, HDAC11 overexpression reduced HCC sensitivity to sorafenib. Collectively, these data propose HDAC11 as a new target for combination therapy in patients with kinase-resistant HCC.
Significance: This study finds that HDAC11 suppresses LKB1 expression in HCC to promote cancer stemness, progression, and sorafenib resistance, suggesting the potential of targeting HDAC11 to treat HCC and overcome kinase inhibitor resistance.

PU-0322

热灭活处理对艾滋病病毒(HIV)核酸检测的影响

张慧、刘子杰
昆明医科大学第一附属医院

目的 探讨热灭活处理对艾滋病病毒(HIV)核酸检测限的影响。
方法 将接近检测限的 HIV 血清样本，将样本稀释后进行 56℃水浴锅内灭活 30min，比较未灭活标本和灭活标本循环阈值（Ct值）及最低检测限，并进行统计学分析。
结果 在高浓度 Ct≤31 样本中未灭活和 56℃、30min 灭活处理基因扩增 Ct 值差异均无统计学意义（P＞0.05）；在中浓度 31＜Ct≤39 样本中未灭活和 56℃、30min 灭活处理基因扩增 Ct 值差异均无统计学意义（P＞0.05）； 在低浓度＞39 样本中未灭活和 56℃、30min 灭活处理基因扩增 Ct 值差异均无统计学意义（P＞0.05）。
结论 使用 56℃、30min 灭活处理和未灭活处理艾滋病病毒样本对核酸检测结果无明显影响，对 Ct 值较大标本无明显影响同时对该方法学的检测限无明显影响，实验室可以采用上述方式处理标本以保护实验人员安全。

PU-0323

Evaluation of the SureX HPV Genotyping Test for the Detection of High-Risk HPV in Cervical Cancer Screening

Baojun Wei、Shengkai Huang、Xueting Yu、Wei Cui
DNational Cancer Center/National Clinical Research Center for Cancer /Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China

Background The SureX HPV genotyping test (SureX HPV test), which targets the human papillomavirus (HPV) E6/E7 genes was compared with the Cobas 4800 and Venus HPV tests for detecting 14 high-risk HPV (HR-HPV) types in clinical referral and follow-up patients to evaluate its value for cervical cancer screening.
Methods Two different populations were enrolled in the study. The first population comprised 185 cases and was used for comparing the SureX HPV test (Health, China) with the Cobas 4800 test (Roche, USA). The second population comprised 290 cases and was used for comparing the SureX HPV test (Health, China) with the Venus HPV test (Zhijiang, China). Polymerase chain reaction (PCR) sequencing was performed for further confirmation of discordant **Results**
Results In the first population, the overall agreement rate was 95.3% for 14 High-Risk HPV types. Eight discordant cases were confirmed by PCR sequencing, which showed that the agreement rates were 75.0% between the SureX HPV test and PCR sequencing and 25.0% between the Cobas 4800 test and PCR sequencing (P<0.01). In the second population, the overall agreement rate was 94.5%. Thirteen discordant cases were confirmed by PCR sequencing, which showed

that the agreement rates were 76.9% between the SureX HPV test and PCR sequencing and 23.1% between the Venus HPV test and PCR sequencing (P<0.01). With cervical intraepithelial neoplasia grade 2+ (CIN2+) as the reference standard, the sensitivity values of the SureX HPV test and the Venus HPV test were 93.5% and 92.0%, (P>0.05), while the specificity values were 43.3% and 46.7%, respectively (P>0.05).
Conclusion The SureX HPV test had good consistency with both the Cobas 4800 and Venus HPV tests for 14 HR-HPV types. In addition, it avoided some false negatives and false positives. Therefore, the SureX HPV test can be used for cervical cancer screening.

PU-0324

Research progress of testis associated highly conserved oncogenic long non coding RNA (THOR) in tumors

wenjie pu
North SiChuan Medical College

Long non coding RNA is a class of RNA molecules with a length of more than 200 nt and lacking protein coding potential. At first, lncRNA was considered as a by-product transcribed by RNA polymerase II and had no biological function. With the development of transcriptome sequencing technology, large-scale lncRNAs have been identified. More and more evidence shows that lncRNA is involved in a variety of biological processes, including gene imprinting, genome rearrangement, chromatin modification, cell cycle regulation, transcription, splicing, mRNA degradation and translation. Abnormal expression of lncrna is associated with a variety of human diseases. Among them, testis associated highly conserved oncogenic long non coding RNA (THOR) is a very conserved non coding RNA, which is specifically expressed in testis and widely exists in a variety of human tumor tissues, such as liver cancer, gastric cancer,nasopharyngeal carcinoma, renal cell carcinoma, osteosarcoma, retinoblastoma, etc Melanoma, non-small cell lung cancer and tongue squamous cell carcinoma play an important role in their occurrence and development. This article reviews the biological function and mechanism of THOR in human cancer, in order to provide molecular basis for the potential evaluation of THOR as a target for early diagnosis and treatment of cancer.

PU-0325

Fluorescent quenching probes based SAA 1 genotyping with a fully automated system.

Jie Zhang、Yishuai Wang、Yan Zhang
DiaSys Diagnostic Systems (Shanghai) Co., Ltd.

Objective The aim of the present study is to develop and validate a reliable and simple application for genotyping serum amyloid A1 (SAA1).
Methods The specific nested PCR was performed to amplify a product of *SAA1* gene. Two quenching probes (QPs) were designed for detecting two single nucleotide polymorphism (SNP) sites, rs1136743(C/T) and rs1136747(C/T) respectively for *SAA1* genotypes. The specific nested PCR and QPs of *SAA1* genotying was introduced into a fully automated genotyping system (I-densy, ARKRAY, Inc.), which enables the genotyping of *SAA1* from whole blood.
Results Six genotypes of *SAA1* ($\alpha^{+/+}$, $\beta^{+/+}$, $\gamma^{+/+}$, αβ, αγ and βγ) could be determined by monitoring the fluorescence intensity of two QPs with melting temperature (TM) analysis. Total 121 clinical samples were *SAA1* genotyped in the fluorescent quenching probes based method with a fully automated I-densy system and were further sequence confirmed with a PCR direct sequencing approach.

Conclusion This fully automated system is a rapid and reliable strategy for the *SAA1* genotyping and for its future clinical application.

PU-0326

含整合酶抑制剂方案治疗云南省 HIV/AIDS 患者常规血液生化指标变化及不良反应分析

马莎、刘家法
云南省传染病医院

目的 研究接受含整合酶抑制剂（INSTIs）DTG 和 RAL 方案治疗 HIV-1 成年患者 48 周的血液和生化指标变化及不良反应情况。
方法 采用回顾性性研究的方法，以云南省传染病医院从 2008 年 1 月至 2019 年 1 月收治的使用含 INSTIs 方案治疗的 148 名 HIV/AIDS 患者为研究对象。按照不同抗病毒治疗方案分为使用含 DTG 方案组和 RAL 方案组，分析其在治疗前基线和治疗后 4 周、8 周、12 周、24 周和 48 周的血常规、血脂和肝肾功指标变化的差异；分析所有入组患者在 48 周内有记录的不良反应发生率。
结果 根据纳入和排除标准，共有 148 例患者符合研究条件，其中使用 RAL 方案有 91 例，使用 DTG 方案有 57 例。48 周 ART 过程中检测到在血液常规、血脂血糖和肝肾功能方面两种方案具有相似的疗效。血液指标方面在 ART 治疗 48 周的 PLT、HGB、RBC、MCV 和 RDW 水平随时间的变化趋势差异无统计学意义（P>0.05），但除 PLT 外，HGB、RBC、MCV 和 RDW 在 5 个随访点与基线比较差异均有统计学意义（P<0.05）；两方案治疗后各指标均数变化比较：与 RAL 组相比，DTG 组的各指标升高更明显。在血脂指标方面，在 ART 治疗 48 周内 TG、TC 和 LDL-C 随时间变化趋势的差异无统计学意义（P>0.05），HDL-C 水平随时间变化趋势两种不同治疗方案差异有统计学意义（F=5.108,P=0.002），在 5 个随访点变化与基线的差异有统计学意义（F=3.612,P=0.014），两方案治疗后均未发现血脂异常。肝脏功能主要指标 ALT、AST 和 TBIL 水平在治疗后 DTG 方案和 RAL 方案间随时间变化趋势及各指标不同随访点变化与基线比较差异都无统计学意义（P>0.05）；肾肝脏功能主要指标 Scr 和 UREA 水平随时间变化趋势差异无统计学意义（P>0.05），UA 随时间变化趋势差异有统计学意义（P<0.05）,各指标在不同随访点变化与基线比较差异无统计学意义（P>0.05）。常见的不良反应是中枢神经系统症状，DTG 组占 14%，RAL 组占 13%；其次是胃肠道不良反应，DTG 组占 11%，RAL 组占 12%。
结论 含 INSTIs 方案治疗 HIV/AIDS 在主要血液和生化指标有变化但均未发现明显异常，DTG 方案和 RAL 方案对 HIV 患者抗病毒治疗 48 周内各系统的变化相似。DTG 方案与 RAL 方案在使用 48 周内出现的不良反应没有明显差异，具有相似的安全性且两种方案发生的不良反应事件级别相似。

PU-0327

某地区中医医院 3025 例女性 HPV 感染情况分析

袁星竹
安岳县中医医院

目的 分析安岳县中医医院就诊的患者（含门诊、住院、体检病人）HPV 感染情况，包括感染人群比例，HPV 各亚型的分布及各年龄组分布特点，为安岳地区宫颈癌的预防和治疗提供科学参考依据。
方法 采用实时荧光 PCR 方法对 2018 年 1 月至 2021 年 5 月来我院就诊的 3025 例女性患者宫颈脱落细胞进行 HPV 分型检测。
结果 3025 例采集样本共检测出 21 种 HPV 亚型，其中 HPV 高危型 18 种（16 18 31 33 35 39 45 51 52 53 56 58 59 66 68 26 82 73），HPV 低危型 3 种(6 11 81)。3025 例采集样本中，检出 HPV

阳性样本 431 例，阳性率为 14.25%，阳性样本以单一感染，高危亚型为主。双重以上感染病人 95 人，占阳性患者 22.04%。2018 年 1 月至 2021 年 5 月 3025 例样本感染阳性率排名前三位的 HPV 亚型分别为 2018 年 52 58 51；2019 年 52 53 16；2020 年 52 58 81；样本中阳性率较高的亚型为 52 16 58，均为高危型。低危型阳性率较高的为 81 6 11。将患者按年龄分组分别 HPV 感染率为 20 岁以下(0.36%)，20-30 岁(1.95%)，30-40 岁(4.07%)，40-50 岁(4.96%)，50-60 岁(1.92%)，60 岁以上(0.99%)6 个组，进行 HPV 亚型差别统计，结果具有统计学意义。

结论 安岳地区 HPV 感染以单纯感染，高危型感染为主，女性高危型感染率明显高于低危型感染率，感染高发年龄段为 30-50 岁女性。建议加强对适龄女性定期检测 HPV 和注射 HPV 疫苗的宣传，从而做到相关疾病的早预防，早发现，早诊断，早治疗，可促进未来宫颈癌的全面防止进程。

PU-0328

2011～2020 年云南省≥50 岁 HIV/AIDS 病例 ART 失败基因型耐药研究

刘家法
云南省传染病医院

目的 本研究旨在对 2011～2020 年间云南省≥50 岁抗病毒治疗失败的 HIV/AIDS 患者进行耐药情况分析，为该人群耐药的预防和治疗提供一定参考依据。

方法 收集云南省 2011 年 1 月～2020 年 12 月期间≥50 岁抗病毒治疗失败患者的人口学信息及耐药检测结果进行综合分析。

结果 本次研究共收集到云南省 2011～2020 年间符合筛选标准的≥50 岁 HIV/AIDS 治疗失败病例 2227 例，累计治疗失败率为 7.88%，其中男性占比较大，为 68.88%；年龄中收集到最多为 50～<60 岁组，占 51.37%；传播途径主要以性接触传播为主，占 85.41%；地区上以红河州为主，占 14.14%；该人群抗病毒治疗失败的耐药率为 57.64%。 对该人群进行耐药与非耐药的特征分析发现，年龄、地区、基因亚型、治疗方案、治疗时长以及病毒载量的分布均存在差异（P<0.05），其中年龄段以 50～<60 岁的病例耐药率相对较高，为 59.26%；地区以临沧市耐药率相对较高，达到 73.08%；基因亚型主要以 CRF01_AE 耐药率相对较高，为 69.05%。治疗方案中以一线治疗方案 TDF+3TC+NVP 的耐药为主，为 72.50%。 基因亚型以 CRF08_BC 为主，占 53.78%，且各年间的主要流行亚型均为 CRF08_BC，URFs 有逐年上升的趋势，特别是云南省的边境地区。

结论 2011～2020 年云南省≥50 岁 HIV/AIDS 入组患者人数占比呈现逐年上升趋势，该人群的累计耐药率较全年龄段人群高，并且呈现一定的上升趋势，应加强对该人群的管理，加强耐药监测，防止多重耐药的发生。该人群 URFs 的分布占比较高，且有逐年增加的趋势，应进一步开展监测，分析其流行病学意义。

PU-0329

胃癌外泌体来源非编码 RNA- X26nt 促进肿瘤血管生成的机制研究及其作为胃癌早筛血清标志物的应用

杨俊瑶[1]、曾亮[3]、沈立松[2]
1. 上海交通大学医学院附属新华医院检验科
2. 上海交通大学医学院附属新华医院检验科
3. 清华大学

目的 胃癌早期无明显特异症状，容易漏诊，有效的血清标志物能提升早期胃癌的检出率，对胃癌的临床治疗具有重要意义。血管生成通过提供氧气和营养物质与肿瘤发生、侵袭和转移密切相关。最近，越来越多的证据表明，含有蛋白质、编码和非编码 RNA (ncRNA) 的癌症衍生外泌体在癌症中具有促血管生成功能。 肌醇需求酶 1 α 诱导的 XBP1 剪接过程中产生 26nt 长度的非编码 RNA——X26nt，在胃癌患者血清和组织中高表达。本研究探索 X26nt 作为胃癌血清标志物的潜力及其在胃癌发展过程中的作用。

方法和结果 首先，我用排阻超滤法提取胃癌（200 例）患者血清外泌体，通过巢式 QPCR 方法检测 X26nt 的表达，发现 X26nt 在胃癌患者血清中表达增高，且早期增高幅度最大，对比传统胃癌标志物，我们发现 X26nt 的敏感性更高。接着，通过探针原位杂交方法，分别检测胃癌组织中剪切型 XBP1 和 X26nt 表达，结果显示 X26nt 在胃癌组织和中的表达水平显着高于邻近组织。其次，我们通过荧光标签，验证了 X26nt 可以通过胃癌细胞外泌体递送到人脐静脉内皮细胞（HUVECs）中，功能实验证明 X26nt 促进 HUVECs 的增殖、迁移和小管形成。此外，我们通过荧光素酶报告基因检测 X26nt 通过直接结合 HUVEC 中 VE-钙粘蛋白 mRNA 的 3'UTR 降低 VE-钙粘蛋白，从而增加血管通透性。最后，通过体内实验， 我们进一步证明 X26nt 在小鼠皮下移植瘤模型中加速肿瘤生长和血管生成。

结论 我们的研究首次揭示 XBP1 来源的非编码 RNA 在胃癌中稳定存在，并通过外泌体分泌，通过促进肿瘤血管生成影响肿瘤的进展，具有很高的胃癌血清标志物应用前景。

PU-0330

Synthesis and Identification of a Novel Visual Peptide Ac-SDK (Biotin) P to Anti-Fibrosis in Rats Silicosis

Jin Wang、Qian Gong
Qingpu Branch of Zhongshan Hospital, Fudan University

Background N-Acetyl-seryl-aspartyl-lysyl-proline (Ac-SDKP) is a short peptide with an anti-silicosis effect. However, the short biological half-life and low plasma concentration of Ac-SDKP hampers discovery of specific targets in organisms and reduces the anti-silicosis effect. A novel peptide, Ac-SDK (Biotin) Proline, termed "Ac-B", with anti-fibrotic properties was synthesized.
Methods Ac-B was detected quantitatively by high-performance liquid chromatography. Phagocytosis of Ac-B by the alveolar epithelial cell line A549 was investigated by confocal laser scanning microscopy and flow cytometry. To further elucidate the cellular-uptake mechanism of Ac-B, chemical inhibitors of specific uptake pathways were used. After stimulation with transforming growth factor-β1, the effects of Ac-B on expression of the myofibroblast marker vimentin and accumulation of collagen type I in A549 cells were analyzed by western blotting. Sirius Red staining and immunohistochemical analyses of the effect of Ac-B on expression of α- smooth muscle actin (SMA) in a rat model of silicosis were undertaken.
Results Ac-B had good traceability during the uptake, entry, and distribution in cells. Ac-B treatment prevented an increase in α-SMA expression in vivo and in vitro, and was superior to

that of Ac-SDKP. Caveolae-mediated uptake of Ac-B by A549 cells led to achieving anti-epithelial–mesenchymal transformation (EMT) effects.
Conclusion Ac-B had an anti-fibrotic effect, and could be a promising agent for the fibrosis observed in silicosis in the future.

PU-0331

血小板膜糖蛋白 GPⅠa（G873A、C807T）在心脑血管疾病及糖尿病患者中基因型分布的调查

焦瑞宝、陈继中
安徽省铜陵市人民医院

目的 调查血小板膜糖蛋白 GPⅠa（G873A、C807T）在心脑血管疾病及糖尿病患者的基因型分布状况。
方法 回顾性收集 2018 年 9 月至 2019 年 9 月在铜陵市人民医院住院、出院主诊断或主要此诊断为心血管疾病、脑血管疾病和糖尿病患者 278 例临床治疗资料，其中心血管疾病组为 58 例，脑血管疾病组为 158 例，糖尿病组为 62 例，采用焦磷酸测序法测定 GPⅠa（G873A）、（C807T）的基因多态性。
结果 两者的野生型、杂合突变型和纯合突变型均同步出现同一个病例，两者三个基因型在三个疾病组中分布及等位基因分布比较，差异均没有统计学意义（c2 =5.203、0.839，P＞0.05），符合 Hardy-Weinberg 遗传平衡，结果见表 2 和表 3。但是 GPIa（G873A）野生型（GG 和 GPIa（C807T）野生型（CC）均不大于 50.00%，而 GPIa（G873A）杂合突变型（GA）和纯合突变型（AA）之和、GPIa（C807T）杂合突变型（CT）和纯合突变型（TT）之和均不小于 50.00%，且等位基因 A 型和 T 型均位于 25%~34%之间。
结论 阿司匹林药效相关基因位点 GPⅠa(G873A、C807T)在人群中存在突变现象较为常见，但基因突变存在个体间差异，不存在群体间差异。

PU-0332

Prostatic aspirated cellular RNA analysis enables fast diagnosis and staging of prostate cancer

Yiwen Sang、Xuchu Wang、Pan Y、Zhihua Tao
The Second Affiliated Hospital of Zhejiang University School of Medicine

Objective The aim of this study is to investigate the potential application of prostatic aspirated cellular RNA analysis technique for fast diagnosing and staging prostate cancer.
Methods Prostatic aspirated cells were obtained immediately after transrectal ultrasound (TRUS)-guided nee_x0002_dle biopsy. Cellular RNA such as glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, prostate specific antigen (PSA) mRNA and prostate-specific RNA (PCA3) mRNA were analyzed by using Reverse Transcription_x0002_Polymerase Chain Reaction (RT-PCR). PCA3 score was calculated as the ratio of PCA3 mRNA to PSA mRNA ex_x0002_pression. Diagnostic performance of the fast-aspirated cellular RNA analysis technique for determining prostate cancer and metastatic status were evaluated by developing receiver operating characteristic curves (ROC), and the correlation between aspirated cellular RNA mRNA expressions and risk grouping was calculated, to investigate the underlying potential for PCa staging.

Results PCA3 score was significantly higher in prostatic aspirated cells obtained from cancerous tissues than noncancerous tissues. The median aspirated cellular PCA3 score was higher in patients with PCa compared to BPH, and presenting an area under the ROC curve (AUC) of 0.87 (95%CI: 0.79–0.94) for PCa diagnosis. Mul_x0002_tivariate regression analysis revealed that baseline median aspirated cellular PCA3 score (OR=9.316, 95%CI: 1.045–83.033, P<0.05) was an independent predictive factor for metastatic status in PCa patients.
Conclusion The ease of use and minimal complexity of fast prostatic aspirated cellular RNA analysis may be a valuable diagnostic technique, providing urgent diagnostic information for accurate PCa diagnosing and staging.

PU-0333

苏州地区女性 HPV 感染状况及 HPV 亚型分布情况研究

韩秀
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 分析苏州地区女性 HPV（human papillomavirus，人乳头瘤病毒）感染情况和 HPV 亚型分布情况，为苏州地区女性宫颈癌防治提供科学依据。
方法 选取 2020 年 1 月至 2021 年 5 月于苏州市独墅湖医院妇科就诊及体检的 769 例妇女，采用江苏硕世生物科技股份有限公司的人乳头瘤病毒核酸分型检测试剂盒（荧光 PCR 法）检测 HPV 分型，分析该地区女性 HPV 感染率、感染亚型分布及年患者年龄分布的特点。
结果 769 例检测者中，HPV 阳性者有 122 例，HPV 感染率为 15.86%(122/769)，其中单一感染 88 例，二重感染 23 例，多重感染 11 例，分别占 11.44%、2.99%、1.43%。高危 HPV 亚型分布前 5 位为 HPV52、HPV58、HPV16、HPV39、HPV31，感染率分别为 3.15%、2.23%、2.23%、1.58%、1.31%。低危 HPV 亚型感染率最高为 HPV81，感染率为 1.97%。分析患者年龄分布情况，结果显示感染阳性者主要集中在 25-35 和 35-45 岁，感染率分别为 0.98% 和 25.41%。
结论 苏州地区 HPV 感染主要为单亚型感染，主要为 HPV52 和 58 亚型，16、39 和 31 次之。HPV 感染分布与年龄有关。HPV 分型检测结果可以为该地区女性宫颈癌的诊断和治疗提供参考。

PU-0334

A review of the Paris system for reporting urinary cytology

Wanru Ma
Affiliated Hospital of Xuzhou Medical University

In recent years, the global incidence of urothelial tumors has increased, and the clinical prognosis is poor. Early detection, screening and diagnosis are particularly important for the prognosis of urothelial tumors. Common detection **Methods** are ureteroscopy, computer tomography(CT) and urinary tract cytology. Before that, the diagnostic criteria we used were usually divided into 5 categories: 1) negative; 2) atypical urothelial cells favoring a reactive process (AR); 3) atypical urothelial cells unclear if reactive or neoplastic process (AU); 4) suspicious for HGUC; and 5) positive for HGUC. This classification scheme lacks specificity and direction. Diagnostic categories for The Paris System for Reporting Urinary Cytology were usually divided into 7 categories:1) Nondiagnostic/unsatisfactory; 2) Negative for high-grade urothelial carcinoma (NHGUC); 3)Atypical urothelial cells (AUC); 4) Suspicious for high-grade urothelial carcinoma (SHGUC); 5) High-grade urothelial carcinoma (HGUC); 6)Low-grade urothelial neoplasm (LGUN); 7) Other: primary and secondary malignancies and miscellaneous lesions. This new reporting system focused on diagnosis of the detection of HGUC and minimized the detection of Low-grade urothelial carcinoma (LGUC), since cytology has a high sensitivity of detecting the HGUC with a poor sensitivity for the LGUC.

PU-0335

来源于肝癌细胞的外泌体 miRNA-622 缺失促进脂肪细胞的脂解

沈钰涛、邓萱
复旦大学附属华山医院

我们发现了肝癌患者血浆中 miR-622 的表达水平与患者的脂肪质量指数呈正相关。本文阐明了 miR-622 在癌变过程当中对脂肪细胞代谢产生的影响。

方法 我们运用 qRT-PCR 检测了脂肪质量指数不同的肝癌患者的血浆，用比色法测定了脂肪细胞培养基中（分别与人肝细胞和肝癌细胞共培养）甘油和游离脂肪酸的含量。我们将外泌体从肝癌患者的血浆和肝癌细胞培养基中分离出来，用 qRT-PCR 检测了其中 miR-622 的表达水平，再用 DiI 标记外泌体与脂肪细胞共培养，测定培养基中的甘油和游离脂肪酸含量，用分子生物学方法研究了 miR-622 的功能机制及其对脂肪细胞代谢的影响。

结果 miR-622 的表达水平与肝癌患者的脂肪质量指数成正比。miR-622 在肝癌细胞及其释放的外泌体中表达下调。与人肝细胞相比，miR-622 表达降低的肝癌细胞可促进脂肪细胞的脂解，而过表达 miR-622 可逆转脂解表型。体外实验证明，从人肝细胞和肝癌细胞中分离出的外泌体可被脂肪细胞吸收内化，而 miR-622 表达含量较低的肝癌细胞外泌体可促进脂肪细胞的脂解。

结论 本研究首次讨论了来源于肝癌细胞外泌体的 miR-622 在体外模型中对脂解代谢的影响。结果表明，来源于肝癌细胞外泌体的 miR-622 可被脂肪细胞吸收并抑制脂肪细胞的脂解。因此，外泌体 miR-622 可作为一种潜在的治疗方案，以减轻与癌症相关的脂解代谢增加并抑制肝癌的进展。

PU-0336

荧光原位杂交技术在骨髓增生异常综合征中的应用

刘燕
吉林金域医学检验所有限公司

目的 骨髓增生异常综合征（MDS）是关于造血干细胞恶性克隆的一种疾病，目前，细胞形态学是诊断骨髓增生异常综合征的主要方法之一，但其与再障性贫血等区分困难。荧光原位杂交(FISH)是一种利用荧光标记的特异性核酸探针与细胞 DNA 结合，检测染色体畸变的方法，可以应用于 MDS 患者中。

方法 1、荧光探针：用于检测 5、7、20、8 和 Y 染色体异常，包括：EGR1/D5S23，D5S721（5q31，5p15.2）；D7S486/CEP7（7q31）；D20S108，MYBL2（20q12，20q13.12）；CEP8；CEPY 四种探针。

2、取全血/骨髓样本 2ml 离心，0.075M KCL 低渗液低渗、吹打、水浴，使红细胞吸水胀破，白细胞胀大，加固定液，冰醋酸：甲醇=1：3 进行固定，调悬液-滴片。镜检：待玻片晾干后 10X 物镜镜检，原则细胞分散，但不重叠。将镜检后的玻片放置晾片板上，56℃烤片 1h。2X SSC 洗涤、梯度酒精脱水，加探针过夜杂交。杂交后用 0.4%NP40 洗涤未结合的探针，然后加 4’，6-二脒基-2-苯基吲哚对细胞核进行复染，最后在荧光显微镜下计数 200 个间期细胞。

结果 5q:红色荧光标记 EGR1(5q31)探针，绿色荧光标记 D5S23，D5S721(5p15.2)探针，正常信号模式为 2G2R(注:G 为绿色信号，R 为红色信号)。

7q:红色荧光标记 D7S486(7q31)探针，绿色荧光标记 CEP7 探针，正常信号模式为 2G2R(注:G 为绿色信号，R 为红色信号)。

20q:红色荧光标记 D20S108(20q12)探针，绿色荧光标记 20q13.12(MYBL2)，正常信号模式为 2G2R(注:G 为绿色信号，R 为红色信号)。

+8:红色荧光标记 CEP8 探针，正常信号模式为 2R(注:R 为红色信号)。

-Y:红色荧光标记 CEPY 探针，正常信号模式为 1R(注:R 为红色信号)。

结论 5q-异常可见于骨髓增生异常综合征及多种恶性疾病如:真性红细胞增多症、急性髓细胞白血病等，这些疾病中 5q-存在标志预后差。
-7/7q-遗传学异常主要在 MDS 中，发生率约为 28%。-7/7q-患者 72％会转为急性白血病，预后较差。
20q-是髓系疾病中常见的再现性异常，见于 4%～5%的 MDS 和 1%～2%的 AML。
CEP8 在 CML、AML、骨髓增生障碍(MPD)、骨髓增生异常综合症(MDS)及其它非特异性造血系统疾病中 8 号三体遗传畸变的发生非常普遍。
Y 染色体缺失约在 5%的 MDS 患者中检测到，孤立的-Y 需结合形态学结果确诊 MDS，部分伴有单纯-Y 的患者免疫抑制治疗有效。

PU-0337

北京地区健康女性人乳头瘤病毒流行及基因型分布

于浩、吴洁
中国医学科学院北京协和医院

目的 人乳头瘤病毒 (HPV) 感染，尤其是高危 HPV (HR-HPV) 基因型感染与宫颈癌的发生密切相关。本研究旨在观察中国北京地区健康女性 HPV 感染的流行病学特征。
方法 收集 2016-2019 年在北京协和医院接受健康查体的 29436 名健康女性的宫颈拭子标本，使用商品化试剂盒检测 15 个 HR-HPV 和 2 个低危 HPV 基因型，分析 HPV 阳性率及基因型分布情况。
结果 共有 3586（12.18%）名参与者检测出 HPV 阳性，其中 3467 人感染了 HR-HPV。最常见检出的基因型是 HPV52、58、16、51 和 56。此外，虽然单一基因型的感染 (9.84%) 更为普遍，但在感染多种 HPV 分型的人群中，HPV16+52 是最常见的组合。此外，在不同年龄组中<25 岁的女性（20.92%）HPV 感染率最高。2016-2019 年期间不同年份 HPV 的流行率无显着差异。除郑州外，北京地区的 HPV 发病率与中国其他地区均存在显著差异（$p < 0.05$）。
结论 我们的研究结果为更好地了解北京地区 HPV 感染的流行病学特征提供潜在的参考。

PU-0338

叶酸代谢能力基因检测不同检测系统比对

李文妮
西安金域医学检验所有限公司

目的 分析两种叶酸代谢能力基因检测试剂对结果的影响，以评估其检测结果的一致性。
方法 检测试剂：苏州旷远人 MTHFR&MTRR 基因多态性检测试剂盒（荧光 PCR 法）和西安金磁 MTHFR C677T、 MTHFR A1298C、MTRR A66G 基因检测试剂盒（PCR－金磁微粒层析法）。检测**方法** 取 5 例临床样本，分别使用两种检测系统提取扩增，对比 MTHFR C677T、MTHFR A1298C、MTRR A66G 基因多态性检测结果。
结果 符合率：苏州旷远与西安金磁叶酸代谢能力基因检测试剂 MTHFR C677T、MTHFR A1298C、MTRR A66G，3 种基因位点结果比对均通过，比对结果符合率为 100%，符合比对标准，可用于临床叶酸代谢能力基因项目检测。
结论 孕妇体内若缺乏叶酸，可造成高同型半胱氨酸血症、胎儿神经管畸形。通过叶酸代谢能力基因检测，可以科学合理的补充叶酸，降低新生儿出生缺陷的风险。上述两种试剂盒均可为高同型半胱氨酸水平或叶酸代谢异常的患者提供辅助诊断及临床用药提供有效的参考。

PU-0339

NIPT、CMA、高分辨染色体核型制备与分析技术在珠海市产前诊断中的联合应用

赵理平
广东省珠海市妇幼保健院

目的 评估无创产前检测（non-invasive prenatal testing，NIPT)、染色体微阵列分析（chromosomal microarray analysis,CMA）、高分辨染色体核型制备与分析技术在珠海市产前诊断中联合应用的临床价值。
方法 对 26882 例符合 NIPT 筛查指征孕妇进行 NIPT 检测，对其中 205 例 NIPT 高风险孕妇进行羊水高分辨染色体核型分析及 CMA 检测。
结果 205 例 NIPT 高风险确诊 124 例，总阳性预测值 60.5% ；高分辨核型分析检出传统技术易漏诊的 3～5Mb 左右结构异常 5 例；CMA 检出正常核型结果中致病或可能致病性微缺失/微重复 3 例，单亲二体（uniparental disomy UPD）2 例，明确不确定染色体结构 1 例，因方法学局限性未检测出核型分析中 4 例倒位、5 例易位、7 例低比例嵌合体。
结论 高分辨染色体核型制备与分析技术较传统技术能有效提高产前诊断中染色体病的检出率。NIPT、CMA、高分辨染色体核型分析三种技术具有互补性，在产前诊断中联合应用可以有效提高胎儿染色体病检出率，减少出生缺陷。

PU-0340

阳泉地区汉族育龄女性亚甲基四氢叶酸还原酶基因多态性分析

赵俊琴、郑礼瑶
阳泉市第一人民医院

目的 调查阳泉地区汉族育龄女性亚甲基四氢叶酸还原酶基因多态性分布情况，为临床医师指导育龄女性合理增补叶酸提供科学依据。
方法 以 2018 年 1 月至 2020 年 8 月在阳泉市第一人民医院进行孕前或孕期检查的汉族女性 1892 例为研究对象，采集血液应用荧光定量 PCR 法检测 MTHFR C677T 位点的基因型，统计分析基因多态性的分布特征，并与文献已经报道的其他地区基因型频率/等位基因频率的分布情况进行统计学比较。
结果 阳泉地区汉族育龄妇女 MTHFR C677T 基因多态性检验结果符合 Hardy-Weinberg 遗传平衡，MTHFR 基因 C677T 位点以纯合突变型(TT)为优势基因型，占 50.2%；野生型(cc)占 18.0%；杂合突变型(TT)占 31.8%。不同年龄组育龄女性的 MTHFR C677T 的等位基因和基因型分布频率差异无统计学意义(P<0.05)。阳泉市育龄女性的 MTHFR C677T 等位基因和基因型分布情况同其他地区相比较，差异有统计学意义(P<0.05)。阳泉地区汉族育龄女性 MTHFR C677T 的基因型与中国七大地理分区比较来看，阳泉市的优势基因型为 TT 型，华南地区优势基因型为 CC 型，其余六大分区（华北、华东、华中、东北、西北、西南）优势基因型均为 CT 型，经比较阳泉市与七大地理分区的差异均具有统计学意义（P<0.05）。
结论 阳泉地区汉族育龄女性的 MTHFR C677T 基因多态性分布具有明显的地域性特征，推荐根据叶酸代谢基因多态性检测结果指导育龄女性合理增补叶酸剂量，预防出生缺陷。

PU-0341

Distributive characteristics of the CYP2C9 and AGTR1 genetic polymorphisms in Han Chinese hypertensive patients: a retrospective study

Keping Chen
Zhongda Hospital, School of Medicine, Southeast University

Background There is an individual variation in response to antihypertensive effect of the angiotensin II receptor antagonist. This study aimed to determine the allele and genotype frequencies of CYP2C9 and AGTR1 genetic polymorphisms and explore the potential role of these polymorphisms in guiding the selection of angiotensinⅡreceptor antagonist in Han Chinese hypertensive patients.
Methods Totally 2419 Han Chinese hypertensive patients and 126 normotensive controls were recruited in this study. Venous blood samples were collected from each patient, and the genetic polymorphisms of CYP2C9 and AGTR1 were assessed using a gene chip platform. The allele and genotype frequency of each gene and the combined genotypes in this study were analyzed respectively.
Results The gene chip analysis identified an allelic frequency of 96.51% for CYP2C9*1 and 3.49% for CYP2C9*3 in the cohort of Han Chinese hypertensive patients. Statistical analysis showed that the frequency of wild-type homozygous for CYP2C9*1/*1 was 93.30%, while the frequency of heterozygous for *1/*3 or mutant homozygous for *3/*3 was 6.41% or 0.29%. Meanwhile, we detected allelic frequencies of 95.06% and 4.94% for the A and C allele of AGTR1, respectively. While the genotype frequency of wild-type homozygous for AA was 90.41%, the frequency of heterozygous for AC or mutant homozygous for CC was 9.30% or 0.29%. Notably, we observed that 84.66% (2048/2419) of the subjects exhibited a combined genotype of CYP2C9 and AGTR1 as *1/*1 + AA, while the combined genotypes *3/*3 + AC or *3/*3 + CC were not detected in hypertension patients. Besides, no significant association was found between normotensive controls and hypertensive patients, or among the three grades of hypertensive patients.
Conclusions These data revealed the polymorphisms characteristics of CYP2C9 and AGTR1 in Han Chinese hypertensive patients, providing valuable information for genotype-based antihypertension therapy in prospective clinical studies in the future.

PU-0342

Analysis of ceRNA networks and identification of potential drug targets for drug-resistant leukemia cell K562/ADR

Yanyan Wang[1,2]、Zhaoping Liu[1,2]、Zhenru Xu[3]、Shunling Yuan[2]、Yanglin Ou[2]、Zeyu Luo[2]、Feng Wen[2]、Jing Liu[4]、Ji Zhang[1,2]
1. Shenzhen Traditional Chinese Medicine Hospital
2. 南华大学附属第一医院
3. 海南医学院第二附属医院
4. 中南大学

Motivation Drug resistance is the main obstacle in the treatment of leukemia. As a member of the competitive endogenous RNA (ceRNA) mechanism, underlying roles of lncRNA are rarely reported in drug-resistant leukemia cells.
Methods The gene expression profiles of lncRNAs and mRNAs in doxorubicin-resistant K562/ADR and sensitive K562 cells were established by RNA sequencing (RNA-seq). Expression of differentially expressed lncRNAs (DElncRNAs) and DEmRNAs was validated by qRT-PCR. The potential biological functions of DElncRNAs targets were identified by GO and KEGG

pathway enrichment analyses, and the lncRNA-miRNA-mRNA ceRNA network was further constructed. K562/ADR cells were transfected with CCDC26 and LINC01515 siRNAs to detect the mRNA levels of GLRX5 and DICER1, respectively. The cell survival rate after transfection was detected by CCK-8 assay.
Results The ceRNA network was composed of 409 lncRNA-miRNA pairs and 306 miRNA-mRNA pairs based on 67 DElncRNAs, 58 DEmiRNAs and 192 DEmRNAs. Knockdown of CCDC26 and LINC01515 increased the sensitivity of K562/ADR cells to doxorubicin and significantly reduced the half-maximal inhibitory concentration (IC50) of doxorubicin. Furthermore, knockdown of GLRX5 and DICER1 increased the sensitivity of K562/ADR cells to doxorubicin and significantly reduced the IC50 of doxorubicin.
Conclusions The ceRNA regulatory networks may play important roles in drug resistance of leukemia cells. CCDC26/miR-140-5p/GLRX5 and LINC01515/miR-425-5p/DICER1 may be potential targets for drug resistance in K562/ADR cells. This study provides a promising strategy to overcome drug resistance and deepens the understanding of the ceRNA regulatory mechanism related to drug resistance in CML cells.

PU-0343

The potential mechanism of PPP2R3A in rat myocardial cells and its interacting proteins

Chunyan Wu [1]、Yuan Liang[2]、Xiaohua Cui[1]、 Liju Ma[1]
1. The first affiliated hospital of kunming medical university
2. 昆明医科大学第一附属医院医学检验科

Background PPP2R3A plays a key role in the cardiac pathological and physiological processes, yet little is known about how the protein involved in normal myocardium formation and the protein-protein interaction pathways involved. To address this, we investigate the role of PPP2R3A in cardiac myocytes and identify PPP2R3A specific protein interaction partners to accelerate the developmental process of the mechanistic studies.
Methods PPP2R3A-silenced primary myocardial cell of neonatal rats and H9c2 cells were established by infecting shRNA lentiviral particles. RT-PCR and western blot were used to determine the expression of PPP2R3A and silencing efficiency. The cell viability was analyzed by CCK-8 kit, then the cell cycles and apoptosis assays were detected by flow cytometry. Novel protein-protein interactions of PPP2R3A were detected by Yeast Two-Hybrid assays using a high quality human primary cardiomyocyte cDNA library.
Results PPP2R3A-silencing rat primary cardiomyocytes and H9c2 cells were established successfully, and the expression of PPP2R3A was downregulated significantly as confirmed by RT-PCR and Western blot. PPP2R3A silencing can inhibit the myocardial cell proliferation, arrest the cell cycle in the S phase and promote the cardiomyocytes apoptosis. 19 potential candidates like COL1A2, GIPC1and BCL6 specifically interact with PPP2R3A, and COL1A2 was the highest screening frequency, covering 12.5% of the 24 clones. These partner are highly enriched in signaling pathways associated with a variety of cellular processes.
Conclusions A series of studies have discovered that PPP2R3A was closely associated with the heart failure and arrhythmia. Our data further confirmed PPP2R3A plays an important role in the cardiomyocytes and PPP2R3A in the regulation of cardiac events via its interaction partners.

PU-0344

采用自上而下的方法评定 HBV-DNA 的测量不确定度

冷丽
曲靖市第二人民医院

目的 对 HBV-DNA 测量不确定度的评估并确保不确定度评定的可靠性和科学性。
方法 采用“自上而下”的方法利用实验室数据从偏倚和复现性两方面来评定 HBV-DNA 测量不确定度。
结果 方法一：HBV-DNA(对数值)低浓度和高浓度合成标准不确定度分别为 0.21、0.22， 相对合成标准不确定度分别为 6.45%、3.82%。扩展不确定度分别为 0.42、0.44，相对扩展不确定度（k=2）分别为 12.9%，7.64%。方法二：室间质量评价数据引入的相对合成标准测量不确定度为 5.58%(k = 2)。相对扩展不确定度为 11.16%(k = 2)。
结论 医学实验室有必要对乙肝 DNA 的测量不确定度进行评定。

PU-0345

Long non-coding RNA Twist1-AS promotes proliferation and migration of colorectal cancer

Feng Zhou
The Second Affiliated Hospital of Nantong University

Objective Increasing evidence has shown that lncRNA plays a critical role in cancer biology, and may serve as biomarkers and promising therapeutic agents for human cancers; however, the role of lncRNA Twist1-AS in colorectal cancer remains unknown until now. This study aimed to examine the contribution of lncRNA Twist1-AS to the biological behaviors of colorectal cancer.
Methods Twist1 and Twist-AS gene expression was quantified in HCT116, DLD-1, HT-29, LS174T, SW480 and SH-SY5Y cells and in colorectal cancer specimens and matched adjacent noncancerous specimens. Cell proliferation was measured with the CCK-8 assay, and cell migration and invasion were assessed using Transwell migration and invasion assays. The relative gene expression was quantified using qPCR assay, and the protein expression was determined using Western blotting assay.
Results qPCR assay detected higher Twist1-AS and Twist1 mRNA expression in HCT116, DLD-1, HT-29, LS174T and SW480 cells than in SH-SY5Y cells, and quantified higher Twist1-AS and Twist1 mRNA expression in colorectal cancer specimens than in adjacent noncancerous specimens ($P < 0.01$). Downregulation of Twist1-AS was found to suppress the proliferation and migration of SW480 cells, and overexpression of Twist1-AS was found to promote the proliferation and migration of HCT116 cells. In addition, Twist1-AS knockdown caused a significant reduction in Twist1 mRNA expression and upregulation of E-cadherin, Vimentin and Fibronectin mRNA in SW480 cells, while Twist1-AS overexpression resulted in elevated Twist1, Vimentin and Fibronectin protein expression and reduced E-cadherin expression.
Conclusion lncRNA Twist1-AS promotes colorectal cancer proliferation and migration via Twist1.

PU-0346

Has2 的缺失介导雌激素受体阳性乳腺癌获得性内分泌治疗抵抗

孙小丹、刘翳雯、何怡青、杜艳、张国良、高锋、杨翠霞
上海交通大学附属第六人民医院检验科

目的 探究雌激素受体阳性乳腺癌获得性内分泌治疗抵抗的发生机制，为内分泌治疗抵抗寻求新的治疗靶点。
方法 通过加入雌激素受体调节剂他莫昔芬(tamoxifen)和雌激素受体降解剂氟维司群(fulvestrant)处理雌激素受体阳性乳腺癌细胞株（MCF7 和 T47D）六个月，分别获得 tamoxifen 和 fulvestrant 耐药细胞株；采用蛋白印迹法和荧光定量 PCR 方法比较天然乳腺癌细胞和耐受细胞中透明质酸合成酶 2(Hyaluronan synthase 2，Has2)的表达水平的差异；通过慢病毒转染构建 Has2 敲降的稳转乳腺癌细胞株，借助增殖实验观察敲降 Has2 后的癌细胞对药物的反应性变化，使用蛋白印迹法检测增殖信号相关分子表达水平的变化；通过蛋白印迹法和免疫荧光实验观察敲降 Has2 对雌激素受体的表达、分布和活性的影响。
结果 我们发现 Has2 的缺失与雌激素受体阳性乳腺癌与 tamoxifen 和 fulvestrant 的耐药性有关；敲降 Has2 的天然细胞对药物的反应性亦下降；Has2 的缺失可能通过影响雌激素受体的表达和活性，进而通过影响雌激素受体相关的增殖相关信号通路诱导内分泌获得性耐药的发生发展。
结论 Has2 的获得性缺失导致内分泌治疗抵抗的发生，且 Has2 介导了雌激素受体阳性乳腺癌发生获得性内分泌治疗抵抗。这表明 Has2 的缺失可能在获得性内分泌治疗抵抗中发挥重要作用，本研究可能为解决获得性内分泌治疗抵抗提供了潜在靶点。

PU-0347

外泌体及肿瘤细胞内 miR-320b 促进食管鳞状细胞癌淋巴结转移的机制研究

刘童、王传新
山东大学第二医院

目的 明确 miR-320b 在肿瘤微环境不同细胞中的生物学功能及其参与调控的靶基因和下游相关信号转导通路，为探寻淋巴结转移治疗靶点提供可靠的理论支撑。
方法 qRT-PCR 检测两个独立样本队列共 366 例 ESCC 患者血清中外泌体 miR-320b 的表达水平并进行对比分析。通过成管实验及 Transwell 实验评估外泌体 miR-320b 对 HLECs 细胞成管能力和迁移能力的影响。小动物成像系统用于探讨荷载 miR-320b 的外泌体是否可以在体内水平促进 ESCC 的淋巴结转移。通过 CCK-8、EdU 以及 Transwell 等实验评估 miR-320b 对 ESCC 细胞系的恶性表型的影响。相关挽救实验明确 miR-320b 促进 ESCC 淋巴结转移的具体分子机制及相关信号通路。Co-IP 实验证明 DGCR8 与 METTL3 之间的相互作用；RIP 和 MeRIP 实验用于探究 METTL3 在 pri-miR-320b 成熟过程中的关键调控作用。
结果 将 LN- vs LN+组对比差异 miRNA 与 N1 期 vs N3 期组对比差异 miRNA 表达谱取交集，并经过两个独立样本队列验证发现，miR-320b 在 LN+患者血清外泌体中的表达水平显著高于 LN-患者。荷载 miR-320b 的外泌体与 HLECs 细胞共培养后，受体细胞中 miR-320b 表达水平显著升高，并且通过靶向 PDCD4 来促进 AKT 的磷酸化，以不依赖 VEGF-C 途径的方式促进 HLECs 细胞的成管能力和迁移能力；体内实验证明，荷载 miR-320b 的外泌体能够促进原位肿瘤组织中淋巴管的生成，使其密度显著增加，显著提高肿瘤细胞的淋巴结转移发生率。此外，高表达 miR-320b 能够显著提高 ESCC 肿瘤细胞的增殖、迁移侵袭能力以及 EMT 相关进程。ESCC 肿瘤细胞内 miR-320b 通过抑制 PDCD4 的表达促进 AKT 通路的激活，从而增强 ESCC 细胞的增殖和迁移侵袭能力。过表达 METTL3 能够促进 miR-320b 的加工过程，降低细胞内 pri-miR-320b 的表达水平，同时增高 pre-

miR-320b 和成熟 miR-320b 的表达水平。Co-IP 实验证明 DGCR8 能够与 METTL3 相互作用，RIP 和 MeRIP 实验证明，过表达 METTL3 能够促进 pri-miR-320b 与 DGCR8 结合以及 pri-miR-320b 的 m6A 甲基化修饰。
结论 血清外泌体 miR-320b 的表达水平在 ESCC 淋巴结转移发生时显著升高，并且与淋巴结转移数量呈正相关。外泌体 miR-320b 能够被 HLECs 摄取，促进淋巴管形成和肿瘤细胞的淋巴结转移，并且 ESCC 细胞中高表达 miR-320b 能够增强肿瘤细胞的增殖和迁移侵袭能力。

PU-0348

Molecular biology analysis of ABO blood group variants caused by natural chimerism

Yuqing Wang[1]、CHENGRUI QIAN[2]、HANG LEI[1]、WEI ZOU[1]、DONG XIANG[2]、XUEFENG WANG[1]、XIAOHONG CAI[1]
1. Ruijin Hospital, Shanghai Jiao Tong University School of Medicine
2. 上海市血液中心

Introduction Natural blood chimerism is an important cause of ABO phenotype discrepancies; however, is not easily diagnosed by routine laboratory testing. Here, a series of natural ABO chimera cases were analyzed by the comprehensive application of a variety of molecular biological **Methods**
Methods 15 suspected individuals (including 2 pedigrees) were tested by standard tube method or column agglutination method，and supplemented with RBC absorption-release test. The ABO gene was analyzed by PCR-SSP genotype and DNA sequencing. Short tandem repeat (STR) analysis and digital droplet PCR (ddPCR) was performed as well.
Results Red blood cells from 11 individuals showed mix-field agglutination with anti-A or anti-B in blood typing; weak A or B antigen on the other four individuals' RBCs was detected by absorption-elution tests. The SSP results provided clues to support chimera deduction in four individuals. An additional ABO allele was identified in 10 individuals by DNA sequencing while 13 individuals by STR analyses. In all 15 individuals, the detection rate of DNA sequencing and STR analysis was 66.7% and 86.7%, respectively. Two probands from two pedigrees were both identified as dispermic chimerism by STR analysis. Two microchimeras were confirmed by ddPCR with extremely low chimerism rates of 0.62% and 0.073%.
Conclusion PCR-SSP/DNA sequencing, STR, ddPCR can be used to identify ABO chimeras step by step to improve the detection rate of natural blood group chimeras, including microchimeras, which have not been identified by many current laboratory **Methods**

PU-0349

异常 DNA 甲基化在胃癌临床诊断中的作用

王景
山东大学第二医院

目的 既往研究发现，异常 DNA 甲基化导致抑癌基因失活和癌基因激活在胃癌（GC）的发生发展中起着至关重要的作用。因此，我们的目的是：1) 分析外周血单核细胞 (PBMCs) DNA 中异常甲基化与胃癌风险之间的关联，以及 2) 确定胃癌与健康对照之间的候选差异甲基化标记，并建立胃基于 PBMC 的 DNA 甲基化的癌症诊断模型。
方法 我们所有的样本都是通过密度梯度离心从外周血中分离出来的单核细胞。首先，我们使用 Illumina HumanMethylation 850k 进行了甲基化分析检测，数据可用于总共 100 个样本：50 个健康对照和 50 个胃癌。然后，基于上述数据，我们筛选了显著的差异甲基化点，并最初使用焦磷酸

测序对其进行了验证。接下来，我们还将依靠焦磷酸测序和甲基化 PCR 来验证大样本中的候选标记。

结果 首先，利用 850 k 甲基化芯片的甲基化分析数据，我们获得了 6000 多个胃癌和健康对照差异的 DNA 甲基化位点。我们还发现胃癌组样本的整体 DNA 甲基化水平低于健康对照组，并且相当数量的 DNA 甲基化位点富含免疫相关通路。此外，胃癌患者 PBMCs 的 DNA 甲基化水平与患者的一些临床病理特征（如胃癌的 TNM 分期和分类）有关。在这 6000 多个位点中，我们选择了 10 个差异最显着且具有统计学意义的位点（包括 6 个高甲基化点和 4 个低甲基化点）作为进一步研究的候选标记。然后，我们从齐鲁医院和山东大学第二医院选取了 20 对胃癌和健康对照 PBMC，通过焦磷酸测序验证了上述候选标志物 DNA 甲基化水平的差异。焦磷酸测序的数据显示所有位点的甲基化趋势与 850 k 甲基化芯片的数据一致，6 个候选标记的结果具有统计学意义。出于临床应用的目的，我们选取了 4 个候选标志物（包括低甲基化点 cg15988552、cg22994883、cg26348226 和 cg02560388）进一步验证，建立胃癌诊断模型。最后，我们计划依靠焦磷酸测序和甲基化 PCR 来验证大样本的诊断模型。

结论 我们已经确定胃癌组的整体 DNA 甲基化水平显著低于正常水平。我们发现并初步验证了可能在胃癌临床诊断中发挥关键作用的候选标志物。

PU-0350

A combined RNA signature predicts recurrence risk of stage I-IIIA lung squamous cell carcinoma

li sun、juan li
The Second Hospital of Shandong University

Objective Recurrence remains the main cause of the poor prognosis in stage I-IIIA lung squamous cell carcinoma (LUSC) after surgical resection. In the present study, we aimed to identify the long non-coding RNAs (lncRNAs), microRNAs (miRNAs), and messenger RNAs (mRNAs) related to the recurrence of stage I-IIIA LUSC. Moreover, we constructed a risk assessment model to predict the recurrence of LUSC patients.

Methods RNA sequencing data (including miRNAs, lncRNAs, and mRNAs) and relevant clinical information were obtained from The Cancer Genome Atlas (TCGA) database. The differentially expressed lncRNAs, miRNAs, and mRNAs were identified using the "DESeq2" package of the R language. Univariate Cox proportional hazards regression analysis and Kaplan-Meier curve were used to identify recurrence-related genes. Stepwise multivariate Cox regression analysis was carried out to establish a risk model for predicting recurrence in the training cohort. Moreover, Kaplan-Meier curves and receiver operating characteristic (ROC) curves were adopted to examine the predictive performance of the signature in the training cohort, validation cohort, and entire cohort.

Results Based on the TCGA database, we analyzed the differentially expressed genes (DEGs) among 27 patients with recurrent stage I-IIIA LUSC and 134 patients with non-recurrent stage I-IIIA LUSC, and identified 431 lncRNAs, 36 miRNAs, and 746 mRNAs with different expression levels. Out of these DEGs, the optimal combination of DEGs was finally determined, and a nine-joint RNA molecular signature was constructed for clinical prediction of recurrence, including LINC02683, AC244517.5, LINC02418, LINC01322, AC011468.3, hsa-mir-6825, AC020637.1, AC027117.2, and SERPINB12. The ROC curve proved that the model had good predictive performance in predicting recurrence. The area under the curve (AUC) of the prognostic model for recurrence-free survival (RFS) was 0.989 at 3 years and 0.958 at 5 years (in the training set). The combined RNA signature also revealed good predictive performance in predicting the recurrence in the validation cohort and entire cohort.

Conclusions In the present study, we constructed a nine-joint RNA molecular signature for recurrence prediction of stage I-IIIA LUSC. Collectively, our findings provided new and valuable clinical evidence for predicting the recurrence and targeted treatment of stage I-IIIA LUSC.

PU-0351

人乳头瘤病毒在女性宫颈病变中的感染情况及 HPV 亚型分布特征分析

沈蓁
潍坊医学院附属医院

目的 分析人乳头瘤病毒（human papilloma virus, HPV）在女性宫颈病变中的感染情况及 HPV 亚型分布特征，以期为当地 HPV 感染的防治提供重要的科学依据。
方法 收集 2018 ~ 2020 年于潍坊医学院附属医院行 HPV 检测的 1850 例女性的临床资料，用宫颈细胞专用取样刷采集宫颈外口及宫颈管脱落细胞，使 用 PCR-反向斑点杂交技术检测患者宫颈细胞中的 23 种 HPV 基因亚型。回顾性分析资料的年龄特征、HPV 感染率及感染的亚型分布。
结果 在 1850 例研究对象中，HPV 检测阳性者 371 例，总体感染率为 20.05%，以高危型 HPV 感染为主，>60 岁年龄组的 HPV 感染率最高，HPV 的感染方式以单一型感染为主，HPV 亚型检出率最高的前三位分别为 HPV16、HPV52、HPV53。共检出 22 种 HPV 亚型（高危型 14 种、低危型 8 种）。高危型 HPV 以 HPV 16 型（17.22%）、HPV 58 型（12.33%）、HPV 18 型（9.25 %）常见，低危型 HPV 以 HPV 6 型（8.22 %）、HPV 11 型（7.05 %）、HPV42 型（6.37 %）常见。HPV 单一亚型感染 251 例（67.65 %），两种亚型感染 55 例（14.82 %）、三种亚型感染 40 例（10.78 %）、四种及以上亚型感染 25 例（6.73 %）。60 岁以上组 HPV 感染率最高，为 23.05 %，各年龄组均以高危型 HPV 感染为主，其中 30-40 岁高危型 HPV 感染率最高，为 16.55%；低危型 HPV 感染率最高的是 50-60 岁，为 5.33%。
结论 女性 HPV 总感染率为 20.05%，以单一高危型感染为主，常见的高危型为 HPV16、HPV52 和 HPV53。HPV 感染亚型及感染者的年龄分布具有一定的区域特征，因此，根据本地区 HPV 的感染特点，结合实际情况，提高相关年龄段人群的 HPV 筛查覆盖率，从而有效减少本地女性宫颈病变的发生率。

PU-0352

A multiplexed circulating tumor DNA detection platform engineered from 3D-coded interlocked DNA rings

Sha Yang
Southwest Hospital, Third Military Medical University (Army Medical University)

Circulating tumor DNA (ctDNA) is a critical biomarker not only important for the early detection of tumors but also invaluable for personalized treatments. Currently ctDNA detection relies on sequencing. Here, a platform termed three-dimensional-coded interlocked DNA rings (3D-coded ID rings) was created for multiplexed ctDNA identification. The ID rings provide a ctDNA recognition ring that is physically interlocked with a reporter ring. The specific binding of ctDNA to the recognition ring initiates target-responsive cutting via a restriction endonuclease; the cutting then triggers rolling circle amplification on the reporter ring. The signals are further integrated with internal 3D codes for multiplexed readouts. ctDNAs from non-invasive clinical specimens including plasma, fecal, and urine were detected and validated at a sensitivity much higher than obtained through sequencing. This 3D-coded ID ring platform can detect any multiple DNA fragments simultaneously without sequencing. We envision that our platform will facilitate the implementation of future personalized/precision medicine.

PU-0353

1828 例男性患者泌尿生殖道病原体感染情况分析

赵美美、姜永玮、孔晓牧、刘怡、高芃、丛笑、杨辉、马亮、曹永彤
中日友好医院

目的 了解北京地区部分男性患者生殖支原体（MG）、沙眼衣原体（CT）、淋病奈瑟菌（NG）及解脲脲原体（UU）的感染情况，为临床诊疗提供依据。
方法 收集 2019 年 12 月- 2021 年 5 月中日友好医院就诊的男性患者尿液标本共 1828 份，采用实时荧光核酸恒温扩增检测技术（SAT）对以上标本分别进行 MG-RNA，CT-RNA，NG-RNA 和 UU-RNA 检测。
结果 所有患者 MG，CT，NG 和 UU 总阳性率分别为 2.24%（41/1828），3.39%（62/1828），1.26%（23/1828）和 17.94%（328/1828），UU 的检出率明显高于其他三种病原体，差异有统计学意义（P＜0.01）。感染人群主要集中在 20～35 岁的年轻男性患者，临床诊断为泌尿生殖道炎症的男性患者检出率最高，差异有统计学意义（P＜0.01）。
结论 解脲脲原体 UU 是北京地区男性患者泌尿生殖道病原体感染的主要病种，在临床诊疗中应加强早期筛查和监测，尽早进行临床治疗。同时 SAT 检测能为临床诊断泌尿生殖道 MG，CT，NG 及 UU 的感染提供依据。

PU-0354

Genome-wide expression profiling and functional analysis of lncRNAs reveal the oncogenic role of CRNDE in acute promyelocytic leukemia and NPM1-mutant acute myeloid leukemia

Xuefei Ma、Wei Zhang、Ming Zhao、Shufen Li、Wen Jin、Xuefeng Wang、Kankan Wang
Ruijin Hospital, Shanghai Jiao Tong University School of Medicine

Background Myeloid differentiation is a precise regulation process of various functional blood cells. The differentiation block of myeloid cells caused by abnormal gene regulation, is critical for the initiation of acute myeloid leukemia (AML). The multi-hit model of AML leukemogenesis has revealed that the development of AML is not only driven by initiating events, including chromosomal translocations and mutations, but also requires other cooperating secondary events. In recent years, with the development of high-throughput techniques and bioinformatic analysis, the roles of long noncoding RNAs (lncRNAs) in gene regulation have attracted much attention. However, most of our knowledge about the cooperating events during AML development and the molecular mechanisms of myeloid differentiation mainly focus on the studies conducted on protein-coding genes, and the roles of lncRNAs involved in the multi-hit model of AML leukemogenesis are still largely unknown.
Methods We first retrieved and analyzed the RNA-seq data of 379 de novo AML samples and 21 normal counterparts from two cohorts of clinical AML patients (TCGA and BEAT AML databases) to explore lncRNAs that may contribute to the pathogenesis of AML. Next, the expression of the pathogenesis-related lncRNA, CRNDE (Colorectal Neoplasia Differentially Expressed), in AML and normal counterparts, was validated by microarray gene expression data. The cooperative function of CRNDE with PML/RARα fusion protein in acute promyelocytic leukemia (APL) was validated using PML/RARα transgenic APL murine model, qRT-PCR and ChIP-seq data. Differentiation of NB4 and OCI-AML3 cells was determined by flow cytometric analysis of CD11b expression after transfection with indicated shRNAs. The cell proliferation was detected by CCK-8 assays. We also addressed the in vivo effect of CRNDE repression using a transplantable murine APL model. Through bioinformatic prediction, and the use of RNA antisense purification assay

(RAP) and dual luciferase activity assay, we discovered the molecular mechanism of the oncogenic effect of CRNDE in APL.
Results Here, we identified one of pathogenesis-related lncRNA CRNDE, highly expressed in APL with t (15;17) translocation and *NPM1*-mutant AML through analyzing RNA-seq data from a large cohorts of AML patients and normal counterpart. Furthermore, we found that CRNDE was high expression in the disease state but not in the preleukemic stage of APL, suggesting that CRNDE might be a secondary event coordinating with PML/RARα to promote APL development. Functional analysis showed that CRNDE knockdown induced differentiation and inhibited proliferation of APL cells, and prolonged survival of APL mice. Further in vivo and in vitro mechanistic studies showed that CRNDE elicited its oncogenic effects through binding the miR-181 family and thereby regulating NOTCH2. Finally, we found that high CRNDE expression was also significantly correlated with *NPM1* mutations and contributed to differentiation block in *NPM1*-mutant AML.
Conclusions By analyzing high-throughput sequencing data, we identified a set of pathogenesis-related lncRNAs in APL and provided a new evidence that CRNDE, as an oncogenic lncRNA, regulates myeloid differentiation and/or cell proliferation in APL and *NPM1*-mutant AML. Moreover, CRNDE can promote leukemogenesis and modulate NOTCH2 level as a miRNA sponge by directly binding miR-181. Our findings shed light on the importance of oncogenic lncRNAs in the development of AML and provide a promising target for AML diagnosis and therapy.

PU-0355

Association between AGTR1 gene polymorphism and the antihypertensive effect of valsartan

Yi Liu、Xiaomu Kong、Yongwei Jiang、Meimei Zhao、Peng Gao、Liang Ma、Yongtong Cao
China-Japan Friendship Hospital

Objective To investigate whether the antihypertensive effect of angiotensin receptor blocker valsartan is associated with angiotensin II type 1 receptor (AGTR1) gene polymorphism (A1166C).
Methods Patients with hypertension who visited China-Japan Friendship Hospital from January 2016 to December 2018 and took only valsartan (80 mg/d) for maintenance therapy in the past month were retrospectively included in this study. Patients'clinical and laboratory data were collected. Real-time PCR was used to genotype the AGTR1 gene polymorphism. Based on the systolic blood pressure (SBP) and diastolic blood pressure (DBP) at the time of visit, patients were divided into good response group (SBP/DBP < 140/90 mmHg, n = 144) and poor response group (SBP/DBP ≥ 140/90 mmHg, n = 137).
Results There were 281 patients with hypertension in this study, including 203 males and 78 females. 164 (58.4%) cases were with grade 3 hypertension, and 117 (41.6%) cases with grade 1/2 hypertension. 247 (87.9%) cases had AA genotype of AGTR1 gene, while 34 (12.1%) cases had AC/CC genotypes. Compared with the patients in poor response group, patients in good response group were older, drank less alcohol, and had a higher proportion of grade 1/2 hypertension and AC/CC genotypes. In multivariate Logistic regression analysis with adjustment for covariates, age (P = 0.033, OR (95%IC) = 0.096 (0.937-0.997)), hypertension grade (P = 0.055, OR (95%IC) = 1.454 (0.991-2.134)) and AGTR1 genotype (P=0.009, OR(95%IC)=0.326 (0.140-0.759)) were the factors influencing the difference in antihypertensive response to valsartan between the two patient groups.
Conclusion Our data suggest that the AGTR1 gene polymorphism (A1166C) can affect the antihypertensive response to valsartan, and valsartan treatment seems to be more effective in hypertensive patients with AC and CC genotypes.

PU-0356

HAS2/HA/CD44 信号轴介导乳腺癌细胞可塑性变化及 PI3Kα 抑制剂耐药的机制研究

盛雨梦、刘鹭雯、何怡青、杜艳、张国良、高锋、杨翠霞
上海交通大学附属第六人民医院检验科

目的 探讨 HAS2/HA/CD44 信号轴对管腔型乳腺癌细胞可塑性变化的调控作用以及在管腔型乳腺癌细胞获得对 PI3Kα 抑制剂耐药性中的作用及机制。
方法 借助慢病毒转染技术，建立透明质酸合成酶 2（Hyaluronan synthase 2, HAS2）过表达的管腔型乳腺癌稳定细胞系，采用 Western blot 和免疫荧光方法观察 HAS2 对管腔型乳腺癌细胞上皮间充质转化(Epithelial mesenchymal transition，EMT)的调控作用；聚焦雌激素受体（Estrogen Receptor，ER）阳性管腔型乳腺癌，通过分析 TCGA 数据库以及建立 PI3Kα 耐药细胞株，分析 HAS2/CD44 在乳腺癌细胞获得对 PI3Kα 抑制剂耐药性中的作用；通过过表达 HAS2 和加入外源性透明质酸（Hyaluronan, HA）激活 HAS2/HA/CD44 信号轴，探究此信号轴在乳腺癌细胞获得对 PI3Kα 抑制剂耐药性中的作用。
结果 研究发现上调 HAS2 显著促进乳腺癌细胞 EMT 的发生；TCGA 数据库分析显示，在管腔型乳腺癌中，PIK3CA 基因突变的乳腺癌的 HAS2 表达水平显著增加，且 HAS2 与 CD44 的表达水平呈正相关关系；Western blot 结果显示 HAS2 及 CD44 在 PI3Kα 抑制剂耐药细胞中的表达显著升高；激活 HAS2/HA/CD44 信号轴，发现此信号轴的激活通过维持 AKT/mTOR 信号通路的重新活化从而介导管腔型乳腺癌细胞对 PI3Kα 抑制剂的耐药性。
结论 HAS2 诱导乳腺癌细胞 EMT 的发生，进而介导管腔型乳腺癌细胞的可塑性变化；在获得对 PI3Kα 抑制剂耐药性的管腔型乳腺癌细胞中，HAS2 与 CD44 的表达均显著增加，由此形成的 HAS2/HA/CD44 信号轴介导管腔型乳腺癌细胞获得对 PI3Kα 抑制剂的耐药性。

PU-0357

去泛素化酶 USP48 在乳腺癌中的表达及其对乳腺癌发生发展的影响

王恬恬、王传新
山东大学第二医院

目的 探讨去泛素化酶 USP48 在乳腺癌中的表达及对乳腺癌发生发展影响。
方法 利用 TCGA 数据库分析 USP48 在乳腺癌中的表达及其与患者预后生存的关系。通过稳转基因沉默技术(sh-RNA)将 USP48 敲低，探究 USP48 在乳腺癌细胞中的作用。通过将乳腺癌特异性 USP48 敲除小鼠与 MMTV-PyMT 驱动的乳腺癌自发成瘤小鼠杂交，探究 USP48 在体内成瘤中的作用。
结果 USP48 在乳腺癌组织中表达下调且低表达 USP48 与较好的预后相关。通过 sh-RNA 抑制乳腺癌 MCF-7 细胞 USP48 表达后，细胞增殖能力显著上调但迁移侵袭能力无明显变化。在体内，USP48 基因缺失加速 MMTV-PyMT 驱动的肿瘤形成，且 PyMT;USP48–/–小鼠的总生存期较 PyMT;USP48+/+ 小鼠明显缩短。
结论 去泛素化酶 USP48 在乳腺癌中表达下调且低表达 USP48 与较好的预后相关。特异性抑制 USP48 基因的表达可增强乳腺癌细胞的增殖能力并加速 MMTV-PyMT 驱动的肿瘤形成，提示 USP48 在乳腺癌发生中的保护作用。

PU-0358

长链非编码 RNA LINC02474 在结直肠癌中的表达特征及对细胞增殖的影响

杜甜甜、王传新
山东大学第二医院

目的 探讨长链非编码 RNA（lncRNA）LINC02474 在结直肠癌组织及循环外泌体中的表达特征及其对结直肠癌发生发展的影响。
方法 利用实时荧光定量 PCR（qRT-PCR）检测 LINC02474 在 30 例结直肠癌患者组织及 128 例结直肠癌患者和 128 例健康对照者血清中的相对表达量；使用电子显微镜检测分离所得外泌体的形态特征；使用纳米粒子跟踪分析（NTA）检测分离所得外泌体的粒径大小；Western blot 检测外泌体表面标志物的表达；CCK-8 实验、平板克隆形成实验和实时细胞分析系统（RTCA）检测干扰 LINC02474 后 DLD-1 细胞的增殖情况；采用生物信息学方法分析预测获得 LINC02474 的潜在靶基因。
结果 qRT-PCR 检测 30 例结直肠癌患者组织及 128 例结直肠癌患者和 128 例健康对照者血清样本均显示，LINC02474 在结直肠癌组织和血清中呈异常高表达，差异有统计学意义（组织样本：t=2.827, p=0.0064；血清样本：t=3.081, p=0.0023）。电子显微镜显示分离所得外泌体呈盘状囊泡结构，大小分布集中于 96.9nm 处，且表达表面标志物 CD9、CD63 和 TSG101。CCK-8 实验、平板克隆形成实验和实时细胞分析系统（RTCA）检测实验表明，干扰 LINC02474 的表达可以抑制结直肠癌细胞的增殖及成瘤能力，差异有统计学意义（p<0.05）。KEGG 和 GO 富集分析显示，LINC02474 的潜在靶基因多富集在 mTOR 及 MAPK 等信号通路。
结论 LINC02474 在结直肠癌患者组织和血清外泌体中呈现高表达特征，干扰其表达可以抑制结直肠癌细胞的增殖及成瘤能力。

PU-0359

Xpert 技术在艰难梭菌检测中的应用

邹红雁
吉林大学第一医院

艰难梭菌（Clostridium Difficile，CDI）是一种革兰氏阳性、产毒素的专性厌氧芽孢杆菌，1978 年首次被证实与疾病有关，可通过粪-口途径传播。CDI 已成为呈世界性分布主要肠道病原体。我国 CDI 的数据较少，这主要是因为缺乏有效的临床诊断工具，导致医疗机构人员没有普遍意识到 CDI 的严重性。Xpert 技术可检测毒素 B 相关基因 tcdB、抑制子基因 tcdC 以及二元毒素基因 cdt，tcdC 和 cdt 与高产毒菌相关，因而可预测高毒力菌株 BI/NAP1/027 型的存在。

我院对 2019 年 1 月-2020 年 12 月住院患者采用该检测技术并结合临床资料进行分析，出现抗生素相关腹泻患者（ADD）占所有抗生素治疗的住院患者 1.0%（317/30532），在这些 ADD 患者中 30.6%（97/317）检出艰难梭菌。ADD 发生频率最高是 ICU（10.7%），ADD 发生比率最高是胃肠内科（37.9%）。临床表现上 CDI 和其他因素导致的 AAD 存在差异，其他因素导致的 AAD 相比 CDI 症状较轻，CDI 患者通常有结肠炎和腹部绞痛，低烧并且白血球升高，而其他因素导致的腹泻通常没有结肠炎。一旦诊断为 AAD，临床医生即停止对患者的抗生素治疗，其中 43 位患者接受了经验性治疗，19 位患者在使用甲硝唑无效后改服万古霉素。约 40% 患者服用了益生菌，与非艰难梭菌导致的 AAD 相比，CDI 患者更多的使用了甲硝唑进行治疗。最终，85.7%(83/97)的 CDI 患者和 92.3%（203/220）的非 CDI 腹泻患者治愈， 3 位 CDI 患者期间复发 1 次。

艰难梭菌感染在我国医院的 AAD 中扮演了重要角色，但由于腹泻程度主要为轻度到中度，临床医生很难区分 CDI 和其他 AAD，建议将艰难梭菌检测纳入腹泻(尤其是 AAD)患者的常规诊断。

PU-0360

Epigenomic State Transitions Characterize Pancreatic Cancer in Mouse

Shujun Zhang、Chuanxin Wang
The Second Hospital of Shandong University

Pancreatic ductal adenocarcinoma (PDA) is one of the most lethal human malignancies. Oncogenic mutations in KRAS are present in over 90% of human pancreatic cancers along with high frequency in pancreatic intraepithelial neoplasia (PanINs), suggesting an initiating role for mutant KRAS. In contrast, missense-mutations of TP53 proteins are sufficient to drive tumor formation. Alteration of epigenetic pathways is an emerging mechanism of PDA progression. However, comprehensively epigenetic landscape at each stage of PDA progression and how mutant TP53 contribute to PDA progression via epigenetic regulatory mechanism remain largely unknown. To address this gap, we developed genetically engineered mouse models of PDA, which preserves the unique biological characteristics of normal (Pdx-1-Cre, known as wide type [WT] mice), PanIN (LSL-KrasG12D; Pdx-1-Cre, known as KC mice) and tumor (LSL-KrasG12D; LSL-Trp53R172H/+; Pdx-1-Cre, known as KPC) and used assay for transposase accessible chromatin using sequencing (ATAC-Seq), H3K27ac chromatin immunoprecipitation (ChIP-seq) and RNA sequencing (RNA-Seq) to characterize how the epigenetic landscape evolves during PDA progression and identified the intrinsic transcriptional regulators associated with mutant TP53 promoting PDA progression in a comparable context. We discover and implicate a novel TF FOSL2 in favor of immunosuppression, which we show can promote tumor growth in vivo. Importantly, we found that mtp53 could promote immune evasion by enhance the transcription of FOSL2. Collectively, our findings suggest that reprogramming of the epigenetic landscape can promote the acquisition of PDA progression traits and delineated for the first time a distinct mechanism by which mtp53 and suggest that mtp53 acts upstream of FOSL2 and regulate FOSL2 expression cistrome to promote cancer growth and evasion of tumor immune surveillance in PDA.

PU-0361

外泌体 microRNA 在食管鳞状细胞癌患者血清中的表达及其在术前淋巴结转移预测中的临床价值研究

刘童、王传新
山东大学第二医院

目的 明确外泌体 microRNA 在 ESCC 患者血清中的表达情况，构建可用于 ESCC 淋巴结转移的预测模型，并评估所构建的模型在 ESCC 淋巴结转移方面的预测效能及临床应用价值。
方法 筛选阶段，选取 10 例淋巴结转移阴性（LN-）ESCC 患者及 10 例淋巴结转移阳性（LN+）ESCC 患者血清外泌体样本进行高通量测序，筛选用于预测 ESCC 淋巴结转移相关的血清外泌体 miRNA 生物标志物。训练阶段，选取 95 例 LN-患者及 83 例 LN+患者血清样本通过 qRT-PCR 验证各候选外泌体 miRNA 的的表达水平并做差异分析；随后，根据表达量数据使用 logistic 回归分析联合血清外泌体 4-miRNA 模型和临床 CT 检查结果构建临床 nomogram 模型，并将预测模型在 91 例 LN-患者及 97 例 LN+患者血清样本中进行验证，ROC 曲线评估该模型在验证组中的淋巴结转移预测效能。ROC 曲线、拟合优度曲线、Hosmer-Lemeshow 检验以及决策曲线分析进一步评估此模型在 ESCC 淋巴结转移预测中的预测效能、校准能力以及临床获益度。本课题进一步分析了该临床模型在 T1 期 ESCC 患者中针对淋巴结转移的预测效能。
结果 筛选阶段共筛选出 4 个候选 miRNA 分子（chr 8-23234-3p、chr 1-17695-5p、chr 8-2743-5p 和 miR-432-5p）。训练阶段，与 LN-患者血清外泌体样本对比，chr 8-23234-3p、chr 1-17695-5p、

chr 8-2743-5p 在 LN+患者血清外泌体中的表达量上调而 miR-432-5p 的表达量显著下调。随后，我们使用 logistic 回归在训练组中构建 4-miRNA 预测模型用于评估淋巴结转移风险系数，随后将验证组中的表达量数据代入公式获得相应风险系数。进一步联合 4-miRNAs 预测模型和临床 CT 检查结果构建临床 nomogram 模型，ROC 曲线分析显示该模型在训练组样本和验证组样本中都显示出良好的淋巴结转移预测效能。拟合优度曲线分析显示，在训练组和验证组中，淋巴结转移实际值与模型预测值之间存在显著的相关性，并且 Hosmer-Lemeshow 检验结果显示二者无显著差异。决策曲线分析显示，训练组和验证组中临床模型在 20%-80%阈值内的临床获益率显著优于“全治疗”、“无治疗”或 CT 检查。针对 T1 期 ESCC 患者，此模型依然能够在训练组和验证组中成功识别患者中的 LN+个体。
结论 ROC 曲线、拟合优度曲线及决策曲线分析结果证明了此临床 nomogram 具有良好的鉴别能力、校正能力以及临床获益度，有望成为 ESCC 淋巴结转移术前预测的新型无创性生物标志物。

PU-0362

LINC01980 促进胃癌细胞的增殖、迁移及侵袭

史爽
山东大学第二医院

目的 揭示 LINC01980 促进胃癌(GC)进展的作用。
方法 通过生物信息学分析，筛选胃癌(GC)组织中差异表达的 lncRNAs,采用 qRT-PCR 检测 GC 组织和癌旁组织中 LINC01980 的表达水平。采用 Kaplan-Meier 法评价 LINC01980 对 GC 的预后作用。检测 LINC01980 胃癌 HGC27 细胞增殖、迁移及侵袭的调控作用。最后，通过在线数据库预测 LINC01980 的分子机制。
结果 LINC01980 在 GC 组织和细胞中表达上调。并且高水平的 LINC01980 提示胃癌患者预后较差。敲除 LINC01980 可降低 HGC27 细胞的增殖、迁移及侵袭能力。LINC01980 在 GC 中表达上调，且其高水平预示 GC 患者预后较好。
结论 LINC01980 在 GC 中表达上调，且其高表达预示预后不良。

PU-0363

新型冠状病毒疫苗接种点环境标本的检测结果分析

刘文静、屈峰、陈雨欣、林泓怡、沈瀚
南京大学医学院附属鼓楼医院

目的 探究南京鼓楼医院新型冠状病毒（新冠，2019-nCoV）疫苗接种点（以下简称“接种点”）是否存在核酸污染问题，是否会影响检验科新冠核酸的正常检测。
方法 分别于 2021 年 1 月 27 日 8：00（接种前）、12：00（接种 3 小时）、18：00（接种 9 小时）、1 月 28 日 8：00（接种完成 14 小时）采集接种点分诊区、接种台以及留观处 12 处位置共 48 份棉拭子标本，另外采集 2021 年 1 月 27 日接受 2019-nCoV 疫苗接种的 4 名检验科分子室核酸检测工作人员接种前、后的皮肤、衣物共 16 份棉拭子标本，采用实时荧光定量 PCR（RT-PCR）方法进行新冠核酸检测。
结果 64 份标本中，共有 15 份新冠核酸检测结果为阳性，其中接种台推车有 10 份标本阳性，接种台桌面有 5 份标本阳性。
结论 在本次疫苗接种点接种过程中存在核酸污染现象，但范围较局限，主要集中在接种台范围，未发现经人携带至检验科分子组的现象，因此不会影响检验科新冠核酸检测的工作。

PU-0364

Long non-coding RNA LINC00310 affects breast cancer cell growth and serves a novel diagnostic biomarker

Juan Li、Chuanxin Wang
The Second Hospital of Shandong University

PURPOSE Recent studies have revealed that long non-coding RNAs (lncRNAs) are involved in different processes of breast cancer. This study was designed to explore the oncogenic roles and diagnostic value of LINC00310 in breast cancer.
METHOD We assessed clinical attributes, prognostic value and potential targets of LINC00310 by TCGA data. The oncogenic roles of LINC00310 were evaluated in vitro and in vivo by dual-gRNA CRISPR/Cas9 system. Furthermore, we detected the expression of serum LINC00310 by qRT-PCR and evaluated its diagnostic significance for breast cancer.
RESULT LINC00310 expression was elevated as breast cancer progress, and the deregulation of LINC00310 was significantly associated with patients' survival. Experiments with KO and rescue approach revealed that LINC00310 promoted cell proliferation by regulating c-Myc expression in vitro. Nude mouse xenograft assay demonstrated that LINC00310 KO significantly suppressed tumor growth in vivo. Furthermore, we found that serum LINC00310 expression was significantly up-regulated in breast cancer patients and ROC curve analysis indicated that LINC00310 had powerful capability for distinguishing breast cancer patients from healthy individuals (the AUC 0.828).
CONCLUSION The results suggest that LINC00310 may play an oncogenic role and serve as a novel diagnostic biomarker in breast cancer.

PU-0365

miR-192-5p 通过 BCL2 通路抑制胃癌细胞的增殖和迁移机制研究

王战豪
成都市第三人民医院

目的 探讨 miR-192-5p 对胃癌细胞增殖和迁移的生物学行为的影响及相关分子机制。
方法 qPCR（Quantitative PCR）检测胃癌组织和癌旁组织及胃癌细胞系中 miR-192-5p 表达水平；基因重组技术构建敲降 miR-192-5p 的慢病毒载体细胞株，miR-192-5p mimic 转染胃癌细胞株，检测细胞株的增殖和迁移；双荧光素酶报告基因检测 miR-192-5p 的靶分子；Western blot 检测敲降 miR-192-5p 的胃癌细胞株的蛋白表达水平。
结果 胃癌细胞 AGS、SGC-7901 的 miR-192-5p 表达显著高于 BGC-823、KATO-Ⅲ、MGC-803，胃癌组织和正常组织的 miR-192-5p 的表达水平没有显著差异；敲降 miR-192-5p 后，细胞增殖和迁移能力较阴性对照组升高；而过表达 miR-192-5p mimic 后细胞增殖和迁移则明显受到抑制。双荧光素酶报告基因结果显示，BCL2 是 miR-192-5p 的靶分子。敲降 miR-192-5p 的胃癌细胞 AGS 和 SGC-7901 中 BCL2 蛋白的表达量显著增加。敲降 miR-192-5p 的胃癌细胞 AGS 和 SGC-7901 中，EMT 相关蛋白 Twist1、Snail2 表达升高，细胞凋亡及细胞周期相关蛋白 Capase3、Bax、PCNA 的表达没有差异。
结论 抑制 miR-192-5p，EMT 相关分子表达增强，并促进细胞迁移和增殖，而 miR-192-5p 模拟物则抑制胃癌细胞的迁移和增殖。miR-192-5p 可能通过对 BCL2 的靶向调控，促使胃癌细胞发生 MET，从而抑制胃癌细胞的增殖与迁移。

PU-0366

单细胞测序技术在脑脊髓液细胞分析中的应用

阮浩宇
江苏省人民医院（南京医科大学第一附属医院）

脑脊髓液（CSF）检测在中枢神经系统疾病的诊断和治疗中具有重要的临床价值，单细胞测序技术为 CSF 的相关研究提供了一个新的切入点。相较于传统方法，该技术可获取 CSF 中单个细胞的表达谱，有利于 CSF 中细胞类群的研究以及低丰度细胞的发现。本文总结了近年来 CSF 单细胞测序的相关研究，主要集中在神经感染性疾病、神经炎性和神经退行性疾病，以及脑膜转移，概括了单细胞测序技术在中枢神经系统疾病研究中的优势和临床价值。

PU-0367

A nomogram combining long non-coding RNA expression profiles and clinical factors predicts survival in patients with bladder cancer

Yifan Wang
The Second Hospital, Cheeloo College of Medicine, Shandong University

Bladder cancer (BCa) is a heterogeneous disease with various tumorigenic mechanisms and clinical behaviors. The current tumor-node-metastasis (TNM) staging system is inadequate to predict overall survival (OS) in BCa patients. We developed a BCa-specific, long-non-coding-RNA (lncRNA)-based nomogram to improve survival prediction in BCa. We obtained the large-scale gene expression profiles of samples from 414 BCa patients in The Cancer Genome Atlas database. Using an lncRNA-mining computational framework, we identified three OS-related lncRNAs among 826 lncRNAs that were differentially expressed between BCa and normal samples. We then constructed a three-lncRNA signature, which efficiently distinguished high-risk from low-risk patients and was even viable in the TNM stage-II, TNM stage-III and ≥65-year-old subgroups (all $P<0.05$). Using clinical risk factors, we developed a signature-based nomogram, which performed better than the molecular signature or clinical factors alone for prognostic prediction. Our three-lncRNA signature-based nomogram effectively predicts the prognosis of BCa patients, and could potentially be used for individualized management of such patients.

PU-0368

基于外泌体的肿瘤诊断新技术研究进展

黄晓明、牛会敏、程少杰、张胜行
联勤保障部队第九〇〇医院

外泌体是细胞分泌的纳米级囊泡，富含特定的蛋白质、脂质和核酸等内容物，具有明显的分子异质性。特定细胞释放的外泌体可以改变细胞外基质微环境，或通过向受体细胞传递信号分子以触发其病理生理功能的变化。这种外泌体介导的细胞与细胞之间的交互通信影响着肿瘤的发生与发展。研究表明，在肿瘤发生发展的极早期，原发部位的肿瘤细胞即可经其外泌体的介导促进远端靶器官预转移微环境的构建以利于循环肿瘤细胞的定植并形成微转移灶。此外，外泌体也被证实可参与肿瘤微环境的血管生成和细胞外基质重塑，它们也是肿瘤生长和转移的关键步骤。鉴于其独特的生物学特性和在机体生理和病理过程中发挥的重要功能，外泌体被认为是包括肿瘤在内的多种疾病诊断的最佳生物标志物之一；相应地，近年来外泌体检测新技术方面的探索正方兴未艾，但目前尚未建

立健全规范的检测方法。究其原因，如何减小其他生物物质如脂蛋白、凋亡小体等细胞外囊泡的干扰以增强检测结果的稳定性是目前亟待解决的现实难题；此外，筛选并鉴定与特定肿瘤发生发展密切相关的肿瘤源性外泌体中更为特异的靶标分子，并基于其开发更为敏感和高效特异的检测方法势在必行。可以预见的是，随着外泌体组学等分析技术的飞速发展，以及单分子检测等技术的开发和应用，基于外泌体的肿瘤诊断新技术将在不久的未来走入临床检验的实践中以造福广大肿瘤患者。外泌体作为肿瘤的非侵入性可检测生物标志物具有广阔的临床应用前景，本文仅就外泌体检测相关新技术及其在恶性肿瘤诊断中的应用等方面的进展作一综述。

PU-0369

鼻咽癌放化疗敏感性的预测标志物

林明樾[1,2]、浣西莎[1,2]、郭立煌[1,2]、程振波[1,2]、李贱成[1,2]、黄玥[1,2]、徐克前[1,2]
1. 中南大学湘雅三医院医学检验系
2. 中南大学湘雅医学院医学检验系

目的 探究鼻咽癌放化疗敏感性的预测标志物。
方法 收集 2019 年 6 月-10 月就诊于中南大学湘雅医学院附属肿瘤医院的 100 例鼻咽癌患者放射治疗前的外周血标本，提取患者外周血白细胞中基因组 DNA，检测 XRCC1 G339A、ERCC1 C118T 以及 hMSH5 C85T 多态性，同时分离外周血淋巴细胞进行彗星试验和 in vitro NHEJ 活性分析，检测血浆 8-羟基脱氧鸟苷（8-OHdG）反映细胞 DNA 损伤修复状况，以研究这些分子标志物在鼻咽癌放化疗中的预测作用。
结果 与 hMSH5 CC 基因型相比，hMSH5 CT 基因型鼻咽癌患者放化疗 3 个月后部分缓解率明显降低，差异具有统计学意义（$P < 0.05$），但是未发现 XRCC1 G339A 和 ERCC1 C118T 与鼻咽癌患者放化疗 3 个月后疗效有关。鼻咽癌患者放疗 3 个月后疾病稳定组的 NHEJ 活性明显高于部分缓解组，差异具有统计学意义（$P < 0.05$），但两组之间的%Tail DNA 和 8-OHdG 水平之间的差异无统计学意义（$P > 0.05$）。
结论 hMSH5 C85T 多态性与鼻咽癌患者放化疗后近期疗效显著相关，NHEJ 活性增高导致鼻咽癌患者放化疗敏感性下降。hMSH5 C85T 多态性和 NHEJ 活性分析可能是预测鼻咽癌放化疗敏感性的检测指标。

PU-0370

The role of lncRNA28 in breast cancer cells on the proliferation、apoptosis and migration

Ruiwei Li[1]、Sai He[1]、Zhifang Liu[2]
1. The Third People's Hospital Of Yunnan Province
2. 云南大学

Objective To investigate the effects of long non-coding RNA (lncRNA) lncRNA28 on the proliferation, apoptosis and migration of breast cancer cells.
Methods The expression of lncRNA28 in breast cancer tissues and breast cancer cells was detected by qRT-PCR. The molecular localization of lncRNA28 was analyzed by cytoplasmic separation method to explore the regulatory mechanism of lncRNA28. After the expression of lncRNA28 was interfered with by siRNA, the effects of lncRNA28 on cell proliferation, apoptosis, migration and invasion were detected by CCK-8, flow cytometry, wound healing assay and Transwell assay.
Results The expression of lncRNA28 in breast cancer tissues and breast cancer cells was significantly higher than that in paracancerous tissues and normal breast epithelial cells, and

lncRNA28 was mainly localized in the nucleus. Knockdown of lncRNA28 significantly inhibited the proliferation, migration and invasion of breast cancer cells.
Conclusions LncRNA28 can promote the proliferation and migration of breast cancer cells.

PU-0371

血清 GGT/ALT 比值与 HBV 基因 BCP 区 1762/1764 突变联合分析对 HB-HCC 的早期诊断价值研究

邱顺华
自贡市第三人民医院

目的 探讨分析血清 γ 谷氨酰转移酶（γGGT）与丙氨酸转移酶（ALT）比值联合乙型肝炎病毒（HBV）基因 BCP 区 1762/1764 突变对乙肝性肝癌（HB-HCC）的临床应用价值。
方法 按照诊疗指南，诊断 HBV 相关性疾病，收集慢性乙肝患者（CHB）、乙肝性肝硬化(HB-LC) 50 例，乙肝性肝癌(HB-HCC) 46 例。血清 HBV-DNA 水平采用荧光定量 PCR 技术检测；血清 γGGT 与 ALT 水平采用全自动生化分析仪检测。乙型肝炎病毒基因 BCP 区 1762/1764 突变采用扩增阻滞突变系统荧光 PCR 法（ARMS-PCR）检测。计量数据和计数数据均采用 SPSS17.0 软件对数据进行统计学分析。
结果 HB-HCC 组患者的血清 γGGT 水平和 γGGT/ALT 比值均高于 HB-LC 组和 CHB 组，差异均具有统计学意义（P<0.05)。HB-HCC 组、HB-LC 组、CHB 组的 HBV 基因 BCP 1762/1764 突变率分别为 91.30%、84.00%、22.22%，HB-HCC 组与 CHB 组比较具有统计学意义（P<0.05），而 HB-HCC 组与 HB-LC 组比较差异无统计学意义（P>0.05）。HBV 基因 BCP1762/1764 突变型与未突变型的 γGGT/ALT 均值比较，差异均具有统计学意义（P<0.05）。诊断 HB-HCC 的 ROC 曲线分析**结果** HBV 基因 BCP 区 172/1764 突变检测联合 γGGT/ALT 比值时，诊断灵敏度 71.7%和特异度 83.2%。
结论 γGGT/ALT 比值和 HBV 基因 BCP 区 1762/1764 突变均与 HBV 相关疾病的病情发展密切相关，同时联合分析二者对 HB-HCC 的早期诊断具有一定的临床应用价值。

PU-0372

Rapid one-tube detection of four prevalent mutations in the SLC25A13 gene by multicolor melting curve analysis

Tong Ou[1]、Qinlong Zeng[2]
1. Medical Laboratory of Shenzhen Luohu Hospital Group
2. 江门市妇幼保健院

Background Citrin deficiency caused by SLC25A13 gene mutations is an autosomal recessive disease with high prevalence among the East Asian population, and SLC25A13 genetic analysis is essential for definite diagnosis. Four prevalent SLC25A13 mutations including c.851_854del, c.1638_1660dup, IVS6+5G>A, and IVS16ins3kb make up over 80% of total pathogenic mutations in the Chinese population. However, suitable assays for detection of the prevalent SLC25A13 mutations are still missing in routine clinical practice.
Methods Here, four primer-probe sets targeting the SLC25A13 mutation regions were designed and a real-time PCR-based multicolor melting curve analysis (MMCA) was developed to detect the four prevalent mutations in one closed-tube reaction. We comprehensively evaluated the analytical and clinical performances of the MMCA assay using 15 artificial templates, 29 clinical samples with known genotypes and a cohort of 5,332 healthy newborns from southern China.
Results All four mutations in the artificial templates and clinical samples were accurately genotyped by their labeling fluorophores and Tm values, and the standard deviations of Tm

values were less than 0.2 °C. The limit of detection was estimated to be 500 diploid human genomes per reaction. A total of 107 carriers were screened from the newborn cohort with a carrier rate of 2%. The MMCA assay of 107 carriers and 112 random noncarriers demonstrated 100% concordance with Sanger sequencing and Long-range PCR.
Conclusions The developed assay can potentially serve as an efficient first-line screening and genetic diagnostic tool for citrin deficiency in routine clinical practice in China.

PU-0373

人偏肺病毒核酸检测试剂盒（PCR-荧光探针法）临床研究

姜习新、梁紫薇、王锴佳
岳阳市人民医院

目的 本临床试验采用盲法、对比试验设计。以核酸序列测定方法（Sanger 测序法）作为对照方法，将入选样本编码后，采用对照方法和待考核试剂盒分别进行盲法检测，待试验结束后揭盲，将待考核试剂盒检测结果与对照方法检测结果进行比较分析，用以评价待考核试剂盒的临床应用性能。
方法 根据《体外诊断试剂注册管理办法》和《体外诊断试剂临床试验技术指导原则》的要求进行临床试验设计。本临床试验采用盲法、对比试验设计。将入选样本编码，用对照方法和待考核试剂盒分别进行盲法检测，试验结束后揭盲，以评价待考核试剂盒的临床应用性能。
结果 本次临床试验根据临床试验方案要求，随机筛选样本 230 例，根据纳入标准入组样本 230 例，根据排除标准和剔除标准，最终纳入统计样本样本 230 例，样本类型为鼻咽拭子。本次研究采用测序方法作为对照方法。
本次临床试验中，经检测鼻咽拭子样本 230 例，对照方法检测结果为阳性的样本 31 例，检测结果为阴性的样本 199 例；待考核试剂盒检测结果为阳性的样本 33 例，检测结果为阴性的样本 197 例。二者阴阳性结果不一致的样本有 2 例。
经统计分析，与对照方法相比，待考核试剂的检测阳性符合率为 100.00%、阴性符合率为 98.99%、总符合率为 99.13%。使用 IBM SPSS22.0 软件进行 kappa 检验，kappa=0.964，P＜0.001。α=0.05 检验水准下，待考核试剂与对照方法检测结果的一致性好，且具有统计学意义。
结论 本次临床试验结果表明待考核试剂盒可靠，准确，安全，简便，稳定，具有较高的临床应用价值。

PU-0374

CMV DNA 和 CMV 抗体在器官移植病人巨细胞病毒感染诊断中的作用

谭伟清
南方医科大学珠江医院

目的 探讨巨细胞病毒（Cytomegalovirus， CMV） DNA 和 CMV-IgM 抗体在诊断器官移植病人巨细胞病毒感染中的作用。
方法 以实时荧光定量聚合酶链反应（PCR）检测 52 例器官移植患者共 56 份尿和外周血单个核细胞 （PBMC） CMV-DNA，同时以酶联免疫吸附分析（ELISA）方法检测血清 CMV-IgM 抗体。
结果 56 份血清标本中 CMV-IgM 抗体阳性 8 例 （14.3%），而尿和 PBMC 的荧光定量 PCR 检测 CMV-DNA 阳性例数分别为 17 例（30.4%）和 21 例（37.5%）。
结论 对于器官移植患者，CMV-IgM 抗体作为 CMV 现症感染的血清学标志物阳性率偏低，检测尿中 CMV-DNA 可以提高阳性率，但依然存在部分漏检的情况，而 PBMC 的 CMV-DNA 则具有较高的阳性率，应该作为器官移植术后患者 CMV 现症感染的首选指标。

PU-0375

优化新型冠状病毒核酸提取方法后的最低检测限评价

宋宇[1,3,4]、罗艳秋[2]、郭文倩[2]、刘子杰[1,3,4]
1. 昆明医科大学第一附属医院
2. 瑞丽市畹町经济开发区人民医院
3. 云南省检验医学重点实验室
4. 昆明医科大学第一附属医院临床检验诊断省创新团队

目的 评价经优化（增大核酸样本提取量）后新型冠状病毒核酸检验程序的最低检测限。
方法 将 SARS-COV-2 定值质控品稀释成 5 个浓度，每个浓度准备 16 份样本，每份样本吸取 1000μl 提取核酸后进行荧光 PCR 检测，计算每个浓度样本的检出率，分别以浓度的对数（以 10 为底）和检出率作 probit 回归分析，得到 SARS-CoV-2 ORF1ab 基因和 N 基因检出率为 95%所对应的浓度。收集 101 例新冠肺炎患者的口鼻咽拭子标本，分别以样本量 1000μl (程序 1）和 200μl（程序 2）分别提取核酸后进行荧光 PCR 检测，比较两种不同检验方法的检出率差异。
结果 SARS-CoV-2 ORF1ab 基因和 N 基因检出率为 95%时所对应的浓度分别为 19.3 copies/mL (95% 置信区间, 15.2-31.1copies/mL), 34.8 copies/mL (95% 置信区间,27.2-54.4copies/mL)。101 例临床样本经检测后，方法 1 检出 65 例阳性，方法 2 检出 54 例阳性，方法 1 的检出率显著高于方法 2。
结论 扩大样本提取量后 SARS-CoV-2 ORF1ab 基因和 N 基因的检测灵敏度明显提高。

PU-0376

新型冠状病毒的研究进展

汪佳婕
盘龙区北京路 1228 号

自 2019 年发现新型冠状肺炎病毒以来，对全球的健康造成了巨大的威胁，至今虽然疫情在我国已经得到了良好的控制，但准确的了解 SARS-Cov2，并快速的诊断新冠病毒至关重要。高通量测序（NGS）和实时荧光定量 PCR（qPCR）技术是目前已知的主要核酸检测技术，现基于 CRISPR 的诊断技术已经在 COVID-19 中得以运用，该技术不仅具有很高的灵敏度和特异度，且大大缩短了检测时间，为新冠病毒的快速诊断提供了有力地依据。本文从新冠病毒的起源开始，对新型冠状病毒检测方法进行概述。

PU-0377

1278 例沙眼衣原体、解脲脲原体和淋球菌核酸检测结果分析

白俊、吴定辉、雷秀琴、刘婷
四川金域医学检验中心有限公司

目的 了解四川 1278 例沙眼衣原体、解脲脲原体和淋球菌的感染情况及其特点，为 STD 预防以及临床治疗提供依据。
方法 采用实时荧光 PCR 法对 1278 例患者的泌尿生殖道分泌物的 CT、UU 和 NG 核酸进行定性检测，对检测结果进行统计分析。
结果 1278 例患者的样本中，UU-DNA 检出阳性 663 例，检出率最高，为 51.88%，CT-DNA 和 NG-DNA 的阳性例数分别为 95、71 例，阳性检出率分别为 7.43%、5.56%；女性 UU 感染率为 59.40%明显高于男性 33.69%（P＜0.01），男性 NG 感染率 12.83%明显高于女性 2.54%（P＜0.01），CT 感染率男性为 10.16%高于女性 6.31%，但无性别差异（P＞0.05）。感染类型以单一

病原体感染为主，阳性率为 52.90%（676 例阳性），其中 UU 阳性率最高为 46.56%，CT、NG 分别为 2.74%、3.60%；混合感染检出率为 5.63%，其中 CT+UU 双重感染的阳性检出率最高，为 3.68%，CT+NG、UU+NG、CT+UU+NG 阳性检出率分别为 0.31%、0.94%、0.70%。不同年龄段的感染情况显示，21-30 岁年龄段感染率最高为 24.49%，其次为 31-40 岁年龄段，阳性检测率为 19.33%,其余年龄段相对较低。

结论 1278 例沙眼衣原体、解脲脲原体和淋球菌检测结果中，三种病原体的阳性检出率不尽相同；女性 UU 感染率明显高于男性，男性 NG 感染率明显高于女性；不同年龄段之间的阳性率有较大差异，其中青壮年（21-40 岁）阳性率最高，所以青壮年应作为性传播疾病防治工作的重点对象；混合感染较为常见，尤其是 CT 合并 UU 感染，因此在性传播疾病筛查诊断时，沙眼衣原体、解脲脲原体和淋球菌三种病原体均需同时检测，为临床治疗提供依据。

PU-0378

Mutation Detection of Mitochondrial DNA D-loop Region in Bone Marrow Cells of Acute Myeloid Leukemia

Songling Huang 、ying zhao
Department of Clinical Laboratory, the First Affiliated Hospital of Kunming Medical University, Kunming, 650032, China

AIM The aim of this study was to detect the mutations in the D-loop region of mitochondrial DNA (mtDNA) in bone marrow cells of patients with acute myeloid leukemia and to analyze their relationship with the pathogenesis of acute myeloid leukemia.
METHODS Twenty-nine newly diagnosed patients with acute myeloid leukemia were selected to extract mtDNA from bone marrow cells and amplify the sequence of mtDNA D-loop region by PCR. The gene sequence of the amplified products was detected by direct forward and reverse sequencing. The results were compared with the revised Cambridge standard sequence and related databases (MITOMAP database, GenBank database, mtDB database).
RESULTS The results showed that the mutation rate of mtDNA D-loop region in acute myeloid leukemia was 82% (24/29 cases), and there was no significant difference in the number of mutations among patients of different ages and types of acute myeloid leukemia (P > 0.05).
CONCLUSION There are high frequency mutations in mtDNA D.1 OOP region of bone marrow cells from acute myeloid leukemia, and the mutations may be related to the pathogenesis of acute myeloid leukemia.

PU-0379

海拔高度对 2 型糖尿病患者循环内皮祖细胞及低氧诱导因子的影响

哈小琴、陈斌泽、李兵、邢媛、张媛媛、胡秦妮
中国人民解放军联勤保障部队第 940 医院（原兰州军区兰州总医院）

目的 探讨不同海拔地区 2 型糖尿病患者循环内皮祖细胞数量及相关指标的变化情况。
方法 选取低海拔地区（咸阳市）和高海拔地区（兰州市）各一家医院内被诊断的 2 型糖尿病患者（共 54 人）和健康体检者（共 40 人），收集基本信息，检测两组人群血脂、血糖、糖化血红蛋白以及低氧诱导因子-1α（HIF-1α）浓度，并用流式细胞仪测定外周血内皮祖细胞（EPCs）数量。
结果 与低海拔地区相较，高海拔地区糖尿病组和健康组循环 EPCs 数量均减少（P＜0.001），HIF-1α 水平显著增高；糖尿病患者体质指数(BMI)、腰臀比(WHR)、甘油三酯（TG）、血糖及糖化血红蛋白（HbAlc）均高于健康组（P＜0.05），而循环 EPCs 低于健康者（P＜0.001）。外周血

EPCs 数量由高到低依次为健康者、2 型糖尿病无血管并发症者、2 型糖尿病伴微血管并发症者，且差异具有统计学意义（P＜0.05）；2 型糖尿病伴大血管并发症者与 2 型糖尿病伴微血管并发症者相比无统计学意义（P＞0.05）。
结论 高海拔地区较低海拔地区人群 HIF-1α 表水平增加，循环 EPCs 数量显著减少，2 型糖尿病患者循环 EPCs 与健康者相比显著减少且与疾病程度相关。

PU-0380

海拔对 2 型糖尿病患者外周血单个核细胞迁移和粘附功能的影响

哈小琴、李兵、王晓辉、邢媛、谢艳芳
中国人民解放军联勤保障部队第 940 医院（原兰州军区兰州总医院）

目的 比较分析不同海拔地区 2 型糖尿病患者外周血单个核细胞功能变化情况。
方法 选取咸阳市和兰州市各一家医院的 2 型糖尿病患者共 54 人，同期健康体检者共 40 人。用密度梯度离心法提取外周血单个核细胞（PBMCs）；用 ELISA 检测血清中反应 PBMCs 迁移、粘附和成血管的因子的浓度：缺氧诱导因子-1a（HIF-1a）、基质细胞衍生因子（SDF-1）、白细胞介素-8（IL-8）和血管内皮生长因子（VEGF）；用荧光定量 PCR 检测 PBMCs 中趋化因子受体 2/4（CXCR2/CXCR4）和白细胞粘连蛋白（LFA-1）mRNA 的相对表达；用蛋白质印迹法检测 PBMCs 中 CXCR2 和 CXCR4 的蛋白量。
结果 血清各因子检测显示，低海拔地区较高海拔地区 SDF-1 和 HIF-1a 表达降低（P<0.05），IL-8 和 VEGF 的表达量升高（P<0.05）；T2DM 高海拔组较低海拔组 SDF-1 和 HIF-1a 的表达升高，IL-8 和 VEGF 的表达降低，差异均有统计学意义（P<0.05）。基因表达量检测显示，低海拔组内 T2DM 者较健康者各基因相对表达量降低，CXCR2 表达差异有统计学意义（P<0.001）；高海拔组 T2DM 者较健康者各基因表达量也均降低，CXCR2 和 CXCR4 基因表达量差异有统计学意义（P<0.001）。蛋白含量测定显示，低海拔组较高海拔 CXCR2 和 CXCR4 蛋白量均较高（P<0.05），健康者 CXCR2 和 CXCR4 蛋白量均高于 T2DM 患者（P<0.05）。
结论 随着海拔的升高，2 型糖尿病患者较健康者缺氧程度加重，外周血 PBMCs 迁移增强、黏附性和成血管能力减弱，调节紊乱。

PU-0381

Sphingosine-1-phosphate does not interfere with HBV replication in hepatocytes in vitro

Weimin Wu
中南大学湘雅二医院检验科

Background/Aim Sphingosine-1-phosphate (S1P) is an important bio-active lipid, and its concentration is significantly increased in the peripheral blood of patients with hepatitis B. S1P activates signaling pathways such as PI3K/Akt and MAPK/ERK by binding to different S1P receptors on the cell surface, and participates in the regulation of various cell functions. Previous studies have shown that PI3K/Akt and MAPK/ERK are involved in regulating HBV replication in hepatocytes. Our previous data showed that the S1P chaperone (apolipoprotein M) was associated with viral replication status in chronic hepatitis B patient. However, the role of S1P in HBV replication in vitro was not clear. The purpose of this study was to determine whether S1P is directly involved in regulating HBV replication in hepatocytes.
Methods HepG2.2.15 cells were treated with different concentrations of S1P and S1P receptor agonist FTY720, and then HBV DNA in the cell supernatant was measured using quantitative PCR , HBsAg and HBeAg in the supernatant were measured using chemiluminescence method.

Results After treating HepG2.2.15 with S1P (up to 3μM) and FTY720 (up to 5μM), the level of HBV DNA, HBsAg and HBeAg in the cell supernatant did not change significantly.
Conclusion Our data indicated that sphingosine-1-phosphate does not interfere with HBV replication in hepatocytes in vitro.

PU-0382

黄芪多糖联合 TPHK 防治低氧水浸复合应激致大鼠肠道损伤微生态的影响研究

杨志华、王晓辉、哈小琴、张全华
中国人民解放军联勤保障部队第九四〇医院

目的 研究携带低氧诱导因子（HIF-1α）与角质细胞生长因子（KGF）双基因真核表达载体的重组减毒沙门菌菌(TPHK) 对低氧水浸复合应激致大鼠肠道损伤微生态的影响研究肠道微生态的作用，为 TPHK 防治应激性损伤提供依据；研究黄芪多糖对低氧水浸复合应激致大鼠胃肠粘膜损伤的微生态的作用以及黄芪多糖与 TPHK 的协同作用，为中药与菌苗联合服用提供依据。
方法（1）通过服用 TPHK 菌苗和黄芪多糖水溶液，在低氧舱内模拟高原低氧水浸复合应激方法制造大鼠应激性溃疡模型，实验分为空白组(N 组)、模型组（M 组）、TPHK 组（T 组）、黄芪组(H 组)、TPHK+黄芪组（L 组）），在造模前，造模后 3 天、5 天、7 天分别取大鼠粪便进行检测，通过 S 高通量测序检测肠道微生态菌群组成与结构的变化。
结果 黄芪多糖组和 TPHK 组经灌胃治疗后，毛色光泽度好转，进食量增加，活动度增加，大便性状有所好转，以联合组恢复最好；与 M 组比较，低氧 3d 时 T、L 组 HIF-1α 蛋白未出现明显变化，低氧 5d、7d 时 T、L 组 HIF-1α 和 KGF 蛋白显著上调（$P<0.05$），L 组大鼠 HIF-1α 蛋白在 7d 时较 T 组显著下调，但仍较 M 组显著增加（$P<0.05$）；低氧 3d 以后，T、L 组 KGF 蛋白的表达与 M 组比显著上调（$P<0.05$）。此外，L 组大鼠 KGF 蛋白在 7d 时较 T 组显著下调（$P<0.05$）。结肠组织 IL-10 在第 3d 至第 7d 时，H 组、T 组及 L 组肠组织 IL-10 表达显著高于 N 组和 M 组（$P<0.01$），且应激 5d 和第 7d 时 L 组 IL-10 的表达显著高于 H 组和 T 组（$P<0.05$）。细菌属的层面分析显示低氧应激可显著降低乳酸杆菌属（Lactobacillus）的丰度， TPHK 与黄芪多糖治疗可以明显提高造模后毛螺科菌与乳杆菌两种益生菌的含量，提高其定植能力，进而发挥保护肠道微生态的作用。
结论 低氧水浸复合应激后，TPHK 与黄芪多糖联合应用能够纠正低氧水浸复合应激致肠道微生态的紊乱，对大鼠胃肠损伤有保护作用。

PU-0383

HIF-1α 和 HGF 双基因修饰大鼠间充质干细胞对高原大鼠股骨缺损模型修复的影响研究

谢艳芳、哈小琴、王晓辉、杨志华、李兵
联勤保障部队第九四〇医院

目的 利用基因治疗和细胞治疗相结合的方法促进低氧条件下高海拔地区骨缺损修复速度和愈合质量。本实验旨在利用低氧诱导因子-1α（hypoxia inducible factor -1，HIF-1α），肝细胞生长因子（hepatocyte growth factor，HGF）联合作用骨髓间充质干细胞（bone marrow-mesenchymal stem cells，BM-MSCs），为低氧条件下改善高海拔地区大鼠股骨缺损模型的修复效果建立新的治疗方案。
方法 将高海拔雌性大鼠股骨缺损动物模型随机分为 5 组：A 组（PBS 对照组）、B 组（BM-MSCs 移植组）、C 组（HIF-1α 基因修饰 BM-MSCs 移植组）、D 组（HGF 基因修饰 BM-MSCs 移植

组）、E 组（双基因修饰 BM-MSCs 移植组），建模后将相应细胞进行局部移植；分别于第 10 d、20 d、30 d 通过 X-ray 检测骨缺损修复情况；于第 20 d 分离出新生骨组织，通过 HE 染色观察其新生股骨厚度和原位杂交法检测组织中雄性 BM-MSCs 的数量及分布；于第 2 d、5 d、10 d、20d 检测股骨组织中 ALP(碱性磷酸酶的含量)；最后通过 Real-time PCR 和 ELISA 法法检测股骨组织中 HIF-1α 和 HGF 的表达情况。

结果 通过 X-ray 检测发现携带双基因的 BM-MSCs 移植组的股骨修复速度较其他组快，且其组织中 ALP 含量高于其他组（P<0.05）；通过原位杂交法检测发现当 HIF-1α 和 HGF 同时高表达时，BM-MSCs 在组织分化的细胞数量明显增多，其抗低氧能力和组织中的存活率明显升高。通过 ELISA 法和 Real-time PCR 法检测 HIF-1α 和 HGF 两种基因在局部组织内均有良好的表达，且 E 组各时间点的浓度均高于其他组（P<0.05）。

结论 将 HIF-1α 和 HGF 双基因修饰的 BM-MSCs 移植到高海拔大鼠股骨缺损动物模型中，均可以检测到 HIF-1α 和 HGF 基因在体内局部有表达，并能够与干细胞共同发挥作用促进股骨缺损的创伤修复。

PU-0384

KGF 联合 HIF-1α 对 BECN1 敲除 IEC-6 细胞缺氧的保护作用及机制

王晓辉、哈小琴、杨志华、李兵
联勤保障部队第九四〇医院

目的 探讨 KGF 联合 HIF-1α 对 BECN1 敲除后的 IEC-6 细胞在缺氧应激状态下的保护作用及相关机制。

方法 利用 CRISPR/Cas9 技术慢病毒转染构建敲除 BECN1 基因的稳定细胞系 IEC-6B-细胞。实验分为空白对照组（Blank control group, BC 组）、阴性对照组（Negative control group, NC 组）、HIF-1α 组、KGF 联合 HIF-1α 组（KH 组），各组细胞 5 %氧浓度培养 24 h。光学显微镜和透射电镜观察细胞形态学改变。CCK-8 法检测细胞存活率。ATP 含量测试盒测定细胞 ATP 含量。流式细胞分析仪检测细胞周期和细胞凋亡率。实时荧光定量 PCR 法检测自噬相关基因 BECN1、SQSTM1 及 LC3 的 mRNA 表达水平。Western blot 法检测凋亡蛋白 Bax/Bcl-2、Caspase3 及自噬相关蛋白 Beclin 1、LC3 II/LC3 I、p62 的表达。

结果 成功构建敲除 Beclin1 蛋白的 IEC-6B-细胞系。低氧处理 24h 后，各组细胞镜下可见梭形、星形及其它异常形态变化。电镜观察 NC 组细胞染色质固缩聚集，胞质内可见大量大小不一的吞噬溶酶体泡；其他各组细胞染色质分散边缘聚集，呈现细胞早期凋亡形态变化，BC 组和 KH 组细胞胞质中可见自噬泡。与 BC 组相比较，各敲除组细胞存活率均显著降低（P<0.01），其中 KH 组细胞存活率高于 NC 组、KGF 组及 HIF-1α 组（P<0.05）。BC 组细胞内 ATP 含量均显著高于其他各组（P<0.05）。与 BC 组和 KH 组比较，NC 组、KGF 组及 HIF-1α 组细胞 G0/G1 期百分比显著增加，细胞凋亡率均显著增加（P<0.05），KH 组与 BC 组之间无显著差异（P>0.05）。与 BC 组相比较，NC 组、KGF 组、HIF-1α 组及 KH 组细胞自噬基因 BECN1、SQSTM1 及 LC3 基因 mRNA 表达均显著降低（P<0.05）。与 BC 组相比较，NC 组、KGF 组、HIF-1α 组及 KH 组细胞 Beclin 1 蛋白及 LC3 II/LC3 I 的比值均显著降低（P<0.05），且 p62 蛋白表达显著增加（P<0.05），NC 组、KGF 组及 KH 组细胞 Bax/Bcl-2 的比值、Caspase3 蛋白表达相比 BC 组显著增加（P<0.05），其中 KH 组的 Bax/Bcl-2 的比值、Caspase3 蛋白表达低于 NC 组（P<0.05）。

结论 KGF 联合 HIF-1α 能促进细胞增殖、增强细胞能量代谢、减少 G0/G1 期阻滞细胞率、抑制细胞凋亡作用，对低氧应激的 IEC-6B-细胞具有保护作用。

PU-0385

新型手性固定相用于检测大鼠血浆中氟比洛芬对映体浓度

孙嘉仪
中国医科大学附属第一医院国家医学检验临床医学研究中心

基于手性固定相的液质联用技术是分离或检测体内手性药物对映体的一个非常有效的方法。这种方法可以根据预分离化合物的结构特点而有目的地制备分离效能高、性能稳定的新型手性固定相，缩短检测时间、提高检测灵敏度、减少检测成本。目的将新制备的手性固定相与液质联用技术相结合，建立大鼠血浆中氟比洛芬对映体浓度检测方法。方法采用氨基键法，通过区域选择性酯化反应、取代反应、加成反应及全衍生化，制备 4-氯苯基氨基甲酸酯取代的 β-环糊精手性固定相。采用固态核磁、红外光谱对手性固定相的化学结构进行确证；采用元素分析法测得固定相表面配体浓度；采用扫描电镜和透射电镜对其微观形貌进行表征；采用热重分析法研究合成手性固定相的热稳定性。通过考察有机改性剂的种类、比例和缓冲盐浓度对分离的影响，优化色谱条件，并将自制固定相上得到的分离结果与商品化固定相上得到的分离结果进行对比。采用固相萃取法处理血浆样品，通过比较不同种类的固相萃取小柱的提取回收率，确定最佳样品预处理方案。结果在优化的色谱条件下，氟比洛芬对映体可获得完全分离，且分离时间及分离度均优于其他商品化固定相。在大鼠血浆中的提取回收率在 92.1%-94.5%之间。测定单一对映体的线性范围在 10.0～20000.0 ng mL-1 之间，定量限为 10.0 ng mL-1。方法的准确度（RE）≤9.4，日内和日间精密度（RSD）≤7.3。结论建立的方法被成功应用于灌胃给予消旋氟比洛芬后药物在大鼠体内的立体选择性药动学研究中。为将来新型手性固定相应用于临床手性药物检测提供可能。

PU-0386

miR-128-3p 在急性冠脉综合征患者血清中的表达水平及其临床意义

刘月娥、关秀茹
哈尔滨医科大学附属第一医院

背景及目的 急性冠脉综合征（ACS）是全球死亡的主要原因之一，给人类带来严重的社会经济负担。ACS 及时准确的诊断有助于患者快速进行缺血再灌注治疗，从而减少并发症以及降低死亡率。循环 miRNAs 因具有许多优势，有望成为 ACS 的潜在生物标志物。有研究发现 miR-128-3p 可通过不同的机制参与心血管疾病的进展，但尚未有循环 miR-128-3p 在 ACS 临床研究中的相关报道。
方法 收集经冠状动脉造影（CAG）的 ACS 患者 60 例和健康体检者 30 例入院 3 小时内的血清，并收集所有受试者的完整病历资料。ACS 患者包括 24 例不稳定性心绞痛（UA）和 36 例急性心肌梗死（AMI）。及时提取总 miRNA 并进行逆转录，血清中 miR-128-3p 的表达水平采用 RT-qPCR 外参法进行相对定量，血清中炎症因子 IL-18 及 IL-1β 的含量采用 ELISA 进行绝对定量。
结果（1）ACS 组血清中 miR-128-3p 的表达水平较对照组显著降低（P<0.001）；UA 组、AMI 组 miR-128-3p 的表达水平较对照组显著降低（P<0.001），且 UA 组 miR-128-3p 的表达水平显著高于 AMI 组（P<0.001）。
（2）ACS 组 IL-1β 的含量相对于对照组显著增高（P<0.05）。
（3）ACS 组血清中 miR-128-3p 的表达水平与 Gensini 分数呈显著负相关（r=-0.6539，P<0.001）。
（4）miR-128-3p 的表达水平与 BNP、CK-MB、NLR、PT、hsCRP、cTnI、NNT 呈负相关（r=-0.288，P=0.025；r=-0.372，P=0.003；r=-0.346，P=0.007；r=-0.301，P=0.019；r=-0.465，P<0.001；r=-0.522，P<0.001；r=-0.689, P<0.001）；miR-128-3p 的表达水平与 EF、PLT 呈正相关（r=0.537，P<0.001；r=0.268，P=0.038）。

（5）miR-128-3p、cTnI、CK-MB 能可靠的区分 ACS 与对照组，AUC 值分别为 0.881、0.899、0.872。指标联合可显著提高诊断性能，miR-128-3p 与 CK-MB 联合的 AUC 值为 0.924，与 cTnI 联合的 AUC 值为 0.920。
（6）PT、DBP、miR-128-3p 均是 ACS 的独立危险因素（P<0.05）。
结论 血清 miR-128-3p 可能是 ACS 患者早期诊断、严重程度及风险评估的新型生物标志物。

PU-0387

尿沉渣 SNORA48 作为肾细胞癌的新型诊断标志物

郑白冰、张悦、尚晓玲、宋兴国、宋现让、谢丽
山东省肿瘤医院

背景 近年来，肾细胞癌发病率逐年升高，但是目前缺乏有效的用于早期诊断肾细胞癌的生物标志物。因此，本研究的目的是验证一种新的诊断肾细胞癌(RCC)的生物标志物。
材料与方法 研究纳入 TCGA 数据库中 516 例透明细胞肾细胞癌以及 71 例病例组织，并从 SNORic 数据库(http: //bioinfo.life.hust.edu.cn/SNORic)获取 SNORA48 的表达水平。然后，我们进一步在 110 例尿沉渣和 30 例血浆及其各自的对照样本中研究了 SNORA48 的表达水平。ROC 曲线用于研究 SNORA48 作为肾癌诊断标志物的诊断效能。
结果 利用 TCGA 数据库，我们发现，与癌旁组织相比，肿瘤组织中 SNORA48 的表达水平明显升高(P< 0.0001)。然后，我们进一步分析了 110 例 RCC 患者和 130 例健康志愿者尿沉渣中 SNORA48 的表达量。结果仍然表明，与正常人相比，在 RCC 尿沉渣中，SNORA48 的表达量明显增加(P< 0.0001)。ROC 曲线显示，尿沉渣 SNORA48 诊断肾癌的 AUC 为 0.71.然而，通过对 30 例 RCC 患者和 30 例健康人的血浆进行分析时，我们未发现 SNORA48 的表达在两组队列中有统计学上的差异。这预示了尿沉渣可能有优于血样本作为生物标志物的潜能。
结论 我们的研究结果表明，尿沉渣 SNORA48 可能是 RCC 患者新的、有前景的非侵入性诊断生物标志物，与肾癌发生密切相关。

PU-0388

TMEM40 在膀胱癌中作用的初步研究

张振飞
南方医科大学珠江医院

目的 深入了解膀胱癌形成的分子机制，完善针对不同膀胱癌患者特异的诊断及治疗方法，寻找膀胱癌特有的分子诊断标志物，以实现基因靶向诊治，从而降低膀胱癌患者的发病率和死亡率，提高患者术后 5 年的生存率及生存质量，是当今医学需要解决的难题。
方法 在当前的研究中我们通过 qRT-PCR 及 WB 检测了膀胱癌细胞及组织中 TMEM40 在 mRNA 及蛋白水平的表达，结果表明 TMEM40 在膀胱癌细胞与组织中表达均上调；其次，通过组织芯片的免疫组化实验，探究 TMEM40 表达水平高低与膀胱癌患者临床病理参数间的关系。
结果 在 115 例膀胱癌患者中，TMEM40 的表达与患者的临床分期、pT 分期、组织病理学分级具有明显的相关性，而与患者的年龄、性别等无显著相关。接下来，我们选取两株人膀胱癌细胞系（5637、EJ），采用不同浓度梯度的 G418 筛选 TMEM40 过表达及敲减的膀胱癌细胞，扩大培养来得到稳定表达的细胞株。最后，通过 CCK-8、EdU、Transwell、细胞周期、凋亡及裸鼠皮下成瘤等一系列功能实验，来进一步验证 TMEM40 对膀胱癌恶性表型的影响。细胞增殖实验结果表明，TMEM40 表达上调促进细胞的增殖，而 TMEM40 下调则在一定程度上抑制了细胞的增殖；Transwell 实验表明，TMEM40 表达上调促进细胞迁移、侵袭，而 TMEM40 敲减则抑制细胞迁移、侵袭；流式细胞仪检测结果表明，过表达 TMEM40 对细胞的凋亡具有一定的抑制作用，而敲减

TMEM40 则促进了细胞的凋亡；过表达 TMEM40 加快 G1/S 期变，而敲减 TMEM40 则细胞周期阻滞在 G1 期。此外，裸鼠体内成瘤实验结果表明，与对照组相比，敲减 TMEM40 能够明显抑制裸鼠体内肿瘤的生长。

结论 研究表明，TMEM40 在膀胱癌组织及细胞中高表达，其表达水平与膀胱癌的迁移、侵袭、增殖等恶性表型密切相关，过表达 TMEM40 还能够抑制 5637 和 EJ 细胞的凋亡并加快 G1/S 转变。因此，TMEM40 在膀胱癌的发生发展过程中发挥着重要的作用，有可能成为膀胱癌患者临床治疗的基因靶点及分子标志物。

PU-0389

高通量测序在疾病诊断中的作用

温金
山东大学第二医院

高通量测序极大地提高了我们确定和诊断人类疾病潜在原因的能力。全基因组测序和全外显子组测序的使用促进了对遗传病新基因的更快、更经济有效的鉴定。它还提高了我们识别遗传病致病突变的能力，这些突变与已知的相关基因有关。这些好处不仅适用于目的是评估成人和儿童遗传疾病风险的情况，也适用于产前基因检测和胚胎检测。高通量测序也影响了我们评估复杂疾病风险的能力，并可能继续影响疾病研究的这一领域，因为越来越多的个人进行测序，我们更好地理解整个基因组中罕见和常见的变异的重要性。

新一代测序的速度和准确性不断提高，对我们识别与疾病风险有关的基因和诊断遗传疾病的能力的速度和范围产生了显著影响，而且改进的步伐并没有放慢。更高通量的技术正在开发和测试，目的是进一步减少处理时间和测序成本。总的来说，我们对高通量测序不同应用的伦理框架和标准的发展，以及我们对各种基因改变对个人健康的影响的理解，在评估遗传疾病风险方面比测序技术的局限性多得多。随着测序技术的进步似乎可能继续超过其他领域的发展，我们将面临有趣的时刻，因为我们将看到这种差异在未来评估遗传疾病风险的努力中如何表现出来。

PU-0390

血浆 SNORD84 作为诊断非小细胞肺癌的新型肿瘤标志物

王世文、王康羽、宋兴国、谢丽、宋现让
山东省肿瘤医院

研究目的 肺癌是世界上发病率最高的肿瘤，每年大约会有 160 万人因肺癌死亡。根据组织类型，肺癌可分为非小细胞肺癌（NSCLC）和小细胞肺癌（SCLC），其中非小细胞肺癌约占 85%。由于其早期无明显症状，通常在晚期才被确诊。据报道，接受有效治疗的 1 期非小细胞肺癌患者一年存活率为 83%，而晚期非小细胞肺癌患者仅为 14%。因此，揭示非小细胞肺癌发生发展的分子机制，寻找新的可反映肿瘤早期发展的生物标志物尤其重要。小核仁 RNA(snoRNAs)是一类广泛分布于真核生物细胞核仁的小分子非编码 RNA，长度为 60～300 个核苷酸，主要参与 rRNA 和其他小 RNA 转录后的成熟加工过程。snoRNAs 主要分为 C /D box snoRNAs 和 H/ACA box snoRNAs 两类,C/D box snoRNAs 主要介导 rRNA 特定位点的 2’-O-甲基化,而 H /ACA box snoRNAs 主要介导 rRNA 特定位点的假尿苷化，二者均能与核糖核蛋白(RNPs) 结合形成稳定的、具有功能的 snoRNPs 复合体。近年来越来越多的证据表明 snoRNA 与肿瘤的发生、发展有关。此外，在肿瘤细胞中部分 snoRNAs 的异常表达以及可在血液中长期稳定存在的特征，也为其成为肿瘤诊断及其预后监测的生物标志物提供了可能。本研究旨在探索 SNORD84 是否可以作为诊断非小细胞肺癌的生物标志物。

研究方法 1.TCGA 数据库筛选差异表达的 SNORNA 基因。

2.数据库及 24 对 FFPE 样本验证 SNORNA 的差异表达。
3.分析 snoRNA 在血浆中的表达特点。
4.收集 107 例肺癌血浆及 110 例健康人血浆样本分离提纯游离 RNA 并通过 RT-PCR 验证 snoRNA 差异表达。
结果 1.SNORD84 在来自数据库配对癌组织与正常组织具有显著的差异表达(P<0.0001)。
2.数据库大样本及 FFPE 样本验证 SNORD84 在肺癌组织中的表达显著高于癌旁组织(P<0.0001)。
3.SNORD84 在血浆中稳定存在。
4.SNORD84 在 107 例肺癌血浆中表达显著高于在 110 例健康人血浆中的表达（P<0.05）。
结论 SNORD84 可作为非小细胞肺癌诊断的循环肿瘤标志物。

PU-0391

尿液中 miRNA 作为恶性肿瘤非侵入性诊断生物标志物的研究进展

吴亚婷[1,2]、李卓林[1,2]、贾如雪[1,2]、张胜行[1,2]、王水良[1,2]
1. 厦门大学附属东方医院福建省适配体技术重点实验室
2. 联勤保障部队第九〇〇医院检验科

全球每年约有 2 千万左右的恶性肿瘤新发病例，而因肿瘤致死的患者近 1 千万人；恶性肿瘤不仅严重危害着人类的健康，也极大地限制了群体的平均预期寿命。鉴于迄今为止，绝大部分中晚期恶性肿瘤患者的综合治疗效果仍然很局限，因此肿瘤的早期诊断对及时有效干预措施的采取以提高患者生存率和改善预后至关重要。肿瘤标志物作为一类与特定肿瘤发生、发展和转归密切相关的生物分子，可存在于患者组织、体液和排泄物，对其的特异检测在肿瘤的早期筛查以及患者治疗反应性的监测中发挥着重要的作用。MicroRNAs（miRNAs）是一类广泛存在且生物学功能多样的小分子非编码 RNAs；越来越多研究表明因遗传或表观遗传学改变所致的特定 miRNAs 的表达失调控在肿瘤恶性进展过程中起着重要的致癌和/或促癌作用。鉴于 miRNAs 可稳定存在血液、尿液、脑脊液或唾液等生物体液中，且与基于血液等液体活检相比，基于尿液的液体活检具有易于处理和无创取样等优势，因此尿液 miRNAs 作为潜在的新型肿瘤分子标志物的研究也吸引越来越多的关注。本综述就近年来尿液 miRNAs 在恶性肿瘤患者中作为非侵入性诊断生物标志物的研究进展作一总结，包括：miRNAs 作为肾细胞癌和膀胱癌等泌尿系统肿瘤、食管癌等消化系统肿瘤、乳腺癌等妇科肿瘤和中枢神经系统肿瘤的潜在生物标志物等方面；同时，对其未来可能的临床实际应用作了初步展望，并提出了一些亟待解决的问题以为未来的相关研究提供有益的启示。

PU-0392

Identification of differentially expressed mRNAs between breast cancer subtype tumor tissues by RNA-sequencing

Yanli Chen、Pengfei Liu、Chang Liu、Fei Xie、Xiaotao Zhao、Shu Wang
Peking University People's Hospital

Background We aim to investigate the different genes expression profiles between breast cancer subtypes. This is significant for deeper understanding of the biology, treatment and prognosis of breast cancer, especially in triple negative breast cancer (TNBC).
Methods Breast cancer tissue samples were obtained from 34 patients. Firstly, based on the ER, PR, Her2 status, the tumor samples were divided into 4 groups: luminal A subtype group, luminal B subtype group, HER-2 enriched subtype group and TNBC group. Then, to further explore the different gene expression profiles between TNBC and other breast cancer subtypes, the tumor samples were also divided into 2 groups: TNBC group and other breast cancer subtypes group.

To obtain differentially expressed mRNAs (DEmRNAs) between breast cancer subtype tumor tissues, RNA-sequencing and bioinformatics analysis were performed. Functional annotation of DEmRNAs were performed.
Results Comparing luminal A subtype and luminal B subtype, a total of 1126 DEmRNAs (325 up-regulated and 801 down-regulated) was obtained. Comparing luminal A subtype and HER-2 enriched subtype, a total of 89 DEmRNAs (6 up-regulated and 83 down-regulated) was obtained. Comparing luminal A subtype and TNBC, a total of 574 DEmRNAs (206 up-regulated and 368 down-regulated) was obtained. Comparing HER-2 enriched subtype and luminal B subtype, a total of 17 DEmRNAs (up-regulated) was obtained. Comparing luminal B subtype and TNBC, a total of 57 DEmRNAs (29 up-regulated and 28 down-regulated) was obtained. Comparing HER-2 enriched subtype and TNBC, a total of 20 DEmRNAs (19 up-regulated and 1 down-regulated) was obtained. Comparing other breast cancer subtypes and TNBC, a total of 273 DEmRNAs (172 up-regulated and 101 down-regulated) was obtained. Response to stimulus, immune system process, cell periphery and plasma membrane are significantly enriched GO terms between luminal A subtype and luminal B subtype tumor tissues. Cell cycle, cell cycle process, mitotic cell cycle and mitotic cell cycle process are significantly enriched GO terms between luminal A subtype and TNBC tumor tissues.Developmental process, anatomical structure development, tissue development and cell cycle are significantly enriched GO terms between other breast cancer subtype and TNBC tumor tissues. Mitophagy-animal, primary immunodeficiency, allograft rejection and asthma are significantly enriched KEGG pathways between luminal A subtype and luminal B subtype tumor tissues. Mitophagy-animal, cell cycle and autophagy-animal are significantly enriched KEGG pathways between luminal A subtype and TNBC tumor tissues. Glycosphingolipid biosynthesis-lacto and neolacto series is significantly enriched KEGG pathway between luminal B subtype and HER-2 enriched subtype tumor tissues. Nicotine addiction, mitophagy-animal, taste transduction and vitamin B6 metabolism are significantly enriched KEGG pathways between luminal B subtype and TNBC tumor tissues.Cell cycle, mitophagy-animal and autophagy-animal are significantly enriched KEGG pathways between TNBC and other subtype breast cancer tumor tissues.
Conclusion This research explore different gene expression profiles between breast cancer subtypes, which expected to present deeper understanding of the biology, treatment and prognosis of breast cancer, especially in TNBC.

PU-0393

Hsa_circ_0000437 enhances tumorigenesis and promotes lymphatic metastasis through exosomes via ERK signaling pathway in gastric cancer

Xianjuan Shen、Shan Kong、Shuo Ma、Lei Shen、Ming Zheng、Shaoqing Ju
Department of Laboratory Medicine, Affiliated Hospital of Nantong University

Background Circular RNAs (circRNAs) play a crucial regulatory role in the occurrence and development of cancer. Exosomes are essential for tumor growth, metastasis, and are used as novel signaling molecules in targeted therapies. Therefore, exosomal circRNAs can be used in new diagnostic and therapeutic approaches due to their involvement in the development of cancers. Exploring their roles and mechanisms of exosomal circRNAs in tumorigenesis and progression may help to identify new diagnostic markers and therapeutic targets. However, the detailed biological function, potential molecular mechanism and clinical application of exosomal circRNAs in gastric cancer (GC) remain unclear. In the present study, we investigated the role and regulatory mechanism of hsa_circ_0000437in gastric cancer (GC)
Methods circRNAs sequencing was performed to verify the significantly high expressed hsa_circ_0000437 in gastric cancer. Hsa_circ_0000437 levels in tissues, serum, cells and exosomes were analyzed using qRT-PCR assays. EdU, CCK-8, flow cytometry analysis, western

blotting and transwell were used to assess the role of hsa_circ_0000437 in cell proliferation, apoptosis, invasion and migration, respectively. The subcutaneous tumor model and popliteal LN metastasis model in nude mice were used to assess the role of hsa_circ_0000437 in vivo. ChIRP assays, parallel reaction monitoring (PRM) and western blotting were used to determine the direct binding of hsa_circ_0000437 to RNA binding protein (RBP) SRSF3. Exosomes were isolated by differential centrifugation and indentified by transmission electron microscopy (TEM) and Nano Sight NS 300 system. Fluorescent PKH67 labeled exosomes were utilized to determine the efficacy of the transfer of exosomal hsa_circ_0000437 between GC cells and recipient cells human lymphatic endothelial cells (HLECs). Tube formation assays was used to evaluate lymphangiogenesis and LN metastasis.

Results We previously performed circRNAs sequencing and verified the significantly high expressed hsa_circ_0000437 in gastric cancer that associated with lymph node metastasis. Mechanistically, hsa_circ_0000437 targets SRSF3 inhibiting PDCD4 to regulate proliferation, apoptosis, invasion and migration of GC cells. More importantly, hsa_circ_0000437 was characteristically enriched in and transferred by GC-secreted exosomes into HLECs to promote HLECs migration and tube formation in vitro, and facilitate lymphangiogenesis and LN metastasis in vivo according to both gain-of-function and loss-of-function experiments. Importantly, the exosomal hsa_circ_0000437 activated the ERK pathway in HLECs independent of VEGF-C. Finally, circulating exosomal hsa_circ_0000437 levels are closely associated with LN metastasis in GC patients.

Conclusions Our findings showed that hsa_circ_0000437 acted as a tumor oncogene in GC by forming a regulatory loop consisting of hsa_circ_0000437/SRSF3/PDCD4. GC-secreted exosomal hsa_circ_0000437 transfers into HLECs to promote lymphangiogenesis and lymphatic metastasis via ERK pathway and may be a potential GC prognosis biomarker, which can be used in precise targeted GC therapy.

PU-0394

Molecular biological correlation of allergic rhinitis and nasopharyngeal carcinoma

Xinying Qiu
Medical Laboratory of Shenzhen Luohu Hospital Group

Objective To obtain biomarkers of allergic rhinitis (AR) and Nasopharyngeal carcinoma (NPC) by performing bioinformatics analysis on gene chips related to allergic rhinitis in the Gene Expression Database (GEO).

Methods From June 2018 to December 2019, we downloaded data (GSE53819) involving 10 NPC patients from the publicallyavailable Gene Expression Omnibus database (http://biokb.ncpsb.org.cn/AlleRGatlas/index.), The test results of 10 patients with allergic rhinitis screened from the rhinitis database all met the requirement of ($P<0.05$)Then, we used the bioinformatics methods, including Gene Ontology (GO) analysis and Kyoto Encyclopedia of Gene, Genome (KEGG) pathway analysis and protein-protein interaction (PPI) network construction to identify key genes in AR and NPC. In the same period, the inferior turbinate mucosa tissues of 10 AR patients and 10 NPC patients controls were collected during operationinthe Department of Otolaryngology Head and Neck Surgery of Shenzhen Luohu Hospital to further verify important genes and pathways and perform real-time quantitative PCR. SPSS9.0 statistical software was used for statistical analysis .

Results A total of 36 differentially expressed genes (DEG) were selected, Among the 36 specific differential genes, four were closely related, namely SSTR1, CXCL8, CCR8, and CCL21. As can be seen from the list of enrichment analysis, inflammatory response、cytokine-cytokine receptor interaction、regulation of cytokine production，These three reactions are the most significant . Pathway and process enrichment analysis reflect which inflammatory response 、regulation of

cytokine production and regulation of cell adhesion， they all from GO Biological Processes. In the, NFKB1 、RELA 、STAT3 and JUN are significant. PPI networkand module analysis of Hub gene was carried out.KEGG pathway enrichment analysis was then performed for the DEGs in the four modules,The module 1 were significantly enriched in S.aureus infections.The module 2 were enriched in chemokine signaling pathways.viral protein interactions with cytokines. The DEGs in module 3 were mainly enriched in ubiquitin-mediated proteolysis. The DEGs in module 4 were enriched in Th1 and Th2 cell differentiation .The DEGs were inriched in chemokine signaling pathways.viral protein interactions with cytokine and cytokine receptors.Summary of enrichment analysis like Pathway and process enrichment analysis ,Th17 cell differentiation,primary immunodefiencicies,and T cell receptor signaling pathways. Both KEGG and GO analysis data were observed to be immune-related factors.

Conclusions a total of 36 genes closely related on the basis of AR and NPC was found in this study, these genes by PPI network and enrichment analysis. in addition to genetic factors, other factors should be considered, such as environment, diet, lifestyle, the immune factors and pathways through the relationship,It creates a better condition and platform for the study of the relationship between allergic rhinitis and nasopharyngeal carcinoma.To provide a better basis for clinical diagnosis and treatment.These genes are involved in the pathogenesis of AR and nasopharyngeal carcinoma, and are expected to become new AR biomarkers, paving the way for further exploration of the relationship between AR and nasopharyngeal carcinoma.

PU-0395

FOXC2 Attenuates LPS-Induced Cell Adhesion by Suppressing ICAM-1 Expression in HUVECs

Pan Li
Laboratory Medicine Center, Nanfang Hospital, Southern Medical University, Guangzhou, Guangdong, China.

Atherosclerosis is a chronic vascular inflammatory disease that involves diverse cell types and circulating regulatory factors, including intercellular adhesion molecule (ICAM)-1, a proinflammatory cytokine. Lipopolysaccharides (LPS) increase ICAM-1 expression and promote cell adhesion, but the mechanism is not clear. We found that LPS induced time- and dose-regulated upregulation of ICAM-1 expression and downregulation of forkhead box protein C2 (Foxc2) expression in human umbilical vein endothelial cells (HUVECs). Overexpression of Foxc2 significantly inhibited both LPS-induced ICAM-1 expression in HUVECs and LPS-induced adhesion of THP-1 cells to HUVECs. Foxc2 siRNA dramatically increased both LPS-induced ICAM-1 expression and LPS-induced adhesion of THP-1 human monocytes cells to HUVECs. We conclude that Foxc2 inhibited LPS-induced adhesion of THP-1 cells to HUVECs by suppressing ICAM-1 expression in HUVECs.

PU-0396

不同 HBV DNA 载量感染患者外周血肝纤维化指标差异分析

雷志萍、李彩东、田鹏飞、张旭强、陈俏丽
兰州市第二人民医院

目的 肝纤维化是一个动态、高度整合分子、细胞的过程，最终导致细胞外基质（Extracellular matrix, ECM）成分的过度积累。任何诱因引起的慢性肝病（Chronic liver disease, CLD）都有可能引起肝实质损伤和持续活动性炎症反应以及肝纤维化，HBV 感染是肝脏慢性炎症进展出现肝纤维化的主要原因之一。本文旨在探讨不同 HBV DNA 载量的慢乙肝（CHB）和肝硬化(LC)患者外周血肝纤维指标的差异。

方法 将我院就诊的 CHB 患者 60 例（男 50 例女 10 例）和 LC 患者 60 例（男 43 例女 17 例）纳入队列，PCR 方法检测 HBV DNA 载量、化学发光法检测肝纤维化透明质酸（HA）、层粘连蛋白（LN）、III 型前胶原（PCIII）、IV 型胶原（IV-C）水平，Mann-Whitney *U* 检验分析各组指标的整体差异。

结果 CHB 组和 LC 组患者整体的 HBV DNA 载量、HA 水平存在显著组间差异（*Z*=-4.35,*P*=0.000;*Z*=-4.56,*P*=0.000）、LN、PCIII 和 IV-C 水平差异无统计学意义（*P*>0.05）。HBV DNA 载量<1.00E+04 IU/mL 时，两组患者肝纤维化指标没有显著组间差异（*P*>0.05）。HBV DNA 载量 1.00E+05<1.00E+07 IU/mL 及≥1.00E+07IU/mL 时，CHB 组和 LC 组 HA 水平差异具有统计学意义（*Z*=-3.21, *P*=0.001；*Z*=-2.82,*P*=0.005）；其余指标组间差异不存在统计学意义（*P*>0.05）。CHB 组患者 HBV DNA 载量不同时，肝纤维化指标不存在显著差异（*P*>0.05），HBV DNA>1.00E+07 IU/mL 较<1.00E+04 IU/mL 的 LC 患者 PCIII 水平显著升高，差异具有统计学意义（*Z*=-2.83,*P*=0.005）；HBV DNA≥1.00E+07 IU/mL 较 HBV DNA 水平 1.00E+05<1.00E+07 IU/mL 的 LC 患者 LN 水平显著升高，差异具有统计学意义（*Z*=-2.12,*P*=0.034）。

结论 CHB 患者与 LC 患者及不同 HBV DNA 载量的 LC 患者肝纤维化指标存在一定差异，提示 HBV DNA 载量可一定程度上反应 LC 患者肝纤维化的可能。

PU-0397

HIV 分子传播网络指导的 MSM 传播风险模型的建立与评估

王真
中国医科大学附属第一医院

目的 2019 年底，我国关于 AIDS 防治“三个 90%”数据依次为：75.7%，89.7%，95.3%，监测数据显示，男男性行为人群中每 100 人中约有 8 人感染艾滋病病毒，重点人群的防治形势仍然严峻。传统流行病学分析存在问题，如隐私泄漏、歧视导致社会期望偏移、无法反映感染者本身的异质性等。分子网络分析是近年来兴起的分子流行病学分析方法，可根据患者携带 HIV 毒株的基因相似性推定毒株在人群间的传播。以往分子网络分析的研究主要是对 B 亚型毒株，我国 HIV 流行毒株复杂，开展分子网络研究更具挑战性，处于分子传播网络中人群的流行病学特点不明确。本研究将分子传播网络分析与流行病学因素相结合，建模型了解 HIV 传播风相关险因素，为控制 HIV 传播提供靶向干预。

方法 1、序列获取：收集 2016-2018 年沈阳市新诊断 HIV 感染者治疗前的血浆样本及基线信息。从血浆中提取出病毒 RNA，巢式 PCR 进行 HIV-1 pol 区基因片段扩增。

2、分子传播网络风险评价：敏感性分析获得 CRF01_AE 与 CRF07_BC 亚型与 B 亚型的基因距离阈值。应用 HIV-TRACE 构建三种主要流行毒株的分子传播网络，计算网络内个体链接数评价传播风险。

3、模型的建立与评估：回归分析建模，评价标准为 H-L 检验、C-statistic、AUC、诊断比值比、内部验证等。

结果 1、2016-2018 年沈阳市主要流行株及分子网络

沈阳市主要流行毒株为 CRF01_AE、CRF07_BC、B 亚型。CRF01_AE 与 CRF07_BC 最佳基因距离阈值为 0.007 替代/位点，B 亚型为 0.013 替代/位点。风险人群判断阈值为个体链接数的第三四分位数（link=2）。

2、建模对象特征

385 例调查问卷中，其中 85.2%（328/385）为 MSM，本研究对 MSM 进行分析建模，经回归分析，风险因素为：有男性偶遇/商业性伴、CD4+T 细胞计数≥350 个/ml、确诊前 HIV 检测次数≥5、不了解性伴感染状态。

3、模型的评价与验证

H-L 检验的卡方值为 4.6；AUC 为 0.763；变量重抽样 Bootstrap 样本中出现的频率均大于 50%。

结论 1、沈阳市的主要 HIV 流行株为 CRF01_AE、CRF07_BC、B 亚型，CRF01_AE 与 CRF07_BC 毒株分子传播网络的最适基因距离阈值与 B 亚型不同。
2、传播风险预测模型包含的风险因素有：有男性偶遇/商业性伴、CD4+T 淋巴细胞计数≥350 个/ml、确诊前 HIV 检测次数≥5、不了解性伴感染状态。
3、基于 HIV 分子传播网络的 MSM 人群 HIV 传播风险预测模型具有较好的预测能力。

PU-0398

基于液相色谱-质谱联用平台（LC-MS）对褪黑素与β淀粉样蛋白（Aβ）亲和力的测定

代雅倩
安徽医科大学

通过对基于液相色谱-质谱联用平台的受体结合分析方法（MS binding assays, MSBA）进行优化，对褪黑素与 β-淀粉样蛋白(Aβ)聚集体的亲和力进行测定。针对褪黑素（melatonin）、氘代同位素（褪黑素-D4，melatonin-D4）以及内标 6-碘-2-（4'-二甲基氨基-）苯基-咪唑并[1,2]吡啶（IMPY）建立液相色谱-质谱（LC-MS）联用方法和定量方法，随后进行基于质谱的饱和结合实验。成功建立了褪黑素的 LC-MS 方法及基于质谱的受体结合测定方法。实验表明褪黑素可与 Aβ 1-40 及 Aβ 1-42 特异性结合，其 Kd 值分别为（814.37±36.62）及（628.33±13.57）nmol/L。

PU-0399

miR-370-3p 靶向调控 FBLN5 在乳腺癌中的作用机制及临床诊断研究

王凌霞、杨欢
苏州大学附属第二医院

目的 乳腺癌作为女性最常见恶性肿瘤，其传统肿瘤标志物诊断效能较低，且病理诊断具有创伤性，诊断周期长，因而需找到一种新型非侵入性诊断标志物。本文旨在探讨 miR-370-3p 在乳腺癌中的生物学作用及分子机制并探讨其作为乳腺癌诊断标志物的可行性及临床应用价值。
方法（1）构建高、低表达 miR-370-3p 的乳腺癌细胞，体外采用克隆形成及 transwell 迁移实验检测增殖转移作用，Western blot 测定增殖转移相关蛋白表达水平；体内构建裸鼠皮下成瘤模型，检测形成肿块体积及重量。
（2）TargetScan 和 PicTar 预测并用双荧光素酶报告基因实验验证靶基因；Western blot 测定靶基因及信号通路蛋白的表达。
（3）试剂盒提取血清 exosome 并鉴定。定量 PCR 检测乳腺癌组织，血清以及血清外泌体中 miR-370-3p 表达量。ROC 曲线分析诊断效能。结合临床病理资料评价 miR-370-3p 在乳腺癌诊断中的价值及临床意义。
结果（1）miR-370-3p 高表达细胞迁移及克隆数显著增加，E-cadherin 表达量明显降低，N-cadherin, Vimentin, PCNA 表达量明显增加；反之结果相反。
（3）miR-370-3p 高表达细胞体内形成肿瘤体积、重量大于对照组，反之结果相反。
（4）miR-370-3p 靶向负调控 FBLN5 且促进 NF-κB P65 表达。
（5）miR-370-3p 在乳腺癌组织，血清及 exosome 表达量显著增加。血清中的 miR-370-3p 与淋巴结的转移程度，TNM 分期成正相关；exosome 中 miR-370-3p 与肿瘤直径大小，淋巴结的转移程度，TNM 分期成正相关。
结论（1）miR-370-3p 促进乳腺癌增殖与转移。

（2）miR-370-3p 靶向负调控 FBLN5, 活化 NF-κB 信号通路。
（3）miR-370-3p 是乳腺癌诊断的潜在新型非创伤性分子标志物，具有重要的临床应用价值。

PU-0400

6620 例 HPV 感染特征及高危分型分析

岳帆、侯向萍、咸敏、魏策
新疆生产建设兵团第一师阿拉尔医院

目的 通过对阿拉尔片区 35-60 周岁已婚健康妇女进行人乳头瘤病毒筛查，了解其感染状况，得出本地区妇女宫颈 HPV 感染情况及亚型分布情况，为本地区宫颈癌的防治研究提供一定的依据。
方法 采用 PCR-反向点杂交法对符合要求的 6620 名妇女进行 HPV 核酸检测及基因分型，对所得数据统计、分析，同时，并对高危型ＨＰＶ感染阳性人群进行液基薄层细胞学（ＴＣＴ）检查。
结果 在受检的 6620 名妇女中，共检出 HPV 阳性感染 969 人，感染率为 14.64%。其中高危型阳性 688 人，感染率为 10.4%；低危型阳性 155 人，感染率为 2.34%；合并型感染 126 人，感染率为 1.9%。1、在高危型感染人群中，本地区 HPV 亚型感染排在前 3 位依次为ＨＰＶ５２（19％，131／688），ＨＰＶ１６（15.98％，110／688），ＨＰＶ５８（10.17％，70／688）；在低危型感染人群中，以 HPV54(25.1%，39/155)，HPV61(18.7%,29/155)最为常见； 混合感染中以二重感染及三重感染最为常见（83.3%，105/126）， 其中 HPV52 易与 HPV16，HPV58，HPV61 发生合并感染，HPV16 型混合感染常见的基因型依次有 HPV31，HPV58，HPV51。2、受检的 6620 名妇女中维吾尔族共计 638 名，检出 HPV 阳性感染 90 人，其高危型 HPV 亚型感染以 HPV16（40%，36/90）最为常见。3、对 HPV 高危型感染者进行液基薄层细胞学（ＴＣＴ）检查，发现合并感染高危型ＨＰＶ人群宫颈上皮内瘤变发生率为 15％-20%。
结论 阿拉尔片区女性 HPV 感染高危亚型主要以 HPV52,HPV16,HPV58 为主,感染率在 45.20%(311/688)，少数民族与汉族亚型分布有一定的差异，且高危型 HPV 感染和合并感染是诱发宫颈癌的重要危险因素。运用 TCT 联合 HPV DNA PCR 检测可提高宫颈癌及癌前病变的检测效果,实现疾病准确诊断,还可帮助临床实现早诊早治的目标,保证患者的治疗效果,延长生存周期。调查显示性生活过早、性生活频率高、宫颈糜烂程度大、吸烟、缺乏免疫力等是女性人乳头瘤病毒感染危险因素。合理制定有效干预措施,大力宣传人乳头瘤病毒和疫苗的健康宣传教育工作是降低女性人乳头瘤病毒感染关键。

PU-0401

基于铁死亡相关 lncRNA 分析的皮肤黑色素瘤预后标志物的研究进展

王楠
山东第一医科大学
山东大学第二医院

目的 近年来，铁死亡作为一种潜在的癌症治疗途径受到了广泛关注。各种研究已经确定了铁死亡在杀死肿瘤细胞和抑制肿瘤生长方面的关键作用。以往的一些研究也证实了铁死亡在胃癌、头颈癌、肝癌和肺癌等治疗和预后的重要意义。皮肤黑色素瘤(Skin cutaneous melanoma, SKCM)是皮肤癌中最恶性的肿瘤类型，在疾病的早期有很强的转移倾向。因此，早期发现是很重要的，并且找到一个早期的预后指标将有助于提高 SKCM 患者的生存率。因此本文探讨 l 铁死亡相关基因与皮肤黑色素瘤(SKCM)预后的关系。
方法 从癌症基因组图谱(TCGA)数据库(https：//portal.gdc.ancer.gov/)获得皮肤黑色素瘤的 RNA 序列(RNA-seq)数据。纳入标准如下：(1)患者被诊断为皮肤黑色素瘤；(2)患者有完整的 lncRNA 数据

和临床资料。根据纳入标准，纳入 470 例皮肤黑色素瘤患者。利用 lncRNAs 和铁死亡相关基因的共表达网络筛选铁死亡相关的 lncRNAs。用单变量 Cox 回归分析铁死亡相关 lncRNAs 的预后价值。将单变量分析中 P<0.05 的铁死亡相关 lncRNA 纳入 Lasso 回归。然后，将 Lasso 的结果纳入多变量 Cox 模型，以建立风险评分。采用 Cox 回归建立独立的预后模型。并绘制 K-M 生存曲线。使用“time ROC”绘制 1 年、4 年和 7 年受试者工作特征曲线（receiver operating characteristic ,ROC)曲线，同时计算 ROC 曲线下面积（area under curve,AUC）,以确认风险评分是否为预后的独立指标。用 Cox 回归和 Lasso 回归估计铁死亡相关的 lncRNA 信号和临床病理数据对预后的影响。
结果 在纳入的 378 例皮肤黑色素瘤样本中，基于 Cox ＆ LASSO 回归算法，预测和构建了 9 个铁死亡相关的(AC009495.1、AC068152.1、EBLN3P、AC009318.2、AC107294.2、SPRY4-AS1、HCP5、AL162171.1 和 USP30-AS1)，并将皮肤黑色素瘤患者分为低风险组和高风险组。基于风险评分是皮肤黑色素瘤患者的显著独立因素(HR=1.333,95% CI=1.213-1.465,P<0.001)。
结论 本研究确定了 9 个与铁死亡相关的 lncRNA 及其标志物可能是皮肤黑色素瘤患者的分子生物学标志物和治疗靶点。

PU-0402

HPV23 分型检测与宫颈病变的相关性分析

程世亮
山东省立第三医院

目的 探讨 HPV23 分型检测与宫颈病变的相关性及临床意义。
方法 选取 2019-2021 年 年在山东省立第三医院妇产科和体检中心就诊患者 1860 例作为研究对象,采集患者宫颈细胞进行 HPV 基因检测并实施宫颈病理活检,组织切片取样行病理学检查,比较 HPV 基因亚型与病理诊断结果并进行相关性分析。
结果 1860 例患者中,正常或炎症宫颈 1616 例,宫颈上皮内瘤变(CIN) Ⅰ 级 58 例, CINⅡ 级 36 例, CINⅢ 级 88 例,宫颈癌 62 例。HPV 阳性检出率随宫颈病变程度不断加重而升高,差异均有统计学意义(P <0.05)。伴随病情不断发展,HPV16 型在不同宫颈病变中的阳性检出率逐渐升高,在宫颈癌患者中同样也是 HPV16 型阳性检出优势明显,为 77.4% (48 / 62)。 HPV 多重感染在不同宫颈病变中的检出情况:正常及炎症 11.3% , CINⅠ 级 17.2% ,CINⅡ 级 27.8% , CINⅢ 级 29.5% ,宫颈癌 9.7% ;宫颈癌中 HPV 多重感染占比明显更少,更多的是单一 HPV 基因型感染,且感染类型全部为高危型。
结论 随着宫颈病变程度不断加重, HPV 阳性检出率随之逐渐升高;宫颈癌中 HPV 基因亚型主要包括: HPV16 、 33 、 52 型。

PU-0403

Molecular network analysis based on baseline HIV pol sequences revealed the transmission of drug-resistant strains in a moderate HIV prevalence Chinese city

Bin Zhao [1]、Wei Song[2]、Wen Tian[1]、mingming Kang[3]、Xue Dong[2]、Xin Li[2]、Lu Wang[2]、Jianmin Liu[2]、Lin Wang[1]、Haibo Ding[1]、Xiaoxu Han[1]、Hong Shang[1]
1. NHC Key Laboratory of AIDS Immunology (China Medical University), National Clinical Research Center for Laboratory Medicine, The First Affiliated Hospital of China Medical University
2. Department of Food Safety and Nutrition, Shenyang Center for Health Service and Administrative Law Enforcement (Shenyang Center for Disease Control and Prevention), Shenyang, 110031, China
3. National Clinical Research Center for Laboratory Medicine, The First Affiliated Hospital of China Medical University

Background Timely collection and molecular network analysis based on HIV pol sequence from all newly diagnosed HIV infections are helpful to obtain the information of transmitted drug resistance (TDR) transmission to guide targeted intervention and ultimately end TDR transmission.
Methods Demographic information (n=2,577) and HIV-positive cryopreserved plasma (n=2,408) from all newly diagnosed HIV infected individuals (n=2,577)of Shenyang from 2016 to 2018 were collected. HIV pol gene was amplified and sequenced. HIV-1 Limiting Antigen Avidity was performed to identify recent HIV infections (RHI). HIV-1 TDR was determined based on Genotypic Resistance Interpretation Algorithm (HIVdb version 9.0). HIV molecular network was inferred by using HIV-TRACE.
Findings A total of 2,173 sequences (90.2%, 2,173/2,408) were acquired. The prevalence of TDR among RHI (8.7%, 65/751) was similar to that among all newly diagnosed HIV-infected individuals (8.4%, 182/2,173) and reached a moderate level (5-15%). The top 5 SDRMs were Q58E(1.9%, 42/2,173), M46I/L (1.2%, 25/2,173)， K103N/S (0.9%, 20/2,173), K103R/V179D (0.5%, 10/2,173), and K65R(0.4%, 8/2,173). HIV molecular network analysis results revealed one CRF07_BC cluster with K103N (66.7%, 8/12), two CRF07_BC clusters with Q58E (100%, 21/21; 100%, 3/3), two CRF01_AE clusters with A98G (100%, 3/3) and K103R/V179D (100%, 3/3), respectively. All of them happened in the men who have sex with men (100%).
Conclusion Our findings demonstrated that HIV molecular network monitoring based on baseline HIVDR testing for all newly diagnosed HIV infections, especially RHI was essential for the precisely targeted intervention for the transmission of TDR.

PU-0404

大动脉炎的遗传因素

晏颂欣
中国医学科学院北京协和医院

大动脉炎（TAK）是一种罕见的系统性血管炎，其特征在于主动脉及其主要分支的肉芽肿性炎症。参与 TAK 发病机制的细胞和生理生化过程开始被逐步了解，并发现细胞和抗体介导的自身免疫机制参与其中。此外，TAK 的潜在病因可以至少部分地通过复杂的遗传因素来解释。该疾病最广为人知的遗传易感基因位点是经典的 HLA 等位基因 HLA-B * 52，已在多个种族中得到证实。在 HLA-B * 52 以及其他经典等位基因和基因座的遗传易感性暗示 HLA I 类和 II 类可能参与 TAK 的发病机制。此外，与编码免疫应答调节因子，促炎细胞因子和体液免疫介质的有关的基因遗传关联可能与疾病机制直接相关。

PU-0405

全外显子组测序鉴定特发性炎症性肌病的罕见变异

晏颂欣
中国医学科学院北京协和医院

目的 特发性炎症性肌病（IIMs）是一组获得性、异质性、全身性疾病，主要累及骨骼肌。本研究旨在利用全外显子组测序（WES）技术研究汉族人 IIMs 中的罕见变异。
方法 对 20 例 IIMs 患者和 20 例汉族健康对照者进行 WES。为病例和对照组生成 WES 数据。变异通过质量、次要等位基因频率和对基因功能的有害性进行注释和筛选。与健康对照组以及中国国家基因库的对照组相比，在患者中确定了候选突变。为了验证，多重聚合酶链反应在另一个独立的队列中进行。
结果 在发现阶段，发现了 7 个在 IIMs 中具有预测蛋白损伤作用的罕见突变，分别存在于 FCRL1、DMBT1、DDX58、DYSF、IL31RA、JAK2、PMS2。随后对这些突变位点进行多重 PCR。DDX58 中的一个新突变（chr9:32487565 T>C）被证实与 IIMs 相关。
结论 本研究结果有助于从全外显子组水平检测和分析 IIMs 的基因突变，为理解 IIMs 的发病机制提供新的思路。

PU-0406

IgG4 相关疾病基因组学研究进展

晏颂欣
中国医学科学院北京协和医院

IgG4 相关疾病（IgG4-RD）是一种免疫介导的纤维炎性疾病，其特征在于受累组织中以 IgG4+浆细胞为主的致密淋巴浆细胞性浸润，常伴有一定程度的纤维化、闭塞性静脉炎和嗜酸性粒细胞增多，约 2/3 的患者伴有血清 IgG4 水平升高。尽管尚不清楚 IgG4-RD 发病机理的确切机制，但一些研究表明遗传因素与 IgG4-RD 的发病具有一定的联系。在本篇综述中，我们将总结相关的研究，分析 IgG4-RD 在基因水平中的研究进展，加深对 IgG4-RD 的认知，期望能为下一步的研究开拓新的思路。

PU-0407

Prognostic role of long non-coding RNA XIST expression in patients with solid tumors: a meta-analysis

毛慧慧
山东大学第二医院

Background The aberrant expression of long non-coding RNA (lncRNA) X inactivate-specific transcript (XIST) has been demonstrated to be involved in the tumourigenesis and the development of various cancers. Therefore, we conducted a meta-analysis to assess the prognostic role of lncRNA XIST expression in solid tumors.
Methods The databases of PubMed, EMBase, Web of Science, Cochrane library (up to Dec 31, 2017) were searched for the related studies and identified 15 eligible studies containing 1,209 patients to include in the meta-analysis. Hazards ratios (HRs) with corresponding 95% confdence intervals (CIs) were pooled to estimate the association between lncRNA XIST expression and survival of cancer patients from Asian.

PU-0408

The mechanism and regularity of quenching the effect of bases on fluorophores: the base- quenched probe method

毛慧慧
山东大学第二医院

目的 阐明碱基导致荧光猝灭的机制及规律。
方法 应用光谱技术研究荧光猝灭的可能机制；应用碱基猝灭探针技术，分析 DNA 分子内核酸碱基与荧光基团之间的电子转移和电子传输规律。
结果 碱基导致荧光猝灭的机制倾向于光诱导电子转移。在单链 DNA 中，荧光基团的电子转移到胸腺嘧啶（Thymine，T）和胞嘧啶（Cytosine，C）的轨道或来自鸟嘌呤（Guanine，G）和腺嘌呤（Adenine，A）的电子占据荧光基团的电子轨道，导致荧光基团的电子不能恢复到基态，从而导致荧光猝灭；在双链 DNA 中，荧光基团的电子在光激发的作用下沿着 DNA 链传输，无法恢复到基态，导致荧光猝灭。此外，研究显示碱基的猝灭效率依次为 G>C≥A≥T；在双链 DNA 中，碱基对的电子传输能力依次为 CG≥GC>TA≥AT（粗体和下划线标识的字母代表探针的互补链上的碱基）；最常见的荧光基团包括 FAM，HEX，TET，JOE 和 TAMRA 均受碱基的影响并且符合以上规律。
结论 在 DNA 分子内，碱基与荧光基团之间的电子转移和传输导致荧光猝灭。

PU-0409

报道一例 4 号染色体父源 UPD 合并 SLC4A4 基因缺陷导致近端肾小管酸中毒

刘晴晴[1]、喻长顺[2,4]、王文红[3]
1. 天津金域医学检验实验室有限公司
2. 广州医科大学金域检验学院
3. 天津市儿童医院肾脏科
4. 天津金域医学检验实验室有限公司

近端肾小管酸中毒是一种遗传性或获得性临床综合征，其表现为近端肾小管碳酸氢盐回收减少，导致正常阴离子间隙高氯代谢性酸中毒。SLC4A4 变异可引起近端肾小管酸中毒伴眼部异常，是一种常染色体隐性遗传病，主要表现为重度低钾血症、高氯血症、代谢性酸中毒、生长迟滞和眼部异常（包括青光眼、白内障和带状角膜病变）；部分可伴有恒牙釉质发育缺陷、精神运动性功能和认知功能受损及基底节钙化。UPD（单亲二倍体）是指在一个正常染色体的个体中，一个染色体区域的两个拷贝仅来自于父母一方，其发病率较低，但可继发隐性基因纯合变异或基因印迹障碍，从而导致各种各样的临床表型。UPD 可分为 hUPD 和 iUPD。从一个亲本遗传一对同源染色体（即同源染色体来自同一个亲本的两条同源染色体）是异源单亲二体（hUPD），反之仅遗传同源染色体中的一条染色体（即同源染色体来自于同一个亲本的同一条染色体）是同源单亲二体（iUPD），同源单亲二体比异源单亲二体更易发生常染色体隐性遗传病。本文描述了一名 4 岁的患儿，临床表现为难以纠正的代谢性酸中毒，高氯低钾血症，语言发育落后，眼部异常以及牙齿釉质发育不全等。临床症状符合肾小管酸中毒表现，因此对该患儿行全外显子组测序，发现 SLC4A4 基因 c.496C>T 纯合变异，并且发现 4 号染色体为单亲二倍体，结合 4 号染色体多个 SNP 位点的分型结果可知，系 iUPD(4)pat（父源性均质性单亲二倍体）。针对父母样本进行 Sanger 测序发现，父亲携带 SLC4A4 基因 c.496C>T 杂合变异，而母亲未携带此变异。SLC4A4 基因的纯合变异可以解释该病例的主要表型。综上，本文首次报道了 4 号染色体父源性均质型 UPD 合并 SLC4A4 基因纯合致病变异导致近端肾小管酸中毒。

PU-0410

Coloring Target and Off-target Effects of Genetically Modified Nucleases by Blue & White Colony Assays

Jing Jiang
huazhong university of sicence and technology union shenzhen hospital

More sensitive evaluation of the off-target effects of gene editing nucleases is crucial for human gene therapy. Here we report chromogenic assays designed for sensitive evaluation of gene editing activities using CRISPR/cas9 test system. Based on beta-galactosidase alpha complementation, qualitative and quantitative evaluations of the target and off-target effects of CRISPR/cas9 were well established through the color alteration of the E. coli colonies. In addition to target effect analysis, these new assays provide extremely sensitive and efficient way to profile the off-target effects with one or more bases mismatched between the targets and the gRNAs. Moreover, these assays allow the identification of gene editing effects for off-targets with one base mismatched PAM sites.

PU-0411

近红外激活时空可控的 miRNA 原位成像

张亮亮[1,2,3]、赵贤贤[1,3]、罗阳[1,3]
1. 重庆大学医学院智慧检验与分子医学中心
2. 重庆大学生物工程学院
3. 重庆大学医学院公共实验中心

In situ spatiotemporal microRNA (miRNA) imaging in mammal cells plays an essential role in illustrating its structures and biological functions. Herein, we proposed a near infrared (NIR) light-activated nanoprobe for high-sensitive in situ controllable miRNA imaging in living cells. The NIR-activated nanoprobe employed an upconversion nanoparticle that acted as a NIR-to-UV transducer to trigger the following photocleavage toward a dumbbell DNA probe tethered on the surface of the nanoparticle. The structure change of the dumbbell probe then induced a catalytic hairpin assembly of target miRNAs, by which in situ readout of the amplified fluorescence signal was enabled. Additionally, both intracellular miRNA imaging and accurate quantification in live cells were realized without damaging the cell membranes. Compared with conventional in situ strategies, the proposed approach remarkedly increases imaging efficiency by eliminating those unfavored intercellular molecular imaging backgrounds.

PU-0412

Detection of simultaneous multi-mutations using base-quenched probe

毛慧慧
山东大学第二医院

The base-quenched probe method for detecting single nucleotide polymorphisms (SNPs) relies on real-time PCR and melting-curve approaches. Here, we applied the most common commercial fluorophores including FAM, HEX, CY5, CY3, TET, JOE, Texas Red and ROX for labeling probes to detect multi-mutations simultaneously according to the different fluorescence channels. Accuracy of the method was confirmed by direct sequencing.The results demonstrated that all above dyes could be influenced by bases and could be applied to detect

SNPs.Furthermore, this method was applied to detect APOM rs707921, APOM rs707922 and MCP-1 rs1024611 simultaneously, which was demonstrated successfully.

PU-0413

Down-regulation of lncRNA OGFRP1 inhibits NSCLC progression through PI3K/AKT pathway

Liping Jing、Xuewei Zhuang
Shandong Provincial Third Hospital

In the past decade, long noncoding RNAs (lncRNAs) displayed important roles in the progression of human cancer. However, function annotations for lncRNAs were still insufficient due to low expression level and tissue specificity. Here we evaluated the function of lncRNA OGFRP1 in non-small-cell lung cancer (NSCLC). We screened the most effectivesi-lncRNA (si-OGFRP1)todown-regulate the expression of lncRNA OGFRP1 in A549 cells. CCK8 assay indicated thatsi-OGFRP1 significantly inhibited cell proliferation in A549. Flow cytometry detection demonstrated that si-OGFRP1inhibited cell cycle arrest and induced apoptosis in A549. Apoptosis associated gene expression was found down-regulated by western blotting assay. Transwell assay indicated that si-OGFRP1 inhibited A549 cell migration and invasion. Then we examined the expression of key proteins in PI3k/AKT pathway. Results revealed that the expression of p-AKT, Raf, p-Erk, P70, CyclinD1 was down-regulated and P53 expression was elevated. Taken together, we demonstrated that down-regulation of lncRNA OGFRP1 inhibited the progression of NSCLC by repressing PI3K-AKT signaling pathway.

PU-0414

UGT2A3 差异表达在结直肠癌发生和早期诊断中的作用机制

李宏峰、赵俊芳、陈雪雯、宋林、部楠
天津市中医药研究院

背景 结直肠癌（CRC）是消化道最常见的恶性肿瘤之一，早期筛查是预防 CRC 的有效手段之一。本研究的目的是研究 UGT2A3 差异表达在在结直肠癌发生中的作用及调控机制。
方法 在 GEO 数据库下载了 8 个 CRC 数据集，并在 TCGA 中下载结直肠癌数据。采用 R 语言分析 UGT2A3 在癌组织和癌旁组织中的差异表达情况。在 TCGA 中根据 UGT2A3 的表达水平，在所有样本、正常组织、癌组织样本中分别选取表达最高和最低的前 20 例样本，比较免疫细胞丰度和免疫富集评分，并筛选差异表达基因和差异表达 miRNA，并进行差异表达基因的通路富集分析。
结果 UGT2A3 在所有 9 个数据集的癌组织中均明显下调。在各样本类型中，与高表达组相比，低表达组的 ImmuneScore、ESTIMATEScore 和 StromalScore 明显较高，且免疫细胞丰度较高（记忆 B 细胞除外）。在正常组织中，UGT2A3 的差异表达主要影响癌症相关通路，而在肿瘤组织中主要影响了代谢途径。miR-194-2、miR-224 和 miR-551b 在所有分组中均显著差异表达，被认为是 CRC 中潜在的 UGT2A3 上游调控基因。
结论 UGT2A3 以及 miR-194-2、miR-224 和 miR-551b 可以作为 CRC 潜在的诊断生物标志物。

PU-0415

Promoter Hypomethylation and Increased Expression of Syncytin-1 in Non-small Cell Lung Cancer

Liping Jing、xuewei zhuang
Shandong Provincial Third Hospital

Purpose In this study, fluctuation of syncytin-1 expression in non-small cell lung cancer (NSCLC) and relative para-cancerous tissues during its prognosis as a plausible pathological mechanism of NSCLC is discussed by statistical analysis of syncytin-1 gene methylation and expression levels.
Methods Syncytin-1 expressions in NSCLC and its relative para-cancerous tissues were verified by immunohistochemistry method. Differentiation of between 5-year survival and death group was analyzed. Survival ratio was calculated by Kaplan-Meier survival curve. Death risk assessment was executed by Cox risk regression model. 5-LTR methylation level of syncytin-1 promoter was detected by EpiTYPER method.
Results Syncytin-1 expression in NSCLC tissue is higher rather than para-cancerous tissues in significant differences with $P<0.01$ and in 5-year survival group is lower than death in significant difference with $P<0.01$ respectively. Based on the average survival period of higher syncytin-1 expression group is significantly lower than the lower one with $P<0.01$, clinical stage and syncytin-1 positive ratio were considered as top risk factors according to Cox ratio risk regression model analysis. The total methylation ratio of NSCLC tissues is lower than para-carcinoma tissues with no significant difference but the CpG-2 site methylation ratio of NSCLC tissue is lower than para-carcinoma tissues in significant difference with $P<0.05$.
Conclusions The low expression level of syncytin-1 is qualified to be an important prognosis standard. Hypomethylation of the syncytin-1 promoter region in non-small cell lung cancer promotes the expression of its gene.

PU-0416

集成式微流控芯片 PCR 阵列用于快速检测多重呼吸道感染病原

刘大渔
广州市第一人民医院

目的 发展一种集成式微流控芯片 PCR 阵列系统，用于资源有限环境下的多重呼吸道感染病原快速检测。
方法 研究设计并加工了一种包含仪器与微流控芯片的 PCR 阵列系统，集成了样本裂解、核酸提取/纯化、扩增/检测功能。微流控芯片通过六个隔膜阀控制流体通路的开放与闭合，以确保流体在芯片内程序性地流动，因而顺序完成一系列分析步骤。核酸 PCR 扩增在预装载引物和探针的 32 阵列微反应室中完成，可同时检测 21 种呼吸道感染病原及内质控（RNase P 基因）。扩增荧光信号被仪器实时采集，依据 Ct 值判定检测结果。研究通过标准样品分析确定了芯片法的检出限、重现性以及特异性，并通过批量临床样本检测对该芯片系统的临床应用价值进行了考察。
结果 该微流控芯片系统能够以全集成方式在 1.5 小时内完成多重呼吸道病原检测。研究通过检测系列稀释阳性对照品确认了芯片法的检出限，基于 Probit 回归分析（$P > 0.05$）计算出各靶标的检出限均在 1.0×103 copies•mL-1 水平。对各靶标的阳性对照品进行重复检测，实验结果显示芯片法对各病原体检测的 Ct 值批间相对标准偏差为 0.08%-0.69%，批内相对标准偏差为 0.9%-2.66%。对多种病原体混合的阳性参考品进行分析，结果显示各病原体之间无交叉影响，芯片法的检测特异性为 100%。批量临床样本检测结果显示芯片法与传统的实时荧光 PCR 法具有一致性。
结论 研究发展的微流控芯片多重呼吸道感染病原体检测方法具有操作简便、通量适宜和分析快速的特点和优势，是资源有限环境下实现病原体快速检测的有力工具。

PU-0417

湖南地区血脂异常患者 APOE 和 SLCO1B1 基因多态性及其与血脂水平的相关性研究

龙璐、易斌
中南大学湘雅医院

目的 分析湖南地区血脂异常人群 ApoE 和 SLCO1B1 基因的多态性及其对血脂水平的影响，并探究 ApoE 和 SLCO1B1 基因与各项血脂指标的相关性。
方法 收集湘雅医院 2020 年 1 月至 2021 年 2 月期间收治的 514 例血脂异常人群的总胆固醇（triglyceride, TC）、甘油三酯（total cholesterol, TG）、低密度脂蛋白胆固醇（low density lipoprotein cholesterol, LDL-C）和高密度脂蛋白胆固醇（high density lipoprotein cholesterol, HDL-C）等数据，将其作为实验组，同时选取 592 名健康体检者作为对照组，采用 PCR 荧光探针法检测实验组和对照组的 ApoE 和 SLCO1B1 基因型，分析 ApoE 和 SLCO1B1 基因的多态性和血脂水平的相关性，比较不同基因型的受试者各项血脂指标的差异。
结果 （1）ApoE 基因多态性分布：实验组 E2、E3 和 E4 基因表型频率分别为 15.18%、66.16%和 18.68%，对照组分别为 16.39%、68.07%和 15.54%，E3 表型频率均为两组最高，E3 表型的 E3/E3 基因型均为两组内最高，其频率分别为 64.20%和 66.72%，组间差异不显著（P＞0.05）。（2）SLCO1B1 基因多态性分布：实验组正常代谢型、中间代谢型和弱代谢型的频率分别为 78.79%、20.43%、0.78%，对照组分别为 79.05%、19.93%和 1.01%，正常代谢型频率均为两组最高，弱代谢型均为两组最低，正常代谢型的*1b/*1b 基因型均为两组最高，其频率分别为 47.86%和 44.26%，组间差异不显著（P＞0.05）。（3）实验组 ApoE 基因 E4 表型的患者 TC 和 TG 水平均大于 E2、E3 表型，E3 基因表型的患者 LDL-C 水平大于 E2、E4 表型，三组表型间 TC、TG 和 HDL-C 的浓度差异不显著（P＞0.05），但 E2 表型的 LDL-C 水平显著低于 E3 和 E4 表型（P＜0.05）。（4）实验组 SLCO1B1 基因正常代谢型受试者的 TC 和 LDL-C 水平大于中间代谢型和弱代谢型，弱代谢型的 TG 水平高于正常代谢型和中间代谢型并且 HDL-C 水平小于正常代谢型和中间代谢型，但三型间各项血脂指标无显著差异（P＞0.05）。
结论 血脂异常患者 ApoE 和 SLCO1B1 基因频率分布存在明显不均，血脂异常患者 ApoE 基因 E2 表型的 LDL-C 水平显著低于 E3 和 E4 表型，ApoE 基因多态性与血脂水平存在相关性，而 SLCO1B1 基因多态性则与其不存在相关性。

PU-0418

Novel multi-fluorine labeled Indanone Derivatives as Potential MRI Imaging Probes for β-Amyloid Plaques in the Brain

Yaqian Dai
The First Affiliated Hospital of Anhui Medical University

A series of novel multi-fluorine labeled indanone derivatives were synthesized successfully on the basis on indanone. In the staining experiment of AD human brain adjacent sections, compound 7d could bind to β-amyloid plaques specifically, showed obvious fluorescence in the green channel of fluorescence microscope. In the in vitro binding experiment, 7d showed a balanced affinity with Aβ1-40 (Kd=367.93±13.72) and Aβ1-42 (Kd=384.80±56.55). 7d exhibited a low toxicity (ID50>50mg/kg) in the acute toxicity experiment. The Log P value of 7d was 3.87, which meant it might have an excellent ability to pass through the blood-brain barrier. In the biodistribution experiment of normal mice, the highest brain uptake could be reached at 1 hours after intraperitoneal injection and cleared from the brain after 24 hours. The imaging capability of

7d increased with the increase in concentration in 19F-weighted mode, showed strong imaging ability at a lower concentration (1.875mg/ml).

PU-0419

甘肃地区乙型肝炎病毒分型和耐药突变分析

陈俏丽、李彩东、田鹏飞
兰州市第二人民医院

目的 分析探讨甘肃地区乙型肝炎病毒(hepatitis B virus, HBV)基因型分布特征及耐药情况，为乙型肝炎患者抗病毒用药提供指导依据。
方法 选择 2018 年 1 月—2019 年 8 月于兰州市第二人民医院就诊的 131 例乙型肝炎患者，通过 Sanger 测序法分析患者乙肝基因型和耐药突变位点分布情况，应用 SPSS 20.0 软件进行统计分析。
结果 131 例乙型肝炎患者共检出 B、C、D 三种基因型，其中 B 型 2 例(1.53%)；C 型 126 例(96.18%)；D 型 3 例(2.29%)。检出 51 例核苷酸类药物耐药，耐药率 39.69%，其中 B 型 1 例，C 型 50 例。耐药突变位点最多见于 M204V/I，以 M204V/I+M204V 联合突变多见，常在此基础上发生三位点、四位点甚至五位点突变。其中与阿德福韦酯(ADV)相关的 A181V/T、N236T、A181V/T+N236T 单药突变最常见，共 15 例(11.45%)。多药突变 36 例(27.48%)，主要以拉米夫定(LAM)和替比夫定(LDT)联合耐药为主，在此基础上多有恩替卡韦(ETV)联合耐药发生。
结论 甘肃地区 HBV 患者基因型以 C 型为主，耐药形式严峻，突变组合模式复杂多样，应及时检测患者 HBV 基因型及耐药突变位点，以评价乙型肝炎患者临床疗效并指导临床抗病毒治疗合理用药。

PU-0420

上海地区妇女宫颈脱落细胞 HPV 感染亚型变化 ——来自单中心的数据分析

孟俊
上海交通大学医学院附属瑞金医院

目的 探讨上海地区人乳头状瘤病毒(HPV) 病毒的分子流行病学特征及亚型感染状况，为预防和治疗 HPV 提供理论依据。
方法 采用多重 PCR 和毛细电泳技术对本院 2017 年 10 月-2020 年 12 月共 58883 例妇科门诊及常规体检妇科门诊的宫颈脱落细胞进行 HPV 分型检测，共检测 25 种型别。
结果 ①58883 例受试者中共检出 HPV 阳性者 9168 例，总感染率为 15.57%（9168/58883），其中单重感染者 6971 例，占比为 76.04%（6971/9168）；多重型感染者 2197 例，占比为 23.96%（2197/9168）。②感染前三位分别为 HPV52、HPV58、HPV16 型，HPV 感染率与女性的年龄因素相关，31-40 岁女性感染率最高，有部分妇女是双重感染、三重感染甚至五重感染。③慢性子宫颈炎、宫颈上皮瘤变、宫颈恶性肿瘤前三位的基因分别是 HPV52、HPV16、HPV58。
结论 高危型 HPV 的检测可发现早期宫颈病变，加强对不同年龄段女性 HPV 感染的监测筛查更有利于宫颈癌的早期预防，为上海地区 HPV 感染的防治提供科学依据。

PU-0421

LncRNA AC010789.1 promotes colorectal cancer progression by targeting microRNA-432-3p/ZEB1 axis and the Wnt/β-catenin signaling pathway

Weili Duan、chuanxin wang
The Second Hospital of Shandong University

Accumulating literatures have indicated that long non-coding RNAs (lncRNAs) are crucial molecules in tumor progression in various human cancers, including colorectal cancer (CRC). However, the clinical significance and regulatory mechanism of a vast majority of lncRNAs in CRC remain to be determined. The current study aimed to explore the function and molecular mechanism of lncRNA AC010789.1 in CRC progression. AC010789.1 found to be overexpressed in CRC tissues and cells. High expression of AC010789.1 was associated with lymph node metastasis and poor prognosis. Moreover, AC010789.1 silencing inhibited proliferation, migration, invasion and epithelial-mesenchymal transition (EMT) in vitro as well as tumorigenesis and metastasis in vivo. Mechanistically, we demonstrated that repression of AC010789.1 promoted miR-432-3p expression, and miR-432-3p directly binds to ZEB1. We then proved the anti-tumor role of miR-432-3p in CRC, showing that the inhibitory effect of AC010789.1 knockdown on CRC cells was achieved by the upregulation of miR-432-3p but downregulation of ZEB1. We also established that silencing AC010789.1 suppressed the Wnt/β-catenin signaling pathway. However, this inhibitory effect was partially counteracted by inhibition of miR-432-3p. In summary, these results reveal that silencing AC010789.1 suppresses CRC progression via miR-432-3p-mediated ZEB1 downregulation and suppression of the Wnt/β-catenin signaling pathway, highlighting a potentially promising strategy for CRC treatment.

PU-0422

肺腺癌转移相关 lncRNAs 标志物的筛选及预后评估模型的构建

张晓时[1]、杜鲁涛[2]、李晓丽[1]、王传新[2]
1. 山东大学齐鲁医院
2. 山东大学第二医院

In the present study, we aimed to develop a prognostic signature which is based on metastasis-associated lncRNAs in patients with lung adenocarcinoma (LUAD). Firstly, the potential metastasis-associated lncRNAs were identified by analyzing high-throughput data from The Cancer Genome Atlas (TCGA), and based on which, an lncRNA signature was constructed for prediction of relapse in LUAD patients using Cox proportional hazards regression analysis. Moreover, the prognostic performance of the lncRNA signature was evaluated using Kaplan-Meier survival analysis, time-dependent receiver operating characteristic (ROC) curve and Cox analysis, respectively. An lncRNA signature consisting of six most important prognostic factors (LINC01819, ZNF649-AS1, HNF4A-AS1, FAM222A-AS1, LINC02323 and LINC00672) was developed. This novel six-lncRNA signature had considerable prognostic value for prediction of relapse in LUAD patients.

PU-0423

鼠尾消化实验传统“经典法”和新技术“快速法”的对比及探讨

刘寒、曾超、陈璐、王君安、凌昉钦、伍均
上海市第一人民医院嘉定分院

目的 以小鼠为模型的模式动物在现代科学研究中发挥着重要的作用。目前对于小鼠的遗传学改造是扩充小鼠品系的重要途径，这也要求对小鼠的基因鉴定应该朝着更快和更准确的方向发展。传统的鼠尾粗 DNA 提取依赖蛋白酶 K，消化时间在 5 个小时左右。本文提出了一种不依赖蛋白酶 K 的快速鼠尾粗 DNA 提取法，并探讨其实验过程及其准确性。
方法 经典鼠尾消化过程，需要在弱碱体系中，经过蛋白酶 K 的水解消化和乙[1]醇洗涤获得粗 DNA 浸出液。我们提出了新的鼠尾粗 DNA 提取的方法，即在强碱、高温环境下，破坏组织裂解细胞，使其核酸片段释放出来，获得粗 DNA 浸出液。该方法不依赖蛋白酶 K 的生物消化过程，是组织和细胞在高温强碱反应下，自然将染色质成分释放出来；在经过酸性缓冲液中和之后，获得可以进行 PCR 反应的鼠尾粗 DNA 提取液。
结果 两种方法联合检测进而对比之后，我们发现，鼠尾消化实验的“快速法”极大的缩短了反应所需时间。传统的“经典法”需 5 个小时左右的时间，但是“快速法”仅仅需要 20 分钟的时间。但“经典法”消化得更为彻底，在经过“快速法”消化后，EP 管底部仍有鼠尾组织。根据两者的实验原理分析，“经典法”获得的是双链粗 DNA，而“快速法”获得的是单链 DNA。由于 DNA 的本质是反向平行的双脱氧核糖核苷酸链，所以双链和单链有等效的遗传信息。对两者获得的粗 DNA 浸出液进行 PCR 反应的结果显示，两者都可对敲除式基因和敲入式基因进行基因鉴定，结果同样稳定可靠，表现为两者条带同样清晰，亮度相似。
结论 通过实践，发现使用“快速法”鼠尾消化可以缩短小鼠基因鉴定所需时间，同时可减少蛋白酶 K 的使用，并且进一步简化实验操作步骤，有一定的应用和推广前景。

PU-0424

DTL inhibits tumor-intrinsic immunity through the cGAS-STING pathway to promote tumorigenesis

Yidan Ren、Yunshan wang
The Second Hospital of Shandong University

Background Evasion of host immunity is characteristic of cancer, the mechanisms linking oncogenic mutations and immune escape are not fully understood. DTL is one of CUL4-DDB1-related factors (DCAFs), which may be involved in tumor development. However, the potential mechanism by which DTL regulates the immunosuppressive state of tumors still needs to be further studied.
Methods Affinity-purification mass spectrometry was used to identify potential DTL interaction proteins. Coimmunoprecipitation (Co-IP) was performed to verify protein interaction between DTL and DAPK3. mRNA levels in cancer cells and tissues were detected by Quantitative real-time PCR. Lentivirus was used to establish stable overexpression and knocking down cell lines for DTL and DAPK3. Transwell and wound healing assays were used to determine migration ability of cancer cells. Matrigel assay was used to determine invasion ability of cancer cells. MTT and colony formation assays were used to evaluate proliferation of cancer cells. Data were analyzed with Chi-square and Student’s t tests. All statistical tests were two sided
Results In this study, we identified DTL as a previously unrecognized driver of anti-tumor immunity through the stimulator of interferon genes (STING) pathway of cytosolic DNA sensing. Overexpression of DTL or kinase activity impaired STING activation and interferon (IFN)-β-stimulated gene induction. DTL deficiency in IFN-β-producing tumors drove rapid growth and reduced infiltration of CD103+ CD8α+ dendritic cells and cytotoxic lymphocytes, attenuating the

response to cancer chemo-immunotherapy. Mechanistically, DAPK3 was identified as a potential substrate of DTL. Co-IP and immunofluorescence assays further confirmed the interaction between DTL and DAPK3. Moreover, DTL overexpression decreased the protein level and accelerated the degradation rate of DAPK3. Through in vitro ubiquitination experiment, we proved that DAPK3 was degraded by DTL through ubiquitination. Clinically DTL was significantly up-regulated in cancer tissues than that in normal tissues. The survival curves showed that cancer patients with higher DTL expression owned lower survival rate. Functional experiments showed that DTL not only enhanced the proliferation and migration abilities of cancer cells, but also promoted the tumorigenesis in nude mice. Rescued experiment results demonstrated that silencing DAPK3 simultaneous with DTL recovered the phenotypes defect caused by DTL knocking down.

Conclusion Thus, DTL is an important tumor-promoting ubiquitin ligase, which can inhibit tumor innate immunity and tumor immune monitoring.

PU-0425

生理性衰老人群肾脏组织中的 RNA 甲基化修饰表达谱研究

徐莉
中国医科大学附属第一医院

目前，人口老龄化给我国带来逐年加重的社会经济负担，健康老龄化成为亟待解决的公共卫生问题，因此研究并探索人口老龄化相关问题具有重大意义。随着年龄增长，肾脏储备功能减退，对外界刺激或损伤的应激反应能力和代偿能力下降，从而导致慢性肾脏疾病发病率增高，同时也可导致急性肾损伤。因此，探索肾衰老的细胞分子结构改变及其发生机制，阐明衰老肾脏相关疾病易感性增加的原因，并寻找有效治疗靶点及预防措施显得尤为重要。本研究选择于中国医科大学附属第一医院泌尿外科因泌尿系局限性肿瘤或肾脏外伤行全肾切除的患者肾皮质组织 6 例（＜45 岁 3 例；＞65 岁 3 例＝，使用 m6A-mRNA&lncRNA 表观转录组芯片检测中青年组和老年组肾组织 mRNA&lncRNA 中 m6A 表观转录修饰水平。RT-qPCR 检测 m6A 甲基化酶的差异性表达。结果发现，随着年龄增长，表达上调 mRNA 1051 个，表达下调 mRNA 269 个；m6A 修饰水平增高 mRNA 23 个，m6A 修饰水平降低 mRNA 113 个。GO 分析与 pathway 分析发现发生明显差异性 m6A 修饰的 mRNA 与钙、钠等离子转运通路、Wnt 信号通路、细胞外基质蛋白受体蛋白等密切相关，有望为肾脏衰老提供早期干预和治疗靶点。

PU-0426

小分子化合物 ABO 提高耐药性卵巢癌对铂类化疗药物敏感性的研究

许瑞
山东第一医科大学附属省立医院

因卵巢癌患者往往发展为化疗耐药，使其死亡率居妇科恶性肿瘤首位。但目前的分子靶向药无法满足临床要求，本项目组初步证明 ABO 能提高耐药卵巢癌对铂类的敏感性，利用耐药卵巢癌细胞 SKOV3/DDP 筛选了一系列具有多种生物活性的苯并噁嗪衍生物并最终寻找到一种苯并噁嗪衍生物—ABO 能够显著逆转该细胞株对顺铂的耐性。BCL2L10 是一个在卵巢癌组织中表达显著降低的因子且与 FIGO 分期显著相关。在耐药卵巢癌细胞 SKOV3/DDP 中过表达后会促进细胞凋亡，说明 BCL2L10 在卵巢癌中是一个凋亡促进因子。发现 ABO 可以诱导耐药卵巢癌细胞 SKOV3/DDP 中 BCL2L10 的表达。BCL2L10 启动子区存在一个 CpG 岛，ABO 能够降低该区域的 DNA 甲基化水平，说明 ABO 通过降低 BCL2L10 启动子的 CpG 甲基化水平从而促进其转录。为了进一步研究

ABO 对 BCL2L10 表达的调控机制，我们检测了 BCL2L10 的邻近基因长非编码 RNA-CERNA1 的 RNA 水平，发现其表达受到 ABO 的诱导。而在 SKOV3/DDP 中过表达 CERNA1 能够显著提高 BCL2L10 的表达。最终证明 ABO 通过 ANXA7 磷酸化 Smad2/3，磷酸化的 Smad2/3 入核后提高 CERNA1 的表达，CERNA1 通过与 DNMT 结合降低 BCL2L10 启动子 CpG 甲基化从而促进其表达，最终提高耐药卵巢癌细胞对铂类化疗的敏感性。

PU-0427

不同来源新冠核酸病毒质控品检测结果的一致性分析

黄献彬、陈宝荣、孙慧颖、郑燕华
北京金域医学检验实验室有限公司

目的 分析 4 种不同厂家的新型冠状病毒核酸检测试剂对不同来源的质控样本的检测能力，并分析其检测结果的一致性。
方法 收集国家卫生健康委临床检验中心、北京市疾病预防控制中心（CDC）及北京市朝阳区疾病预防控制中心的室间质评样本共 30 份。用磁珠法（同一种核酸提取试剂)、3 个不同厂家新型冠状病毒核酸扩增检测试剂及另 1 个厂家生产的新型冠状病毒核酸快速检测试剂进行核酸提取和扩增，根据检测结果比较相关试剂对不同来源的质控品的检测性能。
结果 30 份质评样本中有 16 份为新型冠状病毒核酸阳性样本，14 份为新冠病毒阴性样本。A、C 厂家核酸检测试剂对 16 份阳性质评样本的 ORF1ab 基因检出率为 93.75%，N 基因检出率为 100%，双基因同时检出率为 93.75%，有效检出率为 100.00%；B 厂家核酸检测试剂阳性质评样本 ORF1ab 基因检出率为 87.5%，N 基因检出率为 93.75%，双基因同时检出率为 87.5%，有效检出率为 93.75%。D 厂家快速核酸检测试剂对阳性质评样本的 ORF1ab 基因检出率仅为 18.75%，N 基因检出率为 93.75%，双基因同时检出率为 18.75%，有效检出率为 93.75%。
结论 不同核酸检测试剂对质评样本的检测能力不完全一致，且其检测效能并不能以厂家宣称的检出限作为参考。

PU-0428

M2 型巨噬细胞对前列腺癌细胞迁移的影响

凡慧慧
永州市中心医院

目的 检测 M2 型巨噬细胞在正常前列腺以及前列腺癌组织的分布情况，并体外探究 M2 巨噬细胞对前列腺癌细胞的迁移作用。
方法 采用免疫组织化学染色法，以 CD206+作为 M2 巨噬细胞的分子标记；应用 IL-4 细胞因子诱导出 M2 巨噬细胞，并利用 Transwell 迁移实验检测 M2 巨噬细胞对前列腺癌细胞的迁移作用。
结果 M2 巨噬细胞在前列腺癌组织中的分布高于正常前列腺组织（$P<0.05$）。体外诱导的 M2 巨噬细胞与前列腺癌细胞（DU145,PC3）共培养可促进前列腺癌细胞的迁移活动。
结论 前列腺癌组织中 M2 巨噬细胞浸润增加，在一定程度上增加了肿瘤的侵袭能力。

PU-0429

生姜艾叶洗剂治疗实验大鼠冻伤有效性诊断

陈欣、王战豪 、 杨清、张玲 、郑飞 、刘华伟
成都市第三人民医院

目的 检验生姜艾叶洗剂治疗冻伤的疗效。
方法 ① 40 只大鼠随机分为对照组、模型组、生姜艾叶洗剂组和冻疮膏组，每组 10 只。后三组动物制备冻伤模型，造模成功后，连续给药 10 天，观察大鼠一般情况、皮损伤情况，考察冻伤康复情况。② 通过检测血液流变学特征，及观察冻伤部位皮肤病理改变，验证生姜艾叶洗剂的治疗作用。
结果 生姜艾叶洗剂组治疗给药组总有效率显著高于对照组。
结论 生姜艾叶洗剂治疗冻伤的疗效好，无明显副作用。

PU-0430

外周血 Septin9 基因甲基化联合粪便隐血实验、肿瘤标志物等指标对结直肠癌早期诊断的意义

龙璐
中南大学湘雅医院

目的 探究外周血 Septin9 基因甲基化、粪便隐血试验（fecal occult blood test，FOBT）、癌胚抗原（carcinoembryonic antigen，CEA）、糖链抗原 199（carbohydrate antigen 199，CA199）、及常见的血液检查指标如中性粒细胞淋巴细胞比值（neutrophil lymphocyte ratio，NLR）、血小板与淋巴细胞比值（platelet-to-lymphocyte ratio，PLR）等指标对结直肠癌早期诊断的应用价值。
方法 选取 2019 年 1 月至 2020 年 1 月在中南大学湘雅医院住院的初诊为结直肠癌的患者 140 例为结直肠癌组，其中男性 82 例，女性 58 例。另选取同期健康体检者 110 例为对照组，其中男性 66 例，女性 43 例。取外周血进行 Septin9 基因甲基化、血常规、血清肿瘤标志物水平及粪便隐血试验的检测。SPSS 统计分析比较两组间上述指标的差异。
结果（1）与健康对照组相比，结直肠癌组 Septin9 基因甲基化及 FOBT 阳性率显著升高，RDW、NLR、PLR 及血清肿瘤标志物 CEA、CA19-9 和 CA125 水平也显著升高（P<0.05）。（2）Septin9 基因甲基化检测结直肠癌的敏感性为 86.43%，特异性为 97.27%，准确性为 91.20%，FOBT 检测敏感性为 85.72%，特异性为 98.18%，准确性为 91.20%，Septin9 基因甲基化联合 FOBT 检测敏感性为 97.86%，特异性为 95.45%，准确性为 93.63%；炎症指标检测敏感性为 65.71%，特异性为 82.73%，准确性为 73.20%，Septin9 基因甲基化联合炎症指标敏感性为 90.71%，特异性为 96.36%，准确性为 93.20%；RDW 检测敏感性为 72.86%，特异性为 75.45%，准确性为 74.00%，Septin9 基因甲基化联合 RDW 检测敏感性为 92.14%，特异性为 94.55%，准确性为 93.20%；肿瘤标志物检测敏感性为 60.00%，特异性为 100%，准确性为 77.60%，Septin9 基因甲基化联合肿瘤标志物敏感性为 92.14%，特异性为 97.27%，准确性为 94.40%。
结论 血浆 Septin9 基因甲基化、FOBT、炎症指标、RDW 及肿瘤标志物对结直肠癌有筛查和辅助诊断的作用，Septin9 基因甲基化联合其他指标对结直肠癌结直肠癌的早期诊断有重要作用。

PU-0431

肾移植患者术后 BK 病毒感染的危险因素分析

龙璐
中南大学湘雅医院

目的 研究活体肾移植术后 BK 病毒感染情况，搜集临床资料，分析肾移植术后 BK 病毒感染的危险因素。
方法 选择 2018 年 3 月-2019 年 3 月在中南大学湘雅医院进行同种异体肾移植术的患者 293 例作为研究对象，其中男性 187 例，女性 106 例，并自愿接受 BK 病毒检测，应用实时荧光定量 PCR 检测肾移植术后患者血或尿液的 BK 病毒 DNA 载量，根据检测结果将患者分成两个组：BK 病毒 DNA 阳性组（n=21，尿液或血液及尿液 BK 病毒同时阳性）、BK 病毒阴性组（n=272，血液及尿液 BK 病毒 DNA 均为阴性）。比较两组患者的性别、年龄、巨细胞感染情况、中性粒细胞与淋巴细胞的比值（NLR）、平均血小板（MPV）、血肌酐浓度、血尿素与尿酸浓度、患者有无糖尿病、患者有无肺部感染以及供肾冷缺血时间等临床因素，应用 logistic 回归分析的方法分析影响肾移植术后患者 BK 病毒感染的危险因素。
结果 肾移植患者术后 BK 病毒感染的阳性率为 7.17%，患者的年龄为 15-67 岁，平均年龄为 42.16±10.82，通过 logistic 回归分析显示：患者的年龄（P=0.014）、患者有无糖尿病（P=0.048）、有无肺部感染（P=0.003）、供肾冷缺血时间（P=0.023）与 BK 病毒感染具有显著相关性，将其列为危险因素。
结论 实时荧光定量 PCR 检测 BK 病毒操作简单、易行、灵敏度高，可作为肾移植术后 BK 病毒感染的筛查指标。本研究表明肾移植患者中高龄、有糖尿病史、术后发生肺部感染以及供肾冷缺血时间过长会增加患者 BK 病毒感染的风险。

PU-0432

TMEM206 knockout in mice is associated with loss of corneal transparency

Zi-Jian Yang、Shun-Chang Sun
Ruijin Hospital, Shanghai Jiao Tong University School of Medicine

Purpose To investigate a role for TMEM206 in corneal edema in mice, and to explore the potential mechanisms by which TMEM206 knockout causes corneal edema in mice.
Methods TMEM206-knockout mice were generated line using CRISPR-Cas9 system. The variable ophthalmic pathology was observed using a slit lamp microscope, the corneal edema was observed using optical coherence tomography, the corneal ultrastructure was observed using a transmission electron microscope.
Results Corneal opacity was observed in some homozygous TMEM206−/− mice whereas a similar change was not observed in heterozygous TMEM206+/− mice and wild-type littermates. TMEM206 knockout was associated with corneal edema, which in turn caused the organization disruption of collagen fibrils of the cornea in mice.
Conclusion TMEM206 knockout is associated with corneal edema in mice. TMEM206 may play an important role in chloride ion transport across the corneal endothelium or epithelium under physiological conditions with a pH between 7.2 and 7.5.

PU-0433

湖南地区等候肾移植患者 HLA 等位基因与终末期慢性肾衰竭发生和 PRA 产生的相关性分析

孙谦、苏禅娟
中南大学湘雅医院

目的 通过回顾性分析方法，对湖南地区 347 例等候肾移植慢性肾衰竭终末期患者的 HLA-A、B、DR 基因表达型别和移植前 PRA 抗体的产生情况进行研究，以探讨因为原发性肾脏疾病而导致肾脏衰竭的患者在最终并发 ESRD 进程中，HLA 免疫遗传易感性以及 PRA 产生与自身 HLA 等位基因型的相关性。
方法 对 2015～2019 年间湖南地区 347 例等候肾移植 ESRD 患者的 HLA 等位基因分型和 PRA 抗体筛查结果进行分析，其中采取 PCR-SSP 法对 HLA-A、B、DR 基因分型进行分析，采取 ELISA 法检测患者血清样本中 PRA 抗体并按 PRA 检测结果将患者分为 PRA 阴性组和 PRA 阳性组。应用 SPSS21.0 软件分析 HLA-A，B，DR 三个位点的基因频率、RR、OR 以及 PRA 阴性组和 PRA 阳性组在 HLA-A、B、DR 位点分布频率的差异和不同性别患者 PRA 阳性率的差异。
结果 ESRD 患者共表达 HLA-A 等位基因 14 个，HLA-B 等位基因 25 个，HLA-DR 等位基因 13 个，其中较高频率的等位基因型为 HLA-A2、A11、A24（9）、B60（40）、B46、B13、DR09、DR04、DR12（05）。其中病例组 HLA-A2、B48、B52（05）、B55（22）的基因频率显著高于对照组（P＜0.05）,对照组 HLA-A1101、B60（40）的基因频率显著高于病例组（P＜0.05）。PRA 阴性组和 PRA 阳性组的 HLA 基因频率分布显示，女性 PRA 阳性组基因频率明显高于男性（P＜0.05）；PRA 阳性组 HLA-A2、B38（16）的基因频率明显高于 PRA 阴性组（P＜0.05），PRA 阴性组 HLA-60（40）的基因频率明显高于 PRA 阳性组（P＜0.05）。
结论 研究发现 HLA-A2、B48、B52（05）、B55（22）可能为湖南地区原发肾病患者并发 ESRD 的易感基因，而 B60（40）可能为保护基因；PRA 的产生与 HLA 基因分布具有相关性，HLA-A2、B38（16）可能更易获得 PRA，而 HLA-B60（40）不易获得 PRA。

PU-0434

基于基因表达数据库对胰腺癌患者的生物信息学分析

陈佳益、伍均
上海市第一人民医院嘉定分院

目的 通过生物信息学工具筛选胰腺癌患者相关的差异表达基因，探寻胰腺癌肿瘤的发病机制。
方法 通过 GEO 数据库资料筛查，检索词：胰腺癌（Pancreatic tumor）；探针（array），共筛选 8 个与胰腺癌组织及正常胰腺组织共同相关数据集，GSE15471,GSE16515,GSE28735,GSE32676,GSE56560,GSE62165,GSE62452 和 GSE101448。网络下载相关 mRNA 数据集，使用 R 语言包 sva 合并相关数据集中信息。，其中胰腺癌组织标本 384 个，正常胰腺组织标本 207 个，并寻找差异表达基因。
结果 经过分析，共发现 249 条差异基因（|logFC|>1 且 adjusted p<0.05），其中 173 条上调基因（包含 OLR1），76 条下调基因。接下来进行 GSEA 分析，在脂肪生成(Adipogenesis)中 181 个条目出现了显著富集，在血管生成（Angiogenesis）中 33 个条目出现了富集，在磷酸化作用（Phosphorylation）中 176 个条目出现了富集，在过氧化物酶体(Peroxisome)中 181 个条目上出现了显著富集，表明胰腺癌与非癌组织具有显著差异的基因在这些功能条目上进行了富集，并通过这些功能条目促进胰腺癌的发生发展。我们在此基础上进一步进行通路富集分析，查询这些差异基因共同富集的信号通路（其中包含 PI3K/AKT、KRAS 信号通路）。分析：通过进一步分析 OLR1 在 GEO 数据库中胰腺癌组织和正常胰腺组织的表达水平，我们发现 OLR1 的表达水平在胰腺癌组

织中要显著高于正常胰腺组织（P<0.001）。再下载 TCGA 数据库，使用 survminer R 包做生存分析，采用 KM 分析(log-rank test)，结果显示 OLR1 的表达水平与胰腺癌预后明显相关（P=0.018）。**结论** 氧化低密度脂蛋白受体 1（OLR1），又称为凝集素样氧化低密度脂蛋白受体 1（LOX-1），是一种 II 型跨膜糖蛋白，作为氧化低密度脂蛋白的作用受体（ox-LDL）主要分布于内皮细胞、巨噬细胞及平滑肌细胞表面。OLR1 的表达已经被证实与多种晚期恶性肿瘤相关。我们推测，胰腺癌患者伴有的脂质代谢异常可能与 OLR1 的参与有关。ox-LDL 和炎症刺激反应可以诱导肿瘤表面 OLR1 水平的上调，OLR1 进一步激活信号通路与炎症因子之间形成三者之间的正向反馈，促进胰腺癌脂代谢异常，最终促进恶性肿瘤侵袭与转移的发生。

PU-0435

Identification of the ataxin-1 interaction network and its impact on spinocerebellar ataxia type 1

Jiu-Ming Chen、Shi-Kai Chen、Pei-Pei Jin、Shun-Chang Sun
Ruijin Hospital, Shanghai Jiao Tong University School of Medicine

Purpose To explore the ataxin-1 interaction network and its impact on spinocerebellar ataxia type 1.
Methods Protein-protein interactions were screened using tandem affinity purification (TAP) tagging, and were validated by immunoprecipitation. Direct transcriptional targets of ataxin-1 were identified using chromatin immunoprecipitation high-throughput sequencing (ChIP-seq) and RNA immunoprecipitation high-throughput sequencing (RIP-seq) techniques in HEK-293T cells.
Results We found that wild-type ataxin-1 interacted with MCM2, GNAS, and TMEM206, while mutant ataxin-1 lost its interaction with MCM2, GNAS, and TMEM206 in this study using HEK-293T cells. Two ataxin-1 binding targets containing the core GGAG or AAAT were identified in HEK-293T cells using ChIP-seq. Gene Ontology analysis of the top ataxin-1 binding genes identified SLC6A15, NTF3, KCNC3, and DNAJC6 as functional genes in neurons in vitro. Ataxin-1 also was identified as an RNA binding protein in HEK-293T cells using RIP-seq, but the polyglutamine expansion in the ataxin-1 had no direct effects on the RNA binding activity of ataxin-1.
Conclusions An expanded polyglutamine tract in ataxin-1 might interfere with protein-protein or protein-DNA interactions but had little effect on protein-RNA interactions. This study suggested that the dysfunction of protein-protein or protein-DNA interactions is involved in the pathogenesis of SCA1.

PU-0436

一种新型无酶等温核酸扩增方法

许伟、吴国球
东南大学附属中大医院

目的 建立一种基于核酸分子间自由能差区别驱动的无需酶促的核酸分子扩增体系
方法 该反应类似于酶促反应。待测靶标链 T 触发反应，使得链置换反应启动，通过链置换反应的循环，链 T 在循环末端释放并触发下一个循环。该反应中链 T 并不会被消耗，而是消耗预先加入的复合物 SBO 以及链 F，即该过程中链 T 催化底物复合物 SBO、链 F 生成产物复合物 SF、链 B 和链 O。作为一种类酶促反应，其在待测靶标链 T 存在的情况下可快速高效地将底物转化为产物，实现信号的无酶循环扩增。
反应过程：通过连续三次链置换反应，构建一个闭环的循环扩增方法，当待检测靶标触发第一次反应后即可启动扩增循环，对核酸信号进行扩增，具体原理见图 1。步骤①：链 T 以其功能区 1 与复

合物 SBO 中链 S 中 1’互补结合，且链 S 与链 B 之间结合的吉布斯自由能更低，从而引发链置换反应与复合物 SBO 竞争性结合，导致链 S 从复合物中解离并生成新的复合物 STO；步骤②：因复合物 STO 暴露出 S 链中 3’功能区，所以链 F 可以以其序列中 3 功能区特异性结合至复合物 STO 上，因此其可以通过链置换反应使得链 O 被解离；步骤③：链 F 继续竞争结合在链 S 上的链 T，最终导致链 T 的解离，最终生成复合物 SF。该扩增循环中，链 T 在此过程中充当着核酶的作用，即因为链 T 的存在从而促进了整个反应的进行，而反应前后链 T 并不会消耗。该反应消耗加入体系中的复合物 SBO、链 F，最终生成复合物 SF、链 B 以及链 O。该反应循环系统在不借助酶等物质的帮助下将待测靶标链 T 的核酸信号转化为复合物 SF、链 B 以及链 O 的核酸信号，同时还可以对该信号进行放大。

熵驱动无酶扩增循环示意图. 其中 S, F, T, O, B 分别代表反应体系中所使用核酸链链 S, 链 F, 链 T, 链 O, 链 B. 链 S 为从左至右按 5’-3’顺序, 其它核酸链为从右至左按 5’-3’顺序. 1, 2, 3, 4 代表其中其中的核酸功能区, 1’, 2’, 3’, 4’分别代表功能区 1, 2, 3, 4 的互补序列. 反应按箭头所示方向进行.

结论 核酸按照碱基互补配对规则以氢键相互连接，该反应过程中初始复合物 SBO 以及最终复合物 SF 间互补的碱基对数量相同，仅存在链 O、链 B 间的核酸缺口，可以认为反应的起点以及终点的化学能是相等的。通过以上推导，即可推断该反应过程中体系能量不变，即焓没有变化。

根据吉布斯自由能公式：可知化学反应通过反应熵变以及焓变共同推动，在该反应中焓变，所以我们推断整个过程中反应由反应过程中从初始复合物中释放的分子的熵增益以热力学方式驱动。因此，该方法是一种熵驱动的无酶扩增循环系统。

PU-0437

Age-related Increased Onset and Progression of Prostate Cancer is Revealed in Novel Pten-null Mouse Models

Bing Zhang[1]、Sen Liu[2]、Qiuyang Zhang[2]
1. Medical Laboratory of Shenzhen Luohu Hospital Group , Shenzhen, China
2. Tulane University School of Medicine, New Orleans, Louisiana, United States

Prostate cancer (PCa) is associated with advanced age. To better understand how age impacts PCa, it is critical to use PCa animal models generated at different ages (aged vs. nonaged). The PB-Cre4 driven phosphatase and tensin homolog (Pten) conditional knockout mouse model, which closely imitates human PCa initiation and progression. However, the Pten deletion is triggered in a 2-week-old prostate, when comparing the extent of PCa between aged and non-aged mice, it is difficult to distinguish the extent to which the onset and progression of PCa are due to the acceleration of the normal aging process or due to the manifestation of PCa pathologies over time. We present here a protocol to inject Cre-expressing adenovirus with luciferin tag intraductally into the prostate anterior lobes of Pten floxed mice, thus, the Pten-loss will be triggered at different ages post-Cre expression. The in vivo imaging of luciferin signals following viral infection was conducted to confirm the Cre expression andactivity. Immunohistochemical staining was performed to confirm the Cre expression, Pten loss, and p-Akt and p-S6activation. Prostate weight and histopathology were compared between aged and non-aged mice. The results showed that the virus infection was limited in the prostate glands and aged mice had significantly increased PCa onset and progression compared to young mice. Although technical skill is required to carry out this procedure and the success rate of viral infection is about 80%, this model of PCa is of great use to all investigators in the aging and cancer research field.

PU-0438

BCKDK promotes the proliferation of Tumor by regulating the metabolism of BCAA and Citrate in NSCLC

Li Ren
Tianjin Medical University Cancer Institute and Hospital

Objective Metabolic reprogramming is one of the major characteristics of tumors, Branched-chainα-ketoacid dehydrogenase kinase (BCKDK), the key enzyme of branched-chain amino acids (BCAAs) metabolism, has been reported to play an important role in diabetes, obesity and other diseases. However, much remains unknown regarding BCKDK in No small cell lung cancer (NSCLC). In the current study, we explored BCKDK's role in NSCLC.
Methods Metabolites in serum of NSCLC patients and NSCLC cell culture supernatant were deteted by Nuclear Magnetic Resonance（NMR）.Colony formation, cell proliferation and cell apoptosis were performed to examine BCKDK's role on NSCLC progression. Glucose uptake, lactate production, cellular oxygen consumption rate, extracellular acidification rate and ROS were measured to examine the effect of BCKDK on glucose metabolism. Gene expression was determined by RT-qPCR, Western blot and IHC assay.
Results BCKDK is upregulated in NSCLC tissues, it affects the metabolism of BCAA and citrate in NSCLC cells. Compared with healthy controls and postoperative NSCLC patients, serum BCAA increased and citrate decreased in preoperative NSCLC patients. Knockout of BCKDK decreased NSCLC cell proliferation and apoptosis ex vivo. Further studies demonstrated BCKDK elevated oxidative phosphorylation, ROS level and Inhibited glycolysis.
Conclusion Our results demonstrate that BCKDK may affect glycolysis and oxidative phosphorylation by regulating the degradation of BCAA and citrate, thereby affecting the progression of NSCLC.

PU-0439

丙型肝炎病毒基因分型在临床的应用

李文妮
西安金域医学检验所有限公司

目的 分析丙型肝炎病毒基因亚型的型别分类，以评估其辅助临床治疗丙肝相关疾病的临床价值。
方法 本实验室使用厦门泰普生物 HCV 分型检测试剂盒（PCR--荧光探针法），进行 HCV 基因分型，实时检测临床常见的 HCV 基因亚型，分别为 HCV 1b、2a、3a、3b、6a 5 个亚型。分析本实验室 1613 例 HCV 基因分型结果，对比各亚型的检出率，从而区分临床常见丙型肝炎的感染类型，指导临床用药。
结果 2a 亚型：该型别共检出 495 例，占总样本量的 30.7%。1b 亚型：该型别共检出 388 例，占总样本量的 24.1%。3a 亚型：该型别共检出 179 例，占总样本量的 11.1%。3b 亚型：该型别共检出 92 例，占总样本量的 5.7%。6a 亚型：该型别共检出 67 例，占总样本量的 4.2%。
病毒含量低于检测下限共有 366 例，占总样本量的 22.7%。剩余 26 例样本为极少见型别或无法检测样本，占样本总量 1.6%。通过分析本实验室 1613 例临床样本数据得出 HCV 2a 亚型感染，临床较为常见。
结论 不同亚型的 HCV 感染，其临床表现、肝病严重程度及慢性化病程进展均有差异，抗病毒治疗的效果也不同。临床检测 HCV 基因亚型，有助于区分其感染类型，并判断治疗的难易程度，也可根据病人情况制定个体化抗病毒治疗方案，从而达到治疗效果。

PU-0440

基于分子标记探针的多重 PCR 快速筛查临床高毒力沙门菌方法的建立

肖林林[1]、张李钟蕊[1]、朱雯雯[1]、朱玉[1]、王童[1]、魏取好[1]、董庆利[2]
1. 上海交通大学附属第六人民医院南院
2. 上海理工大学

目的 沙门氏菌是一种常见的食源性病原菌，对公众的生命健康和财产安全造成重大危害。基于此，我们建立并验证了一种基于多重 PCR 结合分子标记探针的检测方法用于快速筛查临床高毒力沙门氏菌，旨在指导临床快速甄别由高毒力沙门氏菌引起的感染，及时采取治疗措施，降低患者负担。
方法 该试验选择沙门氏菌中高保守的分子靶点 invA、常见毒力因子 pagC 基因及肠毒素编码基因 stn，利用已有的基因序列进行引物和探针设计，对设计的 3 套引物和探针进行筛选得到扩增效率最佳的 invAF2、invAR2、invAP3, pagC F3、pagCR3、pagCP2, stnF2、stnR2、stnP1。收集 40 株分离自临床患者标本的沙门氏菌进行灵敏度分析，选择沙门氏菌、大肠埃希菌、阴沟肠杆菌、铜绿假单胞菌、产期肠杆菌、无乳链球菌、金黄色葡萄球菌、肺炎克雷伯菌、变形杆菌、鲍曼不动杆菌、粘质沙雷菌、嗜麦芽窄食单胞菌共 12 种临床常见细菌用于特异性验证。采用磁珠法对所选菌株进行基因组 DNA 提取，将基因组 DNA 浓度稀释至 10-2μg/ml 用于特异性验证，对沙门氏菌基因组 DNA 进行倍比稀释，扩增后依据结果绘制标准曲线，进一步确定灵敏度。
结果 经过系列实验筛查，将 invA、pagC、stn 作为多重 PCR 的 3 个检测靶标具有良好的检测性能，其中以 invA 为沙门氏菌菌种鉴定靶标其检测限可达为 1×10-6μg/ml（目标 DNA 浓度）,特异性 100%，以 pagC、stn 为区分高毒力沙门氏菌鉴定靶标其检测限可达为 1×10-8μg/ml（目标 DNA 浓度）,特异性 100%。3 个检测靶标分别标记不同检测波长的激发荧光基团，相互间无明显干扰。
结论 本研究建立的检测方法具有较高灵敏度和特异性，能够准确鉴定并区分高毒力沙门氏菌菌株，可以用于临床高毒力沙门氏菌的筛查。该方法的建立可以为临床快速判断沙门氏菌毒力大小提供一种高效便捷的手段，为临床早期诊断和治疗提供新的支撑。

PU-0441

Prognostic value of piR-39980 in patients with colorectal cancer

Wei Gao 、Guoqiu Wu
Zhongda Hospital, Southeast University

Objective Colorectal cancer (CRC) accounts for a common gastrointestinal malignancy all over world. Piwi-interacting RNAs (piRNAs) show a substantial role in the oncogenesis of a variety of tumors. The objective of this work was to uncover the expression profile of piR-39980 and its prognostic value in CRC.
Methods The levels of piR-39980 expression in CRC tissues and paired normal tissues was determined by quantitative real-time polymerase chain reaction (qRT-PCR). Association of piR-39980 with CRC clinical feathers was assessed by Chi-square test. Overall survival curve was built via log-rank test by Kaplan–Meier analysis. The prognostic significance of piR-39980 in CRC was measured by Cox regression model.
Results piR-39980 was upregulated in CRC specimens than the paired normal specimens ($P < 0.001$). Importantly, upregulation of piR-39980 was related to tumor size and T stage (all $P < 0.05$). Survival evaluation suggested that CRC folks with high expression of piR-39980 went through poorer overall survival than folks with low piR-39980 expression (log rank test, $P = 0.0429$). piR-39980 could be an independent indicator for CRC patients' prognosis (HR = 3.308, 95% CI = 1.762-6.594, $P = 0.043$).

Conclusions piR-39980 plays oncogenic roles in CRC tumorigenesis and may be an independent indicator for CRC prognosis.

PU-0442

Silvestrol induces cell apoptosis through endoplasmic reticulum stress triggered JAK2/STAT3 pathway inhibition in gastric cancer

Wei Gao 、Guoqiu Wu
Zhongda Hospital, Southeast University

With the increasing of chemotherapeutic resistance in gastric cancer (GC), the discovery of new chemotherapy drugs become extremely urgent. Silvestrol has been found to possess anti-tumor effects recently, but its role and underlying mechanism in GC are still not clear. In the present study, we aimed to explore the effect of silvestrol in GC cells and the underlying molecular mechanism.

Cell viability was evaluated by CCK-8 assay to evaluate whether silvestrol possesses any potential for treatment of GC cells. Apoptotic effects of silvestrol on GC cells were adopted by flow cytometry and western blot. Real-time quantitative PCR was used to clarify whether the endoplasmic reticulum stress (ERS) is involved in silvestrol-induced GC cell apoptosis. To further elucidate the underlying molecular mechanism of silvestrol-induced cell apoptosis, western blotting analyses was also applied to examine the phosphorylation status of JAK2/STAT3 in GC cell treated with various concentrations of silvestrol.

In the research, we found that treatment with silvestrol resulted in a significant inhibitory effect and more apoptotic deaths in GC cells , compared with the control. Our work also revealed that silvestrol play a crucial role in inhibiting the cell proliferation and potently induced the apoptosis of GC cells in vitro in a time- and concentration-dependent manner. Moreover, the addition of silvestrol to GC cells increased the levels of GRP78, ATF4, and CHOP than the control. Furthermore, the phosphorylation of JAK2/STAT3 and the release of caspase-3 proteases in silvestrol-treated cells appeared to be inhibited in a concentration-dependent manner, compared to that in untreated control cells.

In summary, based on the presented data, our results showed that the apoptosis of GC cells induced by silvestrol was mediated by ERS and ERS-triggered JAK2/STAT3 signaling pathway. We provided the support for silvestrol as a potential therapeutic agent for GC, which may facilitate to further development of preclinical anti-tumor drugs.

PU-0443

Hsa_circ_0080145 induces cell proliferation and apoptosis of colorectal cancer via regulation of Akt/NF-kB signaling pathway

Wei Gao 、Guoqiu Wu
Zhongda Hospital, Southeast University

Circular RNAs have been reported to regulate tumorigenesis and served as a tumor target. The functional role and underlying molecular mechanism of circular RNA hsa_circ_0080145 in colorectal cancer (CRC) were still remain unclear. The purpose of this work was to consider the pattern of hsa_circ_0080145 expression, function and its biological significance in CRC.

Thirty cases of CRC tissues and four CRC cell lines of hsa_circ_0080145 mRNA expression were analyzed by RT-PCR. Small interfering RNA (siRNA) were transferred into CRC cells to

target hsa_circ_0080145. MTT assays and flow cytometer were used to analyze the effect of hsa_circ_0080145 on CRC cell growth and apoptosis in CRC cell lines. We also inspected the changes of Bcl-2 and Bax, which is responsible for cell proliferaion and apoptosis. The restraint of hsa_circ_0080145 knockdown on phosphorylation of Akt was verified by western blot.

The outcomes indicated that hsa_circ_0080145 was distinctly overexpressed in all four CRC cell lines. As hsa_circ_0080145 was upregulated in CRC cell lines, RT-PCR demonstrated that hsa_circ_0080145 expression in CRC tissues was overexpressed compared with normal cases. Clinical pathological detection confirmed that high hsa_circ_0080145 expression were highly associated with CRC volume, and the serum content of hsa_circ_0080145 was significantly elevated comparing with healthy control group ($P<0.05$). Hsa_circ_0080145 level also increased in distinguishing CRC compared with normal group ($P<0.01$). In addition, Kaplan–Meier analysis found that increased hsa_circ_0080145 resulted in poor survival ($P < 0.05$). Further experiments illuminated that loss of hsa_circ_0080145 expression repressed tumor proliferation and resulted in apoptosis in vitro. Importantly, we demonstrated that Akt signaling inactivation after loss of hsa_circ_0080145 in CRC.

Taken together, this study supported the first evidence that hsa_circ_0080145 was a promising biomarker and a novel target for treatment of CRC in humans. Hsa_circ_0080145 may be served as a potential target for cancer therapeutics via regulation of Akt signaling pathway.

PU-0444

A Novel Controlled PTEN-Knockout Mouse Model for Prostate Cancer Study

Bing Zhang[2]、Sen Liu[3]、Qiuyang Zhang[1]

1. Department of Structural and Cellular Biology, Tulane University School of Medicine, New Orleans, LA, United States

2. Medical Laboratory of Shenzhen Luohu Hospital Group , Shenzhen, China

3. Department of Structural and Cellular Biology, Tulane University School of Medicine, New Orleans, LA, United States

Prostate cancer (PCa) is associated with advanced age, but how age contributes to prostate carcinogenesis remains unknown. The prostate-specific Pten conditional knockout mouse model closely imitates human PCa initiation and progression. To better understand how age impacts PCa in an experimental model, we havegenerated a spatially and temporally controlled Pten-null PCa murine model at different ages (aged vs. non-aged) of adult mice. Here, we present a protocol to inject the Creexpressing adenovirus with luciferin tag, intraductally, into the prostate anterior lobes of Pten-floxed mice; Pten-loss will be triggered post-Cre expression at different ages. In vivo imaging of luciferin signal following viral infection confirmed successful delivery of the virus and Cre activity. Immunohistochemical staining confirmed prostate epithelial-specific expression of Cre recombinase and the loss of Pten and activation of P-Akt, P-S6, and P-4E-BP1. The Cre-expression, Pten ablation, and activated PI3K/AKT/mTOR pathways were limited to the prostate epithelium. All mice developed prostatic epithelial hyperplasia within 4 weeks after Pten ablation and prostatic intraepithelial neoplasia (PIN) within 8 weeks post-Pten ablation. Some PINs had progressed to invasive adenocarcinoma at 8–16 weeks post-Pten ablation. Aged mice exhibited significantly accelerated PI3K/AKT/mTOR signaling and increased PCa onset and progression compared to young mice. The viral infection success rate is ~80%. This model will be beneficial for investigations of cancer-related to aging.

PU-0445

Aloin affects the apoptosis of oxaliplatin-resistant gastric cancer cells by Akt/NF-kB signaling pathway

Wei Gao 、Guoqiu Wu
Zhongda Hospital, Southeast University

Background Gastric cancer (GC) is one of the most lethal malignancy types with the highest mortality rate and the steadily increasing incidence. Survival of patients with GC remains poor, which is largely attributed to active carcinogenesis. Therefore an enormous amount of research are under to exploit novel strategies for the treatment of gastric cancer. Aloin has recently been shown to have anti-tumor effects, but its functional role and underlying mechanism in GC are rather elusive. The present study is focused on investigating the effect of aloin in GC cell lines and the underlying important cellular signal transduction molecules such as Akt and NF-kB pathway, which play a vital role in cell apoptosis.
Methods To investigate whether aloin possesses inhibitory effect for treatment of gastric cancer, we examined its effect on proliferation of GC cell lines by CCK-8 assay. An annexin V-FITC flow cytometry assay and DNA fragmentation method were performed to analyze the effect on cell cycle assay and apoptosis. Western blot analysis was used to examine the expression of apoptosis related proteins.
Results Aloin treatment group significantly reduced cell viability in a dose-dependent manner compared with control groups. The flow cytometry result showed an increase in sub-G1 phase. Aloin inhibited the nuclear transportation of NF-kB, and downregulated Akt expression. Declined of Bcl-2, activation of caspase-3 and increased of PARP cleavage triggered apoptosis. Besides, DNA fragmentation analyse also displayed apoptotic induction.
Conclusion Taken together, our results suggested that aloin exerted cytotoxicity
against GC cells and could induce apoptosis of SGC-7901. The apoptosis of
GC cells induced by aloin was related to inhibition of Akt/NF-kB signaling pathway. It may become a potential chemotherapeutic therapy strategy for the oxaliplatin-resistantance gastric cancer.

PU-0446

CREB3L4 基因在云南宣威肺癌中的表达及作用机制研究

张艳亮 [1,2,3]、刘肖 [1,2,3]、段友斌 [4]、段勇 [1,2,3]
1. 昆明医科大学第一附属医院
2. 云南省检验医学重点实验室
3. 昆明医科大学第一附属医院临床检验诊断省创新团队
4. 云南昆明血液中心

目的 加强宣威地区肺癌发病的分子机制研究，寻找新的诊断和治疗靶点。
方法 应用 WB 和 RT-qPCR 方法检测 CREB3L4 在宣威肺癌细胞株 JT、普通非小细胞肺癌细胞株 A549 中的表达和其在正常人支气管上皮细胞株 16HBE、Beas-2b 中的表达差异。RT-qPCR、WB、IHC 检测 CREB3L4 在宣威肺癌组织和癌旁组织中的表达情况，并进行临床相关性分析。构建 CREB3L4 过表达、干扰、回复及相应对照稳定转染细胞株，应用 RNA-seq 和 ChIP-seq 对各组细胞进行检测，筛查出差异表达基因。并通过多种等生物信息学方法探讨 CREB3L4 的生物学功能。随后通过 CCK8 实验、Transwell 实验、流式细胞术检测细胞增殖、侵袭、迁移、周期与凋亡等情况，在体外观察 CREB3L4 异常表达对 JT 和 A549 细胞株生物学特性的影响。
结果 无论在转录水平还是翻译水平，JT 和 A549 中的 CREB3L4 的表达都显著高于 16HBE 和 Beas-2b 中的表达（$P<0.05$）。组织实验结果显示，CREB3L4 mRNA 和蛋白水平在宣威肺癌组织中都明显高于癌旁组织。在宣威肺癌组织中 CREB3L4 蛋白的阳性率与患者性别、年龄、吸烟情况

以及肿瘤的 TNM 分期等临床病理特征之间均无明显相关性（P>0.05），但在有淋巴结转移 N1~3 期的肺癌组织中 CREB3L4 蛋白的表达明显高于无淋巴结转移 N0 的肺癌组织（P＜0.05）。CHIP-seq 与 RNA-seq 结果显示在不同组的细胞中均存在一定数量的差异表达基因。GO 和 Pathway 分析结果显示 CREB3L4 涉及的多种与癌症有关的生物学过程和信号通路，提示其在 LCXW 发生发展中的重要作用。功能实验结果显示，CREB3L4 的上调、下调和回复对 JT 和 A549 细胞株的增殖、凋亡、侵袭和迁移都具有一定的调节作用。

结论 CREB3L4 的表达水平在宣威肺癌中发生上调，其表达改变会对宣威肺癌细胞的增殖、凋亡、侵袭和迁移产生影响，CREB3L4 涉及多种与癌症有关的生物学过程和信号通路，以上实验结果为 CREB3L4 在宣威肺癌发生发展中的作用机制研究奠定了一定的基础。

PU-0447

CREB3L4 在宣威肺癌中调控的靶基因筛选及调控方式的探讨

刘肖 [1,2,3]、段勇 [1,2,3]、段友斌 [4]、张艳亮 [1,2,3]
1. 昆明医科大学第一附属医院
2. 云南省检验医学重点实验室
3. 昆明医科大学第一附属医院临床检验诊断省创新团队
4. 云南昆明血液中心

目的 初步探索 CREB3L4 在宣威肺癌发生发展中可能作用的靶基因以及其作为宣威肺癌分子标志物的临床应用价值。

方法 构建 CREB3L4 敲减、过表达宣威肺癌（lung cancer in Xuanwei, LCXW）细胞株，同时应用 RNA-seq 和 ChIP-seq 对各组细胞进行检测，联合分析测序结果筛选出 CREB3L4 可能调控的候选靶基因并在细胞水平进行验证。随后，在新鲜配对 LCXW 组织中通过 RT-qPCR、WB 和 IHC 进一步验证 CREB3L4 与其候选调控靶基因的共表达关系。最后，采用双荧光素酶报告实验验证 CREB3L4 与候选靶基因的结合与调控相关性。同时进行 CREB3L4 及其靶基因的临床相关性分析，评价其作为宣威肺癌诊断标志物的临床应用价值。

结果 联合分析 ChIP-seq 与 RNA-seq，最终筛选出 RASEF 和 SLC38A2 两个候选靶基因进行后续实验。RT-qPCR 结果显示 RASEF、SLC38A2 在 CREB3L4 过表达后存在明显上调（P<0.05）。IHC 和 WB 结果显示，CREB3L4 的蛋白表达量要明显高于癌旁组织（P<0.01），以上结果进一步提示 CREB3L4 与 RASEF 和 SLC38A2 之间的正相关调节。双荧光素酶实验结果显示，抑制 CREB3L4 表达后，RASEF 和 SLC38A2 组的荧光均值比值相对于对照组明显降低（P<0.01），初步证实 CREB3L4 可与 RASEF 和 SLC38A2 直接结合并正向调控它们的表达。临床相关性分析发现，CREB3L4、RASEF 和 SLC38A2 与 LCXW 的淋巴结转移情况和肿瘤病理分期存在相关性（P<0.05）。因此，CREB3L4 及其靶基因 RASEF、SLC38A2 对于 LCXW 的预后评估和治疗可能具有一定意义。

结论 CREB3L4 可能通过调控 RASEF、SLC38A2 的表达而在 LCXW 的发生发展中发挥重要作用。

PU-0448

不同溶血标本对荧光定量 PCR 快速新型冠状病毒核酸检测的影响

杜红飞
成都医学院第一附属医院

目的 2019-nCoV 感染可引起发热、咳嗽、肌痛或疲劳等，重症患者可出现呼吸窘迫综合征等临床表现。2019-nCoV 检测的影响因素众多，其中溶血性状的标本为不可忽视的重要因素。同时，由

于 2019-nCoV 核酸标本采集过程中存在采样人员手法的差异、被采集者鼻腔粘膜破损出血等情况，致血液和标本粘附鼻拭子上，进而可能存在溶血标本的情况。本文就是为了研究分析不同浓度溶血标本对荧光定量 PCR 快速新型冠状病毒核酸检测结果的影响。

方法 利用新型冠状病毒核糖核酸液体室内质控品（中值）模拟阳性标本，实时荧光定量 PCR 方法分别检测非溶血标本与不同模拟溶血标本（依据溶血程度，分为高溶血组，中溶血组，低溶血组）的循环阈值（Ct）值，采用统计学方法进行差异分析。

结果 未溶血与低溶血组的开放读码框 1ab(ORF1ab) 、核衣壳蛋白(N)基因扩增 Ct 值差异均无统计学意义(P > 0.05) ；未溶血与中溶血组的 ORF1ab、N 基因扩增 Ct 值差异均无统计学意义(P > 0.05) ；未溶血与高溶血组比较，溶血组的 ORF1ab、N 基因扩增 Ct 值差异无统计学意义(P > 0.05)，且当血红蛋白浓度达到 142g/L 时，新型冠状病毒核酸标本的 Ct 值>30，被抑制。

结论 通过本文的研究，为指导实验室检验人员在处理患者标本时,能够正确的评价标本因素对 2019-nCoV 核酸检测结果的影响，进而在临床工作中尽量避免对此类标本结果的误判，致临床的漏诊。同时，优化和提高 2019-nCoV 核酸检测标本的质量，对标本的检测结果提供正确、客观分析和合理的解释,避免不必要的临床纠纷。血红蛋白浓度低于 142g/L 的溶血标本对荧光定量 PCR 快速新型冠状核酸检测结果无明显影响。

PU-0449

1351 例地中海贫血基因检测结果及血液学表型分析

周晓萍
成都医学院第一附属医院

目的 地中海贫血是一组不同类型的血红蛋白疾病，其原因是正常珠蛋白链的产生减少或缺失。部分中间型和重型地贫常需规律输血标准治疗方法，如不治疗，患者常表现为中、重度贫血，可伴有肝脾肿大，发育迟缓等，严重者在青少年期死亡。规律输血能够控制住大多数病理状况，但同时也会引发一系列继发性疾病。世界各地对地贫的计划主要是避免重型患儿的出生，许多携带者都是在婚前或早孕阶段进行产前筛查，而近几年本地区地贫筛查才开始普及，成都北部地区地贫流行病学相关报道甚少，本文的目的就是为了了解本地区人群中地中海贫血基因型分布特点，分析 β-地中海贫血杂合子血液学表型与年龄的关系。

方法 选取 2017 年 6 月至 2020 月 12 月于成都医学院第一附属医院检测地贫基因疑似病例 1351 例，采用 PCR-反向斑点杂交法检测常见 α、β 地中海贫血，收集确诊病例的 MCV、MCH、MCHC、Hb 数据。β-地中海贫血杂合子按照年龄分为儿童组、成人组、老人组，比较各组间血液学表型的差异。

结果 在 1351 例检测标本中，确诊 523 例地中海贫血（38.71%），其中 α-地贫 260 例（19.25%），共检出 13 种基因型；β-地贫 252 例（18.65%），共检出 12 种基因型；α 复合 β 地贫 11 例，共检出 9 种基因型。研究发现 MCV、MCH 在儿童组、成人组、老人组呈明显上升趋势，MCHC 呈下降趋势，Hb 在老人组最低，差异具有统计学意义（p<0.05）。

结论 本地区 α-地中海贫血以--SEA/αα 基因型为主，β 地中海贫血以 CD41-42/N、IVS-II-654/N 基因型为主，且在 β-地中海贫血中，年龄与血液学表型呈显著的相关性，可在地中海贫血血常规初筛中提供一定的参考价值。

PU-0450

不同类型地中海贫血对糖化血红蛋白检测干扰的初探

方艳平
南方医科大学珠江医院

目的 高效液相色谱法具有较高稳定性和准确度，为目前临床中公认检测糖化血红蛋白金标准。通过回顾性分析不同类型地中海贫血对 HPLC 检测系统的影响。
方法 收集南方医科大学珠江医院 2017 年 3 月 1 号至 2019 年 4 月 10 号地中海贫血基因检测异常同时又有检测糖化血红蛋白的病例共 284 例，本文中的干扰是指糖化血红蛋白检测不出。
结果 β 地贫基因对糖化血红蛋白的干扰率显著大于 α 地贫基因（P<0.05），不能认为不同类型 α 地贫基因对糖化血红蛋白的干扰有差异（P>0.05），不同类型 β 地贫基因对糖化血红蛋白干扰有明显差异，CD56、CD22、中国型缺失型、SEA-HPFH(东南亚型)和双重杂合突变的干扰率为 100%，但 MCV 和 MCH 的水平却不相同。分析 β 地贫基因检测异常的糖化血红蛋白干扰组和不干扰组的年龄分布，干扰组和不干扰组的年龄有显著差异（P<0.05），干扰组的年龄大于不干扰组。分析不同疾病对糖化血红蛋白的干扰情况，糖尿病肾病组占比最大（45.3%），其他组间占比差异不大。
结论 对于年龄较大的 CD56、CD22、中国型缺失型、SEA-HPFH(东南亚型)和双重杂合突变的检出者，不建议检测糖化血红蛋白反映测定前 120 d 的平均血糖水平。

PU-0451

三种核酸提取方法在六种呼吸道病毒诊断中的比较

谢婷彦、周予婧
中南大学湘雅医院

目的 检测湘雅医院发热儿童呼吸道合胞病毒、腺病毒、副流感病毒Ⅰ型、副流感病毒Ⅲ型、甲型流感病毒和乙型流感病毒的流行率。评估离心柱法、磁珠法(普通型)和磁珠法(快速型)对呼吸道样本的核酸提取效果。
方法 收集 2021 年 3 月 1 日至 4 月 1 日就诊于中南大学湘雅医院的发热儿童咽拭子样本，使用离心柱法提取核酸，用荧光定量 PCR 方法检测六种呼吸道病原体；筛选出阳性样本，分别使用磁珠法(普通型)及磁珠法（快速型）提取核酸，检测核酸浓度和纯度，评估提取方法对六种呼吸道病原体检出的影响。
结果 研究期间，共收集到 236 例发热儿童的咽拭子样本，检测出阳性病毒数 35 例，总检出率为 14.83％。其中呼吸道合胞病毒检出率最高为 14 例（5.93％），其次依次为腺病毒 12 例（5.08％）、副流感病毒Ⅲ型 6 例（2.54％）、副流感病毒Ⅰ型 2 例（2.54％）、甲型流感病毒 1 例（0.4％），未检出乙型流感病毒。三种核酸提取方法获得的核酸浓度（以四分位数表示，单位为 ng/μL）分别为柱提法：22.8（11.86，22.35）、磁珠法(普通型)：12.05（8.12，19.55）、磁珠法(快速型）：14.75（11.85，22.35）（P＜0.05）。三种核酸提取纯度分别为柱提法：1.96（1.91，2.05）、磁珠法（普通型）：1.70（1.62，1.76）、磁珠法（快速型）：2.00（1.87，2.41）（P＜0.05）。离心柱法、磁珠法（普通型）、磁珠法（快速型）提取核酸进行检测的平均 CT 值分别为 28.78、29.95、30.42（P＜0.05）。
结论 六种呼吸道病毒的流行率普遍较低。三种核酸提取方法中离心柱法核酸提取相对完全，浓度及纯度较高，检测灵敏度高。磁珠法（快速型）对胍酸盐的处理能力较弱，影响扩增结果，可造成弱阳性标本的漏检。

PU-0452

一种同时纯化、富集及检测人体血清游离 DNA 的改性水凝胶

张臣、吴国球
东南大学附属中大医院

目的 cfDNA(cell-free DNA)是人体组织排放到血液里的 DNA 片段，不管是正常人还是病人都会发生，现在已经被广泛应用于常见染色体非整倍体无创产前检测(NIPT)、癌症早筛，癌症治疗，治疗后的分子标记物检测等。然而 cfDNA 在血液中含量极低（低至 14-45 ng/mL）以及其已被分解等特性使得临床诊断对其应用进展缓慢，因此对于检测方法的灵敏度及低浓度下定量精确度有较高要求。目前，常规的 cfDNA 纯化和检测方法有磁珠分选法，放射性免疫分析法、实时荧光定量 PCR、测序法等，但这些方法有的检测成本较高，有的方法复杂且需要特殊仪器。因此建立一种简单易行并能够纯化和检测人血清中目标 cfDNA 的方法具很大临床运用前景。
方法 本研究中，研究人员使用一种 DNA 改性水凝胶以及对应的特殊装置实现了人血清样本中的 cfDNA 的同时捕获、纯化、富集以及检测。
结果 该套系统对长度 20-100 bp 的单双链核酸的检测均有良好的灵敏度、特异度，可以检测到低至 10 pg/μL 的 DNA，在多次循环后甚至可以得到极其纯净的核酸。

PU-0453

葡萄球菌核酸酶样结构蛋白 1 在应激刺激下参与加工小体的聚集

邵洁、赵猛、任丽
天津医科大学肿瘤医院

目的 探讨葡萄球菌核酸酶样结构蛋白 1（SND1）在应激刺激下如何参与加工小体（P-body）的聚集以及如何调节应激反应。
方法 利用免疫荧光实验和激光共聚焦显微镜观察 HeLa 细胞中的 SND1 蛋白与 Ago2 蛋白和 Dcp1 蛋白在应激刺激下是否形成共定位加工小体。利用 RNA 干扰技术敲除 HeLa 细胞中 SND1 蛋白表达并利用 Western Blotting 检测蛋白表达水平，从而观察 SND1 低表达是否对加工小体的聚集产生影响。
结果 SND1 蛋白在应激刺激下与 Ago2 蛋白和 Dcp1 蛋白结合共同参与加工小体聚集。SND1 低表达不会抑制 Ago2 聚集到加工小体，但会减少加工小体的数量。
结论 SND1 蛋白在应激刺激下与 Ago2 蛋白和 Dcp1 蛋白结合共同参与加工小体聚集，从而调节细胞应激反应。

PU-0454

叶酸代谢相关酶基因 MTHFR（C677T）多态性与脑梗死的相关性研究

林丽娟
南方医科大学珠江医院

目的 探讨叶酸代谢过程中亚甲基四氢叶酸还原酶（MTHFR）基因 C677T 位点多态性与脑梗死的相关性。
方法 回顾性分析 2017 年 10 月至 2019 年 10 月广州市珠江医院 81 例脑梗死患者的 MTHFR 基因 C667T 位点检测结果，另选择同期本院 81 例进行叶酸代谢相关酶基因检测的健康体检者为对照组，

按 MTHFR 基因多态性分为野生型(C/C 型)、杂合型(C/T 型)、突变型(T/T 型)，分析不同基因型与脑梗死发生的关系。
结果 纯合突变型（T/T）的 MTHFR 在脑梗死组中的频率（30.9%）显著高于对照组（3.7%），差异有统计学意义（P＜0.05）；脑梗死组的亚甲基四氢叶酸还原酶 C/T 型和 C/C 型者和对照组无统计学意义（P＞0.05）
结论 亚甲基四氢叶酸还原酶 C677T 的 T/T 基因型与脑梗死显著相关，T/T 基因型可能是导致脑梗死发生的一个潜在独立危险因素。

PU-0455

G6PD 缺乏症患者基因多态性及与地贫的研究

林丽娟
南方医科大学珠江医院

目的 通过对葡萄糖-6-磷酸脱氢酶（Glucose-6-phoshate-dehydrogenase, G6PD）活性低于 1800 IU/L 的样本进行 G6PD 基因突变分析，了解常见的使 G6PD 酶活性降低的基因突变类型，并探究地贫患者突变与 G6PD 酶活性之间的联系。
方法 收集 2017 年 7 月至 2019 年 1 月在南方医科大学珠江医院酶速率法检测 G6PD 酶活性水平的样本 323 例；从中筛出用 GAP－PCR 法检测 α 地贫基因和反向斑点杂交(RDB) 法检测 β 地贫基因的标本 190 例；并对收集的 323 例的标本一致采用 Taqman 探针荧光定量方法检测 16 种中国人群中常见的 G6PD 基因突变型。
结果 1.在 G6PD 缺乏患者（活性<1300 U/L）中，男女性别比为 103:35；而在 G6PD 酶活性偏低（1300-1800 U/L）人群中，男女性别比为 4:17；两组间的差异有统计学意义。2. 在 130 例单纯一种突变型中分析，其中前四位的基因突变类型分别是 c.1388G>A（67 例，45.6%)，c.1376G>T（46 例，31.2%)，c.95A>G（16 例，4.8%)，c.871G>A（10 例，6.8%)。3. 在 G6PD 缺乏合并地贫的基因检测中，2 例酶活性临界值的女性均检测突变基因型。
结论（1）最常见的两种基因突变为 c.1388G>A 和 c.1376G>T。（2）130 例 G6PD 单纯突变型与 G6PD 酶活性相关性分析，结果发现，不同的基因突变型具有不同水平的 G6PD 酶活性，但没有发现 G6PD 酶活性与突变类型有关联。（3）在收集的 323 例标本中，有 190 例既做了酶法检测 G6PD 酶活性又做了地贫基因筛查的标本，发现无论是 α－地贫、β－地贫或 α+β－地贫，其 G6PD 活性都较无地贫组显著升高(P ＜ 0. 05)，其结果具有显著性差别。

PU-0456

两台荧光定量 PCR 仪检测 HBV-DNA 结果的一致性分析

孙春萍
联勤保障部队第九〇〇医院

目的 对联勤保障部队第 900 医院检验科 PCR 实验室的两台不同型号的荧光定量 PCR 仪（ABI-7500 和 ABI-ViiA7）进行性能评估，在两台仪器精密度，灵敏度，准确度均达到要求的情况下，对两台仪器检测的乙肝病毒 DNA 的结果进行比对分析，评估 ABI-7500 和 ABI-ViiA7 在乙肝病毒 DNA 定量检测方面是否具有一致性的结果。
方法 以 PCR 实验室的 ABI-7500 荧光定量 PCR 仪作为的参比仪器，以该仪器检测的 HBV-DNA 的结果作为参比结果，以 ABI-ViiA7 作为实验仪器，以该仪器检测的 HBV-DNA 的结果作为实验结果。分别通过精密度、灵敏度、准确度等性能验证方法验证这两台定量 PCR 仪器均符合临床检测的要求。其次通过比较两种不同型号仪器所检测的 HBV-DNA 定量值。最后将 30 份无溶血、无黄疸和脂血的新鲜血清标本在这两台仪器上进行扩增，比较分析乙肝 DNA 定量的结果。

结果 ABI-ViiA7 和 ABI-7500 这两台仪器的精密度、灵敏度、准确度均满足临床要求，通过比较 30 份血清标本的结果表明两台仪器检测 HBV-DNA 具有良好的相关性（R2=0.9919），并且两台仪检测的结果偏倚均在<±7.5%的范围。
结论 ABI-ViiA7 检测 HBV-DNA 具有良好的仪器性能，且 ABI-ViiA7 和 ABI-7500 这两种不同型号的仪器检测的 HBV-DNA 具有良好的一致性，ABI-7500 和 ABI-ViiA7 两台荧光定量 PCR 仪 HBV 定量检测的结果能为临床诊断提供一致性和可靠性的保障。

PU-0457

Systematic Analyses of the Role of the Reader Protein of N6-Methyladenosine RNA Methylation, YTH Domain Family 2, in Liver Hepatocellular Carcinoma

Xiangyang Shao
Department of Laboratory Medicine, Nanfang Hospital, Southern Medical University

Background YTH domain family (YTHDF) 2 acts as a “reader” protein for RNA methylation, which is important in tumor regulation. However, the effect of YTHDF2 in liver hepatocellular carcinoma (LIHC) has yet to be elucidated.
Methods We explored the role of YTHDF2 in LIHC based on publicly available datasets [The Cancer Genome Atlas (TCGA), International Cancer Genome Consortium (ICGC), and Gene Expression Omnibus (GEO)]. A bioinformatics approach was employed to analyze YTHDF2. Logistic regression analyses were applied to analyze the correlation between YTHDF2 expression and clinical characteristics. To evaluate the effect of YTHDF2 on the prognosis of LIHC patients, we used Kaplan–Meier (K–M) curves. Gene set enrichment analysis (GSEA) was undertaken using TCGA dataset. Univariate and multivariate Cox analyses were used to ascertain the correlations between YTHDF2 expression and clinicopathologic characteristics with survival. Genes co-expressed with YTHDF2 were identified and detected using publicly available datasets [LinkedOmics, University of California, Santa Cruz (UCSC), Gene Expression Profiling Interactive Analysis (GEPIA), and GEO]. Correlations between YTHDF2 and infiltration of immune cells were investigated by Tumor Immune Estimation Resource (TIMER) and GEPIA.
Results mRNA and protein expression of YTHDF2 was significantly higher in LIHC tissues than in non-cancerous tissues. High YTHDF2 expression in LIHC was associated with poor prognostic clinical factors (high stage, grade, and T classification). K–M analyses indicated that high YTHDF2 expression was correlated with an unfavorable prognosis. Univariate and multivariate Cox analyses revealed that YTHDF2 was an independent factor for a poor prognosis in LIHC patients. GSEA revealed that the high-expression phenotype of YTHDF2 was consistent with the molecular pathways implicated in LIHC carcinogenesis. Analyses of receiver operating characteristic curves showed that YTHDF2 might have a diagnostic value in LIHC patients. YTHDF2 expression was associated positively with SF3A3 expression, which implied that they may cooperate in LIHC progression. YTHDF2 expression was associated with infiltration of immune cells and their marker genes. YTHDF2 had the potential to regulate polarization of tumor-associated macrophages, induce T-cell exhaustion, and activate T-regulatory cells.
Conclusion YTHDF2 may be a promising biomarker for the diagnosis and prognosis of LIHC and may provide new directions and strategies for LIHC treatment

PU-0458

Nasopharyngeal carcinoma diagnosis based on a single-cell Raman-based platform

Dan Xiong、Wei Wu、Dayang Chen、Xiaowen Dou、Xiang Ji、Xiuming Zhang
Medical Laboratory of The Third affiliated hospital of ShenZhen university, Shenzhen, 518001, China;

Nasopharyngeal carcinoma is a kind of head and neck cancer with a high degree of malignancy, which is easy to relapse and metastise. Traditional testing relying on immunofluorescence or fluorescent in situ hybridization were proved to be tedious and expensive. Accurate, quick, and intact diagnosis is important for improving the survival rate of those patients with nasopharyngeal carcinoma. A Raman-based cell assay is a promising tool for evaluating cancer progress. because it can provide abundant varied compound fingerprints of cancer cells in comparison with normal cells, Herein, we developed an efficient and accurate method on a label-free and noninvasive single-cell Raman microspectroscopy (SCRM) platform, to distinguish NPC cell lines 5-8F,6-10B, SUNE1, CNE1, CNE2, C666-1, HK1 from nasopharyngeal normal cell line NPEC1-BMI1. NPC cancer cells and non-cancer cells can be differentiated by analyzing their intrinsic phenotypic Raman spectra at a large scale (5337cm-1 Raman spectra in total). The Raman spectra of glycogen, nucleic acids, and tyrosine in NPC cancer cells were significantly higher than those in non-cancer cells. However, the Raman spectra of lipids in NPC cancer cells were significantly lower than those in non-cancer cells. Those results are consistent with the high expressions of glycogen, nucleic acids, and tyrosine and low expression of lipid in NPC cancer cells. Support Vector Machine (SVM) analysis distinctly differentiates NPC cancer cells from non-cancer cells with 97.85% accuracy. Nasopharyngeal tissues were also clearly distinguished from control tissues with 93.95% accuracy. Together, our study developed an efficient SCRM-based method to evaluate the cells canceration of nasal tissue in advance which shed light on established quick and accurate diagnose during surgery of Nasopharyngeal carcinoma. As a complementary tool, the platform was expected to view the real-time dynamic cancerization status and contributed to improving the diagnosis and operation effects.

PU-0459

实时荧光定量 PCR 检测乙型肝炎病毒 DNA 的方法学性能验证

张鸿娟
昆明医科大学第一附属医院

目的 建立实时荧光定量 PCR 的方法学性能验证方案，并验证实时荧光定量 PCR 检测乙肝病毒 DNA 的方法学性能。
方法 采用试剂厂家所提供的标准品和临床标本进行系列稀释，将所得到的循环阈值与浓度的对数进行直线回归，进行分析测量范围的性能验证；采用接近定量检测限的标本进行倍比稀释，每个浓度标本分为 16 份，分别进行 DNA 提取，以每份浓度样本的检出率和浓度的对数进行概率分析验证最低检出限；选择分析测量范围内高（105IU/mL）、低(103IU/mL)两水平样本，每天平行测定 4 次，连续测量 5 天进行精密度验证。
结果 实时荧光 PCR 检测乙型肝炎病毒 DNA 的分析测量范围为 1.2×103 IU/mL～1.2×107IU/mL；高、低浓度样本批内标准差（浓度取对数）分别为 0.156 和 0.235，总标准分别为 0.221，0.238；最低检出限为 5.2×102IU/mL。
结论 建立的实时荧光定量 PCR 方法学性能验证的方案科学、实用具有可操作性。

PU-0460

Development and internal validation of prognostic nomograms for I-III stage colon cancer patients with preoperative serum normal CEA range

Ming Lei
Yunan Tumor Hospital

Background Although a number of studies have been conducted to investigate factors affecting colon cancer patient overall survival (OS) after surgical treatment, no effective clinical prognostic risk models have been proposed for predicting CC patient with preoperative serum CEA in normal range. We aimed to identify factors affecting the survival of the patients and to construct a nomogram for predicting their survival.
Methods This was a retrospective study. This study used the Colorectal Cancer database of Official Follow-up System of Yunnan Cancer Center, which contains retrospectively collected data of all consecutive patients with stage I to III colorectal cancer who underwent surgical curative resection between 2013 and 2017. We used univariate Cox regression analysis to select the significant prognostic features, which were subjected to the least absolute shrinkage and selection operator (LASSO) regression algorithm for feature selection. Then, the nomogram was used to estimate 1-, 3- and 5-year OS based on the multivariable Cox regression model. Model were established using a training cohort (n=220) and internal testing cohort (n=220). Training cohort stratification was performed by X-tile and Evaluate Cutpoints to assess the predictive capacity of the nomogram. The predictive accuracy was measured by concordance indexes (c-indexes) and calibration values of the nomograms. Evaluation was measured by decision curve analysis (DCA).
Results The multivariate analyses showed that preoperative primary tumor site, differentiation, N stage, and serum CA125 were incorporated into the predictive nomogram. In the training cohort, the preoperative nomogram provided good discrimination, achieved a C-index of 0.811 (95%CI: 0.742-0.882) in predicting OS for training cohort and 0.811 (95%CI: 0.742-0.882) for testing cohort. The timedepended ROC curve was plotted for 1-year nomogram AUC was 0.743, 3-year nomogram AUC was 0.873, and for the 5-year nomogram AUC was 0.823 in the training cohort, while in the testing cohort was 0.863, 0.892, and 0.823. Calibration of the nomogram predicted the probabilities of 1-, 3- and 5-year survival, which corresponded closely with the actual survival rates. The survival curves stratified by the risk score calculated by the nomogram were almost identical for the training and testing cohorts preventing potential loss of information. There was no significant difference at TNM stage I, but there was significant difference at low-risk, intermediate-risk, and high-risk groups in TNM stage II and III.
Conclusion This novel prognostic model showed more accurate predictions of individualized survival in our cohort, but it it recommended to be used in conjunction with AJCC TNM system. In conclusion, this study developed a novel nomogram with good accuracy to aid physicians in estimating the risk of 1-, 3- and 5-year CC in patients starting surgical therapy stratify patients with CC into different risk groups.

PU-0461

叶酸配体靶向 PCR 法定量检测循环肿瘤细胞在非小细胞肺癌临床诊断中的初步研究

刘祥琴
四川省医学科学院·四川省人民医院

目的 循环肿瘤细胞（CTC）的定量检测对肿瘤患者的早期筛查和诊断至关重要。为了研究循环肿瘤细胞对非小细胞肺癌诊断的临床意义，我们采用叶酸配体靶向 PCR 定量检测法对循环肿瘤细胞进行初步研究。
方法 收集 174 例非小细胞肺癌患者和 117 例肺部良性病患者的外周血样本进行实验，以病理检查结果为金标准评估该液体活检方法用于肺癌临床诊断的准确性。通过免疫磁珠筛选去除白细胞使 CTC 得到富集，然后用肿瘤特异性配体——寡聚核苷酸复合物对 CTC 进行标记，洗涤去除多余的未结合复合物，并将与 CTC 结合的复合物洗脱下来进行实时定量 PCR 检测。
结果 按照试剂说明书规定以 8.7CU 作为区分阳性与阴性的阈值，该方法对 I/II 期、III 期和 IV 期患者的检出率分别为 48.3%（29/60）、82.6%（57/69）和 84.4%（38/45）。以肺部良性病患者作为对照组，则该方法对癌症患者的检测灵敏度和特异性分别为 71.3%和 29.6%。
结论 叶酸配体靶向 PCR 定量检测法能够较敏地对非小细胞肺癌患者 CTC 进行定量检测，对肺癌特别是早期患者的临床分期具有潜在应用价值。但特异性较差，需结合病理结果和影像学结果进行进一步确诊。

PU-0462

Prediction of ovarian reserve and clinical pregnancy rates by FSHR Asn680Ser and LHCGR Asn312Ser gene polymorphisms

Xiangqin Liu 、Chun Guo
Sichuan Provincial People's Hospital

Purpose The purpose of this study was to investigate whether the polymorphisms of FSHR (Asn680Ser) and LHCGR (Asn312Ser) can predict ovarian reserve and ovarian response, and the relativity between the polymorphisms and the POSEIDON groups.
Methord 210 infertile women, including 103 low prognosis women were enrolled in this prospective study. The gene polymorphisms were analyzed by Sanger method for direct sequencing. The clinical parameters were statistically analyzed based on genotypes.
Results The frequency of heterozygous and homozygous G allele FSHR Asn680Ser in the low prognosis group was significantly higher than that in normal and high response groups, and there was no significant association between LHCGR Asn312Ser and ovarian response. Moreover, the serum anti-Müllerian hormone (AMH) concentrations, antral follicle count (AFC), oocytes retrieved, MII oocytes, and 2PN oocytes in patients with FSHR Asn/Ser were significantly lower than those with FSHR Asn/Asn. The serum luteinizing hormone (LH) concentrations and clinical pregnancy rate of fresh embryo transfer in patients with LHCGR Ser/Ser were significantly higher than that of the Asn/Ser genotype. In the POSEIDON groups analysis, the low prognosis women with FSHR Asn/Asn were more likely to appear in subgroup 1.
Conclusion In conclusion, our study observed that there was a significant association between the polymorphism of FSHR Asn680Ser and ovarian response. FSHR Asn680Ser Ser/Ser can predict good ovarian reserve, and the LHCGR Asn312Ser gene polymorphisms can be a potential opportunity for all included infertile women to undergo clinical pregnancy for COH. In order to reduce the heterogeneity of POR population, our study adopted POSEIDON groups and

analyzed the correlation between POSEIDON groups and genetic biomarkers. Low-prognosis infertile women with FSHR Asn/Asn genotype were more likely to have better ovarian reserve and prognosis, While using LHCGR Asn312Ser, Asn/Ser is better than Ser/Ser in ovarian response. However, these results are limited owing to the sample size, grouping, ethnicity and region. Larger sample size, and multi-center and multi-ethnic studies are required in future studies.

PU-0463

提升 EB 病毒核酸检测灵敏度对辅助判断鼻咽癌患者疾病进展的意义探讨

杨伊、蔡贞
南方医科大学南方医院

目的 提高鼻咽癌患者血浆 EB 病毒核酸检测灵敏度，初步探究其对患者的疾病进展和治疗效果的临床意义。
方法 使用 EB 病毒核酸检测试剂测定临床确诊的鼻咽癌患者血浆中 EBV DNA 含量。收集 2020 年 9 月至 12 月使用试剂 A 检测结果为 EBV DNA 低于检测下限（500copies/ml）样本 366 例，使用检测下限为 100copies/ml 的试剂 B 进行 EBV DNA 测定，跟踪随访 4~7 个月,记录患者的病情发展及治疗情况并继续监测其血浆 EBV DNA 拷贝数，分析 EBV DNA>100copies/ml 与患者疾病复发或转移的相关性。使用试剂 B 检测 2021 年 3 月至 5 月确诊鼻咽癌患者血浆 EBV DNA，比较以 500copies/ml、100copies/ml 为临界值患者血浆 EBV DNA 阳性率，探讨提高检测灵敏度对临床的指导意义。本次研究采用了磁吸附法对血清中 EBV DNA 进行纯化，实时荧光定量 PCR（qPCR）法对病毒载量进行检测，运用统计学知识对数据进行分析。
结果 使用试剂 B 检测收集到的患者血浆，以 100copies/ml 为临界值，阳性率约为 8.81%（23/261）。通过病例资料随访显示，23 例阳性样本中预后不良者占 56.52%，阴性预后不良者占阴性样本的 4.20%，两组数据的差异具有统计学意义（P<0.01）；男性阳性样本患者比阴性样本患者预后更差；中晚期阳性患者比阴性患者预后更差。试剂 B 检测的 2021 年 3-5 月确诊鼻咽癌患者血浆，以 500copies/ml、100copies/ml 作为临界值，阳性率分别约为 7.81%（31/397）、16.12%(64/397)，提高检测灵敏度后，患者血浆阳性率是提高前的 2.06 倍。
结论 提升 EBV DNA 的检测灵敏度，能更灵敏地反映鼻咽癌患者体内 EB 病毒的变化，及时发现患者体内的病毒残留，有助于临床对鼻咽癌患者复发及转移实施更及时和有效的治疗。

PU-0464

共聚焦显微拉曼光谱鼻咽癌检测中的研究进展

王雪[2]、王萌萌[1]、张秀明[1]、熊丹[3]
1. 深圳市罗湖医院集团医学检验科
2. 深圳市罗湖医院集团医学检验科
3. 深圳市罗湖医学集团医学检验科

中国是鼻咽癌新发病例最高的国家，作为头颈部恶性肿瘤，鼻咽癌严重威胁居民健康。早期鼻咽癌对放化疗敏感，生存率可达 90%。但由于鼻咽癌发病隐匿，现有技术难以实现早期诊断，故灵敏准确的鼻咽癌早期无创检测技术对鼻咽癌的防治及预后评估意义重大。共聚焦显微拉曼光谱技术是将拉曼光谱技术与共聚焦显微分析技术结合起来的一种检测方法，可以提供细胞、组织或体液的化学指纹信息，具有灵敏度高、非侵入性、免标记、水干扰性小等优势。共聚焦显微拉曼光谱在肿瘤细胞间细微差异的检测及肿瘤生物标志物探索方面具有重要的应用价值。本文综述了当前共聚

焦显微拉曼光谱在鼻咽癌检测中的应用现状及研究进展，探讨其成为鼻咽癌临床诊断方法的价值及前景。

PU-0465

Serum exosome concentration as a differential diagnosis marker for pulmonary

Taixue An 、Dehua Sun、Lei Zheng
Nan Fang Hospital

Introduction The 5-year survival rate of Non-small cell lung cancer (NSCLC) patients was less than 16%. Pulmonary tuberculosis (pTB) is the disease most commonly misdiagnosed as lung cancer. A bulk of time and medical resources were consumed on distinguishing two diseases. Previous researches reported that EVs level will increase dramatically in tumorigenesis. However the EVs level in pTB patients has not been determined. We suppose that serum EVs level of pTB patients may be different from cancer patients for their low immunity and weak physical conditions. Serum EVs concentration may sever as a diagnostic marker to distinguish two diseases.
Method We recruited volunteers from the Nang Fang Hospital, including 3 groups: NSCLC (n = 90), pTB (n = 55) and healthy individuals (n = 22). NSCLC patients were diagnosed by pathological biopsy, and pTB patients were diagnosed based on acid-fast staining of sputum smears. Subjects without lung shadows in X-ray tests, a history of tuberculosis, or obvious symptoms of illness were enrolled into healthy group. Chemical reagent was utilized to precipitate EVs from serum. Isolated EVs were characterized by western bloting and electron microscope. The concentration and diameter were measured by the Nanoparticle Tracking Analysis (NTA). Our research was approved and supervised by the Medical Ethics Committee of hospital.
Result We compared levels of serum EVs concentration in pTB, NSCLC, and healthy group. Decreased EVs concentration in pTB patients and smaller EVs diameter in NSCLC patients with advanced stage were observed. With a cutoff of 7.7×1012/ml, the AUC of serum EVs concentration reached 0.83 for discriminating pTB and total NSCLC, which is significant higher than commonly used markers like CEA, CRP and WBC. It seems that serum EVs concentration is not correlated with individual age, sex, CEA, CRP and WBC.
Summary These findings suggest that the serum EVs concentration is significant different among pTB, NSCLC, and healthy individuals, and may serve as a potential marker for the differential diagnosis of two diseases thereby aiding clinicians and decreasing the incidence of misdiagnosis.

PU-0466

43 种白血病融合基因在儿童急性白血病患者中的表达及临床意义

梅 茜
滨州医学院烟台附属医院

目的 本研究通过统计 43 种常见白血病融合基因在儿童白血病患者中的表达情况，分析儿童急性白血病的分子遗传学与临床表现及预后的关系，为进一步加强白血病融合基因用于临床治疗白血病和预后评估提供相应支持。
方法 本研究收集与分析 2018.10.01 至 2019.10.31 一年间医院收治的儿童白血病患者共 52 例患儿的临床资料，主要通过 PCR 实时荧光探针检测方法检测融合基因，采用流式细胞仪检测免疫分型，

以及收集患者骨髓细胞学，血常规等检验结果，（该 52 例患儿均进行了 43 种白血病常见融合基因检测）。
结果 52 例患儿中诊断为 ALL28 例，AML9 例（其中 APL3 例），12 例阴性（另有 3 例无法分型），43 种白血病常见融合基因检测阳性 16 例，总阳性率为 30.7%，包括 TEL-AML1 融合基因 5 例，AML1-ETO 融合基因 3 例，PML-RARα 融合基因 3 例，MLL-AF9 融合基因 2 例，MLL-AF4 融合基因 1 例，E2A-PBX1 融合基因 1 例，NPM-ALK 融合基因 1 例。
结论 采用 PCR 实时荧光探针技术检测融合基因可作为白血病诊断,个体化用药指导，白血病分型、白血病预后评估、临床治疗方案选择，及靶向药物研发的重要依据，也可作为高灵敏度监测 MRD 的分子标志。

PU-0467

Genital human papillomavirus prevalence and genotyping among males in Putuo district of Shanghai, China 2015-2019

Xiaoxiao Li、Fenfen Xiang、 Zixi Chen、Tao Zhang、Zhaowei Zhu、Mengzhe Zhang、Rong Wu、Xiangdong Kang
Laboratory Medicine, Putuo Hospital, Shanghai University of Traditional Chinese Medicine

Background Reports of human papillomavirus (HPV) infection status and genotype-distribution in Chinese men are limited, and men in China have not been recommended for HPV vaccine yet.
Material and Methods We retrospectively reviewed the prevalence and genotyping of male genital HPV in Putuo district of Shanghai, 2015-2019. A total of 1227 male patients (aged 17 to 81 years) attending the dermatology and sexually transmitted disease (STD) clinics at Putuo District Center Hospital were included. Genital exfoliated specimens were obtained for detection and genotyping 27 HPV types by Luminex-based multiplex assay.
Results We found that the prevalence of any HPV was 65.5% (804/1227), and the rate of multiple infection was 25.8% (317/1227). Five main detected types were HPV-6 (32.0%), -11 (23.2%), -16 (5.6%), -43 (4.3%) and -59 (4.0%). In all detected HPV genotypes, 65.5% (875/1336) were nine-valent (9v) HPV genotypes. No significant differences were observed in the detection rate of HPV infection over the studied five years ($P > 0.05$). The ≤24 (70.7%) and ≥55 (72.9%) years old groups showed higher infection rates, and significant differences were detected in rates of low-risk HPV infection in different age-stratified groups ($P < 0.05$). The prevalence of HPV infection among patients with warts (74.4%) was significantly higher than those with other clinical characteristics (40.4%) and physical examination (63.6%).
Conclusions Our study suggested that more than half of Chinese male patients have detectable HPV infections, and penis-genital and anogenital warts were the most common clinical manifestation encountered in patients with HPV infections. Moreover, currently available 9v HPV vaccine covered the most frequently observed HPV types among men.

PU-0468

流行性感冒的季节分布特征分析

张小燕
滨州医学院烟台附属医院

目的 通过探讨本医院 2017 年～2019 年流行性感冒发病的季节分布特征，可进行流行病学的调查研究以及为预防流行性感冒的流行提供参考依据。

方法 收集 2017 年～2019 年医院采用 PCR 核酸检测技术对患者咽拭子进行流感病毒核酸检测的阳性患者共有 351 例，用圆形分布法分析流行性感冒发病的高峰日以及高峰期。
结果 （1）所在实习医院流行性感冒发病有很强的季节性，季节性分布特征为:主要为冬季高发，每年的 1、2、3 月份和 11、12 月份为发病高峰期，其它月份较少或者流感发病患者例数为 0，其中总的流感流行高峰期为 12 月 29 日至次年 4 月 13 日，总高峰日为 2 月 20 日。（2）2017 年和 2018 年所在医院流感发病水平较低，2019 年流感发病人数较多。
结论 2017 年-2019 年所在医院流行性感冒发病存在很强的季节分布特征，每年 12 月至次年 4 月为流行性感冒发病的流行高峰，这段时间正处于冬季，人们容易发病，尤其是学生正处在放寒假回家和返校期间，因此可根据流感发病的高峰期采取有效的预防措施。

PU-0469

烟台地区 PCR 检测 HPV 感染结果分析

邹子涵
滨州医学院烟台附属医院

目的 对烟台地区下生殖道感染女性患者人乳头瘤病毒（Human papilloma virus,HPV）感染的检测结果进行探讨，以了解烟台地区不同年龄的女性 HPV 的感染情况和基因型分布。
方法 选取本医院从 2016 年 1 月至 2019 年 12 月四年的 5599 例女性为研究对象，采集宫颈脱落细胞作为标本，通过多重荧光 PCR 技术对 23 种 HPV 基因型进行分型检测。
结果 HPV 基因检测总阳性率为 16.38%（917/5599），其中高危感染率为 12.95%，感染亚型 52 、16、58 为主分别占总感染人数的 15.28%、15.19%、9.51%。；低危感染率为 2.80%，感染亚型以 42，6，44 为主，分别占中感染人数的 6.59%、4.84%、4.51%。不同年龄组的分布显示 30-40 岁阳性率最高（33.70%）两边呈现下降走向。其中多重感染有 198 人，多集中于 20-30 岁（31.82%；63/198）。
结论 烟台地区女性 HPV 感染以单一感染为主，感染趋势有年轻化的倾向。

PU-0470

GINS2 促进子宫内膜癌增殖和凋亡作用的研究

罗建波
云南省肿瘤医院

目的 本研究旨在从基因和蛋白水平上研究 GINS2 在子宫内膜癌组织中的表达水平，阐明 GINS2 在子宫内膜癌肿瘤细胞增殖和凋亡中可能发挥的作用，为深入研究子宫内膜癌发生发展的分子机制奠定基础，同时为子宫内膜癌的基因诊断和治疗提供新的靶点。
方法实时荧光定量 PCR(RT-PCR）、免疫组织化学法（IHC）。
结论 1 GINS2mRNA、GINS2 蛋白在子宫内膜癌组织中均高表达提示 GINS2 对癌细胞的核酸复制有促进作用，可以调控子宫内膜癌细胞恶性转化，促进子宫内膜癌肿瘤细胞生成过程。
2 子宫内膜癌组织中 GINS2 的高表达与子宫内膜癌患者的年龄、病理类型、病理分级、临床分期、淋巴结转移、肌层侵犯深度和脉管浸润无明显相关性， GINS2 在子宫内膜癌中恒定的高表达，提示 GINS2 可作为子宫内膜癌基因诊断的靶点。
3 Bcl-2、Bax 、CHK2 蛋白在子宫内膜癌组织中的表达水平明显升高，GINS2 与 Bcl-2、CHK2 的表达水平存在正相关，且 GINS2 与 Bcl-2/ Bax 的比值呈正相关。提示 GINS2 通过调节 Bcl-2、CHK2 表达水平，使 Bcl-2、CHK2 表达上调，促进子宫内膜癌细胞增殖抑制其凋亡，发挥促癌作用。其具体的作用机制有待在细胞水平及体外实验进一步探究。

PU-0471

4 个循环 miRNAs 在甲状腺乳头状癌中的诊断意义及与临床病理特征的关系

梁良、李德璇、张晓珺、汪坚、沈乾
云南省第三人民医院

目的 研究 4 个循环 miRNAs 在乳头状甲状腺癌（PTC）中的鉴别诊断的临床意义及与临床病理特征的关系。
方法 选取 2019 年 6 月至 2020 年 6 月在云南省第三人民医院接受甲状腺手术的 PTC 患者 150 例，甲状腺良性病变患者 50 例，健康人 50 例，分别检测外周循环血中 miRNA-21，miRNA-222，miRNA-146b 以及 miRNA-7 的相对表达量。分析 4 个循环 miRNAs 在三组中的表达差异，并分析 4 个循环 miRNAs 与 PTC 临床病理特征的关系。
结果 miRNA-21，-222，-146b 以及 miRNA-7 在 PTC 病变组，甲状腺良性病变组及正常组三组内任意两组之间差异具有统计学意义（P<0.05）。血浆 miR-21、miR-146b 和 miR-7 用于鉴别诊断 PTC 和甲状腺良性病变的诊断价值一般（AUC=0.671、0.629、0.649）；而血浆 miR-222 的鉴别诊断价值良好（AUC=0.953，敏感度 84%，特异性 91.3%）。miR-21、miR-146b、 miR-222 和 miR-7 四者联合指标用于鉴别诊断 PTC 和甲状腺良性病变诊断价值高于 miR-222 单项指标（AUC=0.977，敏感度 90%，特异性 93.3%），特异性高，敏感度强，诊断性较强。miRNA-146b 表达水平与是否有淋巴结转移有相关性（P<0.05）；miRNA-222 与肿瘤分期有相关性（P<0.05）。
结论 miR-146b 与 miR-222 与 PTC 的发展进程相关。血浆 miR-222 可以帮助临床进行 PTC 和甲状腺良性病变的鉴别诊断，减轻病人的痛苦，miRNA-21，-222，-146b 以及 miRNA-7 四者联合指标的诊断效果更好。

PU-0472

MALDI TOF 质谱成像在临床肿瘤组织研究中的应用

卢兆莲
山东大学第二医院

肿瘤是一种高度复杂的组织，由许多不同类型的细胞形成，每种细胞都具有特定的目的，相互之间通过复杂的相互作用而连接，它包含了关于形态、基因组学、蛋白质组学和脂质组学等改变的所有信息。但基于传统的方法很难进行全面评估。基质辅助激光解吸/电离（Matrix-assisted laser desorption/ionization , MALDI）质谱成像（Imaging Mass Spectrometry, IMS）是原位生物分子空间分辨分析的强有力工具。MALDI IMS 能够可视化和测定组织、细胞和微生物区域特异性的、时间性变化的蛋白、多肽、脂质、药物分子和代谢物。这些为研究人员提供了一种新的发现人类疾病潜在生物标志物和解释代谢调节基础生物学的途径，从而使人类健康达到一个新水平。

PU-0473

内皮型一氧化氮合酶增强子 AVE3085 逆转同型半胱氨酸诱导的人乳内动脉内皮功能障碍

张茜、侯敏
天津市胸科医院检验科

同型半胱氨酸(Hcy)是心血管疾病内皮功能障碍的独立危险因素。我们提出假说，eNOS 转录增强子 AVE3085 可以保护人乳内动脉(IMA)中因 Hcy 受损的内皮功能。在肌电图仪中，在不存在/存在 Hcy(100 μmol/L)和/不存在 AVE3085(30 μmol/L)的情况下，使用 U46619(-8 log mol/L)预收缩的冠状动脉手术患者的 IMA 中建立乙酰胆碱（-10 至-4.5 log mol/L）或硝普钠的累积浓度-舒张曲线。RT-qPCR 和 ELISA 定量 eNOS 的 mRNA 和蛋白水平。采用比色法检测一氧化氮(NO)的生成。Hcy 可显著减弱人乳内动脉的最大舒张。与 AVE3085 共孵育可保护内皮免受 Hcy 的损害，并增加 NO 的生成。Hcy 作用 24h 下调 eNOS 蛋白表达($P < 0.05$)而在 mRNA 水平上调 eNOS 的表达($P < 0.05$)。除 Hcy 外 AVE3085 的存在显著增加 eNOS 蛋白($P < 0.05$)，轻微降低 mRNA 水平。该研究首次揭示，在人血管(IMA)中临床相关的高浓度 Hcy 通过下调 eNOS 蛋白生成直接引起内皮功能障碍，可能被 AVE3085 逆转。这些发现不仅为冠状动脉搭桥术中保护内皮，提高移植物的长期通畅率提供了新的方向，而且为 eNOS 增强子在各种病理状态下内皮功能障碍患者中的应用提供了证据。

PU-0474

清远地区生殖道沙眼衣原体和淋病奈瑟菌感染情况分析

周鹏、罗瑛、周美芳、刘艳枚、林金端、尹卫国
清远市人民医院

目的 探讨清远地区生殖道分泌物沙眼衣原体（CT）和淋病奈瑟菌（NG）感染于生殖道炎症及不孕不育之间的相关性分析。
方法 采用实时荧光定量 PCR 对 28762 例女性妇科炎症患者、不孕不育患者和健康体检者的生殖道分泌物和 12655 例男性尿道感染患者、不孕不育患者和健康体检者的尿道分泌物进行 CT、NG 的检测。
结果 女性 CT 总感染率为 8.00%、NG 总感染率为 1.12%，其中妇科炎症患者中 CT 感染率 10.37%和 NG 感染率 2.39%、不孕不育患者中 CT 感染率 6.34%和 NG 感染率 0.33%、健康体检者 CT 感染率 10.46%和 NG 感染率 1.06%；男性 CT 总感染率为 11.17%、NG 总感染率为 10.21%，其中尿道感染患者中 CT 感染率 30.33% 和 NG 感染率 42.39%、不孕不育患者中 CT 感染率 3.43%和 NG 感染率 0.28%、健康体检者 CT 感染率 9.94%和 NG 感染率 1.47%，三个组份中 CT 感染率和 NG 感染率的差异性具有统计学意义，且均是尿道感染患者组感染率最高；各年龄组 CT、NG 的感染率不论是女性还是男性，其差异性均具有统计学意义，且以 25 岁以下人群感染率较高，同时男性就诊者 CT 感染率和 NG 感染率各年龄段均高于女性。
结论 生殖道 CT、NG 感染是导致生殖道感染性疾病和不孕不育的重要因素，且男性的感染率高于女性，重视 CT、NG 的常规检验对治疗生殖道炎症和不孕不育具有重要意义。

PU-0475

Performance Verification of Five Commercial RT-PCR Diagnostic Kits for SARS-CoV-2

Mei Yang
Department of Laboratory Medicine, Shengjing Hospital of China Medical University

Background Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which has caused a global pandemic, can be detected by reverse-transcription quantitative polymerase chain reaction (RT-PCR). However, owing to the urgent need of these detection kits in large numbers, the duration for research and development with regard to the kits has been shortened during the epidemic, and the kits that are being used commercially have not undergone full and independent evaluation. To ensure the accuracy of the SARS-CoV-2 test results, performance verification of commercial RT-PCR kits is required.
Methods The performance of five commercial RT-PCR diagnostic kits for SARS-CoV-2 used in China, namely, reagents A, B, C, D, and E, was evaluated using a COVID-19 RNA liquid performance verification reference product—manufactured by Guangzhou Bondson (BDS) Biotechnology Co., Ltd—that uses the droplet digital PCR combined with the fluorescence quantitative PCR method. The performance verification criteria included the coincidence rate, limit of detection (LoD), specificity, precision, and anti-interference.
Results The coincidence rate for reagent C was 95%, while that for all the other reagents was 100%. The LoD for reagent A was 5.00E+02 copies/ml, 1.00E+03 copies/ml for reagent B, and 2.50E+02 copies/ml for both reagents D and E. Reagent C was not able to detect its advertised LoD of 500 copies/ml. The results for the cross-reactivity tests were all negative, which indicated specificity. Moreover, all kits had a coefficient of variation less than 5%; however, reagent B kits showed the best precision. Reagents A, B, and D showed higher sensitivity to N gene than they did to ORF1ab. The anti-interference results for all five kits were positive.
Conclusions Except for reagent C, all commercial RT-PCR diagnostic kits for SARS-CoV-2 passed the performance verification. This study can provide guidance for the selection or optimization of RT-PCR diagnostic test kits for SARS-CoV-2.

PU-0476

HCV 核心基因的深度基因组测序用于 HCV / HIV 共感染患者的 HCV 亚型分析

雷胡芯、廖璞
重庆市人民医院

目的 HCV 感染是引起肝炎的重要病原体。随着生活水平和习惯的变化，HCV 的感染率越来越高，甚至出现了更多的亚型，并且发现 HCV / HIV 共感染的患者体内的 HCV 亚型与当前的流行病不一致，合并有多种亚型，这对于诊断和治疗非常不利。通过研究 HCV / HIV 共感染患者的 HCV 亚型和亚型的比例，可以推断出 HCV 流行如何受到 HIV 感染的影响，以及如何为 HCV 引起的并发症提供临床诊断和治疗。
方法 通过收集 HCV / HIV 共感染患者的血清样本，用 RT-PCR 扩增 HCV 核心基因，并通过凝胶回收提高其浓度。首先通过琼脂糖凝胶电泳确定核心基因，然后将其送去纯化和深度测序。最后，用 MEGA 6.0 分析了 HCV 亚型系统发育树和亚分析类型比。
结果 我们发现样本 1、5、9、10、12、14 和 15 中同时存在两种或两种以上的亚型，与 HCV 感染的患者通常通常只感染一种亚型基因并不匹配。 HCV 的各种基因型显示出不同的治疗效果， GT 2 和 GT 3 的患者可以实现 70-80％的较高 SVR，而 GT 1 和 GT 4 的患者具有较低的 SVR（40-50％），这可能是由于不同的 GT 和宿主细胞因子对 HCV 的致病性和复制能力不同所致。

结论 在中国，目前慢性 HCV 感染患者的护理标准（SOC）是聚乙二醇干扰素 α 和利巴韦林的组合。但是，在现阶段，针对囚犯的 HCV 抗感染药物治疗仅是基本治疗。正是因为 HCV 感染后这些囚犯用药的基本性，不合规定性和不合规定性可能导致其亚型感染的多样性。

PU-0477

葛根素减轻顺铂引起的急性肾损伤及上调 MIR-31 相关信号研究

吴镇
山东大学第二医院

目的 顺铂(DDP)是一种常用的化疗药物，但其使用的副作用，特别是急性肾损伤(AKI)，限制了其临床应用。葛根素是从中药葛根中提取的天然黄酮类化合物，已被报道可减轻 DDP 引起的肾毒性。然而，葛根素调控 AKI 微 RNA(MIR)-31 介导的信号通路的机制尚不清楚。
方法 通过逆转录-定量 PCR 和 westernblot 分析，研究葛根素在 DDP 诱导的 AKI 大鼠模型中的作用。结果表明，DDP 在体外和体内均以浓度依赖性的方式上调了 MIR- 31 的水平，此外，DDP 显著提高了血尿素氮和丙二醛含 量、血清肌酐和组织病理学变化，同时显著降低了肾脏组织中超氧化物歧化酶、过氧化氢酶和谷胱甘肽 S-转移 酶的表达水平。 TUNEL 和 westernblot 分析表明，DDP 增加了凋亡蛋白的表达水平，影响了 MIR-31 下游的 Numb/Notch1 信号通路。在葛根素治疗后，DDP 所致的效应被抵消。
结果 本研究的结果表明，葛根素通过上调 MIR-31 的表达和抑制 Numb/Notch1 信号通路，对 DDP 诱导的 AKI 具有肾保护作用。

PU-0478

RAGE 基因启动子甲基化与糖尿病视网膜炎症的相关性研究

吴镇
山东大学第二医院

目的 评价 2 型糖尿病视网膜病变(DR)患者外周血单核细胞(PBMC)中晚期糖氨化终产物(RAGE)基因启动子受体的甲基化状态，以研究 RAGE 基因启动子甲基化与糖尿病视网膜炎症的相关性。
方法 2013 年 10 月至 2015 年 10 月期间，山东大学齐鲁医院收治并诊断为 2 型糖尿病患者。他们为观察组，40 名健康受试者被纳入对照组。使用密度梯度离心法收集患者的 PBMC，并使用甲基化特异性 PCP(MSP)检测 RAGE 基因启动子的甲基化状态。采用酶联免疫吸附法(ELISA)测定了血清中白细胞介素-1β(IL-1β)、IL-6 和肿瘤坏死因子-α(TNF-α)的水平。分离 RAGE 基因启动子甲基化阳性患者的 PBMC，并使用去甲基化剂 5'-aza-2'-脱氧胞苷(5-aza-dC)抑制 RAGE 基因启动子甲基化。通过 MSP 检测到 PBMCs 中 RAGE 基因启动子的甲基化状态。用 ELISA 对 PBMC 培养液上清液中的 IL-1β、IL-6 和 TNF-α 水平进行了评价。MSP 结果显示，在 DR 患者中，PBMCs 的 RAGE 基因启动子有 26 例（32.50%的甲基化）。RAGE 基因启动子在所有正常健康受试者中都被甲基化。阳性 RAGE 基因启动子甲基化组的血清中 IL-1β、IL-6 和 TNF-α 水平明显低于阴性 RAGE 基因启动子甲基化组（$p<0.01$）。5-Aza-dC 抑制了 RAGE 基因启动子甲基化阳性患者 RBMC 的 RAGE 基因启动子甲基化。抑制作用 RAGE 基因启动子的甲基化增加了培养液上清液中 IL-1β、IL-6 和 TNF-α 的水平。
结果 发现 RAGE 基因启动子低甲基化，表明 RAGE 基因启动子甲基化可抑制糖尿病视网膜炎症。

PU-0479

重组酶聚合酶检测破伤风方法的建立

郭铭静
中国人民解放军陆军军医大学第二附属医院

目的 利用重组酶聚合酶技术，建立快速、灵敏、特异、经济的破伤风梭菌的检测方法。
方法 在 Genebank 数据库中检索编码破伤风梭菌毒素的基因序列，采用序列比对软件筛选出保守区域，合成并构建质粒标准品，设计并筛选出引物对及探针，扩增目的片段，对其灵敏度、特异性和抗干扰能力进行评估。用标准菌株对建立的方法进行验证。
结果 RPA 95%检测限为 7copies/μl，与 PCR、LAMP 等方法灵敏度相当，对常见感染菌无交叉反应性。可在 20 分钟内读取结果，能够检测出 195bp 的特异性条带。
结论 重组酶聚合酶扩增技术在破伤风梭菌诊断中应用效果较佳，有理想的灵敏度、特异性以及准确度，有望成为替代传统 PCR 的有效检测方式，能在床旁及基层开展，值得临床推广应用。

PU-0480

数字化重组酶聚合酶技术快速检测 lncRNA HULC

郭铭静
中国人民解放军陆军军医大学第二附属医院

长链非编码 RNA（lncRNA）HULC 的发现与表征揭示了其在肿瘤中调控的多样性，在多种肿瘤的发生发展中起到关键作用。恒温数字化检测系统——重组酶聚合酶扩增联合微流控芯片对 lncRNA 标志物 HULC 恒温数字化检测，系统的解决了 HULC 常规检测技术不能满足临床和实验室应用的问题。37℃恒温扩增条件降低了对加热元件的需求，终点处荧光读数降低了实时监测荧光仪器的需求，数十万 RPA 微小反应单元无需绘制标准曲线即可对低拷贝的靶标进行绝对定量。本方案提供了新的高敏、特异、简便、快速的 HULC 检测新技术和新方法，可以对低丰度靶标 HULC 进行检测，该技术不仅能在大中型医院应用，而且能在更多的中小医院推广。

PU-0481

液相芯片技术检测消化道恶性肿瘤常用药物靶位基因多态性

许红丽、左学礼、段小华、彭云、李了兰、张文斌
武冈市人民医院

目的 基于液相芯片技术，建立一种可同时、快速检测消化道恶性肿瘤常用药物相关靶位基因多态性的方法。
方法 从 Genbank 中查找与二氢嘧啶脱氢酶（DPYD）和亚甲基四氢叶酸还原酶（MTHFR）等与 5-氟尿嘧啶（5-Fu）相关；X 射线修复缺陷基因 1（XRCC1）、着色性干皮病互补基因 D（XPD）、切除修复交叉互补组 1（ERCC1）、6-氧-甲基鸟嘌呤-DNA 甲基转移酶（MGMT）、谷胱甘肽 S 转移酶基因 1（GSTP1）等与铂类相关；多耐药基因 1（ABCB1）与紫杉类相关；二磷酸葡糖醛酸转移酶 lAl（UGT1A1）与伊利替康相关等消化道恶性肿瘤常用药物的 9 个基因中 10 个靶位点附近基因序列，设计特异性引物和探针；通过多重 PCR 扩增，等位基因特异性引物延伸（ASPE），MagPlex-Tag 微球杂交，经液相芯片系统 Luminex 200 检测荧光信号，确定基因型；优化反应体系并进行方法学评价。采用建立的方法检测 48 例消化道肿瘤患者 DNA 样本，与测序结果比较。
结果 本方法检测 48 例样本结果显示：纯合子荧光强度中位值（MFI）比率均>0.85 或<0.1，杂合

子 MFI 比率均在 0.25-0.65 之间；各基因型批内和批间变异系数分别低 8.5％和 11.3％；所需 DNA 最低检测限为 0.65ng；48 例样本的检测结果与测序结果完全一致。
结论 本研究采用液相芯片技术，成功建立了快速检测消化道恶性肿瘤常用药物相关靶位基因多态性的方法。该方法可靠，性能稳定，有潜在的临床应用价值。

PU-0482

南京地区体检人群中女性乳头瘤病毒的基因型与感染情况

张燕
江苏省人民医院（南京医科大学第一附属医院）

目的 旨在研究南京地区体检女性人群中人乳头瘤病毒的感染情况，为南京地区的 HPV 疫苗接种及科学防治提供指导作用。
方法 选取 2017 年 1 月～2019 年 7 月在江苏省人民医院健康体检中心进行健康体检的 8699 名女性，采用罗氏 cobas 荧光定量 PCR 进行 HPV 分型检测，并同时取脱落细胞进行液基薄层细胞检测（TCT），通过结果分析对南京地区健康体检人群的 HPV 感染情况做一定的调研。
结果 本研究表明南京地区高危型 HPV 的总阳性率为 12.29%（1069/8699），感染率较低，其中 HPV-16 型仍是需要重点关注的高危型。就年龄段来看，年龄>50 岁的人群 HPV 感染率高于其他年龄段（P<0.05）。通过对高危 HPV 分型和 TCT 的结果分析来看：HPV-16 型与宫颈细胞学病变存在一定的相关性。
结论 通过对南京地区健康体检人群的 HPV 的筛查，基于其感染特性、年度特性、年龄特性、宫颈细胞学特性等研究为疫苗科学接种与 HPV 防治提供指导作用。

PU-0483

Running affects Achilles tendon health in rats by changing the expression of lubricin

Shufen Li
Nanfang Hospital, Southern Medical University

Background The Achilles tendon transmits mechanical force from the calf muscle to the calcaneus through collagen fibers. Lubricin facilitates the movement of tendon fascicle gliding and recoil against the surrounding tissues. However, little is known about its response under various mechanical loading conditions. This study aimed to determine the effect of treadmill running with different exercise intensities on the alterations of lubricin content in rat Achilles tendon.
Methods In this study, 18 rats were randomly divided into the following groups: strenuous treadmill running (STR), moderate treadmill running (MTR), and control (CON). The rats in the two running groups were subjected to eight weeks' treadmill running protocol. Their Achilles tendons were then harvested for histological observation and biochemical analyses.
Results After eight weeks, the morphologies of the collagen fibers were relatively parallel, crimping, and elastic in the CON and MTR groups, but more ruptured in the STR group. The cell density in the Achilles tendon sections markedly increased in the MTR group compared with the CON group, whereas it markedly decreased in the STR group compared with the CON or MTR group. Additionally, the content of lubricin was dramatically increased in the MTR group compared with the CON group, but substantially decreased in the STR group compared with the CON or MTR group. Furthermore, the expressions of TGF-β1 and lubricin were significantly upregulated in the MTR group in contrast to the CON group, while they were significantly downregulated in the STR group in contrast to the CON or MTR group. Conversely, the expression of IL-1 was statistically downregulated in the MTR group in comparison to the CON

group, but was statistically upregulated in the STR group in comparison to the CON or MTR group.
Conclusions Moderate treadmill running might induce an increase of lubricin through the upregulation of TGF-β1 expression to improve lubrication and enhance the loading transmission efficiency. Meanwhile, strenuous treadmill running could result in a decrease of lubricin as a result of the dramatically increased expression of IL-1, consequently enhancing interfascicular tribology, and predisposing to tendinopathy or even tendon rupture.

PU-0484

LINC00973 在非小细胞肺癌的作用机制及临床价值研究

陈妍柯
江苏大学

目的 高通量测序筛选 NSCLC 中差异表达的长链非编码 RNA(long noncoding RNA, lncRNA)，检测 LINC00973 在非小细胞肺癌(non-small cell lung cancer, NSCLC)中的表达，初步探讨其分子作用机制，为 NSCLC 诊疗提供新的靶点。
方法 对 NSCLC 组织全转录组测序筛选，实时荧光定量 PCR 验证其在 NSCLC 细胞、组织中的表达，受试者工作特征曲线分析其临床价值。分别敲减和过表达 NSCLC 细胞中的 LINC00973，细胞生长曲线和平板克隆形成检测细胞的增殖能力， Transwell 迁移与侵袭检测细胞的转移能力，流式细胞术检测细胞周期变化和凋亡情况。转录组测序分析敲减 LINC00973 后影响的靶基因和信号通路。收集与 LINC00973 结合的蛋白质并通过液相色谱-质谱分析鉴定该结合蛋白，小干扰 RNA 敲减 NSCLC 细胞中的 DTX3L，细胞生长曲线和平板克隆形成实验检测细胞增殖能力，流式细胞术检测细胞凋亡。
结果 全转录组测序结果中 LINC00973 表达上调。LINC00973 在 NSCLC 细胞和组织中呈高表达。敲减 LINC00973 削弱细胞的增殖和转移能力，诱导细胞发生 G1 期阻滞并促进凋亡，LINC00973 基因沉默下调上皮间质转化(epithelial-mesenchymal transition, EMT)相关蛋白和增殖相关蛋白的表达，敲减 LINC00973 导致促肿瘤相关基因下调，Akt-mTOR 信号通路受到抑制。过表达结果相反。LINC00973 能与 DTX3L/PARP9 蛋白复合物结合，且正向调控 DTX3L 蛋白表达。敲减 DTX3L 具有抑制 NSCLC 细胞增殖并促进其凋亡的生物学功能。
结论 LINC00973 在 NSCLC 中表达上调，具有作为诊断标志物的潜力。LINC00973 可能通过与 DTX3L/PARP9 蛋白复合物结合发挥作用。

PU-0485

The role and mechanism of hsa_circ_0007991 in gastric cancer progression

Xueyan Zang
Jiangsu Key Laboratory of Medical Science and Laboratory Medicine, School of Medicine, Jiangsu University

Background Circular RNAs (circRNAs) have recently been proven to affect the initiation and progression of cancers. A particularly abundant circRNA, hsa_circ_0007991, was proposed to be involved in tumorigenesis. However, its molecular mechanism in gastric cancer (GC) remains unclear.
Methods Gene Expression Omnibus(GEO) datasets were used to investigate aberrantly expressed circRNAs in gastric cancer. Gene silencing and over-expression were performed to detect circRNA function. Cell proliferation and transwell assays were used to study cell proliferation and invasion. The expression of circRNAs, miRNA and mRNAs was detected by qRT-PCR. The location of circRNAs was detected using RNA in situ hybridization. Meanwhile, the

underlying mechanism of hsa_circ_0007991 was explored by bioinformatics analysis, mass spectrometry, RNA pulldown, RNA immunoprecipitation, luciferase assays and recue experiments. Lastly, mice xenograft was used to exam the clinical relevance of hsa_circ_0007991 in vivo.
Results In this study, we screened out that hsa_circ_0007991 was decreased in GC tissues and serum and was related to lymphatic metastasis and distant metastasis. Overexpression of hsa_circ_0007991 inhibited cell growth, migration and invasion in vitro and delayed tumor growth in vivo. In mechanism, hsa_circ_0007991 contained multiple miRNA binding sites, functioning as a sponge for miR-4449
Conclusion Take together, our findings revealed that hsa_circ_0007991 regulates miR-4449 contributes to GC progression. Hsa_circ_0007991 might serve as a novel tumor suppressive factor and act as a promising prognostic biomarker and therapeutic target for GC treatment.

PU-0486

A Novel Near-infrared Emissive and Biodegradable Polymer for Fluorescent Imaging of Cancers

yanxia Chen
Jiangsu University

Purpose Two nanoparticles were compared to derive an optimized coating strategy for a needed biological feature in cancer imaging.
Methods In this study a chemically synthetic polymer, benzo [1,2-b:4,5-b'] difuran(BDF)-based donor-acceptor copolymer PBDFDTBO, was individually coated by amphiphilic poly(ethylene oxide)-block-poly(ε-caprolactone) (PEO-b-PCL) and1,2-distearoyl-sn-glycero-3-phosphoethanolamine-N-methoxy(polyethylene glycol) (DSPE-PEG), to form stably fluorescent particles at nano dimension in the near-infrared (NIR) window. The physicochemical properties of synthesized nanoparticles were well characterized and compared, in term of their size, morphology and surface charge. In mouse cancer models, both of the circulation time, tumor accumulation and biodistribution were detected.
Results The physicochemical properties of synthesized nanoparticles were great. The sizes of the two nanoparticles are similar. Besides they possess uniform shape and size, and have good biocompatibility and optical stability. In mouse cancer models both polymeric nanoparticles exhibited prolonged circulation time, desired tumor accumulation and preferred biodistribution, showing great biodegradability and biocompatibility.

PU-0487

The role and mechanism of a novel circRNA, circDIDO1, in gastric cancer progression

Yu Zhang
Department of Laboratory Medicine, Nanjing Drum Tower Hospital, Nanjing University Medical School

Objective Circular RNAs (circRNAs), a subclass of noncoding RNA characterized by covalently closed continuous loops, play emerging roles in tumorigenesis and aggressiveness. Nevertheless, the biological roles and clinical significance of circRNAs in gastric cancer (GC) remain unclear. The purpose of this study is to reveal the mechanism of aberrantly expressed circRNAs in GC progression and provide new targets for the molecular diagnosis and therapy of GC.
Methods We conducted bioinformatic analysis to evaluate differentially expressed circRNAs in GC tissues compared to adjacent tissues. The data were downloaded from the Gene Expression Omnibus dataset. Fold change ≥ 2 and P value ≤ 0.05 were set as the threshold for significantly

differential expression. We detected the expression of circRNAs in tumor tissues of GC patients by qRT-PCR and analyzed its association with clinicopathological parameters. Cell counting, colony formation, transwell migration and matrigel invasion assays, and flow cytometry analyses were used to examine GC cell proliferation, migration, invasion and apoptosis. RNA sequencing, mass spectrometry, tagged RNA affinity purification, RNA immunoprecipitation and luciferase analyses were used to find key interacting proteins and miRNAs for the novel circRNA and identify key downstream target genes and signaling transduction pathways.
Results We identified a novel circRNA (termed circDIDO1) that was down-regulated in GC tissues and its low expression level was associated with tumor size, distal metastasis, and poor prognosis. CircDIDO1 overexpression inhibited GC cell proliferation, migration and invasion while promoted cell cycle arrest and apoptosis. Conversely, circDIDO1 knockdown in GC cells led to the opposite effects. Bioinformatics analysis revealed that there were miR-1307 binding sites in circDIDO1 sequence and the luciferase reporter gene assay showed that miR-1307 could bind to circDIDO1. In addition, circDIDO1 was co-immunoprecipitated with miR-1307 from the Ago2 complex. Furthermore, we found miR-1307 was up-regulated in GC tissues, and could down-regulate the expression of circDIDO1 in GC cells.
Conclusion CircDIDO1 could suppress the proliferation, migration and invasion as well as promote apoptosis in GC cells, indicating that it may serve as a new target for the diagnosis, prognosis and therapy of GC.

PU-0488

肿瘤活化中性粒细胞诱导 MSC 向 CAF 转化促胃癌进展

张家慧
江苏大学

目的 探讨肿瘤活化的中性粒细胞调控 MSC 向 CAF 转化以及在胃癌进展中的作用。
方法 从脐带组织中分离培养 huc-MSC 并鉴定。利用胃癌细胞上清刺激中性粒细胞，收集其培养上清。将培养上清与 MSC 共孵育，采用 qRT-PCR 和 Western Blot 检测 CAF 相关纤维化指标。及相关信号通路活化情况。用中性粒细胞上清处理 MSC 后，收集其培养上清，作用于胃癌细胞株，检测胃癌细胞迁移和增殖能力变化。Western Blot 和 qRT-PCR 检测胃癌细胞 N-cadherin、E-cadherin、PCNA、CyclinD1 等蛋白表达情况。裸鼠皮下荷瘤实验检测对肿瘤生长的影响。采用中和抗体与活化的中性粒细胞培养上清共同刺激 MSC 验证中性粒细胞发挥作用的效应分子。
结果 肿瘤活化的中性粒细胞刺激 MSC 后，CAF 相关纤维化指标 FAP 和 α-SMA 表达增高，明显促进胃癌细胞增殖和迁移。Western Blot 和 qRT-PCR 检测发现胃癌细胞增殖和迁移相关蛋白表达增加，裸鼠荷瘤实验结果表明胃癌细胞体成瘤能力增强。IL-17/IL-23/TNFα 中和抗体作用后，中性粒细胞诱导 MSC 向 CAF 转化和发挥上述作用的能力减弱。
结论 肿瘤活化的中性粒细胞能诱导 MSC 向 CAF 转化并促进胃癌进展。

PU-0489

EFNB1 促进淋巴瘤侵袭的作用机制及 EFNB1 对靶向药物的影响

张晨笑
江苏大学

目的 弥漫大 B 细胞淋巴瘤（diffuse large B-cell lymphoma，DLBCL）是最常见非霍奇金淋巴瘤。研究发现 Ephrin-B1（EFNB1）是导致淋巴瘤侵袭关键基因，但机制尚不明确，本研究旨在探讨 EFNB1 在淋巴瘤发生发展中作用，以及对肿瘤细胞应答靶向药物的影响。

方法 C57/BL6 小鼠尾静脉注射对照和过表达 EFNB1 的淋巴瘤细胞，体内重建淋巴瘤模型观察小鼠生长状态和成瘤情况，对淋巴瘤小鼠解剖检查。生物信息学方法分析 EFNB1 基因在 DLBCL 中表达模式及预后潜能。细胞过表达 EFNB1 流式细胞术检测细胞增殖能力。Western blot 检测 NF-κB 信号通路相关蛋白表达。分离并提取过表达 EFNB1 淋巴瘤细胞的上清外泌体，NanoSight 和 Western blot 检测外泌体大小和表面分子标志物。对 18 种靶向药物药物敏感性实验，分析 EFNB1 对靶向药物影响。

结果 体内实验显示过表达 EFNB1 促进小鼠淋巴瘤恶性化，高度侵犯肺和肾脏。生物信息学结果显示 EFNA3、EFNA4、EFNB1、EPHB4、EPHB6 是 DLBC 的主要表达基因，对 EFNB1 生存分析表明 EFNB1 高表达与预后差相关。过表达 EFNB1 后，IκBα、IKKα、IKKβ 和 p-IκBα-Ser32 的表达下调，NF-κB （p65）表达升高。外泌体上表达 EFNB1 蛋白。有 8 种有效的靶向药，其中 EFNB1 高表达细胞对 CAPE、Erlotinib 和 AZD4547 敏感，对 Axitinib 耐药。

结论 过表达 EFNB1 通过抑制 IκBα 来激活 NF-κB 信号通路在淋巴瘤中发挥作用，对 NF-κB 抑制剂 CAPE 敏感。外泌体表达 EFNB1 蛋白，EFNB1 有可能通过外泌体发挥功能。EFNB1 高表达细胞对 CAPE、Erlotinib 和 AZD4547 敏感，对 Axitinib 耐药，为 EFNB1 高表达患者的临床治疗提供新的方向。

PU-0490

L-PGDS 修饰间质干细胞外泌体抑制肿瘤的实验研究

尤本帅
江苏大学

目的 探究脂质运载蛋白型前列腺素 D 合成酶（lipocalin-type prostaglandin D synthase，L-PGDS）修饰的人脐带间质干细胞（hucMSCs）来源的 exosomes 体内外对胃癌的抑制作用。

方法 编码 L-PGDS（Ad-L-PGDS）和空载体（Ad-Vector）的腺病毒转染 hucMSCs，产生过表达 L-PGDS 的 exosomes（EX-L-PGDS）和空载体 exosomes（EX-Vector）。Western blot、透射电镜、Nanosight 可视型纳米颗粒分析仪对 exosomes 鉴定。共聚焦显微镜检测胃癌细胞对 exosomes 的摄取情况，RT-PCR 和 Western blot 检测胃癌细胞内 L-PGDS 的表达。迁移和侵袭实验、流式凋亡检测体外探寻 EX-L-PGDS 对胃癌细胞的抑制作用；构建 SGC-7901 皮下荷瘤小鼠模型，观察 EX-L-PGDS 体内对肿瘤生长的抑制效果。

结果 EX-L-PGDS 除表达特异性标记 CD9、CD63 和 CD81 外，L-PGDS 的表达量较 EX-Vector 明显增高。EX-L-PGDS 被内吞进入 SGC-7901，并增加细胞内 L-PGDS 的表达水平。EX-L-PGDS 能抑制 SGC-7901 细胞的迁移和侵袭能力。EX-L-PGDS 促进 SGC-7901 凋亡发生。同时，EX-L-PGDS 抑制 SGC-7901 细胞克隆形成能力。裸鼠皮下荷瘤实验显示，EX-L-PGDS 处理的 SGC-7901 肿瘤生长更加缓慢，形成的肿瘤更小。HE 切片显示 EX-L-PGDS 组肿瘤组织更加疏松，有更少的血管形成。EX-L-PGDS 组 PCNA 表达较低，TUNEL 检测可见更多的凋亡细胞。EX-L-PGDS 组肿瘤组织 L-PGDS 表达增高，Bax 表达上调。

结论 EX-L-PGDS 体内外能够有效抑制胃癌进展，这为以 exosomes 为载体的肿瘤治疗提供新思路。

PU-0491

人脐带间质干细胞外泌体转运 CAMKK1 促进脂质代谢抑制非酒精性脂肪肝

杨馥吉
江苏大学

目的 人脐带间充质干细胞来源的外泌体(human umbilical cord MSC derived exosome, hucMSC-Ex)能够减缓急性肝损伤及肝纤维化。hucMSC-Ex 是否能修复 NAFLD 尚不清楚。本研究旨在观察 hucMSC-Ex 抑制脂肪沉积缓解 NAFLD 作用，探讨 hucMSC-Ex 转运 CAMKK1 蛋白调控脂肪酸代谢的机制，为 hucMSC-Ex 在 NAFLD 中的应用提供依据。
方法 游离脂肪酸诱导人肝细胞 LO2 脂肪变性，加入 hucMSC-Ex 共培养，Nile red 染色观察脂质沉积，试剂盒检测脂肪酸氧化率，非靶向代谢组芯片检测 LO2 的脂肪酸代谢产物；构建高脂饮食(HFD)诱导的 NAFLD 小鼠模型，尾静脉注射 hucMSC-Ex，评估 hucMSC-Ex 的 NAFLD 修复效果；转录组芯片和质谱分别分析 hucMSC-Ex 调控的脂肪酸代谢通路和相关蛋白并验证。免疫荧光、Nile red 染色等观察过表达蛋白后脂代谢调控作用及其调控的信号通路。构建调控蛋白敲减 hucMSC-Ex，比较分析调控蛋白在 hucMSC-Ex 抑制脂肪酸代谢中的作用。
结果 hucMSC-Ex 表达外泌体标志蛋白 CD9、CD63、Alix 和 TSG101，具有外泌体典型特征。hucMSC-Ex 呈浓度依赖性减轻 LO2 细胞脂质沉积，增加脂肪酸氧化率，抑制脂肪酸代谢物的生成。hucMSC-Ex 能减轻高脂饮食诱导的 NAFLD 小鼠肝脏脂肪空泡变性和脂质沉积，减轻小鼠体重，改善肝功能。钙调蛋白激酶激酶 α(CAMKK1)通过调控 AMPK/PPARa 和 AMPK/SREBP-1C /FASn 通路，促进脂肪酸氧化，抑制脂肪酸生成。CAMKK1 敲减减弱 hucMSC-Ex 的脂代谢调控功能和脂肪沉积抑制作用。
结论 hucMSC-Ex 通过转运 CAMKK1，促进脂肪酸氧化，抑制脂肪酸合成，延缓 NAFLD 的进展，是 NAFLD 潜在治疗手段。

PU-0492

胃癌干细胞外泌体源 hsa_circ_0000670 在吸烟促进胃癌发展中的作用和机制研究

郭文浩
江苏大学

目的 探讨吸烟通过胃癌干细胞 exosomes 促进胃癌发展的作用及机制，阐明 hsa_circ_0000670 在这过程中的生物学作用的生物学作用。
方法 GEO 数据库筛选胃癌中高表达的 circRNAs; qRT-PCR 检测吸烟胃癌患者者胃癌组织中 hsa_circ_0000670 表达；构建胃癌干细胞培养模型，观察胃癌干细胞球形成；细胞活力实验筛选香烟悬液浓度；显微镜观察 0.5%香烟烟雾悬液处理 2d 后胃癌干细胞球大小以及数量变化，qRT-PCR 和 Western-blot 检测处理前后胃癌干细胞干性基因的表达变化；Western-blot、Transwell 迁移实验和 Matrigel 侵袭实验检测 0.5%香烟烟雾悬液以及两种胃癌干细胞 exosomes 处理后胃癌干细胞和胃癌细胞干性基因；qRT-PCR 检测 0.5%香烟烟雾悬液处理前后胃癌干细胞以及 exosomes 内 hsa_circ_0000670 的表达水平。
结果 吸烟者胃癌组织中 hsa_circ_0000670 的表达水平上调；香烟烟雾促进胃癌干细胞球的自我更新以及干性基因 mRNA 和蛋白表达水平；透射显微镜观察香烟烟雾处理前后胃癌干细胞分泌的 exosomes 均为圆形或椭圆形膜性囊泡，其粒径均在 110nm 左右。香烟烟雾处理后胃癌干细胞分泌的 exosomes 上调胃癌干细胞和胃癌细胞的干性基因和 EMT 进程相关指标的表达，促进胃癌细胞的迁移侵袭能力； hsa_circ_0000670 在香烟烟雾刺激的胃癌干细胞及其分泌的 exosomes 中表

达上调；胃癌干细胞自我更新能力提升，促进胃癌干细胞的干性基因的表达和 EMT 进程，香烟烟雾进一步促进了这个过程。
结论 香烟烟雾促进胃癌干细胞的干性基因干性，胃癌干细胞的 exosomes 以自分泌和旁分泌的方式促进胃癌干细胞和胃癌细胞的干性，、EMT 进程以及迁移侵袭能力。Hsa_circ_0000670 发挥重要作用。

PU-0493

miR-4465 修饰间质干细胞外泌体下调 LOXL2 抑制胶原沉积的作用及机制

王岩金
江苏大学

目的 探讨 miR-4465 修饰的人脐带间质干细胞外泌体(hucMSC-ex)对肝星状细胞（Lx2）活化、肝纤维化组织胶原沉积作用及机制。
方法 ExoQuick-TCTM 沉淀法提取 hucMSC-ex,并通过透射电镜、粒径分析以及表面标记检测进行鉴定。TGF-β 活化诱导，建立人肝星状细胞 Lx-2 细胞株活化模型，活化后细胞过表达 miR-4465，实时定量 PCR 检测 miR-4465 的表达情况，并通过 Western blot 和免疫荧光检测 LOXL2 以及胶原表达。将 25μg/mL 和 50μg/mL 的 miR-4465 mimics 分别经超声转入 hucMSC-ex，并提取外泌体内的 miRNA，通过定量 PCR 检测转入效率。分别加入 25、50μg/ul 浓度的 hucMSC-ex 和相同浓度的 hucMSC-ex-miR-4465 与活化后的细胞共培养，另设对照组(常规培养)，Western blot 和免疫荧光检测 LOXL2 表达以及胶原的表达情况。腹腔注射 CCl4 以构建小鼠纤维化模型，并分为损伤组，hucMSC-ex 组和 hucMSC-ex-miR-4465 组，免疫组化，Masson 染色观察比较纤维化修复效果。
结果 HucMSC-Ex 呈球形膜性囊状结构，直径 40~100nm 左右，表达 CD9、CD63 等表面标志物。转染后，细胞内 miR-4465 表达上调，同时 LOXL2 和相关胶原的表达均下调。定量检测表明 miR-4465 经超声后大量转入外泌体。HucMSC-ex 能明显下调 LOXL2 和相关胶原的表达，而 hucMSC-ex-miR-4465 其下调能力更加明显。在体内实验，hucMSC-ex-miR-4465 修复效果强于 hucMSC-ex，纤维化得到更大程度上的缓解，胶原沉积明显减少。
结论 hucMSC 来源外泌体能够转运 miR-4465，通过下调 LOXL2 抑制胶原沉积，从而抑制肝纤维化。

PU-0494

外泌体 hsa_circ_0000670 在胃癌诊断中的潜在价值及作用机制研究

王妍
江苏大学

目的 筛选胃癌中差异表达 circRNA，检测其在胃癌患者组织、血清及其外泌体中的表达并评价其作为诊断标志物潜在价值；揭示外泌体 circRNA 在胃癌进展中的作用机制，为胃癌治疗提供新靶点。
方法 GEO 数据库筛选出胃癌中高表达的分子 circ670。检测 circ670 在胃癌细胞、组织、血清及其外泌体中的表达，评价 circ670 的诊断价值。运用 ASO 和质粒载体对 circ670 进行敲减和过表达，同时将外泌体与胃癌细胞共培养，开展一系列功能学实验研究。采用生物信息学预测与 circ670 结合的 miRNA 和靶基因并验证。共转染实验、qRT-PCR 及 Western blot 用于验证 circ670、miRNA 与靶基因的相互作用。

结果 Circ670 在各胃癌细胞株、组织、患者血清及血清 exosomes 中均呈高表达，且 circ670 的表达与患者侵袭深度和 TNM 分期有关。血清外泌体中的 circ670 显示出更好的诊断效能。FISH 实验提示 circ670 在胃癌组织和各胃癌细胞株中主要存在于细胞质中。 ASO 敲减 circ670 后，胃癌细胞的增殖、迁移能力下降，细胞周期阻滞，而过表达后呈现相反的结果。富集 circ670 的外泌体与胃癌细胞共培养后，其增殖、迁移和干性能力均增加。荧光素酶实验证明 circ670 能与 miR-4659a/b-3p 结合。MiR-4659a/b-3p 能够逆转 circ670 促进胃癌生长和迁移的能力。肝素样表皮生长因子（HBEGF）是 miR-4659a/b-3p 的靶基因，通过 circ670/miR-4659a/b-3p/HBEGF 信号轴促进胃癌的进展。

结论 Circ670 在血清外泌体中其诊断效能更加具有优势。外泌体 circ670 作为胃癌细胞间通讯重要分子，从而促进胃癌的增殖、转移和干性能力，可能通过靶向 miR-4659a/b-3p/HBEGF 来发挥作用。

PU-0495

hucMSC 源外泌体调控 PGC-1α 延缓糖尿病视网膜病变

王小玲
江苏大学

目的 糖尿病视网膜病变（diabetic retinopathy, DR）是糖尿病最常见的微血管并发症，但尚缺乏理想防治方案。本研究旨在探讨人脐带间充质干细胞源外泌体（human umbilical cord mesenchymal stem cells derived exosomes, hucMSC-Ex）在 DR 治疗模型中的作用及机制，为管控和治疗 DR 提供新策略。

方法 构建 DR 大鼠模型。行玻璃体腔内注射 hucMSC-Ex 干预，检测视网膜细胞增殖、凋亡、氧化应激及 DNA 损伤，综合评估 hucMSC-Ex 对于 DR 的修复作用。人视网膜色素上皮细胞（ARPE-19）作为细胞模型，检测其增殖凋亡、细胞活力及活性氧（ROS）水平。hucMSC-Ex 和 HFL1-Ex 进行了 miRNAs 谱分析，筛选抑制氧化应激的 miRNAs。ARPE-19 细胞转染 miRNAs 的模拟物及抑制物明确其分子机制。电穿孔技术制备 miRNAs 工程化 hucMSC-Ex 应用于体内外模型，探索其增强治疗的效果。

结果 hucMSC-Ex 处理后视网膜组织总体厚度增加，结构清晰，抑制氧化应激及 DNA 损伤，且视网膜血管渗漏得到恢复。在体外 hucMSC-Ex 能逆转高糖引起的 ARPE-19 的增殖抑制及 ROS 的产生。hucMSC-Ex 能活化 PGC-1α 的表达，基于测序结果，筛选出了 hucMSC-Ex 中高表达的 1 种新的调控 PGC-1α 的 miRNA 分子，miR-10228。体内外实验结果表明 miR-10228 在延缓 DR 疾病进展中起关键作用。miR-10228 工程化 hucMSC-Ex 显示出更强的抗凋亡、抗氧化应激及 DNA 损伤、促增殖及保护血-视网膜屏障的作用，能更有效的延缓 DR 进程。

结论 hucMSC-Ex 携载 miR-10228 调控 PGC-1α 延缓 DR 进展，miR-10228 工程化 hucMSC-Ex 有望成为新型治疗方案。

PU-0496

昆明地区妇女 HPV 感染分型情况及其与宫颈病变的关系

洪颖、满宝华、常业飞、温瑾、姜水、田浩
云南省第三人民医院

目的 了解昆明地区女性生殖道人乳头瘤病毒（HPV）亚型感染分布情况及与宫颈病变之间的关系。

方法 收集 2019 年 1 月至 2020 年 12 月云南省第三人民医院共 10046 个标本进行 HPV 基因分型的女性作为研究对象，用 PCR 反向点杂交法进行 HPV 基因分型检测，分析昆明地区女性 HPV 亚型

感染情况。并将其中的 4327 例进行阴道脱落细胞液基细胞学检查，分析 HPV 亚型与宫颈病变的关系。
结果 10046 例检测标本中，检出阳性标本 1637 例，阳性率为 16.30%，其中高危型阳性占 88.72%、低危型 HPV 阳性占 11.28%。单一亚型 1292 例，所占比例最高，为 78.63%。其中 HPV 阳性率最高的 3 种 HPV 亚型依次为 HPV52（20.31%）、HPV39(16.24%)、HPV16（12.33%）。不同年龄段女性 HPV 阳性率进行比较，≥55 岁组的总感染率、单一基因及单纯高危亚型感染率均高于 21~55 岁年龄组，且差异有统计学意义（P<0.05）；癌变组 HPV 高危型感染率明显高于非典型鳞状细胞组及宫颈正常组（P<0.05）。
结论 昆明地区 HPV 感染以单一基因和高危感染为主，HPV52 型、HPV39 型、HPV16 型为前三大亚型，55 岁以上年龄段 HPV 感染率较高，随着宫颈病变程度的增加，高危型 HPV 的感染率也逐渐的升高。

PU-0497

Circ0613 在胃癌进展中的作用和机制研究

王君怡
江苏大学

目的 胃癌（gastric cancer, GC）是常见恶性肿瘤之一，发病率和死亡率高居不下，寻找新的诊断标志物迫在眉睫。我们检测了胃癌患者组织、血清及血清外泌体内 circ0613 的表达，阐明 circ0613 在胃癌发生发展中的作用机制，探索潜在的新型胃癌早期诊断和预后判断的生物标志物。
方法 qRT-PCR 检测胃癌患者组织、血清、血清外泌体中 circ0613 表达水平；绘制 ROC 曲线判断其诊断效能；分析 circ0613 与临床数据的相关性。分别构建 siRNA 和过表达慢病毒载体转染胃癌细胞株敲减和过表达 circ0613， CCK-8 和平板克隆形成实验检测胃癌细胞的增殖能力；Transwell 迁移和侵袭实验检测胃癌细胞的迁移和侵袭能力。qRT-PCR 和 western blot 检测 circ0613 母基因 USP1 的表达水平及两者的相关性；探索 USP1 在胃癌细胞中的生物学效应。此外，结合生物信息学与 RIP 实验筛选出 circ0613 的 RNA 结合蛋白(RNA binding protein, RBP)为 HuR；进一步探索 HuR 具体生物学作用。MG132 和 CHX 实验研究 circ0613 调控 USP1、HuR 蛋白水平的机制。皮下注射 circ0613 过表达胃癌细胞构建裸鼠荷瘤模型，取瘤称重和测量体积。
结果 circ0613 在胃癌患者血清中呈高表达，与胃癌的分化程度和淋巴结转移相关，ROC 曲线下面积为 0.726；但该分子在胃癌患者血清外泌中无显著性差异。敲减 circ0613 抑制胃癌细胞的增殖、迁移和侵袭能力；过表达则相反。circ0613 通过抑制蛋白降解而上调 USP1 和 HuR 蛋白的表达。
结论 Circ0613 在胃癌患者血清中呈高表达，有望成为胃癌诊断的潜在分子标志物。Circ0613 的母基因 USP1 及 circ0613 的结合蛋白 HuR 均能促进胃癌细胞的恶性进展。

PU-0498

脐带间质干细胞外泌体靶向抑制 HIF-1α 防治糖尿病视网膜病变的作用及机制

孙丰田
江苏大学

目的 糖尿病视网膜病变（DR）患病率高是成人致盲的主要原因之一，早期防治是降低 DR 致盲的关键。本研究主要探讨人脐带间质干细胞来源的外泌体（hucMSC-Ex）对 DR 的保护作用。
方法 以滴注或玻璃体腔内注射的方式对糖尿病大鼠进行 hucMSC-Ex 干预。通过 HE 染色、免疫组化、Western-blot 等技术分析视网膜结构变化、视网膜细胞增殖、凋亡、炎症及血管新生能力的改变、HIF-1α 表达、定位等情况，以评价 hucMSC-Ex 调控 HIF-1α 信号通路延缓糖尿病视网膜病变

的作用。用 hucMSC-Ex 处理高糖环境下培养的人视网膜微血管内皮细胞(hRMECs)。应用 CCK8 增殖实验观察细胞增殖能力，transwell 实验观察细胞迁移能力，小管形成实验检测血管形成能力以及 HIF-1α 的表达及核转位情况，以进一步评价 hucMSC-Ex 对高糖刺激下 hRMECs 的作用。
结果 hucMSC-Ex 干预后视网膜各层结构清晰，视网膜明显增厚，western blot 结果显示 BAX、Caspase-3 表达降低，Bcl-2 表达增加，同时 hucMSC-Ex 抑制 DR 动物模型和细胞模型炎症因子和促血管物质释放。体外研究表明，hRMECs 在 hucMSC-Ex 处理后增殖和迁移能力减弱，血管形成减少。在高糖刺激下，HIF-1α 蛋白表达整体水平和核内表达皆显著增加，hucMSC-Ex 干预后 HIF-1α 蛋白下调且入核明显减少；进一步研究证实 hucMSC-Ex 干预后降低 DR 动物模型和细胞模型中糖酵解限速酶 PFKFB3 的表达。
结论 hucMSC-Ex 可延缓糖尿病视网膜病变进程，其作用机制可能是通过抑制 HIF-1α 表达，减弱糖酵解，减少促炎因子与促血管生成物质释放，为临床糖尿病视网膜病变的防治提供新方法和思路。

PU-0499

环状 RNA circ1477 对胃癌进展的作用机制及其临床价值

李荣
江苏大学医学院

目的 阐明环状 RNA circ1477 在胃癌组织和血清及外泌体中的表达变化、生物学作用及分子机制，为胃癌诊断及预后判断提供新的分子标志物，为胃癌治疗寻找潜在的靶点。
方法 收集胃癌患者的胃癌组织及癌旁组织，胃癌患者及健康人血清及外泌体，采用 qRT-PCR 检测分析 circ1477 的表达水平。Fish 和核质分离定量 PCR 确定其亚细胞定位，RNase R 和 Actinomy D 处理检测其成环特性及半衰期。通过 siRNA 和过表达质粒转染在胃癌细胞中分别敲减和过表达 circ1477，检测细胞增殖、克隆形成、迁移、侵袭、等生物学功能变化。利用生物信息学技术预测与 circ1477 结合的 miRNA 及其调控靶基因，并通过荧光素酶报告基因检测和 RNA 免疫共沉淀进行验证。
结果 环状 RNA circ1477 在胃癌组织和胃癌细胞系中显著低表达，但在胃癌患者血清及血清外泌体显著高表达，且胃癌组织 circ1477 的表达水平与淋巴结转移相关，胃癌血清 circ1477 的表达水平与远端转移有关。组织 circ1477 低表达的胃癌患者生存时间显著短于高表达者。circ1477 主要表达于胞质中，能抵抗 RNase R 作用，其半衰期显著高于线性 RNA。敲减 circ1477 抑制细胞迁移和侵袭，过表达 circ1477 则相反，但敲减和过表达 circ1477 对细胞增殖影响不显著。生物信息学分析显示 circ1477 具有多种 miRNA 结合位点，且能与 Ago2 蛋白免疫共沉淀。双荧光素酶报告基因检测结果显示 miR-190a 和 miR-190b 能显著抑制 circ1477 载体 3'UTR 荧光素酶报告基因活性，且 miR-190b 在胃癌组织中显著低表达并与 circ1477 表达呈显著正相关。
结论 环状 RNA circ1477 可以作为胃癌诊断与预后判断的新分子标志物；circ1477 能体外抑制胃癌迁移和侵袭，可能是通过与 miR-190 家族结合发挥作用。

PU-0500

hucMSC-Ex 促进星形胶质细胞极化缓解脊髓损伤的作用及机制

金倩
江苏大学

目的 脊髓损伤（spinal cord injury，SCI）是一种严重的中枢神经系统的疾病，现有的临床治疗方案尚不能根治 SCI。本课题组前期研究发现人脐带间充质干细胞来源的外泌体（human umbilical cord mesenchymal stem cell derived exosomes, hucMSC-Ex）可缓解大鼠 SCI，但具体机制尚未明确。星形胶质细胞是中枢神经系统中一种数量最多的异质性神经胶质细胞，调控着神经微环境。

本研究旨在探讨 hucMSC-Ex 在星形胶质细胞表型极化中的作用及机制，为 SCI 临床治疗提供新思路。

方法 分离提取鉴定 hucMSC-Ex。构建 SD 大鼠撞击性脊髓损伤模型，hucMSC-Ex 进行治疗。术后 2w 根据 BBB 评分、HE 和荧光染色评价修复效果。检测星形胶质细胞表型变化。原代培养并鉴定星形胶质细胞，免疫荧光、western blot 和 qRT-PCR 检测 LPS 与 hucMSC-Ex 同时处理下的细胞表型标志物和炎症因子的表达。质谱分析筛选关键蛋白，利用 western blot、组化和荧光染色进行验证。

结果 hucMSC-Ex 具有外泌体的典型表征。hucMSC-Ex 可以缓解大鼠 SCI，减少脊髓组织结构紊乱，促进神经再生。 hucMSC-Ex 抑制静息型星形胶质细胞向炎症（A1）型极化，促进其向 A2 型极化。A2 型星形胶质细胞的条件培养基可以支持微环境细胞。hucMSC-Ex 富含 AP1B1 蛋白，干预后的组织和细胞高表达 AP1B1 和 S100a10。敲减了 AP1B1 的 hucMSC-Ex 抑制星形胶质细胞 AP1B1 和 S100a10 的表达。

结论 hucMSC-Ex 通过抑制 NF-κB 信号通路的磷酸化减少 A1 型星形胶质细胞极化，抑制炎症。hucMSC-Ex 通过携载 AP1B1 蛋白来促进 A2 型星形胶质细胞极化，支持神经系统微环境细胞并缓解 SCI，将成为治疗 SCI 新方案。

PU-0501

基于单细胞 RNA 测序分析脐带间充质干细胞外泌体抑制纤维化延缓糖尿病肾病的作用机制

纪成
江苏大学医学院

目的 糖尿病肾病是持续高血糖引起的糖尿病微血管并发症，进展性肾间质纤维化为特征。间充质干细胞外泌体在急慢性肾损伤中具有明显的修复效果。旨在基于 10xGenomics 单细胞测序探究间充质干细胞外泌体减轻肾组织纤维化延缓糖尿病肾病的分子机制。

方法 45%高脂饮食联合链脲佐菌素构建糖尿病肾病大鼠模型。尾静脉注射 hucMSC-Ex 观察干预 DKD 效果。评价肾功能组织损伤程度和纤维化沉积。10xGenomics 单细胞测序分析大鼠的肾脏细胞群落，分析巨噬细胞与肾小球系膜细胞间交互作用。蛋白质谱 LC-MS/MS 分析筛选 hucMSC-Ex 的激酶泛素系统。

结果 尾静脉注射的 hucMSC-Ex 能迁移至 DKD 大鼠受损肾组织改善肾功能抑制肾间质纤维化程度。10xGenomics 单细胞测序发现 DKD 中 TGF-β1+巨噬细胞活化 TGF-β1/Smad2/3/YAP 促进系膜细胞向肌成纤维化样改变。hucMSC-Ex 抑制系膜细胞 YAP，α-SMA 表达。免疫共沉淀显示 YAP 发生泛素化降解。质谱显示 hucMSC-Ex 富含 CK1δ/β-TRCP 激酶泛素系统促进 YAP 泛素化降解。

结论 hucMSC-Ex 可以靶向迁移至受损的肾组织部位改善肾功能，减轻胶原沉积抑制肾间质纤维化进展。10xGenomics 单细胞测序和转录组分析发现一群高表达 TGF-β1+巨噬细胞群落极化，通过活化 TGF-β1/Smad2/3/YAP 轴促进系膜细胞向肌成纤维化样改变加速肾间质纤维化进展，而 hucMSC-Ex 递送 CK1δ/β-TRCP 激酶泛素系统促进 YAP 蛋白泛素化降解抑制肾间质纤维化延缓糖尿病肾病进展。本研究为间充质干细胞外泌体防治糖尿病肾病提供了治疗新策略。

PU-0502

人脐带 MSC 外泌体转运 Beclin1 促进肝星状细胞铁死亡抑制肝纤维化

黄燕
江苏大学

目的 人脐带间充质干细胞来源外泌体（human umbilical cord mesenchymal stem cell derived exosomes，hucMSC-Ex）能够有效抑制肝纤维化，但详细机制不明。本研究旨在观察 hucMSC-Ex 促进 HSCs 铁死亡抑制肝纤维化的作用，探讨 hucMSC-Ex 转运 Beclin1 调控 HSCs 铁死亡的机制，为 hucMSC-Ex 修复肝纤维化提供新的依据。
方法 超速离心法分离纯化 hucMSC-Ex。将 hucMSC-Ex 与人 HSCs 细胞株 LX-2 共培养，观察 hucMSC-Ex 作用后 LX-2 的铁死亡。检测经 hucMSC-Ex 处理后的 LX-2 的 Beclin1 mRNA 和蛋白表达。观察经 hucMSC-Ex 处理后的 LX-2 和肝组织的 CD9 和 Beclin1 的表达水平。过表达/敲减 LX-2 的 Beclin1 检测铁死亡相关的 Beclin1/System Xc-/GPX4 信号通路，检测 ROS 水平和线粒体膜电位的变化，观察 LX-2 铁死亡。构建 CCl4 诱导的 ICR 小鼠肝纤维化模型，尾静脉注射 hucMSC-Ex、hucMSC-ExshBeclin1。评估肝组织胶原沉积检测 Beclin1/System Xc-/GPX4 信号通路，明确 hucMSC-Ex 的作用及机制。
结果 HucMSC-Ex 能够促进 LX-2 及肝纤维化小鼠肝星状细胞铁死亡。HucMSC-Ex 通过转运 Beclin1 调控 System Xc-转录促进 LX-2 铁死亡。HucMSC-Ex 可通过促进 HSCs 铁死亡，抑制 HSCs 活化，缓解肝纤维化。Beclin1 敲减 hucMSC-Ex 的肝纤维化抑制作用减弱。
结论 hucMSC-Ex 转运 Beclin1 调控 System Xc-/GPX4 信号通路促进肝星状细胞铁死亡，抑制其活化及胶原沉积，延缓肝纤维化。

PU-0503

Depressive-Like Behaviors Induced by Chronic Social Defeat Stress Are Associated With HDAC7 Reduction in the Nucleus Accumbens

xu jing
The Second Hospital of Shandong University

Persistent symptoms of depression indicate the adaptive involvement of stablemolecules in the brain that may be manifested at the level of chromatin remodeling, such as histone acetylation. Former studies have identified alterations in histone acetylation and deacetylation in several animal models about depression. However, the specific histone deacetylases related with depression are needed to be explored. Here, social avoidance behaviors, anxiety-, and depression-like behaviors were all found in mice suffered from chronic social defeat stress. Moreover, we also discovered that the amount of the class II histone deacetylase, HDAC7 rather than HDAC2, was significantly decreased in the nucleus accumbens of defeated mice, which suggested that HDAC7 might be a crucial histone deacetylase in a chronic social defeat stress model. Our data showed that the depressive-like behaviors induced by chronic social defeat stress were associated with HDAC7 reduction in nucleus accumbens. HDAC7 might be a promising therapeutic target for depression.

PU-0504

Gene deficiency or pharmacological inhibition of PDCD4-mediated FGR signaling protects against acute kidney injury

xu jing
The Second Hospital of Shandong University

Recent studies have shown that programmed cell death 4 (PDCD4) modulates distinct signal transduction pathways in different pathological conditions. Despite acute and chronic immune responses elicited by ischemia contributing to the functional deterioration of the kidney, the contributions and mechanisms of PDCD4 in acute kidney injury (AKI) have remained unclear. Using two murine AKI models including renal ischemia/reperfusion injury (IRI) and cisplatin-induced AKI, we found that PDCD4 deficiency markedly ameliorated renal dysfunction and inflammatory responses in AKI mice. Consistently, upregulation of PDCD4 was also confirmed in the kidneys from patients with biopsy confirmed acute tubular necrosis from a retrospective cohort study. Moreover, we found that overexpression of Fgr, a member of the tyrosine kinase family, dramatically aggravated renal injury and counteracted the protective effects of PDCD4 deficiency in AKI mice. We discovered that FGR upregulated NOTCH1 expression through activating STAT3. Most importantly, we further found that systemic administration of ponatinib, a tyrosine kinase inhibitor, significantly ameliorated AKI in mice. In summary, we identified that PDCD4 served as an important regulator, at least in part, of FGR/NOTCH1-mediated tubular apoptosis and inflammation in AKI mice. Furthermore, our findings suggest that ponatinib-mediated pharmacologic targeting of this pathway had therapeutic potential for mitigating AKI.

PU-0505

An ultrasensitive hybridization chain reaction-amplified CRISPR-Cas12a aptasensor for extracellular vesicle surface protein quantification

Shan Xing、Wanli Liu
Sun Yat Sen University Cancer Center

Introduction Tumor-derived extracellular vesicle (TEV) protein biomarkers facilitate cancer diagnosis and prognostic evaluations. However, the lack of reliable and convenient quantitative
Methods for evaluating TEV proteins prevents their clinical application.
Methods Here, based on dual amplification of hybridization chain reaction (HCR) and CRISPR-Cas12a, we
developed the apta-HCR-CRISPR assay for direct high-sensitivity detection of TEV proteins. The TEV protein-targeted aptamer was amplified by HCR to produce a long-repeated sequence comprising multiple CRISPR RNA (crRNA) targetable barcodes, and the signals were further amplified by CRISPR-Cas12a collateral cleavage activities, resulting in a fluorescence signal.
Results The established strategy was verified by detecting the TEV protein markers nucleolin and programmed death ligand 1 (PD-L1). Both achieved limit of detection (LOD) values as low as 100 particles/μL, which is at least 104-fold more sensitive than aptamer-ELISA and 102-fold more sensitive than apta-HCR-ELISA. We directly applied our assay to a clinical analysis of circulating TEVs from 50 μL of serum, revealing potential applications of nucleolin+ TEVs for nasopharyngeal carcinoma cancer (NPC) diagnosis and PD-L1+ TEVs for therapeutic monitoring.
Conclusion The platform was simple and easy to operate, and this approach should be useful for the highly sensitive and versatile quantification of TEV proteins in clinical samples.

PU-0506

结核分枝杆菌磷酸盐转运系统及其在结核病诊断中的应用

刘培
湖南省人民医院

结核病是危害社会健康的常见传染病，我国是结核病发病率较高的国家之一，每年因结核病死亡的人数居传染病死亡人数的首位。结核病的病原体为结核分枝杆菌，其基因组结构及其功能的研究对阐明结核分枝杆菌的致病机制和有效防治结核病具有重要的意义。磷酸盐转运系统是结核分枝杆菌中的运输系统，在其致病、检测、治疗、耐药中都起着一定的作用。本文概述结核分枝杆菌磷酸盐转运系统及其在结核病诊断中的应用。

PU-0507

Hypoxia and cancer related pathology

熊秋霞
昆明医科大学第一附属医院

Hypoxic environments occur normally at high altitude, or in underground burrows and in deep sea habitats. They also occur pathologically in human ischemia and in hypoxic solid tumors. This review will discuss how hypoxia can influence two aspects of tumorigenesis, namely the direct, cell-intrinsic oncogenic effects, as well as the indirect effects on tumor progression mediated by an altered tumor microenvironment. We will also discuss recent progress in identifying the functional roles of hypoxia-related factors (HIFs), along with their regulators and downstream target genes, in cancer stem cells and therapy. Importantly, we propose, using convergent evolution schemes to identify novel biomarkers for both hypoxia adaptation and hypoxic solid tumors as an important strategy in the future.

PU-0508

NCAPH is negatively associated with Mcl-1 in non-small cell lung cancer

Qiuxia Xiong
The First Affiliated Hospital of Kunming Medical University;Yunnan Key Laboratory of Laboratory Medicine; Yunnan Institute of Experimental Diagnosis

lung cancer has a high mortality rate worldwide. non-SMc condensin i complex subunit H (ncaPH) has been identified to be one of the regulatory subunits of the condensin i complex, which is essential for the correct packaging and segre- gation of chromosomes in eukaryotes. NCAPH is abnormally overexpressed in various types of cancer. a pro-survival member of the Bcl -2 family, myeloid cell leukemia sequence 1 (Mcl-1) is also frequently overexpressed in multiple cancers and is associ- ated with poorer clinical outcomes for patients. The association of NCAPH and Mcl-1 proteins with the clinical and pathological features of non-small cell lung cancer (NSCLC) remains to be elucidated. In the current study, the positive percentage of ncaPH in the non-cancerous lung tissues was revealed to be higher compared with that in nSclc. However, the positive percentage of Mcl-1 in the non-cancerous lung tissues was lower compared with nSclc. in addition, ncaPH high-expression patients had a higher overall survival rate compared with

patients exhibiting low expression, whereas the Mcl-1 high-expression group had a lower survival rate. Pairwise association in 260 cases
of NSCLC revealed that overexpression of the NCAPH protein was negatively associated with Mcl-1 expression and vice versa. The results of multivariate Cox proportional hazard regression analysis also indicated that ncaPH and Mcl-1 demonstrated potential as distinct prognostic factors that may be used in NSCLC. The expression of NCAPH and Mcl‑1 may be associated with, and act as distinct molecular marks for the prediction of apoor prognosis in patients with nSclc.

PU-0509

某三甲医院地贫基因突变及红细胞参数分型研究

刘飞、杜昱志
陆军军医大学第二附属医院检验科

目的 收集 地贫患者基因型与红细胞数据，分析缺陷种类、分布差异，为地贫和干预提供流行病学支持。
方法 收集我院 2019 年 5 月到 2020 年 5 月间 281 例地贫患者基因检测数据，关联患者 Hb、RBC、Hct、MCV、MCH、MCHC 红细胞参数。按照 α 地贫静止型、α 地贫标准型、α 地贫 HbH 病型、β 地贫、复合型地贫进行分组。选取各组基因频率较高的基因型与性别、地区等进行差异统计分析。
结果 α 地贫基因缺失型占比最多，其中--SEA 占比高达 55.28%；余下依次为-α3.7、-α4.2、复合型缺失、纯合缺失；点突变最为罕见。β 地贫中，CD41-42/N 单基因突变最多，占比为 32.93%；其余依次为 CD17/N、IVS-2-654/N、-28 缺失型等。α 地贫的 Hb、MCV、MCH 的平均水平随着类型从静止型、标准型到 HbH 依次减少，病情严重化趋势明显。β 地贫的基因型和临床分度没有显著相关。各类地贫的性别和地区基因频率分布没有显著性差异。
结论 除 α 地贫静止型外，所有病例均呈不同程度的小细胞低色素性贫血，在 α 地贫中，静止型、标准型、HbH 病的红细胞参数显示的小细胞低色素贫血程度逐渐加重，而在 β 地贫中则无法找到基因型与临床表现的关系。α 地贫基因缺失型占比最多，点突变最少；β 地贫 CD41-42/N 单基因突变最多，缺失型则较少；各地区和性别之间的的基因型分布频率基本相似，这在某种程度代表性反应了西南地区的基因分布特征。红细胞参数检测是筛检地贫的一个有效的方法。展望：地贫作为一种遗传性疾病，目前还没有彻底治愈的方法，控制地贫的有效方法始终是预防与完善产前筛查。基因诊断目前是地贫确诊“金标准”，但花费较高，报告周期长，需要的医疗条件较高，在贫困地区不易推行，而红细胞参数检验简单易行，在医疗水平不甚发达的地区，对简化筛查步骤具有意义，值得进一步验证并应用。

PU-0510

纳米粒子四氧化三铁纳米粒子表面定量吸附的实验研究

袁晨燕
东南大学附属中大医院

以四氧化三铁磁性纳米粒子为核心，在其表面修饰聚乙烯亚胺(PEI)以制备一种纳米基因载体．利用扫描电镜、红外光谱仪、zeta 电位仪对其形貌、表面包覆功能团、电位等进行表征。 电镜下修饰后粒子之间的聚集明显减轻、等电点由 pH 7．0 移至 pH 11．5．PEI 质量、介质的 pH 值以及离子强度均可影响 PEI 在 Fe3O4 上的吸附．不同的吸附量也影响了纳米粒子的 DNA 结合、释放与转染能力．本文通过对化学沉淀法制备 PEI-Fe3O4 磁性纳米粒中各种影响因素的优化，制定最优生产条件，获得稳定性优良的水溶性 PEI-Fe3O4 磁性纳米粒，兼具超顺磁性，提出多功能型磁性纳米粒的概念，使后续研究更具潜能。

PU-0511

AFP 启动子调控绿色荧光蛋白在肝癌细胞中特异性表达的研究

袁晨燕
东南大学附属中大医院

肝细胞癌（Hepatocellular carcinoma，HCC）是我国最常见的恶性肿瘤之一，随着现代分子生物学理论和技术的飞速发展利用基因工程的手段，对肝癌进行基因治疗，有可能成为肝癌治疗的突破点之一。基因治疗中利用细胞或组织特异性启动子能够使目的基因在特定的靶细胞中表达，从而最大程度的减少对正常组织的毒副作用。以绿色荧光蛋白为报告基因，研究 AFP 启动子调控的下游基因在肝癌细胞中的特异性表达，为肝细胞癌的靶向基因治疗奠定基础。

方法 构建重组真核表达载体：pcDNA3.1(+)-AFP-EGFP，载体经测序验证后分别用脂质体 Lipofectine 转染至肝癌细胞 HepG2，成纤维细胞 L929，于 37℃，5%二氧化碳，饱和湿度条件下培养 48 小时后，于荧光倒置显微镜下观察绿色荧光蛋白 EGFP 的表达情况。

结果和讨论 重组真核表达载体 pcDNA3.1(+)-AFP-EGFP 构建后，经酶切鉴定，载体大小、插入片段位置均正确（图 1），经测序鉴定 AFP 启动子与已报道序列完全匹配（数据未列出）。使用 AFP 启动子驱动下游基因的表达只能在肝癌细胞中进行[8]，因此我们将 pcDNA3.1(+)-AFP-EGFP 重组载体转染肝癌细胞 HepG2 和成纤维细胞 L929 后，仅能在肝癌细胞中观察到报告基因 EGFP 的表达（图 2）。

结论 AFP 启动子可以调控其下游基因仅在肝癌细胞内表达，而在正常细胞中没有转录活性。

PU-0512

CRISPR/Cas12a 结合 RCA 及 G-四链体/hemin 催化的 ABTS 系统比色检测 EGFR 基因突变

冯春凤
陆军军医大学第二附属医院（新桥医院）

表皮生长因子受体(epidermal growth factor receptor, EGFR)第 19 位外显子的突变状态对于预测酪氨酸激酶抑制剂(tyrosine kinase inhibitors, TKIs)治疗非小细胞肺癌(non-small-cell lung cancer, NSCLC)的敏感性具有非常重要的临床意义。因此，对于 NSCLC 患者，迫切需要一个简单、特异、灵敏的等温平台用于 EGFR 19del 检测。CRISPR/Cas12a 复合物在识别靶标后，对其周围的非特异性单链 DNA 表现出强大的反式裂解活性，在生物传感应用中具有潜在价值。在此，我们将 CRISPR/Cas12a 系统与滚动圆扩增(RCA)和 G-四链体/hemin DNAzymes 相结合，报道了一种新的用于 EGFR 19del 的视觉检测的免清洗和免标记的信号递减型比色传感器。根据溶液颜色的改变可用肉眼定性读取检测结果，当用分光光度计检测 420nm 波长吸光度时，可定量反应样本中的靶标含量。在最佳实验条件下，比色生物传感器表现出超高的灵敏度，检测限低至 20 fM。此外，该方法在识别单碱基不匹配和其他核酸时表现出强大的选择性和抗干扰能力。另外，通过加热人血清的方法灭活 RNase，获得了良好的回收率(93.00%~110.31%)。这种基于裸眼的比色生物传感器为癌症的早期无创诊断和指导临床用药提供了一种有前途的策略。

PU-0513

Large number hexagonal cavities microfluidic digital chip for gene mutation ultrasensitive analysis in lung cancer

Pan Feng
Department of Clinical Laboratory, the Second Affiliated Hospital, Army Medical University

Lung cancer has the highest incidence of malignant tumors in the world. Targeted therapy based on gene mutation detection, including epidermal growth factor receptor (EGFR) gene mutation detection, is one of the first-line treatments. In this work, taking the EGFR gene G719S mutation as a representative object, a large number hexagonal cavity microfluidic chip (LHMC) platform based on digital PCR (dPCR) for the absolute quantification of gene mutations in lung cancer was established. A 113,137-cavity chip was designed to increase the number of absolute quantities, which was 2~5 times higher than the traditional number. The hexagonal shape of the cavities elevates the filling rate and filling speed. A set of primers and probes for G719S with high sensitivity, high specificity and high reliability were designed and screened. Then, the PCR parameters were optimized. The results demonstrated that the chip platform shows good performance. The minimum detection concentration of the gene mutant was 3.01 copies/μL, and a good correlation (Y= 0.725X- 0.581, R2= 0.984) was noted between the measured value and the expected value. This chip sensitively detected positive mutations in G719S and indicated completely negative results when detecting other substances. The developed LHMC-dPCR chip is a rapid and accurate gene mutation analysis platform that has faster speed and lower price than classic detection methods, such as droplet dPCR and DNA sequencing **Methods** Moreover, LHMC-dPCR is not limited by the number of nucleic acids and droplets, and there is no need to estimate the nucleic acid concentration of the sample. This chip platform could also detect other gene mutations, for example, L858R and exon 19 deletions, in other tumors, including lung cancer.

PU-0514

HucMSC derived exosomes attenuate colitis by regulating macrophage pyroprosis via the miR-378a-5p/NLRP3 axis

xiu Cai
Jiangsu University

Background Human umbilical cord mesenchymal stem cells derived exosomes (hucMSC-exosomes) are recognized as novel cell-free therapeutic agents for inflammatory bowel disease (IBD), a condition caused by dysregulated intestinal mucosal immunity. The nucleotide-binding domain and leucine-rich repeat-containing family, pyrin domain-containing 3 (NLRP3) inflammasomes play an important role in regulating innate immune responses. Macrophage pyroptosis is a process of cell death releasing pro-inflammatory cytokines like interleukin (IL)-1β and IL-18, which is believed to partially account for inflammatory reactions. This study aimed at confirming the therapeutic effect and mechanism of hucMSC-exosomes on colitis repair.
Methods In vivo,We used BALB/c mice to establish a dextran sulfate sodium (DSS) induced colitis model and administasted hucMSC-exosomes intravenously to estimate its curative effect. Human myeloid leukemia mononuclear (THP-1) cells and mouse peritoneal macrophages (MPMs) were stimulated by LPS and nigericin to activate NLRP3 inflammasomes which simulated inflammation environment in vitro. The microRNA was used to verify the role of miR-378a-5p/ NLRP3 axis in colitis repair.
Results HucMSC-exosomes inhibited the activation of NLRP3 inflammasomes in the mice colon. The secretion of IL-18, IL-1β and Caspase-1 cleavage were suppressed followed by the reduced cell pyroptosis. The same outcome was observed in the in vitro cell experiments, where the co-

culture of THP-1 cells and MPMs with hucMSC-exosomes caused decreased expression of NLRP3 inflammasomes and increased cell survival. Furthermore, miR-378a-5p was highly expressed in hucMSC-exosomes and played a vital function in colitis repair.
Conclusions HucMSC-exosomes carrying miR-378a-5p inhibited NLRP3 inflammasomes and abrogate cell pyroptosis to protect against DSS-induced colitis.

PU-0515

过表达 LNCRNA 00593 通过 p53 通路调控非小细胞肺癌的顺铂耐药

李峥、任丽
天津医科大学肿瘤医院

目的 探讨 LNCRNA 00593 调控非小细胞肺癌顺铂耐药的机制研究。
方法 实时荧光定量 PCR（Quantitative Real-time PCR，RT-qPCR）检测 LNCRNA 00593 在癌旁正常组织、肺腺癌和肺鳞癌、HEB 细胞、A549 细胞、H1299 细胞、PC9 细胞、H460 细胞和 calu3 细胞中的表达量；CDPP 处理 H1299 细胞后 RT-qPCR 检测细胞中 LNCRNA 00593 的表达量。CCK-8 及流式细胞仪分析过表达及下调 LNCRNA 00593 对 H1299 细胞顺铂耐药的影响。RT-qPCR 及 Western blot 检测过表达及下调 LNCRNA 00593 后，H1299 细胞内 p53 的表达量，RNA-pull down 验证 LNCRNA 00593 和 p53 的结合。p53 通路抑制剂 PFT-α 作用细胞后，检测 LNCRNA 00593 对顺铂诱导的 H1299 细胞活力和凋亡的影响。
结果 LNCRNA 00593 在非小细胞肺癌组织的表达水平明显低于癌旁正常组织（P<0.05）。LNCRNA 00593 在非小细胞肺癌 A549、H1299、PC9、H460、calu3 细胞中的表达水平明显低于 HEB 细胞（P<0.01）。分别用 0μM、5μM、10μM CDPP 处理 H1299 细胞后，LNCRNA 00593 表达量随 CDPP 作用浓度依赖性升高（P<0.01）。用 10μM CDPP 处理 H1299 细胞 12 h、24 h、3 6h、48 h 后，LNCRNA 00593 表达量随 CDPP 作用时间不断增加（P<0.01）。CDPP 作用细胞后，下调 LNCRNA 00593 使 H1299 细胞活力明显上升，过表达 LNCRNA 00593 使 H1299 细胞活力下降。过表达 LNCRNA 00593 激活了 p53 通路。
结论 过表达 LNCRNA 00593 通过 p53 通路调控非小细胞肺癌细胞的顺铂耐药。

PU-0516

circHIPK2 在乳腺癌发展中的生物学功能及其临床诊断价值研究

吴军营、杨欢、王凌霞、吴茜茜
苏州大学附属第二医院

目的 研究 circRNA 分子在乳腺癌组织中的表达情况，验证差异表达的 circRNA 筛选出目标分子；建立 circHIPK2 检测方法，明确其与乳腺癌临床特征相关性，为乳腺癌的诊断、疗效及预后判断提供新的分子标志物；研究 circHIK2 对乳腺癌细胞增殖、迁移和侵袭的影响。
方法 1、采用 LPS 刺激乳腺癌细胞 MDA-MB-231，进行测序分析，筛选出差异表达的 circRNA 分子。对筛选出来的 circHIPK2 分子进行验证。并对其进行表征分析和临床病理资料相关性分析。
2、采用小干扰 RNA 进行 circHIPK2 敲减实验；采用细胞生长曲线及平板克隆实验检测 其对乳腺癌细胞增殖能力的影响；采用 transwell 迁移、侵袭实验检测 circHIPK2 对乳腺癌细胞迁移、侵袭能力的影响。
3、通过检测乳腺癌组、健康组及良性肿瘤组血清中 circHIPK2 表达水平，并进行差异分析，确定其在诊断、疗效及预后方面的价值。

结果 1、circHIPK2 在乳腺癌组织中显著高表达，circHIPK2 高表达与肿瘤大小、淋巴结转移和预后不良相关。设计 circHIPK2 特异性引物，PCR 产物仅能从 cDNA 模板中扩增出来，并且 circHIPK2 可以抵抗 RNase R 消化。
2、采用 siRNA 干扰可抑制乳腺癌细胞增殖、克隆形成、迁移和侵袭；敲减 circHIPK2 可以抑制乳腺癌细胞 EMT 及干性基因表达。
3、乳腺癌患者血清中 circHIPK2 表达水平明显高于健康对照组及良性肿瘤组，手术两周后 circHIPK2 表达水平明显降低。
结论 乳腺癌患者肿瘤组织中高表达的 circHIPK2 水平与乳腺癌大小、淋巴结转移相关，其高表达促进乳腺癌细胞增殖、克隆形成、迁移和侵袭，且该分子在乳腺癌、良性肿瘤及健康对照组血清中的表达水平存在显著差异，可作为乳腺癌诊断分子标志物。

PU-0517

Identification of differentially expressed long non-coding RNAs as potential plasma biomarkers for active tuberculosis

Chao Yuan
The Second Hospital of Shandong University

Background Tuberculosis, one of the deadliest infectious diseases worldwide, is difficult to diagnose. As long noncoding RNAs (lncRNAs) were demonstrated to be promising biomarkers, we aimed to identify lncRNAs in plasma as potential biomarkers for tuberculosis.
Methods We analyzed a GEO dataset (GSE94907) to identify the differential lncRNAs in serum exosomes between active tuberculosis (ATB) patients and healthy controls. To search for promising candidates that can be used for tuberculosis diagnosis, we excluded low-abundance lncRNAs using a cutoff value of FPKM >5. Four lncRNAs were selected for validation using real-time quantitative PCR in 69 ATB patients and 69 healthy individuals. A receiver operating characteristic (ROC) curve was constructed to evaluate the diagnostic value of these lncRNAs for ATB.
Results Integrated analysis of the GEO dataset and NONCODE database identified nine dysregulated lncRNAs in ATB patient serum exosomes. Compared with the heathy controls, NONHSAT101518.2, NONHSAT067134.2, NONHSAT148822.1 and NONHSAT078957.2 were significantly downregulated in ATB patient plasma. ROC curve analysis suggests that these four lncRNAs can discriminate ATB from healthy individuals with high specificity and sensitivity.
Conclusion We identified four differentially expressed lncRNAs in ATB patient plasma that can be used as potential diagnostic biomarkers of ATB.

PU-0518

肺结核病实验室不同检测方法诊断价值分析

吕星、杨欣宇
中南大学湘雅二医院

目的 探讨赛沛结核诊断系统（Xpert MTB/RIF）、液基夹层杯法、γ-干扰素释放定量检测(interferon-γ release assays, IGRAs)三种方法在结核病中的诊断价值，为临床选择肺结核病检测方法提供参考。
方法 选取 2020 年 1 月至 2020 年 11 月期间在中南大学湘雅二医院就诊的 200 例疑似结核病患者，根据《肺结核诊断标准(WS288-2017)》，分为临床确诊组（观察组）和临床未确诊组（对照组）。回顾性分析患者住院期间上述三种实验室检查的结果，并进行评价。

结果 观察组的三种检测方法的阳性率均高于对照组。三种方法单独检测的敏感度分别为 21.3%、36.2%、76.6%、85.1%。IGRAs 敏感度高于 Xpert MTB/RLF 和液基夹层杯法，但无统计学意义（P 均＞0.05）。Xpert MTB/RLF＋IGRAs 组合敏感度高于三种方法单独检测，但仅与 IGRAs 和 Xpert MTB/RLF 差异有统计学意义（P＜0.05）。三种方法单独检测的特异度分别为 96.7%、97.4%、68.6%、68.0%。Xpert MTB/RLF 和液基夹层杯法特异度高于 IGRAs，但无统计学意义（P 均＞0.05）。Xpert MTB/RLF＋IGRAs 组合特异度低于 Xpert MTB/RLF 和液基夹层杯法（P＜0.05），Xpert MTB/RLF＋IGRAs 组合特异度与 IGRAs 没有明显差异。
结论 三种方法各有各的优点，在辅助临床诊断结核病时应该优势互补，根据实际情况选用。组合项目检测可以提高检测的敏感度，但特异度会一定程度降低，可根据实际需要科学地选择组合项目，以满足临床需求。

PU-0519

P66shc 基因在 OSAHS 合并高血压患者中的表达水平

吕星、严镕璇
中南大学湘雅二医院

目的 观察阻塞性睡眠呼吸暂停综合征（OSAHS）合并高血压患者外周血 PBMCs 中 p66shc mRNA 表达和血浆 3-NT 浓度水平变化，探讨 p66shc 在 OSAHS 调节外周血氧化应激中的作用。
方法 选择 25 例单纯 OSAHS 和 13 例 OSAHS 合并高血压患者作为观察组，并选择同期 10 例确诊无 OSAHS 的健康人作为对照组。采用密度梯度离心法分离外周血中 PBMCs，RT-qPCR 检测其中 p66shc mRNA 表达水平变化。同时采用 ELISA 法检测血浆中氧化应激指标 3-硝基酪氨酸（3-NT）浓度。
结果 与正常对照组相比，单纯 OSAHS 组、OSAHS 合并高血压组 PBMCs 中 P66shc mRNA 表达和血浆中 3-NT 浓度明显升高，差异有统计学意义（P＜0.05），并且 P66shc mRNA 表达与血浆中 3-NT 浓度成正相关（r=0.517，P＜0.05）；而单纯 OSAHS 组与 OSAHS 合并高血压组之间 P66shc mRNA 表达和血浆中 3-NT 浓度无统计学差异（P＞0.05）。
结论 OSAHS 合并高血压患者外周血 PBMCs 中 P66shc mRNA 表达水平显著升高，并且血浆中氧化应激指标 3-NT 浓度成正相关，提示 OSAHS 可能通过 P66shc 基因调控循环系统氧化应激水平。

PU-0520

Evaluation of serum exosomal lncRNAs as diagnostic and prognostic biomarkers for esophageal squamous cell carcinoma

Suzhen Yan、Lutao Du、Chuanxin Wang
The Second Hospital of Shandong University

Background Exosomal long non-coding RNAs (lncRNAs) have been recognised as promising stable biomarkers in cancers. The aim of this study was to identify exosomal lncRNA panel for diagnosis and prognosis of esophageal squamous cell carcinoma (ESCC).
Methods Exosomes were isolated from serum by ExoQuick Solution. To validate the exosomes, immunoblotting for exosome markers and characterization of nanoparticle were performed. In training set, exosomal lncRNA profiles from 404 samples was conducted and established new models for ESCC detection. In validation set, the diagnostic performance of panel was further validated with an 222 additional individuals. The correlation between lncRNAs and survival rate of ESCC patients was assessed to explore prognostic potential.

Results A 4-lncRNA panel (UCA1, POU3F3, ESCCAL-1 and PEG10) in exosomes for ESCC diagnosis was developed by logistic regression model. The diagnostic accuracy of panel was evaluated with AUC value of 0.844 and 0.853 for training and validation stage, respectively. The corresponding AUCs for patients with TNM stage I-II and III were 0.820 and 0.935, significantly higher than squamous cell carcinoma antigen (P<0.001), which were 0.652 and 0.642, respectively. Kaplan–Meier analysis indicated that patients with higher level of UCA1 and POU3F3 had lower survival rate (P<0.001). Additionly, POU3F3 might be as an independent prognostic factor for ESCC patients (P=0.004).
Conclusions This findings suggested that serum exosomal 4-lncRNA panel has considerable value for ESCC diagnosis, and POU3F3 may serve as a novel prognostic predictor in clinical applications.

PU-0521

一个 F8 基因第 22 内含子剪接位点突变的血友病 A 家系遗传学分析

邱雪平、郑芳
武汉大学中南医院

目的 检测一个血友病 A 患者家系凝血因子Ⅷ基因（F8）的突变情况，明确 F8 基因的突变类型，以期为家系提供遗传咨询。
方法 联合应用长距离 PCR、二代测序技术（next generation sequencing, NGS）和 Sanger 测序技术对一个血友病 A 家系的先证者进行 F8 基因变异检测。
结果 长距离 PCR 结果显示先证者 F8 基因未检测到第 22 内含子和第 1 内含子倒位；NGS 结果发现先证者 F8 基因第 22 内含子区 c.6429+5 G>A 半合子突变，并经 Sanger 测序技术证实，对于该位点突变的致病性已有相关文献报道。
结论 通过 NGS 确定一例 F8 基因第 22 内含子半合子突变，该位点可能通过影响 mRNA 剪接而影响其蛋白功能，最终导致凝血因子Ⅷ活性降低甚至丧失。

PU-0522

B-raf V600E 基因检测试剂在肿瘤患者中检测的临床性能评价

刘玲、王玲玲
山东大学第二医院

目的 B-raf 基因是人类最重要的原癌基因之一，大约 8% 的人类肿瘤发生 B-raf 基因突变。90%左右的 B-RAF 基因突变发生在 15 外显子的第 1799 位核苷酸上 (V600E)，该突变导致下游 MEK-ERK 信号通路持续激活，对肿瘤的生长增殖和侵袭转移至关重要。该突变患者接受 EGFR-TKI 及 EGFR 单抗药物治疗不敏感。本研究拟对国产 B-raf V600E 基因检测试剂的检测性能进行评价。
方法 收集 2015 年 9 月至 2016 年 12 月山东大学第二医院 315 例的肺癌、结直肠癌、甲状腺癌等患者的病理组织样本。美国罗氏试剂为对比试剂，北京鑫诺美迪基因检测技术有限公司的 B-raf 基因突变检测试剂为考核试剂（鑫诺试剂），通过荧光 PCR-毛细管电泳测序法检测 B-raf 基因 V600E 突变。
结果 鑫诺试剂的 B-raf V600E 试剂突变检测率和罗氏试剂的分别为 43.68%、44.59%（P＞0.05），鑫诺试剂的 B-raf V600E 试剂无突变检测率和罗氏试剂的分别为 56.31%、55.41%（P＞0.05）。在统计学上，两者无差异具有较好的一致性。

结论 鑫诺的 B-raf V600E 试剂的灵敏度高、特异度好，具有较高的临床应用价值，可用于指导靶向药物的合理使用。检测 B-raf V600E 基因可及时发现耐药，辅助临床调整治疗方案，避免资源浪费。

PU-0523

胃腺癌中异常表达的 lncRNAs、miRNAs 和 mRNAs 在竞争性内源性 RNA 网络中的综合分析

朱丹丹、陈杰荣、张喜钦
广东省人民医院

蛋白质编码和非编码 RNA 正成为越来越多的研究热点，这些 RNA 参与了癌症的发展和发生。我们的研究旨在进一步探索胃腺癌中长非编码 RNAs(lncRNAs)、微 RNAs(miRNAs)和 mRNAs 之间的相互作用。为了确定差异表达的 RNAs（DERNAs），我们从 The Cancer Genome Atlas（TCGA）数据库中下载了数据。基于 lncRNAs、miRNAs 和 mRNAs 之间的相互作用，我们构建了一个竞争性内源性 RNA 网络来说明 lncRNAs、miRNAs 和 mRNAs 之间的关系。随后，进行了 GO 和 KEGG 功能富集分析和蛋白质-蛋白质相互作用（PPI）网络分析，以探索与 ceRNA 网络相关的 DEmRNAs 的功能和相互作用。生存分析用于筛选预后相关的 RNAs。通过差异表达分析，在胃腺癌中共发现了 327 个 DElncRNAs，242 个 DEmiRNAs，和 4343 个 DEmRNAs。经过预测、配对和网络分析，构建了一个由 29 个 DElncRNAs、31 个 DEmiRNAs 和 182 个 DEmRNAs 组成的 ceRNA 网络。这些 DEmRNAs 在与胃腺癌的发生和发展相关的途径中明显富集。39 个 mRNAs、4 个 miRNAs 和 3 个 lncRNAs 被鉴定出来，并与胃腺癌的总生存率显著相关（P <0.05）。我们的研究提供了关于 ceRNAs 在胃腺癌中的功能以及开发 STAD 治疗方法的生物标志物的见解。

PU-0524

Serum albumin in furry animals as a cross-reactive component may causes more severe allergic symptoms

Zhifeng Huang、Baoqing Sun
First Affiliated Hospital of Guangzhou Medical University

Background The prevalence of allergies has increased significantly in the past decade. And further research on allergic diseases caused by furry animals is of great importance for clinical prevention, diagnosis and treatment.
Objective To identify the sensitization profile and clinical association of various furry animal crude extracts and components based on CRD.
Methods 211 patients with allergic rhinitis (AR) sensitized to cat and or dog were recruited, and the Specific Immunoglobulin E (sIgE) of various furry animals (such as dog / cat extract and its components, pigeon, parrot, duck, chicken, sheep, rat, mouse, goose, cow and horse extract) were measured to analyze the sensitization profiles, cross reaction and clinical relevance.
Results 91.67% of cat sensitized patients were sensitive to Fel d 1, while only 16.03% of cat sensitized patients responded to Fel d 2. Can f 1 and Can f 5 as the major components of dog, the positive rates were 23.53% and 16.18%, respectively. 20% of patients were sensitized with other 10 furry animal allergens, and the positive rate was between 0-19.12%. There was a significant correlation between components (Can f 1-5 and Fel d 2) and 5 furry animals (mouse, sheep, horse, rat, cow), especially between serum albumin (Can f 3, Fel d 2) and furry animals. The sensitization rate of most of the animal crude extracts and components in patients with serum albumin positive was significantly higher than that of the patients with serum albumin negative. Especially for mouse, sheep, horse, rat and cow, which OR value were more than 10

times. The VAS of symptoms and life quality in the serum albumin sensitized patients was higher than that in unsensitized patients, and lipocalin sensitized patients' quality of life was also worse. **Conclusion** Serum albumin Fel d 2 and Can f 3, rather than lipocalin or prostatic kallikrein, as minor allergens in cats and dogs, significantly cross-reacted with 5 uncommon furry animals. Serum albumin sensitization significantly increases the risk of sensitization to other furry animals and makes allergic rhinitis symptoms worse.

PU-0525

黄河三角洲地区育龄妇女亚甲基四氢叶酸还原酶基因多态性分析

郝静静
滨州医学院烟台附属医院

目的 了解黄河三角洲地区育龄妇女体内亚甲基四氢叶酸还原酶(MTHFR)677 和 1298 两个位点基因多态性的分布情况。
方法 采用荧光 PCR 法检测 2019 年 1 月 1 日至 12 月 31 日全年滨州医学院附属医院的 6135 位育龄妇女的 MTHFR 中 C677T 以及 A1298C 的基因分型，统计分析基因多态性的频率分布特征，并与符合条件的其他地区育龄妇女 MTHFR 分布数据作比较。
结果 黄河三角洲地区育龄妇女的 MTHFR 中 C677T 位点 CC（野生型）基因型频率为 13%（798/6135）、CT（突变杂合）基因型频率为 44%（2699/6135）和 TT（突变纯合）基因型频率为 43%（2638/6135）。MTHFR A1298C 位点 AA（野生型）基因型频率为 76%（4662/6135）、AC（突变杂合）基因型频率为 22%（1350/6135）、CC（突变纯合）基因型概率为 2%（123/6135）。对于 C677T 基因突变统计，黄河三角洲地区 T 等位基因与海南、乌鲁木齐、云南、郑州的统计结果差异具有统计学意义(P＜0.05)，与淄博的统计结果差异无统计学意义(PAF＞0.05)。黄河三角洲地区 T 基因突变频率(65.00%)显著高于海南(26.18%)、乌鲁木齐(49.10%)、云南(37.50%)和郑州(62.35%)，表现出明显的地域差异性。同时黄河三角洲地区、郑州和淄博 CT 与 TT 表现型的基因频率相当，海南、乌鲁木齐、云南等地 CT 与 TT 表现型的基因频率差距较大，CT 基因频率高于 TT，即杂合突变率高于纯合突变。
结论 黄河三角洲地区育龄妇女 MTHFR 基因多态性分布具有地域特异性，MTHFR C677T 位点 T 突变率较高，通过检测 MTHFR 基因多态性来指导育龄妇女适量补充叶酸是进一步降低当地出生缺陷和妊娠期疾病的重要方法。

PU-0526

呼吸道病原菌核酸检测在儿童肺炎诊断中的临床应用

刘玲、赵燕、王玲玲
山东大学第二医院

目的 环介导等温扩增技术是 Notomi 发明的一种核酸扩增技术，基于 LAMP 的检测方法具有检测时间短、灵敏度高和检测结果易于判读等优点，能辅助进行病原早期诊断。本研究拟采用环介导等温扩增技术的呼吸道病原菌核酸检测试剂盒对临床痰液样本进行检测，评价该试剂盒的检测效果和临床适应性。
方法 山东大学第二医院 2019-2020 年收治的儿童肺炎患者 45 例，各病例的痰液样本分别使用细菌学方法和呼吸道病原菌核酸检测试剂盒进行，对两种检测方法的病原检出种类、数量和检测一致性进行对比。
结果 试剂盒检测结果和细菌学检测结果有较好的一致性，肺炎链球菌、肺炎克雷伯氏菌和流感嗜血杆菌检出率分别为 37.5%、 14.6%和 9.98%。以上结果与 2010 年的全国性调查结果接近。对于

临床上肺炎感染率最高的 3 种细菌，肺炎链球菌的检测总符合率为 85.4%，肺炎克雷伯氏菌的总符合率为 97.1%，流感嗜血杆菌的总符合率为 91.2%。

结论 呼吸道病原菌核酸检测试剂盒能一次检测肺炎相关的 8 种常见病原菌，操作简便，能快速获得检测结果，能大大缩短对未知病原的检测时间，在实际使用中更具有时效性，检测结果有临床价值，适用于临床的检测。

PU-0527

分支杆菌核酸检测在疑似结核患及非结核分支杆菌病鉴别诊断中的应用

刘玲、刘军莉
山东大学第二医院

目的 利用基于实时荧光 PCR 技术的分枝杆菌核酸检测区别 MTB 与 NTM，探讨其对疑似结核患及非结核分支杆菌病快速鉴别诊断的应用价值。

方法 收集本院呼吸科疑似结核病患者标本经 BACTECMGIT960 快速培养，培养阳性标本 48 例用 PNB 检测法做菌型鉴定获得结核分枝杆菌 41 株、非结核分枝杆菌 7 株，分别用荧光 PCR 检测并与 PNB 结果对比。

结果 重复检测 6 株菌株的核酸／非核酸分枝杆菌检测，符合率 100％，检测特异性高。41 例结核分枝杆菌使用荧光 PCR 方法检测阳性 39 例，结核分枝杆菌阳性符合率为 95.1％（39／41）；7 株非结核分枝杆菌使用荧光 PCR 方法检测，阳性 7 例，非结核分枝杆菌阳性符合率 100％（4／4）。

结论 本研究建立的实时荧光定量 PCR 的分支杆菌核酸检测检测方法，利用结核分枝杆菌和分枝杆菌特异性的核酸序列，利用双重实时荧光 PCR 技术实现对分枝杆菌和非结核分枝杆菌的快速检测。

PU-0528

HHT 可诱导 PSMD11 蛋白合成并调节胰腺癌干细胞特性

王乐乐
山东大学第二医院

胰腺导管腺癌（PDAC）是美国癌症相关死亡的第三大主要原因。PDAC 患者的 5 年死亡率仍低于 8.2%。胰腺癌发现难易转移等特点使得发现新的靶向治疗药物迫在眉睫。我们前期研究发现胰腺癌细胞发生急性凋亡与短寿命中心蛋白质组中 PSMD11 蛋白的迅速降解密切相关。PD98059 激活 MEK/ERK1/2 信号通路可以 抑制由 HHT 引发的 PSMD11 蛋白的合成。理解 HHT 对 PSMD11 蛋白起作用的机制对于 胰腺导管腺癌及其他癌症的靶向治疗可能会有很大的作用。研究发现高蛋白酶体活性的人胚胎干细胞与 PSMD11 蛋白增加有关。提示 PSMD11 蛋白也有可能通过调节胰腺癌干细胞来影响胰腺癌细胞的生长和增殖。因此深入理解胰腺导管腺癌的作用机制对胰腺癌的靶向治疗具有十分重要的意义。

PU-0529

SHOX2/PTGER4 基因甲基化在肺癌早筛的临床意义

赵敬杰、赵燕、王玲玲
山东大学第二医院

目的 DNA 的甲基化在肿瘤的发生发展中发挥了重要的作用，检测某些 DNA 位点的甲基化可作为肿瘤检测的标记物。最新研究表明 SHOX2/PTGER4 基因甲基化在肺癌肿瘤早期筛查方面具有高度的特异性和敏感性。本研究拟探讨 SHOX2/PTGER4 基因甲基化对早期肺癌患者筛查的意义。
方法 收集山东大学第二医院 2018 年 9 月至 2020 年 12 月已确诊为 I 期和 II 期肺癌患者 134 例，72 例非肺癌患者和 75 例正常人的血液标本。用鑫诺美迪 SHOX2/PTGER4 基因甲基化试剂，提取血液标本中肿瘤 ctDNA，进行 MSP 荧光定量 PCR 方法检测 SHOX2/PTGER4 基因甲基化程度。
结果 I 期和 II 期肺癌患者的检测 SHOX2/PTGER4 基因甲基化阳性率与非肺癌患者的分别为 69.12%， 9.01%（P＜0.05），与正常人的 3.49%（P＜0.05）相比，均具有显著性差异。
结论 采用鑫诺美迪的 SHOX2/PTGER4 基因甲基化试剂，能有效应用于肺癌患者的早期筛查，特异性好，灵敏度高，具有较高的临床应用价值。SHOX2/PTGER4 基因甲基化可以联合组织学和细胞学共同检测，提高确诊率，是确诊肺癌的有效工具。

PU-0530

循环肿瘤 DNA 在乳腺癌中的临床应用

王乐乐
山东大学第二医院

目前，液体活检的三驾马车为 ctDNA，CTC 和外泌体。其中 ctDNA 的发展相较于另外两个更有优势。ctDNA 主要来源于肿瘤中癌细胞凋亡和 / 或坏死。ctDNA 在个体总 cfcDNA 的比例主要取决于肿瘤负荷和增殖速率等因素。ctDNA 的取样和分析已经用于转移性非小细胞肺癌（NSCLC），检测 EGFR 突变。在乳腺癌患者中我们通过检测治疗前和治疗过程中患者 ctDNA 水平，来评估 ctDNA 对乳腺癌患者临床结局的预测价值。

PU-0531

免疫球蛋白基因重排分析在非何杰金淋巴瘤骨髓侵犯监测中的作用

马雨婷
滨州医学院烟台附属医院

目的 探讨免疫球蛋白基因重排分析在非何杰金淋巴瘤骨髓侵犯监测中的作用。
方法 收集 2017 年至 2019 年间本院收治的 192 例非何杰金淋巴瘤患者的骨髓穿刺液标本。采用多重体外扩增手段病人免疫球蛋白重链（IgH）和免疫球蛋白轻链（Igκ 和 Igλ）的核酸系列重组；使用多色流式细胞仪检测淋巴细胞上分化抗原的表达；采用瑞士-姬姆萨染色骨髓涂片并用光学显微镜分类计数骨髓细胞；采用传统细胞遗传学检测染色体易位；采纳应用 DNA 复制时期荧光原位杂交(FISH)手段检验 MYC、BCL-2 核酸系列空间构成改变。
结果 免疫球蛋白基因重排检测发现不同类型淋巴瘤骨髓侵犯的发生率不同，小淋巴细胞淋巴瘤和 Burkitt 淋巴瘤的骨髓侵犯率明显高于弥漫大 B 细胞淋巴瘤（P＜0.05）；与核酸序列重组的检验数据比较，小淋巴细胞淋巴瘤骨髓侵犯骨髓形态学检出率较低（P＜0.05），其它几种淋巴瘤亚型尽管没有统计学分别，但均低于核酸系列重组检验的检出率；对各种类型淋巴瘤，流式细胞仪与基因

重排检测骨髓侵犯结果间没有统计学差异（P＞0.05）；传统细胞遗传学和 FISH 技术可确证其它检测结果不符时的诊断结论。

结论 免疫球蛋白基因重排检测在非何杰金淋巴瘤骨髓侵犯监测中具有重要价值，联合应用流式细胞术、细胞形态学以及分子细胞遗传学技术有助于明确淋巴瘤骨髓侵犯的诊断。

PU-0532

葛根素提高肝癌细胞化学敏感性的影响

吴镇
山东大学第二医院

目的 本研究研究了葛根素(Pu)对 HepG2 人肝癌(HCC)细胞对化疗药物敏感性的影响，以确定可能的机制。

方法 用不同浓度的 Pu 和顺铂(CDDP)单独或联合治疗。用 MTT 法测定不同药物对 HepG2 细胞的抑制作用。通过倒置显微镜观察到细胞形态。用西斑点分析测定了 B 细胞淋巴瘤 2（Bcl-2）和 Bax 蛋白的表达。Pu 和 CDDP，单独或联合使用，可抑制 HepG2 细胞的增殖。CDDP 与 Pu 联合使用对 HepG2 细胞的抑制作用明显高于单一药物治疗方法(p<0.01)。此外，与单个药组相比，细胞形态显著改变，细胞凋亡率和 Bax 蛋白表达显著增加（p<0.01）。然而，在联合给药组中，Bcl-2 蛋白的表达显著降低(p<0.01)。

结果 Pu 可以提高 HCC 对化疗药物的敏感性，提高化疗药物对细胞增殖的抑制作用，协同诱导 HepG2 细胞凋亡。该机制可能与 Bax 蛋白的上调和 Bcl-2 蛋白的下调有关。

PU-0533

人肾癌组织和肾癌细胞株中 MICA 表达的临床意义

赵敬杰、鞠振宇
山东大学第二医院

目的 肾细胞癌是一种肾脏最常见的恶性肿瘤，其特点是高发局部侵袭和远端转移。MHC I 类相关基因 A(MICA)位于 MHC I 类基因区域，具有高度的多态，但当细胞受到感染、应激或恶性转化时可明显上调其表达量。本研究拟揭示人类肾癌细胞系和组织标本中膜结合型 MICA（mMICA）的表达，并确定可溶性 MICA（sMICA）在肾细胞癌患者的血清含量。

方法 应用流式细胞术（FCM）、免疫组化和 RT-PCR 法对肾癌组织中和肾癌细胞株的 mMICA 进行检测和分析；应用酶联免疫吸附试验（ELISA）检测对照组和肾癌患者体内血清中 sMICA 的含量。

结果 应用流式细胞术（FCM）、免疫组化和 RT-PCR 三种方法均显示：与健康成人和人胚胎肾 293（HEK293）细胞系相比较，人肾癌组织和肾癌细胞株（786-O 和 Ketr-3）中 mMICA 的表达百分比明显增加（P＜0.05）。ELISA 分析表明 sMICA 在健康成人中的表达为阴性，但在 76.7%（23/30）的肾癌患者中显著升高（P＜0.05）。

结论 MICA 在人肾癌中呈高表达状态，提示 MICA 可作为人肾细胞癌中潜在的肿瘤相关抗原（TAA）。sMICA 的释放则不仅降低肿瘤细胞表面 MICA 的表达，继而降低肿瘤的免疫原性，可能是肿瘤发生免疫逃逸的又一机制。

PU-0534

HSP90α 在肺癌患者中血浆表达的临床意义

赵敬杰、王玲玲、赵燕
山东大学第二医院

目的 热休克蛋白 90α（HSP90α）是一种细胞质蛋白质，是一类在遗传上高度保守的分子，能保护细胞并促进细胞对各种刺激所造成的损伤进行自身修复。HSP90α 作为肿瘤标志物，在肿瘤筛查、诊断、判断预后、评价疗效和高危人群随访等方面都具有重要的实用价值。本研究拟探讨肺癌患者血浆 HSP90α 的表达及其临床意义。
方法 应用酶联免疫法检测山东大学第二医院 72 例初治肺癌患者及 35 例健康体检者血浆 HSP90α 浓度，并分析患者临床资料。
结果 肺癌组血浆 HSP90α 浓度为（189.62±106.21）ng/mL，明显高于健康对照组（40.14± 20.15）ng/mL（t＝10.480，P＜0.001）；使用 58ng/ml 作为区分癌症和对照组的 cut off 值时，检测灵敏度为 71.24%（95% CI，0.695–0.749），特异度为 77. 89%（95% CI，0.761–0.813）。与 CEA、NSE、CYFRA21-1 相比，HSP90α 灵敏度更高，热休克蛋白 90α 与 CEA、NSE、CYFRA21-1 联合检测，灵敏度达到 96%。热休克蛋白 90α 含量的变化与患者病情有对应关系。
结论 HSP90α 具有辅助诊断肺癌的作用，通过数值的变化判断患者病情发展情况，其联合肺癌三项可显著提高肺癌的检出率。HSP90α 亦可提高其他肿瘤患者的病情监测和疗效评价水平，对实现肿瘤个体化治疗具有重要推动作用。

PU-0535

Circulating Serum Exosomal lncRNA POU3F3 as Potential Biomarker for Esophageal Squamous Cell Carcinoma

Suzhen Yan、Lutao Du、Chuanxin Wang
The Second Hospital of Shandong University

Purpose Esophageal squamous cell carcinoma (ESCC) is one of the most common malignant cancers worldwide especially in Eastern Asia and the prognosis of ESCC remain poor. Exosomes are bioactive vesicles secreted by cells into surrounding body fluids,and have major impact in cancer development. Recent studies have demonstrated that long non-coding RNAs (lncRNAs) were present in the circulating exosomes of cancer patients and have shown great potential as powerful and non-invasive tumor markers. The aim of our study was to identify serum exosomes lncRNA expression in patients with ESCC for diagnosis and prognosis prediction.
Methods Exosomes were isolated from serum of ESCC and healthy subjects by ExoQuick precipitation kit and confirmed by transmission electron microscopy, Western blot, flow cytometer and NanoSight analysis. Then, 24 lncRNAs which previously found to be differently expressed in esophageal cancer were selected as candidate targets to investigate in 34 ESCC and matched adjacent normal tissues via quantitative real-time PCR. Identified lncRNAs were further confirmed in serum exosomes on training and validation sets.
Results Consequently, lncRNA POU3F3 was finally identified by qRT-PCR for the diagnosis of ESCC. The results showed that the expression levels of lnc-POU3F3, was significantly higher in ESCC serum exosomes than in normal controls($p<0.001$), and no other lncRNAs showed significant differential expression between ESCC and normal control samples. Furthermore, the expression level of lncRNA POU3F3 was significantly higher in patients with advanced stage. The areas under the receiver operating characteristic curve (AUC) of the POU3F3 were 0.717 and 0.707 for the training and validation stages, respectively. In addition, Kaplan–Meier analysis showed that patients with high levels of POU3F3 had significantly lower survival rate ($p < 0.001$).

In multivariate Cox regression analysis, POU3F3 was independently associated with tumor prognosis of ESCC (p=0.004).
Conclusions Our study identified serum exosomes lncRNA POU3F3 as a biomarker for ESCC diagnosis and demonstrated POU3F3 as an independent prognostic factor for ESCC prognosis prediction.

PU-0536

全外显子组测序筛选限制性心肌病致病基因: 一例限制性心肌病病例报告

徐嘉欣
成都市第一人民医院

目的 限制性心肌病（RCM）是一种罕见且独特的心肌病，其特征是具有正常的心室腔尺寸和正常的心肌壁厚度，但心肌松弛能力减弱，限制了心脏的正常伸展和充盈，患者预后差，心脏移植是目前唯一的治疗方式。遗传因素是 RCM 发病的主要原因之一，但目前关于 RCM 致病基因的相关研究仍不完善。本文通过对 1 例散发 RCM 患者进行全外显子组测序对 RCM 潜在致病基因进行检测与探讨，以寻找新的 RCM 候选致病基因或致病突变，为进一步探索 RCM 潜在的致病机制提供遗传学依据和靶点。
方法 本研究以 1 例中国女性 RCM 患者为研究对象，收集其临床信息并提取其血液样本基因组 DNA 进行全外显子组测序，通过生物信息软件 SIFT、Polyohen-2 和 HOPE 等软件对变异导致的蛋白功能改变进行致病性预测。
结果 此例 RCM 患者的全外显子组测序结果显示 SMPD1 中存在缺失突变（exon1:c.108_113del:p.36_38del），为一新发缺失突变。通过对比不同物种 SMPD1 蛋白氨基酸序列，结果显示突变位点氨基酸具有高度的保守性，SMPD1 突变使蛋白序列发生改变，且 SIFT、Polyohen-2 和 HOPE 软件均预测此变异导致的蛋白功能改变具有有害性。
结论 本文章报道了 SMPD1 上的新的缺失突变位点，该研究结果丰富了中国人群 SMPD1 基因突变谱。同时，为探索其在限制性心肌病发生发展中的致病机制，进一步的细胞与动物实验十分必要。此外，本文章为全外显子组测序在 RCM 诊断上的应用提供了新思路。

PU-0537

基于双功能发光剂的电化学发光传感器用于无标记法检测 microRNA

宁振强[2]、沈艳飞[1,3,4]
1. 东南大学医学院
2. 东南大学医学院
3. 东南大学附属中大医院临床检验医学中心
4. 东南大学江苏省重症医学重点实验室

微小 RNA（microRNA）是一类长度约为 19 至 23 bp 的单链内源非编码 RNA 分子。相关研究表明，作为基因表达的转录后调节因子，microRNA 参与到人体的多种生理过程，如细胞的分化、增值，其表达水平与肿瘤的发生、发展存在重要联系，因此 microRNA 有望成为新型生物标志物应用于疾病的非侵入性的早期诊断。目前，microRNA 的检测方法主要包括 Northern 印迹法，Real-time PCR、基因芯片法等等，而这些方法存在灵敏度低，操作繁琐，耗时，成本高等缺点，因此无法满足当前疾病诊断的需求。因此，建立针对 microRNA 的简便快捷的超灵敏定量检测技术具有十分重要的临床实践意义。

电化学发光（electrochemiluminescence, ECL）是一种由电化学反应驱动的化学发光现象，通过智能整合电化学及化学发光技术，使其相较于其他光学检测方法其具有更加优越的性能。电化学发光不需要额外的光源，这不仅简化了实验的设备，同时也避免了杂志及散射光源的背景干扰，具有较高的灵敏度，因此被广泛地应用于食品和药品分析、环境监测等领域，是实现 microRNA 超灵敏检测的最有潜力的平台之一。

本文首先采用简便的一步合成法制备了同时负载发光剂 Ru(bpy)32+和共反应剂(二乙氨基甲基)三乙氧基硅烷 （DEAMTES）的二氧化硅纳米粒子，其提升了 ECL 反应过程的电子传输的有效性及速率，相比于传统发光剂具有更强的发光效率。其次，通过设计 Y 字型催化发卡自组装探针用于识别 microRNA 并发挥信号放大的作用，用于构建无标记的 ECL 传感系统。结果显示，该传感器能够实现 0.01-1000 pM 浓度范围的 microRNA-21 的定量检测，其最低检测限达到 8.19 fM，显示出其在未来临床检验诊断领域的强大潜力和应用前景。

PU-0538

Fusobacterium nucleatum is a risk factor for metastatic colorectal cancer

Xin Zhang
Qilu Hospital of Shandong University

Background Increasing evidence has indicated that there is a correlation between the abundance of Fusobacterium nucleatum (F. nucleatum) and poor prognosis of colorectal cancer (CRC). Moreover, tumor metastasis plays a decisive role in the prognosis of CRC patients. Therefore, we hypothesized that the abundance of F. nucleatum in CRC tissue affected tumor metastasis.
Materials and Methods F. nucleatum DNA from 141 resected CRC samples was quantified by qPCR to analyze whether there were differences in F. nucleatum abundance between the groups with and without CRC metastasis. Moreover, in vitro experiments (electron microscopy as well as migration and invasion trials) were performed with CRC cells infected with F. nucleatum to observe the influence of F. nucleatum. Additionally, a meta-analysis was carried out to comprehensively evaluate the correlation between the F. nucleatum abundance and CRC stage based on large cohorts.
Results CRC tissues enriched with F. nucleatum had a higher risk of lymph node metastasis and distant metastasis. The receiver operating characteristic (ROC) curve indicated that F. nucleatum in the CRC tissue could act as an indication marker for CRC metastasis to some extent. Moreover, F. nucleatum was a highly invasive bacterial strain and could significantly enhance the invasion and migration capacities of SW480 and SW620 cells. Besides, the meta-analysis indicated a slight correlation between the F. nucleatum abundance and advanced CRC stage (RR=1.17, 95% CI: 1.00–1.37, P=0.04, random effect).
Conclusions F. nucleatum abundance is associated with CRC metastasis, and it might serve as a metastasis biomarker for CRC patients.

PU-0539

Exosome-mediated Bmi1 promotes cholangiocarcinoma growth and metastasis through the differential regulation of miR-320b and miR-27b-3p

Xin Zhang
Qilu Hospital of Shandong University

Background B-cell specific moloney leukemin virus insertion site 1 (Bmi1) is up-regulated in many human malignancies. However, the role of Bmi1 in the progression of cholangiocarcinoma (CCA) remains largely undetermined. In the present study, we investigated the biological function and potential mechanisms of Bmi1 in the progression of CCA.
Methods The expression of Bmi1 was detected in 2 cohorts of human CCA tissues using immunohistochemistry. Function of Bmi1 or exosomal Bmi1 was investigated using CCK8, colony formation, transwell, vascular tube formation assays and tumor xenograft models. RNA-seq and miRNA-seq were used for identification of downstream targets and upstream regulation miRNAs.
Results Bmi1 was significantly up-regulated in CCA tissues, and associated with tumor size and lymph nodes metastasis, which is an independent prognostic marker for CCA. Overexpresson of Bmi1 promoted CCA cells proliferation, migration, and invasion. And, depletion of Bmi1 could inhibit growth and metastases of CCA cells in vitro and in vivo. QBC-939-derived exosomes transferred Bmi1 to RBE cells and human umbilical vein endothelial cells, thus promoting proliferation, metastasis, and angiogenesis of CCA. Bmi1 is involved in regulation of p53 pathway and EMT in CCA. Based on the next-generation sequencing, we identified and verified Bmi1 was downregulated by miR-320b while upregulated by miR-27b-3p in CCA.
Conclusion Bmi1, or exosomal Bmi1, played a critical role in tumorgenosis and metastasis of CCA by inhibiting p53 and promoting EMT, which could be used as a potential predictive biomarker for CAA prognosis.

PU-0540

ＨＰＶ感染和宫颈癌的病发率与防治

郭文静、王耀东、杨叶
呼和浩特金域检验所有限公司

在国内，宫颈癌的发病率飞速上升，是发病率增长速度最快的癌症之一。近十年，新发现的患者数量增加了 68.8%，宫颈癌患者的年龄以往以四十岁至五十岁为最多，二十岁以下的比较少见一些。世界卫生组织国际癌症探讨所的探讨结果表明人乳头病毒(HPV)感染是宫颈癌的主要病因，宫颈癌是近年来最常见的妇科恶性肿瘤之一，在女性恶性肿瘤疾病中位居第二位，随着最近几年宫颈细胞学筛查的普遍应用，明确了解了子宫颈癌的三级预防策略，通过减少 HPV 感染、早发现、早诊断、早治疗子宫颈癌前病变，以及对子宫颈浸润癌及时治疗降低宫颈癌的疾病负担。

PU-0541

乙型肝炎患者检验指标相关性分析

杨博
雅安市人民医院

目的 探讨乙型肝炎患者 HBV DNA 与乙肝标志物及肝功能的相关性。

方法 选取我院 2020 年 6 月至 2020 年 11 月收治的 82 例乙型肝炎患者，对患者实施 HBV DNA 定量检查、乙肝标志物检查及肝功能检查。根据 HBV DNA 定量结果将研究对象分为阴性组、阳性组，比较两组患者乙肝标志物、肝功能检
查结果。
结果 阴性组、阳性组各项乙肝标志物的阳性率比较，P 均 >0.05，无统计学意义。阳性组 ALT、AST 较阴性组高，组间比较，P 均 <0.05，差异有统计学意义。
结论 乙型肝炎患者 HBV DNA 与乙肝标志物无明显相关性，但能反映肝功能变化，定量越高时，肝功能越差。

PU-0542

云南地区遗传性耳聋相关 21 个基因位点的分子流行病学数据报道

孟博
昆明金域检验医学有限公司

目的 与遗传性耳聋相关的基因位点分布在四个基因（GJB2、SLC26A4、GJB3 和 12SrRNA）上，基于中国人群的耳聋基因位点流行病学分布的数据报道还比较有限，不同地区的分布数据更是缺乏。云南地区少数民族种类较多，通过基于该地区的耳聋基因检测大数据分析可以帮助对于云南地区的耳聋发病的分子特征的了解，进而为当地疾病预防和诊疗提供重要的参考价值。
方法 本研究分析了本医学检验所近 19 个月的耳聋基因检测数据（4 个基因的 21 个位点），采用的方法为基质辅助激光解吸电离飞行时间质谱技术（MassARRAY CPM96/Agena Bioscience），统计分析了各位点在检测人群中的突变频率和突变类型，并且进一步比较了与已有报道的异同。
结果 在 35820 例检测样本中， 一共有 1165 例发现有突变位点，占 3.25%。突变位于 GJB2 基因上的样本数为 613 例 （1.71%总样本数，51.43%阳性突变总数），突变于 SLC26A4 上有 427 例（1.19%总，35.82%阳），于 12SrRNA 上有 90 例 （0.25%总，7.55%阳），于 GJB3 上有 62 例（0.17%总，5.20%阳）。GJB2 基因中的热点突变位点为 c.235delc （1.396%总样本数），slc26a4 基因的热点突变为 c.919-2a>g(常用名 ivs7-2a>g) （ 0.793%）。在 1165 例阳性突变样本中，有 1140 例为单位点突变，占突变比例 97.85%。有 25 例为多位点突变，占突变比例 2.15%，其中 SLC26A4 和 GJB2 共突变的检出最多。
结论 我们的研究数据检测到的各个基因的突变频率排序和基于深度测序方法的报道一致，GJB2 和 SLC26A4 是云南地区耳聋基因检测人群中突变频率较高的基因，值得进一步关注。

PU-0543

子宫颈人乳头瘤病毒感染与阴道环境的关系分析

邬剑
雅安市人民医院

目的 探讨子宫颈人乳头瘤病毒(human papilloma virus,HPV)感染与阴道环境相关的因素。
方法 对 500 例参加两癌筛查的妇女的阴道分泌物进行霉菌、滴虫检测，阴道分泌物清洁度检查,对感染 HPV 人群、感染高危型 HPV 人群以及 HPV 阴性人群的检查结果进行比较分析。
结果 500 个受检已婚育龄妇女,HPV 阳性 32 例(6.4%),其中高危 HPV 感染患者 21 例，低危 HPV 感染患者 11 例，HPV 阴性 468 例(93.6%)。HPV 感染患者、高危 HPV 感染患者以及 HPV 阴性患者在假丝酵母菌感染、滴虫感染以及阴道清洁度方面均无明显差异，根据统计学方法分析计算(P>0.05),不具有统计学意义。

结论 子宫颈人乳头瘤病毒感染与阴道环境中假丝酵母菌感染、滴虫感染以及阴道清洁度这三方面无明显的相关性。

PU-0544

Characterization of eight novel full-length genomes of SARS-CoV-2 among imported COVID-19 cases from abroad in Yunnan, China

Mi Zhang 、cuixian Yang 、xingqi Dong
Yunnan Infectious Diseases Hospital

Recent correspondence in this Journal has highlighted the current threat posed by recently-emerging corona virus disease 2019 (COVID-19) in the world.1 The COVID-19 is infection caused by the severe acute respiratory syndrome coronavirus 2 (SARS-COV-2) and is characterized by fever, dry cough, weak, and so on. Eight COVID-19 patients imported from overseas were admitted to Yunnan Provincial Infectious Disease Hospital from March 15, 2020 to March 26, 2020. Phylogenetic analyses revealed that the six isolates, including one from France (YN_Im02), two from Spain (YN_Im01 and YN_Im03), and three from the United States (YN_Im06-08) were clustered as G clade with a high bootstrap value of 99%, one strain from Cambodia (YN_Im04) was grouped into S clade with a bootstrap value of 80%, and the remaining one from Sri Lanka was classified within other clade, a large unclassified sequences because lack the signature variants. To further characterize the characteristics of virus variation, The results revealed that 15, 12 and 10 nucleotide mutations to clades G, S, and other, respectively, were mapped across the SARS-CoV-2 full-length genome. Corresponding to these nucleotide substitutions, 8, 6, and 5 nonsynonymous amino acid substitutions were detected in clades G, S, and other, respectively.

In summary, we characterized the full-length genomes of SARSCoV-2 strains from eight COVID-19 cases imported from abroad in Yunnan, China. Our results showed that the predominant SARSCoV-2 clade was G (6 cases), followed by S clade (one case) and unclassified clade (one case). Further, comparative genomic analyses revealed that a novel signature amino acid substitution P4715L in nsp12 was found in the G clade strains. Moreover, three novel mutations, including D1962V in nsp3, L1375F in nsp3, and A829T in S protein were first identified in this study.

PU-0545

新冠核酸标本检测中的假阳性及假阴性

王娇
雅安市人民医院

目的 探讨新冠核酸检测过程中的假阳性及假阴性并分析原因
方法 从新冠核酸的各个环节着手，逐一分析其中有可能影响结果的因素，有助于提高结果的准确性和及时性，为临床提供更好更准确的检测结果。
结果 造成假阳性结果的原因主要在实验操作过程，假阴性的原因有标本、实验过程、疾病本身病程

PU-0546

HPV16 E7 upregulated the expression of ACP5 by mediating FoxM1 through activating CDK6 in lung cancer cells

Yunhui Li
General Hospital of the northern theater of the Chinese people's Liberation Army

According to the GLOBAL cancer statistics 2018, lung cancer is the most commonly diagnosed cancer (11.6% of the total cases) and the leading cause of cancer death (18.4% of the total cancer deaths)[1]. Besides a range of environmental and genetic factors, Syrjänen, et al. reported that human papilomavirus (HPV) infection was involved in the development of lung cancer firstly[2]. The persistent infection of high-risk HPV is related to the occurrence of cervical cancer, especially HPV16/18. E6/E7 as the mainly oncogenes have been extensive researched. Although the association between HPV infection and lung cancer has not been established in the Western population[3], a significant number of infection rates (37.22%) were found to be related to the incidence of lung cancer in China[4]. P16 as a cyclin dependent kinase(CDK) inhibitor, performs the function of tumor suppressor genes by down-regulating the activity CDK4 and CDK6 [5], which phosphorylate the retinoblastoma susceptible gene product, pRb. Hypophosphorylated form of pRb binds transcription factor E2F. Incompetent pRb-E2F complexes prevent the cell cycle G1-S transition, then play the role of tumor inhibition[6]. The p16/cyclin D1/cdk4/pRb cell cycle regulatory cascade is central to regulation of the G1-to-S phase transition. Once the cell is infected by HPV virus, oncoprotein E7 binds to pRb, the RB-E2F complex will be disrupted resulting in an increase in the level of free E2F, which will promote the cell cycle from G1 to S. In this way, the tumor cell proceeded, the sequestrated E2F will reflex upregulate p16 [7,8]. P16 is expressed high level in pulmonary small cell carcinoma (SCLC)[9] as well as cervical squamous intraepithelial lesion(HSIL) cases, and may help to distinguish HSIL and the triage of transient infection[10].

Forkhead box M1 (FOXM1) is a transcription factor of the Forkhead box (FOX) protein superfamily, plays a crucial part in the regulation of a diversity of cellular functions, including cell proliferation, cell survival, and immortalisation, which are essential for tumorigenesis, and is expressed only in proliferating cells [11,12]. In adult mammals, FoxM1 expression is detected mainly in the progenitor and regenerating tissues. The FoxM1 gene is a downstream target of E2F[13] and frequently overexpressed in lung cancer[14]. But the mechanism is not clearly claimed. Tartrate-resistant acid phosphatase 5(ACP5) plays a vital role in bone resorption and osteoclast differentiation, it promotes cell motility through the modulation of focal adhesion kinase phosphorylation[15]. Overexpression of ACP5 were detected in hepatocellular carcinoma and lung carcinoma, it was correlated with microvascular invasion, poor differentiation and higher tumor-node-metastasis stage, as well as lymph node status, tumor–node–metastasis (TNM) stage, and differentiation respectively[16]. It was reported that ACP5 is a direct transcriptional and functional target of FoxM1[15]. In our study, we speculated that FoxM1 upregulayed ACP5 is mediated by HPV16 E7-induced CDK6 activation mechanism by investigating the correlation among HPV16 E7, p16, CDK4/6, FoxM1 and ACP5. Further elucidate the molecular mechanism of lung cancer and provide a new target for the treatment.

PU-0547

发热伴血小板减少综合征血常规及凝血功能分析

刘文静[1]、魏红霞[2]、李雷[1]、夏永泉[1]、夏茂[1]、徐学静[1]、沈瀚[1]
1. 南京大学医学院附属鼓楼医院
2. 江苏省南京大学医学院附属鼓楼医院

目的 分析发热伴血小板减少综合征（severe fever with thrombocy-topenia syndrome，SFTS）患者与健康者血常规和凝血指标的差异，为临床诊断与治疗 SFTS 提供更多依据。
方法 收集本院 2020 年 4 月-2020 年 7 月 61 例 SFTS 患者和 61 例健康体检者的血常规和凝血五项结果，对其进行回顾性分析。
结果 SFTS 组血小板计数（PLT）65(43.5~81)×109/L 和白细胞计数（WBC）2.1(1.7~3.5)×109/L 显著低于对照组 192(167~223)×109/L、6.1(5.1~7.7)×109/L，P<0.05。SFTS 组的活化部分凝血活酶时间（APTT）、凝血酶时间（TT）、D 二聚体（DD）显著高于对照组。与治疗前相比，危重组治疗后的 PLT 减少，APTT、TT 延长（P<0.05），轻症组治疗后的 PLT、WBC 显著升高。
结论 PLT、WBC 减少以及 APTT、TT、DD 水平的升高提示可能有发热伴血小板减少综合征布尼亚病毒（SFTSV）感染，PLT 持续减少以及 APTT、TT 和 DD 持续升高提示患者预后不良，根据 PLT、APTT、TT、DD 指标的动态变化可以监控患者的病情进展。

PU-0548

长链非编码 RNA 在肺癌研究中的进展

张蕊
中国人民解放军北部战区总医院

肺癌是人类肿瘤发病率和死亡率最高的恶性肿瘤，筛选可用于早期诊断、疗效评估和预后判断的生物标记物成为了近年来的研究热点之一。随着分子生物学的长足发展，长链非编码 RNA 吸引了越来越多的关注。长链非编码 RNA 可以在转录水平、转录后水平以及表观遗传水平调控基因的表达，发挥促进肿瘤或抑制肿瘤的作用，参与了肺癌的发生、进展、转移和侵袭等生物学过程。本文总结了长链非编码 RNA 在肺癌中最新研究进展，旨在为肺癌的早期诊断、疗效评估和预后判断提供理论依据和新的策略方案。

PU-0549

呼吸道病原菌核酸检测技术在下呼吸道感染快速检测中的应用

刘婷婷
中国人民解放军北部战区总医院

目的 探讨呼吸道病原菌核酸检测技术在临床快速检测下呼吸道感染中的应用价值，为临床呼吸道感染的诊治提供参考依据。
方法 收集 2018 年 8 月～2019 年 10 月在北部战区总医院就诊的 900 例疑似下呼吸道感染者的合格痰标本, 采用恒温扩增芯片法对患者痰标本进行临床 13 种常见呼吸道病原菌的定性检测，并分析相关呼吸道病原菌感染的情况。
结果 在 900 例疑似下呼吸道感染的患者中, 核酸检测的阳性率为 49.3%，其中单一感染占 34%，混合感染占 15.3%。在单一病原菌感染中，流感嗜血杆菌与肺炎支原体的检出率最高，占所有患者的 6.1%和 5.4%。在混合病原菌感染中，主要是肺炎克雷伯菌合并其它感染，占所有患者的 6.6%。不同性别呼吸道病原菌总的核酸检出率之间比较，差异无统计学意义，但女性流感嗜血杆菌与铜绿

假单胞菌的核酸检出率明显高于男性，且差异具有统计学意义(χ^2=13.458，P <0.001）(χ^2=9.912，P =0.002）；而在混合病原菌感染中，男性核酸检出率明显高于女性(χ^2=6.817，P =0.009）。不同年龄组呼吸道病原菌总的核酸检出率之间的比较，差异无统计学意义；而肺炎支原体和流感嗜血杆菌在青年组检出率最高（χ^2=9.340，P =0.009）（χ^2=47.034，P <0.001）；嗜麦芽窄食单胞菌和铜绿假单胞菌在老年组检出率最高（χ^2=8.009，P =0.018）（χ^2=8.918，P =0.012）。

结论 采用恒温扩增芯片法对疑似下呼吸道感染者进行临床常见 13 种呼吸道病原菌核酸检测，具有较高检出率，且操作简便快速，有一定的临床应用价值。

PU-0550

变温和恒温核酸体外扩增技术在流感病毒检测中的应用及进展

王兰
中国人民解放军北部战区总医院

近年来，随着现代医疗技术的发展，一系列分子诊断技术以其灵敏度高、漏检率低、窗口检测时期较短的优点被不断被用于流感的检测，本文就 1991 年来至今出现的变温和恒温体外扩增技术的发展现状、应用场景、最新进展等方面的文献进行整理，探讨恒温体外扩增技术—RAA (Recombinase aided amplification）在流感诊断中的可行性及创新性为 RAA 技术在流感中的应用奠定基础。

PU-0551

MiR-186-5p can target ERK1/2 to reduce myocardial apoptosis in acute coronary syndrome

Wennan Nie
JINLING HOSPITAL

Coronary artery disease is the leading cause of morbidity and mortality in the world. Acute coronary syndrome (ACS), consisting of acute myocardial infarction and unstable angina, is the most dangerous and fatal form of coronary heart disease. MicroRNAs are a class of non-coding small RNA with a length of about 22 nucleotides encoded by endogenous genes, which are involved in the regulation of posttranscriptional gene expression. Growing evidences link microRNAs to the process of cardiovascular disease. Our research group previous study confirmed that miR-186-5p expression level in serum is up-regulated in ACS patients compared with those controls, and gradually decreased within 1 week after percutaneous coronary intervention (PCI). So that serum miR-186-5p may be a candidate for monitoring the clinical condition and assessing the prognosis of ACS patients. But little is known about its role in the process of ACS. So we aimed to investigate the underlying molecular mechanism of miR-186-5p participating in the pathological processes of myocardial ischemia. In this study, we first used three bioinformatic software to predict that ERK1/2 may be the target gene of miR-186-5p. Cell transfection, Western Blot and luciferase reporting assay were used to verify the relationship between miR-186-5p and ERK1/2. And then we established a rat model of AMI, and explored the possible source of miR-186-5p in serum by analyzing the changes and relationship of miR-186-5p content in myocardial tissue and peripheral blood serum of rats. At the same time, we established oxygen-glucose deprivation (OGD) model of cardiomyocyte (H9C2) to simulate myocardial ischemia and hypoxia in vitro. The source of miR-186-5p was further verified by analyzing the content of miR-186-5p in cells and cell medium. In addition, flow cytometry and cell proliferation experiments were used to analyze the specific mechanism of miR-186-5p in the process of glucose deprivation and hypoxia in cardiomyocyte.

PU-0552

lncRNA GAU1 induces GALNT8 overexpression and potentiates colorectal cancer progression

Xuemei Tang[1]、Haoyu Ruan[3]、Liu Dong[3]、Sihan Li[2]、Zhiyuan Wu[1]、Ming Guan[3]
1. Department of Laboratory Medicine, Huashan Hospital, Shanghai Medical College, Fudan University
2. Center for Pharmacogenetics, Department of Pharmaceutical Sciences, University of Pittsburgh
3. 复旦大学附属华山医院

Objective Colorectal cancer (CRC) ranked the third common type of cancer, adding up 10% of all cases. Genetic mutation in APC, TP53, and K-RAS have been intensively studied as major contributors to the tumorigenesis of CRC. However, the non-mutational alteration in CRC was less studied. Massive paralleled sequencing facilitated the genome-wide characterization of the human cancer transcriptome, and identified long non-coding RNA (lncRNA) expression as the most common transcriptional alteration in cancer. Our previous reports revealed that lncRNAs are extensively involved in the CRC development and drug resistance, indicating that more efforts should be encouraged to identify the CRC specific lncRNA expression, and to link the biological "operator" regulated these non-coding "regulators".
RNA-Seq technology empowered by sequence alignment and assembly provides a revolutionary approach for the prediction of full-length transcripts from both the intergenic "gene desert" and protein-coding loci. The MiTranscriptome database applied ab-initio assembly to 7,256 curated RNA-Seq libraries from tumor, normal tissue, and cell lines so as to provide an unbiased method for gene discovery. Here by incorporating this ab-initio assembly based human cancer transcriptome database and experimental validation, we identified a colorectal cancer-related lncRNA GAU1 from 12,382 cancer-associated lncRNA transcripts, and investigated the role of GAU1 in colorectal cancer.
Methods In the human cancer transcriptome library MiTranscriptome, through sample collection enrichment analysis, we identified lncRNAs related to colorectal cancer from 12,382 cancer-related lncRNA transcripts. With colorectal cancer samples collected from hospitals and pathological data/follow-up data of patients, lncRNA expression was analyzed in colorectal cancer and adjacent tissues by real-time fluorescence quantitative PCR. The expression level was measured and analyzed, and then correlation analysis was performed on lncRNA and pathological parameters and survival of patients. And the subcellular localization was used to identify cellular location of GAU1.Lentivirus overexpression method and small interfering RNA are used to regulate the expression of GAU1/GALNT8 in cell lines. PI staining was measured for cell cycle analysis.CCK-8 and colony formation test were used to study the proliferation of cell lines. TMA staining and Immunohistochemistry were used to analyze GALNT8 expression in CRC.
Results By incorporating this ab-initio assembly based human cancer transcriptome database and experimental validation, we identified a colorectal cancer-related lncRNA GAU1 from 12,382 cancer-associated lncRNA transcripts. In the human cancer transcriptome library MiTranscriptome, we identified GAU1 (percentile of overexpression = 99.75%) as one of the highest expressed lncRNAs in colorectal cancer by sample set enrichment analysis. Consistent with the database, GAU1 is highly expressed in cancerous tissues compared to normal tissues in clinical samples collected in hospitals. At the same time, high expression of GAU1 is associated with poor prognosis of patients. Experimental data show that GAU1 is highly correlated with GALNT8 expression in cancer tissue samples. In vitro, GAU1 can regulate GALNT8 expression at the RNA and protein levels.
In hospital samples and tissue microarrays, the expression of GALNT8 in cancer was much higher than that in normal tissues adjacent to the cancer, and the high expression of GALNT8 was related to the poor prognosis of colorectal cancer patients. In the samples collected in the hospital, the high expression of GALNT8 was associated with the large tumor volume. In vitro experiments showed that overexpression of GALNT8 significantly promoted the proliferation of cancer cell lines. Interfering with GALNT8 expression in GAU1 overexpressing cell lines can

inhibit tumor proliferation, which further proves that GAU1 can promote the proliferation of colorectal cancer by regulating GALNT8.
Conclusion We found a lncRNA GAU1 highly expressed in colorectal cancer, and its expression level can be used as a prognostic marker for colorectal cancer patients. In colorectal cancer, GAU1 can promote the proliferation of tumor cells by regulating the expression level of protein encoding gene GALNT8.

PU-0553

miR▪21 联合血清胱抑素 C 对肝硬化急性肾损伤的诊断价值

岳飞利[2]、赵敏[3]、王娇[2]、岳飞廷[1,4]
1. 雅安市人民医院超声科
2. 雅安市人民医院检验科
3. 雅安市人民医院肾内科
4. 雅安职业技术学 院附属医院超声科

目的 探讨血清 miR▪21 联合胱抑素 C（Cys C）检测在肝硬化急性肾损伤中的临床诊断价值。
方法 收集 2017 年 1 月-2018 年 1 月雅安市人民医院收治的 123 例肝硬化患者临床资料，将患者分为急性肾损伤组（n=61）和非急性肾损伤组（n=62），选取同时间段体检健康者（n=57）作为对照组。观察受试者血清 miR▪21、Cys C、血肌（SCr）、尿素氮（BUN）及肾小球滤过率（GFR）水平，采用受试者工作特征曲线（ROC）评价血清 miR▪21、Cys C 对肝硬化急性肾损伤诊断的预测价值。
结果 与对照组、非急性肾损伤组比较，急性肾损伤组患者血清 miR▪21、Cys C、BUN、SCr 水平显著升高，GFR 水平显著下降，差异均有统计学意义（P<0.05）；血清 miR▪21、Cys C、BUN、SCr 水平随病情加重而增高（P<0.05），GFR 随病情加重而下降（P<0.05）。Pearson 相关性分析结果显示，血清 miR▪21、Cys C、BUN、SCr 水平与 GFR 水平负相关（r=-0.710、-0.657、-0.545、-0.674，P<0.05）。ROC 曲线显示，血清 miR▪21、Cys C 水平及二者联合检测对肝硬化患者急性肾损伤诊断的曲线下面积分别为 0.824、0.867、0.947。
结论 血清 miR▪21、Cys C 联合检测对肝硬化急性肾损伤的诊断效能优于单独指标检测，对肝硬化继发急性肾损伤的早期诊断具有一定应用价值。

PU-0554

基于大数据挖掘肺鳞癌中血管生成拟态相关分子机制研究

王芃芃、董树昊
中国医科大学附属盛京医院

目的 肺鳞癌具有丰富的血管结构及肿瘤组织的血液供应，是其临床难以治愈的重要原因之一。本研究旨在深入分析并自检相关数据库锁定肺鳞癌生物学相关潜在基因；利用生物模式识别与数据挖掘等多种生物信息处理技术，构建肺鳞癌中 PECAM1/CDH5/ESAM 等促进血管生成和血管拟态相关基因转录网络，进而评价其作为肺鳞癌早期诊断分子靶标的临床价值，具有潜在的临床意义。
方法 于 TCGA 获得 LUSC 的基因组表达数据,鉴定具有显著性的协同一致的差异基因的表达模式，分析预测不同临床分期中的显著的差异基因协同表达模式。利用 cytoscape 软件筛选基因拓扑网络中重要的节点基因集。利用 GSEA，DAVID，ClueGo 等基因功能和通路富集分析预测节点基因集主要富集在 Notch 通路相关因子和癌症相关的血管生成基因（PECAM1, CDH5,ESAM 等），在显著的节点基因集中利用转录因子数据库识别血管生成基因（PECAM1, CDH5,ESAM 等）特定的区域之间结合构成基因调控网络。

结果 1.通过 TCGA 数据库 LUSC 数据集对肺鳞癌早期、晚期及全期进行 WGCNA 法分析获得相关的网络模块及差异基因。2.三组差异基因取交集后取前 300 degree 进行功能聚类分析，结果显示富集到血管生成通路上三个显著基因 PECAM1、CDH5、ESAM。
结论 基于大数据初步构建肺鳞癌中血管生成拟态分子调控网络，肺鳞癌中 PECAMI/CDH5/ESAM 差异表达能够影响血管生成拟态，参与肺鳞癌的发生过程，为肺鳞癌早期诊断提供了潜在的分子靶标。

PU-0555

hsa_circ_0001708 与 IKZF1 的比值对儿童 B-ALL 的诊断价值及其与 B-ALL 中 MICM 的相关性分析

付立芳[1]、何霞[1]、张航[2]、邹琳[2]
1. 雅安市人民医院检验科
2. 重庆医科大学附属儿童医院

目的 探讨 hsa_circ_0001708 与 IKZF1 的比值在儿童 B-ALL 骨髓细胞中的高低情况及临床意义。
方法 利用 T-A 克隆构建包含 hsa_circ_0001708 反向剪切位点的重组质粒，梯度稀释重组质粒作为标准品建立检测 hsa_circ_0001708 的绝对荧光定量 PCR 方法。收集 2016 年 1 月至 2019 年 1 月重庆医科大学附属儿童医院血液科住院的 159 例 B-ALL 患者骨髓标本为研究对象。对照组为同期住院的 19 例非恶性血液病患儿的骨髓标本。采用绝对荧光定量 PCR 方法检测 B-ALL 患儿和对照患儿骨髓细胞中 hsa_circ_0001708 和 IKZF1 的绝对拷贝数，按患者年龄，性别，外周血白细胞数，分子生物学、遗传学、免疫学特点，以及在随访期是否复发，随访期末是否生存等临床特点进行分组。回顾性分析 hsa_circ_0001708 和 IKZF1 的比值在各组中的表达情况以及与以上各因素的相关性。采用 t 检验、Pearson 相关性检验进行统计学分析。**结果** 建立了能精确定量 hsa_circ_0001708 拷贝数的绝对 RT-qPCR 方法。与非血液肿瘤对照患儿相比，hsa_circ_0001708 与 IKZF1 的比值在儿童 B-ALL 中升高（$p<0.0001$），ROC 曲线下面积为 0.7936。相关性分析结果提示，hsa_circ_0001708 与 IKZF1 的比值在外周血高白细胞数组，外周血高原始细胞数组，免疫分型 pre-B 组和细胞遗传学预后较差组中的比值升高，且差异具有统计学意义（$p<0.05$）。
结论 hsa_circ_0001708 与 IKZF1 的比值对儿童 B-ALL 有中等诊断价值且与 B-ALL 患儿的 MIC 分型密切相关。

PU-0556

Methodology and Application of PCR- Dipstick DNA Chromatography for eight Respiratory Bacterial Pathogens Multiple Detection

Wei Xiao、Liuyang Hu、Liangshan Hu、Yachao Yao、Donglin Cao
Guangdong Second Provincial General Hospital

Background Community-acquired pneumonia mainly caused by Acinetobacter baumanni,Klebsiella pneumoniae, Streptococcus pneumoniae, Haemophilus influenzae, Staphylococcusaureus, Pseudomonas aeruginosa, Mycoplasma pneumoniae and Chlamydia pneumoniae that leadto critical illness and death in developing countries. **Purpose** To establish a rapid, simple,sensitive, high-throughput and accurate point-of-care technique for respiratory bacterial pathogensdiagnose, especially co-infection of respiratory pathogens.

Methods Prospectively collected 182respiratory sputum specimens evaluated by PCR-dipstick DNA chromatography assay and werealso tested by quantitative reference culture.
Results The PCR-dipstick DNA chromatographyhybridization method can specifically identify and semiquantitative analysis the eight pathogenicbacteria within 40 minutes. The limit of detection ranged from 10 to 102 CFU/mL of singlebacterium by using PCR-dipstick DNA chromatography hybridization. Compared with the methodof bacterial culture which was regarded as the gold standard of clinical diagnosis, the positivepredictive value of PCR-dipstick DNA chromatography hybridization was 90.2% and the negativepredictive value was 100%.
Conclusion A PCR-dipstick DNA chromatography hybridizationassay was successfully established for the detection of eight respiratory tract bacterial pathogenssimultaneously and successful applied for clinical samples analysis, indicating that this disposabledevice has great potential in analysis of microbial composition associated with respiratoryinfections, as well as can be used for small laboratories and point-of-care diagnosis.

PU-0557

血浆 Septin9 基因甲基化检测与结直肠癌等消化道肿瘤相关性初探

董晓龙、白深林
中国医科大学附属第一医院

目的 在结直肠癌等消化道肿瘤细胞中，Septin9 基因异常甲基化时，其抑癌基因功能缺失导致肿瘤发生。肿瘤细胞释放游离核酸入血后，可在血浆中检测到 Septin9 基因。因此血浆 Septin9 基因甲基化检测能够成为结直肠癌等消化道肿瘤筛查的理想标志物。**目的** 探究血浆 Septin9 基因甲基化检测与结直肠癌等消化道肿瘤的相关性。
方法 收集门诊住院以及体检患者标本，金标准（镜检）做参比，进行 Septin9 甲基化检测，收集结果，通过计算灵敏度和特异性等来验证血浆 Septin9 基因甲基化检测与结直肠癌等消化道肿瘤筛查的相关性。
结果 在门诊住院患者的标本中，Septin9 检验灵敏度为 76.3%，特异性为 79.2%，诊断符合率：为 76.8%。Septin9 检测在体检人群中准确率为 84.5%。所有标本汇总结果灵敏度为 76.3%，特异性 82.9%，诊断符合率 78.9%。其中结直肠恶性肿瘤检测准确率 78.8%（89/113），符合预期结果；在肝细胞癌中检测准确率 75%（6/8）；在胆管恶性肿瘤中检测准确率 100%（2/2）；在胃恶性肿瘤中检测准确率 50%（2/4）。
结论 Septin9 甲基化作为一种新型无创肿瘤筛查手段，在结直肠癌中应用作用显著，此外，对于肝胆相关肿瘤可考虑应用。Septin9 甲基化检测拥有着优秀的特异性和敏感性，并且样本采集方便、患者依从性好、实验方法稳定从而更适合于临床应用。

PU-0558

山东省不同地区 HPV 感染情况调查及 HPV 新型重组疫苗建议

王青、董苹、彭德志、王佳佳、王丽云、张守都
济南金域医学检验中心有限公司

目的 统计山东省烟威地区与济南地区人乳头瘤病毒（HPV）感染和不同型别分布情况，为 HPV 疫苗接种选择提供参考，为重组不同型别疫苗提供建议。
方法 回顾 2018 年 1 月－2020 年 12 月烟威地区与济南地区送检我中心的 153974 例宫颈脱落细胞标本的 HPV 基因分型结果及分布情况，汇总不同价别疫苗型别 HPV 型别感染人群的比率，对结果间差异进行统计分析。

结果 纳入统计的烟威地区和济南地区的总标本量分别为 108305 例和 45669 例，其中烟威地区 HPV 阳性标本 25678 例（占 23.71%），济南地区 HPV 阳性标本 45669 例（占 20.70%），两地区阳性检出率间差异有统计学意义(χ^2 =165.0，P＜0.05)。不同分型结果如下：烟威和济南地区高危型、低危型、多重感染型分别检出 22066 和 8025、7346 和 2629、3734 和 1200 例，三种类型均存在差异(χ^2 值分别为 160.4、55.8 和 69.6，P 均＜0.05)。另外，两地区 23 种型别均被检出，烟威地区与济南地区 HPV 亚型分布前 5 位分别为 HPV16、HPV68、HPV18、HPV58、HPV59 和 HPV16、 HPV58、HPV52、HPV68、HPV18。现用二价、四价、九价疫苗涉及 HPV 型别的感染人群占比分别为 21.91%、30.64%和 71.95%。而重组九价型别，即 HPV16、HPV18、HPV59、HPV51、HPV45、HPV31、HPV68、HPV58、HPV52，感染人群占比为 83.36%，明显高于现用疫苗型别。

结论 烟威地区与济南地区人群 HPV 总感染率均较高且不同型别分布存在差异，因此早期筛查对 HPV 感染和预防宫颈病变有重要意义。另外，因接种疫苗可有效预防 HPV 感染，九价疫苗因型别覆盖广而广泛应用，疫苗生产厂家应定期对国内 HPV 感染亚型进行跟踪和分析，重组新型别的疫苗，更加有效的控制 HPV 感染。

PU-0559

耦合适配体酶和催化发夹自组装策略用于级联信号放大电化学发光生物传感

尹斐[1]、宁振强[1]、郑永军[1]、杨二利[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学中大医院临床检验医学中心
3. 东南大学危重症医学江苏省重点实验室

三磷酸腺苷（ATP）作为生命有机体中必不可少的分子之一，在许多酶活性和生物过程中起着重要作用，其水平与某些疾病和食品卫生有密切的关系。开发可靠、灵敏的 ATP 检测方法对临床诊断和食品安全至关重要[1-3]。本研究以 Ru(bpy)32+掺杂的二氧化硅纳米颗粒（RuSiO2）为电化学发光探针，二茂铁功能化的发夹 DNA（hairpin-Fc）为猝灭剂，将基于适配体酶和催化发夹自组装（CHA）的信号放大与电化学发光（ECL）耦合，制备了一种超灵敏的 ATP 生物传感器。在 ATP 和 Mg2+共存的情况下，核酸酶被激活并催化裂解 DNA 底物，释放大量的触发 DNA。Au@Fe3O4 促进了触发 DNA 的分离纯化，有效降低了背景信号。同时诱导 CHA 反应，即二茂铁（Fc）的附着也会导致触发 DNA 的释放和再循环，从而产生二次信号放大。适配体酶触发的 DNA 底物断裂和 CHA 反应都触发 DNA 的循环释放，使双信号得到高达 940 倍的显著增强。结果表明，制备的 ECL 生物传感器对 ATP 的检出限比以往报道的要低得多，为 0.054 pm，对加标血清样品和金黄色葡萄球菌的 ATP 检测具有较高的可靠性。本研究为核酸信号放大技术在细菌分析和临床诊断中的应用提供了新的思路。

PU-0560

WO3-x 纳米点在循环肿瘤细胞检测中的应用研究

尹斐[1]、潘登[1]、房正邹[1]、杨二利[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学中大医院临床检验医学中心
3. 东南大学危重症医学江苏省重点实验室

与 TPrA 相比，WO3-x 纳米点的毒性可忽略不计，同时在促进 ECL 反应方面保持了优异性能。因此，基于 WO3-x 纳米点作为 Ru(bpy)32+-ECL 体系共反应剂的优异性能和良好的生物相容性，

以循环肿瘤细胞 MCF-7 为模型靶点，以 WO3-x 纳米点为捕获探针构建了 ECL 细胞传感器。其中 Ru(bpy)32+被用作 ECL 发光剂，并且 Fe3O4@SiO2/Au/WO3-x 纳米点/适体作为捕获探针富集 MCF-7 靶细胞。由于 WO3-x 纳米点对 Ru(bpy)32+的 ECL 有明显的增强作用，因此电极上 Ru(bpy)32+的 ECL 增强可能与捕获 MCF-7 细胞的 Fe3O4@SiO2/Au/WO3-x 纳米点/适体有关。细胞传感器在 10 cells mL-1 到 5.0×105 cells mL-1 范围内 ECL 强度与 MCF-7 浓度对数之间呈现线性关系，检测限（LOD）为 3 cells mL-1，迄今为止性能最佳[1, 2]。细胞传感器的优良性能可归因于 WO3-x 纳米点对 Ru(bpy)32+的 ECL 信号增强。因此，以 WO3-x 纳米点为共反应剂制备的 ECL 细胞传感器在生物分析和临床诊断方面具有很大的应用潜力。

PU-0561

金属有机骨架-适配体分离检测肿瘤 EV 亚群新方法

冯俊杰
南方医科大学南方医院

目的 乳腺癌属于高发性肿瘤，对乳腺癌进行早期诊断、预后判断和疗效评估可改善患者预后和指导用药。而目前对于乳腺癌的早期诊断和疗效评估存在灵敏度低、有创、放射性等问题。因此，亟需寻求一种高效、无创或微创、便捷的早期诊断和疗效评估的方法。在这里，我们开发了一种金属有机骨架@适配体和基于胆固醇的 EV 荧光传感器（MOFs@Aptamer Cholesterol-based EV fluorosensor，MACHINE），以期快速分离和高敏检测肿瘤 EV 亚群。
方法 通过水热法合成 MOF 材料 UiO-66-NH2。在 UiO-66-NH2 表面修饰一段功能化的特异性核酸适配体（PO34--Spaser-PD-L1-Aptamer）PSPA,合成修饰的 MOF@PSPA 平台分离富集 1 表达 PD-L1 膜蛋白的特定 EV 亚群。接着，通过脂质探针识别和核酸等温快速检测法，对捕获的特定 EV 亚群进行荧光信号的放大检测。
结果 MACHEINE 检测的荧光强度和外泌体浓度呈拟合的非线性关系，范围在 2.50 × 105 - 1.00 ×1 08 （Particles/μL)，且相关系数为 0.998。检测限（LOD）为 9.40 × 104 Particles/μL；最后，验证了该平台具有良好的检测性能和临床诊断效能，可显著区分早期乳腺癌患者，健康查体和乳腺良性疾病患者的血浆标本。并且可对乳腺癌病人进行有效的分期诊断。
结论 EV 分离检测一体化平台 MACHEINE 可实现特异肿瘤 EV 的快速分离，同时基于脂质识别和 TaqMan 探针的荧光信号放大检测体系，可实现膜蛋白 PD-L1（+）EV 亚群的分离检测。通过临床实际样本 也验证了该平台的实际检测应用能力。我们相信，该方法可对肿瘤特异 EV 亚群进行高效分离和检测，对临床癌症患者提供有效的早期诊断和疗效评估的手段。

PU-0562

WO3-x 纳米点的合成及作为 ECL 共反应剂的性质研究

尹斐[1]、潘登[1]、房正邹[1]、杨二利[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学中大医院临床检验医学中心
3. 东南大学危重症医学江苏省重点实验室

WO3-x 纳米点的特殊性质引起了人们的广泛兴趣[1, 2]，但关于 WO3-x 纳米点制备的报道很少，而且大多数报道依赖于使用 WCl6 作为典型前体的自下而上的合成方法。[3, 4]因此，如何在不使用不稳定反应物、昂贵设备和复杂合成工艺的情况下合成高质量的 WO3-x 纳米点仍然是一个重大的挑战。在此，我们报道了简单但直接剥离大量 WS2 并进行温和后续化学转化来合成高度分散且富含氧空位的无配体 WO3-x 纳米点。首先，使用 DMF 作为溶剂，在室温下超声处理 WS2 块 4 h，导致 WS2 块剥离成几微米的纳米片。在密闭系统中将空气饱和的 WS2 纳米片分散液在 140 ℃下

进一步加热 6 h，离心得到淡黄色悬浮液。制备的纳米粒子在紫外光下呈蓝色荧光，在水中具有良好的单分散性和分散性。WO3-x 纳米点作为 Ru(bpy)32+电化学发光（ECL）的共反应剂出现，其 ECL 效率与众所周知的 Ru(bpy)32+/三丙胺（TPrA）体系相当，且与 TPrA 相比，WO3-x 纳米点的毒性降低了约 300 倍。这项工作为合成性能优异的 WO3-x 纳米点开辟了一条新的途径。

PU-0563

The identification of a 5-hydroxymethylation signature and its associated pathways in circulating cell-free DNA for the noninvasive detection of colorectal cancer

Hongwei Liu[1]、tao tang[2]、huixian zhang[1]、weiren ding[1]、peng zhou[1]、ying luo[1]、华欣 qi[1]、yanm liu[1]、yongixn liu[1]、meifang zhou[1]、weiguo yin[1]、jinduan lin[1]

1. Department of Laboratory Medicine, The Sixth Affiliated Hospital of Guangzhou Medical University, Qingyuan People's Hospital

2. 中山大学肿瘤防治中心（中山大学附属肿瘤医院、中山大学肿瘤研究所）

Background As a crucial epigenetic modification, DNA 5-hydroxymethylcytosine (5-hmC) plays an important role during colorectal cancer (CRC) carcinogenesis. However, the levels of 5 hmC-related genes in the circulating DNA of CRC remain largely unknown.

Methods and Results In this study, the GSE81314 dataset, in which a sensitive chemical labeling-based low-input shotgun sequencing approach was used to detect 5-hmC in circulating cell-free DNA (cfDNA), was downloaded from Gene Expression Omnibus (GEO). It includes 8 plasma samples from healthy people and 4 plasma samples from CRC patients. These data were used for differentially expressed gene (DEG) analysis and weighted gene coexpression network analysis (WGCNA). DEG analysis identified 19 upregulated and 9 downregulated 5-hmC-related genes. WGCNA showed that the pink, purple and brown modules, which contain 531 genes total, were significantly correlated with CRC (0.66 (p=0.02), 0.61 (p=0.04) and -0.59 (p=0.04), respectively). Gene Ontology (GO) and pathway enrichment analyses were performed to determine the functions and related pathways of the genes that were identified from the DEGs and WGCNA. Genes with a significant log fold change and in the highly correlated modules were input into GeneMANIA, a Cytoscape plugin. We constructed a protein-protein interaction (PPI) network, and 4 nodes (LCN2, LRG1, SP100, TACSTD2) played key roles in the network. We analyzed LCN2, LRG1, SP100 and TACSTD2 expression in the GEPIA database. Consistent with the 5-hmC levels in CRC patient plasma, LCN2, LRG1, SP100 and TACSTD2 were highly expressed in CRC tissue compared with controls in the GEPIA database.

Conclusion Our study suggests that the abnormality of cell free DNA hydroxylation in plasma may be associated with an abnormal immune response to CRC. Current research shows that the 5-hmC levels of LCN2, LRG1, SP100 and TACSTD2 in circulating cfDNA may be used as potential noninvasive markers for CRC.

PU-0564

LINC01094 promote epithelial-mesenchymal transition and metastasis of breast cancer by regulating miR-577/Rab25 axis

Ji Wu
Guangdong Provincial People's Hospital, Guangdong Academy of Medical Sciences

Background LNCRNAs can act as both tumor suppressor genes and oncogenes and participate in cell proliferation, metastasis, and apoptosis. LINC01094, as an identified lncRNA, has been reported in several cancers but not in breast cancer. This study aims to explore the effect of LINC01094 on breast cancer tumor epithelial-mesenchymal transition and metastasis and its underlying mechanism.
Methods Bioinformatics analysis was used to analyze the expression of LINC01094 in breast cancer patient with the TCGA database. MCF-7 cells MDA-MB-231 cells with upregulated LINC01094 and MDA-MB-231 cells with downregulated LINC01094 were established. Transwell invasion assays were used to examine the invasiveness of cells. Epithelial-mesenchymal transition (EMT) markers were evaluated by immunofluorescence and Western blot. CCK8, colony formation and wound healing assays were used to detect the proliferation and migration of breast cancer cell. Xenograft models were used to examine the effect of LINC01094 on BC metastasis. Luciferase report assays were employed to analyzed the relationship of LINC01094 and miR-577.
Results LINC01094 expression was significantly upregulated in BC tissues. Moreover, knockdown of LINC01094 strongly inhibited the invasiveness and EMT of BC cells in vitro. Knockdown of LINC01094 significantly affected breast cancer cells proliferation and migration both in vitro and in vivo. Luciferase report showed that MiR-577 was a directly target of LINC01094. And LINC01094 also affect the Rab25 which is a target of miR-577 in BC. Inhibited of miR-577 in si-LINC01094 BC cells decreased the levels of E-cadherin and increased the levels of Vimentin. However, an increase in Rab25 counteracted the invasive effect of si-LINC01094 in BC.
Conclusion In summary, our data indicated that LINC01094 promote epithelial-mesenchymal transition and metastasis of breast cancer by regulating miR-577/Rab25 axis, and LINC01094 may be a therapeutic target for breast cancer treatment.

PU-0565

PAI-1 基因多态性与动脉血栓的关系研究

胡馨元、郝思嘉、姜艳芳
吉林大学第一医院

目的 血栓栓塞分为动脉血栓栓塞和静脉血栓栓塞，遗传和获得性因素可影响遗传性血栓形成的表型表达。在深静脉血栓形成(DVT)患者中，PAI-1 过量可导致纤溶降低，且 PAI-1 基因 4G/5G 多态性可调节抑制剂 PAI-1 的表达。而 PAI-1 基因多态性与动脉血栓的关系目前结果并不一致。本研究目的 PAI-1 基因多态性是否与动脉血栓相关。
方法 选取吉林大学第一医院 2020 年 10 月至 2021 年 6 月发生动脉血管栓塞患者 56 例，健康对照 97 例。采用原位杂交技术进行 PAI-1 基因多态性检测。
结果 发生动脉血管栓塞的患者中 PAI-1 4G4G 基因型为 18 例，4G/5G 基因型为 28 例，5G/5G 基因型为 10 例。健康对照患者中 4G/4G 基因型为 33 例，4G/5G 基因型为 41 例，5G/5G 基因型为 24 例。采用卡方进行分析，动脉血栓组 4G 纯合子频率与健康对照组 4G 纯合子频率无显著性差异

（P=0.548），动脉血栓组 4G/4G,4G/5G,5G/5G 多态性频率与健康对照组也无显著性差异（P=0.137）

结论 PAI-1 基因多态性与动脉血栓关联无统计学意义，可能与样本量较小相关，可能需要增加样本量研究

PU-0566

利用环介导等温扩增技术检测鸟分枝杆菌

蒋栋能
陆军军医大学第二附属医院（新桥医院）

目的 鸟分枝杆菌与结核分枝杆菌有许多相近的生物学特性，对其进行鉴别诊断很有必要。本文拟用环介导等温扩增技术（LAMP），设计一种快速检测鸟分枝杆菌的方法，以期能应用于鸟分枝杆菌临床检测。

方法 通过基因比对与引物设计，设计针对鸟分枝杆菌的 LAMP 引物和检测试剂；对临床标本进行 DNA 预提取、LAMP 扩增及检测；结合临床表现，对方法的主要性能进行初步评价。

结果 通过基因比对与引物设计，设计出一套针对鸟分枝杆菌的 LAMP 引物，含 F3、B3、FIP、BIP 引物、扩增及检测等一套试剂。对临床标本进行了 DNA 提取、LAMP 扩增和检测。与临床表现对照发现，该方法灵敏度高（检测下限约为 1x10^2CFU/ml）、特异性强、与临床表现完全符合，而且比常规的培养方法快捷、简便，非常适合鸟分枝杆菌的临床检测。

结论 本试验设计出的针对鸟分枝杆菌的 LAMP 检测方法，该检测方法具有良好的特异性和较高的灵敏度，操作流程快捷、简便，能够用于鸟分枝杆菌的临床鉴别诊断。

PU-0567

围产期妇女 B 族链球菌感染的易感因素探究

张宇
重庆市人民医院三院院区

目的 探讨围产期妇女 B 族链球菌易感因素,旨在辅助围产期妇女及新生儿 GBS 感染预防和控制工作。

方法 选择 600 例孕妇，于围产期产前检查时或早产孕妇在入院时取阴道下段 1/3 处分泌物进行实时荧光定量-聚合酶链反应（polymerase chain reaction，PCR）GBS DNA 检测，并对其年龄进行分组。同时对其中住院的 316 例分别按有无甲状腺疾病、糖尿病、细菌性阴道炎、高血压分别分为研究组 1、2、3、4（各研究组仅含对应的一种高危因素）无以上四种基础疾病的为对照组共 159 例。

结果 600 例的 4 个年龄组：＜25 岁（阳性率 0.026）、26-30 岁（阳性率 0.04）、31-35 岁（阳性率 0.058）＞35 岁（阳性率 0.06）研究组 1、2、3、4 的 GBS 阳性率分别是 0.33、0.14、0.15、0.14，对照组 2 阳性率是 0.03。采用两独立样本 χ2 检验进行统计学处理。探究围产期妇女 B 族链球菌易感因素（年龄，糖尿病，甲状腺，细菌性阴道炎，高血压）。

结论 甲状腺异常、妊娠期糖尿病、细菌性阴道炎、高血压阳性率均明显高于对照组，阳性率具有统计学差异 (P < 0. 01）。高血压、妊娠期糖尿病、妊娠期阴道炎和妊娠期高血压是 B 族链球菌感染的危险因素。

PU-0568

Deficiency of NARFL increases transcription of NADPH oxidases and ROS production impairing the function of endothelial cells

柳洪周
成都市第三人民医院

Background NARFL is involved in cytosolic iron-sulfur (Fe–S) protein biogenesis and cellular defense against oxidative stress.
Methods and Results It showed that NARFL deficiency resulted in upregulated expressions of Nox2, Nox4, and p47phox and increased ROSROSlevels in endothelial cells. Nox2 knockdown reduced the upregulated ROS levels and improved endothelial dysfunctions caused by NARFL deficiency. ChIP experiments revealed that NARFL knockdown increased the expressions of RNA polymerase II and Histone acetylase (H3K9ac) at the promoter sites of Nox2 and Nox4.
Conclusion NARFL knockdown induced the transcriptional activation of Nox2 and Nox4, which resulted in increased ROS levels and impaired endothelial function.

PU-0569

Circulating exosomal microRNAs as metastasis-related molecular predictors in non-small cell lung cancer

Zhijun Zhang[1]、Xianrang Song[2]
1. Taian city central Hospital
2. 山东省肿瘤医院

Background The high mortality rates of non-small cell lung cancer (NSCLC) are primarily due to metastases. The aim of this study was to investigate the clinical significance of serum exosomal miRNA-212-5p and miRNA-651-3p as metastasis-related molecular predictors in NSCLC.
Methods Serum exosomes of 226 healthy donors and 233 NSCLC patients (M0: n=173 and M1: n=60) were isolated by ultracentrifugation. Characterization of exosomes were conducted by qNano, TEM, and western immunoblotting. Partly differently expressed miRNAs were demonstrated by RT-PCR. Receiver operating characteristic (ROC) analysis were used to evaluate the diagnostic power.
Results Compared with healthy controls, the expression levels of ExmiR-212-5p and ExmiR-651-3p were decreased apparently in NSCLC patients ($p < 0.0001$ and $p < 0.0001$, respectively). The AUC were 0.699 and 0.745 according to ROC curves. Through the combined analysis of ExmiR-212-5p and ExmiR-651-3p, the AUC could be improved to 0.751. Furthermore, both of these two ExmiRs could distinguished metastatic NSCLC patients (n=60) with non-metastatic NSCLC patients (n=173) (both $p < 0.0001$). From ROC curves, the AUC were 0.682 and 0.674, respectively. The combined analysis could improve the AUC to 0.696. The diagnostic power of these two ExmiRs combined by traditional blood biomarkers CEA and CYFRA21-1 could be raised to 0.862.
Conclusion This study demonstrated that serum exosomal miRNAs are promising non-invasive molecular predictors for metastatic NSCLC.

PU-0570

In situ tumor-triggered subcellular precise delivery of multi-drugs for enhanced chemo-photothermal-starvation combination antitumor therapy

Xinglu Jiang[1]、Guoqiu Wu[2]
1. Medical School, Southeast University
2. 东南大学附属中大医院检验科

Rationale Drug combination therapy for cancer treatment exerts a more potent antitumor effect. The targeted delivery and release of multiple drugs in a patient's body thus presents a more effective treatment approach, warranting further research.
Methods Two antitumor drugs (ICG: indocyanine green and THP: pirarubicin) were successfully screened to sequentially trigger self-assembling peptides (P60) to produce bacteria-sized particles (500-1000 nm, P60-ICG-THP). First, after mixing equal amount of P60 and ICG, trace amount of water (the mass ratio between P60 and water: 100:1) was used to trigger their assembly into P60-ICG. Subsequently, the assembly of P60-ICG and THP was further triggered by ultrasound treatment to produce P60-ICG-THP.
Results P60-ICG-THP constituted a cluster of several nanoparticles (50-100 nm) and possessed a negative charge. Owing to its size and charge characteristics, P60-ICG-THP could remain outside the cell membrane, avoiding the phagocytic clearance of blood and normal tissue cells in vivo. However, after localizing in the tumor, the size and charge switches of P60-ICG-THP, rapidly triggered by the low pH of the tumor microenvironment, caused P60-ICG-THP to segregate into two parts: (i) positively charged nanoparticles with a size of approximately 50 nm, and (ii) negatively charged particles of an uneven size. The former, mainly carrying THP (chemotherapeutic agent), could immediately cross the cell membrane and deliver pirarubicin into the nucleus of tumor cells. The latter, carrying ICG (used for photothermal therapy), could also enter the cell via the endocytosis pathway or accumulate in tumor blood vessels to selectively block the supply of nutrients and oxygen (cancer starvation). Both these particles could avoid the rapid excretion of ICG in the liver and were conducive to accumulation in the tumor tissue for photothermal therapy.
Conclusion Our drug delivery system not only achieves the precise subcellular delivery of two anticancer drugs due to their size and charge switches in the tumor site, but also provides a new strategy to combine chemotherapy, photothermal therapy, and cancer starvation therapy for the development of a highly efficient antitumor therapeutic regimen.

PU-0571

Serum exosomal miRNAs as efficient diagnostic biomarkers for the early-stage non-small cell lung cancer

Zhijun Zhang[1]、Xianrang Song[2]
1. Taian city central Hospital
2. 山东省肿瘤医院

Dysregulated exosomal microRNAs (ExmiRNAs) are potential diagnostic and predicting prognosis biomarkers for human cancers. However, insufficient research has been conducted on early-stage non-small lung cancer (NSCLC). The aim of the present study was to evaluate two ExmiRNAs in the serum of NSCLC patients as a useful tool for the diagnosis of early-stage NSCLC. Ultracentrifugation was employed to isolate exosomes from the serum of healthy donors and NSCLC patients, followed by characterization with qNano, TEM, and western immunoblotting. Differentially expressed exosomal miRNAs were determined by microarrays. RT-qPCR was used

to verify the differentially expressed miRNAs using a large set of specimens (healthy donors, n = 282 and NSCLC patients, n=276, 0 and I stage: n=104). The diagnostic values were evaluated by receiver operating characteristic (ROC) analysis. Herein, we proved that the expression of ExmiR-20b-5p and ExmiR-3187-5p was significantly decreased in NSCLC patients compared with that of the healthy donors ($p < 0.0001$ and $p < 0.0001$, respectively). Based on the ROC curves, the Area under the ROC Curve (AUC) was determined to be 0.818 and 0.690 for ExmiR-20b-5p and ExmiR-3187-5p, respectively. When these two ExmiRs were combined, the AUC increased to 0.848. When CEA and Cysa21-1 were combined, the AUC was further improved to 0.905 and 0.894, respectively. Additionally, both ExmiR-20b-5p and ExmiR-3187-5p could be used to distinguish early stage NSCLC (0 and I stage) from healthy controls ($p < 0.0001$ and $p < 0.0001$, respectively). ROC curves showed that the AUCs were 0.810 and 0.673, respectively. Combination of ExmiR-20b-5p and ExmiR-3187-5p enhanced the AUC to 0.838. When continue to combine CEA and Cysa21-1, the AUC would improve to 0.930 and 0.928, respectively. In conclusion, serum exosomal miR-20b-5p and miR-3187-5p were effective, non-invasive biomarkers for the diagnosis of early-stage NSCLC, and the effects were further improved when the ExmiRNAs were combined.

PU-0572

To evaluate the value of varies molecular detection techniques in diagnosing mosaic polysome 9p

Sufen Zhang
Zhuhai Maternity and Child Healthcare Hospital

Polysomy 9p has been characterized by clinical features of intrauterine growth restriction (IUGR), developmental delay, ventriculomegaly, Dandye-Walker malformation, facial dysmorphism, congenital heart defects, the severity of phenotype associated withpolysomy 9p is influenced by the size of the chromosomeinvolved, the degree of mosaicism, and the presence of tissuemosaicism.Mosaicism for polysomy 9p is a challenging issue interms of prenatal diagnosis as the abnormality may not be detectable in amniotic fluid and fetal ultrasound assessment can be normal throughout the pregnancy. Identifyingthe mosaic level and the size of polysomy9pinvolvedaccurately is important for guiding genetic counseling in prenatal diagnosis. In this study, different molecular detection techniques were used to diagnose 2 cases of mosaic polysomy 9pand the advantages and limitations of varies techniques were compared to evaluate the application value in diagnosis process. According to the noninvasive prenatal testing (NIPT) results in the first trimester,chromosome 9 was duplicated to varying degrees in both two cases.The karyotype of the case 1 was 47,Xn,+der(9)del(9)(q21q34)dup(9)(p12p24)[10]/46,Xn[90], of which the chr9 was 2.2 copies in cultured amniocytes, the mosaic level were 2.43 and2.5 copies with chromosomal microarray analysis (CMA) and fluorescence in situ hybridisation (FISH) in uncultured amniocytes, respectively. The case 2 presented a complex mosaic containing 3 cell lines, the karyotype was 47,Xn,+9[82]/47,Xn,+del(9)(q13qter)[14]/46,Xn[4] with 2.96 copies of 9p and 2.82 copies of 9q in cultured amniocytes. The CMA results of case 2 prompted the status of mosaic of multiple cell lines in chromosomal 9 and the smoothsignal diagram showed 9p with 3copies and 9q with 2.5 copies in uncultured amniocytes. These two cases all provided evidence for the discrepancy in themosaic level of 9pbetween uncultured and cultured amniocytes or varies molecular detection techniques. Different detection technologies have their own advantages and limitations in the prenatal diagnosis of polysomy 9p.It is necessary to choose the detection **Methods** according to the needs and also combined use of molecular diagnostic techniques may be could complement each other and increase the detection rate and accuracyof chr9 mosaicism.

PU-0573

珠海市新生儿 G6PD 缺乏筛查结果分析

张素粉
珠海市妇幼保健院

目的 探讨珠海市新生儿葡萄糖 6-磷酸脱氢酶（glucose 6-phosphate dehydrogenase, G6PD）缺乏、新生儿高胆红素血症发病情况及该地区 G6PD 缺乏基因突变热点。
方法 收集 2015 年 1 月至 2020 年 7 月于珠海市妇幼保健院出生的 42480 例新生儿脐血行 G6PD 酶活性检测，同时回顾性分析同期内 8450 例因新生儿高胆红素血症入院新生儿 G6PD 酶活性及基因位点突变类型。
结果 42480 例新生儿 G6PD 缺乏阳性率 6.39%，女性阳性率高于男性，差异有统计学意义(c^2=54.91，P＜0.001)，8450 例新生儿发生高胆红素血症，发病率为 19.89%，男性发病率高于女性，差异有统计学意义(c^2=6.89，P=0.0086)，G6PD 缺乏所致新生儿高胆红素血症发病率 14.47%，男性明显高于女性，差异有统计学意义(c^2=18.93，P＜0.0001)。男性 G6PD 缺乏患儿残余酶活性以低于 10%为主，女性 G6PD 携带者则以 60%-100%残余酶活性为主，差异有统计学意义(c^2=840.1，P＜0.0001)，本地区热点突变基因型以 c.1388G>A、c.1376G>T、c. 95A>G、871G>A 为主，合并约占比 90.96%。
结论 珠海市新生儿 G6PD 缺乏发病率及 G6PD 缺乏所致新生儿高胆红素血症发病率高且均有性别差异，本地区热点突变基因型以 c.1388G>A、c.1376G>T、c. 95A>G、871G>A 为主。

PU-0574

姜黄素对多发性骨髓瘤 RPMI-8226 细胞 RASSF2A 表达及启动子区甲基化的影响

陈佳琦
丽水市人民医院

目的 探讨姜黄素(Curcumin，Cur) 联合甲基化抑制剂 5 氮杂 2′脱氧胞苷(5 AzaCdR)对多发性骨髓瘤(multiple myeloma，MM) 细胞抑癌基因 RASSF2A 的去甲基化作用。
方法 利用 RPMI-8226 细胞系建立 MM 细胞模型，分别加入一定浓度姜黄素组、5 AzaCdR 组以及姜黄素联合 5 AzaCdR 组(联合用药组)处理。观察各组 MM 细胞的生长情况，采用甲基化特异性 PCR 法(MSP)检测各组 MM 细胞 RASSF2A 的甲基化水平，采用荧光定量 PCR 法和蛋白质印迹法检测 RASSF2A mRNA 和蛋白的表达量。
结果 实验组 RASSF2A 甲基化程度为 35.95±2.59（%）均低于对照组 44.16±4.40（%），RASSF2A mRNA 及蛋白表达均显著高于对照组，其中联合用药组为 0.607±0.076 又显著强于 2 个单独用药组，姜黄素组 0.240±0.046、5 AzaCdR 组 0.433±0.038，差异均有统计学意义(P<0.05)。
结论 姜黄素联合 5 AzaCdR 用药可增强 5 AzaCdR 对 MM 细胞抑癌基因 RASSF2A 的去甲基化作用

PU-0575

肿瘤转移的分子机制及靶向干预研究新进展

贾如雪[1,2]、李卓林[1,2]、吴亚婷[1,2]、张胜行[1,2]、王水良[1,2]
1. 厦门大学附属东方医院福建省适配体技术重点实验室
2. 中国人民解放军联勤保障部队第九〇〇医院检验科

转移是肿瘤历经多阶段恶性进展直至终末期后极具特征性改变的病理过程，它涉及一系列序贯发生的细胞恶性生物学改变：通常始于肿瘤在原发部位的局部浸润和侵袭性生长；继而，部分肿瘤细胞经上皮-间质转化（EMT）后获得游离原发部位并侵入邻近的血管或淋巴管道的能力；侵入循环系统的肿瘤细胞可长期处于休眠状态，一旦条件成熟即可从脉管腔穿出并侵入远端靶器官实质组织形成微转移灶，微转移灶再进一步克隆性生长并最终发展成肉眼可见的转移瘤。肿瘤转移是导致病人综合治疗效果差和生存预后不佳的最主要原因；大量统计数据表明，约 90%以上肿瘤患者系死于远端靶器官转移。鉴于转移过程的每一阶段均有赖于肿瘤细胞表型的特征性改变，而这种表型改变又与肿瘤细胞本身遗传和表观遗传改变以及微环境中诸多因素的综合调控密切相关。本综述概要介绍了恶性肿瘤转移多步骤过程中所涉的分子调控新机制以及基于新分子机制而开发的肿瘤转移靶向干预新措施等方面的当前研究进展，主要包括：（1）肿瘤转移起始阶段 EMT 表型改变的转录水平、表观遗传修饰和转录后水平的调控；（2）肿瘤转移中间过程包括肿瘤细胞侵入循环系统及在其中存活等方面的调控；（3）肿瘤转移终末阶段即预转移微环境的构建及转移瘤的克隆性生长的调控；（4）基于新分子机制的肿瘤转移靶向干预新措施的开发。同时，就未来肿瘤转移研究相关的新技术和新方向作一简单的展望。

PU-0576

Tumor-Derived Exosomal miRNAs as Diagnostic Biomarkers in Non-Small Cell Lung Cancer

Zhijun Zhang[1,2]、shuping zhao[1]、Xianrang Song[2]
1. Taian city central Hospital
2. 山东省肿瘤医院

Background Delayed diagnosis is the main obstacle to improve prognosis of non-smallcell lung cancer (NSCLC). Novel biomarkers for the diagnosis of NSCLC are urgentlyneeded. This study aimed to identify the specific exosomal miRNAs with diagnostic andprognostic potential in NSCLC patients.
Materials and Methods Transmission electron microscopy (TEM), qNano and westernblots were used to characterize the exosomes isolated from the serum of NSCLC patients(n=330) and healthy donors (n=312) by ultracentrifugation. Exosomal miRNAs wereprofiled by miRNA microarrays and verified by quantitative PCR (qPCR). The diagnosticaccuracy was determined by receiver operating characteristic (ROC) analysis.
Results A total of differential 22 miRNAs were screened out based on $P < 0.05$ and folddifference>2.0 by miRNA microarrays, among which, exosomal miR-5684 and miR-125b-5p were significantly down-regulated in NSCLC patients compared to healthy donors,processing favorable diagnostic efficiency for (early) NSCLC. Importantly, the exosomalmiR-125b-5p were associated with metastasis ($P < 0.0001$), chemotherapeutic effect($P=0.007$) and survival ($P=0.008$).
Conclusion Exosomal miR-5684 and miR-125b-5p levels are significantly downregulated in NSCLC patients, and serve as the promising diagnostic and prognosticbiomarkers for NSCLC

PU-0577

Role of NRG-1 signaling in regulating tumor biology

Ruxue Jia[1,2]、Zhuolin Li[1,2]、Yating Wu[1,2]、Shenghang Zhang[1,2]、Shuiliang Wang[1,2]
1. 厦门大学附属东方医院福建省适配体技术重点实验室
2. 中国人民解放军联勤保障部队第九〇〇医院检验科

Over the past two decades, tumor has increasingly been recognized as organ that results from the co-evolution of malignant cells and their direct environment. The tumor microenvironment (TME) encompasses extracellular matrix (ECM) and various non-transformed cells including fibroblasts, immune infiltrates, and vascular vessels recruited from nearby local or distant tissues. Through providing matrices, cytokines, growth factors, as well as vascular networks for nutrient and waste exchange, the TME plays an essential role in tumor initiation, progression, invasion, metastasis, and resistance to therapy. Cumulative studies have demonstrated that the cross-talk between cancer cells and their TME involves reciprocal juxtacrine and paracrine signaling pathways. Among them, neuregulin (NRG) signaling has long been recognized as an important player in regulating tumor progression. Neuregulins are members of the largest subclass of growth factors of the epidermal growth factor family, mediate a myriad of cellular functions including survival, proliferation, and differentiation in normal tissues through binding to receptor tyrosine kinases of the ErbB family. However, aberrant neuregulin signaling in the tumor microenvironment is increasingly recognized as a key player in initiation and malignant progression of human cancers. In this review, we summarize the progress in the role of neuregulin signaling in the hallmarks of cancer, including cancer initiation and development, metastasis, as well as therapeutic resistance. Moreover, role of neuregulin signaling in the regulation of tumor microenvironment and targeting of neuregulin signaling in cancer from the therapeutic perspective are also briefly discussed.

PU-0578

一例 46,X,+mar[33]/45,X[67]羊水标本的 STRs 位点分析

龙若庭、陈淑霞、林萃、罗华玉、李恋湘、李淑娜
珠海市妇幼保健院

目的 通过对相关 STR 位点检测，判断 X 染色体上基因的拷贝数，对一例核型为 46,X,+mar[33]/45,X[67]的羊水标本进行遗传分析。
方法 采用达瑞生物、瑞典 Devyser 紧凑型 V3 非整倍体检测试剂盒和中德美联 AGCU19X-STRs 多重荧光扩增试剂盒扩增羊水细胞 DNA，检测 X 染色体上各 STR 相关位点，分析 X 染色体上基因的拷贝数，并用传统方法进行细胞核型分析。
结果 经检测，有 2 个 X 染色体 STR 位点扩增出两个不平衡峰，其余 X 染色体 STR 位点均为单峰。AGCU19X-STRs 检测的 19 个 X-STRs 中有 14 个位点为单峰，DXS10159、DXS10164、DXS10162、DXS10079、DXS10074 等 5 个 X-STRs 为双峰。细胞染色体核型分析结果为 46,X,+mar[33]/45,X[67]。
结论 羊水细胞丢失一条 X 染色体，此条染色体仅残留着丝粒至 q13 区域，形成 46,X,+mar 与 45,X 两种核型的嵌合，联合应用 STRs 分析可对嵌合型染色体数目异常提供诊断支持，为临床咨询提供线索。

PU-0579

造血干细胞移植术后 BK 病毒感染与免疫重塑之间的关联研究

刘胜男[1]、廖建枫[1]、冯舒欣[2]、郑有为[1]、黄革[1]、顾兵[1]
1. 广东省人民医院
2. 广州医科大学

目的 分析造血干细胞移植术（HSCT）后 BK 病毒感染与各淋巴细胞亚群免疫重塑之间的关联。
方法 回顾性分析 2014 年 1 月至 2020 年 8 月广东省人民医院血液科及骨髓移植科行造血干细胞移植术 214 例患者的临床资料，采用实时荧光定量 PCR 技术检测患者尿液或血液中的 BKV-DNA，采用流式细胞术检测患者行移植术后 1 年内（3、6、9、12 月）外周血中淋巴细胞亚群的动态变化。根据 BKV-DNA 定量结果分为 BKV 感染组（>2000copies/mL）和 BKV 未感染组（<2000copies/mL），比较分析 HSCT 后 BKV 感染与淋巴细胞亚群重塑之间的关联。
结果 214 例患者中，HSCT 后有 145 例患者出现 BKV 感染，首发感染多发生在 30d 内（66.3%）。术后 3 个月内 CD3+T 细胞、CD4+CD28+T 细胞、CD8+CD28+T 细胞、CD3+CD16+CD56+NK 细胞恢复迅速，中位重建时间接近 3 个月，CD19+B 细胞中位重建时间接近 6 个月，CD3+CD4+和 CD3+CD8+T 细胞恢复速度慢，12 个月内未恢复正常水平。未感染组的整体重塑时间（225d）略长于感染组（196d）。术后 3 月内 BKV 感染组 CD19+B、CD3+CD4+T 细胞低于未感染组，而 CD3+CD8+T 细胞水平高于未感染组（P＜0.05）；在术后第 6、9 个月 BKV 感染组 CD3+T 细胞和 CD3+CD8+T 细胞高于未感染组，而 CD3+CD8+T 细胞水平低于未感染组（P＜0.05）；移植后 12 月时 BKV 感染组 CD3+T 细胞水平高于未感染组，而 CD19+B 细胞水平低于未感染组（P＜0.05）。P＜0.05，差异具有统计学意义。HSCT 后 NK 细胞、CD19+CD5+和 CD19+CD5-B 细胞免疫重建快组的感染率显著高于慢组（P＜0.05）。
结论 BKV 感染患者存在免疫重建受损和延迟，免疫重建快慢对 BKV 感染情况有影响。

PU-0580

Increased expression of GINS2, Bcl-2, CHK2 and their correlation in endometrial carcinoma

Xi Zhang
Department of Clinical Laboratory, Caner Hospital of Yunnan Province, the Third Affiliated Hospital of Kunming Medical University

Endometrial cancer (EC)is a group of epithelial malignant tumors that occurs in the endometrium. Although a great deal of studies has shown that GINS2 is abnormally expressed in many solid tumors, and plays a key role in cell proliferation and apoptosis, there is no relevant report on its expression and correlation with Bcl-2 apoptosis regulator, and checkpoint kinase 2(CHK2) in endometrial cancer. The purpose is to study the expression level of GINS2 in EC from gene and protein level, and detect the expression and location of GINS2, CHK2 and Bcl-2 in EC tissues by immunohistochemistry, and analyse the correlation between GINS2 with CHK2 and Bcl-2. The results showed that the gene and protein levels of GINS2 in malignant group were significantly higher than those in benign group and normal control group. GINS2 protein was mainly located in the nucleus of EC tissues, CHK2 was mainly expressed in the nucleus, while Bcl-2 protein was mainly expressed in the cytoplasm. The positive rates of GINS2, CHK2, and Bcl-2 in malignant group were significantly higher than those in benign group and normal control group. In addition, the expression of GINS2 was positively correlated with the expression of CHK2 and Bcl-2 in EC tissues, suggesting that GINS2 could promote the development of EC by regulating the expression of CHK2 and Bcl-2.

PU-0581

Identification of a potential autophagy-related prognostic signature involved in colorectal cancer using bioinformatics analysis

Xi Zhang
Department of Clinical Laboratory, Caner Hospital of Yunnan Province, the Third Affiliated Hospital of Kunming Medical University

Background Autophagy is an extremely conservative degradation mode in eukaryotes, aberrant activation or deregulation of autophagy promotes tumorigenesis in various preclinical models of cancer. Although overall survival (OS) rates for colorectal cancer (CRC) has significantly improved in recent years, however, the exact predictive value of autophagy for the prognosis of CRC has not yet been recognized. The purpose of the present academic work was to identify an autophagy-related prognostic signature in CRC and their potential mechanisms.
Material/Methods The gene expression profiles (HTSeq-FPKM) of patients with CRC and normal controls were available from The Cancer Genome Atlas (TCGA) datasets. Differentially expressed autophagy-related genes (ARGs) were further screened out, and then gene ontology (GO) and Kyoto Encyclopedia of Gene and Genome (KEGG) analysis were performed to establish functions of the identified ARGs in CRC. At the same time, Search Tool for the Retrieval Interacting Genes (STRING) 11.0 was used to construct protein-protein interaction (PPI) network and screen relative hub genes. Besides, ARGs and clinic/pathological parameters involved in the OS of CRC were confirmed by Cox proportional hazards regression models. Based on the independent prognostic ARGs, a prognosis risk score of individual patients was calculated using the regression coefficients and responding expression value. Moreover, we also analyzed the correlation between clinic/pathological parameters with autophagy-related gene expression.
Results A total of 206 ARGs were significantly related with CRC, of which 36 ARGs were differentially expressed in CRC. Most of ARGs were mostly involved in biological process including autophagy, utilizing autophagic mechanism, and responding to oxygen levels. Univariate and multivariate Cox proportional hazards regression analyses revealed that 6 ARGs (PELP1, RAB7A, MAP1LC3C, ULK3, WIPI2, and DAPK1) had independent prognostic significance for the OS of CRC. Next, the survival rate of high-risk patients was significantly lower than that of low-risk patients. Besides, T stage and risk score have independent prognostic significance for CRC patients. What's more, PELP1, ULK3, MAP1LC3C, RAB7A, WIPI2 gene and risk score were significantly correlated with clinic/pathological parameters.
Conclusions Our research suggests that six genes autophagy-related signature could serve as an independent prognostic indicator, and may become a new target for the prevention and treatment of CRC.

PU-0582

一种新型的用于外泌体 microRNA-181 检测的分步聚合发卡催化装置

张如意、胡秀梅、郑磊
南方医科大学南方医院

目的 为了更好的检测体液中的外泌体 microRNA，我们设计了一种基于分步聚合的发卡催化组装生物传感器。
方法 外泌体 miR-181 作为激发剂，可以诱导分步聚合催化步骤（SP-CHA），从而生成众多 T 字型的产物，该产物长度不一，可聚集在电极表面。

结果 这种分步聚合的发卡催化传感器所产生的产物可以提高检测信噪比，且它的检测线性范围为 10fM 至 100nM 之间，最低检测限位 7.94fM。另外，这种方法可以鉴别区分冠脉患者及正常健康人的外泌体 miR-181 水平，且结果与 qRT-PCR 的结果相仿。其对冠心病的诊断效能高，曲线下面积可达 0.9867。
结论 SP-CHA 对外泌体 miR-181 检测具有较高的灵敏度及特异度，具有心血管疾病床旁检测试剂开发的前景。

PU-0583

乙型肝炎病毒 C 区基因突变试剂盒临床检测性能评价

刘军莉、刘玲、王玲玲、赵燕、李顺子
山东大学第二医院

目的 HBV 在机体的免疫力压力和药物治疗影响下可出现变异，其中 C 区基因突变在慢乙肝中较为常见。本研究拟对国产乙型肝炎病毒(HBV) C 区基因突变检测试剂盒的检测性能进行评价。
方法 以罗氏公司的乙型肝炎病毒突变检测试剂盒作为对比（以下简称罗氏试剂），以北京鑫诺美迪基因检测技术有限公司的 B 乙型肝炎病毒(HBV) C 区基因突变检测试剂盒为考核试剂（以下简称鑫诺试剂），收集 2018 年 2 月至 10 月山东大学第二医院 569 例临床血清标本，通过荧光 PCR-毛细管电泳测序法，对 HBV C 区的前 C/BCP 区进行突变检测。
结果 569 例临床样本的检测中，鑫诺试剂的灵敏度、特异度分别为 94.50%、96.67%；罗氏试剂的灵敏度、特异度分别为 95.50%、97.17%。Kappa 值为 0.95，U 值为 31.16，P<0.01，两者具有较好的一致性。鑫诺的灵敏度和特异度与罗氏试剂无显著性差异（P＞0.05）。
结论 鑫诺基因的乙型肝炎病毒(HBV) C 区基因突变检测试剂盒的灵敏度高、特异度好。通过检测 HBV C 区耐药基因突变点有助于帮助选择初治药物，判断治疗的效果，及时发现基因型耐药，从而采取预防措施，避免发生病毒反弹，利于临床及时调整用药方案，从而辅助临床诊断和指导临床用药，制定个体化抗病毒治疗方案。

PU-0584

HLA-Ⅰ类基因的多态性与肾小球膜增生性肾小球肾炎的相关性

刘军莉、刘玲、王玲玲、赵燕、程娜娜、赵敬杰
山东大学第二医院

目的 人类白细胞抗原（human leukocyte antigen, HLA）就是一组密切连锁的基因群。HLA 可以作为某些疾病的遗传标志，也可以将 HLA 抗原多态性用于群体关联分析和家系连锁分析，从而推断出人类患某种疾病的相对风险率。本研究旨在探讨 HLA-Ⅰ类基因多态性与肾小球系膜增殖性肾小球肾炎（MsPGN）的相关性，找到相关的基因。
方法 以山东大学第二医院十年间 2641 例 MsPGN 患者为病例组，中国造血干细胞捐献者 6542 例健康志愿捐献者为对照组，采用聚合酶链反应序列特异性引物方法（SSP-PCR）对两组的 HLA 基因多态性进行基因频率（GF）和 odds ratio（OR）分析比较，找出 MsPGN 的易感基因和保护性基因，并对携带易感基因的患者进行预后评价。
结果 HLA 等位基因 A * 23，A * 25，B * 15，B * 40 和 B * 53 的 GF 在 MsPGN 患者中比对照组高（P＜0.05），认为这些等位基为 MsPGN 的易感基因（SSG）。携带这些易感基因与没有携带的患者预后没有差异（P＞0.05）。MsPGN 患者 HLA-A * 32，A * 33，B * 50，B * 58，B * 60，B * 71 的 GF 比对照组低（P＜0.05）。另外，等位基因 A * 20，A * 22，A * 35，A * 36，A * 38，B * 21，B * 73 和 B * 78 在 MsPGN 患者中没有表达，这些基因可被认为是 MsPGN 的保护基因。

讨论 HLA - Ⅰ类基因多态性与 MsPGN 存在相关性，研究发现了 MsPGN 相关的易感基因和保护性基因，为 MsPGN 的临床治疗、预后及预防措施提供了理论依据。

PU-0585

在肾细胞癌中川穹嗪对 MICA-NKG2D 信号通路的影响

刘军莉、刘玲、赵燕、王玲玲、赵敬杰
山东大学第二医院

目的 肾细胞癌是起源于肾实质泌尿小管上皮系统的恶性肿瘤，MICA 与 NKG2D 配受体间信号途径可在肿瘤的免疫监视中具有重要作用，川穹嗪对肿瘤细胞有生长抑制作用。本研究拟揭示人透明细胞（ccRCC）中川穹嗪（TMP）通过 MICA 与 NKG2D 信号途径的抗癌效果及机制。
方法 采用 MTT、流式细胞术、划痕和肿瘤侵袭实验检测 TMP 对 ccRCC 细胞的活力、增殖、凋亡、侵袭和迁移功能的影响；并通过逆转录聚合酶链反应（RT-PCR）、蛋白质印迹和免疫荧光方法检测 TMP 作用后对 MICA-NKG2D 信号通路的影响。
结果 MTT 实验表明 TMP 显著抑制 ccRCC 细胞的活力（抑制率 75.63%，P＜0.05）；流式细胞检测 TMP 可抑制 ccRCC 细胞增殖，促进凋亡；划痕和肿瘤侵袭实验均表明 TMP 可显著抑制 ccRCC 细胞侵袭和迁移功能，并上调 NKG2D 配体（NKG2DLs）MHC Ⅰ类链相关分子 A 和 B（MICA / B）和 E-钙粘蛋白的表达，下调波形蛋白和纤连蛋白的表达。
结论 TMP 对 ccRCC 细胞的抑制可能是通过抑制 NKG2D 相关信号通路，从而进一步抑制上皮间质转化（EMT），抑制肾细胞癌的生长。 NKG2D 与其配体的结合可激活 NK 细胞，为临床有效防治 RCC 提供药物新靶点。

PU-0586

LncRNA AC105942.1 downregulates hnRNPA2/B1 to attenuate vascular smooth muscle cells proliferation

Ruyi Zhang 、Xiumei Hu、Lei Zheng
Southern Hospital, Southern Medical University

Objectives The abnormal proliferation of vascular smooth muscle cells (VSMCs) is crucial in the atherosclerosis. Although long noncoding RNAs (lncRNAs) are implicated in a variety of diseases, their roles in activation of VSMCs proliferation and vascular disorder diseases are not well understood. In addition, heterogeneous nuclear ribonucleoprotein A2/B1 (hnRNPA2/B1) was reported to participate in lncRNAs-mediated function. Herein, we propose to investigate the role of lncRNA AC105942.1 and hnRNPA2/B1 in pathological VSMCs proliferation and the possible mechanisms in vitro.
Methods qRT-PCR analysis and immunohistochemistry staining were used to measure the expression of lncRNA AC105942.1 and hnRNPA2/B1 in atherosclerotic plaques and normal artery tissues. CCK-8 assay and EdU staining were used to evaluate the proliferation ability of VSMCs. The expression of hnRNPA2/B1, CDK4 and p27 were measured by qRT-PCR and western blot.
Results We have identifified that lncRNA AC105942.1 was downregulated and hnRNPA2/B1 was upregulated in atherosclerotic plaques compared with normal artery tissues. Enhanced lncRNA AC105942.1 could noticeably inhibit Ang II-induced VSMCs proliferation. Further investigation suggested that lncRNA AC105942.1 could downregulate the expression of hnRNPA2/B1 and then regulate the level of CDK4 and p27.
ConclusionsTaken together, our study indicated that lncRNA AC105942.1 downregulated hnRNPA2B1 to protect against the atherosclerosis by suppressing VSMCs proliferation. LncRNA

AC105942.1 and hnRNPA2/B1 could represent potential therapeutic and diagnostic targets to atherosclerosis-related diseases.

PU-0587

基于催化发夹自组装偶联免疫荧光试纸条检测 HCV 核酸

苏菲娅
东南大学医学院

目的 HCV 的感染已成为全球公共卫生问题，我国为高危地区，将近 80％的感染者发展成慢性肝炎并引起肝硬化。由于 HCV 的疫苗尚未研发，因此丙型肝炎病毒的检测对 HCV 感染防治具有重要意义应用催化发夹自组装（CHA）偶联免疫荧光试纸条检测 HCV 核酸，为 CHA 技术应用于现场检测探究新技术,早日实现 HCV 现场即使检测（POCT）。
方法 根据 CHA 原理设计发夹探针 H1 和 H2，当目标链存在的情况下，通过吉布斯自由能的驱动，H1、H2 可形成双链杂交产物，随后将反应产物滴加于试纸条加样区后，核酸双链会和修饰有抗生物素的荧光纳米微球结合；当核酸产物进入试纸条检测区后，双链复合物被抗地高辛抗体捕获，从而在试纸条上形成一条荧光线，目的是通过对目标核酸的检测信号进行二次放大并检测其荧光值。通过聚丙烯凝胶电泳以验证 CHA 反应，根据设计系统优化实验条件，设计不匹配探针验证所设计探针的特异性，并通过检测稀释的模板以验证系统的灵敏度。
结果 荧光检测值与 PAGE 电泳相当，以证实反应可行性，优化的试验条件系统表明 CHA 反应在 37℃，30 分钟具有较强特异性，反应较稳定：HCV 核酸灵敏性最低可检测至 1fmol/L。
结论 发夹自组装偶联免疫荧光试纸条检测 HCV 核酸具有较好的特异性和灵敏度，操作简便，具有在现场或基层医院的应用前景。

PU-0588

Nitidine chloride suppresses epithelial-mesenchymal transition and stem cell-like properties in glioblastoma by regulating JAK2/STAT3 signaling

Mingbo Jia、Ying Wang、Yingxue Guo、Pengyue Yu、Ying Sun、Yanke Song、Liyan Zhao
Jilin University Second Hospital

Background Based on the poor prognosis of glioma, new drugs that suppress the rapid progression and aggressive growth of glioma are urgently needed. Nitidine chloride (NC), an active ingredient extracted from plants, has been shown to inhibit the proliferation of a variety of tumor cells and epithelial–mesenchymal transition (EMT). The present study investigated the inhibitory effects of NC on the EMT process in glioma cells and the formation of gliospheres.
Methods Transforming growth factor (TGF)-β1 was used to induce EMT in the U87 and LN18 glioma cell lines. Scratch and invasion assays were used to analyze the migration and invasion abilities of treated cells flow cytometry was used to detect the promotion of glioma cell apoptosis treatment with NC, the second generation of gliosphere formation test, Limiting dilution assay were used to test cancer stem cell self-renewal ability, Western blotting was used to explore the expression of markers related to epithelial mesenchymal transformation, apoptotic proteins, stem cell-related markers, and JAK2/STAT3 signaling pathway proteins.
Results U87 and LN18 glioma cells showed increased migration and invasion after induction of EMT, and these effects were inhibited by NC in a concentration-dependent manner. NC treatment also promoted glioma cell apoptosis, and altered expression of EMT markers after NC treatment indicated the suppression of EMT in glioma cells. Moreover, NC inhibited the EMT-induced enhanced self-renewal capacity of gliospheres as well as the EMT-induced expression of

stem cell markers. Western blotting results indicated that these effects of NC were achieved via the alteration of Janus kinase 2 (JAK2)/Signal Transducer and Activator of Transcription 3 (STAT3) signaling.
Conclusion NC can inhibit the EMT process and glioma stem cell characteristics of glioma cells via modulation of JAK2/STAT3 signaling, suggesting that NC may be a potential anti-glioma drug.

PU-0589

448 例无创产前基因检测(NIPT)高风险胎儿回顾性分析

陈艺升、王菲菲、陆娄恺奕、倪颖华、王强、应春妹
复旦大学附属妇产科医院

目的 探讨无创产前基因检测技术(NIPT) 在胎儿染色体异常筛查中的应用价值。
方法 收集复旦大学附属妇产科医院 2017 年 5 月-2021 年 1 月 NIPT 筛查高风险孕妇 448 例，采用胎儿染色体核型分析和染色体微阵列分析技术(CMA)进行产前诊断，回顾性分析结果，随访妊娠结局。
结果 448 例孕妇产前诊断结果显示 NIPT 筛查对 21、18、13 三体(T21、T18、T13)、性染色体非整倍体(SCAs)、染色体微缺失/微重复综合症的阳性预测值(PPV)分别为 86.0%（86/107）、79.5%（35/44）、54.5%（12/22）、39.5%（75/190）和 41.7%（30/72）。研究表明，NIPT 对高龄孕妇的预测性能优于年轻孕妇（$p<0.05$），而基于特定年龄段（间隔 5 年）的比较分析，T21、T18、T13 和 SCA 的阳性预测值没有明显的上升趋势，这表明无论产妇年龄大小，NIPT 高风险都应被重视。此外，45,X、47,XXY、47,XXX 和 47,XYY 的终止妊娠率分别为 100%（11/11）、91.7%（22/24）、20%（3/15）和 7.1%（1/14），这表明孕妇对胎儿不同 SCA 型别的妊娠决策有很大差异。
结论 NIPT 能有效筛查高危人群, 显著降低侵入性诊断比例，但对 NIPT 高风险的孕妇仍需要胎儿染色体核型分析进行诊断。

PU-0590

新生儿坏死性小肠结肠炎及自发性肠穿孔调控枢纽基因筛选

郭彬瀚、江咏梅
四川大学华西第二医院

目的 新生儿坏死性小肠结肠炎（Necrotizing enterocolitis, NEC）及新生儿自发性肠穿孔（Spontaneous intestinal perforation, SIP）是新生儿期常见胃肠道急症，在早产儿中具有较高发病率及死亡率，但由于该疾病发病原因多样化，因此其确切分子机制尚不明确。本研究通过生物信息学挖掘并分析了两种疾病的潜在分子机制。
方法 通过 NCBI-GEO 公共数据库下载 GSE46619 基因表达芯片数据，使用 R 语言软件对原始数据进行整理，清洗，过滤；应用加权基因共表达网络分析算法构建基因共表达网络，分别识别与 NEC 和 SIP 发病相关的基因模块，利用可视化分析工具筛选枢纽基因，并针对枢纽基因进行基因功能富集分析及互作网络构建。
结果 基于共表达网络分析发现，某些枢纽基因确实与 NEC 和 SIP 两种疾病的发生发展存在显著的关联。基因功能分析提示，与细胞黏附功能相关的一些信号通路诸如细胞黏附分子（Cell adhesion molecules, CAMs）、补体途径与凝血级联等与 NEC 发病具有较高相关性；同时互作网络的分析结果表明，JAK3、KNG1、MMRN1 等枢纽基因在该病的潜在发病分子机制中扮演重要的角色。此外，我们发现补体途径与凝血级联可能也参与了 SIP 的发病过程，但其中还涉及到了血小板激活相

关信号通路。基于此，基因与基因之间互作分析表明，FGA、FGB 以及 FGG 可能作为核心基因在 SIP 发病过程中起了决定性作用。
结论 该研究为严重威胁新生儿健康的消化道疾病 NEC 和 SIP 发病的潜在分子机制提供了新的研究方向及治疗思路。

PU-0591

MAZ 诱导 lncRNA AC005355.2 调控 Ezrin 促进 Luminal 乳腺癌进展的作用机制研究

孟玥
广东省人民医院

Luminal 乳腺癌是女性最常见的恶性肿瘤，其特异的 lncRNA 可能在该肿瘤进展中起到重要作用，但功能机制尚不清楚。我们前期发现 lncRNA AC005355.2 在 Luminal 乳腺癌中特异高表达；MYC 相关的锌指蛋白（MAZ）可结合其启动子区刺激其表达；CHIRP-MS 筛选确认 lncRNA AC005355.2 可与膜细胞骨架蛋白（Ezrin）结合，数据库预测三者表达呈正相关。故我们推测：MAZ 诱导 lncRNA AC005355.2 转录，并促使其在 Luminal 乳腺癌中特异高表达，而 lncRNA AC005355.2 可直接结合 Ezrin 蛋白调控活化下游信号通路从而促进 Luminal 乳腺癌进展。本项目拟从分子、细胞、组织水平全面阐明 lncRNA AC005355.2 在 Luminal 乳腺癌中的功能及上下游调控机制，为研发 Luminal 乳腺癌新型生物标志物及靶向药物提供新方向。

PU-0592

Bioinformatics-based Analysis Identifies Potential Key Genes in the Pathogenesis of Membranous Nephropathy

Yue Zhang、xiaosong Qin
Shengjing Hospital of China Medical

Background Membranous nephropathy (MN) is one of the most common causes of nephrotic syndrome in adults, however, the studies of the mechanisms of pathogenesis in membranous nephropathy are far from enough. Research on the pathogenesis of MN will help clinicians to better prevent the occurrence and delay disease progression.
Methods Data from GSE73953 were downloaded from Gene Expression Omnibus (GEO) datasets to identify differentially expressed genes (DEGs) between MN patients (MNs) and healthy controls (HCs),Then, enrichment analysis included Gene Set Enrichment Analysis (GSEA), FunRich analysis, Gene Ontology (GO) analysis, Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways analysis, and Protein-Protein Interaction (PPI) network analyses were applied. Finally, circRNAs-miRNAs-mRNAs networks were constructed and the key genes related to MN were identified.
Results A total of 1096 mRNAs were differentially expressed between the MNs and NCs. Enrichment analysis showed multiple roles of the DEGs enriched in MN, such as signaling events mediated by HDAC Class III and p53 signaling pathway. Fourteen circRNAs seemed potentially involved in MN via regulation of HDAC3 and HIST1H2AJ expression.
Conclusions Our study found that several mRNAs-miRNAs-circRNAs interaction chains play a crucial part in the pathogenesis of MN, and several mRNA-related molecules including hsa-miR-362-5p, hsa-miR-760, and 14 circRNAs were identified that may be helpful to further understand the mechanisms of MN and provide novel ideas for the development of drug targets.

PU-0593

早期糖尿病肾病病变的生物信息学研究

张悦[1]、司徒成彪[2]
1. 中国医科大学附属盛京医院
2. 中国医科大学

目的 利用生物信息学手段筛选出与人类早期糖尿病肾病（Early Diabetic Nephropathy，EDN）病变差异表达基因,早期糖尿病肾病潜在调控机制,为早期糖尿病肾病的诊断和治疗提供帮助。
方法 在基因表达公共数据库 GEO 中筛选出与人类 EDN 相关的基因芯片数据集（GSE111154），使用 GEO 数据库页面在线提供的 GEO2R 工具筛选出实验组和对照组中符合条件的差异表达基因，使用 DAVID 数据库对已得到的差异基因进行 GO 功能富集分析和 KEGG 信号通路进行进一步的分析
结果 1、利用生物信息学手段筛选获得符合要求的人类 EDN 差异表达相关基因共 123 个，其中包含上调基因 103 个，下调基因 20 个。
2、利用 GO 富集分析，在分子功能的 GO 分析中差异基因主要表现为：结合蛋白、细胞外基质、丝氨酸型内肽酶活性、单加氧酶活性；在细胞组分的 GO 分析中，差异基因主要表现为：细胞外泌体、质膜、细胞外基质；在生物学过程的 GO 分析中差异基因主要表现为：细胞外基质、蛋白水解、免疫反应、补体激活、细胞黏附、血小板脱粒。
3、利用 KEGG 通路分析，差异基因主要表现在：补体和凝血通路、金黄色葡萄球菌感染、药物代谢-细胞色素 P450、酪氨酸代谢、在癌症中的蛋白聚糖、疟疾、细胞色素 P450 代谢异种生物、百日咳、系统性红斑狼疮、PI3K-Akt 信号通路。
结论 1、本次研究获得人类 EDN 差异表达相关基因共 123 个，其中包含上调基因 103 个，下调基因 20 个。
2、 本次研究探明多种信号通路与 EDN 有关，其中包括 PI3K-Akt 信号通路、补体和凝血通路、免疫反应、细胞外基质等等。讨论着重研究了 PI3K-Akt 经典信号通路与 EDN 的相关性。

PU-0594

探究他汀对结核合并Ⅱ型糖尿病患者预后的影响

程宇慧、王义莉、周妍冰、赖红历、吕梦媛、应斌武
四川大学华西医院

目的 探究他汀药物对于结核合并Ⅱ型糖尿病患者（TB-T2DM）预后的影响，并构建预后的预测模型，为临床治疗 TB-T2DM 患者提供可靠依据。
方法 收集 2013 年 12 月至 2019 年 9 月就诊于华西医院的患者的临床病例数据，以 2 月末痰菌阴转率（2SS）、复发、死亡为预后指标。对其进行单多因素分析，探究 TB-T2DM 的危险因素，使用 Logistic 回归、弹性网络、KNN、SVM、RVM 五种模型构建预后的预测模型，并计算相对危险度和相应的 95%置信区间。计算敏感性、特异度及曲线下面积以评估模型效能，$p \leq 0.05$ 时认为差异有统计学差异。
结果 共纳入 927 名患者，其中使用他汀 463 例，未使用他汀 464 例。分析发现是否使用他汀药物为 2SS 独立危险因素（OR=0.603，95%CI：0.463-0.784，P=0.000），吸烟、体重减轻、HbA1c、肺部结节/钙化灶、血糖、肌酐也是危险因素。基于上述结果，成功构建 TB-T2DM 患者预后的五种预后预测模型。训练集中，弹性网络模型 AUC 为 0.663（敏感度：68.4%，特异度：56.1%）；测试集中，弹性网络模型 AUC 为 0.672（敏感度：72.6%，特异度：53.3%）。
结论 他汀药物是 TB-T2DM 患者预后的独立保护因子，服用他汀有助于提高预后。在临床诊治中，可使用弹性网络构建的模型预测 TB-T2DM 患者预后，辅助指导临床医师用药。

PU-0595

河北石家庄地区 HBV 基因分型及耐药突变分析

杨莉、侯军良、冯爱东、刘腾飞、许怡、张海丛
河北省石家庄市第五医院

目的 探讨石家庄地区经各种核苷(酸)类似物治疗的 CHB 患者 HBV 基因型、基因耐药突变位点分布和基因耐药情况进行分析。
方法 选择 2014 年 10 月-2019 年 3 月在石家庄市第五医院就诊的 CHB 患者 1157 例，收集患者基本资料，并采用基因测序技术对患者基因分型和基因耐药突变位点进行检测，对检测结果进行统计分析。
结果 石家庄地区 CHB 患者的基因分型以 C 型为主，少量为 B 型，在不同的 HBV 基因型在不同性别间的分布差异无统计学意义
($\chi2=0.676$, $P>0.05$),不同年龄间的分布差异有统计学意义($\chi2=11.797$, $P<0.05$). 不同的 HBV 基因分型在 14 种不同耐药模式检出率、基因耐药位点突变率及 4 种核苷（酸）类似物的耐药情况分布差异无统计学意义(P>0. 05). C 型患者数随基因突变位点增多而占比不断增高，B 型患者数随基因突变位点增多而占比不断降低,；在对 LAM、ADV、ETV 及 LDT 四种核苷(酸)类似物耐药的 11 种模式中，对 LAM、LDT 及 ETV 均发生耐药的患者占比达到 54.8%；其次是对 ADV 耐药的患者，占比达 21.6%；位于第三位的是对四种药物均耐药的患者占比达 12%。
结论 石家庄地区 CHB 患者感染的基因分型以 C 型为主，男性多见，且发生的基因耐药突变以多重耐药为主。

PU-0596

血清外泌体 SIRT4 在结直肠癌中的表达及临床意义

李宁
山东大学第二医院

目的 SIRT4 作为疾病调控的关键分子备受关注。在这项研究中，我们拟确定 SIRT4 在结直肠癌（CRC）患者肿瘤组织及血清中的表达水平并明确其临床诊断价值。
方法 收集 80 对 CRC 患者的癌组织及癌旁正常组织，通过实时荧光定量 PCR 的方法，检测 SIRT4 在组织中的表达水平，分析其与患者临床病理信息的关系。收集 125 例 CRC 患者的血清，同时纳入 125 例健康对照血清，提取血清外泌体，并对外泌体中的 SIRT4 水平进行检测，通过受试者工作特征(ROC)曲线分析 SIRT4 的诊断价值。
结果 SIRT4 在 CRC 组织和血清外泌体中表达显著降低，此外血清外泌体 ROC 曲线分析发现，其 ROC 曲线下面积（AUC）为 0.841，灵敏度为 84.4％，特异性为 76％（95％ CI = 0.770-0.898），具有较高的临床诊断价值。
结论 SIRT4 有望成为 CRC 诊断和预后的生物标志物

PU-0597

Long Noncoding RNA ADAMTS9-AS1 Suppresses Colorectal Cancer by Inhibiting the Wnt/β-catenin Signaling Pathway, and is a Potential Diagnostic Biomarker

Ning Li
The second hostipal of Shandong university

Long noncoding RNAs (lncRNAs) have come out as critical molecular regulators of human tumorigenesis. In this study, we sought to identify and functionally characterize lncRNAs as potential mediators of colorectal cancer progression.We screened and identified a novel lncRNA, ADAMTS9-AS1, which was significantly decreased in colorectal cancer tissues and was correlated with clinical outcomes of patients according to The Cancer Genome Atlas (TCGA) database. In addition, ADAMTS9-AS1 regulated cell proliferation and migration both in vitro and in vivo. Bioinformatics analysis revealed that overexpression of lncRNA-ADAMTS9-AS1 preferentially affected genes that were linked to proliferation and migration. Mechanistically, we found that ADAMTS9-AS1 obviously suppressed β-catenin, suggesting that Wnt signaling pathway participates in ADAMTS9-AS1-mediated gene transcriptional regulation in the suppression of colorectal tumorigenesis. Finally, we found that exosomal ADAMTS9-AS1 could serve as a diagnostic biomarker for colorectal cancer with AUC = 0.835 and 95% confidence interval = 0.777-0.911. Our data demonstrated that ADAMTS9-AS1 might play important roles in colorectal cancer by suppressing oncogenesis. Targeting ADAMTS9-AS1 may have potential clinical applications in colorectal cancer prognosis and treatment as an ideal therapeutic target. Finally, exosomal lncRNA-ADAMTS9-AS1 is a promising, novel diagnostic biomarker for colorectal cancer.

PU-0598

血清外泌体 lncRNA AL109955.1 在结直肠癌中的表达及临床意义

李宁
山东大学第二医院

目的 长链非编码 RNA（lncRNA）作为疾病调控的关键分子备受关注。在这项研究中，我们拟确定 lncRNA AL109955.1 在结直肠癌（CRC）患者肿瘤组织及血清中的表达水平并明确其临床诊断价值。
方法 收集 80 对 CRC 患者的癌组织及癌旁正常组织，通过实时荧光定量 PCR 的方法，检测 lncRNA AL109955.1 在组织中的表达水平，分析其与患者临床病理信息的关系。收集 125 例 CRC 患者的血清，同时纳入 125 例健康对照血清，提取血清外泌体，并对外泌体中的 lncRNA AL109955.1 水平进行检测，通过受试者工作特征(ROC)曲线分析血清外泌体 AL109955.1 的诊断价值。
结果 AL109955.1 在 CRC 组织和血清外泌体中表达显著降低，此外血清外泌体 ROC 曲线分析发现，其 ROC 曲线下面积（AUC）为 0.841，灵敏度为 84.4%，特异性为 76%（95% CI = 0.770-0.898），具有较高的临床诊断价值。
结论 血清外泌体 AL109955.1 有望成为 CRC 诊断和预后的生物标志物。

PU-0599

鼠尾消化实验的传统“经典法”和新技术“快速法”的对比及探讨

刘寒、曾超、陈璐、王君安、王欣、凌昉钦
上海市第一人民医院嘉定分院

目的 以小鼠为模型的模式动物在现代科学研究中发挥着重要的作用。目前对于小鼠的遗传学改造是扩充小鼠品系的重要途径，这也要求对小鼠的基因鉴定应该朝着更快和更准确的方向发展。传统的鼠尾粗 DNA 提取依赖蛋白酶 K，消化时间在 5 个小时左右。本文提出了一种不依赖蛋白酶 K 的快速鼠尾粗 DNA 提取法，并探讨其实验过程及其准确性。
方法 经典鼠尾消化过程，需要在弱碱体系中，经过蛋白酶 K 的水解消化和乙醇洗涤获得粗 DNA 浸出液。我们提出了新的鼠尾粗 DNA 提取的方法，即在强碱、高温环境下，破坏组织裂解细胞，使其核酸片段释放出来，获得粗 DNA 浸出液。该方法不依赖蛋白酶 K 的生物消化过程，是组织和细胞在高温强碱反应下，自然将染色质成分释放出来；在经过酸性缓冲液中和之后，获得可以进行 PCR 反应的鼠尾粗 DNA 提取液。
结果 经过对比我们发现，“快速法”大大缩短了反应时间。“经典法”还是需要 5 个小时左右的时间，但是“快速法”仅仅需要 20 分钟的时间。“经典法”消化得更为彻底，在经过“快速法”消化后，EP 管底部仍有鼠尾组织。根据两者的实验原理分析，“经典法”获得的是双链粗 DNA，而“快速法”获得的是单链 DNA。由于 DNA 的本质是反向平行的双脱氧核糖核苷酸链，所以双链和单链有等效的遗传信息。对两者获得的粗 DNA 浸出液进行 PCR 反应的结果显示，两者都可对敲除式基因和敲入式基因进行基因鉴定，结果同样稳定可靠，表现为两者条带同样清晰，亮度相似。
结论 通过实践，发现使用“快速法”鼠尾消化可以缩短小鼠基因鉴定所需时间，同时可减少蛋白酶 K 的使用，并且进一步简化实验操作步骤，有一定的应用和推广前景。

PU-0600

Identification of two Novel HIV-1 Second-generation Recombinant Forms (CRF01_AE/CRF07_BC) in Hebei, China

Ying Xing、Erhei Dai
the Fifth Hospital of Shijiazhuang

Homosexual contact is one of the main transmission routes of HIV-1 epidemic in Hebei, China. Several subtypes of HIV are prevalent simultaneously in the population, which always leads to the emergency of unique recombinant forms (URFs). Here we reported two new URFs from two HIV-1 positive subjects (HB030009, HB030021) infected through homosexual contact route in Hebei, China. RNA was extracted from 200μL of plasma samples. Then, extracted RNA was reversely transcribed into cDNA . The NFLG was obtained in two halves by nested PCR amplification. The positive products were detected by 1% agarose gel electrophoresis, then purified and sequenced with a series of special primers. phylogenetic tree and subregion tree were constructed using the Neighbor-joining method based on Kimura two-parameter model with 1000 bootstrap replications by Mega6. Recombination breakpoints were identified by Recombination Identification Program and jpHMM. Phylogenetic and recombinant analyses based on the near full-Length genome (NFLG) of the two URFs both revealed the two URFs are the second generation of recombinant strains originated from CRF01_AE and CRF07_BC. The CRF01_AE segments of two URFs lacated in cluster 4 of CRF01_AE strains in the phylogenetic tree. The emergence of the novel CRF01_AE/CRF07_BC recombinant forms with complicated genomic structures indicated the importance of the continuous monitoring of the HIV-1 epidemic and new URFs among the MSM populations.

PU-0601

Individualized prediction of survival by a 10 long non-coding RNA based prognostic model for patients with breast cancer

Xuemei Yang、Juan Li、Yifan Wang、Peilong Li、Yinghui Zhao、Weili Duan、ABAKUNDANA NSENGA Ariston Gabriel、Yingjie Chen、Haiting Mao、Yunshan Wang、Lutao Du、Chuanxin Wang
The Second Hospital, Cheeloo College of Medicine, Shandong University

Deregulations of long non-coding RNAs (lncRNAs) have been implicated in the progression of breast cancer (BC). However, the prognostic values of those lncRNAs in BC remain elusive. This study aimed at constructing a lncRNA-based prognostic model to improve the clinical management of BC. Systematic investigation of lncRNA expression profiles and clinical data from The Cancer Genome Atlas (TCGA) database were utilized to establish a 10-lncRNA signature. The prognostic signature efficiently discriminated patients with significantly different prognosis regardless of intrinsic molecular subtypes and Tumor-Node-Metastasis (TNM) stage. A combined model was constructed by multivariate Cox proportional hazards regression (CPHR) analysis, which combined the lncRNA-based signature with certain clinical risk factors (TNM stage, age and human epidermal growth factor receptor 2 status). This model predicted a survival probability that closely corresponds to the actual survival probability. With respect to the entire set, the time-dependent receiver-operating characteristic curves revealed that the area under the curve of this model was the highest than any of the clinical risk factors. Moreover, functional enrichment analysis indicated that the molecular signature was mainly involved in DNA replication, which was firmly related to BC tumorigenesis. Consistent with the discovery, the knockdown of LHX1-DT, one of the 10 prognostic lncRNAs, attenuated the proliferation of BC cells in vitro and in vivo. Taken together, our study constructed a novel 10-lncRNA signature for prediction prognosis and the signature-based model could provide new insight into accurate management of BC patients.

PU-0602

Individualized prediction of survival by a 10 long non-coding RNA based prognostic model for patients with breast cancer

Xuemei Yang、Juan Li、Yifan Wang、Peilong Li、Yinghui Zhao、Weili Duan、ABAKUNDANA NSENGA Ariston Gabriel、Yingjie Chen、Haiting Mao、Yunshan Wang、Lutao Du、Chuanxin Wang
The Second Hospital, Cheeloo College of Medicine, Shandong University

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firmly related to BC tumorigenesis. Consistent with the discovery, the knockdown of LHX1-DT, one of the 10 prognostic lncRNAs, attenuated the proliferation of BC cells in vitro and in vivo. Taken together, our study constructed a novel 10-lncRNA signature for prediction prognosis and the signature-based model could provide new insight into accurate management of BC patients.

PU-0603

6-lncRNAs 模型评估三阴性乳腺癌患者预后结局

杨雪梅
山东大学第二医院

目的 通过大数据挖掘，构建可预测三阴性乳腺癌患者预后情况的 lncRNA 预后模型。
方法 基于 R 语言软件包，获取 TCGA 数据库中三阴性乳腺癌和正常乳腺组织的 lncRNA 表达谱及临床病理信息。单因素 Cox 回归和 Kaplan-Meier 曲线，鉴定三阴性乳腺癌中差异表达并与预后相关的 lncRNAs。利用多因素 Cox 逐步回归模型在训练集中构建 lncRNA 预后模型，Kaplan-Meier 曲线评估此模型在训练集、验证集中的预测效能。
结果 116 例三阴性乳腺癌和 113 例正常乳腺组织的 RNA 表达谱差异分析得到 1548 个在三阴性乳腺癌中差异表达的 lncRNAs，单因素 Cox 回归分析联合 Kaplan-Meier 生存曲线发现其中 24 个 lncRNAs 与预后相关，经多因素 Cox 逐步回归模型构建了基于 6-lncRNAs 的预后预测模型：风险评分=0.33× 表达量 LINC02685 + 1. 69 × 表达量 LINC01614 + 0.92 × 表达量 AC112250.2 + 0.57× 表达量 AL355483.2 + 0.16 × 表达量 FAM83A-AS1 + 0.43 × 表达量 LINC00377。Kaplan-Meier 曲线结果表明该模型可有效区分三阴性乳腺癌人群中预后高风险组和低风险组，且高风险组生存率明显低于低风险组。同时，该模型的时间依赖性受试者工作特征曲线下面积高达 0.811。
结论 基于 LINC02685、LINC01614、AC112250.2、AL355483.2、FAM83A-AS1 和 LINC00377 的预后预测模型可有效预测三阴性乳腺癌患者的预后结局，为三阴性乳腺癌的临床决策提供参考依据。

PU-0604

5-lncRNAs 模型用于预测乳腺癌患者预后生存

杨雪梅
山东大学第二医院

目的 长链非编码 RNA 表达失调已被证明与癌症的发生和发展有关，其表现出更高的组织、疾病、发展阶段的特异性表达。 然而，lncRNAs 在乳腺癌中的预后价值仍不清楚。 这项研究通过联合大数据分析及功能实验验证，以寻找新颖的 lncRNA 模型来预测乳腺癌患者的临床结局。
方法 通过大数据分析基因表达谱，以鉴定来自 TCGA 数据库的乳腺癌样品和正常样品之间的差异表达 lncRNAs。然后使用单变量 Cox 比例风险回归筛选鉴定预后相关的 lncRNAs，并通过 Cox 回归模型（逐步回归）进行进一步评估。最后，我们通过多变量 Cox 比例风险回归基于这些与预后相关的 lncRNAs 建立了 lncRNA 模型，并通过 Kaplan-Meier 方法、时间依赖性受试者工作特征曲线（ROC 曲线）在两个不同的数据集中进一步对其进行了验证。我们开发了一种 5-lncRNAs 模型，以预测乳腺癌的 3 年和 5 年 OS。
结果 依据 TCGA 数据库中乳腺癌样品和正常样品的 lncRNA 表达谱，我们确定了 5 种差异表达的 lncRNAs，它们与患者的总体生存率明显相关。然后，我们根据训练数据集中的 5 个预后相关 lncRNAs 的表达值及系数构建风险评分公式，风险得分=（0.244×AC007128.1 表达量）+（0.498×AL445647.1 表达量）+（0.441 ×LINC01574 ）+（0.617×CARMN 表达量）+（0.541×MME-AS1 表达量）。在其他验证集进行了进一步验证，Kaplan-Meier 曲线及时间依赖性

受试者工作特征曲线结果表明高风险评分的乳腺癌患者的生存时间明显低于低风险评分的乳腺癌患者（p 值<0.05）。

PU-0605

DNAzymatic Molecular Beacon Probe for colorimetric Detection of Nucleic Acids

Ying Ping、Xuchu Wang、Zhihua Tao
The Second Affiliated Hospital of Zhejiang University School of Medicine, Hangzhou, China

Nucleic acids are promising biomarkers for disease diagnosis and therapeutic decision-making. Herein, we employ a label-free molecular beacon probe to achieve easy and sensitive detection of nucleic acids. Specifically, a peroxidase-mimicking DNAzyme sequence is linked to the 3' end of molecular beacon that greatly enhances hemin peroxidation with an initial state. Introduction of target nucleic acid opens the stem-loop conformation of molecular beacon exposing the complementary region for DNAzyme sequence binding. The DNAzyme sequence is then extended to displace the target into next cycle, resulting in an embedded conformation that shows less peroxidase activity. This proposed probe is capable of discriminating varieties of gene mutations with high resolution, and detecting target nucleic acid as low as 0.105 nM in an isothermal manner, showing capacity to further exploit a simple and portable biosensor for nucleic acid detection.

PU-0606

Near Full-Length Genomic Characterization of Two Novel HIV-1 Unique Recombinant Forms (CRF01_AE/CRF07_BC) among MSM in Shijiazhuang, Hebei, China

Leilei Han、Erhei Dai
the Fifth Hospital of Shijiazhuang

Multiple subtypes were found to be co-circulated among men who have sex with men (MSM) populations in Hebei province, China, which always result in the emergence of unique recombinant forms (URFs). In the current work, two novel unique recombinant forms (URFs) were identified from two near full-length genomes (NFLG) that were obtained from two HIV-positive subjects (HB010014, HB010063) in Shijiazhuang, Hebei province, China. Both patients signed informed consent before investigated, then, their plasma samples were collected. RNA from plasma was extracted and transcribed into cDNA. the NFLG was amplified in two halves with High Fidelity Taq (Invitrogen) as described previously. PCR positive products were purified and sequenced by SinoGenoMax (Beijing, China) with several specific primers. Phylogenic analyses showed that both two sequences formed a distinct monophyletic cluster. The genomic recombination analysis based on the NFLGs revealed that the genome of HB010014 and HB010063 was composed of CRF01_AE and CRF07_BC. Further subregion phylogenetic analysis indicated that CRF01_AE segments were traced back to cluster 4 of CRF01_AE strains which are mainly circulating among the men who have sex with men (MSM) population in China. The emergence of two novel second-generation recombinant strains indicates the increasing complexity of the HIV-1 epidemic among MSM in Hebei, China.

PU-0607

烟台地区 PCR 检测呼吸道病毒感染结果分析

安 彤
滨州医学院烟台附属医院

目的 研究烟台地区近段时间内呼吸道病毒的流行趋势，从而做到更好地预防感染呼吸道感染以及防控其广泛流行。
方法 利用烟台地区 2019 年以及 2020 年至今的流感样病例的样本，采用实时定量荧光 PCR 法对采集的标本进行扩增，最后对实验结果进行综合分析。
结果 本篇论文就甲、乙型流感病毒(FluA、FluB)和人腺病毒 B 型（AdV-B）的核酸检测结果来进行分析，总体来看，从 2019 年到 2020 年至今甲型流感病毒的阳性率最高，其次是乙型流感病毒和人腺病毒 B 型，其阳性率分别是 17.79%、13.39%和 5.68%。
结论 从现有标本检测结果可分析得知烟台地区呼吸道感染具有明显季节性，对儿童和青少年感染性较强，但根据计算结果显示，并没有证据表明三种病毒的感染与性别之间有统计学意义。

PU-0608

Sox2 inhibits Wnt-β-catenin signaling and metastatic potency of cisplatin-resistant lung adenocarcinoma cells

Kangjian Zhang
The Second Hospital of Shandong University

Lung cancer remains one of the most common cancerassociated mortalities worldwide, and platinumbased doublet chemotherapies are recommended as the firstline treatment for advanced nonsmall cell lung cancer (NSCLC). However, the frequent development of multidrug resistance, to cisplatin regimens in particular, is a major cause of chemotherapy failure in patients with aggressive NSCLC. Wnt/βcatenin signaling and sexdetermining region Y box 2 (Sox2) have been implicated in the development and progression and resistance to epidermal growth factor receptortargeting therapy in lung cancer. The present study aimed to explore the effects of Wnt/βcatenin and Sox2 signaling on the chemoresistance of cisplatinresistant lung cancer cells. This study explored the effects of Wnt/βcatenin and Sox2 signaling on the chemoresistance of cisplatinresistant lung cancer cells by assessing the effects of Sox2 on Wnt/βcatenin signaling activity, cell migration, invasion and clonogenicity, and susceptibility to cisplatin in lung adenocarcinoma A549 cells and cisplatinresistant A549/DDP cells. The results demonstrated that an enforced expression of Sox2 led to inhibition of Wnt/βcatenin signaling activity, potentially by upregulating glycogen synthase kinase 3 β in A549 and A549/DDP cells. An overexpression of Sox2 promoted cell migration and invasion, in addition to enhancing the clonogenic capacity in A549 cells. Notably, knockdown Sox2 using short hairpin RNA led to an enhanced susceptibility of A549 and A549/DDP cells to cisplatin, along with increased cell apoptosis. The present study thus suggests that Sox2 may be an important regulator in development of chemoresistance of lung cancer cells and may be a novel therapeutic target for treatment chemoresistant lung cancer.

PU-0609

适配子在检测 CD64 蛋白中的应用

李卫滨[1]、严烨炜[2]
1. 中国人民解放军联勤保障部队第 900 医院(原福州总医院)
2. 中国人民解放军联勤保障部队第九〇〇医院

目的 中性粒细胞上的人 FcγRI（CD64）是早期诊断脓毒血症的新标志物。目前临床检测技术为流式仪法，仅有部分医院开展项目，尚未有在大部分医院广泛开展的检测方法。适配子是从含有大量随机序列的 ssDNA 或者 RNA 文库中筛出能与蛋白质或其他小分子物质等靶标特异性结合的短链分子。ELAA 法是将适配子代替双抗夹心 ELISA 法中的酶标抗体适配子，用于检测 CD64 浓度，此法有价格低、无需昂贵仪器等优点，易广泛推广。本研究使用固相重组人 FcγRI-适配子结合，对比三条适配子和混合适配子与 CD64 蛋白的结合力，并探索最佳实验条件和抗体最佳包被量，以期为后续研究 ELAA 法测 CD64 蛋白奠定基础。
方法 （1）所购抗体、重组人 FcγRI 特异性分析。（2）在高吸附 96 微孔板上包被 600ng/孔的重组人 FcγRI，分别结合 LW7-1、LW7-9、LW7-27 三条适配子和 250nM、500nM、1000nM 的混合适配子，用酶标仪检测 OD 值，对比选取其中最优的一条适配子。（3）在高吸附 96 微孔板上包被 0nM、100nM、200nM、300nM、400nM、500nM、600nM、700nM 的 CD64 抗体，与辣根酶标山羊抗兔 IgG 抗体结合，用酶标仪检测 OD 值，得到抗体最佳包被量。
结果 （1）所购抗体、重组人 FcγRI 特异性较好。（2）三条适配子中 LW7-9 与重组人 FcγRI 结合力较好，OD 值为 1.052。LW7-1 孔 OD 值为 0.598，LW7-27 孔 OD 值为 0.203。（3）抗体最佳包被量为 200ng/孔。
结论 （1）三条适配子中 LW7-9 与 CD64 蛋白的结合力较好，LW7-1 次之，LW7-27 结合力较低。（2）后续做 ELAA 实验时，抗体最佳包被量为 200ng/孔。

PU-0610

LncRNA NEAT1 受 m6A 甲基化调控并通过 miR-766-5p/CDKN1A 轴介导慢性粒细胞白血病进展

姚芳苡、王小中、黄波、刘静
南昌大学第二附属医院

目的 本研究探讨 LncRNA NEAT1 在 CML 中的生物学功能，并初步探索 METTL3 通过 m6A 修饰调控 NEAT1 表达参与 CML 发生发展的作用机制。
方法 采用 RT-qPCR 检测 20 例健康对照者、20 例 CML 初发期患者及 20 例 CML 急变期患者外周血单个核细胞（PBMC）和 CML 细胞系（K562、KCL22）中 NEAT1 表达水平。采用 NEAT1 过表达载体及对照载体分别转染 K562 和 KCL22 细胞，采用 CCK8 法和流式细胞术检测细胞增殖和凋亡水平变化。生物信息学预测 NEAT1 的靶基因。使用双萤光素酶报告基因实验、RNA 免疫沉淀实验、RT-qPCR 和 Western blot 测定 NEAT1 对 miR-766-5p 和 miR-766-5p 对 CDKN1A 的靶向调控作用。采用 SRAMP 软件预测 NEAT1 基因 m6A 修饰位点，并用 MeRIP 实验进行验证。
结果 与健康对照者相比，CML 患者 PBMC 和 CML 细胞系中的 NEAT1 表达水平均显著下调，CML 急变期患者显著低于 CML 初发期患者。K562 和 KCL22 细胞中过表达 NEAT1 后，细胞增殖降低，凋亡增加。NEAT1 可通过海绵吸附的方式负调控 miR-766-5p 的表达；CDKN1A 是 miR-766-5p 的靶基因，受其负调控。沉默 CDKN1A 可部分逆转过表达 NEAT1 和沉默 miR-766-5p 对 K562 和 KCL22 细胞增殖和凋亡的影响。SRAMP 预测显示 NEAT1 上存在多个 m6A 修饰位点，MeRIP 证实 NEAT1 的表达水平同 M6A 修饰相关，RIP 实验发现 METTL3 可以富集 NEAT1 的表达，沉默 METTL3 可降低 NEAT1 在细胞中的半衰期。

结论 本研究阐明了 NEAT1 以依赖 m6A 修饰方式，通过 METTL3/NEAT1/miR-766-5p/CDKN1A 作用轴，影响 CML 发生发展的作用及其机制。

PU-0611

突变型 SMOC2 基因诱导多能干细胞系的构建

龙逢
山东大学第二医院

目的 构建突变型 *SMOC2* 基因诱导多能干细胞系并检测其增殖凋亡情况。
方法 从患者和正常对照者体内抽取静脉血后分离其单个核细胞（PBMCs）并进行培养。使用电转仪将相关质粒转入 PBMCs 进行重新编程，使其成为诱导多能干细胞（hiPSCs）。对 hiPSCs 传代培养并进行核型分析和 STR 连锁分析，确定该 hiPSCs 的来源。随后进行三胚层分化并提取 RNA 进行实时定量 PCR 检测和免疫荧光染色检测，检测其是否具有与胚胎干细胞相同的分化能力。确定成功构建突变型 SMOC2 基因 hiPSCs 细胞系后，使用 EdU 染色和脱氧核糖核苷酸末端转移酶介导的缺口末端标记法（TUNEL）检测其增殖和凋亡能力。
结果 本研究通过电转成功将 *OCT4*、*SOX2*，*c-Myc* 和 *KLF4* 基因导入 PBMCs 中，将其重新编程为 hiPSCs。核型分析和 STR 连锁分析显示其来源于原始样本。在该 hiPSCs 中，对表达于 ES 细胞的特异性蛋白标志物进行检测，发现 hiPSCs 中这些特异性转录因子在 mRNA 水平和蛋白质水平的表达量与 ES 细胞相似。对其进行三胚层分化后，可高表达内胚层、中胚层和外胚层的标志物。EdU 染色和 TUNEL 检测发现，突变型 *SMOC2* 基因 hiPSCs 的增殖能力没有改变，凋亡能力减弱。
结论 本研究成功构建了来源于患者和对照者的具有多能干性的 hiPSCs，并发现突变型 *SMOC2* 基因 hiPSCs 的增殖能力没有改变，凋亡能力减弱。

PU-0612

SPARC 相关模块钙结合蛋白基因功能的研究

龙逢
山东大学第二医院

目的 探究 *SMOC2* 基因变异导致骨骺发育不良的致病机制。
方法 构建野生型和突变型 *SMOC2* 基因病毒表达载体以及稳定过表达野生型和突变型 *SMOC2* 基因的细胞系，通过蛋白免疫印迹（Western blot，WB）检测 BMP 信号通路和 MAPK 信号通路相关分子的表达水平，利用免疫共沉淀（Co-Immunoprecipitation，Co-IP）、固相结合实验（Solid Phase Assay，SPBA）实验检测分子间相互作用。
结果 本研究成功构建稳定表达野生型和突变型 *SMOC2* 基因的 HEK293 细胞系。WB 检测发现过表达野生型和突变型 *SMOC2* 基因后，HEK293 细胞的磷酸化 SMAD1/5/9 表达量明显降低，使用 BMP 重组蛋白刺激后表达量没有恢复。在过表达野生型 *SMOC2* 基因的 HEK293 细胞系中，使用 WB 检测 MAPK 信号通路的相关分子发现其表达水平没有升高。随后使用活化的 BMP 受体进行拯救实验，发现 SMAD1/5/9 的磷酸化水平得到恢复。此后进行的 Co-IP 实验结果显示野生型和突变型 SMOC2 蛋白均能与 IB 型 BMP 受体（BMPRIB）进行结合。同时，Co-IP 和 SPBA 实验显示突变型 SMOC2 蛋白与 COL9A1 蛋白和 HSPG 结合能力下降，而与 COMP 蛋白和 MATN3 蛋白的结合能力不变。
结论 突变型 SMOC2 蛋白在软骨细胞外基质分子网络中的结合能力下降，使大量 SMOC2 蛋白释放出来，与 BMP 受体结合，阻碍 BMP 配体与受体的结合和 BMP 受体的活化，进而抑制 BMP 信号通路的传导。

PU-0613

突变型 Smoc2 基因敲入小鼠模型的构建及表型分析

龙逢
山东大学第二医院

目的 成功构建突变型 *Smoc2* 基因敲入小鼠并对其表型进行分析。
方法 通过胚胎干细胞（ES）打靶技术构建突变型 *Smoc2* 基因敲入小鼠，并使用 Sanger 测序进行验证。利用 X 光测量小鼠的身长，使用游标卡尺测量小鼠股骨和胫骨长度，应用 micro-CT 检测膝关节形态、骨密度和骨量，通过透射电子显微镜观察软骨细胞的超微结构。制备小鼠胫骨石蜡切片后，通过苏木素-伊红染色，番红固绿染色。免疫染色和脱氧核糖核苷酸末端转移酶介导的缺口末端标记法（TUNEL）检测骨骺生长板的形态和软骨细胞的增殖、分花费大、凋亡情况以及相关标志物的表达水平。
结果 本研究通过 ES 细胞打靶技术承购构建了突变型 *Smoc2* 基因敲入小鼠。突变型 *Smoc2* 基因敲入小鼠的身长、体重、股骨和胫骨的长度均小于野生型小鼠。对小鼠的胫骨生长板进行病理学分析，发现突变型 *Smoc2* 基因敲入小鼠的增殖区软骨细胞所占比例缩小，肥大区软骨细胞所占比例增大，而且软骨细胞排列松散、紊乱。对其软骨细胞的 PCNA、Collagen X 和 Runx2 检测发现突变型 *Smoc2* 基因敲入小鼠的 PCNA 表达量减少，Collagen X 和 Runx2 的表达量增加。
结论 突变型 *Smoc2* 基因敲入小鼠出现明显的骨骼发育不良表现，而且其软骨细胞增殖能力减弱，肥大分化能力增强，导致其骨骺生长板结构异常。

PU-0614

Construction of a circRNA-miRNA-mRNA network reveals the key pathways and central genes of osteosarcoma in vivo and immune cell infiltration characteristics in osteosarcoma

Haifang Zhang、Hong Du
Department of Clinical Laboratory, The Second Affiliated Hospital of Soochow University, Suzhou, Jiangsu, 215004, China.

The potential functions and detailed mechanisms of circular RNAs (circRNAs) in osteosarcoma (OS) have not been fully elucidated. In this study, the circRNA, micro RNA (miRNA), and messenger RNA (mRNA) expression profile of human OS was investigated based on the raw microarray data from Gene Expression Omnibus (GEO) datasets, and seven differentially-expressed circRNAs (DEcircRNAs), 166 differentially-expressed miRNAs (DEmiRNAs), and 175 differentially-expressed mRNAs (DEmRNAs) were identified in total. After bioinformatics analysis, we identified 185 statistically-significant transcription factors and revealed the pattern of tumor-infiltrating immune cells in OS. And we found that post-translational protein modification, collagen-containing extracellular matrix, and single-stranded DNA binding were the most significant pathways in GO annotation analysis, whereas complement and coagulation cascades, RNA transport and drug metabolism-other enzymes were the most significantly enriched pathways in KEGG pathway enrichment analysis. In addition, we constructed circRNA-miRNA-mRNA and protein-protein interaction (PPI) networks that may be associated with pathological processes of OS. Moreover, the expression of targets in competitive endogenous RNA (ceRNA) network constructed was confirmed by RT-qPCR. Finally, we further explored the potential value of the ceRNA networks, and found that COL1A1 and RAN were promising biomarkers which were significantly correlated with overall survival. More importantly, circ_0010220–miR-338-3p–COL1A1 and circ_0010220–miR-324-5p–RAN, the novel

regulatory axes in OS, were firstly highlighted in this study. To our knowledge, this study provides the first profile analysis of DEcircRNAs, DEmiRNAs, and DEmRNAs with OS in vivo and reveals a novel idea for understanding the pathogenesis of OS.

PU-0615

Long non-coding RNA SNHG14 enhances pancreatic-β-cell function by sponging microRNA-206 and thereby upregulating IGF1

Zheng Mao、Zhen Li、Zengkun Qian、Jingjing Zhou、Xiaoqin Li、Fan Cui
The First People's Hospital of Wuhu

OBJECTIVE Diabetes mellitus (DM) characterised by pancreatic β-cell dysfunction and insulin resistance is already prevalent worldwide, and the complications of DM increased the mortality of diabetic patients. More and more reports showed that long non-coding RNA (lncRNA) plays key roles in DM, and in this study we explored the effect of long non-coding RNA SNHG14 (SNHG14) in DM.
STUDY DESIGN Quantitative reverse transcription PCR (qRT-PCR) was used to analyze the expression of SNHG14 and microRNA (miR)-206 in peripheral blood from 60 pairs of healthy and DM samples. Then the effect of SNHG14 on the insulin secretion of pancreatic β-cells was investigated. Moreover, the effects of SNHG14 on the viability and apoptosis of pancreatic β-cells were determined by 3-(4,5)-dimethylthiahiazo (-z-y1)-3,5-di- phenytetrazoliumromide (MTT) assay and flow cytometry (FCM) respectively using INS-1 cells transfected with SNHG14-plasmid and/or miR-206 mimic. Bioinformatics and Daul luciferase reporter assay were used to confirm the direct target of miR-206.
RESULTS Our data showed that SNHG14 level was decreased but miR-206 was increased significantly in the peripheral blood of DM patients. Furthermore, over-expression of SNHG14 enhanced insulin secretion and cell viability but inhibited apoptosis of pancreatic β-cells, whereas, miR-206 over-expression reversed these effects. In addition, insulin-like growth factor-1 (IGF1) was proved to be regulated by miR-206 negatively and over-expression of SNHG14 increased the expression of IGF1 and IGF1R in pancreatic β-cells.
CONCLUSION In conclusion, we found that SNHG14 was significantly down-regulated in DM patients, and SNHG14/miR-206/IGF1 may serve as a potential candidate for the clinical target of DM.

PU-0616

肿瘤坏死因子 α 基因多态性与强直性脊柱炎的相关性研究

杨越、吉阳涛
中国医科大学附属第一医院

目的 探讨肿瘤坏死因子(tumor necrosis factor)-α 启动子区 857C/T 基因多态性与强直性脊柱炎之间的关系,为临床上科学的预防干预和治疗强直性脊柱炎提供新的思路和治疗方案。
方法 通过在计算机中检索 CBM、CNKI、 万方数据库、维普数据库，PubMed、Cochrane Library、OvidSP、Wiley Online Library、 EBSCO、Elsevier Science Direct、Springer Link、Goolge scholar 数据库，文献检索 时间都选择从建库开始到 2021 年 5 月。检索 TNFα857 位点的 SNPs 与 AS 易感性的病例-对照研究，采用 Review Manager 5.4 软件进行 Meta 分析，我们选择使用固定效应模型 或者随机效应模型进行 Meta 分析，然后再通过一定的运算合并 OR 值及其 95%CI，借此来判断 TNFα857 的 SNPs 与 AS 易感性的关联情况,分析强直性脊柱炎与 TNF-α 启动子区 857C/T 基因多态性。

结果 经过筛选，最终选定 6 篇文献，来进行 Meta 分析，其中涉及到 571 例患有 AS 的患者，615 例健康人群对照组病患，Meta 分析的结果最终显示，CC 基因型[OR=0.24, 95%CI (0.31, 0.17), P=0.13]，TT 基因型[OR=0..02, 95%CI (0.03, 0.07), P=0.40],C 基因型[OR=0.14, 95%CI (0.19, 0.08), P=0.04],T 基因型[OR=0.14, 95%CI(0.08, 0.19), P=0.40]。
结论 TNF-α 启动子区 857C/T 基因多态性与强直性脊柱炎发病率存在相关性；携带 C 等位基因人群可能 AS 的发病风险低，而携带 T 等位基因人群可能 AS 的发病风险高。

PU-0617

探讨新冠核酸检测的风险评估与生物防护

胡瑞国
山东第一医科大学第一附属医院

在医学快速发展的当下，医学实验室也在与时俱进，检验项目多元化，检验仪器多品牌化，相应的检验标本种类及数量也越来越多，生物防护就显得尤为重要。PCR 实验室为做好生物防护，加强生物安全管理监控工作，联合相关职能部门（医务处、护理部、感染管理科、总务处）及临床重点科室（新生儿科、产房、血液透析室、重症医学科、呼吸重症监护室、心外监护室、外科监护室、危急重症神经外科、颅脑肿瘤神经外科、脑血管病神经外科、消毒供应室、手术室、内镜诊疗科、发热门诊的科主任及护士长）对新型冠状病毒的生物防护进行风险评估并制定相应的防护措施，本文就 PCR 实验室检测新冠核酸时生物防护现状进行探讨，同时结合工作中的实际问题，提出改进措施进行有效防护。

PU-0618

一多发性骨骺发育不良家系致病基因的分离

龙逢
山东大学第二医院

目的 分离一多发性骨骺发育不良家系的致病基因。
方法 通过系谱分析确定该家系疾病的遗传方式，STR 连锁分析发现该家系的发病是否与已知致病基因相关，使用全外显子组测序技术发现该家系的候选致病基因，通过 Sanger 测序，保守性分析以及生物信息学软件确定该家系的致病基因。
结果 通过对该家系的系谱分析，我们发现该家系的遗传方式为常染色体显性遗传，STR 连锁分析发现该家系的发病与已知致病基因无关。通过对该家系三名患者的全外显子组测序，筛选出 *INSL5*，*MRPS5*，*ANXA5*，*KAT6B*，*MYO15A*，*LRRC48*，*DSCAM*，*PABPC3* 和 *SMOC2* 基因为候选致病基因。在 EXAC 数据库中的检索结果发现位于 *INSL5*，*MRPS5*，*ANXA5*，*KAT6B*，*MYO15A*，*LRRC48* 和 *DSCAM* 基因的变异在正常人群中是存在的。通过对该家系中患者和正常人的 Sanger 测序，我们未检测到 *INSL5*，*MRPS5*，*ANXA5*，*KAT6B*，*MYO15A*，*DSCAM* 和 *PABPC3* 基因的变异与家系中患者表型共分离。对 SMOC2 蛋白和 LRRC48 蛋白在进化中的保守性进行分析，发现 LRRC48 蛋白的突变位点氨基酸在进化中并不保守，而 SMOC2 蛋白的突变位点氨基酸在进化中是高度保守的。
结论 该常染色体显性遗传性多发性骨骺发育不良家系的致病基因为 *SMOC2* 基因。

PU-0619

新型冠状病毒核酸检测比对结果分析

朱艳
西安金域医学检验所有限公司

目的 通过对新型冠状病毒核糖核酸（2019-nCOV）检测的技术人员及检测仪器比对结果分析，确保本实验室新型冠状病毒核酸检测技术人员及检测仪器的稳定性，保证检测结果的准确性和可靠性。
方法 使用广州邦德盛 2019-nCOV 定值质控物 S2（批号 2021004，浓度均值为 1.93E+04 copies/ml）原液 E4、稀释 10 倍至 E3、E3 稀释 5 倍至 E2、及 2 例临床阴性样本，作为 5 例比对样本。人员比对：本实验室 15 名持 PCR 上岗证的技术人员分别提取扩增 5 例样本及阴阳性质控品，阴阳性质控品结果必须在控，之后检测结果与预期结果进行比对。仪器比对：本实验室目前有 4 台提取仪和 12 台扩增仪，由 1 名持 PCR 上岗证的技术人员分别在 4 台提取仪上提取 5 例比对样本及阴阳性质控品，之后分别在 12 台扩增仪上扩增，如提取仪 1 号分别对应扩增仪 1、2、3...12 号，提取仪 2 号再分别对应扩增仪 1、2、3...12 号，以此类推，阴阳性质控品结果必须在控，之后检测结果与预期结果进行比对。
结果 人员比对：15 名持 PCR 上岗证的技术人员检测结果均符合预期，比对通过。仪器比对：4 台提取仪分别对应 12 台扩增仪，共 48 份检测结果均符合预期，比对通过。
结论 本实验室新型冠状病毒核糖核酸（2019-nCOV）检测的技术人员及检测仪器比对结果分析均一致通过，表明本实验室人员及设备的检测质量均有所保障，从而保证检测结果的准确性和可靠性，在新冠疫情中发挥应有的社会价值。

PU-0620

第三方质控品在新型冠状病毒核酸检测中的应用

朱艳
西安金域医学检验所有限公司

目的 通过检测新型冠状病毒核糖核酸（2019-nCOV）第三方质控品，来进行本实验室新型冠状病毒核酸检测的室内质量控制，保证检测结果的准确性和可靠性。
方法 本室使用的广州邦德盛 2019-nCOV 液体质控品，是以新型冠状病毒假病毒培养液为原料，用阴性稀释液稀释，添加适量的稳定剂制备而成。该质控品有不同浓度，本实验室检测浓度为 2-3 次方，通过连续近 200 次的批间测试，计算出 ORF 基因 Ct 值均值为 32.59，SD 为 1.36，CV 为 4.19%，N 基因 Ct 值均值为 33.57，SD 为 1.34，CV 为 4.98%。
结果 ORF 基因、N 基因 Ct 值统计的 CV 结果，均符合试剂盒精密度的变异系数≤5%的要求，检测精密度较好。
结论 ORF 基因、N 基因为新型冠状病毒核糖核酸的主要检测目标，对于新型冠状病毒感染的临床诊断有非常重要的意义。本实验室通过对广州邦德盛 2019-nCOV 液体质控品的检测，提示本实验室的检测精密度较好，室内质量控制有所保障，从而保证检测结果的准确性和可靠性，在新冠疫情中发挥应有的社会价值。

PU-0621

HBV-DNA 定量不同检测系统比对结果分析

朱艳
西安金域医学检验所有限公司

目的 分析 HBV-DNA 定量不同检测系统比对结果的一致性，以辅助指导临床医生对于 HBV 患者的诊治。
方法 采用 HBV-DNA 定量检测系统 1｛设备：罗氏 COBAS® Ampliprep /COBAS® Taqman®全自动核酸纯化/分析仪，检测试剂：罗氏乙型肝炎病毒核酸检测试剂盒，检测**方法** Real-time PCR（内标法）}检测过的 20 例覆盖测量区间且不同浓度的 HBV-DNA 定量临床样本，使用 HBV-DNA 定量检测系统 2（设备：DP1000 半自动核酸提取仪、ABI7500 荧光定量扩增仪，检测试剂：上海科华乙型肝炎病毒核酸检测试剂盒，检测**方法** 磁珠/PCR-荧光探针法）进行检测，比对结果的一致性。
结果 根据 CNAS-CL02-A009：2018《医学实验室质量和能力认可准则在分子诊断领域的应用说明》要求，比对结果的通过标准为线性相关系数 R2≥0.980，总样本数 95%的检测结果偏倚<±7.5%。本室两套检测系统比对结果的线性相关系数 R2 =0.9923，总样本数（19/20) 95%的检测结果偏倚<±7.5%，比对通过。
结论 本室两套检测系统比对结果通过，可同时用于临床 HBV-DNA 定量项目的检测，从而辅助指导临床医生对于 HBV 患者的诊治。

PU-0622

核酸检测联合细菌培养在肾移植术后呼吸道感染早期诊断中的应用

吕星
中南大学湘雅二医院

目的 研究基因芯片检测联合细菌培养的对肾移植术后患者呼吸道感染诊断的临床价值。
方法 本研究选取 2018 年 5 月～2019 年 1 月在湘雅二医院就诊的肾移植术后患者呼吸道来源的标本（痰、肺泡灌洗液、咽拭子）共 132 例作为研究对象。回顾性分析其基因芯片及痰培养的数据，对比分析两种方法的检测结果。
结果 细菌培养共检出 15 例阳性，117 例阴性，阳性率为 11.36%，其中 15 例检出革兰阴性菌，0 例检出革兰阳性菌。基因芯片共检出 53 例阳性，79 例阴性，阳性率为 40.15%，其中革兰阴性菌 44 例，革兰阳性菌 7 例，抗酸杆菌 2 例，未检出嗜肺军团菌、支原体和衣原体。两者共 14 例标本检测结果一致。与细菌培养相比，基因芯片检测结果的灵敏度为 93.3%，特异性为 66.7%，总符合率为 70.7%，两者比较差异有统计学意义(P<0.05)，基因芯片的阳性率明显高于细菌培养。
结论 常规的细菌培养容易贻误治疗时机并可存在一定程度的漏检现象，细菌培养联合基因芯片检测可以有效提高病原菌的检出速度和检出率。

PU-0623

新型冠状病毒核酸快速检测系统性能验证方案建立的探讨

吕星、胡敏
中南大学湘雅二医院

目的 建立适用于新型冠状病毒核酸快速检测系统的性能验证方案,以确保检测系统性能满足临床检测需要。
方法 按照 ISO15189《医学实验室质量和能力认可准则（2012 年）》和《医疗机构新型冠状病毒核酸检测工作手册（试行第二版）》以及厂家声明，采用第三方阳性定值参考品、企业阳性定值参考品以及企业阴性参考品对国产某型新冠核酸快速检测系统的重复性、准确度、特异性、最低检测限、抗干扰能力等进行验证及评价，并与实验室使用的常规新冠核酸检测 RT-PCR 方法比较，了解两种检测方法性能差异。
结果 待评价新冠核酸快速检测系统重复性验证，符合厂家申明和相关国家要求；准确性验证，与常规 RT-PCR 检测系统相比较总符合率为 95%；待评价新冠核酸快速检测系统最低检出限为 7×102 copies/mL。10%（体积比例）的全血、10%（体积比例）鼻分泌液、100 μg/mL 浓度曲安奈德溶液、100 μg/mL 浓度莫匹罗星溶液对检测结果未产生干扰。与冠状病毒（OC43、NL63、229E、HKU1、MERS、SARS）、甲型流感病毒、乙型流感病毒、腺病毒、肺炎支原体不产生交叉反应。
结论 本研究选择的新冠核酸快速检测系统的检测性能基本能够满足厂家申明要求；最低检测限与厂家试剂盒说明书相比有差异，值得临床实验室关注。

PU-0624

胶体金法在诊断甲/乙型流感病毒中的临床应用

吕星、胡敏
中南大学湘雅二医院

目的 评估广州万孚甲/乙型流感病毒抗原检测试剂（胶体金法）对 A、B 型流感病毒的临床诊断价值。
方法 获取中南大学湘雅二医院 2019 年 1 月-2019 年 3 月期间符合流感样症状的 95 例门急诊患者及 226 例住院患者的咽拭子标本，使用甲/乙型流感病毒抗原检测试剂进行咽拭子 A、B 型流感病毒检测，同时取咽拭子经聚合酶链反应（RT-PCR）进行验证。
结果 胶体金免疫层析法的阳性检出率为 19.6%（63/321），与 PCR 方法比较，检测 A 型流感病毒的灵敏度和特异度分别为 31.5%（39/124）和 94.9%（187/197），阳性预测值及阴性预测值分别为 79.6%（39/49）和 68.8%（187/272）；检测 B 型流感病毒的灵敏度和特异度分别为 20.0%（1/5）和 95.9%（303/316），阳性预测值及阴性预测值分别为 7.1%（1/14）和 98.7%（303/307）。
结论 甲/乙型流感病毒抗原检测试剂诊断 A、B 型流感病毒灵敏度低，特异度高，容易出现误诊，故对于流感病毒抗原检测为阳性的患者建议行核酸聚合酶链反应（RT-PCR）进行确诊。

PU-0625

长沙市某医院 2018-2020 年流感流行病学分析及抗原检测方法评价

吕星、胡敏
中南大学湘雅二医院

目的 分析长沙市某医院 2018-2020 年流行性感冒病例的流行病学特征，评估流感病毒抗原检测试剂（胶体金法）对流感病毒的临床诊断价值，为长沙市流感防控措施提供依据。
方法 收集 2018 年 1 月至 2020 年 4 月在中南大学湘雅二医院就诊的 53510 份流感样病例信息，采用卡方检验比较不同流感型别，性别特征，年龄分布，时间分布和科室分布等流行特征。评价流感病毒抗原检测（胶体金法）与核酸检测（PCR 法）比较的一致性、灵敏度和特异度。
结果 43116 例流感抗原检测阳性结果为 3374 例（甲流 2680 例，乙流 694 例），总阳性率为 7.82%。10394 例流感核酸检测阳性结果为 652 例（甲流 504 例，乙流 148 例），总阳性率为 6.27%。流感好发于 15 岁以下的儿童和青少年。、因 2020 年 1 月出现新冠疫情，人们居家隔离以及佩戴口罩，与 2019 年同期比较，流感阳性率出现明显下降。（2）与 PCR 技术相比，胶体金检测甲型/乙型流感病毒一致性较差，Kappa 值分别为 0.283 和 0.275。甲流抗原检测灵敏度为 28.37%，特异度为 94.68%，差异有统计学意义（P=0.000）。乙型抗原检测灵敏度为 30.76%，特异度为 96.74%，差异有统计学意义（P=0.000）。
结论 长沙市地区 2018—2020 年流感发病率呈上升趋势，需加强防控措施。甲型和乙型毒株混合流行，但以甲型为主。科学佩戴口罩以及减少人员聚集可遏制流感病毒传播。抗原检测与核酸 PCR 检测结果一致性较差，甲、乙流感抗原检测（胶体金法）的敏感度较差，特异度较好，临床应根据检查目的合理选择检测方法。

PU-0626

p300 对结肠癌细胞增殖凋亡和迁移的影响及机制研究

唐金霞
中南大学湘雅三医院

目的 探讨 p300 蛋白对结肠癌细胞增殖、凋亡和迁移能力的影响，并对其分子机制进行研究。
方法（1）利用 DNA 测序技术，检测结肠癌患者和正常人外周血 p300 基因 rs20551 的基因型；（2）检测结肠癌细胞系 DLD-1、HT29、HCT116、SW480 和 SW620 与正常结肠细胞系 FHC 的 p300 蛋白表达水平及乙酰转移酶（HAT，histone acetyltransferase）活性；（3）p300 HAT 特异抑制剂 C646 作用结肠癌细胞 HT29、SW480 和 SW620 后，CCK8 实验和克隆形成实验检测结肠癌细胞的增殖能力，Hoechst 染色及流式细胞术检测结肠癌细胞的凋亡水平，划痕实验检测结肠癌细胞的迁移能力；（4）Western Blot 检测 C646 处理结肠癌细胞 HT29、SW480 和 SW620 后 53BP1、p53、乙酰 p53、MMP9、p21 和 Bax 蛋白表达水平变化。
结果（1）p300 rs20551 的基因型在结肠癌患者和正常人之间无明显差异；（2）HT29、SW480 和 SW620 细胞的 p300 蛋白表达以及 p300 蛋白 HAT 活性比 FHC 细胞高，且 C646 处理 HT29、SW480 和 SW620 细胞后，结肠癌细胞的增殖和迁移能力下降，凋亡水平增高；（3）C646 处理结肠癌细胞可下调 HT29、SW480 和 SW620 细胞的 53BP1、p53 和乙酰 p53 蛋白，下调 SW480 和 SW620 细胞的 MMP9 蛋白，上调 HT29 和 SW620 细胞的 Bax 蛋白，HT29 细胞 p21 蛋白上调，SW620 细胞 p21 蛋白下调。
结论 靶向抑制 p300 蛋白 HAT 活性可抑制结肠癌细胞的增殖、迁移，并促进凋亡，这可能与 p300 对 p53 通路的表观遗传学调控和乙酰化调节有关，以及对凋亡蛋白 Bax，迁移蛋白 MMP9 和增殖抑制蛋白 p21 的表达调控有关，这些结果均提示 p300 有望成为结肠癌治疗的潜在靶点。

PU-0627

人乳腺癌细胞系 MCF7 中 FOXM1 调控 SYK 转录

冯鹭
山东大学第二医院

目的 探讨人乳腺癌细胞系 MCF 7 中叉头框转录因子 M1(FOXM1)对脾酪氨酸激酶(SYK)表达的调控机制。
方法 从 MCF 7、T47D、SK BR3 和 MDA MB 231 中提取 RNA 和蛋白质，分别用 PCR 和 Westernbloting 检测 SYK 的表达水平，并检测 SYK 基因启动子区 CpG 岛甲基化。在 MCF 7 中过表达 FOXM1，采用 Westernblot ting 和实时荧光定量 PCR 检测 FOXM1 和 SYK 的表达。利用染色质免疫沉淀(ChIP)技术和荧光素酶报告基因检测转录因子 FOXM1 对 SYK 基因转录水平的调控作用。
结果 SYK 在 MCF 7 中呈阳性表达，而在 T47D、SKBR3 和 MDA MB 231 中呈阴性表达;MCF 7 细胞中 SYK 基因启动子区 CpG 岛甲基化水平低于对照细胞(P<0.05)。在 MCF 7 中过表达 FOXM1 能下调 SYK 表达，在 SK BR3 细胞系中沉默 FOXM1 基因能激活 SYK 表达。ChIP 结果显示 FOXM1 直接参与调控 SYK 的转录;基因沉默 FOXM1 激活 SYK 基因启动子活性，过表达 FOXM1 抑制 SYK 基因启动子的活性。
结论 在人乳腺癌细胞系 MCF 7 中，SYK 是 FOXM1 的靶基因，FOXM1 可能通过调节 SYK 的表达来调控乳腺癌的发生发展。

PU-0628

Ten years of prevalence and clinical laboratory features of HCMV infected children in a hospital of Jiangsu Province

Wenwen Shang、Lei Wu、Hong Zhao、Guodong Rong、Ting Xu、Yan Zhang
Jiangsu Province Hospital

Human cytomegalovirus (HCMV) is prevalent worldwide and causing lifelong infection. We conducted a retrospective study to determine the epidemiology and clinical laboratory characteristics of CMV infection. Urine CMV-DNA load test was intensively ordered in 2012 for infants under 1 month but the rate continuously dropped ever since. In fact, infants under 1 month had the lowest detection sensitivity and children aged between 3 to 24 months had the highest positive rate. Analysis of blood routine test showed that the absolute counts of leukocytes, monocytes, neutrophils and platelets were significantly decreased in CMV+ group. The percentages of neutrophils were decreased while the percentages of lymphocytes were increased. Moreover, NLR, MLR and SII were also decreased. The hospitalization of cases in CMV+ group was significantly longer. CMV survey has not drawn much attention and the combined application of urine CMV detection and blood routine test should be benefit when assessing CMV infections.

PU-0629

MiR-204-5p knockdown increases betaB2-crystallin expression in the lens by targeting Wnt2

Hanxiao Ren
the Second Hospital of Shandong University

Objective To investigate the role of miR-204-5p in regulating betaB2-crystallin during the occurrence and development of cataract, and provide new ways for the early intervention and treatment of cataract.
Methods Real-time PCR and bioinformatics analysis were performed to compare the expression of miRNAs between knockout (KO) mice and wild-type mice (WT). Luciferase reporter assay was used to confirm the target of miR-204-5p. A miR-204-5p mimic and an inhibitor were constructed and co-transfected into HLEC-B3. While the expression of Wnt2 and betaB2-crystallin were detected by quantitative RT-PCR and western blot.
Results Real-time PCR and bioinformatics analysis showed that miR-204-5p was significantly down-regulated after betaB2 had been knocked out. Wnt2 was confirmed to be a novel target of miR-204-5p through luciferase reporter assay. Overexpression of miR-204-5p in HLEC-B3 could reduce the expression level of Wnt2 and betaB2-crystallin, on the contrary, they were apparently up-regulated when the miR-204-5p inhibitor was transfected into HLEC-B3.
Conclusions This study confirms that miR-204-5p could inhibit the expression of betaB2-crystallin by targeting Wnt2. To down-regulate miR-204-5p temperately may alleviate even reverse the development of cataract to some extent, and provide new ways for the early intervention and treatment of cataract.

PU-0630

miR-326 调控晶状体浑浊的机制研究

任含笑
山东大学第二医院

目的 探讨 miR-326 调控 betaB2 晶体蛋白在白内障发生、发展中的作用机制，为老年性白内障的早期干预提供靶点和治疗新途径。
方法 采用基因芯片筛选可能调控 betaB2 的 miRNA 分子，并进行 betaB2 基因 KO 鼠和 WT 鼠之间以及老年性白内障患者与正常人血清之间的差异 miRNA 的筛查。明确 miR-326 的下游靶基因。通过体外荧光素酶报告基因系统验证 miR-326 调控 betaB2 表达的作用靶点。并验证靶点对 betaB2 的调控作用。通过细胞增殖、周期、凋亡等明确晶状体上皮细胞中 miR-326 对 betaB2 表达以及细胞生物学功能的调控作用。
结果 betaB2 基因敲除后 miR-326 的表达显著降低；荧光素酶报告基因实验证实 miR-326 的靶基因为 FGF1；miR-326 模拟物转染 HLEC-B3 细胞后 FGF1 和 betaB2 的表达量均降低，而转染 miR-326 抑制体后 FGF1 和 betaB2 晶体蛋白的表达同步升高。
结论 本研究证实 miR-326 通过与靶基因 FGF1 的 3′-UTR 结合而特异性抑制 FGF1 的表达，从而抑制 betaB2 晶体蛋白的表达。通过 miR-326 的抑制载体靶向上调 FGF1 的表达，进而促进 betaB2 晶体蛋白的表达，促进该蛋白在晶状体中发挥特殊结构蛋白及类伴侣蛋白作用，以利于稳定晶状体正常功能、延缓晶状体老化，为老年性白内障的“未病先防”提供理论及实验依据。

PU-0631

小胶质细胞极化在精神分裂症发病机制中的研究进展

李博慧[1]、刘春梅[2]
1. 大庆市第三医院
2. 江苏省苏北人民医院

目的 小胶质细胞的活化是精神分裂症发病的主要原因之一，其参与精神分裂症的生理病理过程。小胶质细胞可以活化为功能完全不同的两个极化表型。本文旨在分析精神分裂症时小胶质细胞的极化状态及其研究进展。
方法 使用中国知网、PubMed、Embase、Web of Science 网站进行检索，关键词设置为“精神分裂症”和“小胶质细胞”、“Schizophrenia”and“Microglia”
结果 共检索出中文文章 14 篇、英文文章 239 篇，去除重复文章后，最后文章 210 篇，根据文章题目及摘要筛选出与小胶质细胞极化相关的文章共 49 篇。
结论 在精神分裂症的发生发展过程中，存在小胶质细胞的极化过程。其中，M1 极化表型分泌诱导型一氧化氮合酶、肿瘤坏死因子 α、白介素 6 等促炎细胞因子和大量活性氧自由基、引起神经毒性、破坏神经元，使神经递质释放异常，导致精神和行为改变；而 M2 极化表型则分泌精氨酸酶 1、白介素 10 等抗炎因子，同时分泌胶质细胞源性神经营养因子、神经生长因子以及细胞生长因子，促进神经元的再生和修复，并清除中枢神经系统损坏的神经及感染性物质。因此，精神分裂症时，调节小胶质细胞从 M1 极化表型向 M2 极化表型转变，有助于改善疾病状态，为精神分裂症的治疗提供了新方向。

PU-0632

SDC2 基因甲基化检测技术在结直肠癌中的应用

朱艳
西安金域医学检验所有限公司

目的 验证 SDC2 基因甲基化试剂盒的分析性能，以评估其诊断结直肠癌的临床价值。
方法 在西安金域医学检验所分子诊断室，使用 SDC2 基因甲基化检测试剂盒检测 SDC2 基因甲基化阴阳性标本，进行性能验证。灵敏度：检测临床结直肠癌患者的粪便样本 10 例，采用肠镜检查或/和病理诊断结果结合的金标准方法为对照方法进行试验。特异性：检测临床非结直肠癌的粪便样本 9 例，采用肠镜检查或/和病理诊断结果结合的金标准方法为对照方法进行试验。
结果 灵敏度：10 例样本的 SDC2 基因甲基化检测结果均为阳性，与对照方法一致。特异性：9 例样本的 SDC2 基因甲基化检测结果均为阴性，与对照方法一致。总符合率：通过检测 19 例临床粪便样本，结果显示 SDC2 基因甲基化检测结果与对照方法完全一致。
结论 SDC2 基因甲基化检测试剂盒的灵敏度、特异性 2 项性能指标均合格，表明该试剂盒对结直肠癌有较高的辅助诊断价值，可用于临床结直肠癌的辅助诊断。

PU-0633

TCT 联合 HR-HPV DNA 在维吾尔族妇女宫颈癌前期筛查中的应用

佟晓洁、刘静、高婷、孙亚红、胥翠合
新疆金域医学检验所有限公司

目的 宫颈癌是女性两癌之一，是严重影响女性健康的肿瘤疾病。维吾尔族是新疆人数最多的少数民族，该民族的妇女宫颈癌患病率较高。单一的宫颈液基薄层细胞学（TCT）筛查或人乳头瘤病毒（HPV）的感染及基因亚型分析筛查，很难确保诊断的精确性，采取 TCT 联合 HR-HPV DNA 筛查，能够降低漏诊以及误诊的风险，为临床诊断提供更多依据。
方法 收集 2021 年 1-5 月送至新疆金域医学检验所有限公司的育龄维吾尔族妇女受检者 500 例，年龄 18-58 岁，平均年龄 (32.35±4.52) 岁，均进行 TCT 检测和 HR-HPV DNA 检测， 最终以病理活检结果为金标准，统计并比较不同检查方法的检出情况。分析 TCT 联合 HR-HPV DNA 检测在维吾尔族妇女宫颈癌癌前病变筛查中的应用价值。
结果 500 例受检者中，经病理活检确诊宫颈低级别鳞状上皮内病变 175 例，宫颈高级别鳞状上皮内病变 108 例，宫颈癌 13 例；TCT 联合 HR-HPV DNA 检测筛查宫颈癌及癌前病变的准确度为 92.18%， 灵敏度为 93.83%， 特异度为 87.65%。
结论 HPV 与 TCT 的联合使用，极大降低了宫颈癌筛查的漏诊率 ,能够有效、精准地筛查出维吾尔族妇女宫颈癌及癌前病变，为社区医疗服务提供精准治疗的参考依据。同时，结合实际实验中收集的维吾尔族妇女宫颈病变中 HPV 的亚型感染的特点，针对新疆地区维吾尔族妇女 HPV 疫苗的研制提供研发依据，进而为维吾尔族妇女宫颈癌的预防、诊断及治疗提供可靠的参考依据。

PU-0634

Remarkable inhibition effects of afatinib alone or in combination with paclitaxel in esophageal squamous cell carcinoma

Liyan Yang[1]、Zhijian Cheng[2]、Na Zhang[1]、Zhilu Fan[1]、Jiajie Hao[1]、Mingrong Wang[1]
1. National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College
2. 黄山市人民医院

Background and Aim Esophageal squamous cell carcinoma (ESCC) is a serious threat to the life and health of people. To date, chemotherapy drugs do not work well in ESCC, and none of the targeted drugs have been applied in the clinical therapy. Thus, it is urgent to develop targeted therapy for the treatment of ESCC. This study was performed to identify effective small-molecule inhibitors or combinations and to explore the suitable biomarkers associated with the inhibitor in esophageal squamous cell carcinoma.
Methods The effect of of 40 FDA approved small-molecule inhibitors were first tested in five ESCC cell lines. CCK8 assays and xenografts derived from ESCC cell lines were performed to evaluate the anti-ESCC effects of inhibitors or chemotherapeutic agents in vitro and in vivo, respectively. Immunohistochemistry was utilized to analyze the p-EGFR expression in tissues. Western blot combining with gray analysis was conducted to detect the expression of interest protein. Flow cytometry and immunofluorescence assay were used to analyze apoptosis, cell cycle, and mitotic changes after drug treatment.
Results Afatinib showed remarkable effects on inhibiting ESCC cells with higher expression of p-EGFR. Results from combinatorial screening in ESCC cells expressing lower phosphorylation level of EGFR showed that paclitaxel and afatinib presented a significant synergistic inhibitory

effect (P < 0.001). Molecular analysis revealed that paclitaxel sentisized afatinib by activating EGFR, and afatinib in combination with paclitaxel effectively blocked MAPK pathway, induced G2/M cell arrest and apoptosis which is an indicator of mitotic catastrophe.
Conclusions Our data demonstrate that afatinib is an effective drug for patients with ESCC expressing higher phosphorylation level of EGFR. And for patients with lower p-EGFR in tumors, paclitaxel in combination with afatinib might be a promising therapeutic strategy in ESCC.

PU-0635

河南地区肺癌 EGFR 基因突变分型临床特征分析

朱丽蒙、韩雪莹、马楠、任晓妮、王小乐、张暨
郑州金域临床检验中心有限公司

目的 研究河南地区肺癌患者表皮生长因子受体（epidermal growth factor receptor,EGFR）基因突变分型特征，探讨其临床意义。
方法 收集 895 例来自河南省各地市的肺癌患者的诊断资料，用 NGS 技术检测 EGFR 基因全外显子区域的突变状态，包括点突变、小片段插入和缺失、拷贝数扩增等突变类型。统计 EGFR 基因各突变分型阳性率，阐述 EGFR 突变分型特征。
结果 河南地区肺癌 EGFR 基因各突变分型的总阳性率为 53.97%，其中单突变占 83.4%，复合突变占 16.5%；常见突变分型 L858R、19DEL 、20INS、T790M、扩增，阳性率分别为：24.02%、22.12%、1.56%、2.46%、3.91%，突变阳性率之间，有统计学差异（P<0.05）。肺腺癌与肺鳞癌相比，EGFR 基因突变型总阳性率和 L858R、19DEL 阳性率，均有统计学差异（P<0.05）；而 20ins 和扩增的阳性率，无统计学差异（P>0.05）。转移性肺癌的 L858R、19DEL、扩增阳性率与肺癌总体水平相比，有统计学差异（P<0.05）。男性和女性肺癌患者之间，只有 EGFR 基因扩增阳性率无统计学差异（P>0.05），其他突变分型的阳性率有统计学差异（P<0.05）。组织 FFPE 样本和血浆样本之间，各突变分型阳性率和总阳性率无统计学差异（P>0.05）。
结论 河南地区肺癌样本中，EGFR 基因突变阳性率 53.97%；EGFR 基因突变分型在肺腺癌、肺鳞癌、转移性肺癌中分布特征不同；采用 NGS 检测肺癌 EGFR 基因，阳性率在性别之间和不同病理分型之间存在统计学差异，但组织 FFPE 和血浆样本之间无统计学差异，后者提示液体活检对没有足够组织检测的患者是一种有效的辅助诊断方法。

PU-0636

Serum microRNAs as biomarkers for the noninvasive early diagnosis of biliary tract cancer

Yueting Han、Li Ren
Tianjin Medical University Cancer Institute and Hospital

Background Biliary tract cancers (BTCs) are aggressive malignancies with difficult early diagnosis and poor prognosis. Studies have shown that microRNAs (miRNAs) are expected to be biomarkers of the disease, which indicates that we can diagnose cancers according to the miRNAs that have significant changes. The aim of this study was to explore miRNA biomarkers of BTCs.
Methods A total of 163 samples were collected and divided into the control group, the benign group and the malignant group. High-throughput low density chips were used to screen miRNAs with significant changes. Then, the preliminary screening test and the verification test were performed by quantitative real time PCR (qRT-PCR). Finally, the level of miRNAs in serum exosomes was measured.

Results MiR-10a, miR-21, miR-135b, miR-221, and miR-214 were upregulated in the BTCs group compared to the control group. The change in the miR-221 level was statistically significant when the malignant group was compared with the benign group (P<0.01). Meanwhile, miR-135b and miR-214 were enriched in serum exosomes.
Conclusion Five miRNAs in the serum were found to be significantly upregulated in patients with BTCs. Among them, miR-221 can serve as an early diagnostic marker for BTCs patients. MiR-10a, miR-21, miR- 135b and miR-214 can be used as biomarkers for the diagnosis of biliary diseases.

PU-0637

外泌体 miR-214 调控肝脏间质细胞 NKRF/NF-κB/IL-6 通路促进胆管癌肝转移的机制研究

韩月婷、任丽
天津医科大学肿瘤医院

目的 探索胆管癌细胞来源的外泌体 miR-214 通过调控肝脏巨噬细胞中的 NKRF/NF-κB/IL-6 通路产生炎症因子，形成肿瘤转移微环境，从而促进胆管癌肝转移的分子机制。
方法 本研究选取了胆管癌细胞系（HCCC-9810）和肝脏巨噬细胞系（THP-1 细胞诱导）。首先，用 miR-214 mimic/inhibitor 转染 HCCC-9810 细胞后，检测用 HCCC-9810 源性外泌体处理 THP-1 细胞中 miR-214 的水平。然后，在巨噬细胞系中分别上调和下调 miR-214 的表达，利用 western blot、ELISA 方法测 NF-κB 和 IL-6 的表达情况，将其与胆管癌细胞系非接触式共培养，采用 transwell、CCK-8 等方法检测肝脏间质细胞对胆管癌的迁移、增殖能力的影响。
结果 通过生物信息学预测 miR-214 和 NKRF 存在相互作用，并且胆管癌细胞源性外泌体 miR-214 可被 THP-1 细胞摄取。western blot 实验发现转染 miR-214 mimic 的 THP-1 细胞内 NF-κB 的表达量明显高于对照组，而转染 miR-214 inhibitor 的 THP-1 细胞内 NF-κB 的表达量明显低于对照组，P<0.05；ELISA 实验发现转染 miR-214 mimic 的 THP-1 细胞对 IL-6 的分泌量明显高于对照组，而转染 miR-214 inhibitor 的 THP-1 细胞对 IL-6 的分泌量明显低于对照组，P<0.05。此外，CCK8 和 transwell 实验显示胆管癌细胞与活化的 THP-1 细胞共培 48h 后，其增殖和迁移的数量差异均具有统计学意义。
结论 胆管癌细胞分泌的外泌体 miR-214 能够调控胆管癌细胞和肝脏间质细胞的相互作用，负调控 NKRF 的表达并激活 NF-κB/IL-6 通路使肝巨噬细胞活化，产生炎症因子形成肝脏转移前微环境，促进胆管癌的肝转移。

PU-0638

PAX1 基因甲基化检测在宫颈癌筛查中的应用

袁超、赵敬杰
山东大学第二医院

目的 检测配对盒家族基因 1（PAX1）基因启动子区域甲基化修饰，初步探讨 PAX1 基因甲基化在宫颈癌早期筛查中的临床应用价值。
方法 收集山东大学第二医院 2017 年 6 月至 2019 年 4 月已有宫颈病理结果的宫颈脱落细胞样本 606 例，其中 CINⅢ和宫颈癌样本共 224 例，CINⅡ、CINI 和健康女性共 382 例，提取 DNA，采用 PAX1 基因甲基化检测试剂盒进行样本甲基化水平检测。利用 ROC 曲线分析评估 PAX1 基因甲基化水平区分 CIN3、宫颈癌与 CIN2、CIN1、健康个体的能力。

结果 与 CIN2，CIN1 和健康个体相比，CIN3 和宫颈癌中 PAX1 基因甲基化水平显着增加。PAX1 基因甲基化检测侦测 CINⅢ+的灵敏度和特异度分别为 76.2% (95% CI: 69.4%-82.5%)和 90.6%（95%CI: 86.1%-93.3%)。

结论 PAX1 基因甲基化检测能有效检测宫颈癌前病变 CINⅢ及宫颈癌，具有较高的灵敏度和特异度，可联合细胞学检查提高确诊率；亦可作为 HR-HPV(+)后分流管理宫颈，降低阴道镜转诊率。

PU-0639

食管癌患者血清 LINC00189 表达及其临床意义

袁超、赵敬杰
山东大学第二医院

目的 检测食管癌患者血清中 LINC00189 表达水平，评估其表达水平与临床病理参数的关系，并探讨其临床诊断价值。

方法 利用 Kaplan-Meier Plotter 分析 LINC00189 表达水平与肺癌患者生存率关系，实时荧光定量 PCR（qRT-PCR）检测癌组织与相应癌旁组织中 LINC00189 的表达以及体检健康者及食管癌患者血清中 LINC00189 的表达水平，分析其与食管癌患者临床病理参数的相关性，并用 ROC 曲线分析其诊断效能。

结果 Kaplan-Meier Plotter 结果表明 LINC00189 表达水平与肺癌患者的生存率呈负相关。我们收集了 60 例新鲜的食管癌组织，qRT-PCR 的方法检测了癌组织与相应癌旁组织中 LINC00189 的表达，结果表明，癌组织中 LINC00189 的表达水平显著高于癌旁组织。LINC00189 在食管癌患者血清中的平均含量较体检健康者均明显升高(P＜0.01)，且与淋巴结转移、浸润深度和 TNM 分期相关(r 分别为 0.632、0.518 和 0.447，P 均＜0.01)；食管癌患者血清 LINC00189 的 ROC 曲线下面积为 0.873，95％可信区间(CI)为 0.806～0.939。

结论 LINC00189 在食管癌患者癌组织及血清中呈高表达，且与淋巴结转移、浸润深度和 TNM 分期相关，具有食管癌诊断潜在应用价值。

PU-0640

Snail/PRMT5/NuRD complex contributes to DNA hypermethylation in cervical cancer by TET1 inhibition

Jie Gao
The Second Hospital, Cheeloo College of Medicine, Shandong University
山东大学

The biological function of PRMT5 remains poorly understood in cervical cancer metastasis. Here, we report that PRMT5 physically associates with the transcription factor Snail and the NuRD(MTA1) complex to form a transcriptional-repressive complex that catalyzes the symmetrical histone dimethylation and deacetylation. This study shows that the Snail/PRMT5/NuRD(MTA1) complex targets genes, such as TET1 and E-cadherin, which are critical for epithelial-mesenchymal transition (EMT). This complex also affects the conversion of 5mC to 5hmC. This study demonstrates that the Snail/PRMT5/NuRD(MTA1) complex promotes the invasion and metastasis of cervical cancer in vitro and in vivo. This studyalso shows that PRMT5 expression is upregulated in cervical cancer and various human cancers, and the PRMT5 inhibitor EPZ015666 suppresses EMT and the invasion potential of cervical cancer cells by disinhibiting the expression of TET1 and increasing 5hmC, suggesting that PRMT5 is a potential target for cancer therapy.

PU-0641

Phosphorylation of islet-1 serine 269 by CDK1 increases its transcriptional activity and promotes cell proliferation in gastric cancer

Qiong Shi [1]、Xiaomei Ni[1]、Ming Lei[1]、Quansong Xia[1]、Yan Dong[1]、Qiao Zhang[2]、Weiping Wang[3]
1. Clinical Laboratory, School of Clinical Oncology, Kunming Medical University & Yunnan Cancer Center, Yunnan, Kunming, P. R. China.
2. 昆明医科大学
3. 北京大学

Background Despite recent advances in diagnostic and therapeutic approaches for gastric cancer (GC), the survival of patients with advanced GC remains very low. Islet-1 (ISL1) is a LIM-homeodomain transcription factor, which is upregulated and promotes cell proliferation in GC. The exact mechanism by which ISL1 influences GC development is unclear.
Methods Co-immunoprecipitation (co-IP) and glutathione S-transferase (GST)-pulldown assays were employed to evaluate the interaction of ISL1 with CDK1. Western blot and immunohistochemistry analyses were performed to evaluate the ability of CDK1 to phosphorylate ISL1 at Ser 269 in GC cell and tissue specimens. Chromatin immunoprecipitation (ChIP), ChIP re-IP, luciferase reporter, and CCK-8 assays were combined with flow cytometry cell cycle analysis to detect the transactivation potency of ISL1-S269-p and its ability to promote cell proliferation. The self-stability and interaction with CDK1 of ISL1-S269-p were also determined.
Results ISL1 is phosphorylated by CDK1 at serine 269 (S269) in vivo. Phosphorylation of ISL1 by CDK1 on serine 269 strengthened its binding on the cyclin B1 and cyclin B2 promoters and increased its transcriptional activity in GC. Furthermore, CDK1-dependent phosphorylation of ISL1 correlated positively with ISL1 protein self-stability in NIH3T3 cells.
Conclusion ISL1-S269-p increased ISL1 transcriptional activity and self-stability while binding to the cyclinB1 and cyclinB2 promoters promotes cell proliferation. ISL1-S269-p is therefore crucial for tumorigenesis and potentially a direct therapeutic target for GC.

PU-0642

纺锤体检查点蛋白 Cenp-E 过低表达是肝癌细胞染色体数目异常的重要原因

刘斌
南华大学附属第二医院

目的 在肝癌细胞系（HepG-2）和正常肝细胞系（LO2）中研究 Cenp-E（纺锤体检查点蛋白 E）基因在肝癌细胞中的定位和作用。为进一步阐明肝癌细胞染色体数目异常的机理奠定基础。
方法 利用 FQ-PCR 检测 Cenp-E 基因在用 Nocodazole（诺考达唑）同时处理 HepG-2 细胞和 LO2 细胞中 mRNA 的表达水平。同时用间接免疫荧光技术观察 Cenp-E 蛋白在其中的定位及表达。在 LO2 细胞中用 RNAi 技术干扰 Cenp-E 基因来进一步评价细胞功能情况。
结果 Nocodazole 处理前 cenp-E 基因和蛋白在 LO2 和 HepG-2 细胞中表达无显著差异，处理后 cenp-E 基因和蛋白在两种细胞表达都增高，但 LO2 细胞上调水平大于 HepG-2 细胞。间接免疫荧光结果显示 Cenp-E 在出现异常分裂的细胞核内 Cenp-E 蛋白的表达明显低于正常分裂的细胞核。在干扰 Cenp-E 的 LO2 细胞中出现核异常比例明显高于正常细胞。
结论 Cenp-E 过低表达可能是肝癌细胞染色体数目异常重要原因之一。

PU-0643

CircBCBM1 promotes breast cancer brain metastasis by modulating miR-125a/BRD4 axis: a novel diagnostic and therapeutic target

Bo Fu、Wei Liu、Li Pan、Anqi Zhang、Wenqiang Tang、Meng An
Liaocheng People's Hospital

Circular RNAs (circRNAs) play critical roles in tumorigenesis and the progression of various cancers. We previously identified a novel upregulated circRNA, circBCBM1, in the context of breast cancer brain metastasis. However, the potential biological function and molecular mechanism of circBCBM1 in breast cancer brain metastasis remain largely unknown. In this study, we confirmed that circBCBM1 was a stable and cytoplasmic circRNA. Functionally, circBCBM1 promoted the proliferation and migration of 231-BR cells in vitro and growth and brain metastasis in vivo. Mechanistically, circBCBM1 acted as an endogenous miR-125a sponge to inhibit miR-125a activity, resulting in the upregulation of BRD4 (bromodomain containing 4) and subsequent upregulation of MMP9 (matrix metallopeptidase 9) through Sonic hedgehog (SHH) signaling pathway. Importantly, circBCBM1 was markedly upregulated in the breast cancer brain metastasis cells and clinical tissue and plasma samples; besides, circBCBM1 overexpression in primary cancerous tissues was associated with shorter brain metastasis-free survival (BMFS) of breast cancer patients. These findings indicate that circBCBM1 is involved in breast cancer brain metastasis via circBCBM1/miR-125a/BRD4 axis. CircBCBM1 may serve as a novel diagnostic and prognostic biomarker and potential therapeutic target for breast cancer brain metastasis.

PU-0644

GFPT1 基因复合杂合突变引起的先天性肌无力综合征

刘思文、姜艳芳
吉林大学第一医院

目的 鉴定 1 例先天性肌无力综合征患者的致病基因并分析突变带来的疾病表型。
方法 对先证者及其父母进行家系全外显子组分析,并用用一代测序进行验证。
结果 发现两种杂合错义突变(c.331C>T;p。Arg111Cys c.1428G > C;p.Lys476Asn)。GFPT1 基因编码谷氨酰胺-果糖-6-磷酸转氨酶 1，在这例常染色体隐性遗传的 CMS 患者中， c.1428 g > C;p.Lys476Asn 是一个以前没有文献报道过的新的突变体，在 ClinVar 数据集和 gnomAD 全球人口数据集中也没有记录过。我们在此报告 1 例患有 CMS 的患者的遗传变异和临床随访。先证者表现为肢体无力，在肢体活动后症状加重。此外，在先证者中，重复性神经刺激可导致肌肉动作电位下降。因此，最初怀疑是重症肌无力，但他从未出现眼睑下垂和视力模糊。先证者的表型与既往关于 CMS 和 TAs 的报道一致。
结论 本研究为 CMS 患者提供了一个新的 GFPT1 基因突变。本研究为 CMS 患者的诊断和治疗提供了重要信息。

PU-0645

PARP1 rs1136410 Val762Ala contributes to an increased risk of overall cancer in the East Asian population: a meta-analysis

yi juan xin、liu yang、mingquan su、xiaoli cheng、lin zhu、jiayun liu
Air force medical uiversity xijing hospital

Objectives To investigate the association between poly(ADP-ribose) polymerase 1 (PARP1) rs1136410 Val762Ala and cancer risk in Asian populations, as published findings remain controversial.
Methods The PubMed and EMBASE databases were searched, and references of identified studies and reviews were screened, to find relevant studies. Meta-analyses were performed to evaluate the association between PARP1 rs1136410 Val762Ala and cancer risk, reported as odds ratio (OR) and 95% confidence interval (CI).
Results A total of 24 studies with 8 926 cases and 15 295 controls were included. Overall, a significant association was found between PARP1 rs1136410 Val762Ala and cancer risk in East Asians (homozygous: OR 1.19, 95% CI 1.06, 1.35; heterozygous: OR 1.10, 95% CI 1.04, 1.17; recessive: OR 1.13, 95% CI 1.02, 1.25; dominant: OR 1.13, 95% CI 1.06, 1.19; and allele comparison：OR 1.09, 95% CI 1.03, 1.15). Stratification analyses by race and cancer type revealed similar results for gastric cancer among the Chinese population.
Conclusion The findings suggest that PARP1 rs1136410 Val762Ala may be significantly associated with an increased cancer risk in Asians, particularly the Chinese population.

PU-0646

Clinical features and genetic variations in five neonates with severe hyperbilirubinemia: case report

Fen Lin [1]、liye yang[2]
1. Laboratory Medical Center, Chaozhou Central Hospital Affiliated to Southern Medical University, Chaozhou, China
2. 阳江市人民医院

Background Neonatal hyperbilirubinemia is a common problem faced by pediatricians. The role of genetic factors in neonatal jaundice has been gradually recognized. This study aimed to identify genetic variants which influence the bilirubin level in five representative cases by next-generation sequencing (NGS).
Case presentation We present five neonates with severe hyperbilirubinemia, they exhibited bilirubin encephalopathy, hypothyroidism, ABO hemolysis, glucose-6-phosphate dehydrogenase (G6PD) deficiency and premature, respectively. A customed 22 genes panel was designed and NGS was carried out in the neonates. Eight variations (G6PD c.G1388A, HBA2 c.C369G, SPTB c.A1729G, ABCC2 c.C3825G, UGT1A1 c.G211A, EB41c.G520A, c.1213-4T>G and c.A1474G) were identified in five patients, which involved in genetic mutations associated with hereditary elliptocytosis, thalassemia, Gilbert syndrome, G6PD deficiency and Dubin-Johnson Syndrome. One of the patients was found with variants combined EPB41 splice site c.1213-4T>G and c.G520A (p.E174K) mutation but no elliptocyte was seen on his blood smear.
Conclusions Pathological factors of severe neonatal hyperbilirubinemia were very complicated, genetic variants may play an important role for an increased risk of neonatal hyperbilirubinemia, and severe jaundice in neonates may be potentially related to the cumulative effect of genetic variants.

PU-0647

氯化两面针碱对胶质瘤细胞 LN18 上皮-间质转化的抑制作用

李峣、贾茗博、孙莹、宋燕珂、汪敏、赵丽艳
吉林大学第二医院

有研究表明，氯化两面针碱(nitidinechloride, NC)能抑制肿瘤细胞的 EMT(epithelial-mesenchymal transition, EMT)过程，从而抑制肿瘤生长。但 NC 在胶质瘤细胞中扮演的角色及有关机制尚未被揭示，本文对这一问题进行探讨。本文应用划痕愈合实验、Transwell 侵袭实验和 Western blotting 法分别检测细胞迁移、侵袭能力及蛋白表达水平。划痕愈合实验和 Transwell 侵袭实验结果显示，与对照组相比，经 TGF-β1 刺激后的 LN18 细胞划痕距离明显缩小，穿膜数量明显增多，说明诱导 EMT 使细胞迁移和侵袭能力增强(P<0.01）。加入 NC 后，与 EMT 组的 LN18 细胞相比，细胞划痕距离增大，穿膜数量减少，说明 NC 可以抑制 LN18 细胞 EMT 引起的细胞迁移和侵袭能力的增强(P<0.01），并且这种抑制能力与 NC 浓度相关。Western blotting 结果显示，与对照组相比，TGF-β1 处理后的 LN18 细胞上皮标志物表达降低，间质标志物表达升高，加入不同浓度 NC 后，与 EMT 组相比，LN18 细胞上皮标志物表达增加(P<0.05），间质标志物表达降低(P<0.01），说明 NC 对胶质瘤 LN18 细胞 EMT 有明显抑制作用，且与 NC 浓度有关。对 JAK2/STAT3 蛋白表达水平检测结果显示，加入不同浓度 NC 后，与 EMT 组相比，JAK2、p-JAK2、STAT3 和 p-STAT3 蛋白表达水平明显降低(P<0.01），说明 NC 可以抑制 LN18 细胞 JAK2/STAT3 信号通路。用 STAT3 抑制剂 WP1066 阻断 JAK2/STAT3 信号通路的效果与 NC 相同，说明 NC 可以通过阻断 JAK2/STAT3 信号通路抑制 LN18 细胞 EMT 过程。以上实验结果表明，NC 可以抑制胶质瘤 LN18 细胞的 EMT 过程，并且这种作用可能与 JAK2/STAT3 信号通路有关。

PU-0648

IL-35 通过调节乳腺肿瘤细胞来源外泌体的 mRNA 表达谱促进肿瘤血管生成

刘佳、董娜娜
山东大学第二医院

目的 研究表明，肿瘤细胞可通过分泌各种生物活性介质促进肿瘤血管的生成。外泌体（exosomes）是具有双层磷脂分子膜的细胞外囊泡，能够由大多数细胞分泌并被受体细跑吞噬。对乳腺 TME 的研究表明，肿瘤细胞来源的外泌体可以通过与周围的基质细胞交流向受体细胞传递特定信息，从而改善肿瘤细胞的生长环境，促进肿瘤的生长。研究表明，乳腺肿瘤细胞和肿瘤局部浸润淋巴细胞均可表达抑制性细胞因子 IL-35。因此我们着重探讨 IL-35 影响乳腺肿瘤细胞分泌的外泌体在 TME 中的血管生成作用。

方法 1、超速离心法分离乳腺肿瘤细胞外泌体；透射电子显微镜和纳米颗粒跟踪分析技术鉴定外泌体的形态和直径；Western-blot 检测外泌体表面标志蛋白 CD9 和 TSG101。激光共聚焦显微镜观察 HUVECs 对外泌体的摄取。

2、用乳腺肿瘤细胞来源的外泌体(con-Exos)和 IL-35 刺激后的肿瘤细胞分泌的外泌体(IL-35-Exos)分别诱导 HUVECs，CCK8 及流式细胞术检测 HUVECs 的增殖活性及细胞周期变化，成管试验及鸡胚绒毛尿囊膜血管试验分析 HUVECs 成管能力。

3、基因芯片技术分析 con-Exos 和 IL-35-Exos 内 mRNA 表达谱，筛选出显著差异的基因。

结果 与 con-Exos 相比，IL-35-Exos 显著促进 HUVECs 增殖且显著增强了 HUVECs 细胞的成管能力。分析 con-Exos 和 IL-35-Exos 内 mRNA 表达谱，GO 和 KEGG 结果显示，差异基因参与血管生成和细胞增殖，并在 RAS 和 PPAR 信号通路中发挥作用。

结论 本部分的研究表明，乳腺肿瘤细胞来源的外泌体可以被 HUVECs 内吞，并促进肿瘤微环境中的血管生成。IL-35 通过改变乳腺肿瘤细胞来源外泌体的 mRNA 增强其血管生成作用。

PU-0649

The clinical significance of UBE2C gene in progression of renal cell carcinoma

zhiping chen
First affiliated Hospital of Gannan Medical University

Purpose This study proves that UBE2C is an important gene in RCC and is essential to proliferation and migration of RCC.

Methods Bioinformatics analysis and TCGA mining In order to analyze the differential expression levels of UBE2C in RCC and normal renal tissues, TCGA database was extracted. The mRNA expression level of UBE2C from a total of 525 cases of RCC and 72 cases of normal renal tissues was downloaded from the TCGA database (https://cancergenome.nih.gov/). Then, RStudio (Version 1.1.442), a free and open-source data analysis software, was used to analyze the differential expression of UBE2C and to deduce the overall survival (OS) and disease-free survival (DFS) curves. Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) were used in conjunction with DAVID 6.8 and Enrichment Map plug-in Cytoscape to visualize the significant pathways and differential expression genes (DEGs) in RCC.

RCC tissues and pathological information of patients A total of 90 RCC tissues and matched normal tissues were retrospectively collected to perform RT-qPCR analysis. All the patients had received radical operation in our hospital from July 2006 to December 2010.The last follow-up time was August 2017. The pathologic diagnosis of all cases was renal clear cell carcinoma after operation. This study was approved by the Ethics Committee of First affiliated Hospital of Gannan Medical University and written consent was collected from all patients.

RT-qPCR Total RNA of renal cancer tissues and matched normal tissues was extracted with TRIzol (Invitrogen, USA) and treated with RNase-free DNase (Promega, USA). SYBR Green quantitative real-time PCR was performed by Stepone Real-time PCR system (Applied Biosystems 7000, USA). Beta-actin was used as the internal control. Relative expression level of each gene was calculated by the 2-△△Ct method, in which △△Ct=Test group △Ct (CTinterested gene-CTBeta-actin) - Control group △Ct (CTinterested gene-CTBeta-actin)

Immunohistochemical analysis Human tumor tissues were fixed in 4% paraformaldehyde, embedded in paraffin and sectioned as 5 μm. Each sectioned tissues were incubated with antibody against UBE2C (1:500, ab252940, Abcam, NY, USA) diluted with 0.01 M PBST buffer (0.01 M PBS, 0.001×Triton X-100)for 12 h at 44°C followed by HRP-conjugated secondary antibody (1:100, Beyotime, Shanghai, China). Peroxidase conjugates were determined using 3,3′-diaminobenzidine solution.

RNA interference assay (RNAi) siRNA fragments targeting human UBE2C gene (siUBE2C: 5'-TCCTTTTTGTGATTTCTGTATAG-3') was designed and synthesized. Random sequence was designed as negative control (NC). Then RCC typical cells 786-O cells were cultured in a 6-well plate and transduced with siUBE2C or NC (General Biosystems, Anhui, China) by Lipo reagent (Yeasen, Shanghai, China) for 4-6 h according to the manufacture's instruction. The knockdown efficiency of siUBE2C was tested by RT-qPCR method.

Cell proliferation assay Treated cells were seeded into a 96-well plate at 5×103 cell/well and cultured consecutively for 96 h. At each designed time point, 10 μL of CCK-8 agent was added and cultured for another 1-2 h. Then OD value at 450 nm was detected on microplate reader (Molecular Devices, CA, USA). The proliferation rate of cells was calculated according to the negative control.

Cell invasion assay Transwell rooms with 8-μm-pore size membrane were pre-treated with 0.2 mL Matrigel 12 h before seeding tumor cells. Then a total of 2×104 cells/well was seeded into upper room and DMEM medium without FBS was added. DMEM medium containing15% FBS

was added in the lower room. After culture for 24 h, cells on the upper room were removed and cells in the lower surface of upper room were fixed by 4% paraformaldehyde for 30 min and dyed with 0.5% crystal violet for 10 min. Then stained cells were observed under a microscope and counted.
Statistical analysis SPSS 16.0software (SPSS, Inc., Chicago, IL, USA) was used to analyze the experimental data. All data was expressed as mean±SD. TCGA data were analyzed by the independent samples t-test to compare the differential levels of UBE2C mRNA between RCC and control. Chi-square test or Fisher's exact test was employed to analyze the relationship between UBE2C expression and clinicopathological factors of RCC patients. Kaplan-Meier analysis was used to produce the survival curve. Univariate and Cox multivariate survival analyses were performed to analyze the prognostic significance of UBE2C in RCC patients. The difference was considered statistically significant when the p-value was less than 0.05.
Results UBE2C was highly expressed in RCC. UBE2C was correlated to clinicopathological factors in RCC patients. UBE2C showed prognostic value in RCC. Identification of potential signaling pathways associated with UBE2C in RCC. UBE2C is important for cell proliferation in RCC. UBE2C contributes to cell migration in RCC.
Conclusion This study proves the clinical role of UBE2C and suggests it to be an important prognostic factor in RCC. UBE2C contributes to the proliferation and migration in RCC.

PU-0650

纳米孔测序技术在病原微生物感染检测中的应用评价

何沛
新疆生产建设兵团第六师医院

目的 利用纳米孔三代测序技术，对临床样本中的病原微生物进行靶向测序检测，探讨纳米孔三代测序在病原微生物感染检测中的应用价值，为临床早期诊断与治疗提供支持。
方法 1.采用收集临床样本对该技术进行临床评价：1）104 份收集临床阳性样本评价检测灵敏度，包含血流感染相关的 5 种病原微生物。2）用不同浓度的病原微生物灵敏度质控品评价最低检出限。3）模拟 30 例临床阴性样本评价检测特异性。采用纳米孔检测对样本和质控品进行测序检测，采用 qPCR 和三代测序方法做同步验证。纳米孔测序检测流程包括：①提取病原微生物核酸；②设计针对细菌和真菌高度保守序列的通用引物及特异性靶向引物，多重靶向扩增病原微生物特定序列；③对扩增产物进行靶向文库构建和纳米孔测序；④生信分析。 2. 用所建立的方法和传统的细菌培养方法，分别对 23 例下呼吸道感染患者的肺泡灌洗液标本进行病原体检测，并进行一代测序验证，比较检出率及病原种类。
结果 1）104 例阳性样本中检出大肠埃希氏菌 34 例、金黄色葡萄球菌 15 例、白色念珠菌 43 例、EB 病毒 6 例、巨细胞病毒 6 例，与 qPCR 和三代测序法检测结果一致性为 100%。2）最低检出限为：大肠埃希氏菌和金黄色葡萄球菌 100cps/mL，白色念珠菌 100cps/mL，EB 病毒和巨细胞病毒 500cps/mL。3）30 例模拟阴性样本中，检测特异性为 100%。从样本处理到出分析报告全流程于 8h 之内完成，单个样本数据量达 50M 左右，测序序列矫正检测准确度大于 99.2%。 2. 23 例患者的测序病原检出率高于细菌培养[73.9%，43.4%，P<0.05]。测序检出病原种类多于细菌培养。不同的 7 例样本使用一代测序验证，结果与纳米孔检测结果一致。
结论 同传统方法相比，纳米孔测序技术具有更短的检测周期、更高的检测灵敏度、同时检测多种病原体、检测特异性高等特点，为临床感染病原体的快速准确检测提供了新技术。

PU-0651

RNA M6A 修饰在肝癌治疗的研究现状与展望

周英杰、尹文君
南华大学附属第一医院

RNA 的甲基化 N6-甲基腺苷 m6A（N6-methyl-adenosine)修饰是指发生在 RNA 分子(包括 mRNA 和非编码)上不同位置的甲基化修饰现象、是真核生物信使 RNA(MRNAs)中丰度最高的内部修饰，作为一种可逆表观遗传修饰，m6A 不仅存在于信使 RNA 中，而且还存在于非编码 RNA 中，影响修饰 RNA 分子的命运，在几乎所有重要的生物过程中发挥重要作用，包括癌症的发生。其他 mRNA 修饰，包括 N1-甲基腺苷(M1A)、5-甲基胞嘧啶(M5C)和假尿苷，与 M6A 一起形成表位编码组，共同编码控制蛋白质合成的新信息层。M6A 修饰的 mRNA 的作用依赖于识别它们的不同蛋白(即阅读器)的功能，取决于不断扩大的 m6A 阅读器和 m6A 编写器复合体以及潜在的擦除器影响，这些潜在的擦除器目前与转录组中 m6A 的流行丰度尚不清楚。M6A 修饰由由 METTL3、METTL14 和 WTAP 组成的 M6A 甲基转移酶复合物(MTC；即 WRITER)沉积，也可能由 Virma 和 RBM15 组成，并且可以被诸如 FTO，ALKBH5 和 ALKBH3 的 M6A 去甲基酶(即擦除器)去除，并与 m6A 结合蛋白相互作用，如 YTHDF1/2/3, IGF2BP1/2/3, HNRNP, eIF3 (读取器)。RNA 甲基转移酶、去甲基化酶和 m6 结合蛋白在来自不同人类器官的癌症组织中经常上调，增加癌基因转录和癌蛋白的表达，促进癌细胞的增殖、存活、影响肿瘤的启动、进展和转移。近来多项研究结果也表明 m6A 修饰及其相关蛋白的失调通过调节肿瘤相关基因的表达参与肝癌的发生与转移。越来越多的小分子抑制剂已被确定为靶向 m6A 调节剂，并具有治疗各种肝病的潜力。本文将会对 m6A 修饰(编码和非编码 RNA)基因异常修饰的生物学功能、潜在分子机制及在肝癌中的发病机制，靶向 m6A RNA 修饰如何成为治疗肝病的有效新策略等方面的最新研究成果进行综述。

PU-0652

基于四种生物标志物建立急性髓系白血病预后风险评分体系

匡野、高辉、曹向红、王杨、董玉琳、李红燕、程云、孔凡斌
昆明市延安医院

目的 根据生物信息学筛选的生物标志物，建立急性髓系白血病（AML）预后评分系统。
方法 从 UCSC Xena 和 GTEx 下载 151 例 AML 患者和 337 例健康人的 RNA 表达数据和临床资料。我们利用 R3.6.2 中的 dprir 和 tidyr 包，从 RNA 表达数据中筛选出差异表达的 mRNAs（DEmRNAs）。在这些 DEmRNAs 中，使用 R3.6.2 中的 survival 和 glmnet 包，采用单变量和 Lasso 回归筛选预后相关的 mRNAs。采用多变量 Cox 回归分析对这四种核心 mRNAs 与 AML 预后效果综合进行预测评分。我们进一步用 R3.6.2 中的 ESTIMATE 包对核心基因表达水平与肿瘤纯度的关系进行了比较。应用 QRT-PCR 和 western blot 方法，验证了核心 mRNAs 在 AML 细胞模型和临床标本中的差异表达。
结果 筛选了 4 个与 AML 预后相关的核心 mRNAs（FAM124B、HPDL、MPO 和 P2RY1），并与之建立预后评分系统。进一步证实了 4 个核心 mRNAs 在 AML 细胞模型和临床标本中的差异高表达。同时发现具有高免疫性和间质评分的样本，其 HPDL 和 MPO 的表达较高。
结论 本研究发现了与 AML 患者预后密切相关的 4 种 mRNAs（FAM124B、HPDL、MPO 和 P2RY1）。并在此基础上，用 4 个预后 mRNAs 构建了 AML 预后评分系统，其研究结果有助于对于 AML 的预后评估。

PU-0653

CRP 在 EBV 感染儿童中的诊断意义

王新颖
泰安市中心医院

目的 探讨 CRP 对 EBV 感染儿童诊断的临床价值
方法 选取 2018 年 1 月到 12 月在泰安市中心医院确诊的 856 例 EBV 感染的儿童和 240 例健康体检儿童，两组均检测 CRP，EBV 感染儿童检测 EBV-DNA 载量。
结果 EBV 感染儿童组的 CRP 水平显著高于健康对照组，差异有统计学意义（$p<0.05$）,EBV 低载量组患儿与高载量组的 CRP 差异无统计学意义（$p<0.05$）。
结论 CRP 的检测可作为 EBV 感染的一个诊断指标。

PU-0654

长沙 1 092 例急性下呼吸道疾病患儿病毒感染的流行病学特征分析

周杰英
郴州市第一人民医院

目的 了解长沙地区急性下呼吸道感染患儿的呼吸道病毒谱和流行病学特征，为疾病的预防和临床诊疗提供科学依据。
方法 用实时荧光定量 PCR 方法筛查 1 092 份小儿呼吸道标本，对 12 种常见呼吸道病毒进行核酸检测。
结果 1 092 例样本中，呼吸道合胞病毒阳性 437 例（40%）、副流感病毒 3 型 337 例（30.9%）、博卡病毒阳性 263 例（24.1%）、腺病毒阳性 228 例（20.8%）。男性患儿总检出率为 82.26%,女性患儿总检出率为 83.42%。呼吸道合胞病毒在≤6 月组感染率较高、副流感病毒 3 型和博卡病毒在≤2 岁患儿中感染率较高、腺病毒在 6 月～5 岁这一年龄阶段感染率较高。春季、夏季、秋季和冬季病毒感染检出率分别为 90.48%、83.50%、62.26%和 82.80%，差异有统计学意义。
结论 长沙地区急性下呼吸道患儿病毒感染以呼吸道合胞病毒和副流感病毒 3 型为主,混合感染常见。男女童感染检出率差异无统计学意义。2 岁以下患儿更容易获得急性下呼吸道感染。病毒有季节流行趋势，多在春秋季流行。

PU-0655

禽呼肠孤病毒治疗肝癌的基因表达谱及相互作用途径

蔡瑞敏、李毅、冯强、王文洋
泰安市中心医院

Background Primary liver cancer(PLC) has unquestionably been a major public health challenge which is the second most common cause of cancer-associated death worldwide. The reovirus is being investigated as an anti-cancer therapy, and has proven oncolytic effects on many types of cancers.
Methods and Results We utilized the microarray data to analyze the GRCh38 gene expression profile in 6 specimens, Gene ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis and the protein–protein interaction (PPI) network were conducted among the of DEGs, and six genes were validated using RT-qPCR analysis,and FOS, EGR2, IFIT2 and AGTR1 were identified as the hub nodes in the PPI network.

PU-0656

转录组学分析 1 型糖尿病潜在生物标志物的探讨

康建华、沈兴娅、杨立顺、冯绍华、李德来、袁海生
天津市北辰区中医医院

目的 转录组学是研究机体转录的技术，是所有 RNA 转录的总和，可以研究不同生物体的基因表达。本研究对 T1DM 患者进行转录组分析，以揭示其发病机制和进展。
方法 从基因表达（GEO）数据库中下载 GSE55098、GSE72492、GSE55099 和 GSE97123 表达谱。mRNA 表达谱 GSE55098 包括来自 12 例新 T1DM 患者和 10 例对照组的 22 个外周血单核细胞样本（PBMC）；GSE72492 包括 17 例 T1DM 患者和 7 例健康人群的胰腺组织标本。miRNA 表达谱 GSE55099 包含 12 个新 T1DM 患者和 10 个正常对照的 PBMC 样本；表达谱 GSE97123 中有 12 例 T1DM 患者和 12 例健康人血浆来源于外泌体样本，这些患者至少有 25 年的 T1DM 病史。通过不同检测平台筛选了差异表达基因（DEGs）、差异表达 miRNA，进行功能富集、通路、DEMs 靶点和 miRNA-基因对、DEGs 的蛋白-蛋白对分析和 PPI 网络构建。
结果 根据 mRNA 表达谱分别鉴定出 37 个和 110 个 DEGs，命名为短期 DEGs 和长期 DEGs。根据 miRNA 表达谱分别鉴定出 15 个和 6 个 DEMs，命名为短期 DEMs 和长期 DEMs。短期 DEGs 被富集在 6 个基因本体和 4 个通路中，长期 DEGs 被富集在了 40 个基因本体和 10 个通路中。短期 DEMs 中筛选出 17 对 miRNA-基因对，hsa-miR-181a 和 hsa-miR-181c 包含在最多对基因中。长期 DEMs 中获得了 20 对 miRNA-基因对，hsa-miR-338-3p 包含在所有的基因对中。KLRD1 参与了短 DEGs 的 PPI 网络中更多的配对。在长期 DEGs 的 PPI 网络中，ACTA2 和 USP9Y 的配对数较多。
结论 KLRD1、hsa-miR-181a 和 hsa-miR-181c 是 T1DM 致病性的生物标志物；ACTA2、USP9Y 和 hsa-miR-338-是 T1DM 进展的生物标志物。

PU-0657

Isolation of circulating fetal trophoblasts by a four-stage inertial microfluidic device for single-cell analysis and noninvasive prenatal testing

yifang huang[1]、sheng yu[2]、guofeng guan[3]、lei zheng [4]
1. Department of Clinical Laboratory, The First Affiliated Hospital of Guangxi Medical University, Nanning, China.
2. 深圳市第三人民医院
3. 深圳 Genflow 科技
4. 南方医科大学南方医院

Noninvasive detection of circulating fetal cells carrying the entire fetal genome is a promising way for prenatal testing of genetic diseases. However, ideal approaches for efficient separation of these valuable cells are not available. Here, a novel inertial microfluidic chip (CelutriateChip 1) is developed for ultra-fast, label-free enrichment of circulating trophoblasts (CTBs) from the whole blood samples of pregnant women. The unique structural design of the four-stage curved channel in CelutriateChip 1 enables CTBs with larger size to be efficiently separated from the blood samples under the effect of inertial and Dean drag forces. The transition of the target cells among the stages enables CelutriateChip 1 to achieveone or two orders of magnitude higher throughput compared to single channel inertial microfluidic chips. After optimization of conditions, CTBs can be recovered from 2 mL of whole blood within 5 min with an average recovery efficiency ranging from 52.3% to 65.8% and high white blood cell depletion (99.95%). CTBs collected from the chip can be isolated at the single-cell level and used for downstream immunofluorescence staining and genetic genotyping. Clinical tests are performed on 30 pregnant women and the results

demonstrate that CTBs are obtainable in 86.67% of pregnancy cases. A single-base variant in the HBB gene can be accurately detected by sequencing of rare CTBs. This simple, antibody-free and low-cost holds promise for obtaining rare CTBs for prenatal detection of various genetic diseases.

PU-0658

Clinical Application of Third-Generation Sequencing Technology in Precise Molecular Detection of Rare α and β-thalassemias

SHIQIANG LUO[1]、XINGYUAN CHEN[2]、DINGYUAN ZENG[1]、NING TANG[1]、DEJIAN YUAN[1]、QINGYAN ZHONG[1]、AIPING MAO[3]、RUOFAN XU[3]、TIZHEN YAN[1]
1. Liuzhou Maternity and Child Healthcare Hospital
2. 广西壮族自治区人民医院
3. 北京贝瑞和康生物技术有限公司

Objective To compare the screening effect of the third generation sequencing technology and traditional genetic diagnostic technology on rare types of thalassemia genes, and analyze the molecular characteristics and phenotypes of rare thalassemia gene variants.
Methods Taking the 434 cases of Guangxi Zhuang Autonomous Region in China with positive hematology screening as the research object, using the third generation sequencing technology (research group) and traditional gene diagnosis technology (control group) for thalassemia gene screening.
Results Through third generation sequencing and traditional genetic diagnosis technology, a total of 361 cases of genetic testing were confirmed as positive (83.18%), of which 264 cases (60.83%) of α-thalassemia gene, 68 cases (15.67%)ofβ-thalassemia gene, and 29 cases (6.68%) of α and β compound thalassaemia gene. Among them, 318 cases (73.27%) were identified in the control group and 361 cases (83.18%) were detected in the research group. The results of testing 353 cases (81.34%) of conventional thalassaemia genes in the research group were essentially the same as those in the control group. However, the research group detected 76 more cases of 30 gene mutation types that were not detected in the control group, which are completely consistent with the verification results of Sanger sequencing or Gap-PCR. In addition, there are 5 rare cases (3 cases are diagnosed by MLPA technology. 2 cases are unclear mutations) are not in the detection range of third generation sequencing can be detected. The differences in hematological phenotypic parameters of 33 sporadic cases among 81 cases were analyzed.
Conclusion The third generation sequencing technology can increase the detection rate of thalassemia genes, with a comprehensive screening range and high efficiency, and can find rare thalassemia cases with multiple phenotypes, which is conducive to clinical thalassemia gene screening.

PU-0659

FBXW7/mTOR axis as novel biomarkers for diagnosis and metastasis prediction of colorectal cancer

Yuli Wang [1]、Yueyong Liu[1,2]、Jian Mao[2]、Guangwei Wei[3]
1. The Second Hospital of Shandong University
2. Life Sciences Division, Lawrence Berkeley National Laboratory
3. 山东大学

Purpose F-box and WD repeat domain containing 7 (FBXW7) encodes a substrate adaptor for an SCF E3 ubiquitin ligase complex and lies at the nexus of many pathways which control cell

growth, cell differentiation, and tumorigenesis by negatively regulating the abundance of different oncoproteins. Increased cell migration and invasion lead to cancer metastasis and are crucial to cancer prognosis. In this study, we explore whether FBXW7 plays any role in metastatic process.
Methods Wound healing assay, transwell assay and matrigel assay were used to detect the migration and invasion of colorectal cancer cells. Spheroid formation assay was used to detect the capability of self-renewal of colorectal cancer cells. Rapamycin was used to inhibit the mTOR signaling.
Results Depletion of FBXW7 induces epithelial-mesenchymal transition (EMT) in human colorectal cancer cells along with the increase in cell migration and invasion. Moreover, FBXW7 deficiency promotes the generation of colorectal cancer stem-like cells in tumor-sphere culture. mTOR inhibition by rapamycin suppresses FBXW7 loss-driven EMT, invasion and stemness, suggesting accumulation of mTOR in FBXW7-depleted cells play a role in induction of stem-like properties.
Conclusions EMT and stem cell-like properties are essential for tumor cells to disseminate from adjacent tissues and seed new tumors in distant sites. Our results demonstrated that FBXW7 regulated these two essential characteristics of metastatic disease through mTOR signaling pathway.

PU-0660

吉林地区非小细胞肺癌 RET 基因变异分析

何佳雪、胡欣彤、陈立国、姜艳芳
吉林大学第一医院

目的 探讨吉林地区非小细胞肺癌(NSCLC)患者 RET 基因变异情况及其基因变异特征。
方法 回顾性分析吉林地区 NSCLC 患者 RET 基因变异情况。应用高通量基因测序（NGS）技术检测 NSCLC 患者血浆、组织、FFPE、胸水样本中提取的 DNA，检测范围包括 122 个基因的点突变、插入/缺失，拷贝数变异和基因融合/重排。
结果 1060 例非小细胞肺癌患者中检出 RET 基因变异阳性 35 例，检出率为 3.3%，其中 RET 基因突变阳性 12 例，基因融合阳性 23 例，有临床意义的变异占比为 46%。最常见的 RET 融合伴侣是 KIF5B（52.1%），其中 KIF5B-RET（39.1%），RET-KIG5B（13%）。其他主要融合伴侣为 NCOA4（8.7%）、CCDC6（8.7%）、CCDC88C（4.3%）等。女性患者 RET 变异率高于男性（20 vs 15）。RET 突变阳性样本中，共检出突变 251 个，突变个数排名前 11 的突变总数为 107 个，占总数的 42.63%，最高的是 EGFR 共突变（7.7%）。RET 融合阳性样本中，共检出突变 26 个，最高的是 EGFR 共突变（23%），其次是 TP53 共突变（15%）。
结论 吉林地区 NSCLC 患者 RET 基因变异以融合突变为主，常见的 RET 融合伴侣是 KIF5B 和 NCOA4、CCDC6。

PU-0661

Assessing MicroRNA-375 Levels in Type 2 Diabetes Mellitus (T2DM) Patients and Their First-Degree Relatives with T2DM

Xu Wu
the Third Hospital of Yunnan Province, China.

Purpose The pancreatic islet specific microRNA-375 (miR-375) is over expressed in type 2 diabetes mellitus (T2DM) patients suppressing the glucose-induced insulin secretion. Thus, miR-375 may serve as a biomarker for the early prediction of T2DM among high-risk individuals. We

conducted this clinical study to assess the significance of miR-375 among type 2 diabetes mellitus (T2DM) patients and their first-degree relatives.
Patients and Methods We included 56 Han Chinese individuals (N: NGT = 21, T2DM =10, FD-NGT =13 and FD-T2DM = 12) who received medical health check-ups from January 2018 to September 2018 at The Third Hospital of Yunnan Province, China. They were categorized as normal glucose tolerance (NGT), T2DM, first-degree relatives with normal glucose tolerance (FD-NGT) and first-degree relatives with T2DM (FD-T2DM). OGTT, C-peptide and Insulin tests were performed to confirm the diagnosis. The miR-375 levels were determined by Quantitative real-time RT-PCR (qRT-PCR).
Results The OGTT test showed a significant difference in T2DM and FD-T2DM groups compared with NGT and FD-NGT ($p< 0.05$). Similar results were observed during C-peptide and insulin tests. Interestingly, the 2-hour insulin test showed FD-NGT group having a significantly higher mean ± standard error of (64.240 ± 12.775) compared to NGT (28.836 ± 10.875). Assessment of miR-375 expression levels in 4 groups showed a significant up-regulation in T2DM and FD-T2DM compared with NGT and FD-NGT groups. A slight increase in miRNA expression was observed in FD-NGT compared with NGT group but was not statistically significant.
Conclusion The OGTT, C-peptide and insulin tests revealed a statistically significant difference in T2DM and FD-T2DM compared with NGT and FD-NGT groups.
A significantly higher miR-375 expression was also observed in T2DM and FD-T2DM groups compared with NGT and FD-NGT and thus, miR-375 may serve as a stable biomarker for the early prediction of T2DM among high-risk individuals.

PU-0662

As a biomarker for gastric cancer, circPTPN22 regulates the progression of gastric cancer through the EMT pathway.

Shuo Ma、Shan Kong、Xinliang Gu、Yanhua Xu、Mei Tao、Lei Shen、Xianjuan Shen、Shaoqing Ju
Affiliated Hospital of Nantong University

Background Gastric cancer (GC) is one of the most common cancers in the world. Due to the lack of specific symptoms, more than 80% of patients are diagnosed as the advanced stage with a high mortality rate, so the early diagnosis of GC is incredibly essential. Circular RNAs (CircRNAs) are a kind of endogenous non-coding RNA with stable structure, the long half-life, and tumor specificity. It can be used as a diagnostic marker for tumors.
Method Using circRNA sequencing technology screened three pairs of GC and adjacent tissues, and circRNAs with significant expression differences were screened out. The circular structure and characteristics of circPTPN22 were determined by RT-qPCR, agarose gel electrophoresis, Sanger sequencing, RNase R, and actinomycin D assays. Cell Counting Kit-8, colony formation, Transwell, Wound healing, tumor formation in mice and western blotting assays were used to detect the effects of circPTPN22 on the proliferation, invasion, migration, tumor growth of GC cells in vitro and protein expression.
Result CircPTPN22 is up-regulated and positively correlated with metastasis in GC tissues, cells, and plasma. RTqPCR results showed that circPTPN22 had good diagnostic efficacy and could be used to predict the prognosis of GC patients. In vitro and vivo experiments showed that the downregulation of circPTPN22 could inhibit cell proliferation, migration, and invasion through the epithelial-mesenchymal transformation (EMT) pathway. CircPTPN22 may regulate GC progression through the competitive binding of miRNAs.
Conclusion CircPTPN22 can be used as a potential diagnostic and prognostic marker for GC and can inhibit cell proliferation and metastasis through the competitive binding of miRNA to inhibit the EMT pathway.

PU-0663

CircHAS2 通过调控 hsa-miR-944 介导的 PPM1E, 促进胃癌的增殖、迁移和侵袭

马硕、顾新亮、沈蕾、陈垠豪、钱晨、申娴娟、鞠少卿
南通大学附属医院

目的 胃癌被认为是世界上最常见的胃肠道恶性肿瘤之一，并且引发胃癌的原因众多。尽管近年来对胃癌的诊断和治疗都取得了较大进展，但胃癌患者的总体生存情况仍然不令人满意。CircRNAs 是一类新的内源性非编码 RNA，其被证明广泛分布在真核细胞中，可作为众多肿瘤的生物标志物和治疗靶点。但 circRNAs 在胃癌中的作用和潜在调控机制仍不清楚。
方法 利用 qRT-PCR 筛选目标 circRNAs 并检测 circHAS2，hsa-miR-944 以及 PPM1E 的表达水平。利用琼脂糖凝胶电泳、桑格测序、RNase R 和放线菌素 D 等方法检测了 circHAS2 的环状结构和性质。利用体外细胞实验检测了 circHAS2 对胃癌细胞增殖、迁移、侵袭和 EMT 关键蛋白表达的影响。利用 circAtlas，starbase，circBank 和 circinteractome 数据库预测 hsa-miR-944 与 circHAS2 的结合情况。利用 miRDB, miRWalk，miRPathDB 和 Targetscan 数据库预测 hsa-miR-944 和 PPM1E 的结合情况。利用双荧光素酶实验验证 hsa-miR-944 与的 circHAS2 和 PPM1E 的相关性。
结果 circHAS2 在胃癌组织和细胞中表达上调，与肿瘤转移呈正相关。体外实验证明，敲除 circHAS2 可抑制胃癌细胞的增殖、迁移和侵袭能力并可能影响 EMT 过程。此外，hsa-miR-944 与 PPM1E 相互作用，是 circHAS2 的靶基因。加入 hsa-miR-944 的模拟物可抑制胃癌细胞的增殖、迁移和侵袭能力。PPM1E 的上调逆转了敲除 circHAS2 后对胃癌细胞的影响。
结论 circHAS2/ hsa-miR-944/PPM1E 轴可参与胃癌的进展。提示 circHAS2 可充当胃癌的潜在生物标志物和治疗靶点。

PU-0664

伴骨髓异常 T 细胞增多的弥漫性大 B 细胞淋巴瘤一例

朱靖、李良梅、彭子秘、周宇、杨利群
四川金域医学检验中心有限公司

目的 探讨一例伴骨髓异常 T 细胞增多的弥漫性大 B 细胞淋巴瘤的实验室特征。
方法 回顾性分析一例伴骨髓异常 T 细胞增多的弥漫性大 B 细胞淋巴瘤患者的临床资料、骨髓细胞形态学、骨髓活检、流式细胞学、分子生物学检查及淋巴结活检的结果并文献复习。
结果 骨髓细胞形态学分析查见形态异常淋巴细胞，疑为淋巴瘤细胞骨髓侵犯；骨髓活检及免疫组化结果提示：CD3 散在极少数（+）、CD5 局灶（+）、CD79a 散在极少数（+）、CD20 散在极少数（+）、CD34 小血管（+），圆核细胞（-）、CD117 散在极少数（+）、E-cad 红细胞（+）、MPO 粒细胞系统（+）；淋巴结活检提示淋巴结结构完全破坏，弥漫中等偏大异型淋巴细胞浸润，核分裂易见，可见星空现象，累及周围脂肪组织，诊断为侵袭性 B 细胞淋巴瘤，符合弥漫性大 B 细胞淋巴瘤，非特指型（CD5+、CD30+），多系非生发中心来源（Non-GCB）；淋巴结活检标本 EBV 原位杂交显示肿瘤细胞部分阳性；骨髓流式检测到异常 T 淋巴细胞占有核细胞总数约 9.58%（占淋巴细胞总数约 53.82%），表达 cCD3、CD4、CD5、CD2、HLA-DR、CD38 部分，不表达 CD30、CD57、CD3、CD8、TCRab、TCRcd、CD7、CD56、CD19、CD20、CD10、CD34、CD117、CD33；淋巴结活检标本分子生物学检测到 RHOA 基因 p.G17V 突变、STAT3 基因 p.E616K 突变、TET2 基因 p.N275Ifs 和 p.I1349Lfs 突变，突变频率分别为 20.5%、21.2%、10% 和 43.3%；未检测到 BCL2/BCL6/MYC 基因重排；结合临床表现（全身多发淋巴结肿大）综合诊断为弥漫性大 B 细胞淋巴瘤伴骨髓异常 T 细胞增多。

结论 病理结果和流式结果不一致，伴骨髓异常 T 细胞增多的弥漫性大 B 细胞淋巴瘤患者罕见，诊断需结合临床表现和全面的检查，后期密切随访。

PU-0665

新型冠状病毒标本采集、运输、保存及提取对结果的影响

赵娅婷
昆明市中医医院

在新型冠状病毒检测过程中，标本的采集，运输，保存以及提取，在后续的实验过程中至关重要，它将直接影响实验结果的准确性，因此每一个步骤，我们必须严格按照实验室标准操作规程进行操作，严格控制标本采集的有效量，运输环节，样本保存及提取的有效性，确保实验结果准确性，避免操作不当对实验结果造成影响。

PU-0666

Serum hsa_tsr016141 as a kind of tRNA-derived fragments is a novel biomarker in gastric cancer

Xinliang Gu[1,2,3]、Shuo Ma[1,2,3]、Bo Liang[4]、Shaoqing Ju[1]
1. 南通大学附属医院检验科
2. 南通大学附属医院临床医学研究中心
3. 南通大学医学院
4. 南通大学附属医院超声科

Background Gastric cancer (GC) is one of the most common malignant tumors globally and the third leading cause of cancer-related death. GC can occur in any part of the stomach. The vast majority of GC is adenocarcinoma, originating from the most superficial glands or mucous membrane of the stomach. The early symptoms of GC are not obvious, and the symptoms of benign gastric diseases such as gastritis and gastric ulcers are easy to be ignored. Currently, the sensitivity and specificity of diagnostic markers for GC are low, patients often miss the best opportunity for treatment, so it is urgent to find new biomarkers with higher sensitivity and specificity. tRNA-derived small RNAs are a kind of small non-coding RNAs derived from tRNAs. Their stable structure and high abundance in body fluids show their potential to be used in liquid biopsy and become a new generation of tumor biomarkers. At present, most of the studies on tsRNAs have described the effects of tsRNAs on tumor cell proliferation, invasion, and migration, as well as their internal pathways and mechanisms. It is abundant in cancer cells and body fluids. However, there are still few studies on whether tsRNAs can be applied as biomarkers. Our goal is to find the differentially expressed tRNA-derived small RNAs in GC to explore their potential as a GC biomarker.
Methods Quantitative real-time PCR was used to detect the expression level of hsa_tsr016141. The molecular characteristics of hsa_tsr016141 were verified by agarose gel electrophoresis, Sanger sequencing, Actinomycin D Assay, and Nuclear and Cytoplasmic RNA Separation Assay. The diagnostic efficiency of hsa_tsr016141 was analyzed through receiver operating characteristic.
Results The expression level of hsa_tsr016141 in GC tissues and serum was significantly increased. The serum expression level showed a gradient change between GC patients, gastritis patients, and healthy donors and was positively correlated with the degree of lymph node metastasis and tumor grade, which has high diagnostic efficacy for GC. Besides, the elevated serum hsa_tsr016141 has good stability and specificity, which makes it have the potential to be used as a good biomarker for GC. Meanwhile, the elevated serum hsa_tsr016141 can effectively

track the postoperative situation of GC, dynamically monitor GC patients. Its detection method also has good clinical application value. The ROC curve of GC patients and healthy donors showed that the AUC of hsa_tsr016141 was 0.814 (95% confidence interval (CI): 0.760-0.867), which was higher than 0.705 (95% CI: 0.637-0.774) of CEA and 0.607 (95% CI: 0.535-0.678) of CA199. Meanwhile, the sensitivity (75%), specificity (78%), accuracy (76%), positive predictive value (80%), and negative predictive value (72%) of hsa_tsr016141 were also higher than those of CEA and CA199. Moreover, the AUC increased to 0.830 after the combination of hsa_tsr016141 and CEA, and 0.854 after combining hsa_tsr016141 and CA199. The AUC of the combination of the three was the highest, reaching 0.864. Compared with CA724, the AUC of hsa_tsr016141 was 0.820 (95% CI: 0.759-0.881), which was slightly higher than 0.780 of CA724 (95% CI: 0.712-0.848). The sensitivity (66%) and specificity (89%) of hsa_tsr016141 were also slightly higher than that of CA724. ROC analysis showed that the serum expression level of hsa_tsr016141 could significantly distinguish GC patients from healthy donors or gastritis patients. Besides, the expression level of hsa_tsr016141 in GC patients decreased significantly after the operation (P<0.0001).

Conclusions Serum hsa_tsr016141 has good stability and specificity and can be used for dynamic monitoring of GC patients, suggesting that serum hsa_tsr016141 can be a novel biomarker for GC diagnosis and postoperative monitoring.

PU-0667

Diagnostic Value of Detection of Pregenomic RNA in Sera of Hepatitis B Virus-Infected Patients with Different Clinical Outcomes

Ni Lin[2]、Qishui Ou[1]
1. 福建医科大学附属第一医院
2. 福建医科大学医学技术与工程学院

Pregenomic RNA (pgRNA) is a direct transcription product of hepatitis B virus (HBV) covalently closed circular DNA (cccDNA), and it plays important roles in viral genome amplification and replication. This study was designed to investigate whether serum pgRNA is a strong alternative marker for reflecting HBV cccDNA levels and to analyze the correlation between serum pgRNA, serum HBV DNA, and hepatitis B surface antigen (HBsAg). A total of 400 HBV-infected patients who received nucleos(t)ide analog (NA) therapy with different clinical outcomes were involved in this research. Case groups included asymptomatic hepatitis B virus carrier (ASC), chronic hepatitis B (CHB), liver cirrhosis (LC), and hepatocellular carcinoma (HCC) patients, with 100 patients in each group. The results showed that the levels of HBV pgRNA had significant differences between these 4 groups. Serum pgRNA levels correlated well with serum HBV DNA and HBsAg levels (HBV pgRNA levels versus HBV DNA levels, $r = 0.58$, $P < 0.001$; HBV pgRNA levels versus HBsAg levels, $r = 0.47$, $P < 0.001$). In addition, we focused on the 108 HBV-infected patients with HBV DNA levels of <500 IU/ml; it was surprising to find that in 17.57% (13/74) of cases, HBV pgRNA could be detected even when the HBV DNA level was below 20 IU/ml. In conclusion, HBV pgRNA levels in serum can be a surrogate marker for intrahepatic HBV cccDNA compared with serum HBV DNA and HBsAg. The detection of serum HBV pgRNA levels may provide a reference for clinical monitoring of cccDNA levels and the selection of appropriate timing for discontinuing antiviral therapy, especially when HBV DNA levels are below the detection limit.

PU-0668

长链非编码 RNA 调控糖尿病肾病的研究进展

李宇宸[1]、袁芸[1]、杨璐瑶[1]、胡琼英[2]
1. 成都中医药大学医技学院
2. 成都中医药大学附属医院（四川省中医医院）

糖尿病肾病是糖尿病病人最严重的并发症之一。糖尿病肾病在我国的发病率呈上升趋势，已成为终末期肾脏病的主要原因，仅次于肾小球肾炎。由于糖尿病肾病存在复杂的代谢紊乱，一旦发展为终末期肾脏病，往往比其他肾脏疾病的治疗更加棘手，因此早期诊断对糖尿病肾病的防治意义重大。深入了解糖尿病肾病的发病机制，以期早期筛选高危患者是糖尿病肾病治疗的关键。糖尿病肾病病理分期主要是基于肾组织活检，但活检是一项复杂的有创检查，难以早期开展推广，因此临床上希望能找到新的标志物早期诊断、鉴别诊断及指导糖尿病肾病用药。已有研究表明 lncRNA 与氧化应激、凋亡与自噬、炎症反应、细胞肥大与增值、肾纤维化和糖代谢异常等糖尿病肾病发病机制有关，lncRNA 通过这些分子机制来调节糖尿病肾病的发生发展，是糖尿病肾病检测的新型实验室指标。随着基因测序和分析技术的发展，将会有更多与 DN 相关的 lncRNA 被研究者发现，通过研究其生物学及在糖尿病肾病中的发生机制，可筛选出诊断 DN 效能更高的标志物及治疗靶点。然而，lncRNA 与 DN 的研究仍面临诸多挑战，大多数研究尚未建立适当的疾病对照组确认这些 lncRNA 对于 DN 是特异性标志物，因此寻找特异度强的 lncRNA 是有必要的。总之，lncRNA 的出现为临床 DN 的预防及治疗提供新的思路和方法，我们需要更多的研究进一步了解 lncRNA 在 DN 中的作用机制。

PU-0669

Mutational characterization of HBV reverse transcriptase gene and the genotype-phenotype correlation of antiviral resistance among Chinese chronic hepatitis B patients

Ya Fu、Qishui Ou
Fujian medical university

Background and Aims The drug resistance of hepatitis B virus (HBV) originates from mutations within HBV reverse transcriptase (RT) region during the prolonged antiviral therapy. So far, the characteristics of how these mutations distribute and evolve in the process of therapy have not been clarified yet. Thus we aimed to investigate these characteristics and discuss their contributing factors.
Methods HBV RT region was direct-sequenced in 285 treatment-naive and 214 post-treatment patients. Mutational frequency and Shannon entropy were calculated to identify the specific mutations differing between genotypes or treatment status. A typical putative resistance mutation rtL229V was further studied using in-vitro susceptibility assays and molecular modeling.
Results The classical resistance mutations were rarely detected among treatment-naive individuals, while the putative resistance mutations were observed at 8 AA sites. rtV191I and rtA181T/V were the only resistance mutations identified as genotype-specific mutation. Selective pressure of drug usage not only contributed to the classical resistance mutations, but also induced the changes at a putative resistance mutation site rt229. rtL229V was the major substitution at the site of rt229. It contributed to the most potent suppression of viral replication and reduced the in-vitro drug susceptibility to entecavir (ETV) when coexisting with rtM204V, consistent with the hypothesis based on the molecular modeling and clinical data analysis.
Conclusions The analysis of mutations in RT region under the different circumstances of genotypes and therapy status might pave the way for a better understanding of resistance evolution, thus providing the basis for a rational administration of antiviral therapy.

PU-0670

MTHFR C677T 基因多态性与原因不明复发性流产的相关性研究

张光辉、蔡少玲、刘卫民
深圳恒生医院

目的 探讨 MTHFR C677T 基因多态性与原因不明复发性流产（URSA）的相关性，为进行原因不明复发性流产的预防、诊断、治疗奠定基础。
方法 采用病例对照的研究方法，对来自深圳恒生医院 350 位孕周小于 12 周有复发性流产史的患者和 350 名孕周大于 28 周且无并发症的孕妇或者生育大于 1 个小孩的妇女进行 MTHFR C677T 位点基因分型检测，使用 SPSS 26.0 对病例组和对照组中的 MTHFR C677T 基因分型进行统计分析，分析 MTHFR C677T 基因多态性与 URSA 的相关性。
结果 MTHFR C677T 位点多态性与 RSA 明显相关，MTHFR C677T TT 基因型个体 RSA 风险是 CC 型个体的 3.7 倍（P＜0.0001，95％CI：2.5～5.4）；CT 基因型个体 RSA 风险是 CC 型个体的 2.6 倍（P＜0.0001，95％CI：1.7～3.8），携带 T 等位基因个体，RSA 风险增加 140％（P＜0.0001，95％CI：1.9～2.9）。
结论 MTHFR C677T 基因多态性与原因不明复发性流产具有高度相关性。

PU-0671

2021 年 4 月乌鲁木齐 943 批国内冷冻冷藏食品外包装 SARS-CoV-2 核酸检测结果分析

刘静、帕尔吾杂提·阿合苏木、 张雪庆、高婷、佟晓洁
新疆金域医学检验所有限公司

目的 新型冠状病毒 SARS-CoV-2 传染力强、传播途径多样化、不易被阻断、易感人群普遍，可通过气溶胶、接触、粪口等途径广泛快速传播且致死率较高。冷链物流食品是否会成为新型冠状病毒的传染源，其被污染的风险水平目前还缺乏足够的文献资料支撑。为了准确评估冷冻冷藏食品被 SARS-CoV-2 污染的风险大小，分析其可能存在的感染来源，食品表面的新冠病毒核酸检测是当下疫情风险防控的必要手段。
方法 采集 2021 年 4 月 1 日至 2021 年 4 月 30 日，新疆维吾尔自治区乌鲁木齐市不同经营场所、不同产地来源、不同品类的 943 批次冷冻冷藏食品外包装样本，对其采用实时荧光 PCR 法，以新型冠状病毒 2019-ncovdeORF1ab 和 N 基因设计特异性引物和 TaqMan 探针，通过荧光定量 PCR 仪进行 RT-PCR 扩增并检测荧光信号，自动绘制出实时扩增曲线，从而实现对新型冠状病毒 2019-nCOV 核酸的检测。
结果 本实验研究涉及到的 943 批冷冻冷藏食品外包装 SARS-CoV-2 核酸检测结果均显示阴性。
结论 本研究结果表明，乌鲁木齐市冷冻冷藏食品外包装被 SARS-CoV-2 污染的风险较低，其作为 SARS-CoV-2 传染源的可能性也相对较低。本研究实验样本数据充足，实验方法科学得当，检测数据准确可靠，样本来源广泛、食品种类丰富，结果可供参考；但由于本实验样本调查范围仅限于乌鲁木齐的销售环节，并不涉及其他运输、加工环节，未来应扩大研究食品全产业链范围，以便开展长期新型冠状病毒流行病学在食品之间污染概率的监测工作。

PU-0672

MiR-124 is a potential molecular marker in breast cancer

Yi Yang、Tongbao Feng
The Affiliated Changzhou No. 2 People's Hospital of Nanjing Medical University

Purpose MiR-124 acts as tumor-suppressive role in human cancer. However, the clinical significance of miR-124 in BRCA remains unclear. The aim of this study was to evaluate the role of miR-124 in breast cancer cells and investigate the association of hsa-mir-124 expression and the clinicopathological characteristics in breast cancer progression.
Methods MiR-124 expression in breast cancer tissue was measured by quantitative real-time PCR (RT-qPCR). CCK-8 assays were used to detect the role of miR-124 on the breast cancer cell proliferation. The expression profiles of hsa-mir-124 were obtained from the cancer genome atlas for BRCA. Then, we used Cox Regression test, Kruskal-Wallis test and Wilcox test to investigate the prognostic value of hsa-mir-124, the association of hsa-mir-124 and pathology TNM stages and pathologic stages in breast cancer.
Results We found that the expression of miR-124 was significantly downregulated in breast cancer tissues compared with matched adjacent non-neoplastic tissues and significantly inhibited breast cancer cell proliferation. In addition, we observed that miR-124 was associated with the clinicopathological characteristics of breast cancer. Moreover, the expression of miR-124 was also associated with the overall survival of breast cancer patients.
Conclusion Our findings demonstrated that miR-124 acted as tumor-suppressive gene in breast cancer and indicated that hsa-mir-124 expressions were associated with overall survival, TNM stages, pathologic characteristics and tumor molecular phenotype in breast cancer, providing a new biomarker and a potential therapeutic target for breast cancer patients.

PU-0673

Andrographis Enhances 5-Fluorouracil-Induced Anti-Tumor Effect in Colorectal Cancer through Inhibition of DKK1

Yinghui Zhao、Chuanxin Wang
The Second Hospital of Shandong University

Background Colorectal cancer (CRC) ranks as the third leading cause of cancer-related deaths in the US. In this malignancy, 5-fluorouracil (5FU)-based treatment remains the mainstay as first-line chemotherapy. Unfortunately, ~50-60% of patients treated with 5FU eventually develop resistance, leading to increased mortality. Hence, a better understanding of the molecular mechanisms underlying 5FU-resistance will lead to development of more effective therapeutic strategies. Our previous studies have shown that, andrographis, a botanical with diverse biological activities, synergistically enhanced 5FU-induced pro-apoptotic effects by mediating Wnt/β-catenin pathways. However, a more comprehensive knowledge of andrographis-mediated synergism with 5-FU remains largely unclear.
Methods We first established 5FU resistant isogenic cell lines of HCT116 and SW480 CRC cells (HCT116 5FUR and SW480 5FUR). To determine the synergistic anti-tumor effects of andrographis and 5FU, we performed cell viability, proliferation and colony formation assays by treating parental and 5FUR cells with andrographis, 5FU and their combination. To explore the molecular mechanisms responsible for the synergistic anti-tumor efficacy, we next performed gene expression microarrays to identify candidate pathways and genes that mediated anti-tumor efficacy of andrographis in 5FUR cells. We analyzed an expression profiling dataset from CRC patients (GSE52735) who either responded or did not respond to 5FU. We also studied the andrographis-mediated synergism with 5FU in a xenograft animal model, and in 3D patient-derived tumor organoids.

Results Combined treatment with andrographis and 5FU exhibited significantly superior effects on cell viability ($P<0.01$), proliferation ($P<0.001$) and colony formation capacity ($P<0.001$), compared to treatment with individual treatments. In line with our in vitro findings, the combined treatment also significantly reduced tumor growth in mice xenografts ($P<0.0001$) as well as patient-derived tumoroids ($P<0.001$). By analyzing gene expression profiling data from cell lines and CRC patients, we identified that overexpression of DKK1 gene was a critical event for 5FU resistance in CRC. Moreover, qRT-PCR and western blotting data revealed that andrographis resulted in downregulation of 5FU-induced DKK1 overexpression accompanied with the synergistic anti-tumor effects in animal xenografts ($P<0.001$) and patient-derived tumor organoids ($P<0.001$), which were reversed following siRNA-mediated silencing of DKK1 ($P<0.01$).
Conclusions Our data provide novel evidence for andrographis-mediated anti-tumor synergism with 5-FU through DKK1, highlighting that in addition to its preventive efficacy, andrographis may serve as a potential adjunctive treatment to conventional chemotherapeutic drugs in patients with CRC.

PU-0674

Identification of circulating miR-22-3p and let-7a-5p as novel diagnostic biomarkers for rheumatoid arthritis

Jifeng Tang、Jinpiao Lin
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Objectives Early and correct diagnosis would be beneficial for outcomes of rheumatoid arthritis (RA), but there are some limitations in current diagnostic tools. In this study, we aimed to evaluate the diagnostic value of circulating miR-22-3p and let-7a-5p in RA.
Methods Seventy-six RA patients, 30 systemic lupus erythematosus patients, 32 Sjögren's syndrome patients and 36 healthy donors recruited at the First Affiliated Hospital of Fujian Medical University (China) were included in this study. Circulating miR-22-3p and let-7a-5p in plasma were measured using reverse transcriptase quantitative PCR (RT-qPCR) and serum cytokines were detected by cytometric bead array (CBA). The participants clinical materials were also collected. Receiver operating characteristic (ROC) curve analysis and correlation analysis were performed to assess the potential value of circulating miRNAs in RA.
Results Circulating miR-22-3p and let-7a-5p are significantly increased in RA patients and able to distinguish RA patients from other populations. Circulating let-7a-5p has been shown to improve the diagnostic ability of current laboratory indicators anti-cyclic citrullinated peptide antibodies (anti-CCP) and rheumatoid factor (RF). Moreover, the discriminatory capacity of both circulating miRNAs contribute to complement the diagnosis for seronegative RA. Meanwhile, correlation analysis reveals that circulating miR-22-3p positively correlates with hemoglobin, serum bilirubin, albumin and IL-17 but negatively correlates with mean platelet volume as well as let-7a-5p.
Conclusions The increased circulating miR-22-3p and let-7a-5p levels in RA patients, especially in seronegative RA patients, may provide a potential promising diagnostic biomarkers for RA in clinical practice.

PU-0675

Notoginsenoside R1-Induced Neuronal Repair in Models of Alzheimer Disease Is Associated With an Alteration in Neuronal Hyperexcitability, Which Is Regulated by Nav

Tao Hu
Department of Laboratory Medicine, The Third People's Hospital of Yunnan Province

Alzheimer's Diseaseis characterized by a progressive cognitive deficit and may be associated with anaberrant hyperexcitability of the neuronal network.Notoginsenoside R1 (R1), a major activity ingredient from Panax notoginseng (PNS), has demonstratedfavorable changes in neuronal plasticity and induced neuroprotective effectsin brain injuries resulting from various disorders; however, the underlying mechanisms are still not well understood. In the present study, we aimed to explore the possible neuroprotective effects induced by R1 in a mouse model of AD and the mechanisms underlying these effects. Treatment with R1 significantly improvedlearning and memory functions and redressed neuronal hyperexcitability in APP/PS1 mice by altering the numbers and/or distribution of the members of voltage-gated sodium channels (Nav). Moreover, we determined whether R1 contributed to the regulation of neuronal excitability in Aβ-42-injured cells. Results of our study demonstrated that treatment with R1 rescued Aβ1-42-induced injured neurons by increasing cell viability. R1-inducedalleviation in neuronal hyperexcitability might be associated with reduced Navβ2 cleavage, which partially reversed the abnormal distribution of Nav1.1a. These results suggested that R1 played a vital role in the recovery of Aβ1-42-induced neuronal injury and hyperexcitability, which is regulated by Nav proteins. Therefore, R1 may be a promising candidate in the treatment of AD.

PU-0676

The efficacy of addition of tenofovir disoproxil fumarate to Peg-IFNα-2b is superior to the addition of entecavir in HBeAg positive CHB patients with a poor response after 12 weeks of Peg-IFNα-2b treatment alone

Yongbin Zeng、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

Background There are limited data regarding the efficacy of addition of entecavir (ETV) or tenofovir disoproxil fumarate (TDF) to Peg-IFNα-2b in HBeAg positive chronic hepatitis B (CHB) patients without early response to Peg-IFNα-2b. In this study, we aimed to evaluate the efficacy of ETV and TDF in HBeAg positive CHB patients who had a poor response to Peg-INFα-2b at the end of 12 weeks of monotherapy.
Methods A total of 40 HBeAg-positive CHB patients who were naive to antiviral therapy were recruited. The patients received a subcutaneous injection of Peg-IFNα-2b (180 μg) once a week for 12 weeks. However, the patients had a poor response to Peg-INFα-2b at the end of the 12-week-period monotherapy. The patients were then divided into two therapeutic protocol groups: (1) Group A: Patients received Peg-IFNα-2b (180 μg) subcutaneously weekly and ETV (0.5 mg) orally once daily for 48 weeks; (2) Group B: Patients received Peg-IFNα-2b (180 μg) subcutaneously weekly and TDF (300 mg) orally once daily for 48 weeks. The therapeutic efficacy was evaluated. Blood samples were collected at baseline and every 12 weeks. Routine biochemical tests including ALT, AST, etc. were measured by automated biochemical technique. HBV DNA was quantified using the TaqMan PCR assay. The

levels of HBsAg, HBsAb, HBeAg, HBeAb and HBcAb were measured using a commercial chemiluminescent microparticle immunoassay.
Results The HBsAg level declined rapidly in both two treatment groups during the first 12 weeks and declined gradually in the next 36 weeks. At week 48, the mean △HBsAg level in Peg-IFNα-2b+TDF group was significantly higher than that in Peg-IFNα-2b +ETV group (-1.799 ± 0.3063 vs. -1.078 ± 0.2028, P=0.0491). The HBeAg loss rate was significantly higher in TDF add-on group than that in ETV add-on group at week 48 (40% vs. 10%, P=0.028). At week 48, the proportions of patients with undetectable HBV DNA (<500 IU/mL) were 80% (16 out of 20) and 95% (19 out of 20) in Peg-IFNα-2b+ETV group and Peg-IFNα-2b+TDF group, respectively.
Conclusions This real world study demonstrated that the efficacy of addition of TDF to Peg-IFNα-2b is superior to the efficacy of addition of ETV to Peg-IFNα-2b in HBeAg positive CHB patients with a poor response after 12 weeks of Peg-IFNα-2b treatment alone. However, this present study also requires a larger sample size study to verify in the future.

PU-0677

3 例 CD5+的弥漫大 B 细胞淋巴瘤实验室检测和临床特征分析

汪玲[1]、杨利群[1]、林芝[2]、唐梅[1]、黄林林[1]
1. 四川金域医学检验中心有限公司
2. 宜宾市第二人民医院

目的 探讨 CD5+的弥漫大 B 细胞淋巴瘤（DLBCL）实验室检测和临床特征。
方法 收集到初诊为 CD5+的 DLBCL 患者 3 例，结合 HE 片及免疫组化对其进行 Hans 分型，检测 C-MYC、BCL2 蛋白表达情况，并应用 FISH 技术检测 MYC、BCL2 和 BCL6 基因结构异常，同时利用二代测序（NGS）对其进行淋巴造血相关基因突变分析。
结果 3 例 DLBCL 病例均表现为 CD5 阳性，主要的免疫组化抗体结果为 CD20（+）、CD10（-）、BCL-6（+）、MUM-1（+）、BCL-2（+）、C-MYC（+），Ki67（+）、CD5（+）等，根据 Hans 分型均为活化 B 细胞亚型（ABC 亚型）。第一例为 65 岁女性，病变部位为回肠，BCL-2（+，90%）、C-MYC（+，60%）、Ki67（+，90%），提示为 BCL-2、C-MYC 双表达；FISH 结果为阴性。第二例为 70 岁男性，病变部位为左颈部，Ki-67（+，70%），且 EBER（+）；但未进行 FISH 检测。第三例为 52 岁男性，病变部位为扁桃体，Ki67（+，90%）；FISH 结果为 BCL6 阳性，MYC 和 BCL2 为阴性。3 例病例 NGS 检测结果均为阳性，但检测到突变的基因各不相同，除了第三例病例检测到提示预后较差的 TP53 基因突变以外，其余基因突变的临床意义尚不明确，分子检测仍需进一步研究。
结论 在原发性 DLBCL 病例中 CD5 阳性的发生频率较低（约 5-10%），我们收集的 3 例病例均为 ABC 亚型，Ki67 指数均较高。CD5+DLBCL 通常很少继发于慢性淋巴细胞白血病/小淋巴细胞淋巴瘤,且与套细胞淋巴瘤的母细胞样或多形性变异型的区别在于缺乏细胞周期蛋白 CyclinD1 和/或 SOX11 表达。CD5+DLBCL 患者多为老年人，常具有高风险的临床特征，特别是在亚洲国家，并且 CD10 通常阴性，根据免疫组化 Hans 法则分型多为 ABC 亚型。

PU-0678

Xpert MTB/RIF 在结核性脑膜炎中的研究进展

徐婷、张燕、张祥、黄珮珺
江苏省人民医院（南京医科大学第一附属医院）

随着上世纪结核标准化用药的建立，结核病得到了有效控制，但目前全球仍有近百万的感染者，依然是一项世界性公共卫生问题。而结核性脑膜炎是肺外结核中最常见、最严重的类型，其病死率、致残率居高不下，如何进行早期快速诊断对结核性脑膜炎患者的治疗和预后具有十分重要的意义。

近年来越来越多的免疫学和分子生物学方法被运用在结核分枝杆菌检测上，其中，Xpert MTB/RIF 的出现为包括结核性脑膜炎在内的结核病提供了快速有效的诊断方法，是基于一体化的全自动实时 PCR 检测技术。本文就 Xpert MTB/RIF 检测的原理，在结核性脑膜炎中的临床应用和进展作一综述。

PU-0679

4206 例手足口病病毒核酸检测结果分析

唐笑、代冰、唐春燕、刘岱璿、李玲锦
长沙金域医学检验实验室有限公司

目的 分析 4206 例疑似手足口病患儿的肠道病毒核酸检测结果，为湖南地区手足口病原的预防控制提供病原学依据。
方法 选取 2019 年 1 月~2020 年 12 月送检长沙金域医学检验实验室的疑似手足口病患儿的标本作为研究对象，采用实时荧光 PCR 的方法进行肠道病毒通用型（EV）、柯萨奇病毒 A 组 16 型（CA16）和肠道病毒 71 型（EV71）核酸检测，统计分析检测结果，包括性别、年龄、月份的分布情况。
结果 4206 例疑似手足口病患儿检出肠道病毒通用型 1502 例、CA16 型阳性 166 例、EV71 型阳性 1 例，检测阴性 2537 例。其中，肠道病毒通用型阳性检出率明显高于其它两种肠道病毒，各类肠道病毒相比较，差异具有统计学意义（$\chi2=1193.678$，$P<0.01$）。2019 年肠道病毒检出总阳性率与 2020 年相比，差异有统计学意义（$\chi2=54.819$，$P<0.01$）。手足口病患儿男、女病例比例为 1.71:1，男性发病率高于女性。5 岁及以下年龄组手足口病病例占总阳性数的 90.29%。CA16 型手足口病患儿以 1~4 岁儿童为主，通用型感染主要发生在 0~3 岁儿童。湖南手足口病发病有明显的季节性，3~4 月和 9~11 月为湖南地区 2 个发病高峰。
结论 针对疑似手足口病患儿开展肠道病毒核酸检测具有较高的临床意义，可辅助临床诊断并为治疗提供依据。尽早发现并治疗病毒感染引起的手足口病，是疫情防控的关键环节，也是降低其导致的死亡率的有效手段。

PU-0680

The role of autophagy in hepatic fibrosis

Mei Sun
the Second Xiangya Hospital, Central South University

Hepatic fibrosis is a chronic liver injury process, and its continuous development can lead to cirrhosis, hepatic failure or hepatocellular carcinoma (HCC). Autophagy has attracted much attention because of its controversial role in the course of hepatic fibrosis. In this review, we separately introduce the mechanism related to noncoding RNAs and some of the signaling pathways that promoting or inhibiting fibrosis by affect autophagy. Finally, we list some targets related to autophagy that enable hepatic fibrosis therapy and forecast its prospect in hepatic fibrosis. This review will provide new ideas in diagnosing or curing hepatic fibrosis, which will be helpful to reduce the incidence of cirrhosis and its complications.

PU-0681

综合分析人类食管癌中家族性基因 E2Fs 的预后和免疫浸润价值

刘畅
四川省肿瘤医院

背景 E2Fs 是一组高等真核生物中编码转录因子家族的基因。通过调节 G1 / S 和 G2 / M 细胞周期的起始和过渡来调节基因表达。目前在哺乳动物中，已经鉴定出 E2F 家族的八个成员（E2F1-E2F8）。在某些人类恶性肿瘤中，E2F 家族基因表达异常。有研究表明 E2F 家族基因通过参与细胞分化，凋亡和 DNA 损伤反应和细胞死亡来影响肿瘤细胞的生长和侵袭。随着研究深入人们发现 E2F 家族基因可作为某些癌症（包括乳腺癌和胃癌）的诊断和预后生物标志物。然而，不同 E2F 家族基因在食管癌中的表达水平、遗传变异、分子机制、生物学功能以及与食管癌患者预后和免疫浸润的关系尚未完全阐明.
方法 采用 Oncomine、GEPIA、cBioPortal、GeneMANIA、STRING 和 Metascape 数据库，研究 E2Fs 在食管癌中的 mRNA 表达水平、临床相关性分析、预后价值、遗传变异、基因-基因相互作用网络以及功能富集分析。利用 TIMER 数据库研究 E2Fs 表达与食管肿瘤免疫侵袭及 PD-1、PD-L1、CTLA4 的关系。
结果 食管癌患者 E2F1 和 E2F7 的转录水平明显上调，E2F8 的高表达与食管肿瘤患者的肿瘤分期有关。E2F7 的异常表达与食管癌患者的临床预后有关。E2Fs 及其邻近基因的功能主要与 RNA 聚合酶 II 启动子的转录启动有关。E2Fs 及其邻近蛋白的功能主要与细胞周期等有关。我们还发现 E2Fs 的表达与免疫浸润（包括 B 细胞、cd8t 细胞、cd4t 细胞、中性粒细胞、巨噬细胞和树突状细胞）有相关性。与 PD-1 有一定的相关性
结论 本研究为食管癌患者免疫治疗靶点的选择和预后标志物的选择提供了新的思路。

PU-0682

Positive association between MIC gene polymorphism and tuberculosis in Chinese population

En Chen
The First Affiliated hospital of University of South China

The disease progression and morbidity of tuberculosis(TB) infections are determined by virulence of the micro-organism, host genetic factors and environmental factors. The highly polymorphic MHC class I chain-related gene (MIC) could serve as a potential host genetic candidate. To investigate the association of MIC polymorphism with TB infection, 124 patients and 191 ethnically matched controls from Hunan province, Southern China, were genotyped for the MIC polymorphism using polymerase chain reaction-sequence specific priming and sequencing-based typing. The results showed that allele frequencies of MIC-sequence and MICA-STR were different in TB patients in comparison to normal controls (both P<0.05). MICA-A4 and MICA*012:01 alleles were positive associated (OR=2.42, 95% CI: 1.69-3.87; OR=3.41, 95% CI: 2.19-5.33, respectively, both Pc<0.05) while MICA -A5 were inversely associated (OR=0.59, 95%CI: 0.41-0.94, Pc<0.05) with TB. Homozygote MICA*012:01/012:01 was observed to have significant risk effects on TB (OR =4.76，95% CI: 1.94-11.69, Pc<0.05). Additionally, MICB*008 allele conduct a significant risk effect for TB (OR=3.17, 95%CI: 1.80-5.61, Pc<0.05). All the data showed that MIC polymorphism was associated with the variable susceptibility to TB in Chinese population.

PU-0683

BK 病毒试剂盒性能验证

戎国栋、徐婷、张燕
江苏省人民医院（南京医科大学第一附属医院）

BK 病毒为直径约 45nm 的无包膜双链环状 DNA 病毒。其原发性感染多在 10 岁之前，成年人感染率高达 82%。病毒易潜伏在泌尿系统上皮细胞中。正常人因为免疫功能正常，因此绝大部分人群不会出现症状和体征。当人免疫能力下降（如肾移植后），BK 病毒被激活，进入肾小管上皮细胞并复制大量子代病毒，引起细胞坏死，破坏移植肾组织，导致移植肾的功能受损（BKV 肾病）。BK 病毒进入尿液或血液时，分别引起 BKV 尿症和 BKV 血症。国内外数据显示，BKV 肾病、BKV 尿症、BKV 血症的发生率分别为 5.6%、45.6%、22.2%，BK 病毒感染的早发现、早诊断，对于防止肾移植人群发生 BKV 肾病甚至病情恶化，具有重要意义。

我院肾移植人群具有相当数量，因此临床上对 BK 病毒检测的需求也比较大。检验学部分子室为满足临床需求，拟开展 BK 病毒 DNA 定量检测。根据医院试剂采购相关规定，以及检验学部 ISO 15189 质量体系要求，需要对试剂盒进行性能验证。然而目前，国内 BK 病毒 DNA 定量检测试剂盒无统一验证方案及评价标准。本实验室参照我国卫生行业标准 WS/T 492-2016、WS/T 408-2012 及 WS/T 420-2013 中推荐的定量项目精密度、正确度、线性、检出限、特异性验证方案，以乙肝病毒定量检测试剂盒验证的判断标准作为评价依据，验证并确立了 BK 病毒 DNA 核酸检测试剂盒性能验证方案及评价标准。

PU-0684

MICA 基因多态性与海南人群 HBV 易感关联性研究

陈恩
南华大学附属第一医院

目的 研究 MICA 等位基因多态性与海南人群 HBV 感染易感性之间的关联性。
方法 采用 PCR-SSP 和 PCR-SBT 方法对样本 MICA 等位基因的多态性进行检测。
结果 HBV 感染患者中共检出 10 种 MICA 等位基因和 5 种 MICA-STR等位基因，和对照组相比较，MICA* 010、MICA-A5 等位基因可能对 HBV 感染易感(MICA* 010: OR = 3. 88，95% CI: 2.19～6.85，P = 0.000; MICA-A5: OR=1.27，95% CI: 0.92～1.77，P = 0.0068) 。MICA* 008 /045 基因型可能对 HBV 感染不易感，MICA * 010 /010 纯合子基因型可能对 HBV 易感(MICA * 008 /045: OR = 0.09，95% CI: 0.01～1.74，P = 0.0071; MICA* 010 /010: OR = 4.41，95% CI: 1.26～15.46，P = 0. 0106) 。
结论 MICA 等位基因多态性与海南人群 HBV 感染的易感性间存在关联性。

PU-0685

PDZK1 acts as a tumorigenic gene in glioma via interacting with AKT1

Xing Ren
the First Affiliated Hospital of University of South China

Glioma is the most frequently diagnosed primary brain tumour and typically manifests poor prognosis because of malignant proliferation and invasion. It is urgent to detect the mechanisms driving glioma tumourigenesis and develop novel treatments to address this deadly disease. PDZK1 is a multidomain protein with four PDZ domains observed at the apical membrane of renal

proximal tubular cells. Here, we first revealed that PDZK1 is expressed at high levels in gliomas. Knockdown of PDZK1 inhibits glioma cell proliferation and invasion in vitro. Mechanistically, further investigations found that PDZK1 interact with AKT1 and loss of PDZK1 expression by siRNA inhibited the activation of the AKT/mTOR signalling pathway, leading to cell cycle arrest and apoptosis. Clinically, high expression of PDZK1 predicts a poorer prognosis for glioma patients than low expression of PDZK1. Altogether, our study revealed that PDZK1 acts as a novel and potentially selective target for glioma.

PU-0686

尿液外泌体长链非编码 RNA MALAT1 和 HIF1A-AS2 对膀胱癌诊断的价值

高娟、王青、王云杰、马梦影、王科勇、李卓
西安医学院第一附属医院

目的 探讨尿液外泌体中 lncRNA MALAT1 和 HIF1A-AS2 水平与膀胱癌发生和发展的关系及对膀胱癌诊断的价值。
方法 分别测定 40 例膀胱癌患者、膀胱良性疾病患者及健康人尿液外泌体中 MALAT1 和 HIF1A-AS2 的水平。比较 3 组尿液中 MALAT1 和 HIF1A-AS2 水平的差异，并分析膀胱癌患者 MALAT1 和 HIF1A-AS2 水平与肿瘤病理分级、分期及肿瘤大小的关系。应用 ROC 曲线分析 MALAT1 和 HIF1A-AS2 诊断膀胱癌的敏感度和特异度。
结果 膀胱癌组尿液外泌体中 MALAT1 和 HIF1A-AS2 水平显著高于膀胱良性疾病组和健康对照组，差异具有统计学意义 (P<0.01)；膀胱癌 G1 级组 MALAT1 和 HIF1A-AS2 水平与 G2-G3 级组比较，差异无统计学意义（P＞0.05）。膀胱癌不同分期的比较结果显示，Ta 期、T1-T2 期和 T3-T4 期 3 组之间 MALAT1 和 HIF1A-AS2 水平差异无统计学意义（P＞0.05）；而肿瘤直径≥3.0cm 组患者 MALAT1 和 HIF1A-AS2 水平明显高于直径＜3.0cm 组，且差异具有统计学意义（P＜0.05）。结果表明，MALAT1 的 ROC 曲线下面积(AUCROC) 为 0.777，当 cut-off 值为 398.64 时，其筛查膀胱癌的敏感性为 77.5%，特异性为 70.0%；HIF1A-AS2 的 ROC 曲线下面积(AUCROC) 为 0.797，当 cut-off 值为 350.21 时，其筛查膀胱癌的敏感性为 72.5%，特异性为 80.0%；MALAT1 和 HIF1A-AS2 联合检测的 AUCROC 为 0.862，敏感性为 80.0%，特异性为 92.5%，均高于两项指标的单独筛查价值。
结论 膀胱癌患者尿液外泌体 MALAT1 和 HIF1A-AS2 表达水平明显升高，MALAT1 和 HIF1A-AS2 有望成为膀胱癌诊断的潜在生物学标志物。

PU-0687

Targeting of VPS18 by the lysosomotropic agent RDN reverses TFE3-mediated drug resistance

Huanmin Niu
the Second Hospital of Shandong University

Transcription factor E3 (TFE3) is a critical stimulator to enhance the lysosomal biogenesis. Here, we demonstrated a novel role of TFE3 in mediating multidrug resistance (MDR). We found that chemotherapeutic agents such as docetaxel significantly activated TFE3, which resulted from the calcineurin-mediated TFE3 dephosphorylation in resistant cells. Activation of TFE3/lysosome facilitated multidrug resistance-associated protein-2 (MRP2) expression and lysosomal localization rather than promoting the migration of MRP2 to cellular membrane, which contributed to the development of MDR via the enhancement of drug sequestration in lysosomes. TFE3

deficiency reduced MRP2 lysosomal distribution and drug trapped in lysosomes, which significant restored the sensitivity of drug-resistant cells to chemotherapeutics. Importantly, the targeting of lysosomal vacuole protein sorting 18 (VPS18) by a lysosomotropic agent RDN, a novel derivative of bisbibenzyl riccardin D that directly interacted with the RING domain of VPS18, predominantly suppressed the resistant cell survival with no detectable toxicity. Further analysis revealed that the VPS18 was overexpressed in several cancer types and could be noticeably induced after chemotherapy. A high level of VPS18 exhibited drug resistance, associated with the poor survival, whereas VPS18 silencing dramatically inhibited tumor growth in animal study. In conclusion, TFE3-induced MRP2 translocation in lysosomes promotes the development of chemoresistance, and the VPS18 is emerging as a novel biomarker for predicting cancer prognosis and a potential target to overcome therapeutic resistance in cancer treatments.

PU-0688

基于催化发夹自组装和杂交链式反应的可视化传感器快速检测粪便中幽门螺杆菌的研究

邹海民、王东生
四川省肿瘤医院

目的 建立一种快速、灵敏检测粪便中幽门螺杆菌的可视化生物传感检测方法。
方法 采用 NUPACK 软件设计了 HP1、HP2、HP3 和 HP4 四条单链 DNA 发夹结构，其中 HP3 和 HP4 的 5’端用纳米金修饰。当幽门螺杆菌菌体与核酸适配体特异结合后将挤下与核酸适配体互补的催化链（C*），游离的催化链（C*）触发 HP1、HP2 的催化发夹自组装反应（catalytic hairpin assembly，CHA），形成含游离 Toehold 端的 HP1-HP2 复合物，游离 Toehold 端接着触发 HP3、HP4 的杂交链式反应（hybridization chain reaction，HCR）形成 HP2-HP1-[HP3-HP4]n 长链复合物。最后，根据纳米金团聚后溶液颜色变化及溶液吸收光谱波长的位移对幽门螺杆菌进行快速可视化半定量检测。研究对纳米金的制备条件进行了优化，同时对 CHA 反应条件（包括 HP1、HP2 序列，缓冲液种类等）和 HCR 反应条件（包括 HP3、HP4 序列，HP3、HP4 与纳米金的连接，缓冲液种类等）进行了优化。
结果 实验考察了方法的灵敏度、特异性、检出限等方法学参数，并采用构建的传感器对 15 例幽门螺杆菌感染者及 20 例对照人群（所有 35 人均进行 14C 尿素呼吸试验及快速尿素酶试验）粪便样本进行检测，结果显示建立的可视化传感器能够快速、准确从粪便样本中检测出幽门螺杆菌。
结论 研究建立的基于催化发夹自组装和杂交链式反应的可视化传感器具有可靠、特异、敏感的特点，适用于粪便中幽门螺杆菌的快速可视化检测。

PU-0689

新冠标本冷冻保存对病毒核酸检测结果的影响

顾春荣、刘京萍、穆原
江苏省人民医院（南京医科大学第一附属医院）

目的 分析 3 种类型新冠标本冷冻保存对病毒核酸检测结果的影响。
方法 收集 38 份-80℃保存的灭活新冠病人标本（18 份口咽拭子、4 份鼻咽拭子、16 份痰液），江苏科德新冠病毒核酸检测试剂盒和华大基因新冠病毒核酸检测试剂盒同时检测。
结果 18 份口咽拭子江苏科德和华大基因新冠病毒核酸检测试剂盒检测阳性率分别为 61.1%和 50%，4 份鼻咽拭子江苏科德和华大基因新冠病毒核酸检测试剂盒检测阳性率均为 100%，16 份痰液江苏科德和华大基因新冠病毒核酸检测试剂盒检测阳性率分别为 43.8%和 25%。

结论 -80℃保存的鼻咽拭子标本可用于病毒核酸检测，而口咽拭子和痰液标本却不能在-80℃保存后用于病毒核酸检测。

PU-0690

NGS 快速分析系统的临床应用

韩雪莹、朱丽蒙、张暨
郑州金域临床检验中心有限公司

目的 建立并探讨二代测序（NGS）快速分析系统在肿瘤测序数据分析中的临床实用效果。
方法 选取 500 例郑州金域 2020 年临床样本，以下机数据为研究对象，对分析人员和 NGS 快速分析系统筛选出致病位点的准确度、重复性和耗时进行比对并分析金域核心系统导出的报告单与 NGS 快速分析系统导出报告单内容的一致性。NGS 快速分析系统分为两个模块：模块一对生信分析的表格进行条件筛选，排除多态性突变及良性位点并生成格式正确、可被软件识别的有效样本 Excel 表以备后续进行串行或并行的数据检索和处理。模块二借助 cBioPortal，Cosmic，NCBI Pubmed 等多个数据库进行综合分析，通过机器人学习方法进一步提高分析的准确性及可信度。该模块主要识别该位点是否处于蛋白的功能区，有无功能研究，有无小型研究结果提示其有辅助诊断和（或）提示预后的意义，有无良性证据并根据检索结果进行临床分级并给出诊断建议。
结果 快速分析系统分析 500 例下机数据的结果与人工分析一致，准确定和重复性均达标，在耗时方面进行三因素三水平的正交试验分析，分析方法这一因素对分析时间的影响显著（$P<0.01$），选择系统分析为最优方案，其次限制分析的主要时间为标本量，影响因素最小的为检测项目类型。另 PRD 系统与 NGS 快速分析系统导出报告单的内容差异不明显。
结论 NGS 快速分析系统可一次性处理大批量实验数据并快速检出有临床意义的突变以实现结果快速报告，同时降低人员操作主观出错率，替代了人员的重复性工作，不失为一种新型的一体化数据分析解决模式。

PU-0691

LINC01559 promote colon cancer cell proliferation and promotes apoptosis by regulating β-catenin signaling pathway

Ji Wu[1]、Dehui Deng[2]、Wensheng Gong[2]
1. Guangdong Provincial People's Hospital, Guangdong Academy of Medical Sciences
2. 深圳市人民医院

Objective Long ncRNAs (lncRNAs) play an important role in carcinogenesis. LINC01559, as an identified lncRNA, has been reported in several cancers but not in colon cancer. This study aims to explore the effect of LINC01559 on colon cancer tumor growth and metastasis and its underlying mechanism.
Methods Bioinformatics analysis was used to analyze the expression and prognosis of LINC01559 in colon cancer patient with the TCGA database. RT-qPCR was performed to determine the expression of LINC01559 in colon cancer cells. CCK8, colony formation, wound healing, transwell and flow cytometry, assays were used to detect the proliferation, migration, invasion and apoptosis of colon cancer cell. Gain-and loss-function assays were applied to verify the effects of LINC01559 in Wnt/β-catenin signaling. Western blotting assay was used to detect the effects of LINC01559 on the key point protein in Wnt/β-catenin signaling.
Results LINC01559 was upregulated in colon cancer tissues and its high expression was associated with the poor prognosis. knockdown of LINC01559 significantly affected colon cancer

cells proliferation, migration, invasion and apoptosis. To investigate the underlying mechanisms of LINC01559 in colon cancer, we found that LINC01559 can activate the Wnt/β-catenin signaling. Rescue results revealed that the inhibition of the Wnt/β-catenin signaling pathway in LINC01559-overexpressing colon cancer cells suppressed cellular proliferation, migration and invasion.
Conclusion In summary, our data indicated that LINC01559 might serve as an oncogene by regulating β-catenin signaling pathway and may be a therapeutic target for colon cancer treatment.

PU-0692

高胆红素对丙肝病毒核酸定量检测结果的影响

闫静
宝鸡高新医院

目的 探讨不同浓度的胆红素对 HCV-RNA 定量检测结果的影响。
方法 将已知 HCV-RNA 定量检测结果为阴性的不同浓度的高胆红素血清标本加入丙肝病毒定量不同浓度梯度血清标本中，采用实时荧光定量 PCR 方法对其 HCV-RNA 进行定量检测，通过与原始结果比较分析，评价高胆红素对血液标本中 HCV-RNA 检测结果的影响。
结果 加入不同浓度高胆红素的血标本后，HCV-RNA 阴性无影响；HCV-RNA 三次方结果偏倚>7.5%；其余 HCV-RNA 载量大于 103 方结果偏倚<±7.5%。
结论 高含量胆红素对 HCV-RNA 定量检测临界阳性样本有一定的影响，病毒载量较低的高胆红素样本进行 HCV-RNA 定量检测会引起较大的正向偏倚。

PU-0693

TGF-β1 及其基因单核苷酸多态性（SNP）与心房颤动相关性研究进展

聂清美
贵阳市云岩区第二人民医院

房颤（atrial fibrillation，AF），是一种最为常见的快速性心律失常类型，房颤的发病机制极其复杂，是心律失常领域尚未攻克的顽固性疾病。转化生长因子 β1（transforming growth factor beta 1, TGF-β1）是房颤发生、发展和维持的结构基础之一，与房颤的发生发展息息相关。TGF-β1 基因型和 TGF-β1 血浆浓度存在相关性，其位点有 TGF-β1 -800G/A、TGF-β1 -509C/T，同时检测 TGF-β1 基因-800G/A 和-509C/T 位点的有着重要的临床意义，TGF-β1 基因-800G/A 和-509C/T 位点存在明显的连锁不平衡，其基因多态性和相关因子的研究将有利于我们进一步了解房颤发生发展的危险因素，为临床对房颤的诊断及治疗提供理论依据。

PU-0694

lncRNA-ANKRD36BP2 在肺腺癌中诊断预后研究

陈少婷、曹鹏驹、郭嘉晶、曾艳芬、陈发林
福建省立医院

肺癌是全球最常见的恶行肿瘤之一，更有效的诊疗手段目前仍然在不断探索，长链非编码 RNA(Long non-coding RNA, lncRNA)参与肺腺癌（lung adenocarcinoma，LUAD）的演变，而 lncRNA-ANKRD36BP2 对其的影响还不清楚，本文将探究 lncRNA-ANKRD36BP2 在 LUAD 中的

潜在价值。收集 TCGA 中 lncRNA-ANKRD36BP2 表达水平数据和患者临床数据；收集我院 LUAD 和癌旁样本，采用荧光定量 PCR 技术检查其相对表达水平。利用生存分析探究 lncRNA-ANKRD36BP2 表达水平与患者预后的关系；ROC 曲线（receiver operating characteristic curve）评价其诊断价值；COX 逻辑回归分析影响患者预后的独立危险因素。**结果** lncRNA-ANKRD36BP2 于肺腺癌组织中异常低表达（P = 0.008）。通过 TCGA 数据可知其表达水平和 M 分期(P = 0.254)、年龄（P = 0.765）及性别（P = 0.429）无关，和 T 分期（P = 0.009）、N 分期（P = 0.044）、TNM 分期（P = 0.001）及吸烟（P = 0.004）有关。而我们临床验证样本尚未发现其表达水平与临床参数显著相关。通过生存分析发现低表达 lncRNA-ANKRD36BP2 患者预后较高表达 lncRNA-ANKRD36BP2 患者更差。多因素 COX 逻辑回归显示 T 分期及 TNM 分期可作为肺腺癌患者预后的独立危险因素。诊断效能显示 lncRNA-ANKRD36BP2 曲线下面积为 0.6463。lncRNA-ANKRD36BP2 在肺腺癌组织中异常低表达，其表达水平对于肺腺癌的诊断具有一定价值，低表达 lncRNA-ANKRD36BP2 患者其预后越差，其具有成为肺腺癌治疗靶点的可能性，可为将来提高肺腺癌患者预后提高新思路。

PU-0695

常见肿瘤标志物在肺癌血清外泌体中的表达及临床意义

陈良远、周欢、杨国溜、康艳丽、陈发林
福建省立医院

目的 肺癌的主要实验室诊断指标包括神经元特异烯醇化酶（NSE），细胞角质蛋白 19 片段 21-1（CYFRA21-1），癌胚抗原（CEA），他们都有一定的局限性，本次研究探讨了常见肿瘤标志物 NSE 在肺癌患者和健康人血清外泌体中的差异表达，探究其临床意义。
方法 从 68 个肺癌患者和 35 个健康人的血清中提取外泌体，从外泌体中提取外泌体蛋白，采用 Roche Cobas 602 电化学发光分析仪检测外泌体 NSE 在肺癌患者和健康人血清样本中的表达水平。
结果 实验结果显示，健康人血清外泌体 NSE 高表达，肺癌患者血清外泌体 NSE 低表达，具有明显的差异性。
结论 肺癌患者和健康个体的血清外泌体中 NSE 的表达有较大差异，差异表达的外泌体 NSE 有可能作为潜在的肿瘤诊断标志物，值得进一步深入研究。

PU-0696

血清外泌体的 ENST00000422944 作为肺癌诊断标志物的筛选与验证

陈良远、康艳丽、杨国溜、尤剑彬、陈发林
福建省立医院

背景 肺癌是一种常见肿瘤，以其高发病率和高死亡率为特征。最近已有多项研究表明，许多外泌体中的长链非编码 RNA（lncRNA）在肺癌患者与健康人群中具有差异表达的现象。本研究旨在之前研究的基础上，验证 ENST00000422944 在肺癌诊断中的诊断价值。
方法 提取肺癌患者与健康人血清中外泌体中的 lncRNA，筛选出需要验证的 lncRNA 后，进一步通过实时荧光定量 pcr（qPCR）以及统计学分析来对其进行验证。
结果 经统计学分析，ENST00000422944 在肺癌患者以及健康人群中的血清表达水平有明显差异，且对于 TNM 分期也有一定的临床意义。通过 qPCR 验证后，更加进一步证明 ENST00000422944 对于肺癌早期筛查有着巨大潜力。
结论 ENST00000422944 在健康人群与肺癌患者的血清中有着差异表达，其有望作为新型的肺癌诊断与筛查的标志物。

PU-0697

肺癌患者血清外泌体中 hsa_circ_0001492 和 hsa_circ_0002490 诊断性能的初步分析

陈良远、康艳丽、杨国溜、尤剑彬、陈发林
福建省立医院

目的 探讨环状 RNA（circRNA）在肺腺癌患者和健康人血浆外泌体中的差异表达，通过分析特异性外泌体 circRNA 的表达谱为研究肺腺癌的发病机制建立一定的基础。
方法 从前期研究筛选出差异表达的 circRNA 中挑选其中两个 circRNA：hsa_circ_0001492 和 hsa_circ_0002490 进行进一步研究，通过扩大分析样本量并通过实时荧光定量 PCR（qPCR）进行验证。
结果 在早期肺腺癌患者和健康人血清外泌体中 hsa_circ_0001492 和 hsa_circ_0002490 差异表达，其中 hsa_circ_0001492ROC 曲线下面积（AUC）为 0.8167；hsa_circ_0002490ROC 曲线下面积（AUC）为 0.8588。
结论 肺腺癌患者和健康个体的血清外泌体中 hsa_circ_0001492 及 hsa_circ_0002490 的表达有较大差异并具有表达特异性，具备成为肺腺癌早期诊断标志物的潜力。

PU-0698

分子诊断技术虚拟仿真实验教学平台的构建与应用

杨柳、辛毅娟、程晓丽、李蕊、张翔、周磊、刘家云
空军军医大学西京医院

新冠疫情的暴发凸显了分子诊断技术的重要性。如何做好分子诊断技术规范化操作及实验室生物安全相关培训工作，提高操作培训的教学质量，是做好疫情防控工作的前提和保障。
目的 为提高分子诊断技术的实验培训效果，依托省级临床检验研究中心、省级 PCR 上岗培训基地的建设，在新冠核酸检测的操作技术培训中，采用虚拟仿真技术，使学生通过人机交互的方式对技术原理和实验操作流程进行“探究式、参与式”学习，并探讨平台的建设方法、效果及应用价值。
方法 1.情景化实验：我们开发的虚拟仿真实验平台实现全交互式场景教学。教学中根据实际工作的不同情景设计每项实验，学生可根据自己的学习进度自主学习，通过操控 3D 虚拟人完成实验操作流程。2.模块化教学：实验教学分为演练和考核两个模块。集“学、测、评”于一体，使学生即时了解对知识点的掌握情况并有重点地进行学习。3.线上线下结合的实训体系：虚拟仿真实验与实体单个训练相结合，提高学习效果。同时，学生在线学习遇到疑问时，教师在线解答，做到线上线下相结合的混合式教学。

PU-0699

Has_circ_0002490 可作为肺癌检测新的生物标志物

杨国溜、康艳丽、陈良远、尤剑彬、陈发林
福建省立医院

目的 探讨环状 RNA(circRNA)作为肺癌检测的新生物标志物，对肺癌的诊断价值。
方法 收集 2018 年 10 月至 2020 年 1 月福建省立医院收治的肺部肿瘤患者 5 例，通过高通量测序技术筛选出 5 个表达差异的 circRNA。扩大样本量，收集 79 对肺癌组织和邻近正常肺组织，分为肿瘤组和对照组。检测受试者组织中 circRNA2490、4891、74368、87357、0896 的相对表达水平。用受试者工作特征(ROC)线的相关参数分析。

结果 肿瘤组、对照组中 circRNA2490、4891、74368、87357、0896 的相对表达水平比较，差异均有统计学意义(P<0.05)。曲线下面积 AUC 分别为 0.832、0.679、0.809、0.743、0.683，circRNA2490、74368、0896 联合的曲线下面积 AUC 为 0.855。
结论 circRNA2490、4891、74368、87357、0896 的相对表达量检测对肺癌诊断均有诊断价值，其中 circRNA2490 预测价值最高，另外，circRNA2490、74368、0896 联合检测的诊断效能更佳，有望成为诊断肺癌新的诊断生物标志物。

PU-0700

重度子痫前期孕妇胎盘组织中 TMEM16A 表达的研究

王学翔
山东大学第二医院

目的 检测正常孕妇、重度子痫前期孕妇胎盘组织中 TMEM16A 的表达，分析 TMEM16A 在这二者之间的表达差异，探讨 TMEM16A 在重度子痫前期疾病发生发展中的作用。
方法 选取近 3 年在山东大学第二医院生产的孕妇，其中重度子痫前期孕妇 20 例，正常孕妇 20 例。利用实时荧光定量 PCR 技术（Real time PCR）和免疫印迹法(Western blot)分别检测两组孕妇胎盘中 TMEM16A 的 RNA 相对表达量和蛋白的表达水平，进行统计学分析。
结果 与正常孕妇胎盘组织中 TMEM16A 表达相比，重度子痫前期患者胎盘组织内 TMEM16A 的表达水平（RNA 和蛋白）显著增加。
结论 TMEM16A 在孕妇胎盘组织中有表达，与正常孕妇胎盘组织相比，重度子痫前期孕妇胎盘组织中 TMEM16A 的表达水平高。

PU-0701

Smoothened loss is a characteristic of neuroendocrine prostate cancer

Lili Wang
Shandong Provincial Qianfoshan Hospital

Purpose Hedgehog (Hh) signaling promotes castration-resistant prostate cancer (CRPC) by supporting androgen-independent prostate cancer cell development and growth; however, its role in neuroendocrine prostate cancer (NEPC) has not yet been explored. In this study, we assessed the expression of key genes involved in Hh signaling in prostate cancer and investigated the potential role of smoothened (SMO) in the pathogenesis of NEPC.
Methods Six public datasets, each containing cases of prostate adenocarcinoma (AdPC) and NEPC, were analyzed to compare the differential mRNA expression of 6 classic Hh signaling genes. The SMO, synaptophysin (SYP), chromogranin A (CHGA) and androgen receptor (AR) proteins were evaluated in human tissues from 5 cases of NEPC, 2 cases of AdPC mixed with NEPC, 2 cases of AdPC with neuroendocrine differentiation and 22 cases of high-grade AdPC as determined by an immunohistochemistry assay. Gene set enrichment analysis (GSEA) was performed to identify relevant genetic signatures associated with SMO expression based on the public datasets. Stable SMO-knockdown LNCaP and C4-2B cells were established with a lentiviral system, and the expression of SMO, Gli1, AR, PSA, and REST was assessed by real-time PCR and western blot. Secreted PSA in the conditioned medium was assessed by ELISA. Gli1 was ectopically expressed performed by the transfection of Gli1 cDNA into SMO-knockdown LNCaP cells, and western blot was used to assess of AR and PSA expression.
Results The mRNA level of SMO was dramatically downregulated in NEPC samples compared with AdPC samples in all 6 public datasets. SMO protein loss was observed in 100% of NEPC

samples but in only 9% (2 of 22) of high-grade AdPC samples. GSEA results showed that SMO loss was closely correlated with AR signaling activity. Stable SMO knockdown significantly attenuated AR signaling activity and suppressed AR expression, while Gli1 overexpression partially reversed the inhibitory effects of SMO knockdown on AR signaling activity and AR expression in LNCaP and C4-2B cells.
Conclusion These results demonstrate that SMO loss is a characteristic of NEPC and that detecting SMO by IHC could aid pathologists in NEPC diagnosis. SMO loss may promote NEPC pathogenesis by modulating AR signaling.

PU-0702

Clinical laboratory evaluation of COVID-19

Li Zhang
The First Affiliated Hospital of Shandong First Medical University & Shandong Provincial Qianfoshan Hospital

COVID-19, caused by SARS-CoV-2, is a highly infectious disease, and clinical laboratory detection has played important roles in its diagnosis and in evaluating progression of the disease. Nucleic acid amplification testing or gene sequencing can serve as pathogenic evidence of COVID-19 diagnosing for clinically suspected cases, and dynamic monitoring of specific antibodies (IgM, IgA, and IgG) is an effective complement for false-negative detection of SARS-CoV-2 nucleic acid. Antigen tests to identify SARS-CoV-2 are recommended in the first week of infection, which is associated with high viral loads. Additionally, many clinical laboratory indicators are abnormal as the disease evolves. For example, from moderate to severe and critical cases, leukocytes, neutrophils, and the neutrophil-lymphocyte ratio increase; conversely, lymphocytes decrease progressively but are over activated. LDH, AST, ALT, CK, high-sensitivity troponin I, and urea also increase progressively, and increased D-dimer is an indicator of severe disease and an independent risk factor for death. Severe infection leads to aggravation of inflammation. Inflammatory biomarkers and cytokines, such as CRP, SAA, ferritin, IL-6, and TNF-α, increased gradually. High-risk COVID-19 patients with severe disease, such as the elderly and those with underlying diseases (cardiovascular disease, diabetes, chronic respiratory disease, hypertension, obesity, and cancer), should be monitored dynamically, which will be helpful as an early warning of serious diseases.

PU-0703

G6PC 基因复杂杂合突变致糖原累积病 Ia 型合并先天性心脏病一例及诊断思路探讨

王晶、陈健康、高倩、周磊、刘家云
空军军医大学西京医院

糖原累积病（Glycogen storage Disease, GSD）是糖原和脂质在肝、肾内的异常累积导致肝脏和肾脏的肿大为特点的一种常染色体隐性遗传病。其中Ⅰ型又称 von Gierke 病，主要包括Ⅰa 和Ⅰb 两种亚型,Ⅰa 为葡萄糖-6-磷酸酶缺乏症，Ⅰb 为葡萄糖-6-磷酸转移酶缺陷[1]。2018 年 GSD Ⅰ型被国家卫生健康委员会等 5 部门联合制定的《第一批罕见病目录》纳入，以低血糖、高乳酸血症、高尿酸血症、高脂血症和肝腺瘤为特征。现报道临床检验工作中发现的糖原糖原贮积病 Ia 型合并先天性心脏病一例。

PU-0704

CRISPR/Cas9 系统构建 TSC1 基因敲除的 HEK293 稳定细胞株

王晶、刘家云
空军大学第一附属医院

目的 利用 CRISPR/Cas9 基因编辑系统在 HEK293 细胞系中对 TSC1 基因稳定敲除，并对其敲除效果进行鉴定。
方法 根据 TSC1 基因的序列设计 sgRNA，将 sgRNA 克隆到载体 lentilCRISPRv2 上，将连接产物转化至 Stbl3 感受态细胞，对菌液进行测序鉴定。将鉴定成功的 lentiCRISPRV2-sgTSC1 质粒转染至 HEK293 细胞，加入嘌呤霉素进行筛选，筛选后制备单细胞悬液铺板于 15cm 培养皿，挑选单细胞克隆进行 PCR 鉴定，选取条带单一的细胞株用蛋白免疫印迹法鉴定 TSC1 基因的表达。
结果 成功构建 lentiCRISPRV2-sgTSC1-1/2 重组质粒，并利用该质粒完成对 TCS1 基因的定点切割，蛋白免疫印迹法结果显示细胞中无 TSC1 表达。
结论 用 CRISPR/Cas9 系统成功构建 TSC1 基因敲除的稳定细胞株，为后续实验奠定了基础。

PU-0705

CREB-TFDP3 Promotes Prostate Carcinoma Cell Growth by inhibiting E2F1-Dependent Apoptosis

rui li、liu yang、juan wang、xiaoke hao、yueyun ma
Air force medical uiversity xijing hospital

Background The cAMP-responsive element-binding protein (CREB) is a transcription factor that controls cell differentiation and survival. CREB is overexpressed and constitutively phosphorylated in several human cancers, including prostate cancer (PCa). However, the regulation of CREB in PCa remains to be deciphered. We previously demonstrated that TFDP3 negatively regulates E2F1 transactivation, which is important in PCa carcinogenesis. And 5 CREB binding sites were found in the upstream of TFDP3 promoter.
Methods Luciferase and chromatin immunoprecipitation assays were used to determine the association between CREB and TFDP3. Immunohistochemical staining andimmuno-cytofluorescence assays were performed to determine the expression of CREB and TFDP3 in a prostate cancer tissue microarray and cell lines. Cell lines stably expressing the wild-type, overexpression or knockout of CREB and TFDP3 were established. The protein expression of CREB and TFDP3 were detected by western blot analysis. CCK-8, TUNEL staining and cell cycle analysis were used to analyze the proliferation and apoptosis of the stable cell lines in vitro. The tumor growths were evaluated using nude mice xenograft models.

PU-0706

实时荧光核酸恒温扩增技术在检测分泌物中 MRSA 的应用

张维清、杨滨
福建医科大学附属第一医院

目的 对实时荧光核酸恒温扩增技术（simultaneous amplification and testing method,SAT）检测创面分泌物中耐甲氧西林金黄色葡萄球菌（MRSA）核酸试剂盒（RNA 恒温扩增）应用进行评价。
方法 收集我院临床各科室于 2016 年 12 月至 2017 年 1 月送至检验科微生物室 347 份分泌物标本,分别用实时恒温扩增技术和 ChromID MRSA 产色平板筛选 MRSA。当 SAT 法和 MRSA 培养结果不相符时,进行冻存的备用标本 PCR 扩增、第三方测序,以 MRSA 培养结果加 PCR 测序结果作为本

次试验"扩大金标准",计算 SAT 的灵敏度、特异性、阳性预测值、阴性预测值,并进行相应的统计学分析。
结果 以 ChromID MRSA 产色平板筛选加 PCR 测序作为"扩大金标准",SAT 法检测 MRSA 的敏感度为 90.91%、特异度为 99.40%、阳性预测值为 83.33%、阴性预测值为 99.40%,对 MRSA 的最低检出下线为 102 拷贝/mL,Kappa 系数为 0.85。
结论 SAT 技术在检测分泌物中 MRSA 具有很高的灵敏度、特异性,而且准确、可靠,与传统的细菌培养相比耗时短,为 MRSA 的实验室诊断提供新的检测方法。

PU-0707

Long noncoding RNA LINC00511 promotes gastric cancer progression via regulation of p21 and activation of the AKT and STAT3 pathways

Shengkai Huang 、Hong Lin、Ruo-Xuan Ni、Mei Zhao、Dong-Dong Li、Yan Li、Ke-Xin Li、Qiao Zhang、Chang-Zhi Huang
National Cancer Center/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, 100021, China

Aims Multiple studies suggest that long intergenic noncoding RNA 00511 (LINC00511) plays an important role in all kinds of human cancers. However, the molecular role of LINC00511 in gastric cancer (GC) is still poorly understood and remains largely unexplored.
Methods The expression level of LINC00511 in human serum was determined by reverse transcription and quantitative polymerase chain reaction (qRT-PCR) experiments. CCK-8 assays were used to examine cell proliferation. Cell cycle progression was detected by flow cytometry. BALB/c nude mice were used for tumor transplantation experiments. Protein expression was detected by western blots.
Results In this study, we found that the expression of LINC00511 was upregulated in the serum of patients with gastric cancer and in cell lines derived from gastric cancer. Functional gain and loss experiments showed that overexpression of LINC00511 could promote the proliferation and invasion of gastric cancer cells in vitro, while depletion of LINC00511 inhibited cell growth and induced cell cycle arrest. Mechanistically, we found that LINC00511 downregulated p21 and activated the AKT and STAT3 pathways.
Conclusion Our findings show that LINC00511 accelerates gastric cancer progression by targeting p21 and activating the AKT and STAT3 pathways, and it could be a potential target for future treatments.

PU-0708

长春地区 1593 例人群解脲脲原体感染情况分析

刘明珠
吉林金域医学检验所有限公司

目的 了解本地区 2020 年内 1593 例人群泌尿生殖道解脲脲原体感染情况，为本地区解脲脲原体感染患者诊治提供参考依据。
方法 本实验所用试剂购于上海科华生物工程股份有限公司
1.核酸提取
1.1 吸取 100ul 样品处理液 A 于 0.5ml 离心管中，再加入 100ul 被测样本。
1.2 震荡混匀 13000rpm 离心 10min。
1.3 吸弃上清加入 50ul 样品处理液 B，震荡混匀 2000rpm 离心数秒，100℃干浴 10min。

1.4 3000rpm 离心 10min，取 2ul 上清为 PCR 反应模板。
2.PCR 试剂准备
根据待扩增样品数将 UU 反应液分装至 PCR 反应管中，每管分装 28ul。
3.加样
在 PCR 反应液管中分别加入处理好的样本及阴性、阳性对照各 2ul。
4.PCR 扩增
4.1UNG 酶反应：温度 50℃，时间 2 分钟，循环数 1。
4.2 预变性：温度 94℃，时间 2 分钟，循环数 1。
4.3 变性：温度 94℃，时间 10 秒，60℃时荧光检测，检测通道：FAM。
4.4 退火、延伸：温度 60℃，时间 30 秒,步骤 3 和 4 循环数 40 个。
结果 经检测 1593 例人群样本，其中检测到 UU-DNA673 例，未检测到 UU-DNA920 例，阳性率 42.24%。
结论 长春地区 1593 例样本中，感染解脲脲原体数量为 673 例，阳性率为 42.24%，因此通过实时荧光 PCR 的技术手段可以对解脲脲原体进行检测，可辅助临床进行早诊断、早治疗,并为性传播疾病的流行病学研究提供可靠依据。

PU-0709

福建省汉族乙型肝炎病毒感染者胆固醇 7α-羟化酶基因的多态性分析

吴文楠、欧启水
福建医科大学附属第一医院

目的 探讨胆固醇 7α-羟化酶（CYP7A1）基因多态性与福建汉族人 HBV 感染后不同临床结局之间的相关性,为了解 HBV 相关疾病的发生发展机制奠定基础。
方法 病例对照研究。收集 2015 年 5 月至 2016 年 6 月在福建医科大附属第一医院肝病中心未经抗病毒治疗的 HBV 持续感染者 586 例,乙型肝炎康复者 225 例（年龄在 35～55 岁之间）。未经抗病毒治疗的 HBV 持续感染组包括慢性乙型肝炎患者亚组（246 例）、乙型肝炎相关性肝硬化亚组（177 例）和乙肝相关性肝癌亚组（163 例）。采用改良的多重高温连接酶检测反应技术（iMLDR）对 CYP7A1 基因的 rs3824260、rs4738687 和 rs8192871 位点进行检测,在 HBV 持续感染组、乙型肝炎康复组以及慢性乙型肝炎亚组、肝硬化亚组和肝癌亚组之间进行两两比较,校正年龄性别因素运用二分类 Logistic 回归模型和卡方检验分析基因分型结果。
结果 rs3824260 位点各基因型在各组间的分布差异无统计学意义（X2=1.565,P=0.459）,相较于肝癌组,rs4738687 的突变型 GG 基因型频率在非肝癌组中显著增高（X2=4.403,P=0.041;X2=6.940,P=0.009）,性别分层结果显示男性分组的 rs4738687 的各基因型在 HBV 持续感染组间的分布差异有统计学意义（X2=10.697,P=0.030）。
结论 CYP7A1 基因多态性与福建汉族 HBV 感染者的不同临床结局有关。rs3824260 位点突变具有一定的性别倾向,在男性患者中突变等位基因检出比例更高,携带 rs3824260 C 等位基因的男性乙型肝炎患者更有机会转为乙肝康复;rs4738687 位点可能与福建汉族人肝癌的发生有关,尤其是在男性分组中,GG 基因型可能会延缓肝癌的发生发展;未发现 rs8192871 位点与 HBV 感染的不同临床结局存在相关性。

PU-0710

Long non-coding RNA LINC00662 promotes proliferation and migration of breast cancer cells via regulating the miR-497-5p/ EglN2 axis

Long Cheng、Zihe Xing、Peng Zhang、Wuqin Xu
The First Affiliated Hospital of Wanan Medical College

Previous reports indicated that ong intergenic non-protein coding RNA 662 (LINC00662) plays a crucial role in several human cancers. Here, we studied the expression pattern of LINC00662 and explored its function in human breast cancer. The expression level of LINC00662 was determined in human breast cancer cell lines and tissues by real-time quantitative polymerase chain reaction (RT-qPCR). Cytoplasmic and nuclear RNA from MDA-MB-157 cells were extracted to analyze the subcellular location of LINC00662. Moreover, the MTT assay, wound-healing assay, colony-forming assay and transwell assay were employed in MDA-MB-157 cells to detect the effect of LINC00662 on cell apoptosis, invasion, migration and proliferation, respectively. LINC00662-specific miRNA and miRNA-gene axis were examined in a dual-luciferase reporter assay and Western blot. We found that LINC00662 was overexpressed in both breast cancer cell lines and tissue compared to normal breast cell lines and healthy breast tissue. Analysis of subcellular localization revealed that LINC00662 was mainly found in the cytoplasm. Furthermore, LINC00662 silencing reduced cell viability and inhibited the proliferation, migration and invasion of MDA-MB-157 cells. Bioinformatics analysis predicted that LNC00662 binds to miR-497-5p. A series of studies confirmed that LINC00662 directly interacted with miR-497-5p and downregulated its expression in MDA-MB-157 cells. MiR-497-5p knockdown significantly reversed the inhibitory effect of shLINC00662. Moreover, egl-9 family hypoxia inducible factor 2 (EglN2) was verified as a target of miR-497-5p. Overall, our results demonstrated that overexpression of LINC00662 accelerated the malignant growth of breast cancer cells via sponging miR-497-5p and upregulating EglN2 expression, and indicate that targeting LINC00662 may represent a novel strategy for breast cancer therapy.

PU-0711

Urinary cell-free microRNA-106b as a novel biomarker for detection of bladder cancer

Xuanjun Zhou、Chuanxin Wang
The Second Hospital of Shandong University

Background Cell-free microRNAs (miRNAs) stably and abundantly exist in body fluids and emerging evidence suggests cell-free miRNAs as a novel class of non-invasive disease biomarkers. In this study, we hypothesized that the quantitative detection of the oncogenic miR-106b-25 cluster in urine could be a useful clinical biomarker for bladder cancer (BCa).
Methods Three members of the miR-106b-25 cluster (miR-106b, miR-93 and miR-25) were quantified by real-time RT-PCR in urine supernatant of 112 BCa patients and 78 age-matched controls.
Result In our study, the urinary levels of miR-106b were significantly higher in BCa patients than controls ($P<0.001$). No significant difference was observed in the urinary levels of miR-93 and miR-25 between two groups. Furthermore, the levels of urinary miR-106b were significantly reduced in postoperative samples compared with the levels in the preoperative samples ($P=0.007$). With respect of clinicopathological characteristics, the level of urinary miR-106b was associated with advanced tumor stage. Receiver operating characteristic (ROC) analysis revealed that urinary miR-106b had considerable diagnostic accuracy, yielding an AUC (the areas

under the ROC curve) of 0.802 with 76.8% sensitivity and 72.4% specificity in differentiating BCa from controls.
Conclusions Our data indicate that urinary cell-free miR-106b might provide new complementary tumor biomarkers for BCa.

PU-0712

石墨烯场效应晶体管生物传感器免扩增、快速检测 SARS-CoV-2 核酸

吴丁[1]、喻轶[2]、李听弦[2]、李坤[2]
1. 武汉大学中南医院
2. 湖北中医药大学

目的 现在主流的 SARS-CoV-2 RNA 检测方法为 RT-PCR，然而其检测具有检测周期长、灵敏度低等缺点。因而本研究旨在构建一种新型 SARS-CoV-2 RNA 生物传感器，以实现 SARS-CoV-2 RNA 的免扩增、直接快速检测。
方法 将与 SARS-CoV-2 RdRp 片段特异性互补的磷酰二胺吗啉寡核苷酸探针固定在该芯片表面，直接构建 SARS-CoV-2 RNA 生物传感器。随后，将其用于各种环境中 SARS-CoV-2 RdRp 基因的直接检测，以考察该传感器的灵敏度、特异性等性能。同时，选取 SARS-CoV RdRp 等干扰物考察该传感器的方法特异性。
结果 该传感器检测 PBS、咽拭子保存液、血清中 SARS-CoV-2 RdRp 的灵敏度分别为 0.37 fM(223 copies/μL)、2.29 fM、3.99 fM。在检测不同干扰物时，其信号分别为 6.7 mV（PBS）、18 mV（完全不互补 RNA）、23 mV（SARS-CoV RdRp）、37 mV（单碱基错配 RNA），与 133.4 mV（SARS-CoV-2 RdRp）之间均有显著性差异。在检测实际临床样品时，20 例阳性标本与 10 例阴性标本的检测信号之间的差异具有统计学意义（P<0.0001）。绘制受试者工作曲线后，其曲线下的面积可达 0.995。在该方法与金标准 RT-PCR 之间的一致性结果比较中，其 Kappa 指数可达 0.92；在实时检测中，该传感器可在 2 min 内产生特异性电流响应。
结论 本研究成功构建了一种用于免 PCR 扩增、直接检测 SARS-CoV-2 RNA 的高性能生物传感器。该生物传感器具有良好的方法特异性、出色的灵敏度（223 copies/μL）、抗干扰能力及准确性。该平台可在 2 min 内产生特异性信号响应，极大地缩短了检测周期，因而有望成为快速诊断 COVID-19 的全新检测平台。

PU-0713

血清外泌体 CircRNA 在桥本氏甲状腺炎中差异化的初步研究

吴亚彬、秦晓松
中国医科大学附属第二医院

目的 本研究重点探索桥本氏甲状腺炎（Hashimoto'sthyroiditis, HT）的病理机制，应用微阵列人 circRNA 基因杂交技术发现 HT 患者血清外泌体 circRNAs 的变化，为研究血清外泌体中的 circRNAs 在桥本氏甲状腺炎中的作用机制奠定基础。
方法 通过超高速离心法，提取 3 例 HT 患者及 3 例健康对照者血清中的外泌体。将外泌体中 circRNAs 利用微阵列人 circRNA 基因杂交技术进行分析，发现其差异表达 circRNAs。从上述差异的 circRNAs 中，选取 3 个上调和 1 个下调的 circRNAs，在 7 个 HT 和 8 个健康对照组中，使用逆转录定量聚合酶链反应（reverse transcriptase-quantitative polymerase chain reaction,RT-PCR）进行验证。预测并构建 circRNA/microRNA 之间的相互作用网络，并利用 GO 和 KEGG 途径分析并预测差异基因的潜在功能。

结果 与健康对照组血清中外泌体 circRNAs 相比，发现 HT 血清外泌体中有 162 个 circRNAs 表现出显著差异。所选定的 4 个差异的 circRNAs，经 RT-PCR 验证，统计学分析，hsa_circ_0038416 确实在 HT 患者血清外泌体中表现出上调。经 GO 和 KEGG 基因富集分析表明，这些显著差异表达的 circRNAs 与 29 种基因功能和 1 种信号通路相关。
结论 此项研究结果表明，可以对 HT 血清外泌体 circRNAs 进行基因调控机制研究，支持进一步研究外泌体 circRNAs 在 HT 中的作用。

PU-0714

女性宫颈上皮细胞端粒相对长度与高危型人乳头状瘤病毒感染的相关性

王丽娜
山东大学第二医院

目的 端粒在炎癌转换中发挥重要作用，高危型人乳头状瘤病毒（hrHPV）感染会引起女性宫颈炎、宫颈癌等。在 hrHPV 感染的宫颈癌上皮中端粒长度显著增加，但在 hrHPV 感染的宫颈炎上皮组织中端粒长度的变化研究不多。
方法 收集 2019 年 1 月至 2020 年 6 月在山东大学第二医院进行子宫颈癌筛查女性宫颈上皮组织，排除患有尖锐湿疣等生殖系统感染性疾病、宫颈上皮内瘤变、宫颈癌以及其他系统肿瘤等疾病。留取子宫颈脱落细胞标本，放入 SurePathTM 细胞保存液中，同时进行薄层液基细胞学检查、cobas 4800 HPV DNA 检测高危型 HPV 分型，并提取上皮细胞 DNA，qRT-PCR 检测上皮细胞相对端粒长度，分析相对端粒长度与 hrHPV 感染的关系。
结果 留取了 1434 份无其他生殖系统感染、无宫颈上皮内瘤变、宫颈癌以及其他系统肿瘤的女性宫颈上皮细胞标本，其中 608 例无 HPV 感染，826 例 hrHPV 感染阳性（其中 HPV16/18 感染阳性患者 306 例）；与 HPV 感染组相比，hrHPV 感染组端粒长度明显缩短（$p<0.05$），其中 HPV16/18 感染组与其他 hrHPV 感染组相比端粒长度更短,但无统计学意义。（$p>0.05$）
结论 感染 hrHPV 尤其是感染 HPV16/18 女性的宫颈上皮细胞相对端粒长度明显比未感染女性缩短，因此，宫颈上皮细胞相对端粒长度有望成为宫颈病变早期筛查标志物。

PU-0715

microRNA-206 通过靶向 IGF1 调节胰腺 β 细胞功能

李振、钱增堃、周敬敬、朱文娟、茆政、崔凡
芜湖市第一人民医院

糖尿病是一种常见的代谢性疾病，以慢性高血糖和胰腺 β 细胞功能障碍为特征。多种证据表明，microRNA-206 (miR-206)与糖尿病的发生密切相关，可在胰腺 β 细胞中调控。 然而，miR-206 是否影响 DM 的发展，其具体机制尚不清楚，我们设计本研究是为了阐明 miR-206 通过胰岛素样生长因子 1(IGF1R)/磷脂酰肌醇 3-激酶(PI3K)/蛋白激酶 B(AKT)信号通路在胰腺 β 细胞中的功能和相关的潜在机制，这可能为 DM 提供新的诊断或治疗。
方法 采用定量逆转录 PCR(qRT-PCR)检测 miR-206 和胰岛素样生长因子 1(IGF1)的水平。采用生物信息学和双荧光素酶报告分析方法，阐明了 miR-206 与 IGF1 的关系。 用刺激葡萄糖(16.7mM)或基础葡萄糖(3.3mM)刺激 INS-1 细胞 1h，用酶联免疫吸附试验(ELISA)检测胰岛素含量)。此外，还进行了 3-（4，5）-二甲基噻唑(-z-y1)-3，5-二苯甲酰肼(MTT)测定和流式细胞术(FCM)测定 INS1 细胞活力和凋亡，并分别用 Westernblot 法检测 IGF1R/PI3K/AKT 通路(IGF1R、p-AKT 和 AKT)中的相关蛋白。

结果 DM 患者血液样本中的 miR-206 水平高于健康献血者，表明 IGF1 为 miR-206 的直接靶标。此外，我们还发现 miR-206 负调控 IGF1 在 INS-1 细胞中的表达。证实了 miR-206 抑制剂导致胰岛素总含量增加，INS-1 细胞活力增加，细胞凋亡减少。因此，miR-206 抑制剂显著增强了 INS-1 细胞中 IGF1R 和 p-AKT 蛋白的表达。
结论 miR-206 可以通过靶向 IGF1 调节 IGF1R/PI3K/AKT 通路，从而调节胰腺 β 细胞的细胞活力和胰腺 β 细胞分泌胰岛素的能力。

PU-0716

Prevalence, Antibiotic Resistance and Molecular Characterization of Campylobacter Isolated from Children with Diarrhea in Guangzhou, China

Shouyi Chen、peng mei
Guangzhou Center for Disease Control and Prevention, Guangzhou 510440, China;

Diarrhea is a leading cause of morbidity and mortality in children around the word. Campylobacter, as a food-borne zoonotic pathogen, has been proved the most common pathogen that causes human gastroenteritis in developed countries, while there is a lack of information on the prevalence and antibiotic resistant profile in Guangzhou, China. In this study, stool samples from children with acute diarrhea were collected. The syringe filtration with enrichment method was used for the Campylobacter isolation. The isolates were characterized using molecular approaches and tested for antibiotic resistance. A total of 53 Campylobacter strains, including 42 C. jejuni and 11 C. coli, were isolated from 1197 samples. The most frequently observed resistance agents were ciprofloxacin, tetracycline and nalidixic acid. Overall, 43 different sequence types belonging to 13 clonal complexes and unassigned were identified, and 39.2% Campylobacter isolates representing 19 STs were reported for the first time in the MLST database. The dominant clonal complexes of C. jejuni and C. coli were CC-464 and CC-828, respectively. This study provides detailed information about the prevalence, molecular characterization and antibiotic susceptibility of Campylobacter infections in diarrheal children, which may facilitate the development of pathogen tracking and Campylobacter infection prevention in Guangzhou.

PU-0717

FBN1 基因 c.4336G>A 突变在马凡综合征家系中的致病性研究

李金洁
空军军医大学西京医院

目的 对 1 例马凡综合征患者及其家庭成员进行基因检测，并探究检出突变 FBN1（c.4336G>A）的致病性。
方法 采用多重 PCR 联合二代测序技术对先证者进行遗传性胸主动脉瘤/夹层相关的 15 个基因的组合检测，应用 Sanger 测序技术对检出位点进行验证并对其家庭成员进行同一位点的检测，通过反转录 PCR 及 Sanger 测序等体外实验研究突变对 pre-mRNA 剪接过程的影响，根据 ACMG 指南判读位点致病性。
结果 基因组合检测结果显示先证者携带有 FBN1 基因杂合变异 c.4336G>A，生物学软件预测该位点可能影响剪接；Sanger 测序对患者家庭成员检测发现该家系中存在 4 例携带者，其中 3 例已出现胸主动脉瘤/夹层表现；体外实验表明，该突变位点导致 FBN1 基因 35 号外显子缺失；根据 ACMG 指南该位点致病性判读为可能致病的突变。

结论 FBN1 基因 c.4336G>A 位点首次被证实影响剪接过程，导致 FBN1 基因 35 号外显子缺失，携带该突变将导致严重的胸主动脉瘤/夹层表现，建议对家系中突变携带者加强随访，尽早进行手术治疗或药物干预。

PU-0718

A de novo sSMC(22) characterized by High-Resolution chromosome microarray analysis in a Chinese boy with Cat-Eye Syndrome

Jinjie Li
Air force medical university xijing hospital

We report a 15-year-old boy with Cat-eye syndrome (CES) withoutshortstature or intellectual disorder. The boy was confirmed by cytogenetic and high-resolution chromosome microarray analysis(CMA). The G-banding karyotype confirmed the de novo of thepatient. And the CMA result showed 1.76Mb tetrasomy of proximal 22Q11.1→22Q11.21 consistent with CES {arr22q11.1q11.21(16,888,899-18,644,241)X4}, a typical small type I CES chromosome. The patient has many of the basic characteristics of CES, however, he is taller but not shorter than peers. It is rarely reported in the past since short stature is a common feature of this syndrome. Furthermore, the boy has no intellectual disorder and attends a normal school since he was six years old. What bothered him most were recurrent respiratory infections, retromicrognathia and heart defects.

PU-0719

Human umbilical cord mesenchymal stem cell-derived extracellular vesicles promote the proliferation of Schwann cells by regulating PI3K/AKT signaling pathway via transferring miR-21

Yongbin Ma 、Dan Zhou 、Huanyan Zhang、Jianhua Su
Jintan Affiliated Hospital of Jiangsu University

As an alternative mesenchymal stem cells (MSCs) based therapy, MSC-derived extracellular vesicle (EVs) have shown promise in the field of regenerative medicine. We previously found that human umbilical cord mesenchymal stem cell-derived EVs (hUCMSC-EVs) improved functional recovery and nerve regeneration in a rat model of sciatic nerve transection. However, the underlying mechanisms are poorly understood. Here, we demonstrated for the first time that Schwann cells were effector targets of hUCMSC-EVs, which promoted the proliferation of Schwann cells by activating PI3K/AKT signaling pathway. Furthermore, we showed that hUCMSC-EVs mediated Schwann cell proliferation via transfer of miR-21. Our findings highlight a novel mechanism of hUCMSC-EVs in treating peripheral nerve injury and suggest that hUCMSC-EVs may be an attractive option for clinical application in the treatment of peripheral nerve injury.

PU-0720

IGF2BP2 recognizes the m6A modification of YAP and activates the expression of ErbB2 to promote colorectal cancer progression

Anquan Shang
Tongji Hospital of Tongji University

Objective To explore the effect of insulin-like growth factor 2 mRNA-binding protein 2 (IGF2BP2) on colorectal cancer (CRC) by recognizing the m6A modification of YAP mRNA thus activating ErbB2 expression.
Methods The expressions of IGF2BP2, YAP, and ErbB2 in human CRC tissue, paracancerous tissue, normal human intestinal epithelial cells (HIECs), and three CRC cell lines were analyzed by RT-qPCR and Western blot analysis. Cell proliferation, migration, and invasiveness were detected by CCK-8 assay, scratch test and Transwell assay. The apoptosis was detected using flow cytometric analysis. YAP binding on the ErbB2 promoter was measured by dual-luciferase reporter assay. Enrichment of TEAD4 in the ErbB2 promoter region was measured by the ChIP assay. The level of YAP m6A modification in CRC cells was determined by Me-RIP. The xenograft tumor mice model was established and the tumor volume and weight were recorded.
Results High expressions of IGF2BP2, YAP, and ErbB2 promoted the proliferation, migration and invasion of CRC cells and reduced their apoptosis. IGF2BP2 recognized the m6A on YAP mRNA and promoted the translation of mRNA. YAP regulated ErbB2 expression by promoting TEAD4 enrichment in ErbB2 promoter region. Therefore, IGF2BP2 promoted the expression of ErbB2 to enhance the proliferation, invasion and migration of CRC cells, to repress cell apoptosis, and to promote solid tumor formation in nude mice.
Conclusion IGF2BP2 activates the expression of ErbB2 by recognizing the m6A of YAP, thus affecting the cell cycle of CRC, inhibiting cell apoptosis, and promoting proliferation.

PU-0721

LINC00936 regulate cell proliferation, migration and invasion and tumor angiogenesis in ovarian cancer by interacting with LAMA3 via binding to microRNA-221-3p

Anquan Shang
Tongji Hospital of Tongji University

Objective Ovarian cancer remains to be a leading cause of high mortality in women. Long non-coding RNA (lncRNA) are known to regulate the underlying biological processes and pathogenesis of numerous diseases including ovarian cancer. We aimed to explore whether LINC00936 influences ovarian cancer mediating laminin alpha 3 chain gene (LAMA3) throughmicroRNA-221-3p (miR-221-3p).
Methods Firstly, we identified the differentially expressed lncRNAs related to ovarian cancer in datasets. Subsequently, the expression of LINC00936, miR-221-3p and LAMA3 in ovarian cancer tissues and adjacent tissues was determined following RNA isolation. Next, ovarian cells were transfected with over-expressed LINC00936, miR-221-3p mimic, miR-221-3p inhibitor, and si-LAMA3 respectively, to elucidate their roles in cell proliferation, migration, invasion, angiogenesis, as well as tumorigenesis of ovarian cancer. To further investigate the underlying mechanism of LINC00936 in ovarian cancer, the relationships between LINC00936 and miR-221-3p, and between miR-221-3p and LAMA3 were identified using luciferase activity detection and RIP assays.

Results In cancer tissues, LINC00936 and LAMA3 were poorly expressed, while miR-221-3p was highly expressed. LINC00936 was found to bind to miR-221-3p. Over-expression of LINC00936 led to reduced miR-221-3p, while enhanced LAMA3 expression. Over-expression of LINC00936 significantly decreased ovarian cancer cell proliferation, migration, invasion, angiogenesis and tumorigenesis. Over-expression of LINC00936 reversedthe cancer progression caused byoverexpression of miR-221-3p or silencing ofLAMA3.
Conclusion In summary, over-expression of LINC00936 reduced the progression of ovarian cancer by competitively binding to miR-221-3p. Therefore, LINC00936 or miR-221-3p as therapeutic targets, could provide a novel sight for the treatment of ovarian cancer.

PU-0722

基于 CRISPR-Cas13a 快速高灵敏度检测甲型流感 H1N1

李锦潮[1]、肖斌[2]、李林海[2]
1. 中国人民解放军南部战区总医院
2. 广州医科大学附属第六医院，清远市人民医院检验医学部

目的 将成簇的规律间隔短回文重复序列及其相关蛋 13a （CRISPR-Cas13a）与等温扩增（Recombinase Polymerase Amplification，RPA）结合，即 SHERLOCK 技术，建立快速、高灵敏度以及高特异度的甲型流感 H1N1 检测方法。
方法 以甲型流感病毒 H1N1 特异性基因 H1 的保守序列设计 4 对 RPA 特异性引物，通过扩增和 H1 基因 dsDNA 片段，利用琼脂糖凝胶电泳筛选出扩增效率最高的一对引物，并设计相应扩增片段特异性的 crRNA（CRISPR RNA）；利用梯度稀释的甲型流感病毒 H1N1 核酸标准品评价该方法的检测极限；以 real-time PCR 法为金标准，通过检测临床样本，评价该方法的灵敏度与特异度。
结果 不同的 RPA 引物扩增效率差异明显，筛选出扩增效率最高的一对 RPA 引物，并设计相应的 crRNA，成功构建快速检测甲型流感病毒 H1N1 的 SHERLOCK 检测方法；该方法对甲型流感病毒 H1N1 标准品的检测极限为 10 拷贝，与其它流感病毒无交叉反应；以 real-time PCR 法为金标准，通过检测 30 份临床样本，该 SHERLOCK 检测法的灵敏度达 90%，特异度达 100%。
结论 建立的 SHERLOCK 检测法，具有快速简单、高灵敏以及高特异等优点,为甲型流感病毒 H1N1 的快速检测提供了新的工具。

PU-0723

Detection of EVs RNA Biomarkers by TCLN Chip for Early Diagnosis of Prostate Cancer

Yanjun Diao 、ani nan、weixiao fan、lijuan yu、zhou li、rui li、jinjie li、bingbing zhu、shan wang、lei zhou、liu yang、xiaoke hao、jiayun liu
Department of Clinical Laboratory Medicine, Xijing Hospital, Fourth Military Medical University, Xi'an, China

Extracellular vesicles (EVs) RNA are widely recognized as a good source of tumor biomarkers, because ithasbeenprovedselectivelysortedintoEVs and its detection technique hasrelatively loose requirements for EVs purity compared with protein biomarkers. Serological PSA test, as the only screening method for prostate cancer (PCa), has been abolished in Europe and America from 2012 because of its poor diagnostic specificity.Exploring new diagnostic biomarkers is the key to improve early diagnosis status of PCa. Currently, approximately 90% (17/19) EVs-RNA biomarker studies focus on early diagnosis of PCa, which means to select differentially expressed EVs RNA to distinguish PCa and benign prostate disease. Therefore, this experiment aims to explore and establish a new early diagnosis method for PCa, based on a new EVs detection technology "Tethered Cationic Lipoplex Nanoparticle"(TCLN) chip.

PU-0724

Tumor-Derived Extracellular Vesicles Nucleic Acids as Promising Diagnostic Biomarkers for Prostate Cancer

Yanjun Diao 、weixiao fan、ani nan、lijuan yu、rui li、jinjie li、bingbing zhu、lei zhou、liu yang、xiaoke hao、jiayun liu
Department of Clinical Laboratory Medicine, Xijing Hospital, Fourth Military Medical University, Xi'an, China

Liquid biopsy as a non-invasive method has a promising future in the field of cancer, and extracellular vesicles (EVs) as one of the new areas have drawn much attention. Tumor-derived EVs could mediate immune responses, antigen presentation and intracellular communication through serving as vehicles for intercellular proteins, nucleic acids and lipid transfer. An improved understanding of the role of EVs could lead to a powerful new strategy for diagnosing and preventing prostate cancer (PCa). Among all the components, nucleic acids seem to be the most promising biomarkers which show with potential for the detection and stratification of PCa. In this review, we summarize the current understanding of the topic. The literature points out two aspects of EVs in PCa: 1) biological function of EVs in PCa; 2) summarizing the recent research status of EVs RNA and DNA as PCa diagnosis biomarkers.

PU-0725

Limited diagnostic value of microRNAs for detecting colorectal cancer: A meta-analysis

Xuanjun Zhou、Chuanxin Wang
The Second Hospital of Shandong University

Background MicroRNAs have been demonstrated to play important roles in the development and progression of colorectal cancer. Several studies utilizing microRNAs as diagnostic biomarkers for colorectal cancer (CRC) have been reported. The aim of this meta-analysis was to comprehensively and quantitatively summarize the diagnostic value of microRNAs for detecting colorectal cancer.
Methods We searched PubMed, Embase and Cochrane Library for published studies that used microRNAs as biomarkers for the diagnosis of colorectal cancer. Summary estimates for sensitivity, specificity and other measures of accuracy of microRNAs in the diagnosis of colorectal cancer were calculated by using the bivariate random effects model. A summary receiver operating characteristic (SROC) curve was also generated to summarize the overall effectiveness of the test.
Result Thirteen studies from twelve published articles met the inclusion criteria and were included. The overall sensitivity, specificity, positive likelihood ratio, negative likelihood ratio and diagnostic odd ratio of microRNAs for the diagnosis of colorectal cancer were 0.81 (95%CI: 0.79-0.84), 0.78 (95%CI: 0.75-0.82), 4.14 (95%CI: 2.90-5.92), 0.24 (95%CI: 0.19-0.30), and 19.15 (95%CI: 11.65-31.48), respectively. The area under the SROC curve was 0.89.
Conclusions The current evidence suggested that the microRNAs test might not be used alone as a screening tool for CRC. Combining microRNAs test with other conventional tests such as FOBT may improve the diagnostic accuracy for detecting CRC.

PU-0726

结直肠癌特异性血清外泌体蛋白质标志物的筛选与应用

王恬恬、王传新
山东大学第二医院

目的 肿瘤细胞来源的外泌体蕴含丰富的核酸和蛋白等物质，能够实时反映原发肿瘤的动态变化，为肿瘤早期诊断提供了一条新途径。本研究旨在利用高通量蛋白质组技术检测分析结直肠癌特异性血清外泌体蛋白质表达变化，为结直肠癌早期诊断外泌体蛋白标志物的研究提供科学数据。
方法 随机选取 pTNM 分期 I-II 期结直肠癌患者及健康对照者血清样本各 8 例，超速离心法提取血清外泌体，采用 Label free 蛋白质谱分析技术鉴定差异表达蛋白，并利用生物信息学工具分析差异表达蛋白的功能。
结果 在健康人血清外泌体中鉴定出 4235 个蛋白分子，结直肠癌血清外泌体中鉴定出 4131 个蛋白分子，其中结直肠癌特有蛋白分子 181 个。基于 FC＞2.0 且 p＜0.05 的标准，共筛选出 367 个差异表达的蛋白分子，包括 136 个上调和 231 个下调蛋白分子。这些差异表达的蛋白质主要来自于胞外区、细胞质膜及细胞质，参与免疫反应、代谢、信号转导等生物学过程。
结论 利用血清蛋白质组学技术可以筛选出结直肠癌血清外泌体蛋白标志物,为结直肠癌的血清学诊断提供依据。

PU-0727

11 例惠普尔养障体阳性检出患者的临床特征分析

张玮佳、邓方芳、谭筱醴、冯敏
四川金域医学检验中心有限公司

目的 探讨宏基因二代测序技术检出惠普尔养障体阳性患者的临床特征。
方法 回顾性分析 2020 年 8 月至 2021 年 5 月通过宏基因二代测序技术检出的 11 例惠普尔养障体阳性患者的临床特征，包括性别、年龄、实验室检查、影像学表现、临床症状等，为惠普尔养障体的研究和临床诊疗提供依据。
结果 11 例阳性检出患者中男性共 5 例，占 45.4%，女性 6 例，占 54.6%；年龄范围为 27-90 岁，其中 60-90 岁占 36.4%。阳性检出患者普遍存在呼吸道症状，其中 3 例出现咳嗽，3 例出现呼吸困难，个别出现胸痛、下肢浮肿等症状。6 例阳性检出患者（54.5%）C 反应蛋白高于正常值范围（12.08-190.94mg/L），4 例阳性者（36.3%）降钙素原略微升高（0.43-0.65ng/mL），3 例（27.3%）表现为白细胞计数升高（>10×10^9 个/L），7 例（63.6%）中性粒细胞比率升高。影像学方面，共 9 例（81.8%）存在 CT 异常表现，包括间质病变、多发结节、异常密度影等。9 例（81.8%）合并检出其他病原体，如肺炎链球菌、金黄色葡萄球菌、结核分枝杆菌复合群、耶氏肺孢子菌等。
结论 惠普尔养障体阳性检出患者男女比例及年龄分布较为平均，反映人群普遍易感。临床表现为 C 反应蛋白正常或升高，降钙素原正常或略微升高，白细胞计数和中性粒细胞正常或升高。影像学多表现为肺部炎性改变，部分存在咳嗽、呼吸困难等症状。随着宏基因二代测序技术的普及，更多的惠普尔养障体检出阳性患者被发现，但由于惠普尔养障体感染导致的惠普尔病多为慢性病，且患者仍存在其他病原体合并感染情况，因此阳性检出是否代表致病有待进一步研究。

PU-0728

A Biomimetic Drug Delivery System by Integrating Surface-Engineered Exosomes and Doxorubicin-Loaded Nanoparticles for Glioma Dual-mode Therapy

yang zhang[1,2]、weiling fu[2]、lixiang wu[1]
1. Chongqing University cancer hospital
2. 陆军军医大学第一附属医院

Background Existing nanoparticle-mediated drug delivery systems for glioma systemic chemotherapy remain a great challenge due to poor delivery efficiency resulting from the blood brain barrier/blood-(brain tumor) barrier (BBB/BBTB) and insufficient tumor penetration. To address this issue, Exosomes, naturally derived nanovesicles secreted from various cell types, can serve as an outstanding drug platform for delivery for the reason that they have excellent biocompatibility, near nonimmunogenicity, and long blood circulation ability, all of which result from their endogenous origin. Moreover, exosomes also can traverse the blood-brain barrier, penetrate dense structural tissue. To date, various gold nanomaterials,
including gold nanoshells, gold nanorods (AuNRs), and gold nanocages, have been shown to absorb light in the NIR region (700–900 nm) and kill cancer cells locally without harming the healthy tissues via transforming optical energy into heat. These nanomaterials show promise for biomedical applications, especially tumor therapy.
Method and Results In this work, or the first time, We demonstrated a reproducible and bio-friendly strategy to combine Doxorubicin-Loaded Gold Nanorods (AuNRs) with engineered exosomes via a donor cell-assisted membrane modification strategy. We proposed using sulfhydrylated exosomes as a platform for efficiently conjugating natural exosomes with targeting biomolecules. RGD, which has a certain affinity for combining with integrins overexpressed on the tumor neovasculature and tumor cells. Furthermore, to improve the tumor cellular uptake efficiency, the surface of GD-Exos was functionalized with another tumor-specific targeting ligand (folic acid, FA) through covalent bonds. Because of the synergistic effect of the dual ligands, a high local exosome concentration could accumulate at the tumor site, generating better therapeutic outcomes. Moreover, to promote DOX release in the tumor acidic microenvironment, we prepared DOX-loaded AuNRs nanoparticles with pH-sensitive property (pH-sensitive DNs). Thus, The drug release behavior, which is IR-enhanced, could be rapidly, selectively, and locally activated by remote stimuli. Furthermore, because tumor cells have a lower heat tolerance than normal cells, localized hyperthermia would selectively eliminate the tumor cells without affecting surrounding normal tissues.
Conclusion The designer exosome effectively accumulates at target tumor sites via dual ligand-mediated endocytosis. followed by the near-infrared irradiation triggered drug release from exosomes, thus inhibiting tumor relapse in a programmable manner. The designer exosome can provide functional platforms by engineering with more multifarious functionalities from synthetic materials to achieve individualized precise cancer therapy in the future, especially Glioma.

PU-0729

高病毒载量 HBsAg 阳性孕妇 HBV 母婴传播多因素分析及控制策略

朱博[1]、吕小静[2]、田红霞[1]、赵玉婵[1]、戴二黑[1]
1. 石家庄市第五医院
2. 石家庄妇幼保健院

目的 探讨高病毒载量乙肝孕妇发生母婴传播的危险因素，为完善乙肝母婴阻断策略提供科学依据。
方法 回顾性收集石家庄市妇幼保健院和石家庄市第五医院高病毒载量（HBV DNA≥2×105IU/mL）乙型孕妇的资料，根据入排标准筛选并分为 TDF、TBV 和对照组，对可能影响 HBV 母婴传播的因素进行单因素分析及多因素 logistic 回归分析。
结果 共纳入 545 例孕妇，分娩 545 例婴儿。TDF 组、TBV 组和对照组 HBV 母婴传播率分别为 0.00%（0/174）、0.30%(1/331) 和 5.00%(2/40)，TDF 组与 TBV 组差异无统计学意义（P>0.999），但均低于对照组（P<0.05）。三组均无新生儿畸形等严重不良事件发生。单因素分析结果显示孕妇分娩时 HBV DNA 水平和孕期是否接受抗病毒治疗是发生母婴传播的影响因素（P<0.05），多因素 logistic 回归分析显示分娩时 HBV DNA 水平是发生母婴传播的危险因素（P=0.007）。多因素线性回归分析显示分娩时 HBV DNA 水平受基线 HBV DNA 水平、抗病毒治疗和抗病毒治疗时间影响。在 TDF 组中，孕妇孕中期服药分娩时 HBV DNA 水平显著低于孕晚期服药（P<0.001），但 TBV 组无此统计学差异（P>0.05）。
结论 高病毒载量乙肝孕妇分娩时 HBV DNA 高水平是导致免疫失败的主要原因，孕期接受抗病毒治疗可有效降低孕妇分娩时 HBV DNA 水平，提高母婴阻断成功率且安全性良好。孕中期服用 TDF 降低分娩时 HBV DNA 水平效果显著。因此，强烈推荐孕中期服用 TDF 进行抗病毒治疗以预防 HBV 母婴传播。

PU-0730

集成式微流控核酸检测系统用于生殖道感染病原现场快速检测

刘大渔
广州市第一人民医院

目的 发展一种便携式全集成多靶标核酸检测系统，用于生殖道感染病原现场快速检测。
方法 研究利用 3D 打印快速成型技术和消费电子器件极简地构建了一种低成本自动化“多重样品进快速结果出”核酸分析平台，以阵列芯片锚定液滴序列来构建试剂存储与反应单元，通过芯片相对磁、热、光等作用区域的宏观空间运动完成时间序列上的系列微观质量-能量输运过程，从而实现复杂微分析涉及的样品处理、信号放大及检测在芯片上串联集成和高度并行。研究通过将核酸分析涉及的裂解、富集、纯化、扩增检测试剂以油包水液滴形式预装载在多通道液滴阵列芯片上，将多通道核酸分析所需的系列操作转化为平行化的基本液滴操作组合，通过简单地耦合芯片一维线性运动与可变阵列磁场作用即可实现核酸分析操作的无缝集成与高效执行。该平台上还集成有基于无线视频摄像头的宽场荧光成像模块，结合荧光扩增曲线校正算法可提供基于空间多重分辨实时荧光定量检测且通道间的阈值时间 RSD<5%。
结果 研究优化了液滴平台上 RNA 提取的操作参数，可在 12 分钟内完成快速 RNA 提取，从而将实验室标准操作流程所需的时间相对缩短了近 2/3。进一步，以病原菌细胞内特异性且丰度高的 16S rRNA 为检测对象，通过等温 RNA 同时扩增检测（SAT）反应可以检出含量不低于 102 RNA copies/反应的样品。批量（n=41）临床尿液标本测试结果显示，该平台在 42 分钟完成疑似生殖道感染标本中 4 种病原体的快速定量检测，且结果与实验室标准方法的一致性良好。

结论 研究发展了一套集成式微流控核酸检测系统，并展示了其用于临床标本快速病原筛查的可行性。

PU-0731

基于核酸分子杂交的新型电化学传感器用于 circ RNA 定量检测

孟凡飞、张立群
陆军军医大学第二附属医院（新桥医院）

目的 构建基于核酸分子互补杂交电化学生物传感器，实现肝癌患者血清样本 circ RNA 的超敏快速精准检测。
方法 捕获探针通过氨基羧基作用被固定在磁珠表面，肝癌患者样本中被剪切的特异性片段与捕获探针结合，探针发卡结构被打开，信号探针可识别发卡结构序列并与其特异性结合，信号探针也被固定到磁珠表面。磁吸作用下使磁珠被有效清洗和富集。将磁珠加入电化学工作站区域，通过检测电化学物质分子的信号实现对 circ RNA 的定量分析，采用循环伏安、DPV 等不同检测方法对传感器表面的修饰过程进行电化学表征。
结果 该生物传感器对 circ RNA 有很好的电流响应，在最优的检测条件下，对传感器循环伏安法连续扫描 50 圈，峰电流值下降 3.9%，MB 的氧化峰电流值变化与 circ RNA 的浓度在 1 pmol/L 至 100μmol/L 时范围内呈良好的线性关系，检测限为 0.2 pmol/L。
结论 成功制备了基于核酸分子互补杂交的新型 circ RNA 电化学传感器，建立了 circ RNA 极微量精准检测新方法，该电化学传感器具有电流响应快，灵敏度高，稳定性好，特异性强和可再现性等优点，可应用于 circ RNA 的检测。该方法使用的设备简单方便，不需复杂的配套设施和条件，在微量物质的现场快速检测中具有很好的应用前景。

PU-0732

血液传染病筛查核酸检测与化学发光法比较评价

李广波
上海市东方医院（同济大学附属东方医院）

目的 评价血液传染病筛查三项（HBV、HCV、HIV）核酸检测在临床应用的可行性及与化学发光的比较。
方法 收集检测血液传染病筛查三项的血清标本 500 例，化学发光法检测乙肝五项、抗-HCV、HIV 抗原抗体，提取核酸定性检测 HBV DNA、HCV RNA、HIV RNA。比较三种病原体抗原、抗体筛查化学发光检测与核酸检测结果。结果不一致的标本用罗氏 CobasTaqMan 检测系统检测病毒载量确认最终结果。
结果 检测出 11 例 HBV 化学发光与核酸定性结果不一致标本，未检出 HCV 和 HIV 化学发光与核酸定性结果不一致标本。2 例 HBsAg 阳性 HBV DNA 定性阴性检测标本检测载量均小于 20IU/mL。9 例 HBsAg 阴性 HBV DNA 定性阳性样本中 2 例标本未检测到 HBV DNA 载量，6 例标本检测到 HBV DNA 载量小于 20IU/mL，1 例标本 HBV DNA 载量为 23.6IU/mL。7 例 HBsAg 阴性 HBV DNA 检测到载量标本中 1 例乙肝五项结果全阴，其余 6 例存在 HBsAb、HBeAb、HBcAb 中 1 至 3 项阳性。
结论 血液传染病三项使用核酸检测有利于检测出窗口期和免疫状态异常的感染者，有利于临床对手术病人及输血等患者的评估和管理，核酸检测与化学发光检测结合可为病人的感染确诊及管理追踪提供重要依据。

PU-0733

性病门诊就诊者 HPV 基因检测结果分析

李春花
四川省医学科学院·四川省人民医院

目的 了解统计分析成都地区性病门诊患者就诊者人乳头瘤病毒(Humanpapilomavirus, HPV)感染情况、及亚型分布及不同性别分布特征。
方法 采用导流杂交基因芯片技术对 2018 年 3303 例我院性病门诊就诊者进行 HPV 的 21 种分型检测，包括 15 种高危型和 6 种低危型。
结果 我院 3303 例性病门诊就诊者 HPV 感染率阳性率为 54.56%(1802/3303)，其中男性 1119 例，占 62.1%感染率为 53.16%(1119/2101)，女性 683 例，占 37.9%。感染率为 56.82%(683/1202)，两者比例差异有统计学意义($\chi2=3.912$, $P < 0.05$)。单一型别感染为主，占 58.44%以 58.44%（1053/1802）的单一型为主，其中 6 型(27.04%),11 型(19.06%),16 型(6.71%),52 型(6.35%),58 型(5.11%)最常见，而在多重感染中，以二重感染最为常见 434 例，占 57.94%（434/749）。不同年龄组的 HPV 感染率差异有统计学意义（$\chi2=12.937$, $P < 0.05$），其中，＞60 岁的感染率 63.57%（82/129）最高。
结论 本研究可反应出本地区人群 HPV 感染的基因型分布，不同年龄段和不同性别的 HPV 感染特征，对研制适合本地区特异性 HPV 疫苗，以及宫颈癌的筛查与防治具有参考价值。

PU-0734

Expression and Prognosis of Shelterin genes in Human Colorectal Cancer

Xiaowu Zhong[1]、Shuqi Wang[1]、Dongsheng Wang[2]、Xiaolan Guo[1]
1. Affiliated Hospital of North Sichuan Medical College
2. 四川省肿瘤医院

Background Mammalian chromosomes have a repetitive sequence at the end to prevent the loss of essential genetic information during end-replication. The shelterin genes are a protein complex that prevents recognition of telomere sequences as sites of DNA damage. Changes in telomeres can lead to a variety of human diseases, such as progeria and cancer. However, the distinct roles of each shelterin subunit involved in colorectal cancer (CRC) tumorigenesis remain unknown. In the current study, the mRNA expression and prognostic value of six shelterin subunits in CRC are elucidated.
Methods The transcriptional levels and clinic pathological of shelterin genes were analyzed via the ONCOMINE and UALCAN database. The sequence alteration data related to shelterin genes were obtained from c-BioPortal. The prognostic values of shelterin genes were performed in Kaplan-Meier Plotter. Database for Annotation, Visualization and Integrated Discovery (DAVID) were used to evaluate gene functional enrichment.
Results The result showed higher shelterin mRNA expression in CRC tissues than in normal tissues except TINF2. The higher expression of TERF1, TERF2, POT1, TINF2 and ACD showed in CRC patients with a more advanced cancer stage. The CRC patients with high mRNA levels of the POT1 and ACD were predicted to have poor prognosis. Moreover, the mutation rate of TERF1, TINF2, and POT1 was relatively high in CRC patients. Functional enrichment analyses confirmed that the expression levels of cell cycle genes were closely affected by shelterin genes alterations.
Conclusions This study implied that POT1and ACD could act as potential prognostic markers for the improvement of CRC, especially for high-risk subgroups of patients with CRC, as well as may be potential therapeutic targets for CRC.

PU-0735

METTL3 通过 mTOR 信号通路参与食管鳞状细胞癌细胞的糖酵解

钟晓武、邹江、周锡、郭晓兰
川北医学院附属医院

食管鳞状细胞癌(Esophageal squamous cell carcinoma, ESCC)是人类最致命的癌症之一，5年生存率较低。N6 -甲基腺苷(N6-methyladenosine，m6A)甲基化是一种重要的表观遗传修饰，已被报道与肿瘤的生理和病理过程有关。然而，它在 ESCC 中的作用仍不清楚。在本研究中，我们发现在 ESCC 癌组织和 ESCC 细胞中 m6A 水平升高。此外，我们发现 METTL3 mRNA 和蛋白在 ESCC 组织中显著上调。组织中 METTL3 mRNA 表达水平与 ESCC 分化程度和性别有关($p<0.05$)。组织 METTL3 mRNA 表达水平，诊断 ESCC 的敏感性为 75.00%，特异性为 72.06%，ROC 曲线下面积为 0.8030。METTL3 的缺失显著降低了人 ESCC 细胞系中 m6A 的水平，而 METTL3 过表达恢复了 m6A 水平的降低。这些结果表明 METTL3 是调控 m6A 甲基化的主要酶，是 ESCC 中一个关键的调控因子。此外，在细胞模型和动物模型中，METTL3 敲低显著抑制 ESCC 细胞增殖，而 METTL3 过表达显著促进 ESCC 细胞增殖。这些结果表明 METTL3 促进了 ESCC 的发展。同时也发现 METTL3 可通过 mTOR 信号通路参与 ESCC 细胞的糖酵解，进而促进 ESCC 的进展。我们的研究首次报道了 METTL3 介导的 m6A 甲基化在 ESCC 肿瘤发生中起着至关重要的作用，并强调了 METTL3 可能是 ESCC 患者潜在的生物标志物和治疗靶点。

PU-0736

NIPT 在筛查非目标染色体异常中的应用

叶松道、王晓欧
温州医科大学附属第二医院、育英儿童医院

目的 探讨无创产前筛查（non-invasive prenatal test，NIPT）在筛查常见非整倍体以外的其他染色体异常中的价值。
方法 选择 2018 年 1 月至 2020 年 12 月在温州医科大学附属第二医院产前诊断中心进行 NIPT 的孕妇 12726 例，对提示为 21、18 和 13 非整倍体之外的罕见常染色体数目异常及性染色体异常的孕妇，在知情同意前提下进行介入性产前诊断，获取胎儿染色体核型及染色体微阵列分析结果。回访所有孕妇的妊娠结局及胎儿出生 3 个月后的情况。统计 NIPT 检测胎儿非目标染色体异常的可靠性和准确性。
结果 NIPT 共筛查出胎儿罕见常染色体数目异常及性染色体异常 77 例，筛查阳性率 0.61%。其中 65 例孕妇通过介入性产前诊断，确诊胎性染色体异常 16 例（15 例数目异常、1 例复杂异常），罕见常染色体数目异常 2 例，阳性预测值（positive predictive value,PPV）分别为 43.24%、7.14%。在提示性染色体异常的孕妇中，性染色体增多（XXX、XXY 和 XYY）的 PPV 高达 81.25%，性染色体减少（XO）的 PPV 为 13.33%，性染色体复杂异常的 PPV 为 33.33%，一例复杂异常的核型为 45, X[30] / 46, XY, idic(Y)(q11.22)[23] / 46, XY[47]。
结论 NIPT 可用于筛查胎儿性染色体数目异常，对性染色体结构等复杂异常也有一定的提示作用；NIPT 对筛查罕见常染色体数目异常的阳性预测值不高，存在一定的局限性。

PU-0737

Prediction value of serum HBV large surface protein in different phases of HBV infection and virological response of chronic hepatitis B patients

Can Liu、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

Background Serum HBV large surface protein (HBV-LP) is an envelope protein that has a close relationship with HBV DNA level. This study is to explore the prediction value of HBV-LP in different phase of HBV infection and during antiviral therapy in chronic hepatitis B (CHB) patients.
Methods A retrospective study was conducted in 2033 individuals, which included 1677 HBV infected patients in different phases and 356 healthy controls. HBV-LP, HBV serum markers and HBV DNA were detected by ELISA, CMIA and qRT-PCR, respectively. 85 CHB patients receiving PegIFNα or ETV were divided into virological response (VR) and partial virological response (PVR). The dynamic changes of HBV DNA and HBV-LP were observed.
Results The level of HBV-LP in 2033 individuals was shown as: HBeAg-positive hepatitis > HBeAg-positive infection > HBeAg-negative hepatitis > HBeAg-negative infection > healthy controls. HBV-LP was positive in all patients whose HBV DNA > 1.0E + 06 IU/ml. When HBsAg was <0.05 IU/ml or >1000 IU/ml, HBV DNAs were all negative if HBV-LP < 1.0 S/CO. When HBsAg was between 0.05 IU/ml and 1000 IU/ml, the consistency of HBV-LP with HBV DNA was 100% in case of HBV-LP > 4.0 S/CO in HBeAg-positive patients and HBV-LP > 2.0 S/CO in HBeAg-negative ones. During antiviral therapy, baseline HBV-LP was lower in VR patients than that in PVR patients. The optimal cut-off points to predict VR by baseline HBV-LP were 32.4 and 28.6 S/CO for HBeAg-positive and HBeAg-negative hepatitis patients, respectively.
Conclusions HBV-LP may be a useful marker for distinguishing the different phases of HBV infection. Moreover, baseline HBV-LP level can be used for predicting VR of CHB patients.

PU-0738

Polymorphisms of CYP27B1 are associated with IFN efficacy in HBeAg-positive patients

Yongbin Zeng 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

Background Host single nucleotide polymorphisms were associated with antiviral therapy in CHB patients. The CYP27B1 gene, encoding 25(OH)D3 -1α hydroxylase, might activate 25(OH)D3 to 1,25(OH)2 D3 in kidney resulted in influencing the efficacy of interferon (IFN). The aim of the study was to investigate the association between CYP27B1 polymorphisms and the response to IFN in HBeAg-positive patients.
Methods Eighty-seven HBeAg-positive CHB patients infected with HBV genotype B or C were included in the study. All patients were treated with IFN at least 1 year. According to the response to PEG-IFN therapy, they were divided into three groups: 16 complete responses (CR), 42 partial responses (PR), and 29 nonresponses (NR). Sanger-sequencing was utilized to genotype the CYP27B1 SNPs(rs4646536 and rs10877012).
Results In logistic regression analysis, the frequency of rs4646536 CC genotype was observed to be higher in the NR group. Besides, the GG genotype of rs10877012 differed significantly among the three groups. The GG genotype was prevalent in patients with CR, and patients with TT genotype result in NR at the end of IFN treatment. The most common haplotype TG was independently associated with CR, after adjustment, and haplotype CT appeared to be

associated with NR and PR, rather than CR. The data also showed that patients with baseline 1,25(OH)2 D3 > 39.39 pg/mL had higher CR rates at the end of IFN therapy.
Conclusion These results suggested CYP28B1 gene polymorphisms may be independently associated with the efficacy of IFN in HBeAg-positive patients.

PU-0739

Genetic variants in NTCP exon gene are associated with HBV infection status in a Chinese Han population.

Wennan Wu、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Aim Sodium taurocholate co-transporting polypeptide (NTCP) plays an important role in the enterohepatic circulation of bile acids. Recently, NTCP was identified as a hepatitis B virus (HBV) receptor. The aim of this study is to investigate the association of NTCP polymorphisms with HBV clinical outcomes and investigate the relationship between NTCP polymorphisms and the serum bile acid level in a Chinese Han population.
Methods The single nucleotide polymorphisms rs2296651 and rs4646285 were genotyped in 1619 Chinese Han individuals. Improved multiple ligase detection reaction was utilized to genotype. The level of bile acids was measured by the enzymatic cycling method. Quantitative polymerase chain reaction analysis was carried out to analyze the potential function.
Results In logistic regression analysis, the frequency of rs2296651 (S267F) CT genotype was higher in HBV immune recovery and healthy control groups than in the chronic HBV infection group ($P = 0.001$ and $P < 0.001$, respectively). Patients who carried allele T showed a higher bile acid level than patients who did not carry allele T ($P = 0.009$). The rs4646285 AA genotype was more common in the immune recovery group than in the chronic HBV infection group ($P = 0.011$). No difference in serum bile acid was detected between the rs4646285 wild-type patients and mutant-type patients. Quantitative reverse transcription-polymerase chain reaction showed the NTCP mRNA levels were lower in rs4646285 variants than wild types.
Conclusion NTCP gene polymorphisms may be associated with the natural course of HBV infection in a Chinese Han population. The S267F variant may be a protective factor to resist chronic hepatitis B progression which showed a higher bile acid level in Chinese Han chronic HBV infection patients. The rs4646285 variants could influence the expression of NTCP at the level of transcription, and ultimately may be associated with HBV infection immune recovery.

PU-0740

Evaluation of the performance of four Methods for detection of hepatitis B surface antigen and their application for testing 116,455 specimens

Can Liu、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

Hepatitis B surface antigen (HBsAg) is a crucial serum marker for the diagnosis of hepatitis B virus (HBV) infection. It is imperative to compare test results from different detection **Methods** based on different principles. Four methods, chemiluminescent microparticle immunoassay (CMIA), electrochemiluminescent immunoassay (ECLIA), enzyme-linked immunosorbent assay (ELISA) and golden immunochromato-graphic assay (GICA) were applied to test the HBsAg level in 250 specimens. According to the EP12-A2 and EP15-A2 documents from Clinical and Laboratory Standards Institute (CLSI), the concentration at which repeated results are 50% positive (C50) of HBsAg detected by CMIA, ECLIA, ELISA and GICA was 0.05, 0.08, 0.15 and

15.0IU/ml, respectively. When the detection concentration of HBsAg was 0.5IU/ml, the imprecision degree of CMIA, ECLIA and ELISA was 8.1%, 5.9% and 14.9% respectively. When detecting high HBsAg level (≥20.0IU/ml) and HBsAg negative specimens, the consistency of the four **Methods** was high, while for the low level (0.05-20.0IU/ml), the consistency was poor (except for the CMIA and ECLIA, P<0.05). When evaluation of the four **Methods** in qualitative diagnosis of HBsAg level in the 116,455 specimens, there was no significant discrepancy among CMIA, CMIA and ECLIA, however, GICA was significantly different from the other 3 **Methods** Compared with CMIA, the false negative rate of ECLIA, ELISA and GICA was 0.2%, 1.3% and 12.3% respectively. In conclusion, GICA was only suitable for the preliminary screening of HBsAg positive individuals and ELISA can be applied to the qualitative diagnosis of HBsAg. Both CMIA and ECLIA were suitable for the quantitative determination of HBsAg.

PU-0741

广东地区下呼吸道标本分枝杆菌菌种鉴定及结核分枝杆菌耐药基因检测结果回顾性分析

张磊、吴业鑫、党文强、王秀、黄亚梅、黄韵
广州金域医学检验中心有限公司

目的 了解广东地区下呼吸道标本分枝杆菌的检出率及菌种分布情况，以及结核分枝杆菌的耐药基因突变模式，为分枝杆菌感染的防治提供依据。

方法 采用 *PCR*-反向点杂交法对本中心 2020 年全年收集的 2131 份来自广东地区的下呼吸道标本进行分枝杆菌菌种鉴定（1138 份）和结核分枝杆菌耐药基因突变检测（993 份），分析其菌种分布特征及结核分枝杆菌的耐药基因突变模式。

结果 1138 份菌种鉴定标本中，分枝杆菌阳性 439 例（38.58%），其中结核分枝杆菌 285 例（占阳性标本的 64.92%），非结核分枝杆菌 154 例（占阳性标本的 35.08%）；混合感染 7 例。在 285 例结核分枝杆菌感染患者中，男性 220 例（占 77.2%），检出率显著高于女性，差异有统计学意义（χ^2=33.59，*P*=0.000）。非结核分枝杆菌菌种分布达 9 种，以胞内分枝杆菌和脓肿分枝杆菌脓肿亚种为主；其中胞内分枝杆菌 75 例（46.58%），男性 38 例，性别分布差异无统计学意义（χ^2=3.64，*P*=0.0564）；脓肿分枝杆菌脓肿亚种 53 例（32.92%），女性 41 例，检出率明显高于男性，差异有统计学意义（χ^2=13.49，*P*=0.0002）。485 份阳性标本结核分枝杆菌耐药基因突变检测结果显示，利福平耐药基因突变 80 例（16.49%），以 *rpoB* 531 位点为主（58.75%）；异烟肼耐药基因突变 89 例（18.35%），以 *katG* 315 位点为主（83.15%）；链霉素耐药基因突变 56 例（11.55%），以 *rpsL* 43 位点为主（75%）；乙胺丁醇耐药基因突变 35 例（7.21%），以 *embB* 306 位点为主（62.86%）。

结论 广东地区分枝杆菌感染以结核分枝杆菌为主，且耐药基因突变情况较严重，应重视药敏检测并关注利福平和异烟肼的耐药变化。非结核分枝杆菌感染率明显高于内陆地区，且种类多样，应普及分枝杆菌菌种鉴定。

PU-0742

Detection of hepatitis B virus genotypic resistance mutations by coamplification at lower denaturation temperature-PCR coupled with sanger sequencing

Can Liu、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

Mutations in the reverse transcriptase (rt) region of the DNA polymerase gene are the primary cause of hepatitis B virus (HBV) drug resistance. In this study, we established a novel method that couples coamplification at lower denaturation temperature (COLD)-PCR and Sanger sequencing, and we applied it to the detection of known and unknown HBV mutations. Primers were designed based on the common mutations in the HBV rt sequence at positions 180 to 215. The critical denaturation temperature (Tc) was established as a denaturing temperature for both fast and full COLD-PCR procedures. For single mutations, when a melting temperature (Tm)-reducing mutation occurred (e.g., C-G → T-A), the sensitivities of fast and full COLD-PCR for mutant detection were 1% and 2%, respectively; when the mutation caused no change in Tm (e.g., C-G → G-C) or raised Tm (e.g., T-A → C-G), only full COLD-PCR improved the sensitivity for mutant detection (2%). For combination mutations, the sensitivities of both full and fast COLD-PCR were increased to 0.5%. The limits of detection for fast and full COLD-PCR were 50 IU/ml and 100 IU/ml, respectively. In 30 chronic hepatitis B (CHB) cases, no mutations were detected by conventional PCR, whereas 18 mutations were successfully detected by COLD-PCR, including low-prevalence mutations (<10%), as confirmed by ultradeep pyrosequencing. In conclusion, COLD-PCR provides a highly sensitive, simple, inexpensive, and practical tool for significantly improving amplification efficacy and detecting low-level mutations in clinical CHB cases.

PU-0743

一例与常染色体隐性脊髓小脑共济失调伴轴突神经病 2 型有关的 SETX 基因新突变

文霞、罗庆、刘靳波
西南医科大学附属医院

目的 本研究旨在确定一例共济失调患者的遗传学病因。
方法 对先证者进行详细的临床资料采集。通过动态突变及全外显子组测序寻找可能的致病变异，采用多种在线生物信息学软件对变异进行致病性分析及保守性评估。
结果 先证者主要表现为进行性加重的小脑性共济失调，头颅 MRI 提示小脑萎缩，电生理检查提示双下肢感觉神经受损。基因检测结果发现先证者存在 SETX 基因 c.3247T>C、c.5267T>C 复合杂合变异，父亲携带 c.3247T>C，母亲携带 c.5267T>C，且父母均无异常，符合常染色体隐性遗传模式。弟弟携带同样的复合杂合突变，但除了左眼有轻微水平眼球震颤外没有任何表现。多种生物信息学软件预测两个变异均具有致病性、且变异位点保守。
结论 常染色体隐性脊髓小脑共济失调伴轴突神经病 2 型具有极大的临床和遗传异质性，基因检测有助于该病的确诊。SETX 基因 c.3247T>C 与 c.5267T>C 变异可能为该患者的致病原因，其中 c.3247T>C 是未报道过的新变异，扩展了 SETX 基因的变异谱。

PU-0744

Clinical significance of periodic detection of hepatitis B virus YVDD mutation by ultrasensitive real-time amplification refractory mutation system quantitative PCR during lamivudine treatment in patients with chronic hepatitis B

Yongbin Zeng 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

Monitoring hepatitis B virus (HBV) mutants periodically during nucleoside analogue treatment is of great clinical significance, particularly in persistently HBV DNA-positive patients. However, few studies have investigated the dynamic changes of HBV YMDD (Tyr-Met-Asp-Asp) and YVDD (Tyr-Val-Asp-Asp) populations in chronic hepatitis B (CHB) patients whilst undergoing lamivudine (LMV) treatment. In this study, we sought to investigate the dynamic changes of HBV YMDD and YVDD variants by ultrasensitive real-time amplification refractory mutation system quantitative PCR (RT-ARMS-qPCR) and evaluate its significance for changes in the treatment of CHB patients. RT-ARMS-qPCR was established and evaluated with standard recombinant plasmids. Fifteen CHB patients receiving LMV (100 mg daily) were consecutively recruited and followed up for 60 weeks. Serum samples were obtained from each patient at baseline and every 12 weeks. The total HBV DNA, HBV YMDD DNA and YVDD DNA levels were measured using RT-ARMS-qPCR at all given time points after treatment. Routine liver biochemistry parameters, including aspartate aminotransferase and alanine aminotransferase, were also measured every 12 weeks. The linear range of the assay was between 1×10(12) and 1×10(5) copies ml(-1). The low detection limit was 1×10(4) copies ml(-1). After 60 weeks of LMV treatment, nine patients experienced virological breakthrough. The YVDD variant could be detected 12-48 weeks before virological breakthrough. The YVDD variant was detected as the predominant population (range 69.4-100 %) in patients by the time virological breakthrough appeared. We concluded that RT-ARMS-qPCR was sensitive for the detection and quantification of low levels of HBV mutation. Periodic detection of HBV YM(V)DD every 12 weeks during LMV treatment is helpful for therapeutic decision making.

PU-0745

Application strategies of serum HBV DNA detection in HBV infection patients: A retrospective study of 5611 specimens

Can Liu、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

The detection of hepatitis B virus (HBV) DNA plays a critical role in determining the level of viral replication in HBV-infected patients. However, how to select appropriate HBV DNA detection method, low-sensitivity (ls) and hypersensitivity (hs) remains unclear. In this study, hepatitis B surface antigen (HBsAg), hepatitis B e-antigen (HBeAg), alanine transaminase (ALT), aspartate transaminase (AST), and hs HBV DNA titers in serum of 5611 cases with suspected HBV infection were reviewed. Besides, the dynamic changes of HBV DNA and HBsAg in 85 chronic hepatitis B (CHB) patients receiving peginterferon α (PegIFNα) or entecavir (ETV) were observed. The results showed the positive rate of HBV DNA was 32.8%, of which low viral load (20 to 500 IU/mL) accounted for 51.8%. In the 5611 cases, when the HBsAg was less than 1000 IU/mL, the proportion of low viral load was 76.3%. Moreover, in patients receiving antiviral treatment, when HBsAg was less than 2000 IU/mL (PegIFNα) or HBsAg was less than 3500 IU/mL (ETV), the

proportion of patients with low viral load was 79.5% or 78.0%, respectively. We developed a strategy of serum HBV DNA detection in HBV-infected patients. When HBsAg was negative, HBV DNA detection should be unnecessary. When HBsAg was 0.05 to 1000 IU/mL, hs HBV DNA should be detected in patients with abnormal level of ALT, AST, or HBeAg. While HBsAg was greater than or equal to 1000 IU/mL, ls HBV DNA was recommended. Moreover, the cutoff value of HBsAg increased during antiviral therapy of CHB patients. In conclusion, hs HBV DNA is of great value in HBV-infected patients with low viral load. HBV DNA detection **Methods** should be selected reasonably according to the levels of HBsAg, HBeAg, ALT, and AST.

PU-0746

A Circulating Long Noncoding RNA Panel Serves as a Diagnostic Marker for Hepatocellular Carcinoma.

Jinlan Huang、Qishui Ou
Department of Clinical Laboratory, First Affiliated Hospital of Fujian Medical University

Background Circulating long noncoding RNAs (lncRNAs) have been demonstrated to serve as diagnostic biomarkers for various cancers. We aimed to elucidate the diagnostic efficacy of eight serum lncRNAs HULC, MALAT1, Linc00152, PTENP1, PTTG3P, SPRY4-IT1, UBE2CP3, and UCA1 and their combinations for the diagnosis of hepatocellular carcinoma (HCC).
Methods A total of 129 patients with HCC, 49 patients with liver cirrhosis, 27 patients with chronic hepatitis B, and 93 healthy controls were enrolled in this study. The levels of serum lncRNAs were assessed by quantitative real-time polymerase chain reaction. The correlations between serum lncRNAs and clinicopathological characteristics were further analyzed. The receiver operating characteristic (ROC) curve and area under curve (AUC) were utilized to estimate the diagnostic capacity of serum lncRNAs and their combination with AFP for HCC. A logistic regression model was performed to establish a multiple-lncRNA panel.
Results The levels of serum HULC, MALAT1, Linc00152, PTTG3P, SPRY4-IT1, UBE2CP3, and UCA1 were significantly higher in HCC patients than in patients with benign liver diseases and healthy controls, whereas serum PTENP1 was significantly decreased in HCC patients compared with healthy participants. Positive correlations between serum Linc00152 and GGT, serum PTTG3P and GGT, and serum SPRY4-IT1 and ALT were noted in HCC patients. ROC analysis revealed that all these lncRNAs had a significantly predictive value for HCC except for PTENP1. The best performance of single lncRNA was obtained by Linc00152 with an AUC of 0.877. When combined with AFP, the combination of Linc00152 and AFP gained the highest accuracy, yielding an AUC of 0.906. Through logistic regression analysis, the panel consisting of serum linc00152, UCA1, and AFP provided the greatest predictive ability, obtaining an AUC of 0.912 with 82.9% sensitivity and 88.2% specificity.
Conclusion The panel of serum Linc00152, UCA1, and AFP demonstrates a novel and noninvasive biomarker with relatively high sensitivity and specificity for HCC diagnosis.

PU-0747

细胞因子与糖尿病视网膜病变的相关性研究

卢宇萌
徐州市第一人民医院

随着经济社会的迅速发展，生活方式的改变， DR 患者逐渐增多，正日益突显，但 DR 的确切病因和发病机制尚不明确。近年来有研究发现 DR 的发生发展过程与部分细胞因子存在一定程度的相关性，其中 VEGF 是目前已知的最强的内皮细胞有丝分裂原和诱导血管生成的细胞因子，也是目前认为与 DR 新生血管形成联系最紧密的一个细胞因子；IGF-1 作为一种多功能细胞增生调控因子，

与视网膜多种细胞生长繁殖密切相关。目前，已有研究表明，在 DR 患者中血清 SIL-2R、LECT-2 水平显著升高，而血清 IL-35、IL-6 水平显著降低。但这些细胞因子在 DR 中的具体作用尚不明确。迄今为止，国内外对 DR 与细胞因子相关性的研究众多，但大多数都是进行单一细胞因子的检测，很少有研究进行多种细胞因子的检测。因此，本研究拟以徐州市第一人民医院就诊的 PDR 患者和 NPDR 患者为研究对象，以健康体检者作为健康对照组，采用多重微球流式免疫荧光发光法检测血清中 12 项细胞因子（IL-1β、IL-2、IL-4、IL-5、IL-6、IL-8、IL-10、IL-12、IL-17、IFN-α、IFN-γ、TNF-α）的含量及其水平变化，运用统计学分析 12 项细胞因子与 DR 的相关性，评估 DR 患者的发病风险及患病程度，明确 DR 发生和发展过程中相关细胞因子的作用并探讨其临床意义。为我国 DR 的预防和诊治提供新的思路和方向。

本研究拟表明 DR 患者的血清中部分细胞因子表达水平存在差异，揭示炎症反应在 DR 发生和发展中起到重要作用。DR 的病变程度与部分细胞因子含量呈正相关，病变的严重程度逐渐加重，血清中的细胞因子含量呈递增趋势。因此，细胞因子有可能成为 DR 临床早期预警的标志物。

PU-0748

LncRNA-IMAT1 promotes invasion of meningiomas by suppressing KLF4/hsa-miR-22-3p/Snai1 pathway

Yu Ge、Tao Zhang
Huashan Hospital, Fudan University

Objective Meningiomas originate from the arachnoid cap cells and are the most common primary central nervous system (CNS) tumors. Although majority meningiomas are benign and can be completely resected by surgery, some others has high risk of recurrence and poor prognosis, especially WHO Ⅱ/Ⅲ grade tumors (high-grade meningioma). Compared to benign meningiomas, the prognosis of malignant meningioma is poor, and it seriously affects the survival and quality of life of the patients. Meningiomas with certain molecular characteristics, are prone to be aggressive, for example, NF2 mutation, loss of chromatin 22. Nevertheless, there is no effective molecular marker which has the appreciated value to predict the risk grade and prognosis of meningiomas invasiveness, especially in some benign tumors. Therefore, it is of urgent need to explore novel invasion-related molecule which can assist physicians to decide more precise therapy for patients. Recently lncRNAs are the hot topic in diseases researches，they regulate tumorigenesis and progression in a great many of tumors，which provide a new prospect of studying malignant meningiomas. Now this study is to illuminate the function of a new discovered lncRNA in high-grade meningiomas.

Methods The levels of IMAT1, KLF4, and Snai1 were detected by RT-qPCR and calculated according to the comparative Ct (2 -ΔCt) method using β-actin as an internal control, and hsa-miR-22-3p levels were normalized by U6 as reference. The protein level of KLF4, α-SMA, E-cadherin, MMP2, MMP9 and Snai1 were detected by Western blotting. β-actin was used as an endogenous reference for normalization. The expression of IMAT1 and hsa-miR-22-3p was also analyzed using FISH. The binding of KLF4 and has-miR-22-3p, as well as has-miR-22-3p and Snai1 were confirmed by Luciferase assay. Meningioma cell's viability was analyzed by CCK-8 assay, invasion ability was detected using Cell Invasion Assay and migration ability was assessed using wound healing assay.

Results Our studies indicated that the expression of IMAT1 in invasive meningiomas showed a significant increase compared with that in noninvasive meningiomas. In vitro studies showed that IMAT1 promoted meningioma cells invasion through inactivation of the tumor suppressor Krüppel-like factor 4 (KLF4) by acting as a sponge for hsa-miR-22-3p. IMAT1 knockdown effectively restored the tumor suppressive properties of KLF4 by preserving the KLF4/hsa-miR-22-3p/Snai1 pathway. In vivo experiments have confirmed that IMAT1 silencing could significantly inhibit the proliferation of subcutaneous tumors and prolong the survival period of malignant meningioma tumor-bearing mice.

Conclusion Our research shows that the high expression of IMAT1 is the inherent reason why KLF4 gene loses its tumor suppressor properties during meningioma progression. Based on its function model, we believe that IMAT1 may be a potential target for the treatment of meningioma and has the potential to become a new screening marker of diagnosis, grading, and prognosis for meningiomas.

PU-0749

西南地区 120 例男性不育症患者染色体原因分析

罗庆、李亚兰、刘靳波
西南医科大学附属医院

目的 探讨西南地区 120 例男性不育患者的临床特征与细胞及分子遗传学原因。
方法 收集西南四川地区 120 例男性不育症患者的临床资料并对其进行相应的实验室检测。精液检查按照世界卫生组织指南操作，外周血淋巴细胞按常规染色体培养 G 显带行核型分析，Y 染色体微缺失检测选取 EAA 和 EMQN 推荐的 6 个 Y 染色体特异标签序列位点采用多重 PCR 技术检测 Y 染色体 AZFa（sY84, sY86）、AZFb（sY127， sY134）和 AZFc（sY254, sY255）区的微缺失情况。
结果 120 例男性不育症患者中无精子症患者 62 例、严重少精子患者 21 例及精液质量正常的患者 37 例。采用核型分析与 Y 染色体微缺失检测发现异常 37 例，占总数 31.67%，其中 3 例患者结果均异常。检出染色体异常 30 例，占总数 25%，其中染色体数量异常 20 例，17 例为 47,XXY，2 例为 47,XXY,9qh+。染色体结构异常 11 例，包括了 5 例 46,X,Yqh-，2 例 46,X,inv(Y)(p11q11)，2 例 46,XY,inv(9)(p12q13)，1 例 46，XX, 1 例为 45,X[30]/46,X,Yqh-[20]，1 例 46,XY,15p+。检出 Y 染色体微缺失 10 例，均发生在无精子组及严重少精子组，占总数 8.3%，其中 AZF（a、b、c）缺失 1 例，AZF(b、c)区缺失 2 例，AZFc 区缺失 7 例。
结论 西南地区男性不育症患者中核型异常 47,XXY 与 Y 染色体 AZFc 位点缺失的发生率最高。对不育症患者进行核型分析与 Y 染色体微缺失检测等有助于病因的诊断及遗传咨询，必要时还应进行相关基因检测来进一步寻找遗传学病因。

PU-0750

Association between mitochondrial DNA content and baseline serum levels of HBsAg in chronic hepatitis B infection

Zhen Xun 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Recent studies have demonstrated a potential link between mitochondrial DNA (mtDNA) content and cirrhosis or hepatocellular carcinoma (HCC). However, there are few studies evaluating mtDNA content as a noninvasive marker of chronic hepatitis B infection (CHB). In this study, we conducted a case-control study to determine mtDNA content in peripheral blood leukocyte (PBL) samples from 76 CHB cases naïve to antivirus therapy and 96 healthy controls, and then evaluated the association between mtDNA content and baseline serum concentration of HBV markers. Consequently, CHB cases had significantly higher mtDNA content than healthy controls (1052.85 vs 618.98, $P < 0.001$). Pearson's correlation analysis revealed that mtDNA content was negatively correlated with the baseline levels of hepatitis B surface antigen (HBsAg) ($r=-0.291$, $P=0.011$) in CHB patients. In a trend analysis, a statistically significant association was detected between lower mtDNA content and increasing levels of HBsAg ($P=0.015$). In conclusion, our study provides the first epidemiological evidence that mtDNA content of CHB cases naïve to antivirus therapy is significantly higher than healthy controls and the levels of

mtDNA content is negatively associated with HBsAg. mtDNA content may serve as a potential noninvasive biomarker of CHB which may need more researches to validate.

PU-0751

非小细胞肺癌患者基因突变情况及与肺结节患者的比较

赵冉[1]、伍潇怡[1]、陈颖玮[1]、王雪亮[1]、何章勇[2]、黄维纲[1]
1. 上海市临床检验中心
2. 上海奕检医疗科技有限公司

目的 探讨 15 种肺癌相关基因在非小细胞肺癌（NSCLC）患者中的突变情况及与肺结节患者的差异。
方法 采用二代测序（next-generation sequencing，NGS）技术靶向检测 650 例 NSCLC 患者及同期 29 例肺结节患者石蜡包埋组织中肺癌相关 *BCL2L11*、*BRAF*、*EGFR*、*ERBB2*、*FGFR*、*KRAS*、*MAP2K1*、*MET*、*NRAS*、*NTRK*、*PIK3CA*、*RET*、*TP53*、*ROS1* 共 15 种基因的突变情况。
结果 在 NSCLC 组及肺结节组患者中，检测到基因突变的频率分别为 61.23%及 55.17%（P>0.05）；在所有检测到的基因突变位点中，位于表皮生长因子受体 *EGFR* 基因上的突变位点个数最多，占所有基因突变位点的比例分别为 67.65%和 59.09%（P>0.05）；两组患者中携带至少 1 个 *EGFR* 基因突变的患者分别为 313 例（48.15%）和 11 例（37.93%）（P>0.05）；中国 NSCLC 人群中 EGFR 基因变异频率远高于已报道的西方人群。在 *EGFR* 基因变异的 NSCLC 患者中，除外显子 19DEL、外显子 20INS、T790M 和 L858R 外，还发现了 24 种不同的非常见 *EGFR* 突变。在 NSCLC 患者中 *EGFR* 合并其他基因突变的情况较常见，且 *EGFR* 合并 2 个及 2 个以上其他基因突变的比例也较高，占所有 EGFR 合并突变的 16.13%（10/62）。此外，女性肺腺癌患者发生基因突变的频率更高。
结论 应用 NGS 技术揭示了中国 NSCLC 患者群体肺癌相关基因变异的更多独特特征，比其他分子检测方法更具可行性和必要性，可为后续 NSCLC 患者的药物开发和靶向治疗需要提供特殊策略。

PU-0752

Association study of hypertension susceptibility genes ITGA9, MOV10 , and CACNB2 with preeclampsia in Chinese Han population

Qian Xin
The second hospital of Shandong university

Objective Preeclampsia (PE) is a disorder that occurs during the pregnancy and could affect the maternal and perinatal mortality as well as morbidity. The aim of our study is to investigate the associations between the hypertension susceptibility genes ITGA9 , MOV10 and CACNB2 with PE in Chinese Han population.
Methods A case – control study including 178 PE patients and 202 healthy controls was conducted to assess the associations between three loci (ITGA9 rs155524, MOV10 rs2932538 and CACNB2 rs4373814) and PE. The TaqMan probe assay was applied for genotyping in our study. Quantitative real-time PCR was performed to detect the mRNA expression levels of ITGA9, MOV10 and CACNB2. ELISA was carried out to detect the concentration of serum sFlt-1 or PLGF.
Results Our study detected no significant differences in allelic frequencies of three SNPs between PE patients and healthy controls. In the genetic model, the results showed that the patients with ITGA9 rs155524 GA or AA genotypes had a higher risk of PE development compared to those with GG genotype in codominant model. And PE patients had a higher frequency of GA þ AA genotypes based on the dominant model. Subgroup analysis showed ITGA9

rs155524 was associated with early-onset PE but not with late-onset PE. No association was observed between MOV10 and CACNB2 with PE in any genetic model and subgroup analysis. Quantitative real-time PCR results showed that ITGA9 mRNA expression level was apparently increased in the placental tissues of PE patients. In addition, ITGA9 expression levels of GA þ AA subjects were apparently higher than that in the genotype GG of placental tissues. sFlt-1/PLGF ratio was higher in GA þ AA subjects than that in GG subjects. Regression analysis revealed that ratio of sFlt-1/PLGF was positively correlated with ITGA9 mRNA expression level.
Conclusion This study has identified ITGA9 is a promising candidate susceptibility gene for early-onset PE. Our findings demonstrated that the high expression of ITGA9 might be associated with an increased risk of PE.

PU-0753

Real-time PCR for quantitative detection of mitochondrial DNA from peripheral blood mononuclear cell in patients with HBV-related hepatocellular carcinoma

Zhen Xun 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

The alteration of mitochondrial DNA (mtDNA) content could affect the expression of genes which causes many tumor diseases. However, the association between mtDNA content in peripheral blood mononuclear cell (PBMC) and hepatitis B virus (HBV)-related hepatocellular carcinoma (HCC) remains undetermined. First of all, establishing a reliable assay to detect mtDNA content is of great clinical significance. In this study, the method of real-time quantitative polymerase chain reaction (RT-qPCR) with SYBR Green I was established to evaluate mtDNA content in PBMC of healthy controls (n=23) and non-surgical HBV-related HCC cases (n=46). Receiver operating characteristic (ROC) curve analysis was carried out to assess the clinical significance of mtDNA content for diagnosing HCC. Consequently, linear range of the assay was between 1×1010 copies/μl and 1×103 copies/μl. Sensitivity was 800 copies/μl. Besides, HCC cases had a significantly lower mtDNA content than healthy controls (378.55[58.20–784.85] vs 715.48[292.00–1280.00]; P<0.001). When 489.90 copies/μl was set as the cut-off point, the sensitivity and specificity of mtDNA content to diagnose HCC were 82.6% and 71.7%, respectively. In conclusion, a simple, cost-effective, highly sensitive and specific method to detect mtDNA content is established. This method can be applied to clinical laboratory for detecting mtDNA content. Moreover, our study provides the first epidemiological evidence that mtDNA content in PBMC is significantly associated with HCC. MtDNA content in PBMC could serve as a novel clinical diagnostic indicator for HCC which may need more researches to validate.

PU-0754

医学检验技术在血液肿瘤诊治中的支持作用

胡玎玉
南华附属第一医院

血液检验技术极大地影响了不同形式的血液系统恶性肿瘤患者的诊断和临床管理。早期对血液肿瘤的检测主要根据光镜及电镜下观察细胞形态以及化学染色，此方法易于在基层单位推广，无论新技术如何发展，这一方法仍有不可替代的价值。随着免疫学、细胞遗传学及分子遗传学、分子生物学技术的飞速发展与临床应用，使多种检验方法被综合起来法对血液肿瘤进行诊断和分型。免疫学分析主要包括 IHC 和 FCM, 细胞遗传学主要采用染色体核型分析，分子遗传学分析主要采用荧光原位杂交技术。与 FISH 技术比较，染色体核型分析反映了全基因组的遗传学改变，可同时发现多

种染色体异常，与其他基因分析技术比较，对整条染色体或较大片段染色体的丢失或增加或易位的发现更直观、快速、便捷。血液肿瘤是由于造血干/祖或前体细胞染色体异常或基因突变，导致细胞增殖、分化或凋亡异常，恶性血液细胞大量增加的疾病。目前临床应用的基因检测技术主要有融合基因检测、基因测序和基因芯片技术。目前全基因组测序、全外显子测序、目标基因的测序等多种技术的也相继开展，也从技术层面上进一步推动了血液肿瘤分子检测在实验室的开展和临床的广泛应用。尽管有这些好处，但新突变的识别在临床环境中也面临挑战。在细胞减少不清楚和可能代表芯片的克隆性突变存在的情况下是需要谨慎的。在淋巴系统恶性肿瘤方面，正在尝试建立淋巴瘤的液体活检诊断方法，并最终在骨髓瘤中建立液体活检诊断方法，从而改善治疗监测。不仅如此，临床医生和分子生物学家都需要深入培训，以便对下一代测序结果进行合理的解释，他们的跨学科交流比以往任何时候都更加重要。这样的联合努力最终将有助于最大化发挥这些新的诊断方法的优势，并勾勒出未来的需求和战略，以造福于血液恶性肿瘤患者。

PU-0755

Evaluation of cell-free DNA variables including gene mutations as prognostic biomarkers in breast cancer

Juan Xu[1]、Hailin Peng[1]、Yongmei Meng[1,2]、Chenglin Zhou[1]
1. Department of Laboratory Medicine, Taizhou People's Hospital
2. School of Laboratory Medicine, Dalian Medical University

Objective Cell-free DNA (cfDNA) has recently been recognized as a biomarker of cancer progression. In this paper, we evaluated the prognostic potential of cfDNA variables in breast cancer.
Methods A total of 92 breast cancer (BC) patients were enrolled. The concentration of plasma cfDNA was represented by the qPCR result with LINE1-97 bp primers, and integrity index was calculated as the ratio of the LINE1-259 and LINE1-97. Next generation sequencing (NGS) was used to examine cfDNA to detect copy number variation (CNV) and single nucleotide variant (SNV).
Results The cfDNA concentration, cfDNA CNV index were higher and cfDNA integrity index were lower in metastatic patients than in no metastatic ones ($P < 0.05$). The concentration (OR = 3.877, 95% CI: 1.043-14.413, $P = 0.043$) was associated with metastatic status of BC patients. CNV index of cfDNA was associated with metastatic (OR = 2.895, 95% CI: 1.129-7.424, $P = 0.027$) and distant metastatic status (OR = 4.055, 95% CI: 1.225-13.424, $P = 0.022$) of BC patients. Cases with high cfDNA concentration showed worse progression-free survival (PFS) compared with cases with low cfDNA concentration ($P < 0.05$). Nineteen mutant genes were validated in enrolled breast cancer patients. Among these patients, 27 patients (29.3%) have TP53 mutations, 14 patients (15.2%) have PIK3CA mutations, and 9 patients (9.8%) have KRAS mutations. TP53 mutation was closely related to tumor stage and distant metastatic status of breast cancer ($P < 0.05$). In addition, patients with TP53 mutation showed shorter PFS than those without mutation ($P < 0.05$). In the multivariate analysis, TP53 mutation were significant associated with the poor PFS ($P = 0.035$, HR = 2.094, 95% CI: 1.052-4.167).
Conclusion Assessment of cfDNA concentration, cfDNA integrity index, CNV index and TP53 mutation could be useful in predicting prognosis for breast cancer. These cfDNA variables carry important clinical information for breast cancer monitoring.

PU-0756

GABRD 表达增强预测结肠腺癌患者预后不良

伍模鑫
九江学院附属医院

据报道，神经递质与肿瘤的发生和进展有关。本研究旨在阐明使用来自癌症基因组图谱 (TCGA) 数据库的数据，研究 γ-氨基丁酸 A 型受体 δ 亚基 (GABRD) 在结肠腺癌 (COAD) 中的预后价值。使用 Wilcoxon 秩和检验比较 COAD 和正常组织中的 GABRD mRNA 表达水平。通过 Wilcoxon 秩和检验或 Kruskal-Wallis 检验和逻辑回归分析临床病理特征与 GABRD 表达之间的相关性。使用 Kaplan-Meier 曲线和 Cox 回归分析确定 GABRD mRNA 表达在 COAD 患者中的预后价值。最后，通过基因集富集分析（GSEA）预测了 GABRD 在 COAD 中的分子机制。COAD 组织中 GABRD mRNA 表达水平高于正常组织。Logistic 回归分析显示 GABRD mRNA 表达与 TNM 分期、N 分期、M 分期和微卫星不稳定性（MSI）状态相关。 Kaplan-Meier 生存曲线和对数秩检验显示，表现出高 GABRD mRNA 表达的 COAD 患者与较差的总生存期 (OS) 相关。多变量分析表明，GABRD mRNA 表达的增加是一个独立的预后因素，并且与较差的 OS 相关。 GSEA 揭示 GABRD 参与信号通路，包括细胞粘附分子、间隙连接、黑色素生成和 mTOR 信号通路，以及与基底细胞癌或膀胱癌发展相关的信号通路。总之，增强的 GABRD mRNA 表达可能是 COAD 潜在的独立预后生物标志物。

PU-0757

Genetic polymorphisms in MAPK4 are associated with clinical response to methotrexate in patients with psoriasis

Zhijia Fan、kexiang yan、zhicheng wang
Department of Laboratory Medicine, Huashan Hospital, Fudan University, Shanghai

Background Although methotrexate (MTX) is widely applied to treat psoriasis, significant heterogeneity of efficacy exists among individuals.
Objectives We aimed to investigate the relationship of MAPK4 genetic variants with the efficacy of MTX in psoriasis patients.
Methods Patients treated with MTX were classified as responders or nonresponders if the Psoriasis Area and Severity Index (PASI) at week 12was reduced greater than 75% or lower than 50%, respectively. The genotypes of 14 MAPK4 single nucleotide polymorphisms (SNPs) in 310 patients with MTX treatment were analyzed. The associations of polymorphisms of MAPK4 gene with clinical response were analyzed using both allelic and genotypic models. The expression levels of relative proteins were detected by western blot.
Results Multiple SNPs significantly influenced the clinical response in the univariate analyses. Only rs751114 and rs9949644 polymorphisms were associated with the efficacy followed by adjusting for the confounding factors. Besides, the haplotype analysis of the SNPs revealed the strong differences of frequencies in some haplotypes between responders and nonresponders, as of H5-TA and H6-AGCT haplotypes were significantly higher, whereas the frequencies of H3-GG, H7-GATC, and H11-AT haplotypes were significantly lower in responders. The expression levels of MAPK4 were down-regulated in responders but up-regulated in nonresponders.
Conclusions By demonstrating the significant association of MAPK4 with the clinical efficacy of MTX, this study indicates that MAPK4 may be involved in drug metabolism as a predictor of therapeutic response.

PU-0758

18 个代谢相关基因的肺腺癌预后模型的建立及验证

张文婷[1,2]、刘亚峰[1,2]、胡春晓[1,2]、胡东[2]、邢应如[1,2]
1. 淮南东方医院集团肿瘤医院
2. 安徽理工大学医学院

目的 基于代谢基因的生物信息学分析构建肺腺癌预后模型及验证。
方法 获取 TCGA 和 GEO 数据库中肺腺癌相关临床数据，LASSO 回归构建 TCGA 多基因预后模型并形成风险评分公式以计算患者风险值（risk score,RS）。单因素 Cox 独立预后分析联合多因素 Cox 独立预后分析判断肺腺癌独立的预后因子。通过 ROC 曲线获取模型的 AUC 面积用以评价模型的准确性。根据 RS 的中位值将患者分为高风险、低风险组，在两组间进行 Kaplan-Meier 生存分析判断预后差异。为辅助临床评价患者的生存预后，利用肺腺癌患者的临床信息和 RS 构建诺莫列线图。通过 GSEA 对高低风险组间预后代谢基因进行功能富集分析，探索肺腺癌相关代谢基因的生物学功能和机制。通过 TIMER 数据库分析患者的 RS 与 6 种免疫细胞的浸润以及与 8 种免疫检查点分子表达的相关性。
结果 运用 TCGA 数据库基于 18 个代谢相关基因构建肺腺癌预后模型，GEO 验证集验证预后模型效应良好。RS 可以作为独立的预后因子(HR=4.242,95%CI=3.040-5.919，P＜0.001)。ROC 曲线下面积为 0.713。K-M 生存分析显示，与高风险组相比，低风险组总体生存率显著更高(P＜0.001),预后模型与免疫细胞的浸润以及与免疫检查点分子的表达具有相关性。
结论 基于 18 个代谢相关基因构建的肺腺癌预后模型对患者的预后有良好预测价值，预后模型的 RS 是独立的预后因子，预后模型可以对肺腺癌病人的个体化治疗和早期评估给予一定帮助，同时为指导免疫精准治疗提供了新方向。

PU-0759

血清外泌体 miR-218-5p 在结直肠癌中的表达水平及临床应用价值

常文婧[1]、李冬[2]
1. 上海市同济医院
2. 李冬

目的 探讨外泌体 miR-218-5p 在结直肠癌（CRC）患者血清中的表达水平及其与患者临床病理特征的相关性，评价其在 CRC 中的诊断效能。
方法 选择同济大学附属同济医院 2016 年 10 月至 2018 年 10 月确诊的结直肠癌病例组 78 例，术前采血并保存血清；选择同期健康体检者 40 例作为对照组。采用 ExoQuick 试剂盒提取血清外泌体，应用透射电镜、NTA、Western blot 对外泌体进行形态学和分子表型鉴定；利用 miRNeasy 试剂盒提取血清外泌体中总 RNA，实时荧光定量 PCR 法（RT-qPCR）检测各组血清外泌体 miR-218-5p 的表达水平。以 miR-218-5p 相对表达水平的中位数为截断值，将 CRC 患者分为高表达与低表达组，利用四格表卡方检验（χ2 检验）判断其与临床病理特征的关系；受试者工作特征曲线（ROC）判断其在结直肠癌中的诊断效能。
结果 试剂盒法成功提取到血清中的外泌体。结直肠癌患者血清外泌体 miR-218-5p 的表达水平较正常健康人明显降低（P＜0.001）；其低表达程度与肿瘤大小、TNM 分期、肿瘤淋巴结转移和浸润深度显著相关（P 均＜0.05）；ROC 分析表明血清外泌体 miR-218-5p 诊断结直肠癌的曲线下面积（AUC）为 0.827（95%CI=0.754～0.900），明显优于常规的肿瘤标志物癌胚抗原 CEA（AUC=0.718, 95%CI=0.626～0.811)和糖类抗原 CA199（AUC=0.661,95%CI=0.564～0.758）。
结论 结直肠癌患者血清外泌体中 miR-218-5p 的表达下调与多个不良临床病理学因素相关，具有成为结直肠癌诊断生物标志物的潜力。

PU-0760

无创 DNA 基因检测技术在产前筛查中的应用价值

陈敏
陆军特色医学中心（大坪医院）

目的 通过对比分析无创基因检测技术、血清学唐氏筛查技术和羊水细胞核型分析，探讨无创 DNA 基因检测技术应用于产前筛查中的临床价值和意义。
方法 回顾性分析在我院 2018 年 1 月至 2018 年 12 月 3175 例孕妇进行无创基因检测，包括预产期年龄≥35 岁，唐筛结果为高风险、临界风险或单指标异常、超声软指标等孕妇。在充分知情同意后选择无创 DNA 产前检测，对检测结果为高风险孕妇进一步进行染色体核型分析，对低风险孕妇进行电话追踪随访。
结果 3187 例孕妇外周血中，3175 例低风险，12 例高风险，其中 8 例提示 21 号染色体异常，3 例 18 号染色体异常，1 例 13 号染色体异常，另有 17 例提示性染色体或其他常染色体异常；无创 DNA 检测结果为异常的 29 例孕妇，25 例进行了羊水穿刺核型分析，7 例染色体核型为 47，XN，+21；0 例染色体核型为 47，XN，+18；0 例染色体核型为 47，XN，+13，4 例性染色体异常，3 例其他常染色体异常，11 例染色体无整倍体异常。并对无创 DNA 检测低风险的出生新生儿进行随访，未述明显异常。应用无创 DNA 检测技术诊断胎儿染色体疾病的敏感度为 100%（14/14），特异度为 99.62%（3175/3187），假阳性率为 0.35%（11/3187），假阴性率为 0（0/3187）。
结论 无创 DNA 检测技术在产前筛查中敏感性和特异性高，假阳性和假阴性低的优点，可提高产前筛查效率，减少染色体疾病患儿的出生，是快捷、安全、较介入性产前诊断易于接受、值得推广的安全可靠的产前筛查方法。

PU-0761

Long non-coding RNA IGF2-AS represses breast cancer tumorigenesis by epigenetically regulating IGF2

Yanan Zhang
Ben Xi central hospital

Long non-coding RNAs (lncRNAs) are a kind of endogenous ncRNAs with a length of more than 200 bp. Accumulating evidence suggests that lncRNAs function as pivotal regulators in tumorigenesis and progression. However, their biological roles in breast cancer remain largely unknown. Here, we found that IGF2 antisense RNA (IGF2-AS) was significantly decreased in breast cancer tissues, cell lines and plasma. Patients with low IGF2-AS were more likely to develop larger tumor size and later clinical stage. Overexpression of IGF2-AS evidently inhibited the proliferation and induced apoptosis of MCF-7 and T47D cells in vitro, as well as retarded tumor growth in vivo. Further investigation revealed that IGF2-AS inhibited the expression of its sense-cognate gene IGF2 in a epigenetic DNMT1-dependent manner, resulting in the inactivation of downstream oncogenic PI3K/AKT/mTOR signaling pathway. Enforced expression of IGF2 could significantly block the tumor inhibitory effect of IGF2-AS. Importantly, we found that IGF2-AS could be used as an effective biomarker for breast cancer diagnosis and prognosis. Taken together, our study indicates that IGF2-AS is a tumor suppressor in breast cancer, restoration of IGF2-AS may be a promising treatment for this fatal disease.

PU-0762

Retinoic acid-induced gene G (RIG-G) as a novel monitoring biomarker in leukemia and its clinical applications

quan wenqiang、Li Dong
ShanghaiTongji Hospital

INTRODUCTION Retinoic acid inducible gene G (RIG-G) is an inducible gene produced during the treatment of acute promyelocytic leukemia with all-trans retinoic acid (ATRA). The expression level of RIG-G gene in the peripheral blood of healthy subjects and patients with acute promyelocytic leukemia (APL or AML-M3) is unclear. A TaqMan-MGB fluorescent probe qPCR (real-time polymerase chain reaction) method was established to detect the expression of RIG-G (retinoic acid induced gene G) in APL.
METHODS we used this method to analyze the expression level of RIG-G in the peripheral blood of normal population and APL patients, and further explore its clinical value in APL. Twenty clinical patients with APL were selected and their RIG-G expression was quantified to evaluate the relevance between peripheral blood and bone marrow samples. U test was used to analyze the expression level of RIG-G in the peripheral blood of 40 normal specimens and 20 APL patients to observe the prognostic monitoring effect of RIG-G gene in the ATRA treatment process, and use ROC (receiver operating characteristic curve) Analyze and test the diagnostic efficiency of RIG-G gene for APL patients.
RESULTSThere is a strong positive correlation between the expression of RIG-G in peripheral blood and bone marrow of APL patients. The expression level of RIG-G in peripheral blood of APL patients is significantly lower than that in healthy controls ($p<0.001$). The changes inthe expression level of RIG-G in peripheral bloodchanged indicates the remission and recurrence of APL patients after ATRA treatment, and the ROC curve shows that it has a better diagnostic power for APL.
CONCLUSIONS The TaqMan-MGB real-time PCR method we established functioned successfully, deeming it suitable for the detection of RIG-G gene expression in peripheral blood. This method could provide necessary help for diagnosis, prognosis judgment and relapse monitoring of clinical APL patients.

PU-0763

结直肠癌患者血浆外泌体 miRNA-139-3p 的表达及其临床应用价值

杨滇宇、李冬
上海市同济医院(同济大学附属同济医院)

目的 探讨结直肠癌患者的血浆外泌体 miRNA-139-3p 水平的变化及其在结直肠癌辅助诊断中的临床应用价值。
方法 利用外泌体试剂盒提取 80 例结直肠癌患者和 23 例健康人血浆中的外泌体，分别使用透射电镜、Western Blot 和纳米颗粒示踪法进行鉴定。采用 RT-qPCR 法检测血浆外泌体中 miRNA-139-3p 的表达 水平，并分析其与患者临床病理学特征的关系。
结果 结直肠癌患者血浆外泌体 miRNA-139-3p 的表达水平较正常健康人明显降低（$P<0.001$），其低表达程度与肿瘤转移和浸润深度显著相关（$P<0.05$）；受试者工作特征曲线（ROC）分析表明，血浆外泌体 miRNA-139-3p 诊断结直肠癌的曲线下面积（AUC）为 0.726（95%CI=0.603～0.848），血浆外泌体 miRNA-139-3p 鉴别诊断结直肠癌是否有转移和是否浸润至粘膜下层的曲线下面积（AUC）分别为 0.766（95%CI=0.662～0.869）和 0.733（95%CI=0.602～0.863）。

结论 结直肠癌患者血浆外泌体中 miRNA-139-3p 的表达下调与多个不良临床病理学因素相关，具有成为诊断结直肠癌的生物标志物的潜力。

PU-0764

A nomogram from the SEER database for predicting the prognosis of patients with non-small cell lung cancer

Bingjie Zeng 、Zujun Sun
Shanghai Tongji Hospital

Objective The purpose of this study was to establish and validate a nomogram to predict the prognosis in patients with non-small cell lung cancer (NSCLC) from multiple perspectives.
Methods A total of 98,640 eligible patients were randomly divided into a training set (n = 69,048) and a validation set (n = 29,592). The base line characteristics of the two sets were similar. We used clinical data from patients in the training set for univariate and multivariate Cox regression analyses. Twelve independent risk factors were incorporated for constructed a prognostic nomogram.
Results And the nomogram with a concordance index of 0.777(95 % CI, 0.775 to 0.779) for overall survival. The calibration curve results showed that the actual survival rate was consistent with the predicted survival rate. The area under curve of the receiver operating characteristic curves demonstrated that the nomogram has a high prediction of the overall survival rate in patients with NSCLC.
Conclusion We have developed a nomogram with high prediction accuracy and discrimination ability, which can help cliniciansmaking personalized survival predictions for NSCLC patients.

PU-0765

p62 在肺腺癌中的表达及其临床诊断价值

曾冰洁、李冬
上海市同济医院(同济大学附属同济医院)

目的 探讨 p62 蛋白在肺腺癌(lung adenocarcinoma，LUAD)中的表达情况及其在肺腺癌中的临床诊断价值。
方法 收集 2011 年 12 月至 2013 年 5 月上海市同济医院收治的 60 例肺腺癌患者组织标本进行石蜡包埋和组织芯片制作，采用免疫组织化学技术(immunohistochemistry，IHC)检测肺腺癌患者癌组织和癌旁组织中 p62 的表达，综合分析 p62 表达与肺腺癌患者临床病理特征及生存预后的关系；收集 2018 年 4 月至 2019 年 10 月同济医院初诊的肺腺癌住院患者术前检查标本和健康体检者血浆标本，酶联免疫吸附法(enzyme linked immunosorbent assay，ELISA)分别检测肺腺癌患者和健康体检者血浆中 p62 的表达情况，应用 ROC 曲线评估血浆 p62 在肺腺癌中的诊断价值。
结果 IHC 结果显示癌组织中 p62 水平明显高于癌旁组织，具有统计学意义(P<0.05)；p62 表达与患者肿瘤大小、临床病理分期及有无淋巴结转移具有统计学相关（均 P<0.05）。p62 高表达的肺腺癌患者总生存期差于 p62 低表达患者(P<0.05)，提示 p62 高表达与肺腺癌患者不良预后有关。肺腺癌患者血浆中的 p62 蛋白水平显著高于健康对照组，差异具有统计学意义(P<0.001)，受试者工作特征曲线下面积为 0.835(P<0.05)，单项指标中 p62 的 AUC（0.835）、阴性预测值（82.02%）和准确度（76.67%）优于 CEA、CA125、CA153 等传统指标；四项指标联合检测敏感度（86.67%）、准确度（81.67%）和 AUC（0.920）则最高。
结论 p62 在癌组织和血浆中高表达，与肺腺癌患者总生存期及不良预后相关，与传统肿瘤标志物联合检测能明显提高对肺腺癌的诊断效能，具有一定的辅助诊断价值，有望成为评估肺腺癌患者生存预后的肿瘤标志物。

PU-0766

人类转导蛋白（β）-2（TBL2）在泛癌中的表达分析研究

刘阳阳
柳州市柳铁中心医院

肿瘤作为人类致死率最高的疾病之以其的发生与遗传、能量代谢、环境等多种因素相关，肿瘤标志物也一直是肿瘤学的研究重点之一。人类 TBL2 目前多认为是与威廉姆斯伯伦综合征、血脂调节和代谢综合征等疾病相关，但与肿瘤的发生及预后之间的关系尚缺乏相关研究。

目的 探究 TBL2 与泛癌的发生及预后间是否存在关联，探寻其作为肿瘤标志物及预后指标的可能。

方法 通过 TCGA、Oncomine、TIMER、GEPIA2、UALCAN 及 cBioportal 等在线数据库对 TBL2 在不同肿瘤中的表达水平和突变情况进行分析，并探究其表达水平对肿瘤患者生存情况的影响及遗传变异情况。

结果 1.TBL2 的 mRNA 表达水平在 BLCA、BRCA、CHOL、COAD、ESCA、GBM、HNSC、KICH、KIRC、KIRP、LIHC、LUAD、LUSC、PRAD、READ、STAD、LGG、DLBC、OV、SKCM 及 THYM 中均呈高表达,在 LAML 及 TGCT 中则呈低表达状态（P<0.01）。在蛋白水平上则在结肠癌、乳腺癌、透明细胞癌、RCC、UCEC 及 LUAD 中呈高表达（P<0.01）。同时在 IV 期的 CESC 中呈高表达状态（P<0.01）。2.在 LGG、LUAP、SARC、GBM 及 UVM 中均存在随 TBL2 表达升高患者整体生存率降低的情况（P<0.01），同时在 LGG、LIHC 及 UVM 中存在随 TBL2 表达升高患者无病存活率降低的情况（P<0.01）3.TBL2 在在 TCGA 数据库中各肿瘤中的遗传变异情况表现为：在 UVM 病例中均表现为突变，在 ESCA、DLBC、TGCT、PRAD、CSCC 及 KRCC 中则均表现为扩增。突变位点中则是以错义突变为主。在 SKCM、LGG 及 GBM 中 TBL2 的突变水平与患者整体生存率相关（P<0.05）。

结论 人类 TBL2 与多种肿瘤的发生及预后均具有一定的相关性，是作为新的肿瘤标志物的有力候选。

PU-0767

人体表征分子 SNP 位点在群体个体识别方面的初步研究

赖力
福建省立医院

目的 通过对 DNA 遗传信息和表型特征进行关联分析，在人体外貌特征（EVC）的特定表型与第三代遗传标记单核苷酸多态性(Single nucleotide polymorphisms，SNPs)位点之间建立对应关系，评价分子遗传标记在人体表征鉴定识方面应用价值。筛选与特定群体虹膜颜色、发色等人体表征具有高度相关性的 SNPs 位点，为构建针对群体的 EVC 鉴识体系提供依据。

方法 以 100 名福建地区汉族无血缘关系个体为研究对象，采集研究对象个人头面像及虹膜照片，由人工读取 2D 照片并对色素表型进行分类的方法来提取色素特征。同时采集研究对象血样并提取基因组 DNA，构建 EVC 中与虹膜及毛发颜色相关的 24 个 SNPs 复合检测体系，来源于 11 个不同的基因：MClR， HERC2，OCA2，SLC24A4，SLC45A2，IRF4，EXOC2， TRYPl，TYR，KITLG 和 PIGU / ASIP。通过 PCR 复合扩增、产物消化、电泳体系纯化、毛细管电泳和荧光检测基因分型等方法获得 24 个 SNPs 位点的基因分型。将 SNPs 分型结果上传色素表型在线推断模型（https://HIrisPlex.erasmusmc.nl/）进行表型分析，计算后可得到眼睛颜色（中间色、棕色）和头发颜色（棕色、黑色、深色）的推断概率。依据推断模型使用说明及相关文献对眼睛头发颜色进行判读。判读结果与人工图片判读结果进行比较。

结果 福建地区汉族人群的虹膜和毛发颜色为棕色瞳孔和深色头发，体系预测的平均准确度为深色头发 93.3%和棕色瞳孔 95.8%，基于 SNP 位点基因型的色素表型推断结果与人工判断结果基本一致。

结论 24 个虹膜与毛发颜色相关的 SNP 位点构建的色素表征推断体系具有较高的可靠性，具有一定的适用性，能够在群体个体识别尤其是眼睛和毛发颜色预测中有重要作用。

PU-0768

HPV genotypes distribution in cervical intraepithelial neoplasia and invasive cervical cancer: a population-based study in Beijing

Xiao Han、Jie Yi、Yaling Dou、Yong Gan、Lingjun Kong、Jie Wu
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences

Background Human papillomavirus (HPV) has been proved to be a major risk in the occurrence of cervical cancer. Therefore, it is critical to understand the distribution of HPV genotypes in a specific region. This study aimed to investigate the distribution and prevalence of HPV genotypes among women with cervical intraepithelial neoplasia (CIN) and invasive cervical cancer (ICC) in Beijing.
Methods A total of 2133 women with HPV-positive infection and pathological abnormalities were enrolled in Beijing from January 2014 to November 2019. The obtained data were used to analyze the prevalence rates of HPV genotypes based on all grades of pathological diagnosis (CIN1, CIN2, CIN3, and ICC). Frequency tables were evaluated using the chi-squared test ($\chi 2$). The multivariate logistic regression method was used to analyze the association between the multiple HR-HPV types and cervical lesions of CIN3 and ICC.
Results The top five overall prevalence of HPV genotypes were HPV16 (28.22%), HPV58 (19.64%), HPV52 (19.32%), HPV66 (9.47%), and HPV56 (9.14%) among HPV-positive women with all grades of pathological abnormalities in Beijing. The overall prevalence of HPV was higher in the under 35 and 35-44 age groups than in other age groups ($P<0.001$). As a single type of HPV infection, HPV16 had a significantly higher percentage in CIN3/ICC than in the CIN1 group ($P<0.05$). Considering infection with the single HPV genotype as a reference, adjusted odds ratio (OR), (95% CI) was 0.94 (0.70-1.25) in CIN3 in the case of individuals with ≥2 HPV infection. The corresponding result in ICC was 0.81 (0.56-1.17).
Conclusion HPV detection and pathology diagnosis were important screening programs in patients under the age of 45, who should take cervical precancerous lesions seriously. Moreover, there was no significant association between the multiple HR-HPV types infection and the pathological diagnosis of CIN3/ICC (versus CIN2) in this study.

PU-0769

宁夏地区尖锐湿疣患者人乳头瘤病毒基因分型检测及分析

赵倩颖、师志云、乔霞
宁夏医科大学总医院

检测与分析宁夏地区人乳头瘤病毒（HPV）基因型的感染情况。利用 HPV 液态芯片流式荧光杂交法对已确 525 例尖锐湿疣（CA）患者进行 HPV-DNA 分型检测与分析。525 例患者中 HPV 阳性 245 例，检出率为 46.7%，27 种亚型全部检测出。排名前 6 的亚型检出分别为 HPV-6（19.4%，102/525），HPV-11（7.4%，40/525），HPV-39（4%，21/525），HPV-53（4%，21/525），HPV-16 （3%，16/525），HPV-18（2.9%，15/525），其中高危型检出率为 34.8%，低危型检出率为 37.3%。单一感染有统计学意义占 63.3%，多重感染占 36.7%。不同性别间，单一低危型和单一高危型感染差异（P ＜0. 05），但多重感染差异无统计学意义（P＞0. 05）。宁夏地区 CA

患者以低危型 HPV -6、HPV -11 和高危型 HPV -39、HPV -53 为主，高危型与低危型存在混合感染或交叉感染，为宁夏地区 CA 患者 HPV 感染预防提供参考依据。

PU-0770

Quantitative Proteomics Reveals Dormancy-related Proteins Mediated Attenuation Program in Mycobacterium Strain

hong wang、Er hei Dai
The Fifth Hospital of Shijiazhuang,

More evidences show that Mycobacterium tuberculosis complex (MTBC) exhibit >99.95% identity over genome sequence and closer genetic relationship, but different virulent, immune response, and transmissibility. To better understand the mechanisms of MTB virulence and search new potential targets, we systemically investigated the total cell protein among virulent H37Rv, attenuated H37Ra, and avirulent M. bovis BCG vaccine strain in log and stationary-phase by tandem mass tag (TMT) quantitative proteomics. Data analysis showed that we obtained deep-coverage protein identification (three quarters of annotated proteins) and higher quantification (>99% labeling efficiency). Among the quantified proteins in log-phase, total 611 protein groups were dysregulated including 227 groups from H37Rv and H37Ra, 381 from BCG and H37Rv, and 414 from BCG and H37Ra group. More differentially expressed proteins (DEPs) were found in stationary-phase, total 1365 protein groups showed statistically significant differences including 61 groups from H37Rv and H37Ra, 1177 from BCG and H37Rv, and 1124 from BCG and H37Ra, respectively. Similar protein abundance was observed between H37Ra and BCG in log-phase, while more similar protein expression was showed between H37Rv and H37Ra in stationary-phase. Bioinformatics analysis revealed that the upregulated DEPs from H37Rv or H37Ra in log-phase were virulence factors, which mainly enriched in VII secretion system, pathogenesis, sulfolipid biosynthesis, growth of symbiont in host cell, and active evasion of host immune response. Whether in log or stationary phase, the DEPs of BCG were enriched in fatty acid metabolism, lipid metabolism of cell wall, carbon flux, arginine synthesis, and stress response (hypoxia, NO, nutrient starvation, deficiency of metal ions, low pH, etc.), which are also the MTB response proteins under dormancy condition. This study described the proteomic portrait of H37Rv, H37Ra and BCG by precise quantitative proteomics, which may provide a better understanding of H37Rv pathogenesis, H37Ra attenuation and BCG inmmuno-protection.

PU-0771

Diagnostic value of dysregulated microribonucleic acids in the placenta and circulating exosomes in gestational diabetes mellitus

Lina Wang
Laboratory Medical Center, The Second Hospital of Shandong University, Jinan, Shandong Province, China

Aims/Introduction Differentially expressed microribonucleic acids (miRNAs) in the placenta and circulating exosomes are of diagnostic value for gestational diabetes mellitus (GDM). In a cross-sectional study, we identified miRNAs expressed both in the placenta and circulating exosomes of pregnant women with GDM, and estimated their diagnostic value.
Materials and Methods Next-generation sequencing was used to identify miRNAs in the placenta that were differentially expressed between GDM and normal glucose tolerance

pregnancies. Quantitative polymerase chain reaction was used to validate the identified targets. Western blot and transmission electron microscopy were used to validate exosomes. Univariate logistic regression analysis was used to establish diagnostic models based on miRNAs expression, and the diagnostic value was estimated using the receiver operator characteristic curve.
Results We identified 157 dysregulated miRNAs in the placental tissue obtained from GDM pregnancies. Of these, miRNA-125b was downregulated ($P < 0.001$), whereas miRNA-144 was upregulated ($P < 0.001$). The patterns of these two miRNAs remained the same in circulating exosomes from GDM pregnancies (all $P < 0.001$). miRNA-144 levels in the circulating exosomes negatively correlated with body mass index both before pregnancy ($P = 0.018$) and before delivery ($P = 0.039$), and positively correlated with blood glucose at 1 h, estimated using the oral glucose tolerance test ($P = 0.044$). The area under curve for the established diagnostic model was 0.898, which was higher than blood glucose levels at 0 h.
Conclusions These findings suggest that miRNA-125b and miRNA-144 are consistently dysregulated in circulating exosomes and the placenta from GDM pregnancies, and are of excellent diagnostic value for GDM.

PU-0772

Y 染色体 STR 基因座分型与 AZF 区基因微缺失的相关性研究

赖力
福建省立医院

目的 对个体识别和父源关系鉴定中的 Y 染色体 STR（Y-STR）基因座分型缺失现象进行分析，探讨其与 AZF 区基因微缺失的相关性。
方法 采用三种 Y-STR 基因座检测系统共检测样本的 43 个 Y-STR 基因座，分别为 AGCU Y24 检测系统、GFS 24Y 检测系统以及 Promega Y23 检测系统（美国 Promega 公司），对存在 Y-STR 基因座分型缺失的样本进一步采用 Y 染色体微缺失试剂（荧光 PCR-毛细管电泳法）（北京阅微基因技术公司）进行 AZF 区 STS 位点检测，对 AZF 区基因缺失情况进行判断。
结果 本研究共发现 3 例样本存在 Y-STR 基因座分型缺失现象，其中 1 例样本（编号 1）采用 GFS 24Y 检测系统发现 DYS459 和 DYS527ab 基因座分型缺失，用 AGCU Y24 检测系统发现 DYS527ab 基因座同样存在分型缺失（见图 1）。进行 Y 染色体微缺失 STS 位点检测，结果显示该样本丢失 sY255/sY1191/CDY1/sY254/DAZ 等位点，经过分析该样本为 AZFc 区缺失（b2/b4）（见图 2）。本研究还发现 2 例存在父子亲缘关系的样本（编号 2,3）的 Y-STR 基因座分型结果一致，均存在 DYS522、DYS570 和 DYS576 等三个基因座分型缺失，其余基因座分型为单倍型（见图 3）。对两份样本进行 Y 染色体微缺失分析，结果提示两份样本检测结果一致，AZF 区均未发现缺失以及 SRY 基因均正常（见图 4）。
结论 在个体识别和父源关系鉴定中发现 Y-STR 基因座缺失的个体有可能存在 Y 染色体 AZF 区基因微缺失，部分 Y-STR 基因座如 DYS459、DYS527ab 等与 Y 染色体 AZF 区 STS 位点存在对应关系,在对男性不育症基因检测方面具有一定应用价值，而在遗传关系鉴定方面应避免使用。

PU-0773

Understanding the functional effects of ZEB2 and RBM38 in determining the liver cancer stem cell proliferation

Xiaowan Yu、Wei Wang
Department of Laboratory Medicine, Second Affiliated Hospital of Fujian Medical University

Purpose Liver cancer stem cells are associated with tumor progression, metastasis and resistance development and therefore it is important to understand the key proteins that supports the tumor microenvironment. There are reports available that suppression of ZEB2 results with inactivation of Wnt/βcatenin pathway. As in case of RBM38, it suppresses tumor outgrowth and helps to improve the longevity of tumor patients. But still the direct role of ZEB2 and RBM38 in favoring tumor microenvironment is not studied.
Methods Initially, we develop an initial and advanced stage of liver cancer mice model using CD133+ cells injection, which mimics the natural form of liver cancer in all aspects. Histology, Immunohistochemistry and Western blotting analysis are carried out to understand the cancer progression.
Results Histologically, the developed initial liver cancer is observed with the microfoci structure formation; in an aggressive stage of liver cancer, it is observed with distinct morphological changes with enlarged nucleolus and clumping nature. Immunohistochemical and Western blotting analysis of CD133 and ZEB2 proteins shows the similar upregulated expression pattern as the tumor progress with initial and advanced stage of liver cancer. But the expression of RBM38 is enormously increased in initial liver cancer stage, but noted with a remarkably downregulated expression in advanced stage of liver cancer.
Conclusions In overall, from our result, we conclude that ZEB2 favors the tumor microenvironment which supports liver cancer stem cells proliferation. But RBM38 expression negatively regulates the tumor microenvironment that restrict the proliferation of liver cancer stem cell.

PU-0774

GPR183 在 T-ALL 中的表达及对 T-ALL 细胞系作用

张航
成都市第三人民医院

目的 研究 GPR183 在 T-ALL 患者细胞及细胞系中的表达，并探索过表达 GPR183 及应用其激动剂后对 T-ALL 细胞的影响。
方法 收集 T-ALL 患者骨髓分离肿瘤细胞，提取 mRNA 及蛋白质，qPCR 及 Wsetern blot 检测 GPR183 表达；GEO 数据库查询 T-ALL 患者全基因组测序结果，分析 GPR183 表达水平；过表达 GPR183 及使用激动剂后检测对 T-ALL 细胞增殖及凋亡的影响。
结果 GPR183 在 T-ALL 患者细胞中 mRNA 及蛋白质表达明显降低，GEO 数据库中亦证明 GPR183 在 T-ALL 中表达下降；使用 GPR183 激动剂 7α,25-OH 胆固醇及过表达 GPR183 后 T-ALL 细胞系增殖明显被抑制且凋亡明显增加。
结论 GPR183 在 T-ALL 中表达下降，过表达和激动 GPR183 后 T-ALL 细胞增殖被抑制凋亡增加，说明 GPR183 在 T-ALL 发生发展中可能起重要作用，并可能成为其治疗靶点。

PU-0775

lncRNA RMST Suppressed GBM Cell Mitophagy through Enhancing FUS

Changhong Liu
Central South University

Long non-coding RNAs (lncRNAs) play a significant role in post-translational modifications of proteins, yet the importance of lncRNAs for SUMOylation is unknown. rhabdomyosarcoma 2 associated transcript (RMST) expression in glioma tissues and normal brain tissues was measured by quantitative real-time PCR and in situ hybridization. The functional roles of RMST in astrocytomas were demonstrated by a series of in vitro experiments. The potential mechanisms of RMST for SUMOylation were investigated by RNA immunoprecipitation, RNA pull-down, western blotting, and coimmunoprecipitation assays. We first demonstrated the oncogenic activity of lncRNA RMST by inhibiting glioma cells mitophagy. We also first determined that RMST is an enhancer of FUS SUMOylation, especially boosting SUMO1 modification at K333. SUMOylation induced by RMST contributes to the interaction between FUS and heterogeneous nuclear ribonucleoprotein D (hnRNPD) and stabilized their expression and cells mitophagy. Importantly, lncRNA RMST could serve as a promising prognostic factor for glioma patients. Our results demonstrated a previously unknown function of lncRNAs worked as an enhancer in FUS SUMOylation, and RMST will be a significant guide for the development of medications targeting gliomas.

PU-0776

外泌体 miRNAs 作为代谢相关脂肪性肝病诊断标志物

陈豪、曾玉萍、何訸
四川大学华西医院

目的 代谢相关脂肪性肝病（metabolic associated fatty liver disease, MAFLD），全球患病率高达 25%，未来十年可能超过乙型肝炎成为终末期肝病和肝移植的主要原因，而早期诊断是控制 MAFLD 疾病进展的关键。肝活检、影像学和生物标志物评分在中国人群中存在较强异质性。大量证据显示血浆外泌体中的 miRNA 更能准确反映肝脏病变情况，因此，它有潜力成为 MAFLD 的新型无创性诊断分子标志物。
方法 收集 MAFLD 患者、疾病对照（非代谢相关肝纤维化，酒精性脂肪肝，病毒性肝炎）以及健康对照血浆，差速离心法提取血浆外泌体，采用高通量测序技术检测筛选队列中外泌体 miRNA 的差异表达谱，通过生物功能学分析筛选目标 miRNA，利用 qRT-PCR 方法在验证队列中进行验证。
结果 共纳入 143 例受试者，其中 MAFLD 患者 81 例，健康对照 51 例，疾病对照组 11 例。实验室指标提示 MAFLD 组出现不同程度的肝损伤以及脂糖代谢紊乱。测序检测在 MAFLD 患者和健康对照间共发现了 1125 个差异表达的 miRNAs，其中，697 个 miRNAs 的表达水平上调，428 个下调；最终选择 miR-122-5p、miR-148a-3p 和 miR-192-5p 进行下一步验证； qRT-PCR 方法在验证队列中检测 3 种候选 miRNAs 发现：与健康对照组相比，miR-148a-3p 仅在 MAFLD 组中高表达；miR-192-5p 在 MAFLD 组和疾病对照组中均上调；miR-122-5p 在 MAFLD 组和疾病对照组中都出现上调。
结论 本研究在中国汉族人群中发现 3 种血浆外泌体 miRNAs（miR-148a-3p、miR-192-5p 和 miR-122-5p）在 MAFLD 患者中较健康对照组明显上调，可能是 MAFLD 潜在的新型诊断标志物。

PU-0777

基于 MALDI-TOF MS 技术的乳腺癌蛋白质组学研究

许小雨
中国人民解放军联勤保障部队第九六〇医院

目的 应用基质辅助激光解吸电离飞行时间质谱（MALDI-TOF MS）发现乳腺癌血清中潜在的肿瘤标志物，为乳腺癌类型的筛查以及术后疗效的评估提供新的策略和方法。
方法（1）收集 2020 年 8 月至 2021 年 3 月中国人民解放军第九六〇医院经组织病理学活检确诊的 61 例乳腺癌女性患者及 44 例健康女性体检者血清。使用弱阳离子交换磁珠（WCX-MB）富集蛋白质/多肽，MALDI-TOF MS 上机检测，筛选出乳腺癌组与健康体检对照组之间的差异蛋白/多肽峰，使用 GA、SNN、QC 三种算法建立乳腺癌诊断预测模型并选择最佳效能模型。（2）收集接受了手术治疗的乳腺癌患者 12 例，并保存其术前血作为对照数据。使用统计学方法筛选术前术后蛋白质/多肽差异峰，分析乳腺癌患者与健康对照者之间存在的差异峰，寻找与乳腺癌相关的潜在血清生物标志物。（3）将乳腺癌组分为三阴性乳腺癌组（8 例）和非三阴性乳腺癌组（53 例），筛选两种不同类型乳腺癌之间的差异峰。
结果（1）将乳腺癌组与健康体检对照组的血清蛋白质谱进行对比，成功筛选出 26 个差异显著的蛋白/多肽峰（P<0.000001），三种算法中，GA 模型具有最优的诊断性能，其敏感性为 93.8%，特异性为 90.9%，准确性为 92.6%。（2）与健康组对照组相比，差异峰 m/z 4220.9、5920.36 在乳腺癌组中低表达，此外，术后组这两个峰的表达水平明显高于术前组；与非三阴性乳腺癌患者组相比，三阴性乳腺癌组峰 m/z 4220.9、5920.36 的表达水平升高。
结论 MALDI-TOF MS 联合 ClinProTools 能为区分乳腺癌患者和健康人、乳腺癌患者术前术后以及三阴性乳腺癌患者与非三阴性乳腺癌患者提供新的发展方向。

PU-0778

分子诊断在肝癌诊疗中的探究

王宏
烟台市烟台山医院

分子诊断是指利用 DNA 或 RNA 作为生物标记进行临床检测的诊断技术，包括多种扩增技术的精细探测方法。分子诊断依托其准确、便捷、灵敏、无创和自动化的优势，在疾病的诊断、预后评估及疗效监测中也发挥着极为重要的作用。临床上，分子诊断广泛应用于感染性疾病,肿瘤以及遗传性疾病的检测。

1. MK 与肝癌

肝癌标志物的研究中出现了一种中间因子(Midkine，MK)。MK 是一个肝素结合性生长因子, 其基因最初鉴定是在视黄酸诱导分化早期的胚胎瘤细胞中获得。成年后除肾脏外,其它正常组织几乎测不出 MK mRNA 表达[1,2] 。RT-PCR 研究表明，MK mRNA 在肝癌患者中成高表达，而在肝良性病变组织均未见其表达[3]。MK 的高表达可能可以作为肝癌诊断过程中的一个早期指标，并可能参与肝癌细胞局部浸润、转移，对术后制定进一步治疗方案有参考价值。

2. miRNA 与肝癌

微小 RNA（microRNA，miRNA） 是一类短的单链内源性非编码 RNA，可与靶 mRNA 的 3’非编码区部分序列不完全或完全互补配对， 引起靶向 mRNA 的翻译抑制或特异性降解， 调控基因表达，从而调节细胞增殖、分化、凋亡等生命过程。YANG 等人[4] 利用 miRNA 芯片以及 qRT-PCR 技术，对肝癌标本以及各细胞株 HepG2、Hep3B、 Huh7、 L-O2（正常肝细胞株）进行分析研究，并通过双荧光素酶和 Western-Blot 验证。得出结论， miRNA-590 的 2 个臂的 miRNA 在 HCC 恶变中发挥着至关重要的作用。在不久之后，Zhang 等人[5]对肝硬化发育不良结节、分化良好的肝细胞

癌组织、晚期肝癌以及对应的肝硬化组织进行实时荧光定量发现，miRNA-96-3p 表达水平是 HGDN 和 HCC 鉴别诊断的良好标志物。

PU-0779

XpertMTB/RIF 和 T-SPOT.TB 在诊断艾滋病合并肺结核中的临床应用分析

王晓敏
长春市传染病医院

目的 对 XpertMTB/RIF 和 T-SPOT.TB 在诊断艾滋病合并肺结核中的临床应用分析，以期两种方法能联合应用及时准确诊断出艾滋病患者患有潜伏结核分枝杆菌感染及利福平耐药情况。
方法 对 2017 年 12 月—2020 年 7 月期间内收治的，获得明确诊断的艾滋病患者，并疑似肺结核感染，共计 108 例研究对象进行回顾性分析。108 例均做 XpertMTB/RIF 诊断性试验（HIV 合并肺部感染组 44 例， HIV 合并肺结核感染组 64 例），其中有 91 例做 XpertMTB/RIF 和 T-SPOT.TB 两种方法的诊断性试验，有 17 例单独做 XpertMTB/RIF 诊断性试验。
结果 认为在艾滋病合并肺结核患者中女性平均年龄要比男性平均年龄高，本组年龄和性别间差异有统计学意义($p<0.05$，$p=0.013$)。91 例患者同时做 XpertMTB/RIF 和 T-SPOT.TB 两种方法的诊断性试验，T-SPOT.TB 检测方法敏感度 76.60%（36/47）优于 XpertMTB/RIF 检测方法敏感度 53.19%（25/47），差异有统计学意义（$p<0.05$,$p=0.017$）。XpertMTB/RIF 检测方法特异度 100%（44/44）优于 T-SPOT.TB 特异度 84.09%（37/44），差异有统计学意义（$p<0.05$,$p=0.012$）。64 例 HIV 合并肺结核组 XpertMTB/RIF 检测到 22 例阴性、22 例利福平耐药、20 例利福平敏感。

PU-0780

不良孕产患者宫颈分泌物解脲脲原体、沙眼衣原体和生殖道支原体核酸的检测及临床意义

杨佳佳、张彦懿、黄江渝
成都市第三人民医院

目的 分析不良孕产患者宫颈分泌物中解脲脲原体（UU）、沙眼衣原体（CT）和生殖道支原体感染情况及临床意义，比较实时荧光聚合酶链反应（FQ-PCR）和实时荧光核酸恒温扩增检测(SAT)技术检测 UU、CT 核酸的性能差异。
方法 应用 FQ-PCR 检测 98 例不良孕产患者（观察组）和 38 例健康妇女（对照组）宫颈分泌物中的 UU-DNA 和 CT-DNA，应用 SAT 检测观察组和对照组 UU-RNA、 CT-RNA 和 MG-RNA，并进行统计学分析处理。
结果 1：观察组 UU-DNA、CT-DNA 阳性检出率和总检出率均高于对照组（$P<0.05$）。2：在<35 岁年龄段，观察组 UU-DNA、CT-DNA 阳性检出率和总检出率均高于对照组（$P<0.05$）；在≥35 岁年龄段，观察组 UU-DNA 阳性检出率和 UU-DNA 及 CT-DNA 总检出率均高于对照组（$P<0.05$）。3：观察组 MG-RNA 阳性检出率高于对照组（$P<0.05$）。在<35 岁年龄段，观察组 MG-RNA 阳性检出率高于对照组（$P<0.05$）。4：在自发性流产、异位妊娠和不孕症患者中，UU-RNA、CT-RNA 和 MG-RNA 阳性检出率较一致，差异无统计学意义（$P>0.05$）。5：观察组中 UU-RNA 与 UU-DNA 检出率相当、CT-RNA 与 CT-DNA 检出率相当（$P>0.05$）；但在对照组中，UU-RNA 检出率明显高于 UU-DNA（$P<0.05$），CT-DNA 与 CT-RNA 检出率无明显差异（$P>0.05$）。

结论 不良孕产患者宫颈分泌物中 UU 检出率较高，并随年龄增加有增高趋势。FQ-PCR 和 SAT 检测均能为临床诊断 UU、CT 或 MG 感染提供依据。SAT 检测无症状感染人群中的病原微生物更具优势。

PU-0781

血浆 hsa_circ_0005397 检测作为肝癌潜在生物标志物的研究

王峰
南通大学附属医院

目的 环状 RNA（circRNA）在肝细胞癌（HCC）的发生发展中起着重要作用。然而，有关血浆 circRNA 在 HCC 中的表达模式及临床应用价值的报道较少。我们探讨了血浆 hsa_circ_0005397 在 HCC 诊断和预后中的作用。
方法 采用实时定量聚合酶链反应（qRT-PCR）检测血浆 hsa_circ_0005397 表达水平。通过受试者操作特征（ROC）曲线评价血浆 hsa_circ_0005397 以及联合血清 AFP、AFP-L3 对 HCC 的诊断价值，并通过动态监测和 Kaplan-Meier 曲线分析评价血浆 hsa_circ_0005397 对 HCC 的预后价值。
结果 HCC 患者血浆 hsa_circ_0005397 的表达高于良性肝病患者和健康对照组（均 P<0.05）。与 HCC 患者肿瘤大小（P=0.020）和 TNM 分期（P=0.006）密切相关。血浆 hsa_circ_0005397 诊断 HCC 的 ROC 曲线下面积为 0.737，95%可信区间为 0.671-0.795。血浆 hsa_circ_0005397、血清 AFP 和 AFP-L3 联合检测可提高 HCC 的诊断灵敏度。此外，动态监测血浆 hsa_circ_0005397 可能有助于预测 HCC 患者手术切除后的复发或转移；且血浆 hsa_circ_0005397 升高与 HCC 患者总生存期缩短密切相关（P=0.007）。
结论 血浆 has_circ_0005397 有望成为一个新的 HCC 生物标志物；其与血清 AFP、AFP-L3 联合检测可提高对 HCC 的诊断价值。

PU-0782

S100A6 和相关 lncRNAs 作为原发性胆汁性胆管炎诊断和分期生物标志物的分析

董西华
中国医科大学附属第一医院

目的 探讨血浆 S100A6 mRNA、LINC00312、LINC00472 和 LINC01257 对原发性胆汁性胆管炎（PBC）的诊断及分期价值。
方法 采用胆管结扎（BDL）小鼠模型模拟 PBC；免疫荧光双标记法验证 BDL 小鼠肝内胆管细胞中 S100A6 蛋白表达是否上调；纳入 145 例 PBC 患者和 110 例健康对照者(HCs)，其中 80 例 PBC 患者和 60 例 HCs 作为训练集，65 例 PBC 患者和 50 例 HCs 作为验证集；采用 qRT-PCR 方法分析血浆 S100A6 mRNA、LINC00312、LINC00472 和 LINC01257 的相对表达量；用甘氨酸鹅脱氧胆酸（GCDC）处理人肝内胆管上皮细胞（HiBECs）模拟 PBC 肝内胆管上皮细胞胆汁淤积环境。
结果 S100a6 蛋白在 BDL 小鼠肝内胆管上皮细胞中表达上调；PBC 患者血浆和 GCDC 处理的 HiBECs 中 S100A6 mRNA、LINC00472 和 LINC01257 的相对表达量均上调，LINC00312 的相对表达量下调；S100A6 mRNA 在 PBC 晚期（III 期和 IV 期）的相对表达高于 HCs 和早期；晚期 LINC00312 表达水平低于早期和 HCs，早期 LINC00312 相对表达低于 HCs；LINC00472 在晚期的相对表达高于早期和 HCs；与 HCs 相比，LINC01257 在早期和晚期相对表达均上调；S100A6、LINC00312、LINC00472 和 LINC01257 对 PBC 诊断的曲线下面积(AUC)分别为 0.759、0.7292、

0.6942、0.7158；对 PBC 分期的 AUC 分别为 0.666、0.661、0.839 和 0.5549；验证集数据的 AUC 与训练集接近。
结论 S100A6、LINC00312、LINC00472 和 LINC01257 可作为 PBC 诊断的潜在生物标记物；LINC00472 可作为 PBC 分期的潜在生物标志物。

PU-0783

血清外泌体 MT1-MMP 对胃癌的早期诊断价值研究

董召刚、张义
山东大学齐鲁医院

目的 检测血清外泌体 MT1-MMP 在胃癌、不典型增生、慢性萎缩性胃炎、健康对照中的表达。
方法 收集山东大学齐鲁医院胃癌（119 例）、不典型增生（33 例）、慢性萎缩性胃炎（31 例）患者及 31 例健康对照血清。试剂盒提取血清外泌体 RNA，RT-PCR 检测 MT1-MMP 表达。电化学发光法检测 CEA、CA19-9、CA72-4。
结果 成功分离并鉴定了血清外泌体，MT1-MMP 在胃癌中表达(4.819 (1.748–8.023))高于不典型增生(2.725 (1.566-4.878))、慢性萎缩性胃炎(1.886 (0.779–3.631))及健康对照(0.694 (0.066–2.464))（P 均<0.05），而不典型增生高于慢性萎缩性胃炎（P=0.022）及健康对照（P=0.001），慢性萎缩性胃炎高于健康对照（P=0.019）。胃癌 CEA (2.31ng/ml)高于不典型增生(1.77ng/ml)、慢性萎缩性胃炎健康对照(1.65ng/ml)，P<0.05），而健康对照、胃炎及不典型增生表达无差异（P 均>0.05）。CA19-9 和 CA72-4 在三组表达无显著差异（P >0.05）。胃癌患者血清外泌体 MT1-MMP 表达与肿瘤大小(P=0.002)、分化(P=0.013)、分型(P=0.012)、浸润深度(P<0.001)、转移(P<0.001)、TNM 分期(P<0.001)密切相关。ROC 曲线显示 MT1-MMP 与 CEA 诊断胃癌的 cut-off 值为 2.89 和 2.10 ng/ml，其曲线下面积、灵敏度、特异度、分别为 0.788 和 0.655、63.9%和 63.0%、87.1%和 87.1%。二者联合灵敏度、特异度、曲线下面积为 75.6%、83.9%、0.821。
结论 血清外泌体 MT1-MMP 在胃癌时表达升高，与分期转移密切相关，对胃癌早期诊断价值较高。

PU-0784

TNIP1 gene polymorphisms associated with susceptibility to rheumatoid arthritis in the Chinese population

Qian Xi
Department of Laboratory, Medicine, Sichuan Provincial People's Hospital

BACKGROUND The tumor necrosis factor alpha inducible protein 3 interacting protein 1 (TNIP1) is involved in inhibition of nuclear factor-κB (NF-κB) activation. Recently, TNIP1 is regarded to associate with systemic lupus erythematosus (SLE) susceptibility, while the role of TNIP1 in RA is obscure. Thus, we conducted this study, aiming to precisely estimate the correlation.
METHODS A case-control study was conducted on TNIP1 single nucleotide polymorphisms (SNP) rs3792783 in Chinese population including 151 RA patients and 209 healthy controls. The presence of disease-related autoantibodies in RA were assessed.
RESULTS TNIP1 rs3792783 was found to be associated with RA susceptibility (recessive model, OR=0.55, 95%CI: 0.32-0.93) and anti-CCP antibody positive RA (recessive model, OR=0.53, 95%CI: 0.30-0.94). In accordance, TNIP1 haplotype CTC* favored the risk of RA development (P=0.011).
CONCLUSION TNIP1 rs3792783 was strongly correlated with RA inChinese population.

PU-0785

在中国人群中 C 反应蛋白启动子（rs3091244）的功能性基因变异与癌症风险无关

苏海翔[1]、王铭宇[2]、周海红[1]、武一[2]
1. 甘肃省医学科学研究院，甘肃省肿瘤医院
2. 兰州大学生命科学院

目的 在欧洲人群中，循环 C 反应蛋白（CRP）基因水平升高与癌症风险的关系已被广泛研究，但结论有很多矛盾。三等位基因 rs3091244 是一种功能验证的基因变体，其等位基因频率在欧洲和亚洲人群中存在显著差异。本项目研究中国人群中 rs3091244 与癌症风险的关系。
方法 采用 Sanger 测序法对 4971 例癌症患者和 2485 例正常人进行 rs3091244 基因分型，同时，在亚组中使用 TaqMan 分析对 rs1205 和 rs2794521 基因变异进行分型。
结果 无论是否区分癌症类型，在中国人群中 CRP 基因型变异都与癌症风险之间没有相关性。
结论 在中国人群中，循环 CRP 与肿瘤发生没有因果关系。

PU-0786

RASSF1A 及 SHOX2 基因甲基化水平对肺癌和良性肺部疾病的鉴别诊断研究

任静
广元市中心医院

目的 评价肺泡灌洗液（BLAF）中 SHOX2、RASSF1A 甲基化水平对肺癌和良性肺部疾病的鉴别诊断的临床价值。
方法 选取广元市中心医院 2018 年 10 月—2020 年 2 月经病理初次确诊的 162 患者，其中肺癌 65 例，良性肺部疾病 76 例，非肺部的恶性肿瘤 21 例。将良性肺部疾病和非肺部的恶性肿瘤患者共 97 例，分别作为对照组。对全部 162 例患者的 BLAF 样本，进行修饰纯化脱氧核糖核酸 (DNA)后采用实时荧光 PCR（RT－PCR）检测 BALF 中 SHOX2 和 RASSF1A 两种基因甲基化情况，比较二者在肺癌和良性肺部疾病的鉴别诊断的临床价值。
结果 1）肺泡灌洗液中 SHOX2 和ＲASSF1A 基因甲基化联合检测在肺癌组的诊断灵敏度为 0.836，高于良性疾病组(0.189) (P＜0.05)；高于非肺部的恶性肿瘤（0.210）(P＜0.05)。2）肺癌组 BALF 中 SHOX2、RASSF1A 基因甲基化联合检测阳性率在小细胞肺癌和肺鳞癌中分别是 100%和 91.4%，高于肺腺癌(75.0%)。
结论 对肺泡灌洗液中 SHOX2、ＲASSF1A 基因甲基化的 PCR 检测在肺癌诊断中有良好的灵敏度及特异性，是肺癌病理学诊断的有效补充工具。

PU-0787

高危型 HPV 感染与阴道微生态及性病感染情况的相关性研究

任静
广元市中心医院

目的 探讨阴道微生态与高危型人乳头瘤病毒（HR-HPV）感染及性病感染情况的关系。
方法 选择 HR-HPV 阳性受试者 296 例、HR-HPV 阴性受试者 306 例作为研究对象，进行阴道微生态、性病三项核酸（CT、UU、NG）及 HPV 分型检测，分析这三者之间的关系。

结果 HR-HPV 阳性与 HR-HPV 阴性比较，HR-HPV 阳性菌群多样性明显高于 HR-HPV 阴性($\chi2=7.602$，$P<0.05$)，HR-HPV 阳性组较 HR-HPV 阴性组的过氧化氢、白细胞酯酶和唾液酸苷酶的阳性率均明显升高($\chi2$ 分别为 8.560，8.431，10.907，$P<0.05$)；两组 pH 值无明显统计学意义($\chi2=0.079$，$P>0.05$)。与 HR-HPV 阴性组相比，HR-HPV 阳性组沙眼衣原体检测，解脲支原体，淋球菌检出率均高于对照组，差异均有统计学差异($\chi2=6.357$，$P<0.05$)；

结论 阴道微生态失调与 HR-HPV 感染及宫颈病变密切相关，阴道微生态平衡被打破，可增加 HR-HPV 感染及宫颈病变风险。此外，部分病原体诸如沙眼衣原体检测，解脲支原体，淋球菌对于 HR-HPV 的感染具有协同作用。

PU-0788

Further delineation of bone marrow failure syndrome caused by novel compound heterozygous variants of MYSM1

Niu Li[1]、Yufei Xu[1]、Tingting Yu[1]、Ru-en Yao[1]、Jing Chen[1]、Chengjuan Luo[2]、Jian Wang[1]
1. Shanghai Children's Medical Center, Shanghai Jiaotong University School of Medicine
2. Shanghai Children's Medical Center

Myb-like SWIRM and MPN domains (MYSM1) is a chromatin-binding transcriptional regulator that mediates histone 2A deubiquitination, which plays a vital role in hematopoiesis and lymphocyte differentiation. Biallelic variants in MYSM1 cause a rare bone marrow failure syndrome (OMIM #618116). To date, only three pathogenic variants (E390*, R478*, and H656R) of MYSM1 have been reported in nine patients, and all variants are homozygous. Here, we describe a Chinese female patient who mainly presented with leukopenia, granulocytopenia, thrombocytopenia, severe anemia, and B-cell and natural killer cell deficiency in the peripheral blood, and was diagnosed with bone marrow failure. Trio whole-exome sequencing revealed a novel compound heterozygous variant in MYSM1 (c.399G>A, p.L133L, and c.1467C>G, p.Y489*). The c.399G>A synonymous variant is located at the 3′-end of exon 6, which is predicted to affect MYSM1 mRNA splicing. Analysis of the products obtained from the reverse transcription-polymerase chain reaction revealed that the c.399G>A variant leads to exon 6 skipping, resulting in a premature termination codon (c.321_399 del, p.V108Lfs*13). cDNA sequencing suggested that the c.1467C>G variant triggered nonsense-mediated mRNA degradation. Moreover, we identified a novel transcript of MYSM1 mRNA (missing exons 5 and 6) in human blood cells. Our results expand the mutation spectrum of MYSM1; additionally, this is the first report of a synonymous splicing variant that induces post-transcriptional skipping of exon 6 leading to a bone marrow failure syndrome phenotype.

PU-0789

Exosomal miR-222-3p contributes to AIPC transformation and confers resistance to AR inhibition via activating mTOR signaling

Weiwei Liu、Piaoping Kong、Zhihua Tao
The Second Affiliated Hospital of Zhejiang University School of Medicine

Background/Aims Prostate cancer (PCa) remains the most common urologic malignancy and the second leading cause of male cancer-related deaths in developed countries. As PCa growth is initially dependent on androgens for survival, androgen deprivation therapy (ADT) has been the mainstay of treatment for PCa. However, these tumors will eventually progress to an androgen-

independent phenotype and fail to respond to ADT treatment, becoming the major obstacle of clinical therapy. Understanding the molecular mechanisms that underlie the progression of androgen-independent PCa will shed considerable lights on possible treatment strategies for PCa. MicroRNAs (miRNAs) or exosomes have recently been shown to play vital regulatory or communication roles in cancer biology. However, the roles and mechanisms of exosomal (Exos) miRNAs in AIPC remain unclear. In the present study, we aimed to investigate the detailed roles and mechanisms of tumor-generated exosomal miRNAs in the progression of AIPC.

Methods High-throughput sequencing was used to characterize the whole transcriptome profiles in both the androgen dependent and independent PCa cell line. Exosomes were isolated using ultracentrifugation and characterized using transmission electron microscope (TEM). The effects of Exos-miR-222-3p on PCa cell viability, apoptosis, EMT, motility were evaluated by CCK8, flow cytometry, transwell and wound healing assays, immunofluorescence. The regulatory mechanisms of miR-222-3p were investigated by qRT-PCR, WB, dual-luciferase assays and immunofluorescence.

Results 1. In our previously established stable ADT treatment-resistant LNCaP cell lines, cell growth was stabilized and can grow well in androgen-depleted environment. Our CCK-8 and transwell migration/invasion results showed that LNCaP-AI cells exhibit stronger proliferation, metastasis and invasiveness activity than LNCaP cells.

2. High-throughput RNA sequencing results found that miRNA-222-3p was mostly elevated in LNCaP-AI compared to LNCaP. In addition, exosomes secreted by AIPC cell line LNCaP-AI were successfully ingested by LNCaP, which dramatically promoted the growth activity and enhanced the migration and invasion ability of LNCaP cells in androgen-free complete medium. Interestingly, we further found that miRNA-222-3p expression was significantly enhanced in LNCaP-AI exosomes than that of LNCaP exosomes. Moreover, overexpression of miRNA-222-3p can significantly promote the proliferation ability of LNCaP. These results strongly suggested that Exos-miR-222-3p plays a paramount role in facilitating AIPC transformation.

3. What's more, the underlying mechanisms by which Exos-miR-222-3p contributes to AIPC transformation were investigated. Firstly, based on the results of full transcriptome sequencing, GO pathway and KEGG analysis showed that mTOR signalling pathway was markedly activated in LNCaP-AI cells compared to LNCaP-AI. In line with the predictive results, p-mTOR was obviously increased after miR-222-3p overexpression both in LNCaP and LNCaP-AI cells. Secondly, the target mRNAs of miR-222-3p were investigated. miRWalk 3.0 online predictive results showed that MIDN, BMF, BCL2L11, TP53BP2, ZFYVE16, PHACTR4, TMCC1 are potential target mRNAs of miR-222-3p. Considering the fuctions (oncogenes or tumor supressors) of these 7 potential targets, MIDN, a tumor supressor, was highly suspected to be a novel target of miR-222-3p. Dual-luciferase assays further demonstrated that miR-222-3p significantly supressed MIDN expression by combining with the 3' untranslated region (3'UTR) of the target gene mRNA, in addition, this result was also verified by RT-qPCR. Taken together, our results suggested that Exos-miR-222-3p mediated AIPC transformation was, at least in part, by activating mTOR signalling pathway via targeting MIDN.

4. Exos-miR-222-3p confers resistance to androgen receptor (AR) inhibition. In addition to androgen deprivation therapy, AR blocking is also an effective therapeutic strategy for prostate cancer. We found that either MDV3100 or AR shRNA mediated AR inhibition significantly decreased the proliferation activity of LNCaP, however, this anti-tumor effect was dramaticlly impaired after treatment of LNCaP-AI exosomes. Moreover, dual inhibition of miR-222-3p and AR led to synergistic cytocidal effects both in LNCaP and LNCaP-AI.

5. Exos-miR-222-3p may be a potential biomarker for castration-resistant prostate cancer (CRPC) diagnosis. Circulating exosomes from androgen dependent PCa (ADPC) and CRPC patients were isolated using ultracentrifugation, qPCR results indicated that miR-222-3p was more abundant in ADPC-exosomes compared to CRPC-exosomes, suggesting it could be a promising non-invasive biomarker for identifying ADPC and CRPC.

Conclusion In summary, our findings show that Exos-miR-222-3p plays a paramount role in promoting AIPC transformation and confers resistance to AR inhibition, which is mediated, at least in part, by activating mTOR signalling pathway via targeting MIDN, suggesting it could be a promising non-invasive biomarker for facilitating CRPC treatments.

PU-0790

人类白细胞抗原基因分型方法研究进展

蒲丹
昆明市第一人民医院

人类白细胞抗原（HLA），又称人类主要组织相容性复合物。HLA 分型过去主要采用分辨率及准确性较低的血清学和细胞学方法。随着 PCR 技术，基因芯片技术和基因测序技术等分子生物学技术的发展，HLA 分型技术也得到了很大的提高与完善。本文对 HLA 基因分型方法的进展进行综述。

PU-0791

Malignant Assesment of Mutant KRAS Circulating Cell-Free DNA in Pancreatic Cancer

Zheying Wang[1]、Xiaorong Pan[2]、Jianhua Tong[2]
1. Qilu Hospital of Shandong University
2. 上海交通大学医学院附属瑞金医院

Objective The research on circulating tumor DNA (ctDNA) in pancreatic cancer (PC) has emerged recently. Although the detection rate of the c in ctDNA was relatively consistent with that in tumor tissue, whether the KRAS mutant allele fraction (MAF) differed was still not reported. In this study, we aim to explore the clinical application of mutant KRAS ctDNA detection in clinical staging and differential diagnosis of PC.
Methods Plasma samples were collected from 110 PC and 52 pancreatic benign (PB) disease patients. The detection of KRAS mutation in ctDNA was performed using droplet digital PCR and compared with that in matched tumor tissue. We assessed the utility of KRAS MAFs in ctDNA and tissue for pancreatic malignancy assessment.
Results We found that KRAS MAF in ctDNA of PC patients was higher than that of PB patients, and was obviously associated with tumor staging and distant metastasis. However, KRAS MAF in ctDNA was significantly different from that in matched tissue. KRAS MAF in tumor tissue had no significant correlation with the clinical status. In addition, a ROC curve analysis revealed that mutant KRAS ctDNA combined with CA19-9 could increase the sensitivity rate of early-stage PC prediction, compared with CA19-9 test alone.
Conclusion The MAF of KRAS in ctDNA was related to the clinical stage of PC. Mutant KRAS ctDNA could improve the sensitivity in early diagnosis of PC as a complement to CA19-9. Our study suggested that KRAS mutation in ctDNA could be a valuable circulating biomarker for the malignancy assessment in PC.

PU-0792

Performance comparison of commercial kits for isolating and detecting of circulating tumor DNA

MENGYAN WANG、XIA HUANG、XIN LI、QIAOMEI GUO、WANXING XU、MINGNA ZHAO、XUEQING WANG、LIN WANG、JIATAO LOU
SHANGHAI CHEST HOSPITAL

Circulating tumor DNA (ctDNA), a fraction of cell-free DNA (cfDNA) in the circulatory system, is released from tumor cells and thus carries tumor-specific genetic signatures. Using blood-derived ctDNA to detect somatic mutations has shown great value in guiding cancer targeted

therapy. Isolation and detection efficiencies are the key factors affecting the performance of ctDNA detection.

To optimize and standardize our clinical practice, in this study, we analyzed the isolation efficiency of four commercial cfDNA purification kits: QIAamp circulating nucleic acid kit, AmoyDxVR Circulating DNA kits, MicrodiagVR circulating DNA isolation kit, and MagMAX cell-free DNA isolation kit; and the detection efficiency of two mainstream domestic EGFR gene mutation detection kits: MicroDiag EGFR gene mutation detection kit and Fluorometric real-time PCR Detection Kit for the analysis of EGFR gene mutations. Reference materials and plasma samples collected from lung cancer patients and healthy volunteers were used for the analysis. Our results showed that QIAamp circulating nucleic acid kit and MicrodiagVR circulating DNA kit had the highest recovery rate (up to 21.25 ng/mL) for short DNA fragments of about 173 bp which is the peak length of ctDNA. For ctDNA detection, the MicroDiagVR EGFR gene mutation detection kit showed the highest detection rate and sensitivity for detecting EGFR mutations at a mutant frequency of 0.5%. This work provides a reliable choice of commercial kits for the clinical application of ctDNA.

PU-0793

Non-small cell lung cancer cell–derived exosomal miR-17-5p promotes osteoclast differentiation by targeting PTEN

MENGYAN WANG[2]、MINGNA ZHAO[1]、QIAOMEI GUO[1]、JIATAO LOU[1]、LIN WANG[1]
1. SHANGHAI CHEST HOSPITAL
2. 上海市胸科医院

Aberrant activity of bone resorbing osteoclasts plays a key role in the development of osteoporosis and cancer bone metastasis. The identification of novel and specific targets will be helpful for the development of new therapeutic strategies for bone metastasis in lung cancer. Herein, we examined microRNAs in tumor cell-derived exosomes to investigate the communication between the bone environment and tumor cells. TCGA database analysis showed that the level of miR-17-5p increased in non-small cell lung cancer tissues compared with non-tumor tissues. To investigate the function of exosomes in inducing osteoclastogenesis, osteoclast precursors were incubated with exosomes isolated from non-small cell lung cancer cell line, as well as receptor activator of NF-KB ligand and M-CSF to induce osteoclastogenesis. We found that exosomal miR-17-5p is upregulated in a non-small cell lung cancer cell line with bone metastasis compared with the original cell line. Overexpression of miR-17-5p enhanced the osteoclastogenesis of RAW264.7 cells. PTEN was identified as a direct target of miR-17-5p and showed negative effects on osteoclastogenesis. Importantly, treatment of LY294002 (an inhibitor of the PI3K/Akt pathway) attenuated miR-17-5p-mediated osteoclastogenesis effects. Taken together, our findings demonstrated that miR-17-5p promotes osteoclastogenesis through the PI3K/Akt pathway via targeting PTEN in lung cancer.

PU-0794

JAK/STAT3 信号通路特异性抑制剂 AG490 对膀胱癌细胞侵袭能力的影响

张彦懿
成都市第三人民医院

目的 探讨 JAK/STAT3 信号通路特异性抑制剂 AG490 对 MMP-2、MMP-9、VEGF 和 P-STAT3 蛋白表达以及膀胱癌细胞侵袭能力的抑制作用，以验证 PLCε 是否是通过 JAK/STAT3 通路来抑制膀胱癌细胞侵袭能力。
方法 分别用高、中、低三种药物浓度的 AG490 处理 BIU-87、T24 细胞株,transwell 侵袭试验检测 AG490 对细胞侵袭能力的影响，采用 Western blot 法分别检测 AG490 处理前后 STAT3 总蛋白、磷酸化形式蛋白和 MMP-2、MMP-9 和 VEGF 蛋白表达变化。
结果 AG490 对膀胱癌细胞侵袭力具有抑制作用，且抑制作用呈浓度依赖性，AG490 同样抑制 P-STAT3、MMP-2、MMP-9 和 VEGF 蛋白的表达(P<0.05)。
结论 AG490 可能通过抑制 JAK/STAT3 信号通路的激活，从而抑制下游 MMP-2、MMP-9 和 VEGF 的表达既而达到下调膀胱癌侵袭能力的作用。

PU-0795

2016-2020 年成都某医院门诊女性 HPV 感染情况及基因亚型分析

张彦懿
成都市第三人民医院

目的 了解四川省成都市某医院女性人乳头瘤病毒（human papilloma virus，HPV）阳性感染情况，为宫颈癌防治策略提供参考依据。
方法 收取 2016 年 1 月至 2020 年 12 月门诊就诊的 9635 例女性的宫颈脱落上皮细胞样本，采用宫颈刷取法，用 PCR 及导流杂交方法对 21 种 HPV 亚型进行分型检测，分析各型感染阳性率。同时，将受检者年龄分为 6 组（≤20 岁，21-30 岁，31-40 岁，41-50 岁，51-60 岁，≥61 岁），分析各年龄段感染情况。用卡方检验对结果进行统计分析。
结果 共检出 HPV 阳性 4322 例，阳性率 44.9%，其中单一型感染占 32.46%，多重感染占 12.44%；所有 21 种基因亚型均被检出，其中高危型占 73.82% ，低危型占 26.18%，检出率前三位的亚型依次为 52 型、16 型、53 型；各年龄段的检出率分别为：≤20 岁 32.67%，21-30 岁 28.49%，31-40 岁 10.26%，41-50 岁 5.81%，51-60 岁 1.19%，≥61 岁 21.58%，单一型别及多重感染率最高的组均为≤20 岁年龄组。
结论 2016-2020 年成都该医院女性 HPV 感染以单一型、高危型为主，以 HPV 基因亚型 52 型、16 型、53 型多见，预防接种时宜选用涵盖这 3 种亚型的疫苗。

PU-0796

Protective effect and mechanism of miR-216a silencing on carbon tetrachloride-induced liver fibrosis in rats

Shuaijun Lu 、fang wang、burong zhang、weihua wang
The AffiliatedHospitalof Medical School，Ningbo University

Objective To explore the effect and mechanism of microRNA (miRNA) 216a silencing on carbon tetrachloride-induced liver fibrosis in rats.
Methods Ten of the fifty rats were randomly selected as the normal group, and the remaining 40 rats were intraperitoneally injected with olive oil solution containing CCl4 to establish the liver fibrosis model rats. Thirty rats were randomly divided into model group, control group and silent group, with 10 rats in each group. Adenovirus containing empty plasmid was injected into the control group through tail vein, and adenovirus containing plasmid si-miR-216a was injected into the silent group through tail vein. The levels of hyaluronic acid (HA), laminin (LN), type Ⅲ

procollagen (PC Ⅲ) and type Ⅳ collagen (C Ⅳ) were detected by enzyme-linked immunosorbent assay. The expression levels of miR-216a, phosphatase and tensin homolog deleted on chromosome 10 (PTEN) mRNA and mothers against decapentaplegic homolog 7 (Samd7) mRNA were detected by real-time fluorescence quantitative PCR method. The expression levels of PTEN and Samd7 were detected by Western Blot.

Results Compared with the normal group, the levels of HA, LN, PC Ⅲ, C Ⅳ, and miR-216a in the model group increased, while the levels of PTEN mRNA, Samd7 mRNA, PTEN, and Samd7 decreased, the differences were statistically significant (P<0.05). Compared with the model group and control group, the levels of HA, LN, PC Ⅲ, C Ⅳ, and miR-216a in the silent group decreased, while the levels of PTEN mRNA, Samd7 mRNA, PTEN, and Samd7 increased, and the differences were statistically significant (P<0.05).

Conclusions miR-216a silencing can reduce the levels of HA, LN, PC Ⅲ and C Ⅳ in liver fibrosis rats, and improve the liver fibrosis injury induced by carbon tetrachloride. The mechanism may be related to the regulation of PTEN/Smad7.

PU-0797

基于多重 RT-PCR 检测法的儿童呼吸道病原体流行特征

刘文渊、张艺之、卢文波
宁波市妇女儿童医院

目的 了解区域儿童呼吸道感染病原体的流行特征，为临床防控和诊治提供参考依据。
方法 收集 2019 年 7 月～10 月间宁波市妇女儿童医院就诊急性呼吸道感染患儿的标本共 3 103 例，通过基于毛细电泳的多重 RT-PCR 法检测常见的 13 种呼吸道病原体，并对结果进行统计分析。
结果 3103 例患儿中 2 053 例呼吸道病原体检测阳性，总阳性率为 66.16%。检出率前 3 位分别为肺炎支原体（mycoplasma pneumoniae, MP）33.19%（1030/3 103）、鼻病毒（human rhinovirus, HRV）24.20%（751/3 103）和腺病毒（human adenovirus, HADV）8.77%（272/3 103）。病原体在男性患儿和女性患儿中的检出率分别为 65.70%（1 157/1 761）和 66.77%（896/1 342），差异无统计学意义；在年龄≤1 岁组、1～≤3 岁组、3～≤6 岁组和 6～≤16 岁组检出率分别为 58.02%（626/1 079）、74.37%（589/792）、73.78%（543/736）和 59.48%（295/496），组间差异具有统计学意义；7 月～10 月份检出率依次为 71.64%（341/476）、68.81%（536/779）、67.01%（648/967）和 59.93%（528/881），差异具有统计学意义；单一感染率为 52.30%（1 623/3 103），两种及以上病原体混合感染率为 13.86%（430/3 103），其中以 2 种病原体混合感染多见。
结论 本区域儿童呼吸道病原体检出以 MP 和 HRV 为主，病原体检出率在不同年龄阶段和不同月份间存在一定差异。

PU-0798

YTHDF1 promotes Cyclin B1 translation through m6A modulation and contributes to the poor prognosis of Lung adenocarcinoma with KRAS/TP53 co-mutation

Xiaoying Lou、Kexin Li、Danfei Xu、Yue Wu、Wei Cui
National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital

Background KRAS and TP53 mutations are the two most common driver mutations in patients with lung adenocarcinoma (LUAD), and appear to reduce latency and increase metastatic

proclivity when KRAS and TP53 co-mutation (KRAS/TP53-mut) occur. This raises the question of whether co-mutations impact the prognosis of LUAD. N6-methyladenosinde (m6A), the most abundant RNA modification in mammal mRNAs, plays a critical role in tumorigenesis. YTHDF1, as m6A reader protein, directly promotes the translation of methylated mRNAs. Recently studies have revealed that YTHDF1 depletion restrains LUAD progression. However, the molecular mechanism involved is unclear for LUAD patients with KRAS/TP53-mut.
Methods Transcriptome, somatic mutation, and clinical data for LUAD patients was extracted from public database to investigate the impact of KRAS and TP53 co-mutation in LUAD. Differential expression of the 15-m6A-related genes were analyzed in LUAD with different mutations. Moreover, bioinformatic analysis was applied to screen the potential targets of YTHDF1. The specific binding between YTHDF1 and presumed target was verified by m6A-RIP and YTHDF1-RIP assays. Furthermore, cell proliferation assays were performed to discover the functional role of YTHDF1 and its target in LUAD with KRAS/TP53-mut. Finally, 70 LUAD tissues were collected from patients with KRAS and/or TP53 mutation to confirm the association between YTHDF1 and Cyclin B1 expression.
Results We first found that only LUAD patients with KRAS/TP53-mut, but not individual mutation appeared to poor overall survival, when compared with patients without KRAS and TP53 mutation (Wild-type). Interestingly, YTHDF1 was the most upregulated in KRAS/TP53-mut patients and associated with their adverse prognosis. RNA level of YTHDF1 was positively correlated with the protein level and translation efficiency of Cyclin B1. Cyclin B1 is high expressed in LUAD patients with KRAS/TP53-mut, and its high expression is closely correlated with shorter overall survival. Experimental evidence indicated that protein levels of YTHDF1 and Cyclin B1 were significantly elevated in the KRAS/TP53-mut cell lines. Elevated YTHDF1 functionally promoted the translation of Cyclin B1 in an m6A-dependent manner, thereby facilitating the tumor proliferation and poor prognosis of LUAD with KRAS/TP53-mut. Furthermore, the correlation between YTHDF1 and Cyclin B1 expression was confirmed in patients with co-mutant KRAS/TP53, and upregulation of YTHDF1 was found to be associated with an unfavorable pathological stage and tumor size.
Conclusion In this study, we found that YTHDF1 promotes the translation of Cyclin B1 through m6A regulation and contributes to the poor prognosis of LUAD with KRAS/TP53 co-mutation by combining bioinformatics and experimental **Results** Thus, YTHDF1-targeted therapy might be a potential target for KRAS/TP53-mut lung cancer therapy.

PU-0799

Identification of Thearpeutic Targets and Prognostic Biomarkers Among CDKs in the Renal Cell Carcinoma Microenvironment

Chenggui Zhao
Zhongda Hospital,Southeast University

Background Renal cell carcinoma (RCC), which is one of the most common malignances, hasa continuous growing incidence and mortality.
Methods ONCOMINE, GEPIA, UALCAN, cBioPortal, GeneMANIA, DAVID 6.8,Metascape, TRRUST, LinkedOmics and TIMER were utilized in this study.
Results The mRNA levels of CDK1/2/4/5/8/13/16 in RCC tissues were significantly elevated while the mRNA levels of CDK3/9/17 were significantly reduced. The transcriptional levels of CDK1/2/3/4/5/7/9/10/13/17/18/19 in RCC tissues were significantly elevated while the transcriptional levels of CDK6/8/14/16 were significantly reduced. A significant correlation was found between the expression of CDK1/4/5/6/8/9/15/19/20 and the pathological stage of RCC patients. RCC patients with low transcriptional levels of CDK1/3, high transcriptional levels of CDK9/14/15/18/19/20 were significantly associated with a better prognosis. The functions of

differentially expressed CDKs are primarily related to the cell cycle, serin/threonine protein kinase complex, cyclin-dependent protein serin/threonine kinase activity. It's suggested that IRF1, MYC, TP53, NR3C1, AR and RREL were key transcription factors for CDKs. Significant correlations were found between the expression of CDKs and the infiltration of six types of immune cells (B cells, CD8+ T cells, CD4+T cells, macrophages, neutrophils, and dendritic cells). 19 drug-gene interaction pairs were obtained in DGIdb.
Conclusions This study provides novel insights for the selection of immunotherapeutic targets and prognostic biomarkers for renal cell carcinoma.

PU-0800

HOTTIP contributes to cisplatin resistance by sponging miR-216a-5p in gastric cancer

Rui Zhao
Qilu Hospital, Shandong University

Background Gastric cancer (GC) is a significant public health burden worldwide, and cisplatin resistance is the leading cause for the failure of chemotherapy in this disease. Previous studies have revealed that HOXA transcript at the distal tip (HOTTIP) is involved in the pathology of GC and is associated with poor overall survival. Recent studies have revealed that autophagy plays an important role in regulating response to chemotherapy. However, the functional role of HOTTIP in GC cisplatin resistance and whether HOTTIP can modulate cisplatin resistance in GC by regulating autophagy remains largely unknown. Our study aims at investigating the important roles of HOTTIP in GC cisplatin resistance.
Methods 1. Expression levels of HOTTIP in GC cells (GES-1, SGC7901 and SGC7901/DDP) were detected by RT-qPCR. 2. The HOTTIP coding sequence was amplified and cloned into pcDNA3.1 vector. The resulting construct, named pcDNA3.1-HOTTIP, was used to overexpress HOTTIP. Si-HOTTIP was used to silencing HOTTIP expression. Transfection was performed using Lipofectamine 2000. 3. A xenograft tumor model was established to evaluate the effect of HOTTIP on chemoresistance in vivo. 4. The effect of HOTTIP expression levels on cisplatin resistance in GC was detected by CCK-8 proliferation assay, apoptosis assay (TUNEL assay and flow cytometric analysis) and autophagy assay. 5. The interaction among HOTTIP, miR-216a-5p and Bcl-2 were predicted by StarBase v2.0 and confirmed by double luciferase reporter system and western blot.
Results 1. SGC7901/DDP expressed higher level of HOTTIP than SGC7901 ($p<0.001$), and these two GC cell lines showed 1.473- and 2.042-fold upregulation of HOTTIP compared to GES-1. 2. HOTTIP overexpression notably increased cisplatin resistance of SGC7901 cells compared to control cells ($p<0.001$) while silencing of HOTTIP significantly inhibited cisplatin resistance of SGC7901/DDP cells compared to cells transfected with the empty vector ($p<0.001$). 3. In vivo experiment, HOTTIP overexpression group displayed larger tumor size and weight than those in the NC group. 4. Overexpression of HOTTIP in SGC7901 cells significantly decreased cell apoptosis while silencing of HOTTIP in SGC7901/DDP cells significantly increased cell apoptosis. 5. Knockdown of HOTTIP inhibits chemoresistance of SGC7901/DDP by promoting autophagy. 6. HOTTIP could sponge miR-216a-5p to promote the expression of Bcl-2, then decrease the release of Beclin1 from Bcl-2/Beclin1 complex, and finally inhibit autophagy.
Conclusion HOTTIP could affecte the cisplatin resistance of GC cells by regulating miR-216a-5p/Bcl-2 /Beclin1 pathway, which provides a novel strategy to overcome resistance to chemotherapy in GC.

PU-0801

Exosomal long noncoding RNA HOTTIP as potential novel diagnostic and prognostic biomarker test for gastric cancer

Rui Zhao
Qilu Hospital, Shandong University

Aim Gastric cancer (GC) is a huge burden worldwide with high morbidity and high mortality, especially in Eastern Asia. Blood-based examination is an ideal examination for GC diagnosis, butcurrent serum tumor biomarkers, like CEA, CA 19-9 and CA 72-4, have a low positive rate. Long noncoding RNA HOTTIP (HOXA transcript at the distal tip) plays important roles in the generation and progression of human cancers and has gained growing attention among cancer-related lncRNAs. Exosomes participate in cellular communication by transmitting moleculars between cells and are regarded as suitable candidates for non-invasive diagnosis. However, the existence of HOTTIP in the circulating exosomes and the potential roles of exosomal HOTTIP in GC was poorly understood. This study aims at estimating the potential novel diagnostic and prognostic values of exosomal HOTTIP for GC.
Methods 1. Serum exosomal HOTTIP from 246 subjects (126 GC patients and 120 healthy people) were detected by reverse transcriptionreal-time quantitative polymerase chain reaction (RT-qPCR) and serum CEA, CA 19-9 and CA 72-4were measured by electrochemiluminescence method on Cobas E601. 2. Receiver operating characteristic curve (ROC) was built to estimate the diagnostic values of exosomal HOTTIP, CEA, CA 19-9 and CA 72-4. 3. The Kaplan–Meier analysis was used to analyse the relationship between exosomal HOTTIP, CEA, CA 19-9 and CA 72-4expression levels and overall survival (OS) of GC. 4. Cox proportional hazards models were performed to identify independent prognostic factors for GC.
Results 1. Exosomal HOTTIP was directly released by GC cells. And RT-qPCR results showed that the expression levels of exosomal HOTTIP in serum were typically higher in GC than in normal control ($P < 0.001$) and its expression levels were significantly correlated with tumor invasion depth ($P = 0.0298$) and TNM stage ($P < 0.001$). We also proved the stability ofexosomal HOTTIP by treated serum samples with prolonged exposure to room temperature or mutiple freeze-thaw cycles. 2. The area under the curve (AUC) for exosomal HOTTIP was 0.827 ($P < 0.001$), which was significantly higher than the AUCs for CEA, CA 19-9, CA 72-4 with 0.653, 0.685 and 0.639, respectively ($P < 0.001$), indicating that exosomal HOTTIP was superior to them in GC diagnosis. 3 The Kaplan–Meier analysis showed a correlation between increased exosomal HOTTIP levels and poor overall survival (OS) ($P < 0.001$) and there was no significant relationship between CEA, CA 19-9, CA 72-4 and OS ($P > 0.05$). The online (www.kmplot.com) survival analysis results, basing on the detection data from GC tissues, demonstrated that expression levels of HOTTIP were increased above the optimal cutoff point in 71.8% of patients with GC and these patients had a poor OS, with the pooled HR of 1.63 (95% CI 1.19-2.23, logrank $P = 0.0022$), which supported our
Conclusion 4 Univariate and multivariate COX analysis revealed exosomal HOTTIP overexpression was an independent prognostic factor in GC patients (HR = 2.037, 95% CI = 1.085-3.823, $P = 0.027$).
Dissucion Exosomal long noncoding RNA HOTTIP may be a potential biomarker for GC in diagnosis and prognosis.

PU-0802

应用加权基因共表达网络分析筛选结肠腺癌干性指数相关核心基因

丁志祥、史兵伟、葛贤
南京中医药大学附属常州市中医医院

目的 利用加权基因共表达网络分析挖掘结肠腺癌（colon adenocarinoma，COAD）转录组干性指数相关核心基因。
方法 从 TCGA 官网下载 COAD 相关转录组数据及临床资料，应用逻辑回归机械学习法则计算基于转录组表达数据的干性指数（mRNA expression-based stemness indices，mRNAsi）。应用加权基因共表达网络分析（weighted gene co-expression network analysis，WGCNA）获取与 mRNAsi 密切相关的模块及基因。对相关模块基因进行 GO 富集分析和 KEGG 通路分析。利用 STRING 在线数据库分析 mRNAsi 相关基因的蛋白质相互作用网络（PPI），并通过 Cytoscape 筛选核心基因（Hub gene）。分析各 Hub 基因之间的相关性及其在 COAD 组织和正常组织中的表达差异。
结果 COAD 组织中 mRNAsi 评分显著高于正常组织（t=14.145，P<0.001），mRNAsi 高评分组生存率高于低评分组（P=0.041）。应用 WGCNA 共筛选出 3 个 mRNAsi 相关模块及 178 个相关基因。通过 PPI 分析筛选出的 Hub 基因包括 COL1A2、COL1A1、COL3A1、POSTN、THBS2、COL5A1、COL5A2、DCN、BGN 及 LOX。经 TCGA 数据库验证 COL1A2、COL1A1、COL3A1、POSTN、THBS2、COL5A1、COL5A2、BGN 及 LOX 在 COAD 组织中表达显著高于正常结肠组织（P<0.01），而 DCN 在癌组织中表达显著低于正常组织中的表达（P<0.01）。
结论 通过 WGCNA 筛选到与结肠腺癌 mRNAsi 相关的 10 个潜在 Hub 基因，对结肠腺癌的分子机制研究提供了新靶点。

PU-0803

Comparative analysis of QS3D and droplet digital PCR for detection of plasma EGFR T790M mutation at disease progression

QIAOMEI GUO、XIA HUANG、LIHUA QIAO、MINGNA ZHAO、MENGYAN WANG、LIN WANG、JIATAO LOU
Department of Laboratory Medicine, Shanghai Chest Hospital

Objectives Numerous studies have demonstrated the ability of QuantStudioTM 3D (QS3D) and droplet digital PCR (dPCR) platforms in the successful detection of EGFR mutations from plasma. However, no prospective data on quantitative comparative analysis of the two **Methods** are available. Here we directly compared the performance of the two platforms in the detection of the EGFR T790M mutation in cell-free DNA (cfDNA) samples from lung cancer patients.
Methods cfDNA was isolated from plasma samples of 72 non-small cell lung cancer patients who initially received tyrosine kinase inhibitor treatment and acquired drug resistance. Identical cfDNA samples were subjected to T790M mutation analysis using QS3D and droplet dPCR in parallel.
Results The T790M mutation was detected in 15/72 (20.8%) cfDNA samples by QS3D dPCR and 21/72 (29.2%) cfDNA samples by droplet dPCR. The overall concordance between the two **Methods** was 91.7% (66/72). The median allele frequency of the T790M mutation detected by QS3D dPCR and droplet dPCR was 2.01% and 2.62%, respectively. The partition number of QS3D dPCR is much higher than that of droplet dPCR, while the mutation abundance detected by the two platforms is similar. Furthermore, a strong correlation was observed in allele frequencies and copy numbers between the two methods, with R2 of 0.98 and 0.97, respectively.

Conclusion Our study demonstrated a high level of concordance between the QS3D and droplet dPCR platforms for the detection and absolute quantification of the EGFR T790M mutation in cfDNA.

PU-0804

Exosomal miR-92b-3p Promotes Chemoresistance of Small Cell Lung Cancer Through the PTEN/AKT Pathway

李明
安徽省立医院（中国科学技术大学附属第一医院）

Resistance to fifirst-line chemotherapy drugs has become an obstacle to improving the clinical prognosis of patients with small cell lung cancer (SCLC). Exosomal microRNAs have been shown to play pro- and anti-chemoresistant roles in various cancers, but their role in SCLC chemoresistance has never been explored. In this study, we observed that the expression of exosomal miR-92b-3p was signifificantly increased in patients who developed chemoresistance. Luciferase reporter analysis confifirmed that PTEN was a target gene of miR-92b-3p. The PTEN/AKT regulatory network was related to miR-92b-3p-mediated cell migration and chemoresistance in vitro and in vivo in SCLC.

PU-0805

The subtype-specific molecular function of SPDEF in breast cancer and insights into prognostic significance

Ting Ye、Jinbo Liu
The Affiliated Hospital of Southwest Medical University

Background Breast cancer (BC) is a molecular diverse disease which becomes the most common malignancy among women worldwide. There are four BC subtypes (Luminal A, Luminal B, HER-2 enriched and Basal-like) robustly established following gene expression patterns based characterization, behave significant differences in terms of their incidence, risk factors, prognosis and therapeutic sensitivity. Thus, there is an urgent need to provide mechanism research, treatment strategies and/or prognosis evaluation based on the patient stratification of BC subtypes. The prostate-derived ETS factor SPDEF was first identified as an activator of prostate specific antigen and then the involvements in many aspects of BC has been proposed. However, the subtype-specific molecular function of SPDEF in BC and insights into prognostic significance have not been clearly elucidated.
Materials and Methods In the present study, we unveiled the global expression profiles of SPDEF, as well as the clinicopathologic and prognostic importance in different BC subtypes through public datasets and experimental evidences. Subsequently, Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG) and hallmark effect gene sets analysis were performed to explore the potential functions and molecular mechanisms of SPDEF in BC subtyping progression.
Results We conducted the prognostic risk model of SPDEF-related prognosis genes respectively in subtypes of BC, indicating a highly prognostic performance in survival surveillance.
Conclusions In summary, our findings would help to better understand the possibly mechanisms of various BC subtypes and to find possible candidate genes for prognostic and therapeutic usage.

PU-0806

自噬相关 LncRNA 在肝细胞肝癌中的预后价值研究

周亚萍
新疆军区总院
石河子大学

目的 LncRNA 可能通过体内多种自噬相关途径在肝细胞肝癌的发生、转移和生理生化反应中发挥至关重要的作用，本研究的主要目的是探讨肝细胞肝癌中多种自噬相关 LncRNA 的表达情况及其临床意义，并进一步研究其可能的分子机制。
材料与方法 肝细胞肝癌患者和自噬相关基因数据分别从癌症基因组图谱数据库和人类自噬数据库获得，基于比例风险回归模型分析和基因共表达构建预测模型。
结果 最终构建的预后模型中包含 7 个自噬相关的 lncRNA，分别是 PRRT3-AS1,RP11-479G22.8,RP11-73M18.8,LINC01138,CTD-2510F5.4,CTC-297N7.9,RP11-324122.4。对预测模型进行进一步风险评估，整体生存（OS）曲线显示，高风险患者的 OS 显著低于低风险患者（P = 2.292E-10），并且其风险评分预测精准度（AUC = 0.786）显著高于 ALBI 肿瘤分期（AUC =0.532），Child_Pugh 肿瘤分期（AUC =0.573），甲胎蛋白 AFP（AUC =0.5751）和美国癌症委员会肿瘤分期（AUC =0.631）。多因素 COX 分析和风险评分列线图显示，风险评分联合 Child_Pugh 肿瘤分期、患者年龄、TNM 分期和 GRADE 分级进行综合分析时，预测肝细胞肝癌患者 1 年和 3 年的 OS 的准确率明显升高（1 年生存率 AUC =0.87，3 年生存率 AUC =0.855）。此外，这 7 个自噬相关的 lncRNAs 可能参与调节体内剪接体构成、细胞周期、RNA 转运、DNA 复制、mRNA 监控途径等，并且与 RNA 剪接、mRNA 剪接的生物学过程有关。
结论 综上所述，这 7 种自噬相关的 LncRNAs 可能通过体内多种调节途径参与肝细胞肝癌的发生发展过程，也可能是监测肝细胞肝癌的治疗效果和预后情况的理想标志物。

PU-0807

GATA1/SP1 and miR-874 mediate enterovirus-71-induced apoptosis in a granzyme-B-dependent manner in Jurkat cells

Meijuan Zhang、jun zhou
the First Affiliated Hospital of Nanjing Medical University

Enterovirus 71 (EV71)-induced T lymphocyte apoptosis plays an important role in hand, foot, and mouth disease (HFMD), and granzyme B (GZMB) has been shown to be critical for this process. However, the mechanisms underlying GZMB- mediated apoptosis of T lymphocytes remain unknown. In this study, we investigated whether transcription factors and microRNAs (miRNAs) are involved in GZMB-mediated apoptosis of T lymphocytes in response to EV71 infection. Our ndings indicated that EV71 infection signi cantly induced apoptosis in Jurkat cells, a human T lymphocytes cell line, as revealed in ow cytometric analysis. Furthermore, EV71 increased the expression of pro-apoptosis Bcl-2-associated X (Bax) and cleaved caspase 3 but decreased the expression of anti-apoptosis B-cell lymphoma protein 2 (Bcl2). GZMB knockdown decreased cell apoptosis and prevented EV71-induced changes in the expression of Bax, cleaved caspase 3, and Bcl2 in Jurkat cells, highlighting the role of GZMB as a key factor in EV71-induced apoptosis. Our study also indicated that overexpression of the transcription factors GATA binding factor 1 (GATA1) and speci city protein 1 (SP1) signi cantly increased luciferase activity when this gene was inserted in the GZMB 3’ untranslated region (3’UTR). GATA1/SP1 overexpression induced cell apoptosis, increased the expression of Bax and cleaved caspase 3,

and decreased the expression of Bcl2. Finally, our results suggested that miR-874 plays an essential role in GZMB-mediated cell apoptosis, since an miR-874 mimic decreases the expression of GZMB by targeting its 3'UTR. Collectively, these data indicated that GATA1/SP1 and miR-874 mediate EV71-induced apoptosis in a granzyme B-dependent manner. This signaling pathway may provide a new pharmacological target for the prevention and treatment of HFMD.

PU-0808

高危型 HPV 基因分型在妇科保健人群中的分布特征分析

张美娟、周军
江苏省人民医院（南京医科大学第一附属医院）

目的 了解高危型人乳头瘤病毒(high risk HPV, hr HPV)感染的基因分型，为宫颈病变的早期筛查提供依据。
方法 选取 2020 年 4 月~2021 年 3 月江苏某三甲医院妇女保健门诊就诊的 1903 名女性，取宫颈脱落细胞标本进行高危型 HPV 分型检测，了解高危型 HPV 感染状况以及亚型分布规律。
结果 在所收集的 1903 份标本中，共检出高危型 HPV 阳性 396 例，阳性率为 20.8%。hr HPV 感染型别按检出阳性率从高到低依次是 HPV52(5.47%) 、HPV58(3.31%)、HPV16(3.05%)、HPV51(2.05%)、 HPV39(1.94%) 、HPV56(1.58%)、 HPV18(1.31%) 、HPV68(1.26%) 、HPV66(1.10%) 、HPV33(1.00%)、 HPV59(1.00%)、 HPV35(0.84%)、 HPV31(0.79%) 、HPV45(0.58%) 和 HPV82(0.53%)。hr HPV 阳性率从高到低的年龄组分别是: ≥65 岁组(35. 71%)、55~64 岁组(31.71%)、<25 岁组(24.64%)、45~54 岁组(24.14%)、35~44 岁组(20.00%)、25~34 岁组(18.84%)。在 396 例 HPV 阳性检测结果中，以单一感染为主，共 321 例(81.06%)，多重感染 75 例，多重感染率为 18.94％，其中二重感染 57 例，三重感染 13 例，四重感染 3 例，五重感染 2 例。
结论 在妇科保健人群的筛查中，感染率最高的出现在≥55 岁的人群。阳性人群中以单一感染为主，hr HPV 感染以 HPV52、HPV58 和 HPV16 亚型为主。Hr HPV 基因分型检测对于宫颈病变的早期防治有重要的指导意义。

PU-0809

结直肠癌组织高频突变基因与临床病理特征及 MMR 基因突变的相关性分析

吴爱华
宁波市第一医院

目的 利用高通量测序平台分析结直肠癌（colorectal cancer，CRC）热点基因及新发基因突变状况，探讨突变基因与临床病理特征之间的关系。
方法 回顾性分析 2019 年 1 月至 2020 年 12 月宁波市第一医院行二代测序检测的 128 例 CRC 患者的临床病理资料及基因检测结果。分析热点基因和新发基因突变的分布及致病性，分析高频突变基因与临床病理特征及 MMR 基因的关系。
结果 128 例 CRC 患者中，检测出 APC、TP53、KRAS、FBXW7、 PIK3CA 及 MMR 基因的突变率分别为 77.3%（99/128）、73.4%（94/128）、42.2%（54/128）、16.4%（21/128）、15.6%（20/128）和 7.8%（10/128）。共检测到结直肠癌相关的 17 个基因的 224 种突变，其中包括 191 种热点突变和 33 种新发突变。利用生物信息学软件分析基因新发突变的致病性，结果显示有 17 个位点对基因的功能产生重大影响。此外，TP53 基因在有脉管浸润（p=0.035）及发生远处转

移 (p=0.03) 的患者中突变率高。APC 基因突变在左半结肠癌（p=0.01）的患者中突变率较高。KRAS 基因在不同肿瘤原发部位（p=0.002）的突变率有统计学意义。PIK3CA 基因在女性（p=0.019）、肿瘤直径≥ 5 mm（p=0.005）及未发生脉管浸润（p=0.043）的患者中具有较高的突变率。FBXW7 基因在发生淋巴结转移（p=0.023）的患者中突变率较高。TP53、APC、KRAS、PIK3CA、FBXW7 基因突变率与 MMR 基因的突变率没有相关性。

结论 高通量测序平台可作为分析结直肠癌多基因检测的手段，高频突变基因 TP53、APC、KRAS、PIK3CA 和 FBXW7 基因与临床病理参数存在相关性，对临床诊疗提供一定帮助。

PU-0810

通过转录组测序探索生物节律参与 2 型糖尿病肾病的机制研究

孔晓牧、马亮、曹永彤
中日友好医院

目的 生物节律对于维持肾脏生理功能至关重要。已有研究提示生物节律紊乱可能参与糖尿病肾脏疾病的发生发展，机制尚不清楚。本研究旨在通过转录组测序方法探索生物节律参与 2 型糖尿病肾病病理过程的新机制。

方法 购入 36 只 8 周龄雄性 2 型糖尿病 db/db 小鼠及对照组 m/m 小鼠。在各基因型组内，根据基线随机血糖与体重水平将动物进一步分为 6 组（n=6）。采取 12h 光照-黑暗周期（光照从 7:00am~7:00pm）适应性饲养 1 周。其后，分别在环境钟（ZT）为 ZT0（7:00am）、ZT4（11:00am）、ZT8（3:00pm）、ZT12（7:00pm）、ZT16（11:00pm）、ZT20（3:00am）时处死小鼠并取材。肾脏组织进行二代转录组测序、差异表达基因富集分析。

结果 转录组测序初步结果显示，m/m 小鼠 ZT4、ZT8、ZT12、ZT16 和 ZT20 组肾脏相对 ZT0 组的差异基因数目分别为 133、284、278、155 和 46 个；db/db 小鼠各组肾脏相对 ZT0 组的差异基因数目分别为 11、90、161、115 和 18 个，可见其在各 ZT 时间点差异基因数目均显著少于 m/m 小鼠。差异基因富集分析显示，db/db 小鼠与 m/m 小鼠肾脏受到生物节律调控的基因通路存在共同点与差异性，m/m 小鼠肾脏受到生物节律调控的基因通路种类更为丰富。此外，各 ZT 时间点检测到 m/m 与 db/db 小鼠的肾脏间分别存在 347（ZT0）、408（ZT4）、514（ZT8）、453（ZT12）、526（ZT16）及 563 个（ZT20）差异表达基因。我们将对其中受到生物节律调控最为显著的基因及通路进行验证与分析。

结论 转录组测序数据显示 2 型糖尿病小鼠与对照组相比肾脏受到生物节律调控的基因数目与通路的丰富性均显著降低，提示肾脏生物节律调控基因及通路的异常参与了 2 型糖尿病肾脏疾病的病理过程，有可能成为未来防治糖尿病肾脏疾病的新靶点。

PU-0811

Advances in the application of artificial intelligence in solid tumor imaging

Ting Cui
the First Affiliated Hospital of Nanjing Medical University

Background Cancer is currently a worldwide health problem. Early diagnosis and timelytreatment are crucial in reducing cancer-related mortality. Medical imaging is acommon technique used to guide the clinical diagnosis of solid tumors. Accurateinterpretation of imaging data has become an important but difficult task inthe diagnosis process. Artificial intelligence (AI) has greatly relievedclinical workloads and changed the current medical workflows.

Methods Wesearched for recent studies, reports and reviews referring to AI and solidtumors; many reviews have summarized AI applications in the diagnosis andtreatment of a single tumor type.
Results We herein systematicallyreview the advances of AI application in multiple solid tumors includingesophagus, stomach, intestine, breast, thyroid, prostate, lung, liver, cervix,pancreas and kidney with a specific focus on the continual improvement on modelperformance in imaging practice.
Conclusion AI has clear characteristicsof high efficiency, specificity and sensitivity in the classification,identification and diagnosis of solid tumor. After its integration into imagingtechnology, AI optimizes clinical workflows, decreases the discrepancy between thereaders and reduces the misdiagnosis rate, which helps clinicians effectively chooseappropriate therapeutic strategies and accurately predict the prognosis.

PU-0812

Sample-to-Answer and Routine Real-Time RT-PCR：A Comparison of Different Platforms for SARS-CoV-2 Detection

Donghua Wen 、Simin Yang、Guangbo Li、Qiankun Xuan、Wenzheng Guo、Wenjuan Wu
Department of Laboratory Medicine, Shanghai East Hospital, Tongji University School of Medicine, Shanghai, China

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is spreading all over the world and has caused millions of deaths. Several Sample-to-Answer platforms, including Cepheid Xpert® Xpress SARS-CoV-2 (Xpert Xpress), have received emergency use authorization (EUA) for SARS-CoV-2 nucleic acid detection as a point of care test（POCT） in the US. But their application niche is unclear comparing with real-time reverse transcription PCR (rRT-PCR) assays cleared by the National Medical Products Administration (NMPA) in China. In this study, the clinical performance, sensitivity and workflow of Xpert Xpress and two rRT-PCR kits (BioGerm, Shanghai and Sansure, Hunan) were evaluated by the specimens from 86 symptomatic patients. The positive percent agreement (PPA) of Xpert Xpress was 100%, followed by BioGerm Kit (96.15%) and Sansure Kit (90%), respectively. The negative percent agreement (NPA) was 100% for three assays. The limit of detection (LoD) is 100 copies /mL for Xpert Xpress, 500 copies /mL for BioGerm Kit and Sansure Kit. By serially diluting five positive specimens assay, the Xpert Xpress displayed better detection capability. In the workflow and throughput analysis, the turnaround time was 51 min for Xpert Xpress, 150 min for BioGerm kit and 210 min for Sansure kit. This study provides some indication for diagnosis **Methods** selection.

PU-0813

The role of DNA methylation in syndromic and non-syndromic congenital heart disease

jiali cao[1]、qichang wu[2]、yanru huang[3]、lingye wang[4]、zhiying su[5]、huiming ye[4,6]
1. Women and Children's Hospital, School of Medicine, Xiamen University
2. Women and Children's Hospital, School of Medicine, Xiamen University
3. Women and Children's Hospital, School of Medicine, Xiamen University
4. School of Public Health, Xiamen University
5. Women and Children's Hospital, School of Medicine, Xiamen University
6. Women and Children's Hospital, School of Medicine, Xiamen University

Congenital heart disease (CHD) is a common structural birth defect worldwide, and defects typically occur in the walls and valves of the heart or enlarged blood vessels. Chromosomal abnormalities and genetic mutations only account for a small portion of the pathogenic mechanisms of CHD, and the etiology of most cases remains unknown. The role of epigenetics in various diseases, including CHD, has attracted increased attention. The contributions of DNA methylation, one of the most important epigenetic modifications, to CHD have not been illuminated. Increasing evidence suggests that aberrant DNA methylation is related to CHD. Here, we briefly introduce DNA methylation and CHD and then review the DNA methylation profiles during cardiac development and in CHD, abnormalities in maternal genome-wide DNA methylation patterns are also described. Whole genome methylation profile and important differentially methylated genes identified in recent years are summarized and clustered according to the sample type and methodologies. Finally, we discuss the novel technology for and prospects of CHD-related DNA methylation.

PU-0814

Methylation of CYP1A1 and VKORC1 promoter associated with stable dosage of warfarin in Chinese patients

shiwei he[1,2]、yuan wu[3]、shuidi yan[4]、jumei liu[1]、li zhao[1,5]、huabin xie[3]、shengxiang ge[2]、huiming ye[1,2,5]
1. Women and Children’s Hospital, School of Medicine, Xiamen University
2. National Institute of Diagnostics and Vaccine Development in Infectious Diseases (Xiamen University), School of Public Health, Xiamen University
3. Xiamen Cardiovascular Hospital, School of Medicine, Xiamen University
4. Zhongshan Hospital, School of Medicine, Xiamen University
5. School of Medicine, Xiamen University

Objective To investigate the association between DNA methylation and the stable warfarin dose through genome-wide DNA methylation analysis and pyrosequencing assay.
Method This study included 161 patients and genome-wide DNA methylation analysis was used to screen potential warfarin dose-associated CpGs through Illumina Infinium HumanMethylation 450 K BeadChip; then, the pyrosequencing assay was used to further validate the association between the stable warfarin dose and alterations in the methylation of the screened CpGs. GenomeStudio Software and R were used to analyze the differentially methylated CpGs.
Results CpGs surrounding the xenobiotic response element (XRE) within CYP1A1 promoter methylation levels significantly differed between the different dose groups ($P < 0.05$), and these CpGs presented a positive correlation ($r > 0$, $P < 0.05$) with an increase in the stable dose of warfarin. At the VKORC1 promoter, two CpGs methylation level were significantly different statistically between the differential dose groups ($P < 0.05$), and one CpG(Chr16: 31106793) presented a significant negative correlation ($r < 0$, $P < 0.05$) among different dose (low, medium, and high) groups.

Conclusion This is a novel report of the methylation levels of six CpGs surrounding the XRE within the CYP1A1 promoter and one differential CpG at the VKORC1 promoter associated with stable warfarin dosage; these methylation levels might be applied as molecular signatures for warfarin.

PU-0815

Immunogenicity of recombinant protein CPSIT_p6 and its localization in cells infected with Chlamydia psittaci

Mingxing Liang 、 changshun yang
the First People's Hospital of Huaihua

We evaluated the immunogenicity and the localization of CPSIT_p6 in Chlamydia psittaci 6BC-infected cells. The recombinant plasmid pET-30a-CPSIT_p6 was transformed into Escherichia coli BL21 for expressing the His-tagged CPSIT_p6, which was purified using Ni-nitrilotriacetic acid (NTA) beads and was confirmed by western blot analysis. BALB/c mice were immunized with the purified His-fusion protein subcutaneously three times with 2-week intervals. Results displayed that the CPSIT_p6 protein induced not only a strong humoral immune responses to C. psittaci by generating significantly high titers of specific serum IgG antibodies, but also a strong T lymphocyte responses that were recalled by the immunogen CPSIT_p6 in an in vitro restimulation assay. Furthermore, the CPSIT_p6 protein substantially primed secretion of IFN-γ, revealing that induce a strong Th1 response. Finally, a mouse anti-CPSIT_p6 antibody was used to localize the protein in cells infected with C. psittaci using an indirect immunofluorescence assay (IFA), revealed that CPSIT_p6 was localized inside the inclusion of C. psittaci 6BC-infected cells. Although CPSIT_p6 protein is a non-secreted protein, it has good immunogenicity. Therefore, the CPSIT_p6 protein may be useful for developing vaccines against C.psittaci infection.

PU-0816

Association of MTHFR C677T gene polymorphism with neonatal defects: a meta-analysis of 81444 subjects

juan li[1]、danqin feng[2]、shiwei he[3]、hua yang[4]、zhiying su[5]、huiming ye[6]
1. Women and Children's Hospital, School of Medicine, Xiamen University
2. Women and Children's Hospital, School of Medicine, Xiamen University
3. Xiamen University
4. Women and Children's Hospital, School of Medicine, Xiamen University
5. Women and Children's Hospital, School of Medicine, Xiamen University
6. Women and Children's Hospital, School of Medicine, Xiamen University

Objectives Methylenetetrahydrofolate reductase (MTHFR) is one of the enzymes involved in folic acid/homocysteine metabolism. In this meta-analysis, we attempted to clarify controversial associations of the MTHFR C677T gene polymorphism in maternal and fetal tissue with neonatal defects.
Methods We searched the PubMed, Embase, Cochrane, and Wanfang Data electronic databases to identify all case-control studies in English or Chinese that reported the association of MTHFR C677T gene polymorphism with frequencies of neonatal defects including congenital heart disease (CHD), neural tube defects (NTD), nonsyndromic cleft lip and palate (NSCL/P), and Down syndrome (DS). Studies were divided by subject type (neonatal and maternal) . We used a random-effect model or fixed-effect model to estimate overall odds ratios, depending on data heterogeneity.

Results In total, 81444 subjects of 116 qualified studies were included in this meta-analysis, namely 8169 case and 55604 control subjects in the maternal group and 6970 case and 10701 control subjects in the neonatal group. Depending on the neonatal defect subtypes, MTHFR C677T gene polymorphism was associated with NTD, CHD (except for TC/CC and TT+TC/CC modes of inheritance; p = 0.167 and p = 0.054, respectively), DS, and NSCL/P (TC/CC mode of inheritance, p = 0.032) in the maternal group. However, in the neonatal group, the MTHFR C677T gene polymorphism was only associated with the frequency of NTD and CHD.
Conclusions Maternal and neonatal MTHFR C677T gene polymorphisms appear to be associated with neonatal defects, but differ by defect types. More studies are needed to validate the findings of this meta-analysis.

PU-0817

Upregulation of microRNA 181a 5p increases the sensitivity of HS578T breast cancer cells to cisplatin by inducing vitamin D receptor mediated cell autophagy

jianmin lin[3]、xuming chen[4]、mingliang sun[5]、xiaojiao qu[1]、ye wang[6]、chenxi li[7]、xiujuan li[8]、li zhao[2]、zhiying su[9]、huiming ye[10]

1. Cardiovascular Hospital, School of Medicine, Xiamen University
2. Xiamen University
3. Women and Children's Hospital, School of Medicine, Xiamen University
4. Women and Children's Hospital, School of Medicine, Xiamen University
5. Women and Children's Hospital, School of Medicine, Xiamen University
6. Women and Children's Hospital, School of Medicine, Xiamen University
7. Women and Children's Hospital, School of Medicine, Xiamen University
8. Women and Children's Hospital, School of Medicine, Xiamen University
9. Women and Children's Hospital, School of Medicine, Xiamen University
10. Women and Children's Hospital, School of Medicine, Xiamen University

Objective Breast cancer (BC) is the leading cause of death in females worldwide. Although cisplatin is a strong-effect and broad-spectrum chemotherapy drug, resistance to cisplatin remains a significant factor effecting clinical efficacy. The underlying mechanism of cancer cell resistance to cisplatin is not fully understood. MicroRNAs (miRs/miRNAs), as a regulator, are involved in regulating chemosensitivity to numerous chemotherapeutic drugs. The present study aimed to investigate the function of miR-181a-5p as a potential tumor suppressor in improving the efficiency of cisplatin in BC.
Method The IC50 of cisplatin and miR-181a-5p expression were determined in five BC cell lines, and HS578T was selected as an appropriate cell line for subsequent experiments. The sensitivity of HS578T cells to cisplatin was assessed using cell proliferation, migration and apoptosis assays. Western blotting was performed to detect the expression of vitamin D receptor (VDR) and autophagy in HS578T cells.
Result It was found that the increase in autophagy resulted in increased apoptosis and sensitivity to cisplatin in HS578T cells. miR-181a-5p transfection also inhibited the proliferation and migration ability of HS578T cells and induced apoptosis. Meanwhile, HS578T cells have increased sensitivity to cisplatin. VDR, as a target gene and autophagy regulator of miR-181a-5p, was negatively regulated by miR-181a-5p. Upon the decrease in VDR expression, the autophagy in HS578T cells was increased.
Conclusion These results indicate that the increase in autophagy enhanced the chemosensitivity of cisplatin by inducing apoptosis of HS578T cells and by inhibiting proliferation and migration. The present study showed that miR-181a-5p increased the chemical sensitivity of HS578T cells to cisplatin by inhibiting VDR to promote autophagy. The use of miR-181a-5p/autophagy/VDR-based treatment strategies may be a potential method to overcome cisplatin resistance in BC.

PU-0818

Development of a 6-gene model for COVID-19 diagnosis and treatment based on the blood leucocytes sequencing dataset of patients with SARS-CoV-2 infection

Xin Gao、Changshun Yang
怀化市第一人民医院检验科

Objective Coronavirus disease 2019 (COVID-19) is a global epidemic disease caused by a novel virus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), causing serious adverse effects on human health. By analyzing transcriptome sequencing data from peripheral blood samples, we can identify differentially expressed genes (DEGs) associated with host immune and/or inflammatory responses. Studying the changes in gene expression in human immune cells after SARS-CoV-2 infection helps improve understanding of the mechanism of SARS-CoV-2 damage to the human body and helps improve the diagnosis and treatment of the disease. The objectives of this study were to explore aberrantly expressed genes related to SARS-CoV-2 infection in peripheral blood leucocytes and to develop a diagnostic model for COVID-19 using SARS-CoV-2 infection-related genes.

Methods and results In this study, we obtained the COVID-19-related dataset GSE157103 from the GEO database, which consists of human blood leucocytes sequencing data from 100 COVID-19 patients and 26 non-COVID-19 individuals. We identified 245 DEGs in the GSE157103 dataset based on the criteria log2|fold change (FC)| > 2 and false discovery rate (FDR) < 0.05, these DEGs including 226 upregulated DEGs and 19 downregulated DEGs. We further analyzed these DEGs by protein–protein interaction analysis and Gene Ontology enrichment analysis and identified 15 DEGs closely related to SARS-CoV-2 infection. Then, we constructed a 6-gene model (comprising IFIT3, OASL, USP18, XAF1, IFI27 and EPSTI1) by logistic regression analysis and calculated the area under the ROC curve (AUC) for the diagnosis of COVID-19. The risk score of SARS-CoV-2 infection was calculated by the following formula:
risk score = (−0.00318 × ExpressionIFIT3) + (0.01133 × ExpressionOASL) + (0.00015 × ExpressionUSP18) + (−0.02515 × ExpressionXAF1) + (0.00269 × ExpressionIFI27) + (0.05727 × ExpressionEPSTI1) − 0.66853. Therefore, for each patient, we obtained the expression level of these six genes and substituted these values into this formula to calculate the risk value. We then divided the patients into high- and low-risk groups according to the cutoff value 0.5. We found that patients in the high-risk group are more likely to have COVID-19 disease. The AUC values of the training group, testing group and entire group were 0.930, 0.914 and 0.921, respectively. The 6-gene model has a good predictive ability, and the predictive ability of the model was higher than that of individual genes. We also found the predictive ability was higher than some clinical indicators (CRP, ferritin, fibrinogen, D-dimer, lactate and procalcitonin) in the same dataset. The combined diagnostic model obtained by fitting the 6-gene model with ferritin and fibrinogen had a higher AUC value (0.976), indicating that the 6-gene model combined with ferritin and fibrinogen clinical indicators could better identify patients infected with SARS-CoV-2. In addition, the six genes were highly expressed in patients with COVID-19 and positively correlated with the expression of SARS-CoV-2 invasion-related genes (ACE2, TMPRSS2, CTSB and CTSL). The risk score calculated by this model was also positively correlated with the expression of TMPRSS2, CTSB and CTSL, indicating that the six genes were closely related to SARS-CoV-2 infection.

Conclusion We comprehensively analyzed the functions of DEGs in the blood leucocytes of patients with COVID-19 and constructed a 6-gene model that may contribute to the development of new diagnostic and therapeutic ideas for COVID-19. Moreover, these six genes may be therapeutic targets for COVID-19.

PU-0819

4 种方法对比研究 Xpert MTB/Rif 对结核分枝杆菌检测的临床应用价值

褶淑霞、尹卫国、周美芬、杨梦、刘艳枚、汤英贤
清远市人民医院

目的 综合评价 Xpert MTB/RIF 的检测性能及其临床应用价值，寻找结核分枝杆菌（mycobacterium tuberculosis，MTB）的联合检测方案，以更好指导临床结核病的诊断和治疗。
方法 收集清远市人民医院门诊、住院部或体检人群中，被临床诊断为结核病、疑似结核病、肺部感染、发热查因、不明感染、健康查体等患者的痰液、胸水、脑脊液等临床标本，采用抗酸染色、荧光定量 PCR（QPCR）、恒温芯片扩增法 及 Xpert MTB/RIF 4 种不同的检测方法，对同一标本进行检测，比较 4 种方法的阳性检出率。
结果 在 312 例待测标本中，抗酸染色的阳性检出率为 19.23%，QPCR 为 32.69%，恒温芯片法为 27.56%，Xpert MTB/RIF 为 38.14%，3 种分子检测技术与抗酸染色相比均有显著性差异（ P<0.001）。在抗酸染色阳性标本中，Xpert MTB/RIF 与 QPCR 的阳性检出率对比无统计学差异（P>0.05），与恒温芯片法对比有显著差异（P<0.001）。而在涂阴标本中，Xpert MTB/RIF 的阳性检出率为 24.6%，与 QPCR（18.25%）及恒温芯片法（13.49%）对比均有显著性差异（P<0.001）。
结论 Xpert MTB/RIF 对 MTB 的阳性检出率最高，QPCR 次之，恒温芯片法最低。XpertMTB/RIF 检测方法的操作简单，同时能检测利福平耐药，适用于对早期结核病的快速检测，也适用在基层医院推广应用。

PU-0820

Association of aldehyde dehydrogenase 2 gene polymorphism with myocardial infarction Running Title: Association of ALDH2 with MI

Lei Peng[1,2]、Liping Zhu[1]、Peng Zhou[1]、Shuxia Xuan[1]、Ying Luo[1]、Chen Chen[1]、Bin Chen[2]、Jinduan Lin[1]、Yanmei Liu[1]、Fengjun Tan[1]、Weiguo Yin[1]
1. The Sixth Affiliated Hospital of Guangzhou Medical University-Qingyuan People's hospital
2. 广州医科大学附属第六医院

Objective This study explored the correlation between myocardial infarction (MI) and the Glu504Lys polymorphism in the aldehyde dehydrogenase 2 (ALDH2) gene in the Qingyuan area.
Methods The Glu504Lys polymorphism of the ALDH2 gene was analyzed using the polymerase chain reaction and deoxyribonucleic acid microarray analysis for 468 patients diagnosed with MI for the first time and 132 healthy subjects.
Results There was a significant difference in the distribution of the ALDH2 genotype between the MI group and the control group (P = 0.0492), but there was no significant difference in allele frequency between the two groups (P = 0.1363). The clinical data showed that there were statistically significant differences (P < 0.05) in the two groups' gender and age distributions, rates of diabetes and hypertension, levels of alcohol and tobacco use, serological levels of heart markers, blood lipids and glucose. The subgroup analysis of ALDH2 genotypes found that alcohol consumption, high levels of myoglobin, and low levels of high-density lipoprotein cholesterol were significantly associated with a higher incidence of MI (P < 0.05). After adjusting for gender, hypertension, diabetes, and other related influencing factors, logistic regression analysis showed that the ALDH2 genotype GA/AA was an independent risk factor for MI (P < 0.05, OR = 1.479, 95% CI = 1.003–2.179).

Conclusion The presence of risk alleles with the genetic effect (ALDH2 genotype GA/AA) is an independent risk factor for MI.

PU-0821

新型冠状病毒肺炎痰标本 SARS-CoV-2 核酸阳性 3 例报道：对咽拭子检测假阴性问题的思考及建议

马良
长治医学院附属和平医院

由新型冠状病毒(SARS-CoV-2)引起的肺炎(COVID-19)目前疫情仍十分严峻。SARS-CoV-2 的核酸检测是 COVID-19 确诊的必要指标之一。临床对标本类型的选择影响 SARS-CoV-2 核酸检出率。本文报道 3 例 COVID-19 患者的确诊经过，分析采用咽拭子和痰标本检测 SARS-CoV-2 的效果，为临床诊断 COVID-19 时如何选择标本类型和如何提高核酸检出率提供参考。

PU-0822

MassARRAY 在非小细胞肺癌多基因位点检测中的应用

吴彭春、陈欣、李金莲、王淑华、刘敏
昆明金域医学检验所有限公司

目的 MassARRAY 系统是一款定制用于 DNA 分子精准检测的基质辅助激光解吸附电离-飞行时间(MALDI-TOF)质谱仪。本研究通过 MassARRAY 和 NGS（Next Generation Sequencing）在非小细胞肺癌 (non-small cell lung cancer ,NSCLC) 多基因位点检测的方法学比对，以评估 MassARRAY 是否可用于临床非小细胞肺癌多基因位点的检测。
方法 首先通过查阅肺癌相关文献以及中国肺癌人群的基因谱特征，选取 10 个与 NSCLC 发病机制、耐药及转移密切相关的靶向基因，即:BRAF、EGFR、KRAS、ERBB2、PIK3CA、ALK、RET、ROS1、NTRK1、MET，共 107 个突变位点。采用 Assay Design 设计引物 107 条，其中正向和反向扩增引物 107 对，延伸引物 107 条，建立检测方法。从昆明金域病理库中选取 2021 年 4 月至 12 月共 100 例确诊 NSCLC 患者送检的蜡块组织，通过使用 NGS 检测非小细胞肺癌相关基因进行比较和验证，并评估该方法的敏感性和特异性。
结果 基于 MassARRAY 技术的非小细胞肺癌相关 10 基因多重检测方法结果显示:100 例 NSCLC 中，总体突变阳性率为 58%，EGFR 突变阳性占比最多（41%），其次是 KRAS(9%),其余突变为 ALK（4%），ERBB2(2%)、MET(1%)和 BRAF(1%)，检测双基因和双位点共存突变有 EGFR/PIK3CA、EGFR/KRAS、KRAS/PIK3CA、ERFR18 外显子+19 外显子各 1 例。检测结果与 NGS 高度一致，该方法可以用于临床非小细胞肺癌多基因位点的检测。检测灵敏度和特异性分别为 100%和 96.8%。
结论 基于 MassARRAY 技术的多重检测方法较 NGS 实验操作简单，并节省了生信分析环节，可以应用于中国非小细胞肺癌患者多基因位点的检测。

PU-0823

DNA N6-Adenine methylation in Hepatocellular Carcinoma

Zhongling Zhuo[1]、Fei Xiao[2]
1. Beijing Hospital
2. The Key Laboratory of Geriatrics, Beijing Institute of Geriatrics, Beijing Hospital; National Center of Gerontology, National Health Commission

Objective DNA methylation on N6-adenine (6mA) has recently been found to be a potentially epigenetic mark in prokaryotes and several eukaryotes. However, its distribution patterns and potential functions in human tumorigenesis remain largely unknown. Here we reported global profiling of 6mA sites at single-nucleotide resolution in the genome of hepatocellular carcinoma using Nanopore sequencing.
Methods The DNA library was sequenced using the long-read sequencing on GridION. The mRNA was sequenced using next-generation sequencing on Illumina NextSeq. Tombo was used to identify 6mA positions in the human hepatocellular genome at single-base resolution. A variety of bioinformatics analysis **Methods** were used to analyze 6mA modification patterns.
Results 6mA was widely distributed throughout the human genome and was mainly distributed in introns and intergenic regions. The 6mA site was related to the pathway of porphyrin and chlorophyll metabolism in autosomes and was related to oxidative phosphorylation and ATP metabolism in mitochondria. The most prevalent motifs in tumors were mainly distributed in mitochondria, and AGG was the most significantly associated motif with 6mA modification. The density of 6mA was related to the activation of gene transcription.
Conclusion DNA 6mA modification was extensively present in the human hepatocellular genome, related to the activation of gene transcription, and could play a fundamental role as an epigenetic in hepatocellular carcinoma.

PU-0824

中国人群中 UGT1A1 基因型对伊立替康剂量限制性毒性反应的预测价值及疗效的关系

储楚
江苏省人民医院（南京医科大学第一附属医院）

目的 在精准医学分子学基础上探讨 UGT1A1* 6 和 UGT1A1* 28 基因多态性对伊立替康剂量限制性毒性反应的预测价值及疗效的关系，将遗传学信息、治疗两者结合，使疾病的诊治更具有针对性、安全性、靶向性和特异性。
方法 新鲜外周血中抽提 DNA，治疗前采用 PCR 毛细管电泳法分析 300 例中国肿瘤患者 UGT1A1* 6 和 UGT1A1* 28 的基因多态性，合理制定药物配伍及用药剂量。
结果 300 例中国肿瘤患者中, UGT1A1* 6 基因型为野生型(G/G)有 182 例(60.7%)，杂合突变型（G/A）与纯合子突变型（A/A）有 118 例(39.3%)；UGT1A1*28 基因启动子区 TA 序列呈 6 次重复的野生型（TA6/6）有 191 例(63.7%)，TA 序列杂合突变型(TA6/7) 与纯合子突变型（TA7/7）有 109 例(36.3%%)。剂量调整后完全缓解 1 例，部分缓解 53 例，疾病稳定 233 例，疾病进展 53 例；白细胞减少 87 例，中性粒细胞减少 57 例，腹痛腹泻 16 例。调整剂量后，腹痛腹泻及粒细胞减少等副反应发生率与传统治疗的差异具有统计学意义。
结论 在采用含伊立替康方案化疗恶性肿瘤患者中，伊立替康的剂量限制性毒性主要取决于患者个体的 UGT1A1 基因型，要提高伊立替康的临床疗效和安全性，降低其不良反应，重点在于治疗前对患者进行基因型检测，预测患者 UGT1A1 基因型，并合理制定药物配伍及用药剂量等，实现临床抗肿瘤药物的精准化治疗。

PU-0825

HPVE6/E7mRNA 检测对宫颈病变筛查的价值研究

孙佳莹
吉林金域医学检验所有限公司

目的 探讨 HPVE6/E7mRNA 对宫颈病变筛查的临床价值。
方法 选取 2020 年 1 月至 2020 年 10 月送检我公司的 TCT 结果异常的标本进行 HPVE6/E7 mRNA 检测，根据 TCT 检测结果将研究对象将标本分为未见上皮内细胞病变组（NILM）、非典型鳞状细胞组（ASC-US）、低度鳞状上皮内病变组（LSIL）、高度鳞状上皮内病变（HSIL）、鳞状细胞癌组（SCC）5 组。以 TCT 检测结果为金标准,并与组织病理学检测结果比较，计算 HPV E6/E7mRNA 检测方法的灵敏度、特异性及准确性并进行统计学分析，分析 HPVE6/E7 对宫颈病变患者的筛查价值。
结果 HPVE6/E7mRNA 检测提示 NILM 组阳性率为 25.40%,ASC-US 组提示阳性率是 57.89%,LSIL 组提示阳性率是 91.67%,HSIL 组提示阳性率是 100.00%,SCC 组提示阳性率是 100.00%,总阳性率是 42.78%;HPV E6/E7mRNA 的阳性率是 42.78%,灵敏度是 91.42%,特异性是 70.34%,准确性是 74.44%。
结论 HPVE6/E7 mRNA 检测在宫颈病变患者的筛查中，灵敏度、特异性、准确率都较高，对宫颈病变患者的筛查具有重大意义,可以通过 HPVE6/E7 阳性表达来判断宫颈病变严重程度,为临床提供参考依据进而采取相应治疗措施,制定相关预后方案。

PU-0826

宏基因组测序诊断非典型恙虫病 1 例

刘美芳、赵锐
南昌大学第一附属医院

目的 分析非典型恙虫病的临床特点，并探讨宏基因组测序对该病的诊断及应用价值。
方法 回顾性分析南昌大学第一附属医院收治的 1 例非典型恙虫病的临床表现、诊治过程。患者为 52 岁女性，出现连续发热伴寒战、头痛、肌肉酸痛等非特异性症状数十天，皮肤未见焦痂。多次予抗细菌、抗病毒药物治疗，效果不佳。入院后多次行常见病原微生物检测，均未找到致病菌。遂采集患者静脉血行宏基因组测序。
结果 宏基因组测序提示恙虫病东方体感染，检出 7 个序列数，覆盖率为 6%。予恙虫病特效药多西环素，辅以莫西沙星，每 12 小时 100 mg 剂量治疗。用药 24 小时后，患者体温恢复正常，全身症状改善。用药 3 天后患者出院。出院一周后回院复查，各项实验室指标均恢复正常，无并发症发生。
结论 恙虫病在我国南方地区的流行季节为 5～12 月，呈大单峰分布，以夏季型恙虫病为主。患者发病季节为三月，在我国南方地区十分罕见，又无典型焦痂，诊断极为困难，为非典型的恙虫病。而宏基因组测序是一种可用于帮助临床诊断疑难病例的准确快速的诊断方法，包括非典型恙虫病。

PU-0827

高分辨溶解曲线建立 SLCO1B1 和 ApoE 多态性检测的方法

陈欣、张宸源、李金莲
昆明金域医学检验所有限公司

目的 利用高分辨溶解曲线（HRM-PCR）建立一种较为简易灵敏的方法，对他汀类药物代谢相关基因位点 SLCO1B1 和 ApoE 进行检测，通过与实时荧光定量 PCR(RT-qPCR) 比较，以评估高分辨溶解曲线（HRM-PCR)是否可用于临床 SLCO1B1 和 ApoE 多态性检测。
方法 选取 2021 年 1 月至 4 月在诊断为高脂血症或动脉粥样硬化的患者送检昆明金域的 EDTA 抗凝全血共计 89 例，并提取标本基因组 DNA。分别采用 HRM-PCR 和 RT-qPCR 检测 SLCO1B 的 rs2306283(388A＞G) 和 rs4149056(521T＞C) 位点以及 ApoE 的 rs429358(388T＞C) 和 rs7412(526C＞T)位点，并利用 Kappa 系数比较结果的一致性。
结果 利用高分辨溶解曲线（HRM-PCR)可以直接判断 SLCO1B1 和 ApoE 上述基因位点，其检测结果与实时荧光定量 PCR(RT-qPCR) 结果完全一致。
结论 HRM-PCR 可应用于他汀类药物代谢相关基因 SLCO1B1 和 ApoE 多态性的检测，为临床他汀类药物个体化用药提供可靠评估。

PU-0828

白血病抑制因子通过调控支链氨基酸代谢促进胰腺癌增殖的机制研究

蒋文娜、任丽
天津医科大学肿瘤医院

目的 探讨胰腺癌星形细胞分泌的白血病抑制因子（LIF）对于胰腺癌细胞中支链氨基酸（BCAA）代谢的影响。
方法 回顾性收集天津医科大学肿瘤医院收治的 100 例胰腺癌组织标本对 LIF 进行免疫组化染色，分析 LIF 在胰腺癌组织中的表达水平与胰腺癌患者生存预后的相关性，收集血清标本，包括胰腺癌，健康对照组，利用 ELISA 实验验证 LIF 预测胰腺癌的价值，利用共培养技术，检测 PSC 通过分泌 LIF 对于胰腺癌生物学行为的影响，利用核磁及蛋白质谱技术，分析 LIF 对 BCAA 水平的影响及对于 BCAA 代谢酶的影响。
结果 胰腺癌患者均获得随访，胰腺癌组织中 LIF 的表达水平与胰腺癌的生存预后成负相关，血清中 LIF 表达含量在胰腺癌组明显高于正常对照组，并且可以作为预测胰腺癌的分子标记物，PSC 通过分泌 LIF 导致胰腺癌增殖，LIF 通过上调 BCKDK 导致 BCAA 代谢紊乱从而促进胰腺进展。
结论 LIF 是胰腺癌预后的独立风险因素，通过影响 BCKDK 的表达促进 BCAA 代谢紊乱.

PU-0829

LIF 在胰腺癌中作为预测淋巴结转移及远处转移的生物标志物的应用价值

蒋文娜[1]、任丽[2]
1. 天津医科大学肿瘤医院
2. 天津医科大学附属肿瘤医院

目的 本研究旨在探讨 LIF 分子在胰腺癌中与临床病理特征的关系及其表达水平对胰腺癌的诊断价值。
方法 采用免疫组化和 ELISA 法检测组织和血清中 LIF 水平。采用 Kaplan Meier 法分析总生存期(OS)和无复发生存期(RFS)，采用受试者工作特征曲线评价 LIF 的预测价值。
结果 胰腺癌组织中 LIF 水平与话患者的总生存期 OS 和无进展生存期 RFS 呈负相关。此外，LIF 蛋白是胰腺癌的独立预后因素。LIF 的组织或血清水平与淋巴结转移相关。根据受试者工作特征(ROC)曲线下面积(area under the receiver operating characteristic, ROC)，血清 LIF 在预测淋巴结转移和远处转移方面优于其他标记物(CA199 和 CEA)。
结论 LIF 的表达与胰腺癌的预后密切相关且为独立危险因素。该因子可用于诊断淋巴结和远处转移的胰腺癌患者。

PU-0830

新冠病毒检测方法学发展与比较

夏海丹
沈阳金域医学检验所有限公司

目的 评价新冠病毒检测方法的进展以及在感染诊断中的应用。
方法 回顾性评价现有用于新冠病毒的检测手段。
结果 1.荧光 PCR 法
PCR 法指的是聚合酶链式反应，能将微量的 DNA 大幅增加。用于检测新冠病毒时，由于新冠病毒是 RNA 病毒，需要先将病毒 RNA 逆转录为 DNA，再进行 PCR 检测。这是目前新冠病毒核酸检测最常用的方法。
2.联合探针锚定聚合测序法
这种检测主要是用专门的仪器检测测序载片上 DNA 纳米球携带的基因序列。这种检测的灵敏度高，不容易漏诊，但结果也容易受多种因素的影响而不准。
3.恒温扩增芯片法
和 PCR 相比，基因芯片准确率高，时间更短，但价格也更为昂贵、检测通量（单位时间内所能产生的数据量）相对更低。
4.病毒抗体检测
抗体检测试剂是检测血清中由病毒进入人体后刺激人体产生的 IgM 或 IgG 抗体，IgM 抗体出现较早，IgG 抗体出现较晚。目前已获批的 5 个新冠病毒抗体检测试剂，分别采用的是胶体金法和磁微粒化学发光法。
胶体金法是用胶体金试纸进行检测，也就是目前常说的快速检测试纸。这种检查一般在 10~15 分钟左右，就可以得出检测结果。这种检测方法很方便，出结果的速度也很快。但主要的不足在于，检测通量较低，有一定的误判率（主要是受抗体质量影响）。而且，胶体金法检测的新冠病毒抗体是 IgM 抗体。IgM 产生的时间要晚于病毒复制的时间，所以检测的时间窗口比核酸检测窄。

磁微粒化学发光法是在化学发光检测的基础上，加用了磁性纳米粒子，使检测具有了更高的灵敏度和更快的检测速度。不过，磁微粒化学发光法选择性差，会对一个系列的化合物做出反应，而非特定的某一化合物，因此，准确性上相对不够好。而且，环境对检测的影响比较大，容易导致误差。
结论 目前推荐用来确诊新冠感染的只有核酸检测，对于新冠病毒核酸检测阴性的疑似病例，可以采用抗体检测作为补充检测指标。

PU-0831

杭州地区乙肝患者核苷类似物耐药位点分析

许生样
杭州迪安医学检验中心有限公司

目的 检测杭州地区乙型肝炎患者体内 HBV 逆转录酶基因的耐药突变情况，为临床制定合理的治疗方案提供依据。
方法 通过聚合酶链反应（PCR）及 DNA 测序将 2020 年 1 月至 9 月送检杭州迪安医学检验中心的 746 例乙型肝炎患者进行 HBV 耐药突变位点和基因耐药情况检测，并对结果进行统计分析。
结果 在 746 例血清标本中有耐药突变位点产生的有 324 例，检出率是 43.43%（324/746），其中 M204I、L180M+M204V、L180M+S202G/C+M204V 和 L180M+T184L/A/F+M204V 检出率较高，分别占总数的 16.36%（53/324）、16.67%（54/324）、13.89%（45/324）和 11.11%（36/324）。患者对 L-dT、LMV、FTC、ETV、ADV、TDF 耐药比例分别是 95.37%（309/324）、87.04%（282/324）、87.04%（282/324）、38.27%（124/324）、31.17%（101/324）、0.31%（1/324）。单药耐药比例为 4.63%（15/324），多药耐药比例为 95.37%（309/324）。发生耐药突变与患者的性别无关（P＞0.05）。
结论 在杭州地区乙肝患者中，常见的突变模式为 M204I、L180M+M204V、L180M+S202G/C+M204V 和 L180M+T184L/A/F+M204V；耐药情况主要以多药耐药为主。

PU-0832

IMPA2 plays a novel role in AIFM2-mediated mitochondrial apoptosis pathway and enhances paclitaxel resistance in cervical cancer

Min Wang、bingqi wang、sheng yin、lei liu
The Second Xiangya Hospital, Central South University

Background Cervical cancer continues to be concerned and chemoresistance of tumors often lead to treatment failure, which underscores pivotal needs to find novel therapeutic targets. Previously, we firstly identified IMPA2 as a potential oncogene and verified its tumor-promoting role in vitro and in vivo. In this study, we aimed to elucidate the underlying mechanisms of IMPA2 in regulation of tumor apoptosis and to evaluate whether IMPA2 inhibition attenuates chemoresistance to chemotherapy drugs by regulating apoptosis.
Methods Cell apoptosis was assessed by apoptosis-related proteins detecting, flow cytometry, immunofluorescence and immunohistochemical staining. Morphological changes of mitochondria were observed through transmission electron microscopy (TEM) and function changes were evaluated by measurements of mitochondrial membrane potential, intracellular Ca2+ levels and release of Cyto c. Fluorescence microscope was used to analyze ROS generation. The expression of AIFM2 was determined by qRT-PCR, western blot and immunohistochemical staining analysis. Determination of IC50s were calculated according to cell viability detected by CCK-8.

Results Apoptosis of cervical cancer cells was markedly promoted when silencing IMPA2, and IMPA2 knockdown-induced apoptosis was proved to be mitochondria-dependent along with generation of reactive oxygen species (ROS). Also, antioxidant (NAC) treatment successfully rescued IMPA2 deficiency-induced apoptosis. After inhibiting IMPA2 expression, AIFM2 was significantly up-regulated both in mRNA and protein levels, and inhibition of AIFM2 could reserve IMPA2 knockdown-induced apoptosis in a mitochondrial dependent manner. Further mechanistic study revealed that IMPA2 silencing apparently activated p53 and treatment of p53 inhibitor (Pifithrin α) could rescue IMPA2 knockdown-induced cell apoptosis. More importantly, IMPA2 inhibition was shown to increase chemosensitivity to paclitaxel (PTX) by enhancing PTX-induced cell apoptosis.
Conclusion Our findings demonstrated a novel function of IMPA2 in regulating mitochondrial metabolism and apoptosis within cervical cancer cells and inhibitory of IMPA2 greatly improved chemosensitivity to PTX, potentially making it a novel therapeutic target for cervical cancer treatment.

PU-0833

Longitudinal assessment of the bkv-miR-B1-3p in blood and urine concentration for kidney transplant recipients with BK polyomavirus replication-a retrospective study.

Sheng Yin、wang min
The Second Xiangya Hospital of Central South University

Objective In kidney transplant recipients (KTRs), BK polyomavirus (BKV) replication may progress to polyomavirus-associated nephropathy (PVAN). BK polyomaviruses encoded microRNA can better reflect the replication of virus. Here, we studied whether microRNA in urine can become a promising diagnostic indicator.
Method In this retrospective study, we assessed the BKV DNA and bkv-miR-B1-3p in urine and blood samples consecutively acquired from 276 KTRs who displayed different stages of BKV replication and eventually developed PVAN. Besides, we analyzed renal function and blood drug concentration.
Results In all specimens tested for BKV DNA, 36.8% of them were positive for urine and 23.4% were positive for blood. BKV DNA positive mainly occurred in renal transplantat recipients who had taken immunosuppressive agents, and FK506 based therapeutic scheme was significantly increased the positive rate. Correlation analysis showed that the BKV DNA in the blood was related to it in the urine ($r=0.6065$, $P<0.0001$). Urine BKV DNA analysis had a higher sensitivity (92%), while blood BKV DNA method had a higher specificity (85.7%). The bkv-miR-B1-3p results have a good correlation with DNA loads, and might be a better detection performance for BKV infection.
Conclusions Immunosuppressant should be adjusted or replaced when BKV DNA was detected in the blood or urine. MicroRNA detection method showed a good diagnostic efficiency in laboratory detection of BKV replication.

PU-0834

新型冠状病毒患者检验指标的变化及其临床意义

陈升辉
沈阳金域医学检验所有限公司

目的 研究探讨新型冠状病毒感染者（COVID-19）外周血中各项检验指标对于临床的意义。

方法 通过收集 2019 新冠爆发至今的新冠相关检验指标变化相关文献，将搜索到的文献进行归纳整理，得出本文。
结果 新型冠状病毒具有爆发快，易传染，起病急等特点，严重危害人们的健康，COVID-19 根据临床表现可分为普通型、重型、危重型，普通型患者外周血白细胞计数、淋巴细胞百分比、C 反应蛋白（CRP）均升高，且有性别差异，女性患者较男性患者升高幅度高。重症，危重症患者可出现淋巴细胞百分比降低现象，危重症甚至出现大量减低，提示预后不良。对比流感引发的肺炎，新冠相关肺炎肝肾功能指标也均有不同程度的升高。血清中抗体表达水平与疾病转归密切相关，IgM 类抗体可出现于疾病窗口期（即核酸检测阴性但有相关症状），可将抗体检测与核酸检测联合作为疑似患者的筛查手段，有效降低漏诊。疾病早期抗体含量常常与疾病预后成正比，检测抗体含量联合影像学手段可有效判断疾病进程。疾病中晚期 IgG 类抗体水平升高，核酸复制量明显减低，应用 IgG 类抗体检测，可有效防止疾病后期核酸报告“假阴性”。有文章指出，新冠患者血液冻存样本较新鲜样本相比，抗体效力明显下降，因此疑似患者的样本应尽量避免冻存。
结论 本文分析了目前新型冠状病毒患者血中检验指标对于疾病的分期、进程、转归方面的意义，意在更好的服务临床，助力人类早日战胜病魔。

PU-0835

人乳头瘤病毒分型在临床上对女性宫颈癌筛查的诊断价值

李丽兵
沈阳金域医学检验所有限公司

目的 用于女性宫颈癌的筛查
方法 人乳头瘤病毒（Human Papillomavirus，HPV）是一种小的 DNA 双链病毒。目前已经发现的 100 多个基因型中近 40 种能入侵人生殖器官，其中 16、18、31、33、35 及 58 型等高危型的感染是女性宫颈癌的主要病因。而 6、11 等低危型是引起常见性病湿疣的主要病因。本试剂盒是应用 PCR 体外扩增和 DNA 反向点杂交相结合的 DNA 芯片技术，利用 HPV 基因特点设计特异引物，可以扩增出包含 23 种 HPV 基因型的目标片段，再将扩增产物与固定在膜条上的包括 17 种高危型和 6 种低危型的分型探针进行杂交，依据杂交信号的有无来判断是否有这些 HPV 基因型的存在。
结果 根据膜条上显色位点判读相应的 HPV 基因型。可检测 17 种高危型（HPV16，18，31，33，35，39，45，51，52，53，56，58，59，66，68，73，82）和 6 种低危型（6，11，42，43，81 和 83
结论 HPV 有多种基因型，不同基因型的 HPV 感染可导致不同临床病变，HPV 的分型检测可以将 HPV 病毒分为高危型和低危型，高危型 HPV 感染与宫颈癌、癌前病变相关，低危型主要与轻度鳞状上皮内病变和泌尿生殖系统庞、复发性呼吸道息肉相关。高危型 HPV 感染的检测，对于预防和早期发现子宫颈癌及癌前病变有非常重要的意义。

PU-0836

探讨人乳头瘤病毒检测对宫颈癌的诊断意义

刘璐
沈阳金域医学检验所有限公司

目的 探讨人乳头瘤病毒检测在宫颈癌筛查中的临床应用价值，能够让大家更加详细的了解人乳头瘤病毒，能更有效的预防和治疗宫颈癌。
方法 人乳头病毒（简称 HPV）是一种嗜上皮性病毒，有高度的特异性，HPV 病毒的感染可引起人类良性的肿瘤和疣，若该病毒生长在生殖器官附近皮肤和黏膜上会导致尖锐湿疣以及生长在黏膜上的乳头状瘤。HPV 病毒有 130 多种基因型，分高危型和低危型。其中，高危型如 16、18、30、31、

33、35、39、45、51、52、56、58、59、66、68 等与癌及癌前病变相关，低危型主要与轻度鳞状上皮损伤与泌尿生殖系统疣等相关。目前 HPV 病毒检测方法临床主要应用定性和定量两种。我们常用的是反向杂交法，16、18 型是感染 HPV 最危险型别。连续两次（间隔 6-12 个月）检 HPV 为阳性，即可视为持续感染；30 岁以上妇女 1 次 HPV 结果阳性，即可视为高危人群。
结果 若发现 HPV 病毒检测结果阳性不要害怕，大部分妇女感染 HPV 病毒后，在 9-16 个月会被自身免疫力清除，在病毒清除后 3-4 个月时间内转为正常。定期复查就好。从感染 HPV 到发展为宫颈癌需要 9-25 年时间，持续 HPV 感染是子宫颈癌发生的必备条件。
结论 通过对 HPV 病毒检测的了解，明确了 HPV 病毒检测对宫颈癌的筛查和诊断有重要意义。及早的发现病毒感染，做到早检测、早治疗；预防宫颈癌的发生。

PU-0837

阴道菌群与 HPV 感染的相关性

张静
沈阳金域医学检验所有限公司

目的 通过 HPV 分型检测和阴道微生态检查，探讨阴道菌群和 HPV 感染的相关性。
方法 收集患者宫颈分泌物标本和阴道拭子—500 份，采用 PCR—反向点杂交法进行 HPV 基因亚型检测，使用涂片镜检法对阴道菌群进行观察。
结果 通过检测得出，HPV 检测阴性 325 例（65%），主要阴道菌群为乳酸杆菌，偶见加德纳菌；HPV 检测阳性 175 例(35%)，阴道菌群中加德纳菌的检出率为 78%，且为优势菌种，并可见加氏乳酸杆菌等其他菌种。而且，HPV 阳性组的阴道加德纳菌和加氏乳酸杆菌检出率也高于 HPV 阴性组。
结论 由此可见，HPV 感染会造成阴道优势菌群改变，与 HPV 阴性组相比，HPV 阳性组菌群的多样性和组成更为复杂。阴道微生态失衡可能作为 HPV 感染的协同因素，对疾病确诊提供佐证。

PU-0838

对新型冠状病毒核酸检测结果影响因素的探讨

张鑫宇
沈阳金域医学检验所有限公司

目的 2019 年末快速爆发的由新型冠状病毒（SARS-Cov-2）引发的新型冠状病毒肺炎（COVID-19），简称“新冠肺炎”，蔓延至上百个地区，甚至国家。其诊断需要结合临床表现，肺炎影像学，血清学等多方面结果，其中核酸检测阳性或基因测序高度同源是确诊的金标准，核酸检测简便快捷，成本较低，是确诊最主要方法。但核酸检测结果受影响因素颇多，检测结果与临床诊断有差异等问题也引起重视，也是检验人员持续关注并需要解决的问题。本文主要探讨不同标本类型、不同检测试剂、不同提取方法等各方面因素，对新型冠状病毒核酸检测结果的影响。
方法 通过查询新冠肺炎相关文献，结合沈阳金域医学检验所有限公司基因实验室核酸检测的经验，从分析前、分析中、分析后多个方面详细探讨，在便于操作的环节，基于某一影响因素为变量，控制其他因素为定量的方法检测，进行实验后分析。
结果 新型冠状病毒核酸检测受多方面因素的影响：
1. 分析前：1.1 样本采集部位及方法
标本采集部位：鼻咽拭子阳性率最低，其中鼻拭子标本阳性率高于咽拭子，痰标本其次，鼻咽拭子联合痰标本检测阳性率最高；1.2 样本运输及保存；1.3 核酸检测相关设备及试剂；1.4 人员培训；
2.分析中：2.1 提取方法、相关试剂、操作
各厂家试剂盒检测结果差异明显，对比 ORF-lab 基因的 Ct 值及△Rn 可分析出差异明显；2.2 扩增

3.分析后：3.1 结果分析；3.2 环境、物表消杀
结论 在这场战“疫”中，检验人的高效与准确有着至关重要的作用，对于新冠病毒核酸检测的结果的控制，是要综合考量的，相对于其他因素，分析前尤为重要，随着检测的不断完善，检测结果的准确性、稳定性一定会有大幅度提升，进一步对症治疗，控制疫情。

PU-0839

探讨新型冠状病毒检测结果的影响因素

刘爽
沈阳金域医学检验所有限公司

目的 新型冠状病毒肺炎疫情已全球蔓延，在如此严峻的环境下如何对新型冠状病毒检测结果质量保证。
方法 本文详细介绍了不同试剂新型冠状病毒的检测方法，包括抗体检测、核酸检测、抗原检测等
结果 分析了新型冠状病毒核酸检测及特异性抗体检测产生假阳性和假阴性的原因，导致假阴性的原因主要为分析前标本采集、运输和保存，分析中试剂质量和病情进展、用药、内源性和外源性干扰物质等因素；导致假阳性的原因主要为分析中交叉污染、消毒不彻底，标本不合格，操作不规范和方法学缺陷等因素；
结论 新型冠状病毒肺炎传染性极强，人群普遍易感，严重危害了人民健康。本文结合卫健委相关规范性文件和本实验室防控程序，探讨采集人员及检验人员如何规范操作，制定有效的防护措施并通过对三者联合检测结果的分析，建立完备的质量保证方案，为患者的每一份期待的心得到可靠的质量保证。

PU-0840

探究乙肝病毒含量肝脏损伤之间的关系

孔祥峰
沈阳金域医学检验所有限公司

目的 比较 HBV-DNA 含量与该患者肝脏功能损伤程度是否存在某一数量关系，探究 HBV-DNA 含量与携带者传染能力是否具有某种比例关系。
方法 采用回顾性分析方法，在沈阳金域医学检验所有限公司 2019 年 12 月至 2020 年 12 月的乙肝定量样本中抽取 600 人进行数据记录统计分析。并制成二乘二列联表进行独立性检验探究关系。将 600 人按照个体属性分类，设 A 为乙肝相关个体，A1、A2 分别为阳性和阴性；设 B 为肝脏病变相关个体，B1、B2 分别为有明显病变与无明显病变。
结果 由联表得：147、143、155、155 皆大于 5，且 K^2=600（147*155-143*155）²/（147+155）（147+143）（143+155）（155+155）≈0.0212，K^2远远小于 0.45。
结论 经查表可得 0.0212＜0.14，即成立概率小于 1-0.50=0.50，故可认为乙肝病毒含量肝脏损伤之间并无数量关系。

PU-0841

HPV 分型实验杂交仪封盖膜材料探究

霍颖
沈阳金域医学检验所有限公司

目的 杂交决定实验成功与否，材料的不同，对实验有不同影响，合适的材料是至关重要的。

方法 从稳定性的角度出发，探究各种材料对实验的影响情况。

结果 主要从一下几个角度挑选材料①耐热能力、②密封能力、③介电性、④耐臭氧性。大多数固体材料热稳定性较强，然而质地较硬，气密性不好，无法贴合杂交盒形成想多隔离的空间，金属材料更是良导体，硅胶具耐热性、耐寒性、介电性、耐臭氧性等优点。因此硅胶材质最适合用于此实验。

结论 由于材料的种类复杂，也可能由于新材料的诞生而有所改变，随着科技的发展，对材料的研究，更多新型材料的研究，为实验室提供更好的实验条件。

PU-0842

探究人乳头瘤病毒 HPV 分型检测与液基细胞 TCT 检测结果结合分析的意义

尚鑫辉
沈阳金域医学检验所有限公司

目的 探讨 HPV 分型检测结果与液基细胞 TCT 检测结果相结合对宫颈癌及癌前病变早期筛查的临床应用价值。

方法 选取 100 例不同地区不同医院在本公司检测 HPV 分型和液基 TCT 的筛查者，将他们的检测结果结合。HPV 结果 16 型作为高危阳性参考,TCT 高度病变作为阳性参考。

结果 100 例筛查标本中有 76 例为阴性，15 例为低危阳性（不作为参考）1 例因细胞量不足结果不在记录范围内。2 例 TCT 结果高病变但 HPV 分型结果阴性。1 例 TCT 结果低度病变 HPV 分型结果 16 型。其余 5 例 TCT 结果高度病变且 HPV 结果均存在 16 型

结论 液基细胞 TCT 检测结果与 HPV 分型结果二者从一定程度上可以相互印证对方结果的准确性。因为采样时机和方法所以对于有些样本的结果存在影响导致实验结果不准确的可重新实验。二者的实验结果在一定程度上相吻合，所以对于临床上判断宫颈癌以及宫颈癌前病变的筛查提供了有力证明。

PU-0843

新型冠状病毒人源性和非人源性试剂适用性初步分析

周文婧
沈阳金域医学检验所有限公司

目的 本研究目的在于评估人源性和非人源性检测试剂，检测不同类型样本和的适用分析

方法 收集 10 例已知阴性结果样本，5 例物表样本包括（食品表面，环境表面），5 例送检筛查患者样本，样本正常提取后，10 例验证样本，3 份生理盐水阴性对照，1 份弱阳性质控品，共 14 人份分别用人源性试剂和非人源性试剂两种试剂同时扩增。

结果 人源性试剂 5 例送检筛查患者样本 VIC 内标曲线正常，5 例物表样本，3 份生理盐水阴性对照无扩增曲线，弱阳性质控品质控曲线正常；非人源性试剂 10 例样本，3 份生理盐水阴性对照 VIC 内标曲线正常，弱阳性质控品质控曲线正常。

结论 人源性和非人源性检测试剂对于验证样本检测符合性一致。非人源性试剂对物表样本及生理盐水阴性对照样本无法进行有效区分，在检测样本时非人源性试剂可能会出现样本漏检无法检测的情况，人源性试剂可以通过比对 VIC 内标曲线区分物表和送检筛查患者样本，适用临床不同筛查样本的区分。

PU-0844

脂血和溶血样本对 HBV-DNA 定量实验结果的影响

祝蕊
沈阳金域医学检验所有限公司

目的 分析在日常实验中脂血、溶血对于实时荧光定量 PCR 检测乙型肝炎病毒定量项目的结果影响
方法 分组实验观察脂血标本的制备：在分析脂血对 HBV-DNA 定量实验结果的影响时，将几份不同患者的脂血样本混合后，进行分别处理。分为未作任何处理和做高速离心处理，高速离心后样本分离脂质层和血清层后，弃去脂质层，吸取下层血清加入。观察对比同样本在脂血状态下和高速离心后吸取上清进行实验后实验结果的差异。溶血样本的制备：采集 10 份乙型肝炎病毒的血液标本，混合离心后吸取血清，作为无红细胞样本；同样的样本与部分红细胞混合后，适当混匀，作为溶血样本。观察对比样本在两种状态下进行实验后实验结果的差异。HBV-DNA 定量实验的实验操作、反应体系、扩增条件严格按照试剂盒所写进行。
结果 将扩增后的结果转为数值进行分析，可得出结论脂血样本与离心后样本结果无明显差异；溶血样本与空白对照样本结果相比偏低。

PU-0845

人乳头瘤病毒感染和液基薄层细胞检测的关系

张静
沈阳金域医学检验所有限公司

目的 旨在通过数据分析，以液基薄层细胞学（TCT）为参考，提高人乳头瘤病毒（HPV）分型结果的准确性。
方法 本研究选取 2400 例样本，通过 PCR-反向点杂交技术检测 HPV 亚型，同时进行 TCT 检查。
结果 2400 例样本，根据 TBS 分组，HSIL 共 56 例（2.33%），HPV 感染率为 89.3%；LSIL 组共 126 例（5.25%）HPV 感染率为 77.8%；ASC 组共 245 例（10.21%），HPV 感染率为 59.2%。
结论 TCT 阳性患者 HPV 检出率明显高于 TCT 阴性患者，联合 TCT 检测，能更好的提高 HPV 分型检测结果的准确性。

PU-0846

HPV 分型阳性结果亚型分布情况的统计

张佳蓉
沈阳金域医学检验所有限公司

目的 总结近一月内女性 HPV 检测阳性基因亚型分布情况，为本地区 HPV 防治提供参考数据。
方法 所有 HPV 检测通过全自动核酸提取仪采用磁珠法提取核酸，使用 PCR 方法进行扩增，再进行反向点杂交，采用基因芯片法进行基因分型检测；通过公司系统收集 2021 年 3 月-2021 年 4 月本公司检测人群 HPV 分型检测结果，运用 spss 和 Excle 软件进行统计学分析。
结果 2021 年 2 月-2021 年 3 月 HPV 试剂盒所提供的 23 个型均有检出，其中 HPV52、HPV16、HPV53、HPV81、HPV51 型阳性检出率在近一月中占据阳性型别的前五位，阳性率分别为 14.72%、11.99%、9.45%、7.26%、6.07%。、

结论 本统计结果显示近一月 HPV 阳性型别前五位的主要为 HPV52、HPV16、HPV53、HPV81、HPV51，其中 81 型为低危型，其余均为高危型别，说明本地区 HPV 防治应着重注意 HPV 高危型别。

PU-0847

低水平乙型肝炎病毒 DNA（HBV-DNA）载量的临床意义

董艳、周文婧、刘璐、刘爽
沈阳金域医学检验所有限公司

目的 乙型肝炎病毒（Hepatitis B virus ）是引起乙型肝炎（简称乙肝）的病原体，乙型肝炎病毒 DNA（HBV-DNA）载量是判断乙肝病毒感染最直接、特异性强和灵敏性高的指标，HBV-DNA 阳性，提示 HBV 复制和有传染性，HBV-DNA 越高表示病毒复制越多，传染性越强。乙肝病毒的持续复制是乙肝致病的根本原因，HBV 的治疗主要是进行抗病毒治疗，根本目的是抑制病毒复制，促使乙型肝炎病毒 DNA 的转阴。在乙肝诊断领域，国内外最新的乙型肝炎防治指南提到，推荐使用最低检测下限可以达到 20IU/mL 的高灵敏检测方法检测乙型肝炎病毒 DNA（HBV-DNA），以帮助找到更多低病毒血症的患者，指导临床用药，进一步减少肝癌的发生。
方法 采用回顾性分析方法，2020 年 9 月-2021 年 3 月，全自动核酸提取纯化仪（Abbott m2000 sp)/实时荧光定量 PCR 仪（Abbott m2000rt)共检测 3282 例临床标本，根据阴性，临界值，低值，中值和高值分别进行统计。
结果 阴性占 42.07%，临界值占 37.91%，低值占 9.96%，中值占 5.13%，高值占 4.93%。阴性和临界值占比相对较高，确诊 HBV 和评估 HBV 治疗效果时更多选择高灵敏检测方法。高值占比相对比较低，选择其他检测方法。
结论 使用高灵敏检测方法检测 HBV-DNA 对确诊 HBV 和评估 HBV 治疗效果具有十分重要的作用，可了解机体内病毒的数量、复制水平、传染性、药物治疗效果、制定治疗策略等并作为评估指标，也是唯一能帮助确诊隐匿性 HBV 感染和隐匿性慢性 HBV 的实验室检测指标。

PU-0848

基于无效循环反应实现 hNQO1 检测和药物筛选的电致化学发光传感

郑永军[4]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学附属中大医院临床检验医学中心
3. 江苏省重症医学重点实验室，东南大学
4. 东南大学医学院

目的 hNQO1（醌氧化还原酶）是一种参与体内解毒和激活抗肿瘤药物的双电子还原酶，其作为一种潜在肿瘤标志物和药物靶点受到了广泛的关注。近年来，hNQO1 检测取得了极大进展，其检测机制都依赖于 hNQO1 还原激活通过酯键连接的醌修饰的探针底物。然而，大多数基于这种策略的 hNQO1 传感缺乏足够的稳定性，对于提高 hNQO1 检测体系的灵敏性仍然具有十分巨大的挑战。在此，我们首次构建了基于检测 hNQO1 代谢天然底物的产物的电致化学发光（ECL）传感，用于 hNQO1 的高灵敏检测以及相关药物活性的筛选。
方法 我们以三维泡沫镍负载鲁米诺（信号分子）作为工作电极，Ag/AgCl 作为参比，铂丝作为对电极构建了三电极体系。当 NQO1 与底物作用时，产生大量的活性氧分子，在电激活下活性氧可以引起鲁米诺的 ECL 信号变化。该变化可以直接反应酶活性变化。此外，不同底物与酶反应时，产

生的活性氧含量有显著差别，该差别可以直接反映底物的抗肿瘤活性，因此该体系也可以用于药物筛选。

结果和结论 归功于 hNQO1 代谢机制固有的循环放大效应和全新构建的鲁米诺修饰的多孔泡沫镍工作电极，该 ECL 传感器表现出创纪录的 hNQO1 的检测限（10 ng / mL）和信噪比（～460）。另外，利用同样的传感机制，该传感器成功地实现了 hNQO1 相关的抗肿瘤药物的快速筛选。这项全新的 hNQO1 传感策略将引导 ECL 作为一种极具潜力的兼具肿瘤诊断和药物筛选功能的高效肿瘤管理工具。

PU-0849

SORBS1 基因甲基化在 Hcy 诱导人脐静脉内皮细胞氧化应激中的作用

梁雅茹
清远市人民医院

目的 探讨 SORBS1 基因甲基化在同型半胱氨酸(Hcy)诱导人脐静脉内皮细胞(HUVEC)氧化应激中的作用.

方法 将培养冻存的人脐静脉内皮细胞(HUVEC)复苏培养至第三代,分成四组:(1)Hcy 组;(2)叶酸组;(3)叶酸+VitB12 组;(4)空白对照组.用基因芯片法筛选出具有差异的甲基化位点 SORBS1.siRNA 转染 HUVEC,检测转染后三组(SORBS1-siRNA 组,NC-siRNA 组和空白对照组)HUVEC 的 SORBS1、丙二醛(MDA)和超氧化物歧化酶 2(SOD2)的表达水平.

结果 与空白对照组相比,Hcy 组 SORBS1 甲基化水平升高(P<0.05);与 Hcy 组比较,叶酸组、叶酸+vitB12 组 SORBS1 甲基化水平均降低(P<0.05).与 NC-siRNA 组和空白对照组相比,SORBS1-siRNA 组 SORBS1 和 SOD2 表达水平均下降(P<0.05),MDA 含量升高(P<0.05).

结论 Hcy 可通过调节 SORBS1 基因的甲基化水平诱导人脐静脉内皮细胞的氧化应激,为 Hcy 导致 HUVEC 氧化应激的分子机制提供了新思路.

PU-0850

Circular RNA hsa_circ_0089172 Regulates T Helper 17 Cells Response in Patients with Rheumatoid Arthritis

Huiyong Peng、Yingzhao Liu、Shengjun Wang
The Affiliated People's Hospital of Jiangsu University

Circular RNAs (circRNAs) are important transcriptional regulators of gene expression that participate in the pathogenesis of human diseases. Mechanistically, circRNAs, as competitive endogenous RNAs (ceRNAs), can sponge microRNAs (miRNAs) with miRNA response elements (MREs). Previous study has identified hsa_circ_0089172 is abnormally expressed in Hashimoto's thyroiditis and may regulate miR-125a-3p expression. However, the role of hsa_circ_0089172 in Rheumatoid arthritis (RA) remains unclear. A total of 28 RA patients and 28 healthy controls were enrolled in this study. We found that hsa_circ_0089172 was an abundant and stable circRNA in the RA patients and could potentially differentiate the RA patients from the healthy subjects. Additionally, the elevated levels of IL-23R, one of the miR-125a-3p target genes, had positive correlation with hsa_circ_0089172 expression. Knockdown of hsa_circ_0089172 resulted in the reduction of IL-23R+ cells. The proportion of circulating Th17 cells and the transcript levels of IL-17A were increased in the RA patients, which were both positively correlated with IL-23R expression. Moreover, positively correlations between the transcript levels of hsa_circ_0089172 and the percentage of Th17 cells and the transcript levels of IL-17A were indicated in the RA

patients. Down-regulation of hsa_circ_0089172 decreased the proportion of Th17 cells and the transcript levels of IL-17A in human CD4+T cells. Furthermore, hsa_circ_0089172 functioned as a ceRNA for miR-125a-3p in the RA patients. Taken together, our results indicate that the elevated levels of hsa_circ_0089172 contribute to Th17 cells response in the RA patients.

PU-0851

Androgen Receptor is a prognostic biomarker and correlated with clinical pathologic features and immune infiltrates in gastric cancer

nan xia
The first hospital affiliated to China medical university

Backgroud Androgen Receptor (AR) is a critical gene in different human malignancies. However, the correlation of AR to prognosis and immune-infiltrating lymphocytes in different cancers remain unclear.
Methods AR expression was analyzed via the Oncomine database and Tumor Immune Estimate Resource (TIMER) site. We evalueted the influence of AR on clinical prognosis using Kaplan-Meier plotter, the PrognoScan database and Gene Expression Profiling Interactive Analysis(GEPIA). The correlations between AR expression and gene marker sets of immune infiltrates were analyzed by TIMER and GEPIA.
Results High AR expression was associated with poorer overall survival(OS), disease-specific survival(DSS), and disease-free survival(DFS). In addition, AR expression was positvely correlated with inflilltrating levels of CD4+ T and CD8+ Tcells, macrophages, neutrophils, and dendritic cells(DCs) in gastric cancer. AR expression showed strong correlations with diverse immune marker sets in GC.
Conclusion These findings suggest that AR is correlated with prognosis and immune infiltrating level in gastric cancer patients.

PU-0852

The CYP3A5 and ABCB1 gene polymorphisms in kidney transplant patients and establishment of initial daily tacrolimus dosing formula

Yuting He、YiXiao Ma、Qian Fu、Jianbo Liang、Xuegao Yu、Bin Huang
The First Affiliated Hospital, Sun Yat-sen University

Objective To detect the gene polymorphisms of CYP3A5 and ABCB1 of the patients after kidney transplantation at the First Affiliated Hospital of Sun Yat-sen University and establish the initial daily dose formula of tacrolimus based on the clinical information, genotypes of CYP3A5 and ABCB1, and laboratory test results of patients, providing tacrolimus personalized medication for kidney transplant patients.
Methods The patients who underwent a triple immunosuppressive regimen of tacrolimus, mycophenolate mofetil and prednisone after kidney transplantation at the First Affiliated Hospital of Sun Yat-sen University from May 2016 to May 2018 were selected as the research subjects. The enrolled patients were divided into two cohort according to the admission time. One cohort was used to establish the tacrolimus dosage formula, and the other was used to evaluate the feasibility of tacrolimus dosage formula formed previously. PCR-SSP and PCR-RFLP were used to detect the genotypes of CYP3A5 and ABCB1. Meanwhile, blood cell, PCT, CRP and tacrolimus blood concentration were also analyzed. The height, weight, age, gender, type of

transplantation, blood pressure and infection status of the patients were recorded. The effect of each index on tacrolimus dose were analyzed and multiple linear regression analysis were used to establish the initial dose formula of tacrolimus in kidney transplant patients. Then the formula was evaluated by comparing the estimated dose from the formula with the actual clinical dose.
Results 102 cases of kidney transplant patients were enrolled in cohort one to establish the initial daily dose formula of tacrolimus, including 34 female and 68 male patients. Their height, weight and hemoglobin value were 162 ± 14 cm, 55 ± 15 kg and 95 ± 16 g / L respectively and there were 42 cases of infection and 87 cases of hypertension. There were 10 cases of CYP3A5 *1/*1 (9.8%), 28 cases of CYP3A5 *1/*3 (27.5%) and 64 cases of CYP3A5 *3/*3 (62.7%). The mutation frequency of CYP3A5 was 76.5%. The distribution of ABCB1 C1236T genotype were CC 15 (14.7%), CT 45 (44.1%) and TT 42 (41.2%); The distribution of ABCB1 C3435T genotype were CC 36 (35.3%), CT 52 (51.0%) and TT 14 (13.7%); The distribution of ABCB1 G2677T/A genotype were GG 39 (38.2%), GT 40 (39.2%) and TT 23 (22.5%). The allele mutation frequency of ABCB1 C1236T, ABCB1 C3435T and G2677T/A were 63.3%, 39.2% and 42.1% respectively. The multiple linear regression analysis had indicated a linear relationship between body weight, hemoglobin concentration and CYP3A5 genotypes and the daily dose of tacrolimus. Then the initial daily dosage formula of tacrolimus in kidney transplant patients was formed, which was equal to 7.499+0.053×weight-0.029×hemoglobin concentration -1.045×CYP3A5 genotype. (CYP3A5 genotype: *1/*1 type inputs 0, *1/*3 type inputs 1, *3/*3 type inputs 2). 65 cases of kidney transplant patients were enrolled in cohort two to evaluate the initial daily dose formula of tacrolimus formed previously, including 5 cases of CYP3A5 *1/*1 (7.7%),26 cases of CYP3A5 *1/*3 (40.0%) and 34 cases of CYP3A5*3/*3 (52.3%). Their weight and hemoglobin concentration were 54±14 kg and 98±16 g/L respectively. Pearson correlation analysis showed that the predicted dose of tacrolimus formula had a positive correlation with the actual clinical dose. The correlation coefficient r=0.605 (P<0.001). The equation for the linear regression line was Y = 1.072*X - 0.688 and the R2 values for the linear goodness of fit was 0.366.
Conclusions The hemoglobin, weight, and CYP3A5 genotype should be considered comprehensively when using tacrolimus. The dose formula established in our study can make a good prediction for the initial daily dosage of tacrolimus and help the patient reach the reference range of the tacrolimus treatment window.

PU-0853

lncRNA 在冠状动脉粥样硬化性心脏病中的诊断和预测价值

陈则金、江华、郑登滋、魏建威
福建省第二人民医院

目的 探讨 lncRNA 在冠状动脉粥样硬化性心脏病中的诊断和预测价值。
方法 选取我院住院患者 2018 年 6 月~2020 年 6 月期间收治的 68 例冠心病患者和同期接受检查的 70 例健康体检者作为研究对象，分别作为观察组和对照组，所有受试者知晓本次研究的目的与意义，并自愿参与本次研究。采集两组受检者的空腹肘静脉血，提取 RNA（Trizol 法），测定 RNA 浓度，合成 cDNA，应用雅培 Abbott m2000rt 实时荧光定量 PCR 仪，进行 lncRNA UCA1、lncRNA TUG1 表达水平的检测（qRT-PCR 法），比较冠心病患者和健康体检者、不同病变支数冠心病患者以及不同预后患者的 lncRNA UCA1、lncRNA TUG1 表达水平。
结果 冠心病患者和健康体检者对比，观察组患者的 lncRNA UCA1 表达水平[（0.79±0.30）＜（1.02±0.22）]低于对照组（P＜0.05）、lncRNA TUG1 表达水平[（1.79±0.27）＞（1.12±0.32）]高于对照组（P＜0.05）。不同病变支数冠心病患者对比，单支病变患者的 lncRNA UCA1 表达水平最高，双支病变其次，多支病变最低。单支病变患者的 lncRNA TUG1 表达水平最低，双支病变其次，多支病变最高。不同预后患者对比，预后良好患者的[（0.95±0.22）＞（0.74±0.18）]高于对照组（P＜0.05）、lncRNA TUG1 表达水平[（1.19±0.27）＜（1.43±0.22）]低于对照组（P＜0.05）。

结论 在冠心病患者的诊疗过程中，lncRNA 有着重要的应用价值，根据 lncRNA 的表达水平，能够真实、准确的反映出疾病的发生、进展情况，能够为疾病的早期防治提供重要的参考依据。

PU-0854

Screening of novel biomarkers in maternal blood for prenatal screening of Down's syndrome and construction of detection Methods for biomarkers

Yuan Yao
Guigang District, No 923 Hospital, Joint Logistics Support Force of PLA
中国人民解放军陆军军医大学第一附属医院检验科

Chromosome analysis of fetus cast-off cells obtained by invasive procedures is the gold standard for prenatal diagnosis of Down's syndrome (DS), whereas the invasiveness warrants the discovery of novel noninvasive predictive biomarkers. In this study, the liquid chromatography-tandem mass spectrometry analysis and the gas chromatography-mass spectroscopy analysis were employed, and combined with the results of bioinformatics studies, to set up the analysis model of metabonomics in maternal serum from DS-unaffected pregnant women (UP) and DS-affected pregnant women (DP). The principal component analysis (PCA), cluster analysis, and random forest (RF) analysis were performed, and the Welch t-test was used to screened for the metabolic molecules whose levels differed significantly between UP and DP. Total RNA was extracted and purified, and RNA quality and quantity was measured. After that, the cluster analysis, and RF analysis were performed, and the unpaired t-test was used to screened for the microRNA molecules. The western blot test was performed to verify the four proteins including CFHR1, dGTPase, KNG1, and β2-GPI, and the TRFIA **Methods** were established to detect the concentrations of the proteins in maternal serum. Then, the methodological evaluation, including the linear detection ranges, the sensitivity exploration, the precision experiments, the specificity experiments, was conducted, and the concentration ranges of the proteins were preliminarily investigated in serum of UP and DP. The results of PCA for metabonomics in serum showed that the contribution ratios of comp 1, comp 2, and comp 3 were 34.86%, 10.46% and 5.99%, and the RF analysis provided a forecast accuracy of 97%. A total of 193 metabolic compounds expressed significantly differentially were screened out, including the increased levels of 16 molecules and decreased levels of 177 molecules. Results of the cluster analysis for microRNA in plasma showed that the levels of microRNA between samples within a group were homogeneous. A total of 135 microRNA molecules expressed significantly differentially were screened out, including the increased levels of 95 molecules and decreased levels of 40 molecules. Results of western blot tests revealed that levels of CFHR1, dGTPase, and KNG1 in DP were increased significantly, and β2-GPI was decreased remarkably, compared with UP. The TRFIA detection results of dGTPase, KNG1, β2-GPI, and showed that the equation of standard curve was "lg(y) = 0.867lg(x)+lg1789" (R2 = 0.992), "lg(y) = 0.982lg(x)+lg1579" (R2 = 0.994), and "lg(y) = 1.009lg(x)+lg1164" (R2 = 0.991), and the sensitivity was 3.06, 2.16, and 3.91 ng/ml, respectively. Besides, there were significant differences in the levels of dGTPase, KNG1, and β2-GPI between UP and DP, as well as between DS-unaffected high-risk pregnant women group and DP. A total of 193 metabolic compounds whose levels differed significantly between UP and DP were discovered, which might provide the foundation for the screening of potential metabolic markers for DS-affected pregnancies, and the exploration of the metabolic pathways might provide some clues for the exploration of the pathological mechanism of DS. Levels of 135 microRNA molecules differed significantly between UP and DP, which might provide the foundation for the screening of potential microRNA markers for DS-affected pregnancies, and the exploration of microRNA markers and the gene expression might provide some clues for the exploration of the pathogenesis of this disease. Results of western blot tests suggested that CFHR1, dGTPase, KNG1, and β2-GPI might be potential novel protein markers for DS, and establishment of the

TRFIA **Methods** for dGTPase, KNG1, and β2-GPI in maternal serum provided some foundations for the exploration of novel prenatal screening strategies for DS-affected pregnancies.

PU-0855

The Role of Dectin-1-Mediated M1 Macrophage Polarization in Cerebral Ischemia-Reperfusion Injury

Zongyun Chen
Department of Laboratory Medicine, Mindong Hospital Affiliated to Fujian Medical University

Introduction Te advances in cerebral ischemia treatment have resulted in a larger proportion of patients get the benefits of
rebuilding blood flow to the brain. Ten, ischemia-reperfusion injury has emerged as a new essential problem. Dectin-1 plays an
important role in cerebral ischemia-reperfusion injury by regulating the function of immune cells.
Methods C57BL/6 was blindly divided into four groups including the sham-operated group and the three different kinds of middle cerebral artery occlusion (MCAO)groups(after6hours,12hours,and24hoursafterplugremoval).Teproteinexpressionlevelsofdectin-1,proapoptosis
molecule, and antiapoptosis molecule were measured by using western blot analysis. Te brain tissue was analyzed by flow
cytometrytodetecttheM1macrophagelevels.
Results Tecorrelationanalysisofdectin-1andinfarctareasshowedthattherewas an obviously positive correlation in between them (R^{2}0.9603). Dectin-1, cleaved caspase-3, and Bax increased, while anti-apoptosis molecule, Bcl-2, decreased at three appropriate time points (after 6 hours, 12 hours, and 24 hours). Te level of M1 macrophages in the experimental group increased after ischemia-reperfusion injury compared to the control group.
Conclusions Te high expression level of dectin-1 may affect M1 macrophage polarization and brain cell apoptosis in cerebral ischemia-reperfusion injury.

PU-0856

Integrated Analysis of lncRNAs and mRNAs Identifies a Potential Driver lncRNA FENDRR in Lung Cancer in Xuanwei, China

Yanliang Zhang、Yong Duan、Yan Wang、Ying Zhao
First Affiliated Hospital of Kunming Medical University

This study was to screen out potential driver long non-coding RNAs (lncRNAs) in lung cancer in Xuanwei (LCXW) differently expressed mRNAs and lncRNAs were detected by gene expression microarrays in 23 paired lung adenocarcinoma and adjacent tissues. Combined bioinformatics analysis was performed to identify potential driver lncRNAs and their potential regulatory relationships. Transcriptome and clinical data in TCGA-LUAD were used as comparison and validation dataset. The comparison of LCXW and TCGA-LUAD revealed significant differences in expression of some genes, signaling pathways affected by differentially expressed genes, and the 5-year survival rate of patients. We identified 14 consistently deregulated mRNAs and 5 lncRNAs as candidate genes, which affected multiple cancerrelated pathways and influenced patients' overall survival. By combined bioinformatics analysis, we further identified a potential driver lncRNA fetal-lethal non-coding developmental regulatory RNA (FENDRR) and proposed its possible regulation mechanism. The low expression of FENDRR was positively correlated with Kruppel-like factor4 (KLF4), KLF4 down-regulation may loss the

activation function of cyclin-dependent kinase inhibitor 1A (CDKN1A) and cyclin-dependent kinase inhibitor 1C (CDKN1C) and the inhibition function of CyclinB1 (CCNB1), eventually cause excessive cell cycle activation and lead to lung cancer. This study revealed a potential FENDRR-KLF4-cell cycle regulation axis. These results lay an important foundation for further research on the pathogenesis of LCXW and identification of potential novel biomarkers or therapeutic targets.

PU-0857

BRCA1 基因表达和 CXCL16 在乳腺癌诊断中的应用

邓君、洪华、刘蔚、孙昌瑞
四川省医学科学院·四川省人民医院

目的 探讨乳腺癌易感基因 1（breast cancer susceptibility gene 1, BRCA1）和趋化因子 CXCL16 在乳腺癌诊断和治疗监测中的应用。
方法 采用 FQ-PCR 检测 50 例健康女性体检者、102 例良性乳腺肿瘤、157 例乳腺癌和 126 例其他肿瘤组外周血中 BRCA1 mRNA，ELISA 检测 CXCL16，分析与乳腺癌患者临床组织学分期的关系，以及手术前后的差异。
结果 乳腺癌组的 BRCA1mRNA 水平低于正常对照组和良性乳腺疾病组，而 CXCL16 高于正常对照组和良性乳腺疾病组，乳腺癌组的 BRCA1 低于其他肿瘤组，而 CXCL16 则无显著性差异；BRCA1 在手术后显著上升，而 CXCL16 显著下降；在乳腺癌组中,随着临床分期的升高，BRCA1 递减，而 CXCL16 递增；BRCA1 和 CXCL16 联合检测可提高乳腺癌诊断灵敏度。
结论 BRCA1 和 CXCL16 对乳腺癌预后有一定的预测作用，BRCA1 和 CXCL16 对术后随访有意义，联合检测有助于提高对乳腺癌早期诊断。

PU-0858

RMP 通过 ATM/NF-κB 信号途径促进肝癌细胞 DNA 双链损伤修复

周围
常州市第一人民医院

目的 放疗耐受是肝癌治疗中的一大难题，急需从分子水平解析肝癌细胞射线的耐受的原因。目前已有报道表明 RMP 能够维持基因组稳定性，因此 RMP 能否参与肝癌细胞 DNA 损伤修复调值得进一步探究。
方法 经 γ 射线诱导肝细胞和肝癌细胞 DNA 损伤，彗星电泳和免疫荧光染色明确各组细胞在射线照射 0~120 分钟后的 DNA 损伤程度；通过 qRT-PCR 和 Western blot 检测射线诱导后 RMP 的表达水平；评估 RMP 对对肝癌细胞 DNA 损伤后的修复速度的影响。通过 Western blot 分析 DNA 损伤后细胞核和胞浆中 RMP 的表达水平；检测 DNA 损伤断链点上 RMP 的募集； qRT-PCR 检测损伤修复和凋亡基因在射线照射后的表达；Western blot 分析 RMP 对 ATM 和 NF-κB 磷酸化的影响；免疫荧光和免疫共沉淀分析 RMP 与 ATM 在细胞损伤断链点的共定位；ATM 抑制剂和 NF-κB 抑制剂处理后，明确 ATM 和 NF-κB 磷酸化对 RMP 介导的肝癌细胞 DNA 损伤修复的影响。
结果 γ 射线照射后，肝癌细胞的 DNA 损伤修复速度高于肝细胞，且 RMP 表达显著上调；敲减 RMP 表达后，肝癌细胞 DNA 损伤修复明显减慢，DNA 损伤 120min 后细胞核内仍存在较多 DNA 损伤断链点；发生 DNA 损伤后，RMP 蛋白核转位增加，并募集于 DNA 损伤断链点处；同时 RMP 能促进 ATM 磷酸化，且 RMP 在损伤断链点的募集不依赖于 ATM 磷酸化，但 ATM 磷酸化能抑制 RMP，ATM 和 Mre11 损伤修复复合物的形成。RMP 能通过促进 ATM 磷酸化激活 NF-κB 通路，而

NF-κB 介导的损伤修复、细胞周期调控和抑凋亡分子等的表达参与了 RMP 介导的 DNA 损伤修复过程。
结论 肝癌细胞通过上调 RMP 的表达增强 DNA 损伤修复，该过程中，RMP 募集于损伤断链点，形成 RMP/ATM/Mre11 损伤修复复合物，激活下游 NF-κB，促进 DNA 损伤修复的同时，促进抑凋亡基因表达。

PU-0859

RMP 与 IGF1r 协同促进缺氧诱导的胃癌转移的机制研究

周围
常州市第一人民医院

目的 缺氧是肿瘤微环境的一大特征，而缺氧诱导的转移是胃癌治疗中迫切需要解决的难题，急需从分子水平解析缺氧诱导胃癌转移的原因。已有报道表明定位于 mTOR 通路上游和下游的 IGF1r 和 RMP 是肿瘤细胞应答微环境、调控细胞生长和转移的重要分子。因此探讨 RMP 和 IGF1r 调控缺氧微环境诱导的胃癌细胞转移的机制，对我们理解胃癌转移的分子基础具有重要意义。
方法 明确 RMP，IGF1r 和 RMP-Ser371 磷酸化与胃癌转移和患者生存期的相关性；建立体外和体内的胃癌缺氧模型，明确 RMP、IGF1r 和 RMP-Ser371 磷酸化与缺氧的关系；通过划痕、transwell 和小鼠肿瘤转移模型明确单独和共敲减 RMP 和 IGF1r 表达对胃癌细胞转移的影响；通过免疫印迹明确 RMP 和 IGF1r 对迁移相关蛋白表达的影响；建立 RMP 的 Ser371 突变体明确其与胃癌转移的关系；通过敲减 PKN3 表达明确 PKN3 应答缺氧微环境并磷酸化 RMP；通过小分子抑制剂分析 PI3K, mTOR, AMPK 通路对缺氧诱导的胃癌转移的影响；通过抑制剂和激动剂评估 AMPK 对 RMP-磷酸化和 RMP/IGF1r/PKN3 复合体的影响，最终明确缺氧诱导胃癌转移的分子基础。
结果 缺氧微环境能上调胃癌细胞中 RMP 和 IGF1r 的表达，促进 RMP 的 Ser371 磷酸化；RMP 的磷酸化促进胃癌细胞中迁移相关蛋白的表达；IGF1r 能与 RMP 结合并且维持 RMP 磷酸化；缺氧时 AMPK 下游分子 PKN3，能被 AMPK 活化，从而与 RMP/IGF1r 形成三元复合物，进而促 RMP 磷酸化；缺氧时 AMPK 和 PKN3 的活性对于 RMP 的磷酸化和胃癌细胞的转移必不可少，而 IGF1r 作为桥梁分子，促进 RMP 和 PKN3 的蛋白互作。
结论 缺氧通过上调胃癌细胞 AMPK 活性，促进 RMP/IGF1r/PKN3 三元复合物形成，帮助 PKN3 磷酸化 RMP 的 Ser-371 位点，最终诱导胃癌转移。

PU-0860

基于网络药理学的强心益脉汤调治射血分数保留的心力衰竭的分子机制研究

万科幸
自贡市第一人民医院

目的 基于网络药理学方法分析强心益脉汤调治射血分数保留的心力衰竭（HFpEF）的药理机制，为新药研发及经典方剂的临床拓展运用提供参考。
方法 通过 TCMSP 数据库获取太子参、黄芪、猪苓、泽泻、白术、茯苓、桂枝、红花、桃仁、川芎、赤芍的主要化学成分及其靶点，根据 ADME 筛选中药活性组分；通过 Gencards、OMIM、TTD、DRUGBANK 数据库获取射血分数保留的心力衰竭主要靶点，利用 String 平台进行蛋白质相互作用分析，构建 PPI 网络并挖掘网络中潜在的蛋白质功能模块。采用 Metascape 平台分析“药物-成分-靶点”及其参与的生物过程及通路，而后采用 Cytoscape3.7.1 软件构建“强心益脉汤成分-HFpEF 靶点-通路”网络，最后采用 MOE2010 中的分子对接模块进行分子对接验证。

结果 强心益脉汤调治射血分数保留的心力衰竭的核心活性成分为 β-胡萝卜素、豆甾醇、谷甾醇、β-谷甾醇、菜油甾醇、白杨甙、常春藤皂苷元、异黄酮、氢化松苓酸、齿孔菌酸等。强心益脉汤调治 HFpEF 的生物学通路主要作用于癌症相关信号通路，cAMP 信号通路、HIF-1 信号通路、钙信号通路以及 C21-甾体激素的生物合成等通路，其功能主要为调节血压，血液循环等生命活动。
结论 本研究初步揭示了强心益脉汤调治射血分数保留的心力衰竭的多成分、多靶点、多通路的作用机制，为强心益脉汤的临床开发利用提供基础。

PU-0861

Analysis of circular RNA expression profiles of lung cancer in Xuanwei, China

Yan Wang、Ling-Jiao Lu、Yong Duan、Xiao Liu、Yue Mao、Yu Chen、Yan-Liang Zhang
First Affiliated Hospital of Kunming Medical University

Background Mounting evidence indicates that circular RNAs (circRNAs) could play a pivotal role in cancers. However, due to the lack of sensitive biomarkers, most lung cancer in Xuanwei (LCXW) patients are still diagnosed at an advanced stage accom_x0002_pany with distant metastasis.
Methods According to the stage of LCXW patients and tissue sources, circRNAs microarray detection was carried out in six groups. Considering fold change, raw intensity, the length of circRNAs, and P-value, we selected eight circRNAs for fur_x0002_ther study. A total of 50 paired LCXW tissues were carried out real-time quantitative polymerase chain reaction (RT-qPCR) in order to extended sample size to verify the expression of these circRNAs.
Results We designed 13 617 human circRNA probes for the human circular RNA microarray, detected 10 819 circRNA in six groups of samples; 537 circRNAs were differentially expressed consistently in every stage. Through RT-qPCR, we selected 8 circRNAs, three of which were upregulated (hsa_circ_0005927, hsa_circ_0069397 and hsa_circ_0000937) and five were downregulated (hsa_circ_0001936, hsa_ circ_0005255, hsa_circRNA_406010, hsa_circ_0007064, hsa_circ_0000907) in tumor tissues, only hsa_circ_0001936 showed the opposite expression between microarray and RT-qPCR, others were consistent. Additionally, hsa_circ_0005927 and hsa_circ_0001936 were significantly correlated with tumor size, and hsa_circRNA_406010 was related to the prognosis of LCXW patients.
Conclusion Together, these results suggest that hsa_circ_0005927, hsa_ circ_0001936, and hsa_circRNA_406010 may serve as the novel potential biomarkers for LCXW. Moreover, these results may provide a new insight for the pathogenesis of LCXW.

PU-0862

PAPP-A 和 sFlt1/PlGF 对中国人群子痫前期诊断价值的比较

马岩团进[1,2]、张宇航[1,2]、钱源[1,2]
1. 昆明医科大学第一附属医院
2. 云南省检验医学重点实验室

目的 统评价妊娠期 PAPP-A 水平和 sFlt1/PlGF 比值与子痫前期发病的相关性，间接比较 PAPP-A 和 sFlt1/PlGF 在中国人群子痫前期诊断的临床价值。
方法 检索中国知网、万方、维普、中国生物医学文献数据库，收集有关妊娠期 PAPP-A、sFlt1/PlGF 检测子痫前期诊断性实验的相关文献。按纳入与排除标准筛选文献、评价文献质量、提取数据。采用 Meta-Disc1.4 和 Stata15 软件对纳入的文献进行 meta 分析。
结果 总共有 35 项研究纳入。分析结果显示，子痫前期组血清 PAPP-A 水平低于对照组[SMD=-1.688, 95%CI (-2.878～-0.497)]，而子痫前期组的 sFlt1/PlGF 比值明显高于对照组[SMD=1.44,

95%CI (0.876～2.003)]，差异均有统计学意义（P<0.05）；PAPP-A 诊断子痫前期发病的 SEN 合并为 0.69（95%CI 0.66～0.72）,SPE 合并为 0.81（95%CI 0.80～0.82）,DOR 为 10.54（95%CI 6.37～17.43）,SROC 曲线下面积为 0.8017; sFlt1/PlGF 诊断子痫前期发病的 SEN 合并为 0.80（95%CI 0.77～0.84）,SPE 合并为 0.89（95%CI 0.87～0.9）,DOR 为 34.41（95%CI 16.36～72.38）,SROC 曲线下面积为 0.8903。间接比较显示 PAPP-A 与 sFlt1/PlGF 检测的 AUC 有统计学差异（Z=2.16 P<0.05）。

结论 妊娠期 PAPP-A 水平的降低或者 sFlt1/PlGF 比值的提高与子痫前期发病相关，PAPP-A 和 sFlt1/PlGF 检测在诊断子痫前期发病中均具有较好的准确性，但 sFlt1/PlGF 较 PAPP-A 的诊断准确性更高，可作为预测子痫前期发病的方法之一。

PU-0863

Association of Apolipoprotein E gene polymorphisms with type 2 diabetes mellitus and coronary artery disease

Lei Wu
The First Affiliated Hospital of Nanjing Medical University

Apolipoprotein E (APOE) gene mediates lipoprotein clearance in the body and is one of the most studied candidate genes for Type 2 diabetes mellitus (T2DM) and coronary artery disease (CAD). This study was performed to determine the association between APOE polymorphisms and T2DM with and without CAD, as well as its effect on plasma lipid level. A total of 1414 subjects were recruited into four distinct groups, 264 in T2DM group, 401 in CAD group, 204 in T2DM+CAD group, and 545 in normal control group. APOE genotyping was carried out using chip platform. Logistic regression analysis was used to obtain odds ratio (OR) and 95% confidence interval (CI) in predicting the risk probability of APOE. APOE ε3/ε3 genotype was the most prevalent genotype in our studied groups. Genotype frequency ratio of genotype ε3/4 and allele ε4 among the CAD patients with or without T2DM was obviously increased. Compared with ε3/3 genotype, the ε3/4 genotype had a significant increased risk of CAD (adjusted OR = 1.90, 95% CI = 1.30-2.77) and T2DM+CAD (adjusted OR = 1.95, 95% CI = 1.24-3.08). The plasma HDL-C levels of CAD patients with ε4-bearing genotypes were lower than those with ε3/3 genotype. These results indicate that ε4 allele may increase the risk of both CAD with and without T2DM, and has influence on lipid profiles. The detected associations deserve to be definitively validated in larger multi-center studies.

PU-0864

Near a half of PICU patients with unexplained death received genetic diagnosis by exome sequencing and the genotypes and phenotypes of 19 rare diseases were expanded

Yu Zheng、Juan Liu、Jiaotian Huang、Desheng Zhu、Ping Zang、Yongjia Yang、Zhenqing Luo、Zhenghui Xiao、Yimin Zhu、Xiulan Lu
Hunan Children's Hospital

Background Phenotypes of some rare genetic diseases are atypical. A considerable proportion of PICU puzzling cases are still need to be clarified. It is a challenge for pediatric intensive care units (PICUs) to diagnose and manage shortly in emergency.
Methods 58 PICU patients in critical ill status or died shortly without a clear etiology in Hunan Children's hospital from 9/20/2014 to 12/30/2018 were selected. Whole exome sequencing was

performed for 103 samples in 58 families (39 deceased and 19 surviving patients). Disease-causing single nucleotide variants (SNVs) and copy number variants (CNVs) were analyzed using customized bioinformatics pipeline.
Results In total, 27 (46.6%, 27/58) patients received a genetic diagnosis, and six (10.3%, 6/58) patients had uncertain pathogenicity variants (VUS). We identified 34 pathogenic or likely pathogenic SNVs from 26 genes, which relating to at least 19 rare diseases. Each genetic rare disorder involved in an isolated patient, excepting two patients shared underlying disorders from the same gene ACAT1. In addition to two novel CNVs, the genotypic spectrum of genetic disorders was expanded by 23 novel SNVs from gene MARS, PRRT2, TBCK, TOR1A, ECE1, ARX, ZEB2, ACAT1, CPS1, VWF, NBAS, COG4, and INVS etc. Among the 27 patients with genetic diagnosis, 20 patients (74.1%, 20/27) accompanied severe infection, 19 patients (70.1%, 19/27) died. Phenotypes associated with respiratory (n=12), MCA (n=10), neuromuscular (n=8), or metabolic disorders (n=9) were the most common. In addition to the phenotypes associated with the identified genetic diseases, eight patients had clinical features to be clarified.
Conclusion The diagnosed genetic disorders are sporadic in the regional PICU, which resulted in high mortality. Our findings expanded the genotypes and phenotypes of 19 rare diseases from PICU with complex characteristics.

PU-0865

同源重组缺陷检测在肿瘤临床诊疗中的进展与展望

郁俐[1]、沈敏娜[1]、姜惠琴[1]、王蓓丽[1,2]、郭玮[1,2]
1. 复旦大学附属中山医院
2. 复旦大学附属中山医院厦门医 院检验科

目的 总结同源重组缺陷（homologous recombination deficiency, HRD）检测方法，探讨 HRD 检测在肿瘤临床诊疗中的作用。
方法 围绕 HRD 的基本概念，检测方法及临床价值作一综述。
结果 同源重组（Homologous recombination，HR）是修复 DNA 双链断裂、单链 DNA 间隙和停滞或折叠复制叉的主要途径，有助于端粒维持，确保减数分裂过程中染色体的正确分离。同源重组修复（Homologous recombination repair, HRR）通路是 DNA 损伤修复通路之一，在肿瘤中有较高的突变频率。除了 BRCA1/2 基因突变之外，同源重组缺陷（homologous recombination deficiency, HRD）也可以由其他机制引起，例如 HRR 相关基因的胚系突变、体细胞突变、基因组稳定性及 HRR 途径中涉及基因的表观遗传修饰等。最新临床研究数据发现，通过 HRR 基因突变检测和基因瘢痕检测来反应同源重组缺陷状态可有效预测肿瘤患者使用多聚腺苷二磷酸核糖聚合酶（Poly ADP-ribose polymerase, PARP）抑制剂的疗效，帮助患者精准用药及预后判断。
结论 本文回顾了 HRD 的不同检测方法，探讨 HRD 检测在临床运用中的价值，为肿瘤的精准治疗奠定临床基础。

PU-0866

血清 Flt3L 和 Gas6 对非霍奇金淋巴瘤患者化疗后感染的诊断价值

晏黎[1]、黄伟[2]、饶亚华[2]、熊银[2]、姜锐[2]、崔天盆[2]
1. 湖北中医药大学
2. 武汉市第一医院

目的 探讨 Flt3 配体（Flt3L）和生长停滞特异性蛋白 6（Gas6）对非霍奇金淋巴瘤（NHL）患者化疗后感染的诊断价值。

方法 收集 2019 年 7 月至 2020 年 10 月在武汉市第一医院就诊的 NHL 化疗患者 94 例。根据化疗后是否感染，分为感染组 40 例，未感染组 54 例。另选择同期健康者 50 例为对照组，比较三组间血清 Flt3L、Gas6 和一般炎症指标的表达水平及相关性。ROC 曲线分析血清 Flt3L 和 Gas6 对 NHL 患者化疗后感染的预测价值。采用 Kaplan-Meier 曲线分析血清 Flt3L 和 Gas6 水平对 NHL 化疗患者发生医院感染的影响。
结果 NHL 患者化疗后感染组血清 Flt3L［807.80（215.10～1232.00）pg/ml］和 Gas6［20.04（13.14～27.52）ng/ml］水平均高于未感染组和对照组，差异均有统计学意义（P 均<0.05）；NHL 患者化疗后重度感染组血清 Flt3L［887.30（321.60~1367.00）pg/ml］和 Gas6［25.24（17.61~42.86）ng/ml］水平均高于轻度感染组，差异均有统计学意义（P 均<0.05）。血清 Flt3L 浓度与 WBC 呈负相关，与 IL-6 呈正相关；血清 Gas6 浓度与 WBC 呈负相关。ROC 曲线分析表示血清 Flt3L 和 Gas6 预测诊断感染的曲线下面积及 95%CI 分别为 0.811（0.719～0.902），0.643（0.526～0.759）。血清 Flt3L 与 hsCRP、PCT 和 IL-6 联合应用后诊断效能明显提高，曲线下面积分别为 0.956、0.923 和 0.865。Kaplan-Meier 曲线分析表示 NHL 化疗患者血清 Flt3L≥649.8pg/ml 及血清 Gas6≥21.50ng/ml 时，医院感染率显著升高（P 均<0.05）。
结论 早期检测血清 Flt3L 浓度有助于预测 NHL 患者化疗后感染及病情判断。

PU-0867

中药靶向 miRNA、lncRNA 治疗乳腺癌的机制的研究策略及乳腺癌与化学修饰

卢晴晴
湖南中医药大学

乳腺癌是全球发病率第一的癌症，根据免疫组化的结果可将乳腺癌分为四型，不同型别的乳腺癌在肿瘤直径、组织学分级、生存率等上存在差异。miRNA 是一类小的非编码 RNA，lncRNA 是一类长的非编码 RNA，它们对乳腺癌的增殖、迁移、侵袭、凋亡等可能有促进或抑制的作用。根据乳腺癌型别及研究目的的不同常采用不同的研究策略，不论采用何种实验，都必须同时研究过表达和敲减待研 miRNA 对乳腺癌细胞和正常乳腺细胞的影响，以保证实验思路严谨、结果可靠。除了 miRNA 和 lncRNA 以外，乳腺癌的发生发展还与 mRNA 甲基化和蛋白质泛素化等化学修饰有关。

PU-0868

Circulating LncRNA UCA1 and LncRNA PGM5–AS1 act as potential diagnostic biomarkers for early-stage colorectal cancer

Xiaodong Feng、Minghui Wang
The Affiliated Hospital of Qingdao University

Background Colorectal cancer (CRC) is the most common malignant tumor worldwide and is difficult to diagnose. Growing evidence has indicated that long non-coding RNAs (lncRNAs) play a significant role in the occurrence and progression of many cancers. In this study, we aimed to identify lncRNAs in plasma as potential diagnostic biomarkers for CRC.
Methods The common differential lncRNAs between cancer tissues and adjacent tissues were identified by analyzing Gene Expression Omnibus (GEO) datasets GSE102340, GSE126092, GSE109454 and GSE115856. Then the two most differentially expressed lncRNAs were verified by using quantitative real time–PCR (qRT–PCR) in 200 healthy controls and 188 CRC patients.

Receiver operating characteristic (ROC) curve was constructed to evaluate their diagnostic value for CRC.
Results Integrated analysis of the GEO datasets identified three significantly up–regulated and eleven down–regulated lncRNAs in CRC tissues. Compared with healthy control, lncRNA UCA1 was significantly up–regulated in CRC patient plasma and lncRNA PGM5–AS1 were significantly down–regulated. The area under the ROC curve (AUC) was determined to be 0.766, 0.754 and 0.798 for UCA1, PGM5–AS1 and the two lncRNAs were combined. Moreover, these two lncRNAs could be used to distinguish early stages CRC from the healthy controls. The combination of UCA1 and PGM5–AS1 enhanced the AUC to 0.832. When the lncRNAs were administered with either carcinoembryonic antigen (CEA) the AUC was further improved to 0.874.
Conclusion This research identified two differentially expressed lncRNAs in CRC patient plasma. Our data suggest that these two lncRNAs can be used as potential diagnostic biomarkers of CRC.

PU-0869

低密度脂蛋白受体 rs688 位点、AvaⅡ、NcoⅠ基因多态性与缺血性脑卒中的相关性研究

陈雅斌、张志珊
福建医科大学附属泉州第一医院

目的 分析低密度脂蛋白受体 rs688 位点、AvaⅡ、NcoⅠ等基因之间是否存在连锁不平衡，以及连锁不平衡的基因与缺血性脑卒中是否存在相关性。
方法 选取缺血性脑卒中、健康对照、其他脑血管病组各 50 例，进行低密度脂蛋白受体 rs688 位点、AvaⅡ、NcoⅠ等基因多态性的检测。应用卡方分析对组间各基因型频率、等位基因频率进行比较。连锁不平衡和病例/对照研究分析 3 基因之间是否存在连锁不平衡，并分析缺血性脑卒中关联的等位基因。Logistic 线性回归分析连锁不平衡的基因与缺血性脑卒中的相关性。
结果 缺血性脑卒中组中 LDLR rs688 位点基因型频率、等位基因频率存在明显差异；AvaⅡ基因等位基因频率比较亦均有统计学差异；NcoⅠ基因比较差异无统计学意义。连锁不平衡分析显示 rs688 位点基因和 AvaⅡ基因存在高度连锁不平衡（D'=0.940，R2=0.533）。与缺血性脑卒中存在相关等位基因分别为：rs688 位点：T（X2=16.071，P=0.000）、AvaⅡ：C（X2=8.224，P=0.004）。logistic 线性回归分析得出，和野生型 rs688 位点和 AvaⅡ基因（CC/TT）组合相比，双重杂合子突变（CT/TC），增加了缺血性脑卒中疾病发生的概率（OR= 1.361，P=0.000）。
结论 缺血性脑卒中 LDLR rs688 位点、AvaⅡ基因多态性的频率分布明显区别于对照。rs688 位点和 AvaⅡ基因存在高度的连锁不平衡现象。双重杂合子（rs688/ AvaⅡ:CT/TC）提高了缺血性脑卒中发生的风险概率。或可作为缺血性脑卒中的一个遗传标志，用以临床筛查高危人群预防缺血性脑卒中的发生。

PU-0870

4 例新型冠状病毒感染病例鼻拭子、咽拭子病毒核酸检测和血浆抗体检测结果分析

陈荣华、柳丽娟、李勤光
福建医科大学孟超肝胆医院

目前，新型冠状病毒（SARS-CoV-2）核酸检测和血浆抗体检测是确诊新型冠状病毒肺炎（COVID-19）的重要依据。为比较分析 SARS-CoV-2 感染病例鼻拭子与咽拭子的病毒核酸检测及其血浆病毒抗体检测结果，本研究采用实时荧光定量 PCR 方法，分别检测 4 例 COVID-19 确诊病例鼻拭子与咽拭子标本的 SARS-CoV-2 ORF 1ab 基因和 N 基因，并采用胶体金法检测血浆标本中的 SARS-CoV-2 IgM 和 IgG 抗体。结果显示，在 4 例 COVID-19 确诊病例中，鼻拭子中病毒 ORF 1ab 基因及 N 基因的核酸扩增信号均强于咽拭子，Ct 值均低于咽拭子；血浆病毒抗体检测仅发现 1 例标本 SARS-CoV-2 IgG 单阳性。本研究结果提示，鼻拭子标本的病毒含量明显高于咽拭子标本，血浆病毒 IgM 和 IgG 抗体检测是 COVID-19 辅助临床诊断的有效工具。

PU-0871

Elevated Soluble Programmed Death-ligand 1 levels indicate immunosuppression and poor prognosis in hepatocellular carcinoma patients undergoing transcatheter arterial chemoembolization

Wenjing Yang、Xiao-Lu Ma、Xu-Dong Qu、Bei-Li Wang、BAI-SHEN PAN、JIAN ZHOU、JIA FAN、Xin-Rong Yang、WEI GUO
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University

AIMS Soluble Programmed Death-ligand 1 (sPD-L1) is associated with hepatocellular carcinoma (HCC) prognosis after resection; however, this association has not yet been characterized in patients with unresectable HCC. The present study aimed to determine the prognostic significance of sPD-L1 in HCC patients undergoing transcatheter arterial chemoembolization (TACE).
METHODS We treated 114 HCC patients with TACE from 2012 to 2013 and determined their sPD-L1 levels by enzyme-linked immunosorbent assay. We evaluated prognoses according to mRESIST criteria and analyzed prognostic values by Cox regression and Kaplan-Meier analysis. We further evaluated correlations between sPD-L1 and systemic inflammation index (SII), soluble interleukin-2 receptor (sIL-2R), IL-10, hepatitis B virus (HBV)-DNA loads, and C-reactive protein.
RESULTS sPD-L1 levels were significantly increased in patients who developed HCC progression (P=0.002) and death (P<0.001). Patients with higher pre-treatment sPD-L1 levels had a significantly shorter time to progression (10.50 vs. 18.25 months, P=0.001) and decreased overall survival (16.50 vs. 28.50 months, P=0.003). In low-recurrence-risk subgroups, sPD-L1 levels retained prognostic value (P<0.050). Importantly, multivariate regression confirmed that pre-treatment sPD-L1 level was an independent predictor for both progression [hazard ratio (HR) 1.82; P=0.032] and survival (HR 1.84; P=0.009). Moreover, sPD-L1 levels positively correlated with SII (r=0.284, P=0.002), sIL-2R (r=0.239, P=0.010), IL-10 (r=0.283, P=0.002), HBV-DNA loads (r=0.229, P=0.014), and CRP (r=0.237, P=0.011).
CONCLUSIONS sPD-L1 level is a prognostic indicator of poor outcomes after TACE. High sPD-L1 might reflect increased immune activation in an immunosuppressive environment that hindered anti-tumor response activity. Lowering sPD-L1 levels may provide a novel avenue for preventing HCC progression post-TACE.

PU-0872

BCL11B suppresses tumor progression and stem cell traits in hepatocellular carcinoma by restoring p53 signaling activity

Wenjing Yang[1]、YUN-FAN SUN[1]、AN-LI JIN[1]、BEI-LI WANG[1]、TE LIU[2]、BAI-SHEN PAN[1]、JIAN ZHOU[1]、JIA FAN[1]、XIN-RONG YANG[1]、WEI GUO[1]
1. Department of Laboratory Medicine, Zhongshan Hospital, Fudan University
2. 上海中医药大学；上海老年医学研究所

Background Cancer stem cells (CSCs) are a rare subclass of highly tumorigenic cells with self-renewal capacity and differentiation potential. Previous studies identified B cell leukemia/lymphoma-11b (BCL11B) as a novel tumor suppressor with the potential to restrain CSC traits. The implications of BCL11B in hepatocellular carcinoma (HCC) remain unclear.
Methods The prognostic value of BCL11B in patients with HCC was evaluated by immunohistochemistry staining. The effects of BCL11B silencing and overexpression in HCC cell lines were measured. HCC cell self-renewal and proliferation were assessed in vitro and in vivo. CCK-8 and colony-formation assays were conducted to assess proliferation potential. Cell cycle progression and apoptosis were evaluated by flow cytometry. Transwell and wound-healing assays were performed to determine migration capacities. A Cignal Finder Center 10-Pathway Reporter Array was used to identify key downstream pathways.
Results Low BCL11B expression was an independent indicator for shorter overall survival (OS) and time to recurrence (TTR). In vitro and in vivo experiments confirmed BCL11B as a tumor suppressor in HCC with inhibitory effects on proliferation, cell cycle progression, apoptosis, and mobility. BCL11B suppressed CSC traits, as evidenced by dramatically decreased liver spheroid formation and enhanced drug sensitivity. Mechanistically, BCL11B activated P53 signaling by triggering P73 transcription. BCL11B exerted its inhibitory functions on HCC cells regardless of P53 mutation status.
Conclusions BCL11B is a strong suppressor of CSC traits in HCC. Ectopic expression of BCL11B should be investigated as a strategy for anti-HCC treatment with the potential to cure HBV-related HCC regardless of P53 mutation status.

PU-0873

长链非编码 RNA 作为新的诊断标志物在自身免疫病中的进展研究

孙萌、李忠信、王文强
郑州安图生物工程股份有限公司

长链非编码 RNA (Long non-coding RNA, LncRNA)是多种生物学和病理过程中的重要调控分子。已有的研究显示 LncRNA 和 microRNA（miRNAs）作为竞争性内源性 RNA（ceRNA）在控制基因表达及多种疾病发生发展中发挥重要作用。自身免疫性疾病是指机体对自身抗原发生免疫反应而导致自身组织损害所引起的疾病。目前，自身免疫性疾病患病率逐年增加。此外，自身免疫病及其发病机制的研究一直是体外诊断研究的热点和难点。通过 LncRNA 表达水平与自身免疫性疾病的相关研究，可以进一步加深我们对疾病发展及发病机制的了解。因此，考察 LncRNA 作为一种诊断标志物在自身免疫病中的研究进展，可为临床工作者以及体外诊断研究者提供重要的参考资料。

PU-0874

BMP4 过表达诱导阿尔茨海默病 APP/Tau 蛋白的上调和记忆缺陷研究

汪晶、马丽、徐旺旺、程阳
蚌埠医学院

目的 探讨 BMP4 在阿尔茨海默症中所扮演的角色及作用机制
方法 利用神经烯醇化酶（NSE）启动的 BMP4 过表达的转基因小鼠并结合阿尔茨海默症常用的模型细胞株小鼠神经瘤细胞（N2A）、海马神经细胞（HT22）、人神经母细胞瘤（SH-SY5Y）。1.将 BMP4 转基因鼠和野生鼠分为 1 月、3 月、6 月、9 月四个年龄段，用 WB 和 RT-PCR 技术检测不同年龄段海马组织中 AD 诊断标志物及凋亡的变化。2.6 月龄的实验鼠用 Morris 水迷宫实验。3.TUNEL 荧光实验和 HE 染色检测 9 月龄老年实验鼠海马组织凋亡和神经元丢失的情况。4.细胞株通过 RT-PCR 技术检测 3 种细胞株 BMP4 基因的 RNA 水平的表达量，通过 WB、RT-PCR、MTT 细胞增殖实验等方法探究 BMP4 水平的高低是否影响阿尔茨海默病的进展。
结果 1.Morris 水迷宫实验证明 6 月龄的 NSE-BMP4 转基因小鼠记忆出现缺失；2.实验鼠海马组织蛋白和 mRNA 结果证明 NSE-BMP4 转基因鼠 β 淀粉样蛋白和异常磷酸化 TAU 蛋白升高且神经元凋亡增加；3.细胞株实验证明 BMP4 基因升高后 AD 标志物表达升高，BMP4 敲低后则这些标志物表达降低。4.细胞株 MTT 实验证明 BMP4 升高后细胞增殖能力减弱，敲低则增强；流式细胞仪细胞凋亡结果显示 BMP4 过表达后细胞凋亡率增加，敲低则减少；5.9 月龄实验鼠海马组织 TUNEL 实验发现，与野生鼠相比 NSE-BMP4 转基因鼠海马组织 CA1、CA3 区和齿状回 DG 区凋亡率增加。6.9 月龄鼠 BMP4 转基因小鼠海马组织 CA1 和 CA3 区的椎体细胞排列紊乱，出现一定的神经细胞丢失现象。
结论 1.Morris 水迷宫实验证明中年期 NSE-BMP4 转基因小鼠有存在空间记忆障碍；2.BMP4 可对通过 β 淀粉样蛋白沉积机制，PSEN 突变机制和 TAU 蛋白异常磷酸化机制调控阿尔茨海默病；3.BMP4 促进神经细胞的凋亡和抑制神经细胞的增殖。

PU-0875

中枢神经系统淋巴瘤脑脊液中弥漫性大 B 细胞的单细胞转录组分析

阮浩宇
江苏省人民医院（南京医科大学第一附属医院）

弥漫性大 B 细胞淋巴瘤（DLBCL）是中枢神经系统淋巴瘤（CNSL）的主要类型，包括原发性 CNSL 和继发性 CNSL。脑脊液中弥漫性大 B 细胞（CSF-DLBCs）为 CNSL 脑膜转移的诊断和治疗提供了广阔前景。为了探索 CSF-DLBCs 的特征，我们使用 Smart-seq2 单细胞 RNA 测序（scRNA-seq）分析了六名 CNSL-DLBCL 患者 1000 多个 CSF-DLBCs 的转录组。通过分析发现 CSF-DLBCs 高表达 B 细胞标记物，增殖和代谢活跃。CSF-DLBCs 表现出免疫球蛋白轻链限制性（LCR），但值得注意的是，某些 CSF-DLBC 具有 lambda 和 kappa 两种轻链可变区。CSF-DLBCs 异质性较高，病人间异质性高于病人内异质性，且细胞间异质性 CSF-DLBCs 主要表现在细胞周期状态，癌-睾丸抗原的表达以及基于单细胞生发中心（sc-GC）B 细胞特征的细胞分类。另外，与各种正常 B 细胞相比，CSF-DLBC 中基因 CCDC167, EML6, EZH2, HAUS1, LAS1L, METTL26, NCAPH2, NT5DC2, NUSAP1, PHF19, PKMYT1, PTTG1, RRM2, SH3TC1, SMC4, TIMM50 显著上调，这 16 个基因在 CNS-DLBCL 发生发展中具有潜在的重要价值。该研究是首次系统全面地分析 CSF-DLBCs 转录组特征，为 CNSL-DLBCL 的机制研究和诊断提供新的方向。

PU-0876

Circulating tumor cell characterization of lung cancer brain metastases in the cerebrospinal fluid through single-cell transcriptome analysis

Haoyu Ruan
Jiangsu Province Hospital

Background Brain metastases explain the majority of mortality associated with lung cancer, which is the leading cause of cancer death. Cytology analysis of the cerebrospinal fluid (CSF) remains the diagnostic gold standard, however, the circulating tumor cells (CTCs) in CSF (CSF-CTCs) are not well defined at the molecular and transcriptome levels.
Methods We established an effective CSF-CTCs collection procedure and isolated individual CSF cells from five lung adenocarcinoma leptomeningeal metastases (LUAD-LM) patients and three controls. Three thousand seven hundred ninety-two single-cell transcriptomes were sequenced, and single-cell RNA sequencing (scRNA-seq) gene expression analysis was used to perform a comprehensive characterization of CSF cells.
Results Through clustering and expression analysis, we defined CSF-CTCs at the transcriptome level based on epithelial markers, proliferation markers, and genes with lung origin. The metastatic-CTC signature genes are enriched for metabolic pathway and cell adhesion molecule categories, which are crucial for the survival and metastases of tumor cells. We discovered substantial heterogeneity in patient CSF-CTCs. We quantified the degree of heterogeneity and found significantly greater among-patient heterogeneity compared to among-cell heterogeneity within a patient. This observation could be explained by spatial heterogeneity of metastatic sites, cell-cycle gene, and cancer-testis antigen (CTA) expression profiles as well as the proportion of CTCs displaying mesenchymal and cancer stem cell properties. In addition, our CSF-CTCs transcriptome profiling allowed us to determine the biomarkers during the progression of an LM patient with cancer of unknown primary site (CUP).
Conclusions Our results will provide candidate genes for an RNA-based digital detection of CSF-CTCs from LUAD-LM and CUP-LM cases, and shed light on the therapy and mechanism of LUAD-LM.

PU-0877

Role of circulating free DNA in evaluating clinical tumor burden and predicting survival in Chinese metastatic colorectal cancer patients

XIAO-JING XU、YI-YI YU、MIN-NA SHEN、Mengling Liu、SHENG-CHAO WU、Li Liang、FEI HUANG、Chenlu Zhang、WEI GUO、TIAN-SHU LIU
Department of Oncology, Zhongshan Hospital, Fudan University, Shanghai, China;

Background The aim of this study was to explore the utility of circulating free DNA (cfDNA) in the evaluation of clinical tumor burden and survival in Chinese patients with metastatic colorectal cancer (mCRC) and to preliminarily summarize some metastatic characteristics associated with mutational status.
Methods A panel covering a total of 197 hotspot mutations of KRAS, NRAS, BRAF and PIK3CA was used to evaluate the mutational status in plasma by next-generation sequencing (NGS) technology in 126 patients with mCRC. An amplification-refractory mutation system (ARMS) was used to analyze genomic DNA from matched tissue samples.
Clinical markers including carcinoembryonic antigen (CEA), carbohydrate antigen 199 (CA199), carbohydrate antigen 125 (CA125), neuron-specific enolase (NSE) and lactate dehydrogenase

(LDH) in serum and the sum of all tumor diameters on CT or PET/CT were collected to indicate clinical tumor burden. The correlations between cfDNA and clinical tumor burden were analyzed using Pearson correlation and linear regression models. The median progression- free survival (PFS) and 1-year overall survival (OS) rates were calculated by Kaplan-Meier (K-M) survival analysis.

Results Of the 126 enrolled patients, patients who were tested positive for mutations in plasma accounted for 45.2% (57/126). Mutations in KRAS, NRAS, BRAF and PIK3CA were detected in 37.3% (47/126), 1.6% (2/126), 3.2% (4/126) and 13.5% (17/126) of patients, respectively. The overall concordance rate of mutational status between plasma and matched tissues was 78.6% (99/126). Sixteen patients had mutations in plasma that were not detected in tissue, including some rare hotspot mutations. The cfDNA concentration was significantly correlated with the levels of clinical markers, especially CEA ($P < 0.0001$, Pearson $r = 0.81$), LDH ($P < 0.0001$, Pearson $r = 0.84$) and the sum of tumor diameters ($P < 0.0001$, Pearson $r = 0.80$). Patients with a high cfDNA concentration (> 17.91 ng/ml) had shorter median progression-free survival (6.6 versus 11.7 months, $P < 0.0001$) and lower 1-year overall survival rate (56% versus 94%, $P < 0.0001$) than those with a low cfDNA concentration (≤17.91 ng/ml). The most common metastatic site was the liver (77.8%), followed by the lymph nodes (62.7%), lung (40.5%), peritoneum (14.3%) and bone (10.3%), in all patients. There was no significant difference in metastasis between different mutational statuses.

Conclusion Analyzing mutations in plasma could provide a more comprehensive overview of the mutational landscape than analyzing mutations in tissue. The cfDNA concentration could be a quantitative biomarker of tumor burden and could predict survival in Chinese patients with mCRC.

PU-0878

HCV6 型 NS3 基因区域耐药检测方法学的建立

曾征宇、郭晓磊、代艳峰、温俊雄
广州金域医学检验中心有限公司

目的 通过检测已知为 HCV 6 型（6a,6n）的丙肝患者血浆样本 NS3 基因突变位点，建立并评价 HCV 直接抗病毒药物的耐药检测方法，为临床直接抗病毒治疗提供相关依据。

方法 设计针对 HCV 6 型（6a,6n）NS3 区域的扩增及测序引物，收集广州金域医学检验中心有限公司分型为 HCV 6 型（6a,6n）的丙肝患者的血浆样本；从血浆样本中提取 HCV RNA 模板，一步法反转录 PCR 法扩增 HCV NS3 片段，琼脂糖凝胶电泳鉴定扩增片段的正确性及产物大致浓度；满足测序要求时利用 ABI3730xl 测序仪进行测序；未满足测序要求的样本以第一轮扩增产物为模板进行巢式 PCR 扩增并测序。然后使用序列分析软件 Sequencher 将得到的序列与 HCV 6 型参考序列进行比对，进而确定分析位点的氨基酸变异情况。最后对检测数据进行统计分析，评价有效性、重复性和最低检出限三个方法学参数的分析性能。

结果 使用 40 例样本进行有效性验证，经过两轮 PCR，扩增及测序成功率为 100%（40/40）；使用 20 例样本由不同操作人员、在不同时间和不同仪器上进行重复性验证，结果显示该检测方案的重复性为 96.25%（77/80）；使用进行分别梯度稀释后的 5 例 HCV 阳性样本进行最低检出限验证，初步认为，该检测方案的最低检出限为在 1.00E+03IU/mL。

结论 该检测方案在用于 HCV 6 型 NS3 基因区域的耐药检测过程中，方法学性能良好，有望应用于临床相关检测。

PU-0879

Circular RNA hsa-circ_0003945 promotes progression of hepatocellular carcinoma by mediating miR-34c-5p/LGR4/GSK-3β axis

Lihua Lv、CHUN-YAN ZHANG、XIN-RONG YANG、WEI GUO
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University

Aim Accumulating evidence proposed that circular RNAs (circRNAs) play essential roles in regulating cancer progression, but many circRNAs in hepatocellular carcinoma (HCC) remain unknown. In this study, we evaluated the dys-regulated circRNAs in HCC patients and explored the role of hsa_circ_0003945 (circ_0003945) and its underlying mechanism in HCC.
Methods Dysregulated circRNAs in HCC were identified through the bioinformatics analysis of Gene Expression Omnibus data sets. The qRT-PCR, Sanger sequencing, RNase R treatment, and actinomycin D treatment were conducted to confirm the characterization of circRNAs. The CCK-8, wound healing, transwell assay were performed to assess the functional role of hsa_circ_0003945 (circ_0003945) in HCC cells. The subcellular fraction assay and fluorescence in situ hybridization (FISH) assay were performed to locate the circ_0003945 in HCC cells. Dual-luciferase reporter assay was executed to verify the binding of circ_0003945 with miRNAs or the miRNAs with their target genes.
Results In this study, we found that circ_0003945 was upregulated in tissues, and higher circ_0003945 expression was positively correlated with tumor size and CNLC stages. The functional experiments revealed that overexpression or knockdown of circ_0003945 promoted or attenuated tumor growth and invasion, respectively. Mechanically, circ_0003945 might function as miR-34c-5p sponge to upregulate the expression of LGR4, which inactive GSK-3β/phospholating β-catenin pathway and finally facilitated the malignant progression of HCC cells. Additionally, GSK-3β activator or Wnt/β-catenin inhibitor could also reverse the consequence caused by intervening the expression level of circ_0003945.
Conclusion The circ_0003945 exerts a tumor-promoting role in HCC progression by regulating miR-34c-5p/LGR4/GSK-3β axis, which may be a potential target for HCC therapy.

PU-0880

The diagnostic value of plasma exosomal hsa_circ_0070396 for hepatocellular carcinoma

Lihua Lv[1]、WEN-JING YANG[1]、HAO WANG[1]、JIE ZHU[1]、AN-LI JIN[1]、TE LIU[2]、BEI-LI WANG[1]、JIAN ZHOU[1]、JIA FAN[1]、XIN-RONG YANG[1]、WEI GUO[1]
1. Department of Laboratory Medicine, Zhongshan Hospital, Fudan University
2. 上海中医药大学 上海老年医学研究所

Aim We aimed to identify novel exosomal circRNAs for HCC diagnosis.
Methods Exosomes was extracted and characterized. The expression level of exosomal circRNAs were verified via quantitative real-time PCR. The diagnostic value of candidate circRNAs was evaluated according to the receiver operating characteristic curve (ROC) analysis.
Results The exosomal circ_0070396 significantly elevated in HCC patients than other control groups and it performed better in distinguishing HCC patients from healthy donors than that of AFP. Combination of two above markers exerted greater diagnostic performance. Exosomal circ_0070396 could discriminate HCC individuals from patients with chronic hepatitis B and liver cirrhosis. Intriguingly, exosomal circ_0070396 was positively correlated with HCC progression.
Conclusion Exosomal circ_0070396 maybe a potential biomarker for HCC detection and management.

PU-0881

磷酸化酶激酶 β 亚基(PHKB)与肿瘤的研究进展

金安莉、杨文静、郭玮
复旦大学附属中山医院

目的 综述磷酸化酶激酶 β 亚基(PHKB)与肿瘤发生、发展之间的关系。
方法 以磷酸化酶激酶 β 亚基、糖原代谢和肿瘤为关键词进行文献检索，建立网络分析图，进行综述分析。
结果 糖原代谢被认为是癌症代谢重编程的关键途径，肿瘤细胞内糖原代谢重编程的特征表现为调控其合成与分解代谢的关键酶的表达或功能异常。糖原分解是机体内糖原代谢的主要方式之一，为肿瘤细胞的增殖提供能量，促进肿瘤的发生发展。磷酸化酶激酶是参与糖原分解过程的关键酶，其活性受到磷酸化酶激酶 β 亚基的调控。近年研究发现，磷酸化酶激酶 β 亚基在多种类型的肿瘤中异常表达，参与肿瘤细胞的增殖和凋亡，并与肿瘤的预后相关，有望成为一种预示肿瘤发生的新型生物分子标志物。
结论 磷酸化酶激酶 β 亚基有望成为一种预示肿瘤发生的新型生物分子标志物。

PU-0882

HBV RNA 检测试剂盒性能验证及临床应用

马艳婷、黄斐、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 对 HBV RNA 检测试剂盒进行性能验证评估；比较不同乙肝两对半模式患者血清 HBV RNA 水平以及其与 HBV DNA 之间的相关性；探究血清 HBV RNA 水平与抗病毒药物治疗的联系。
方法 对 HBV RNA 检测试剂盒进行性能验证评估（包括精密度、灵敏度以及线性范围）；收集 81 例 HBsAg 阳性患者的血清，并进行分组。通过对比分析 HBV RNA 与其他血清学标志物以及治疗用药情况的联系来探讨其潜在临床意义及应用价值。
结果 HBV RNA 试剂盒的低值和高值的批内精密度 CV 为 2.16%、0.63%，批间精密度 CV 为 5.98%、3.11%；灵敏度达 100%；线性回归方程为 y = 0.9769x + 0.1299，R2=0.9995，线性范围为 102~107 copies/ml，性能验证符合要求；HBeAg 阳性组血清 HBV RNA 水平高于 HBeAg 阴性组（P<0.01），在不同两对半模式患者中，HBeAg 阳性且 HBeAb 阴性组 HBV RNA 水平最高（P<0.01）；未经治疗患者血清 HBV RNA 水平高于治疗组患者（P<0.05）；HBV RNA 与 HBV DNA 及 HBeAg 均有相关性（r=0.348，P<0.05；r=0.544，P<0.05）。
结论 HBV RNA 试剂盒性能验证结果满足临床需求，血清 HBV RNA 是一种潜在的乙肝病毒活性及治疗疗效监测的新型标志物。

PU-0883

多平台检测 cfDNA 肿瘤突变在 NSCLC 患者中的应用评估

高姚怡、黄斐、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 对 NGS 平台检测 NSCLC 患者 cfDNA 肿瘤突变进行性能验证，并进行血浆 cfDNA 突变检测的 NGS、ddPCR、super ARMS 平台比对。
方法 对标准品、初诊未治疗 NSCLC 患者血浆 cfDNA 及自制混合标本进行 NGS 平台的检测，以验证 NGS 平台的空白限、分析灵敏度、精密度、准确性及分析特异性；使用 ddPCR、NGS 平台对

复旦大学附属中山医院的 75 例 NSCLC 患者血浆 cfDNA 突变检测，比较两平台对血浆 cfDNA 突变的检测性能，随机抽取 12 例进行 super ARMS EGFR 突变检测，比较 3 平台对 NSCLC 患者血浆 cfDNA 突变检测的检测性能。

结果 本研究 NGS 平台对血浆 cfDNA 突变检测的空白限统一设置为 0.00%；分析灵敏度为 0.2%；批内精密度、批间精密度均为 100%；检测结果不受血浆内源性血红蛋白、胆红素和甘油三酯或外源性 DNA 干扰影响，分析特异性好。75 例 NSCLC 患者血浆 cfDNA ddPCR 平台、NGS 平台检测突变阳性率分别为 61.33%、60%，完全一致率为 89.33%。

结论 NGS 平台可用于 NSCLC 患者的 cfDNA 突变检测；ddPCR、NGS、super ARMS 对 NSCLC 患者血浆 cfDNA 的突变检测各有优点，可根据临床需要选择。

PU-0884

Chemotherapy-associated clonal hematopoiesis mutations should be taken seriously in plasma cell-free DNA RAS/BRAF genotyping for metastatic colorectal cancer

Fei Huang、YI-HUI YANG、BAI-SHEN PAN、BEI-LI WANG、WEI GUO
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University

Background Genotyping of plasma cell-free DNA (cfDNA) is an increasingly important method to assess the tumor mutation status in colorectal cancer (CRC) patients. Clonal hematopoiesis (CH) releases non-tumor somatic mutations into blood, causing false positive results in cfDNA-based tumor genotyping. Till now, it is still not clear if CH should be examined in all the CRC patients undergoing cfDNA analysis.
Methods We analyzed cfDNA KRAS/NRAS/BRAF genotypes in 236 metastatic CRC patients, who had matched tissue genotyping results, by next-generation sequencing using plasma cfDNA. The cfDNA-only mutations with allele frequencies (AFs) <5% were defined as candidate CH-derived mutations. CH-derived mutations were finally determined by droplet digital PCR (ddPCR) using paired peripheral blood cells (PBCs). A patient with a CH-derived mutation was followed up and the subpopulation of blood cells, in which CH was present, was investigated.
Results Three CH-derived mutations, KRAS Q61H, KRAS G12D and KRAS G12V, were identified in the patient cohort. All the three patients harboring corresponding CH-derived mutations had a prior chemotherapy history. The CH-derived KRAS G12V mutation in a patient was found only present in lymphocytes and persisting under treatment. For all the cfDNA mutations, the CH-derived ones were clustered in the patients with <5% mutation AF and prior chemotherapy.
Conclusion It is recommended for patients with <5% mutation AF and prior chemotherapy to take genotyping analysis of their PBCs following plasma cfDNA genotyping.

PU-0885

Cross-platform comparison of NGS and MALDI-TOF mass spectrometry for detecting RAS/RAF/PIK3CA mutations in cfDNA from metastatic colorectal cancer patients

Fei Huang、MIN-LU CAO、BEI-LI WANG、WEI GUO
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University

Background Examining the tumor RAS/RAF/PIK3CA status in metastatic colorectal cancer (mCRC) is essential for treatment selection and prognosis evaluation. Cell-free DNA (cfDNA) in the circulatory system is a feasible source for tumor gene analysis.

Methods In this study, we recruited mCRC patients and analyzed their KRAS/BRAS/BRAF/PIK3CA status in cfDNA using two platforms, next-generation sequencing (NGS) and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). The performance between the two platforms and the concordance between cfDNA and tissue were analyzed. The relationship between cfDNA-related variables and clinical variables were also assessed. For the patients that carried tumor mutations and received continuous treatments, their cfDNA was monitored in the follow-ups.
Results NGS reported 1 false negative result of 840 reportable ones, whereas MALDI-TOF reported 6 false positive ones and 5 false negative ones. The overall concordance rate of NGS and MALDI-TOF was 98.6%. For the reportable types of mutations in both cfDNA and tissue, the concordance rate was 96.1%. Among 28 tissue-positive patients, the allele frequencies of tumor mutations in cfDNA was significantly higher in patients with primary tumor burden. Both CEA and CA 19-9 were positively correlated with cfDNA concentration. The allele frequencies of tumor mutations changed with disease progression.
Conclusions Compared to MALDI-TOF, NGS showed slightly better performance in detecting cfDNA mutations. cfDNA was a valuable source for tumor mutation detection, with a high concordance rate with tissue. As well as serum biomarkers, cfDNA-related variables reflected the tumor status, showing a promising potential in monitoring disease progression.

PU-0886

卡氏肺孢子虫肺炎患者肺泡灌洗液的免提取 PCR 检测方法的建立及临床应用评估

杨轶慧、王蓓丽、郭玮
复旦大学附属中山医院

参考中国医师协会检验医师分会分子诊断专家委员会《实验室自建分子诊断项目基本要求专家共识》相关要求，验证本实验室自建的卡氏肺孢子虫肺炎患者肺泡灌洗液的免提取 PCR 检测方法各项性能参数。
方法 2016 年 1 月-2019 年 12 月复旦大学附属中山医院已确诊的 10 例肺炎患者的肺泡灌洗液样本及自配标准品质粒。根据卡氏肺孢子虫基因保守序列设计引物和探针，建立一种免提取核酸的荧光 PCR 检测方法。在准确性、精密度、检出限、分析特异性、临床符合率等各方面对检测方法的性能进行评估。
结果 基于肺泡灌洗液样本的免提取 PCR 检测方法的准确性一致性为 100%；精确性符合率为 100%；最低检出限为 500 拷贝/ml；特异性符合率为 100%；临床符合率为 100%。
结论 基于免提取荧光 PCR 反应方法检测卡氏肺孢子虫可用于卡氏肺孢子虫肺炎患者的快速筛查和辅助诊断。

PU-0887

高通量测序生信数据分析提示结直肠癌患者 ERBB2 扩增

沈敏娜、郁俐、陈馨宁、王蓓丽、郭玮
复旦大学附属中山医院

目的 回顾性分析非涵盖 ERBB2 扩增检测的高通量测序检测方法生信数据对 ERBB2 扩增的潜在提示价值。
方法 回顾性分析经病理活检确诊为结直肠癌，并接受外周血 cfDNA 高通量测序检测样本的生物信息学数据 252 例。根据经免疫组织化学（immunohistochemistry, IHC）和荧光原位杂交(fluorescence in situ hybridization, FISH)判断为 ERBB2 非扩增样本的生物信息学数据，初步确定

其提示 ERBB2 扩增的临界值。根据临界值筛选可疑阳性样本，使用数字 PCR、IHC 和 FISH 进行验证。
结果 89 例经 IHC 和 FISH 判定为 ERBB2 非扩增样本的 17 号染色体占检测区域 Reads 数比例范围为 0.188~0.299。以 0.299 作为提示 ERBB2 扩增的临界值分析 163 例样本数据，其中 7 例疑似阳性，比例范围 0.302~0.853。其中 5 例经 IHC 和 FISH 判定为阳性，其中 6 例经数字 PCR 验证为阳性，ERBB2/EIF2C1 比值与 17 号染色体占检测区域 Reads 数比例成正相关，相关性好，r2=0.9498。
结论 高通量测序生信数据对结直肠癌患者 ERBB2 扩增有一定提示价值。

PU-0888

基于 GeneXpert 系统的结核分枝杆菌检测及利福平耐药的研究

郭晓磊、曾征宇、唐耀祖
广州金域医学检验中心

目的 通过回顾性研究广州金域医学检验公司 2015 年 4 月~2018 年 3 月不同标本类型、不同地区、不同性别及不同年龄段人群的结核分枝杆菌(MTB)阳性率及利福平(RIF)耐药率的情况，对临床采样提供指导意义同时对发病率高的人群指导采取干预措施，从而指导疾病防控。
方法 采用 GeneXpert MTB/RIF 方法对 11918 例疑似结核患者的标本进行检测，统计 MTB 阳性及 RIF 耐药的数据，分析其意义。
结果 11918 例患者 MTB 阳性率为 28.51%，RIF 耐药率为 15.27%。其中，痰液的 MTB 阳性率最高，为 34.06%；关节液的 RIF 耐药率最高，为 28.57%；各标本类型的 MTB 阳性率及 RIF 耐药率差异具有统计学意义(χ^2=480.86，P<0.05；χ^2=457.38，P<0.05)；东北地区 MTB 阳性率及 RIF 耐药率均最高，各地区 MTB 阳性率及 RIF 耐药率差异具有统计学意义(χ^2=196.49，P<0.05；χ^2=46.89，P<0.05)；男性 MTB 阳性率显著高于女性，差异具有统计学意义(χ^2=92.05，P<0.05)，RIF 耐药率差异无统计学意义(χ^2=0.73，P>0.05)；20~29 岁年龄段患者 MTB 阳性率最高，40~49 岁年龄段患者 RIF 耐药率最高，各年龄段 MTB 阳性率及 RIF 耐药率差异具有统计学意义(χ^2=143.86，P<0.05；χ^2=52.57，P<0.05)；各年份 MTB 阳性率差异具有统计学意义(χ^2=21.92，P<0.05)，各年份 RIF 耐药率差异无统计学意义(χ^2=7.59，P>0.05)。
结论 各标本类型中，以痰液标本 MTB 阳性率最高，为首选标本类型；在全国七个地区中，以东北地区 MTB 阳性率最高，患者男性多于女性，MTB 阳性主要集中在青年年龄段(21~29 岁)，RIF 耐药主要集中在中年年龄段(40-49 岁)，对于结核的防控，应针对重点人群。

PU-0889

Correlation between steroid levels in follicular fluid and hormone synthesis related substances in its exosomes and embryo quality in patients with polycystic ovary syndrome

LI YU、BEI-LI WANG、WEI GUO
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University, Shanghai

Purpose Polycystic ovary syndrome (PCOS) is a major endocrine and metabolic disorder with heterogeneous manifestations and complex etiology. Follicular fluid (FF) serves as the complex microenvironment for follicular development. However, the correlation between the concentration of steroid in FF and the pathogenesis of PCOS is still unclear.
Methods 20 steroid levels in FF from ten patients with PCOS and ten women with male-factor infertility

undergoing in vitro fertilization were tested by liquid chromatography-tandem mass spectrometry (LC-MS/MS) in order to explore their possibly correlation with PCOS. Meanwhile, the mRNA expression levels of core enzymes in steroid synthesis pathway from exosomes of FF were also detected by qPCR.
Results The estriol ($p < 0.01$), estradiol ($p < 0.05$) and prenenolone ($p < 0.01$) levels in FF of PCOS group were significantly increased, compared to the normal group, and the progesterone levels ($p < 0.05$) were decreased in PCOS group. Increased mRNA levels of CYP11A, CYP19A and HSD17B2 of exosomes were accompanied by the changes in hormonal levels in FF. Correlation analysis showed that mRNA levels of CYP11A and HSD17B2 were negatively and significantly correlated with percent of good-quality embryos and rate of embryos develop to blastocyst.
Conclusion Our results suggest that increased levels of estrogen and pregnenolone in follicular fluid may affect follicle development in PCOS patients, and the mechanism is partially related to HSD17B1, CYP19A1 and CYP11A1 expression change in FF exosomes.

PU-0890

Role of blood mSEPT9 in evaluating tumor burden and disease monitoring in colorectal cancer patients

HUI-QIN JIANG、BEI-LI WANG、WEI GUO
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University.

Purpose This study aimed to investigate the correlation between mSEPT9 and tumor burden and explore the role of mSEPT9 in disease monitoring in CRC patients.
Methods A total of 309 patients were recruited and received mSEPT9 detection in this retrospective study. Clinicopathologic characteristics were collected, including age, gender, differentiation, gene mutation, stage, tumor marker, and so on. The correlations between mSEPT9 and clinical tumor burden were analyzed. A relative mSEPT9 value was determined using the △△Ct method.
Results The overall positivity rate of mSEPT9 was 39.8% in CRC patients. mSEPT9 status was significantly associated with disease status and tumor marker (CEA and CA19-9). The mSEPT9 positivity rate was 15.6%, 50.0%, 64.4%, and 70.0% for P0M0, P1M0, P0M1, and P1M1, respectively ($P<0.001$). Among 137 CRC patients who received mSEPT9 assay before surgery, the pre-operation mSEPT9 positivity rate increased significantly from UICC stage I to stage IV CRC patients (Stage I vs. II vs. III vs. IV 25% vs. 59.1% vs. 57.1% vs. 70.0%, respectively). Consecutive blood samples were available from 26 patients on therapy. The patients with increased mSEPT9 levels after treatment showed a higher progression rate.
Conclusion mSEPT9 was a biomarker reflecting tumor burden, and serial detecting of mSEPT9 could be a promising strategy for disease monitoring in CRC patients.

PU-0891

一种快速、灵敏的 SARS-CoV-2 感染环介导等温扩增试验的研制及临床应用

邓倩昀、胡雪姣、侯铁英
广东省人民医院

目的 开发和验证一种新的反转录环介导的等温扩增（RT-LAMP）方法来检测严重急性呼吸综合征冠状病毒 2 型（SARS-CoV-2）。SARS-CoV-2 的爆发迫切需要敏感、便捷的诊断方法，以遏制疫情和及时治疗患者。

方法 从 2020 年 1 月 26 日至 4 月 8 日，在两家医院招募疑似 COVID-19 患者和密切接触者。采集呼吸道标本，采用 RT-LAMP 检测，并与逆转录定量 PCR （RT-qPCR）检测结果进行比较。两种方法结果不一致的样品进行二代测序确认。RT-LAMP 还应用于无症状 COVID-19 携带者和其他呼吸道病毒感染患者。

结果 共收集 129 例患者（329 例鼻咽拭子）和 76 例患者（152 例鼻咽拭子和痰样本）的样本。RT-LAMP 方法被证实准确度高（总灵敏度和特异度分别为 88.89%和 99.00%）和诊断效能高（阳性和阴性似然比分别为 88.89 和 0.11）。与 RT-qPCR 相比，RT-LAMP 检测 SARS-CoV-2 的灵敏度更高（88.89% vs 81.48%）、一致性更高（kappa, 0.92），且只需要恒温加热和目视判读结果。RT-LAMP 从样品制备到结果所需时间均在 1 h 以内。此外，RT-LAMP 可用于无症状患者，且不与其他呼吸道病原体发生交叉反应。

结论 我们开发的 RT-LAMP 一种提供了快速、敏感和直接的 SARS-CoV-2 感染检测方法，可能有助于在公共领域和医院扩大 COVID-19 检测范围。

PU-0892

基于 COVID-19 确诊患者临床多种生物样本监测 2019-nCoV RNA 比对研究

张驰[1]、王钒[1]、何雯雯[1]、宋玉霞[1]、许珺[1]、舒占钧[1]、张蕊[1]、李远达[1]、王子璠[1]、段丽[1]、屈晓娟[1]、赵豆豆[1]、木尼热·库尔班[1]、何雪[1]、林国跃#[1]、蔺志强[1]、易嘉敏[2]、王珂[3]

1. 新疆医科大学第八附属医院（新疆新冠肺炎医疗救治定点医院）

2. 广州中医药大学第一临床医学院中西医临床，广州市 510006；

3. 广东省广州市天河区黄埔大道石牌村广东省结核控制中心，广州市 510000

目的 探讨冠状病毒病 (corona virus disease 2019，COVID-19) 患者不同部位核酸检测阳性率及其影响因素。

方法 应用 2019-nCoV ORF1ab/N 基因双重实时荧光 PCR 技术对新疆维吾尔自治区第六人民医院 2020 年 1 月 31 日-2 月 19 日定点收治住院的 46 例 COVID-19 患者不同部位样本进行 2019-nCoV 核酸检测，分析比较咽拭子、痰液、粪便的病毒核酸检测阳性率。

结果 46 例 COVID-19 患者共检测咽拭子 246 人次，痰液 18 人次，粪便 15 人次，其核酸检测阳性率咽拭子 43.90% (108/246)、痰液 33.33%(5/15)、粪便 38.89%(7/18),咽拭子检出阳性率高于痰液及粪便，但三者阳性率差异无统计学意义（P ＞ 0.05）；对疑难危重型患者有针对性的重点同时采集 2 种不同生物样本进行 2019-nCoV 核酸检测，发现 10 例咽拭子/粪便样本检测阳性率 80.00%(8/10) /70.00 %(7/10)，比 4 例咽拭子/痰液样本 75.00%(3/4)/ 50.00%(2/4)和 2 例粪便/痰液样本 0.0%(0/2）/50.00%(1/2)同时检测效果明显的高，经 Fisher 精确检验组内比较无统计学意义（P＞ 0.05）。

结论 重点监测 COVID-19 患者选择咽拭子或痰液样本就可以及时明确临床诊断、预估病情进展及预后，对已确诊的 COVID-19 患者同时采集不同部位样本反复监测 2019-nCoV RNA 其临床诊断意义不大。

PU-0893

成骨不全患者临床分型及表型分析

白雪[1]、常小丽[1]、官士诊[1]、任秀智[2]、王毅[1]
1. 天津市天津医院
2. 天津市武清区人民医院

目的 研究 COL1A1/COL1A2 基因突变的成骨不全（osteogenesis imperfecta, OI）患者临床分型及临床表型。
方法 收集天津市天津医院及天津市武清区人民医院就诊的 OI 患者，经基因检测已确诊为 COL1A1/COL1A2 基因突变患者 28 例，其中 COL1A1 基因突变患者 17 例、COL1A2 基因突变患者 11 例，分析这些 OI 患者的临床分型及表型。
结果 28 例 COL1A1/COL1A2 基因突变的 OI 患者中，临床分型为 IV 型的 OI 患者占 57.14%、Ⅰ型 OI 患者占 32.14%、Ⅲ型 OI 患者占 10.71%。Ⅰ型患者与Ⅲ型患者例数比较无显著性差异（χ^2 =3.84，P>0.05），Ⅰ型患者与 IV 型患者例数比较无显著性差异（χ^2 =3.54，P>0.05）。IV 型 OI 患者例数大于Ⅲ型 OI 患者例数（χ^2 =13.46，P<0.01）。在 OI 患者的临床表型中，蓝巩膜占 100%，四肢畸形占 82.14%，牙质形成不全占 67.86%，脊柱及胸部畸形各占 35.71%，影响活动能力，不能自行行走的患者占 42.86%。初次骨折的年龄从出生到 13 岁均有发生，初次骨折的平均年龄为 2 岁。患者骨折次数从 2 次到 80 次均有发生，平均骨折的次数为 18 次。OI 患者身材矮小，但Ⅰ型 OI 患者身高可接近正常水平。
结论 COL1A1/COL1A2 基因突变的 OI 患者临床表型变化多样，临床表型前三位依次为，蓝巩膜、四肢畸形、牙质形成不全。初次骨折时间越早、骨折次数越多，病情越严重。临床表型较严重的患者临床分型以Ⅲ型、IV 型居多。临床分型和临床表型分析有助于 OI 患者的诊断和发病机制研究。

PU-0894

恒温扩增芯片技术在下呼吸道感染性疾病诊断中的应用价值评估

吕阳花
攀枝花市中心医院

目的 评价恒温扩增芯片技术在医院下呼吸道感染性疾病诊断中的应用价值。
方法 纳入于 2020 年 11 月~2021 年 5 月攀枝花市中心医院呼吸科和重症医学科疑似下呼吸道感染住院患者 506 例，在抗生素使用前采集痰液或肺泡灌洗液标本，通过恒温扩增芯片技术（芯片法）检测 13 种呼吸道常见病原菌，同时进行痰培养，比较芯片法和痰培养方法的检出率。
结果 芯片法共检出 167 例样本阳性，阳性率 33.00%（167/506），高于培养法的 17.39%（88/506），差异具有统计学意义；芯片法检出阳性样本中，单一感染 120 例，占比 71.86%（120/167），混合感染 47 例，占比 28.14%（47/167），混合感染以 2 重感染为主，占混合感染的 70.21%（33/47），另外在 4 例样本中分别检出 4 种病原菌混合感染；芯片法检出率排名前五位的病原菌分别为肺炎克雷伯菌（21.65%）、流感嗜血杆菌（16.45%）、结核分枝杆菌（13.85%）、铜绿假单胞菌（10.82%）和肺炎链球菌（7.79%）；同时，芯片法检出 1 例嗜肺军团菌和 3 例肺炎支原体。
结论 恒温扩增芯片技术检测呼吸道病原菌操作简便、快速、灵敏度高，可同时检出 13 种呼吸道常见病原菌，病原体的检出率明显高于培养法，并且在结核分枝杆菌、嗜肺军团菌、肺炎支原体等难培养病原菌感染的诊断方面优于培养法。

PU-0895

血浆 Septin9 甲基化检测在结直肠癌诊断中的临床意义

刘冬雪
吉林金域检验医学检验所有限公司

目的 通过研究血浆中游离 DNA Septin9 甲基化检测灵敏度与结直肠癌诊断及分期的关系，探讨血浆 Septin9 甲基化检测在结直肠癌诊断中的临床意义。
方法 收集 2014 年至 2017 年间权威研究机构收取的大样本 1330 例进行临床研究试验，受试者年龄全部在 30 岁到 80 岁之间，其中有结直肠癌阳性患者 586 例，结直肠癌前病变及早期其它肠道系统疾病患者 744 例。对这 1330 例大样本进行 Septin9 甲基化检测，评价其在结直肠癌诊断中的价值。
结果 通过对 1330 例样本结果进行逐一分析，其中结直肠癌阳性符合率为 76.45%，结直肠癌阴性符合率为 90.32%,总体符合率为 84.21%。在探讨 Septin9 甲基化检测与结直肠癌分期的研究中，1 期结直肠癌阳性符合率为 63.89%，2 期结直肠癌阳性符合率为 75.92%，3 期结直肠癌阳性符合率为 82.82%，4 期结直肠癌阳性符合率为 90.41%。
结论 Septin9 甲基化检测结果与患者的年龄、性别无相关性，检测灵敏度与结直肠癌分期呈正相关。Septin9 甲基化检测在结直肠癌诊断中有比较高的灵敏度与特异度，优势为无创伤、采样方便快捷、样本利用度高、方法稳定等，临床推荐适用于不能或不愿意接受肠镜检查结直肠癌高风险人群，可以与肠镜检测优势互补，提高肠镜的一次阳性检出率，因此可以作为在临床检测中诊断结直肠癌的辅助手段。

PU-0896

Screening and functional prediction of key candidate genes in hepatitis B virus-associated hepatocellular carcinoma

Ling Liao、Shaoli Deng
中国人民解放军陆军特色医学中心

Background The molecular mechanism by which hepatitis B virus (HBV) induces hepatocellular carcinoma (HCC) is still unknown. The genomic expression profile and bioinformatics **Methods** were used to investigate the potential pathogenesis and therapeutic targets for HBV associated HCC (HBV-HCC).
Methods Microarray dataset GSE55092 was downloaded from the Gene Expression Omnibus (GEO) database. The data was analyzed by bioinformatics software to find differentially expressed genes (DEGs). Gene ontology (GO) enrichment analysis, kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis, ingenuity pathway analysis (IPA) and protein-protein interactions (PPIs) network analysis were then performed on DEGs. The hub genes were identified using Centiscape2.2 and Molecular Complex Detection (MCODE) in Cytoscape software (Cytoscape_v3.7.2). The survival data of these hub genes was downloaded from the OncoLnc.
Results A total of 2264 messenger RNA transcripts were differentially expressed, including 764 up-regulated and 1500 down-regulated in tumor tissues when compared to those in the paired normal tissues. GO analysis revealed that these DEGs were related to small molecule metabolic process, xenobiotic metabolic process and cellular nitrogen compound metabolic process. KEGG pathway analysis revealed that metabolic pathways, complement and coagulation cascades and chemical carcinogenesis were involved. IPA analysis showed that canonical pathways, such as LXR/RXR activation, FXR/RXR activation and LPS/IL-1 mediated inhibition of RXR function were involved in regulating the occurrence and development of HBV-HCC. Diseases and bio functions showed that DEGs were mainly associated with the following diseases or biological function

abnormalities: cancer, organismal injury and abnormalities, gastrointestinal disease, and hepatic system disease. The top 10 upstream regulators were predicted to be activated or inhibited by Z-score and identified 25 networks. The 10 genes with the highest degree of connectivity were defined as the hub genes. Cox regression revealed that all the 10 genes (CDC20, BUB1B, KIF11, TTK, EZH2, ZWINT, NDC80, TPX2, MELK and KIF20A) were related to the overall survival.
Conclusion Our study provided a registry of genes that play important roles in regulating the development of HBV-HCC, assisting us in understanding the molecular mechanisms that underlie the carcinogenesis and progression of HCC.

PU-0897

基于 CRISPR/Cas9 全基因文库技术筛选肝癌乐伐替尼耐药基因靶点

孙一帆[1,2]、卢永刚[2]、黄文杰[2]、沈永奇[2]
1. 柳州市柳铁中心医院
2. 广西医科大学附属柳铁中心医院

目的 乐伐替尼（Lenvatinib）是新的中晚期肝癌患者一线靶向药物，但其耐药机制尚未阐述。
材料和方法 使用 GeCKO V2 文库建立 HuH7 Lenvatinib 耐药细胞模型，经高通量测序获得表达差异的 sgRNA。利用 CCK8 和克隆形成实验筛选出影响细胞增殖的耐药关键基因。采用 HuH7 和 PLC/PRF/5 细胞系，通过敲除或敲低耐药基因，通过克隆形成和细胞杀伤实验检测基因缺失后对 Lenvatinib 耐药性的影响。进一步过表达耐药基因回复基因功能后验证对 Lenvatinib 耐药性的影响。Western blot 检测 HuH7 和 PLC/PRF/5 细胞系经敲除或敲低、过表达耐药基因后 AKT、ERK 和 FOXO3 磷酸化水平。选择相关通路抑制剂作为杀伤药物，验证 IC50，获得基因缺失后仍然对癌细胞敏感的药物，并在 HuH7、PLC/PRF/5 细胞系和肝癌小鼠模型中，验证药物对肝癌细胞增殖、肿瘤大小和重量的影响。
结果 经测序和初步验证结果表明 NF1 和 DUSP9 是潜在的耐药基因。敲除或敲低 NF1 和 DUSP9 后，肝癌细胞对 Lenvatinib 耐药性上升；过表达 NF1 和 DUSP9 后，可恢复了肝癌细胞对 Lenvatinib 的敏感性。NF1 缺失导致 AKT、ERK 和 FOXO3 磷酸化；Dusp9 缺失导致 ERK 和 FOXO3 磷酸化，过表达 NF1 和 DUSP9 后，上述磷酸化重新被抑制。NF1 或 Dusp9 缺失后，Trametinib 仍能抑制 AKT、ERK 的磷酸化。动物实验表明 NF1 缺失后，肝癌细胞对 Trametinib 仍然敏感。
结论 NF1 和 DUSP9 缺失后通过磷酸化 AKT、ERK 和 FOXO3，导致 PI3K/AKT/mTOR 和 RAS/Raf/MAPK/ERK 信号通路重新激活，使 Lenvatinib 失去了对肝癌细胞的抑制作用。Trametinib 仍能抑制 NF1 缺失后导致的 AKT、ERK 磷酸化。

PU-0898

LINC02323 参与肺腺癌转移的相关分子机制研究

张晓时[1]、杜鲁涛[2]、韩竟懿[1]、李晓丽[1]、王洪春[1]、王传新[2]
1. 山东大学齐鲁医院
2. 山东大学第二医院

In the present study, we aimed to investigate the underlying roles of LINC02323 in the migration, invasion and TGF-β-induced epithelial-mesenchymal transition (EMT) of lung adenocarcinoma (LUAD) cells.LINC02323 was distributed in the cytoplasm and nucleus. TGF-β-induced EMT process was significantly affected by both RNA interference (RNAi) and over-expression of LINC02323. The predicted results showed that there were binding sites between LINC02323 and miR-1343-3p. The double luciferase reporting system, RT-qPCR and Western

blotting experiments confirmed that LINC02323 could bind to miR-1343-3p, which bound to TGF-β receptor 1 (TGFBR1). Inhibition of miR-1343-3p reversed LINC02323 silencing-mediated suppression of migration, invasion and EMT.

PU-0899

LncRNA SNHG16 通过靶向 miR-106a，上调 KLF9，加重糖尿病肾病中高糖诱导的足细胞损伤

何昕
暨南大学附属第一医院

糖尿病肾病(DN)是糖尿病的主要并发症之一，足细胞损伤在 DN 发病机制中起重要作用。MicroRNA(miR)-106a 被预测为长链非编码 RNA (lncRNA)SNHG16 的靶标，并已被确定为糖尿病肾病的治疗生物标志物。然而，SNHG16/miR-106a 轴在 DN 中的作用尚未得到阐明。本研究旨在探讨 SNHG16 是否可通过 miR-106a 调控 DN 足细胞损伤，并揭示其潜在机制。
方法 MPC5 足细胞经对照或高糖(HG)培养基处理后，检测其 miR-106a 水平。暴露于汞的 MPC5 细胞中，miR-106a 过表达或不过表达，然后 KLF9 或 SNHG16 过表达或不表达。检测细胞活力、凋亡、活性氧种类及 synaptopodin、podocin 蛋白表达。
结果 MiR-106a 在 DN 患者和 hg 诱导的 MPC5 足细胞中均下调。过表达 miR-106a 抑制了高糖诱导的细胞活力、Bcl-2、synaptopodin 和 podocin 表达的降低，ROS、凋亡细胞、Bax 和 cleavedcaspase3 表达的增加。MiR-106a 可与 KLF9 和 lncRNA SNHG16 结合，在 DN 患者和 hg 诱导的 MPC5 足细胞血清中均上调。SNHG16 过表达降低了 miR-106a 水平，而 miR-106a 过表达降低了 KLF9 的表达。此外，过表达 KLF9 或 SNHG16 削弱了 miR-106a 对汞诱导的 MPC5 损伤的保护作用。
讨论 LncRNA SNHG16 可以通过靶向 miR-106a 来增强 KLF9 的表达，从而促进汞刺激的足细胞损伤。SNHG16/miR-106a/KLF9 干预可能是一种治疗 DN 的方法。

PU-0900

Clinical evaluation of Interferon-γ Release Assay, Nucleic Acid Amplification Tests and Culture in the diagnosis of active tuberculosis

Ting Xu[1]、Yan Zhang[2]、Guodong Rong[1]、Hong Zhao[1]、Lei Wu[1]、Peijun Huang[1]
1. the First Affiliated Hospital of Nanjing Medical University
2. Nanjing medical university

Background Interferon-γ release assay (IGRA), nucleic acid amplification tests (NAAT) and culture are recommended as the evidence of diagnosed TB, but still have considerable limitations. This study intended to evaluate the performance of these **Methods** to speed up the TB diagnosis process through the effectively use of routine tests.
Methods A retrospective study was conducted from January 2018 to June 2019 at the first affiliated hospital of Nanjing Medical University. A total of 288 hospitalized patients who were suspected of active tuberculosis were enrolled in this study. Each subject underwent IGRA, NAAT and TB culture tests. The diagnostic performance of these tests was compared.
Results IGRA produced the highest overall sensitivity (87.80%) as compared to NAAT and culture (both 46.34%). NAAT produced an overall sensitivity and PPV of 100%. The comparatively higher overall NPV occurred in IGRA (97.28%), followed by NAAT (91.82%) and culture (91.79%). In extrapulmonary TB, IGRA had a sensitivity of 100%, which outperformed

both NAAT (25%) and culture (8.33%). A substantial agreement between NAAT and culture was revealed with Kappa coefficient of 0.64 (95% CI 0.46-0.82, P<0.001). A trend was also found IGRA simultaneously increased with the positive rates of NAAT and culture (P<0.001). Then a two-step procedure of NAAT-IGRA was suggested benefited 69.44% patients (200/288) who got the test results in about 28 hours with the accuracy of 99% (198/200).
Conclusions IGRA and NAAT displayed complementary advantages in tuberculosis diagnosis, and the two-step principle of NAAT-IGRA can shorten the diagnostic cycle with high accuracy.

PU-0901

血清长链非编码 RNA Linc00511 在胃癌中的表达及临床意义

孙晓杰、李林
齐齐哈尔医学院

目的 探讨长链非编码 RNA Linc00511 在胃癌病人血清中的表达，分析其表达水平与胃癌临床特征的相关性，评估其单项及与糖类抗原 CA72-4 联合检测对胃癌临床诊断的应用价值。
方法 收集 100 例胃癌病人和 76 例健康对照者血清样本，通过实时荧光定量 PCR 技术检测 Linc00511 的相对表达量；Mann-Whitney U 检验方法分析 Linc00511 表达水平与胃癌临床特征的相关性；采用受试者工作特征（ROC）曲线和危险分数分析法评价 linc00511 对胃癌的诊断价值；通过 ROC 曲线下面积（AUC）、灵敏度、特异度、阳性预测值（PPV）及阴性预测值（NPV）评估单项及联合检测的临床诊断效能。
结果 胃癌组和健康对照组血清 Linc00511 的相对表达量分别为 1.871±1.082 和 1.389±1.078，两组比较差异有统计学意义（Z=﹣3.605，p<0.01）。Linc00511 的表达水平与患者的年龄、性别以及肿瘤远处转移等均无关（p>0.05），但其在临床Ⅰ~Ⅱ期胃癌病人血清中的表达水平显著高于临床Ⅲ~Ⅳ期的病人，两组比较差异有统计学意义（Z=-2.203，p<0.05）；此外，Linc00511 在无淋巴结转移病人血清中的表达水平显著高于有淋巴结转移者（Z=-2.138，p<0.05）。Linc00511 诊断胃癌的 AUC 值为 0.659，诊断的灵敏度和特异度分别为 74%和 60.5%，PPV 和 NPV 分别为 71.8%和 64.4%。CA72-4 诊断胃癌的 AUC 值为 0.764，灵敏度和特异度分别为 30%和 81.6%，PPV 和 NPV 分别为 68.2%和 47%。CA72-4 与 Linc00511 联合检测可将灵敏度和 NPV 分别提高至 83%和 69.6%。
结论 血清 Linc00511 的表达水平与胃癌临床分期和淋巴结转移相关，与 CA72-4 联合检测可作为胃癌诊断的潜在血清学标志物。

PU-0902

血管内皮生长因子 VEGF 在肺癌患者血清中的表达及诊断价值的研究

王琳[1]、任丽[2]
1. 天津医科大学肿瘤医院
2. 天津医科大学肿瘤医院

目的 本论文旨在研究血管内皮生长因子（VEGF）在肺癌患者血清中的表达及功能。
方法 收集天津医科大学附属肿瘤医院 2015 年 5 月至 6 月确诊为肺癌的患者病历资料和血清标本 100 例,其中小细胞肺癌患者至少 70 例,非小细胞肺癌患者 20 例，正常对照 10 例。采用酶联免疫吸附法（ELISA）定量检测患者血清中血管内皮生长因子水平,比较肺癌患者血清中血管内皮生长因子水平的表达,明确血管内皮生长因子与肺癌的相关性,根据病理分期、转移情况对 100 例患者进行分组,明确血管内皮生长因子与肺癌病程进展、转移情况的相关性。

结果 (1)比较正常组与肺癌患者血清中的血管内皮生长因子水平,差异有统计学意义（P<0.05）,比较非小细胞肺癌患者与小细胞肺癌患者,差异无统计学意义(P>0.05)。（2）在肺癌患者的不同分期中比较局限期和广泛期的血管内皮生长因子水平,差异有统计学意义（P<0.05）。（3）比较肺癌患者有转移组和无转移组的血管内皮生长因子水平,差异有统计学意义（P<0.05）。（4）血管内皮生长因子与小细胞肺癌、肺癌病程进展、转移情况有显著相关性（P<0.05）。
结论 血管内皮生长因子在肺癌患者血清中的异常表达,对肺癌患者的病程发展及转移情况的判断具有一定的临床价值。

PU-0903

The Roles of GSTT1 in Taxol/Carbo-Resistant Serous Ovarian Cancer Cells

Jing Zhang、Suhong Xie、Lei Zhou、Xiaoyu Tang
Fudan University Shanghai Cancer Center

Objectives To construct a paclitaxel/carboplatin combined drug-resistant cell lines for ovarian cancer (HO8910-TAX/CBP and SKOV3-TAX/CBP), and study the role of GSTT1 in chemotherapy resistant cell lines, which plays an essential role in.
Methods Taxol/carboplatin drug-resistant cell clones (HO8910-TAX/CBP and SKOV3-TAX/CBP) were constructed using the increasing concentration gradient method. The final concentration of each drug was 20 folds than the initial concentration. Examination of drug-resistance related genes expression were used by qRT-PCR and western-blot. The application of immunefluorescence and co-immunoprecipitation confirmed the localization of GSTT1 and Topo I in cells, and figured out the interaction between GSTT1 and Topo I. The expression of GSTT1 in chemotherapy resistant cell lines was down regulated by shRNA.
Results The expression of resistance-related molecules MDR1, Bcl-2, ERCC1, GSTT1 and Topo I was increased in the chemotherapy-resistant cell clones, both at the mRNA and protein level. Cell arrest was observed in the drug-resistant cells at the G0/G1-phase. Then, down-regulation of GSTT1 in the drug-resistant cells significantly depressed cell proliferation and increased cell sensitivity to taxol and carboplatin. In addition, inhibition of GSTT1 induced cell cycle arrest at the G2/M phase and increased cell apoptosis. Finally, down-regulation of GSTT1 resulted in a reduction in DNA damage repair molecules Topo I, and down-regulation of the expression levels of cell cycle-relevant molecules Cyclin B1 and Cyclin E1. Also GSTT1 and Topo I were co-localized in the cell nucleus and GSTT1 co-existed with Topo I.
Conclusion We successed in developing cell clones resistant to taxol/carbo. The expression of GSTT1 is associated with paclitaxel / carboplatin resistance in ovarian cancer. Down-regulation of GSTT1 can increase the sensitivity of ovarian cancer cells to taxol / carboplatin. This study indicates a potential role of GSTT1 as an indicator of drug resistance in serous ovarian cancer.

PU-0904

母体内胎儿游离 DNA 检测在预防新生儿染色体疾病达中的应用研究

徐天天、骆衡
贵州金域检验中心有限公司

无创产前诊断是通过高通量测序技术对母体内胎儿游离 DNA 进行检测以判断其是否存在异常突变，从而对新生儿某些基因疾病起到预防作用。与传统的唐筛相比，孕妇所承受的伤害较小，且检测覆盖范围广泛，是目前前景较好的预防新生儿基因疾病的一种策略。本研究拟通过检测母体内

胎儿游离 DNA 以对新生儿部分染色体疾病达到早预防的作用，减少新生儿的出生缺陷率。对孕妇外周血进行离心得到一定量的血浆，通过磁珠法对血浆中游离的胎儿 DNA 进行提取、筛选以及纯化后，得到胎儿小片段 DNA，进行 PCR 扩增，构建相应的文库，采用高通量测序技术对文库进行测序。结果表明利用高通量测序技术对母体内胎儿游离 DNA 进行检测可发现较多病种，包括临床常见的 13 号、18 号、21 号三个染色体异常的 3 种胎儿染色体非整倍体疾病，及 Turner 综合征、超雌综合征、超雄综合征、克氏综合征 4 种性染色体非整倍体疾病， 21 种胎儿其他常染色体非整倍体疾病，103 种大于 3Mb 的胎儿染色体缺失/重复疾病。正常结果的检测范围 Z 值在负 3 和正 3 之间，超出范围属于异常结果。上述结果表明通过对母体内胎儿游离 DNA 检测可有效预防新生儿部分基因疾病，可满足临床需要，为降低新生儿出生缺陷率，具有一定的临床使用价值。

PU-0905

LncRNA-FA2H-2 attenuates LPS-induced endothelial cells proptosis and inflammation via regulation of the NF-κB/NLRP3 pathway

Fengxia Guo
Henan Provincial People's Hospital

Pyroptosis is a novel form of pro-inflammatory programmed cell death linked to atherosclerosis (AS), but its exact mechanisms are unknown. Long noncoding RNAs (lncRNAs) are important in the etiology of a variety of diseases, such as AS. The relationship between lncRNAs and pyroptosis in AS, on the other hand, is largely unknown. Our previous research showed that LncRNA-FA2H-2 was expressed at low levels in AS plaques and was closely related to the inflammatory response. In this study, we confirmed that the Nod-like receptor protein 3 (NLRP3)-mediated pyroptosis and inflammation was induced by lipopolysaccharide (LPS) and overexpression of LncRNA-FA2H-2 could reduce this effect. Interestingly, the results of our study also indicated that LncRNA-FA2H-2 could inhibit the function of nuclear factor κB(NF-κB) p50 (an NF-κB subunit) and that p50 could interact with NLRP3 in endothelial cells (ECs). In conclusion, these results suggested that LncRNA-FA2H-2 participated in pyroptosis and inflammation in ECs under conditions of LPS stress by activation of the NF-κB/NLRP3 signaling pathway, which could shed light on how LncRNA-FA2H-2 is regulated during the progression of AS.

PU-0906

新疆地区 6-丙酮酰四氢蝶呤合成酶缺乏致四氢生物蝶呤缺乏症的诊断及基因突变分析

何江、杨曦、史清海
新疆军区总医院检验科

目的 探讨新疆地区 6-丙酮酰四氢蝶呤合成酶缺乏症（PTPSD）的临床诊断和基因突变特点，为开展四氢生物蝶呤缺乏症（BH4D）患者的基因诊断和基因携带者筛查提供重要依据。
方法 6 例 HPA 患者经血 Phe、BH4 负荷或 Phe+BH4 联合负荷试验、尿蝶呤谱、DHPR 活性测定，采用基因芯片捕获、二代高通量测序等进行 PTS 基因突变检测，分析基因型与临床表型的关系。
结果 病例 1、3、6 均为经新筛召回复查确诊 HPA，初期症状为皮肤稍白、四肢肌张力正常或稍有降低，偶有惊厥，病例 2、4、5 未接受新筛，呈智力障碍、运动落后、肌张力异常、惊厥等症状，尿新蝶呤（N）明显增加（病例 2、4、5）或者正常（病例 1、3、6），生物蝶呤（B）全部明显降低，B/(B+N)%都<5%甚至<1%，DHPR 酶活性测定基本正常，服用 BH4 或 Phe+BH42h 后，

Phe 浓度逐渐下降至 56.89%~68.75%，4h 后下降至 83.29%-90.26%，4~6h 血 Phe 浓度基本将至正常水平，在 6 例 BH4D 患者 12 个等位基因中都发现 PTS 基因致病突变，最终全部诊断为 PTPSD。5 例患者接受 BH4、左旋多巴、5-羟色氨酸等治疗后逐渐好转，1 例死亡。在 6 例 PTPSD 家系中发现错义突变 5 种：N52S、P87S、K91R、D96N、P98Q，剪切位点突变 1 种（IVS1-129A>G），突变检出率为 83.3%，以错义突变为主（91.7%），突变主要集中在外显子 5（66.7%）、外显子 2（25.0%）和内含子 1（8.3%）中。发现 IVS1-129A>G 为一种国际上尚未报道的新突变。

结论 PTS 基因突变是导致 BH4D 的主要原因，N52S、P87S、K91R 和 D96N 为新疆地区 PTS 基因的热点突变，联合采用基因芯片捕获和二代高通量测序技术可优化 BH4D 诊断策略，提高基因诊断时效。

PU-0907

中国西北地区汉族苯丙酮尿症患者苯丙氨酸羟化酶基因突变分析

何江[6]、强荣[1]、毛新梅[2]、王慧珍[3]、闫有圣[4]、邹红云[6]、史清海[5]

1. 陕西省妇幼保健院医学遗传中心
2. 宁夏回族自治区妇幼保健院新生儿疾病筛查中心
3. 青海省妇幼保健院新生儿疾病筛查中心
4. 甘肃省妇幼保健院医学遗传中心
5. 新疆军区总医院检验科
6. 新疆军区总医院检验科

目的 分析中国西北地区汉族苯丙酮尿症患者苯丙氨酸羟化酶（PAH）基因的突变特征。

方法 应用 PCR 产物直接测序法、基因芯片捕获和二代高通量测序对西北地区 223 例汉族 PKU 患儿及其父母的 PAH 基因启动子、第 1~13 外显子及其旁侧内含子区域进行基因突变分析。

结果 在西北地区 223 例汉族 PKU 患者 446 条 PAH 等位基因中检测出 75 种致病突变，总检出率为 88.6%（395/446），突变以错义突变（66.7%）、剪切位点突变 12 种（16.0%）和无义突变（9.3%）为主；大部分突变主要分布在外显子 7（29.0%）、外显子 6（10.5%）、外显子 3（10.3%）、外显子 11（9.6%）、外显子 12（8.5%）和第 4 内含子（6.7%）中；突变频率较高的 PAH 基因致病突变是 R243Q（22.1%）、IVS4-1G>A（6.7%）、EX6-96A>G（6.5%）、R111X（5.4%）、R53H（4.3%）、Y356X（4.0%）、R413P（3.8%）和 V399V（3.1%）；西北汉族最常见 PAH 基因突变（R243Q）与中国北方基本一致，但显著区别于日本（R413P）、巴西（V388M、德国（R408W）、立陶宛（R408W）和美国（R408W）。发现 7 种国际上未见报道的新突变：N93fsX5、G171E、P225S、Q304K、H107R、F392I 和 N223I。

结论 西北汉族 PKU 患者 PAH 基因致病突变构成与中国北方类似，但显著区别于部分亚洲和欧美国家，西北汉族的 PAH 基因突变谱具有其独特保守的地域特征，推测 R243Q 突变的高处在中国北方地区，而 R408W 突变的高处在欧洲地区。

PU-0908

1 例晚期婴儿型神经元蜡样质脂褐素沉积症的临床诊断及新突变发现

何江
新疆军区总医院
全军临床检验诊断中心
全军计划生育优生优育技术指导中心

目的 探讨新疆地区 1 例晚期婴儿型神经元蜡样质脂褐素沉积症（LINCL）的临床诊断和基因改变，为神经元蜡样质脂褐素沉积症（NCL）患者诊断策略优化和基因携带者筛查提供重要依据。
方法 对 1 例初发症状"癫痫伴进行性小脑萎缩"患者进行头颅 MRI、听觉和视觉诱发电位、运动及体感诱发电位、脑电图、数字视频脑电、SCA 基因动态突变、TPP1 活性和多重连接探针扩增分析（MLPA）、基因芯片捕获、二代高通量测序等辅助检查，分析基因型与临床表型的关系。
结果 本病例发病年龄 4~5 岁，癫痫、小脑共济失调伴萎缩是首发临床症状，后续出现小脑萎缩、共济失调、运动认知功能倒退、语言障碍等，PPT1、TPP1、CLN3、CLN6 和 CLN8 基因未发现存在大片段变异， 全血 TPP1 酶活性测定值（7.2 nmol/day/spot）远低于正常参考范围，患者 CLN2 基因发现 V216M（c.646G>A，p.Val216Met）和 IVS7-17A>G（c.887-17A>G）复合杂合核苷酸变异，其变异分别遗传自生物学父母，患者最终被确诊为两个 CLN2 基因突变所导致的晚期婴儿型神经元蜡样质脂褐素沉积症。IVS7-17A>G 突变经检索相关文献及数据库，是国际上尚未见报道的新突变。
结论 根据患者发病年龄、临床表现、电生理学、组织病理学、影像学进行 NCL 诊断难度较高，尽早进行酶学检查和 NCL 相关基因（CLN1~10 基因）突变测序分析，可显著提高 LINCL 诊断时效，以延缓病程进展或者减轻患者症状。我国 CLN2 基因的突变类型存在与其他国家或地区不同的新基因，为本家系的携带者筛查和产前诊断奠定了坚实基础。

PU-0909

中国西北地区回族苯丙酮尿症患者苯丙氨酸羟化酶基因突变分析

何江 [1]、毛新梅 [2]、王慧珍 [3]
1. 新疆军区总医院
2. 宁夏回族自治区妇幼保健院新生儿疾病筛查中心
3. 青海省妇幼保健院新生儿疾病筛查中心

目的 分析中国西北地区回族苯丙酮尿症患者苯丙氨酸羟化酶（PAH）基因的突变特征。
方法 应用 PCR 产物直接测序法、基因芯片捕获和二代高通量测序对西北地区 67 例回族 PKU 患儿及其父母的 PAH 基因启动子、第 1~13 外显子及其旁侧内含子区域进行基因突变分析。
结果 在西北地区 67 例汉族 PKU 患者 134 条 PAH 等位基因中检测出 40 种致病突变，总检出率为 82.1%（110/134），突变以错义突变（65.0%）、剪切位点突变（15.0%）和无义突变（10.0%）为主；大部分突变主要分布在外显子 7（24.6%）、外显子 6（15.7%）、外显子 3（7.5%）、外显子 11（6.7）中；突变频率较高的 PAH 基因致病突变是 R243Q（13.4%）、R241C（7.5%）、R413P（5.2%）、Q232X（4.5%）、Y356X（3.7%）、EX6-96A>G（3.7%）和 L430P（3.0%）；西北回族最常见 PAH 基因突变是 R243Q，区别于日本（R413P）、巴西（V388M）以及德国、立陶宛、拉脱维亚和美国等欧美国家（R408W）。西北回族 R243Q 突变检出率显著低于中国北方（P<0.05），R413P 突变检出率显著低于日本（P<0.05），EX6-96A>G 在中国北方和韩国的突变检出率显著高于中国西北（P<0.05）。发现 5 种国际上未见报道的新突变：M1I、L430P、D222G、S16fsX10 和 IVS11+1G>A。Y414X、P281L 和 S303fsX38 这三种突变是中国回族中首次报道的突变。

结论 西北回族 PKU 患者 PAH 基因致病突变构成与中国北方类似，但显著区别于部分亚洲和欧美国家，具有自身独特保守的特性。

PU-0910

广西桂北地区人群脂联素及其基因多态性与冠心病的关联研究

向晓华[1]、韦传东[1]、冷俊[2]、李宁[2]
1. 桂林医学院第二附属医院
2. 桂林医学院

目的 探讨桂北地区人群脂联素（APN）水平及脂联素基因两个单核苷酸多态性（SNPs）与冠心病（CHD）的关系。
方法 采用酶联免疫吸附法测定 498 例研究对象(冠心病组 263 例、健康对照组 235 例)血清 APN 浓度，比较两组间 APN 表达差异；采用聚合酶链反应-限制性片段长度多态性结合 DNA 直接测序技术，分析 498 例受试者的 rs1501299 G/T 和 rs266729 C/G 的基因型，比较两组间的分布差异及其与 APN 浓度的相关性。
结果 冠心病组血清 APN 浓度明显低于对照组（$P < 0.001$）。两组间 rs266729 基因分型差异有统计学意义(P<0.001)，但等位基因分布频率差异无统计学意义(P>0.05)。在未对性别及年龄参数做出调整时，突变纯合子 GG 基因型与野生纯合子 CC 基因型之间差异无统计学意义（$P > 0.05$），调整后，GG 基因型较 CC 基因型增加 CHD 的患病风险（OR=2.740,95%CI 1.109-6.768,P=0.029）。rs266729 基因型的显性和隐性模型与冠心病的关系表现为 GG 基因型较 C 等位基因（CG 型+CC 型）增加患 CHD 的风险（OR=2.156,95%CI 1.004-4.631,P=0.049），且在调整性别和年龄参数后仍然存在（OR=2.695,95%CI 1.110-6.540,P=0.028），GG 基因型携带者可能是 CHD 的独立危险因素之一。rs1501299 在两组间无统计学意义（$P > 0.05$）。rs1501299 和 rs266729 对血清脂联素的水平无显著性影响（$P > 0.05$）。
结论 桂北地区 CHD 患者血清 APN 水平低于健康人群，提示低脂联素血症是 CHD 的危险因素之一；rs266729 基因的 GG 基因型增加患 CHD 的风险可作为冠心病的独立危险因素之一；rs1501299 和 rs266729 与 APN 水平无明显相关性，不能作为 APN 水平的预测指标。

PU-0911

缺血性脑卒中患者外周血中 miR-488 表达水平与 NIHSS 评分的相关性探讨

张钦政[1]、马思琦[2]、任晓庆[2]、樊金宇[2]、李晨[2]、李春燕[2]、闫海润[1]
1. 牡丹江医学院红旗医院
2. 牡丹江医学院

目的 缺血性脑卒中发生后，脑组织和外周血中的 miRNA 表达谱出现变化，此前研究表明 miR-488 在脑卒中患者外周血中相对表达水平大概是健康对照组的 2 倍。本文旨在研究 miR-488 在缺血性脑卒中患者外周血血清中的表达水平以及其与美国国立卫生研究院卒中量表（NIHSS）评分之间的相关性，探究 miR-488 能否作为评估缺血性脑卒中患者病情严重程度的指标。
方法 随机选择 2020 年 8 月至 2021 年 2 月于牡丹江医学院附属红旗医院就诊的缺血性脑卒中患者 30 例作为病例组，收集同期来我院体检的健康体检者 30 例作为对照组，收集患者确诊时和健康体检者的血清，采用实时荧光定量聚合酶链反应（qRT-PCR）测定两组外周血血清中 miR-488 相对表达量；记录病例组和对照组的年龄、性别、吸烟史、血糖、血压、血脂等指标，进行统计学分析。收集病例组患者确诊时的 NIHSS 评分，采用 pearson 的相关性分析，分析病例组患者外周血血清中 miR-488 的相对表达量与 NIHSS 评分之间的关系。

结果 病例组和健康对照组之间在年龄、性别、糖尿病、吸烟、血压、血脂等方面的差异无统计学意义（P>0.05）。病例组血清中 miR-488 的相对表达量显著高于对照组（P<0.01）；pearson 的相关分析表明，缺血性脑卒中患者外周血血清中 miR-488 的相对表达量与患者 NIHSS 得分呈正比。
结论 与健康人相比，缺血性脑卒中患者外周血血清中 miR-488 表达量明显增高，并随发病时间呈上升趋势，与 NIHSS 评分呈正相关。检测脑卒中患者外周血中 miR-488 表达水平有助于评估病情严重程度及神经功能受损情况。

PU-0912

结直肠癌中长链非编码 RNA-AL135905.1 的表达及作用的初步研究

李铭杰、伍严安
厦门大学附属翔安医院

目的 研究长链非编码 RNA（lncRNA）AL135905.1 在结直肠癌组织中的表达模式，探讨其对结直肠癌细功能的影响及潜在机制。
方法 本研究通过高通量测序（RNA-seq）的方法，筛选出结直肠癌组织中差异表达的 lncRNAs。扩大样本对结直肠癌组织和细胞系 lncRNAs 表达水平的验证。构建过表达 AL135905.1 的重组质粒，转染低表达该 lncRNA 的结直肠癌细胞 Caco2 和 SW480。应用 CCK8 实验、克隆形成实验检测细胞增殖，Transwell 小室实验检测细胞迁移、侵袭。流式细胞术检测细胞周期、凋亡。通过 TCGA 数据库分析不同 AL135905.1 表达水平的患者总生存时间（OS）和无疾病复发生存时间（RFS）。最后对 AL135905.1 潜在的靶基因及作用机制进行生物信息学分析。
结果 AL135905.1 在结直肠癌肿瘤组织和细胞中显著下调（P < 0.001）。AL135905.1 低表达同患者淋巴结转移、TNM 分期、脉管侵犯、神经侵犯相关（均 P < 0.05），而与患者年龄、性别、肿瘤大小、分化状态、远处转移、浆膜侵犯、KRAS 突变、BRAF-V600E 突变无明显相关（P > 0.05）。体外实验表明过表达 AL135905.1 的细胞株，细胞增殖、克隆形成、迁移和侵袭明显受到抑制，而细胞凋亡显著被促进（P < 0.05）。生存分析提示同时高表达 AL135905.1 和 PHLPP2 的结直肠癌患者 OS 和 RFS 显著高于二者同时低表达患者及单一基因低表达患者。生物信息学分析预测 AL135905.1 可能通过 miR-6838-5p/PHLPP2/ PI3K/ AKT 轴在结直肠癌中起抑癌基因样的作用。
结论 AL135905.1 在结直肠癌肿瘤组织和细胞系中表达下调，AL135905.1 可能通过 miR-6838-5p/PHLPP2/PI3K/AKT 轴在结直肠癌中起抑癌基因样的作用。

PU-0913

TIM-3 与非小细胞肺癌预后的相关性研究

景丽萍、庄学伟
山东省立第三医院

目的 检测非小细胞肺癌组织 TIM-3 和肿瘤浸润淋巴细胞（TILs）表达情况，探讨免疫分子在非小细胞肺癌微环境分布及其预后价值。
方法 HE 染色法检测 TILs，免疫组化法检测 TIM-3 在非小细胞肺癌组织表达，分析 5 年存活组和 5 年内死亡组表达差异。
结果 TIM-3 和 TILs 在非小细胞肺癌组织都有表达；与 5 年存活组相比, 5 年内死亡组 TIM-3 表达高，差异有显著意义(P<0.05)，TILs 细胞表达低，但表达两组差异无显著意义（P>0.05）。
结论 TIM-3 在肿瘤细胞和免疫细胞皆有表达，5 年生存组低于 5 年死亡组，TIM-3 高表达预后差，是独立预后因子。

PU-0914

合胞素在急性髓系白血病患者表达及化疗对其表达的影响

景丽萍、庄学伟
山东省立第三医院

目的 研究合胞素在急性髓系白血病患者表达及化疗对其表达的影响
方法 初诊急性髓系白血病患者 20 例，其中男 17 例，女 25 例，年龄 25～62 岁; 其中包括 M1 2 例，M2 4 例，M3 3 例，M4 5 例，M5 例。首次及第二次化疗前分别收取其外周血标本。健康对照 20 例。实时定量 PCR 法检所有病例及对照单个核细胞合胞素表达。
结果 1、与健康对照组相比，化疗前急性髓系白血病患者外周血单个核细胞合胞素表达明显升高（$P < 0.05$）；2、首次化疗后，急性髓系白血病患者外周血单个核细胞合胞素表达较化疗前表达显著下调（$P < 0.05$），但仍高于健康对照水平（$P < 0.05$）；3、进一步分析发现，未获完全缓解患者（$n =6$）合胞素表达水平显著高于缓解患者（$P < 0.05$）。
结论 急性髓系白血病患者外周血单个核细胞合胞素表达水平明显升高，化疗后随着肿瘤负荷下降，其表达水平下调，且未缓解患者水平高于缓解患者，提示合胞素在急性髓系白血病中发挥重要作用，有望成为白血病诊断治疗中的新型标志物。

PU-0915

Syncytin-1 表达与非小细胞肺癌预后的关系

景丽萍、庄学伟
山东省立第三医院

目的 检测非小细胞肺癌组织 syncytin-1,CD4+,CD8+T 细胞表达情况，探讨免疫分子在非小细胞肺癌微环境分布及其预后价值。
方法 免疫组化法检测 syncytin-1，CD4+和 CD8+T 细胞在非小细胞肺癌组织表达，分析 5 年存活组和 5 年内死亡组表达差异。
结果 Syncytin-1,CD4+T,CD8+T 细胞在非小细胞肺癌组织都有表达；与 5 年存活组相比, 5 年内死亡组 syncytin-1 表达高, 而 CD8+T 细胞阳性率表达低，差异有显著意义($P<0.05$)，CD4+ T 细胞表达两组差异无显著意义（$P>0.05$）。
结论 Syncytin-1，CD8+T 细胞在非小细胞肺癌组织表达，可作为判断预后的指标，CD8+ T 细胞表达高预后好，而 syncytin-1 表达高则预后不良。

PU-0916

H2O2 对 BeWo 细胞 syncytin-1 表达的影响

景丽萍、庄学伟
山东省立第三医院

目的 采用过氧化氢（hydrogen peroxide，H2O2）作为外源性自由基生成系统，观察其对 BeWo 细胞 syncytin-1 基因表达的影响，从细胞及分子水平探讨氧化应激在子痫前期发病中作用及其可能的机制。
方法 实时定量 PCR 法检测不同浓度（50μmol/L、100μmol/L 和 200μmol/L）外源性 H2O2 对培养的 BeWo 细胞 syncytin-1 表达的影响。

结果 50μmol/L、100μmol/L 和 200μmol/L H2O2 三组中 100μmol/L 的 H2O2 对 syncytin-1 基因表达影响最大，外源性 100μmol/L H2O2 组与对照组相比，syncytin-1 表达 24h 升高，48 小时达峰值，72 小时降低。
结论 H2O2 可影响 syncytin-1 基因的表达，可能是子痫前期发病机制之一。

PU-0917

莆田市 HPV 感染的 27 种基因亚型和年龄分布的特征分析

陈展飞[1]、张文娟[2]、涂海健[1]、俞柳敏[1]
1. 莆田学院附属医院
2. 莆田学院药学与医学技术学院医学检验系

目的 研究探讨 2020 年 12 月至 2021 年 4 月期间福建省莆田市女性人乳头瘤病毒（HPV）的感染状况、基因亚型及年龄分布特征，同时也为宫颈癌的早期筛查和临床诊断与治疗提供可靠依据。
方法 选取 2020 年 12 月至 2021 年 4 月期间于莆田学院附属医院（以下用“我院”代替）就诊的女性，共计 3245 例，收集宫颈脱落细胞标本，采用流式荧光杂交法检测女性 HPV27 种基因亚型的感染情况，分析不同年龄阶段女性 HPV 的感染状况和基因亚型、感染的高危型和低危型情况以及单一感染、双重感染和多重感染的情况。
结果 在接受检查的 3245 例患者中，剔除不符合本次统计的标本之后，有效数据共 2950 例，检测结果显示共有 609 人感染 HPV，检出率达到 20.64%：其中处于 20 岁以下有 18 人，感染人数为 6 人，占比为 33.33%，位居第一；处于 61-70 岁有 89 人，感染人数为 27 人，占比为 30.34%；处于 21-30 岁有 521 人，感染人数有 120 人，占比为 23.03%，位居第三；随后依次为 41-50 岁、51-60 岁和 31-40 岁，感染人数分别为：175、82 和 199，占比分别为：20.49%、20.30%以及 18.70%，不同年龄阶段之间 HPV 检出率比较差异有统计学意义（$\chi 2=11.18$，$P<0.05$）。感染 HPV 的 609 人中，单一感染共有 454 例，比例为 74.55%，双重感染共有 110 例，比例为 18.06%，三重感染共 32 例，比例为 5.25%，四重感染共 11 例，比例为 1.81%，五重感染共 2 例，比例为 0.33%。此外，609 例感染人数中检测出 HPV 感染基因共 824 次，其中高危型感染基因检出频数为 503 次，占总感染人数的 82.59%。
结论（1）HPV 感染的基因亚型与年龄分布具有一定的相关性。（2）HPV 感染的基因亚型具有地域性，而 HPV 混合感染与地域差异无明确关联。

PU-0918

Evaluation of low coverage whole genome sequencing as a new method for detecting malignant ovarian mass

Pengqiang Zhong[1]、Ming Chen[1]、Mengzhi Hong[1]、Jingfeng Tan[1]、Xuegao Yu[1]、Hao Huang[1]、Juan Ouyang[1]、Xiaoping Lin[2]、Peisong Chen[1]
1. First Affiliated Hospital of Sun yat-sen university
2. 中山大学肿瘤防治中心

Objective To evaluate whether low coverage whole genome sequencing is suitable for the detection of malignant pelvic mass and compare its diagnostic value with traditional tumor markers.
Methods We enrolled 63 patients with a pelvic mass suspicious for ovarian malignancy. Each patient underwent low coverage whole genome sequencing (LCWGS) and traditional tumor markers test. The pelvic masses were finally confirmed via pathological examination. The copy number variants (CNVs) of whole genome were detected and the Stouffers Z-scores for each CNV was extracted. The risk of malignancy (RM) of each suspicious sample was calculated

based on the CNV counts and Z-scores, which was subsequently compared with ovarian cancer markers CA125 and HE4, and the risk of ovarian malignancy algorithm (ROMA).
Results Receiver Operating Characteristic Curve (ROC) were used to access the diagnostic value of variables. As confirmed by pathological diagnosis, 44 (70%) patients with malignancy and 19 patients with benign mass were identified. Our results showed that CA125 and HE4, the CNV, the mean of Z-scores (Zmean), the max of Z-scores (Zmax), the RM and the ROMA were significantly different between patients with malignant and benign masses. The area under curve (AUC) of CA125, HE4, CNV, Zmax, and Zmean was 0.775, 0.866, 0.786, 0.685 and 0.725 respectively. ROMA and RM showed similar AUC (0.876 and 0.837), but differed in sensitivity and specificity.
Conclusion After all, we develop a LCWGS based method for the identification of pelvic mass of suspicious ovarian cancer. LCWGS shows accurate result and could be complementary with the existing diagnostic **Methods**

PU-0919

BS69 在先兆子痫患者胎盘中的表达

庄学伟、景丽萍
山东省立第三医院

目的 探讨 BS69 基因在先兆子痫患者胎盘与正常胎盘之间的差异表达。
方法 通过收集 8 例先兆子痫孕妇胎盘和 12 例正常胎盘，提取 RNA 后进行实时荧光定量 PCR，观察先兆子痫胎盘与正常胎盘的表达差异。
结果 BS69 作为一种转录抑制因子，先兆子痫患者胎盘中的表达显著下调。
结论 BS69 基因表达下调与先兆子痫密切相关，可作为先兆子痫疾病诊断的潜在生物标志物。

PU-0920

siRNA 干扰下调 DJ-1 的表达对人支气管上皮细胞 HBE 生物学行为的影响

魏旺丽
郴州市第一人民医院

目的 探讨 DJ-1 表达下调对正常人支气管上皮细胞系 HBE 细胞生物学行为的影响。
方法 构建 DJ-1 基因 siRNA 慢病毒载体,感染 HBE 细胞（DJ-1 siRNA 组），并设立慢病毒载体对照组（Control siRNA 组）及空白对照（BC）组，分别进行流式细胞术检测、MTT 实验和克隆形成实验、Transwell 小室实验。
结果 与 Control siRNA 组及空白对照组比较，DJ-1 siRNA 组的 G1 期细胞数量显著增多而 S / G2 期细胞数减少表明细胞周期受阻；细胞增殖能力明显减弱(P<0.01)；细胞体外迁移和侵袭能力显著减弱(P<0.01)。
结论 下调 DJ-1 的表达具有抑制人支气管上皮细胞系 HBE 细胞增殖和体外迁移侵袭的作用。

PU-0921

新冠感染者外周血 lncRNA 和 circRNA 差异性表达研究

吴英萍
浙江大学医学院附属第四医院

为应对新冠肺炎疫情在全球范围内的爆发，围绕新冠肺炎感染、传播和治疗开展了大量研究。然而，circRNA 和 lncRNA 参与调节免疫耐受、免疫逃逸等多种生命活动，可能为 COVID-19 新发感染和复发提供宝贵信息，目前研究较少。此外，外泌体已被报道在 COVID-19 复发中发挥重要作用，因此可能与 circRNA 和 lncRNA 的表达相互作用。在这项工作中，我们对复发性 COVID-19 患者和健康人群的 circRNA、lncRNA 和 mRNA 进行了测序，并比较了两者的差异。GO 和 KEGG 富集分析表明，差异表达的 circRNA 和 lncRNA 主要参与调控宿主细胞周期、凋亡、免疫炎症、信号通路等过程。与外泌体相关数据库的比较显示，有 114 个差异表达的 circRNA, 10 个差异表达的 lncRNA 与外泌体相关。这些研究为探索 circRNA 和 lncRNA 研究 COVID-19 感染机制、诊断和治疗价值以及将其作为生物标志物的可能性提供了参考。

PU-0922

非小细胞肺癌患者呼出气冷凝液中 miRNA34a 和 miRNA21 检测的临床意义

陶国华、万洋洋、宋卫华、陈金亮
南通市第一民医院

目的 探讨非小细胞肺癌（non-small cell lung cancer, NSCLC）患者呼出气冷凝液（exhaled breath condensates, EBC）中 miRNA34a 和 miRNA21 的表达水平及其临床意义。
方法 应用实时定量聚合酶链反应技术检测 50 例病理证实 NSCLC 患者的血清、EBC，及其中 30 例手术患者癌组织、癌旁组织和 50 例健康人群的血清及 EBC 标本中 miRNA34a 和 miRNA21 的相对表达水平。
结果 NSCLC 患者癌组织、血清及 EBC 中 miRNA21 的相对表达量均高于对照组，而 miRA34a 的相对表达量低于对照组（P 均<0.05）。晚期（Ⅲ-Ⅳ期）NSCLC 患者癌组织、血清和 EBC 中 miRNA21 的表达量均高于早期（Ⅰ-Ⅱ期）患者（P <0.05），而 miRNA34a 的表达量均低于早期患者（P <0.05）。.腺癌患者癌组织、血清和 EBC 中 miRNA21 的表达量高于鳞癌患者（P 均<0.05）。
结论 miRNA34a 和 miRNA21 在 NSCLC 患者癌组织、血清和 EBC 中的相对表达水平与非小细胞肺癌患者的 TNM 分期和病理类型相关，可用于临床 NSCLC 患者的诊断和病情严重程度的评估。

PU-0923

乳腺癌 miR-185-5p、c-MYC、NK1R-Tr 的相互表达调控研究

周云丽
天津医科大学肿瘤医院

目的 探讨乳腺癌 miR-185-5p、c-MYC、NK1R-Tr 之间的相互表达调控关系。
方法 选取 2020 年天津医科大学肿瘤医院 100 例乳腺癌患者癌及癌旁组织，分析 NK1R-Tr、c-MYC、miR-185-5p 在癌及癌旁组织和不同乳腺癌细胞系中的表达，并与不同病理特征进行统计分析。采用 CHIP 验证 c-MYC 对 NK1R-Tr 启动子区的结合；采用荧光素酶报告基因验证 c-MYC 对

NK1R-Tr 的调控作用，检测干扰和过表达 c-MYC 后 NK1R-Tr 蛋白/mRNA 水平的改变。在 MDA-MB-231 中利用荧光素酶报告基因验证 miR-185-5p 对 NK1R-Tr 的 3'-UTR 区调控作用；瞬时转染 miR-185-5p，检测 NK1R-Tr 的蛋白及基因表达、miR-185-5p 水平的改变；检测干扰 c-MYC 后，miR-185-5p 表达水平改变；验证抑制 miR-185-5p 是否通过 c-MYC 影响 NK1R-Tr 蛋白及基因表达。
结果 NK1R-Tr、c-MYC 在癌组织中表达明显高于、miR-185-5p 明显低于癌旁组织；转移组 NK1R-Tr 和 c-MYC 的 mRNA 表达高于、miR-185-5p 低于未转移组；TNM 分期Ⅰ-Ⅱ期 NK1R-Tr 和 c-MYC 的表达明显低于、miR-185-5p 明显高于Ⅲ-Ⅳ期组。MDA-MB-231 细胞中 miR-185-5p 表达较低，NK1R-Tr、c-MYC 表达较高。c-MYC 结合于 NK1R-Tr 启动子区并对 NK1R-Tr 起正性调节的作用；干扰 c-MYC 后，NK1R-Tr 的表达降低；过表达则相反。miR-185-5p 靶向作用于 NK1R-Tr 的 3'UTR 区抑制其转录活性。c-MYC 可抑制 miR-185-5p 的表达，并通过 miR-185-5p 间接作用 NK1R-Tr 调控其表达。
结论 c-MYC 可通过调控 miR-185-5p 靶向影响乳腺癌细胞 NK1R-Tr 的表达。

PU-0924

Hepatitis B virus X protein modulates chemokine CCL15 upregulation in hepatocellular carcinoma

Yueguo Li
Tianjin medical university cancer hospital and institute

Background Hepatitis B virus X protein (HBx) is an indispensable progression factor in hepatocellular carcinoma (HCC). CCL15 could be a peculiar proteomic biomarker of HCC with tumorigenesis and tumor invasion.
Objective The aim of study was to explore the relationship between HBx and CCL15 expression in HCC.
Methods HBV–positive HCC pathological tissue samples and corresponding adjacent non-tumor liver tissues were clearly collected. The expression of HBx and CCL15 was analyzed by immunohistochemistry, real-time polymerase chain reaction (PCR) and western blot analysis in tissues or in vitro.
Results The levels of CCL15 mRNA and protein expression in HCC samples were observably higher than the ones of adjacent non-tumor liver tissues. The CCL15 was significantly associated with the expression of HBx in HBV-positive HCC samples. The up-regulation of HBx induced CCL15 expression in vitro. The high expression score of CCL15 was significant associated with the poor prognosis of HCC patients.
Conclusions The CCL15 expression was observably associated with HBx in HCC patients. The CCL15 may be considered as a indicator in clinical managment of HBV-associated HCC.

PU-0925

Rapid and visual detection of Burkholderia pseudomallei using a a lateral flow dipstick recombinase polymerase amplification assay

Jin Li
Department of Clinical Laboratory Medicine, Institute of Surgery Research, Daping Hospital, Army Medical University

Burkholderia pseudomallei is an important infectious disease pathogen, which mainly causes melioidosis. The melioidosis is mainly prevalent in Thailand, northern Australia and southern China, which has become a global public health problem. Early detection of

B. pseudomallei infection is vital for prognosis of a melioidosis patient. In this study, we evaluated the utility of a lateral flow dipstick recombinase polymerase amplification (LFD-RPA) assay for detecting B. pseudomallei and other non-B. pseudomallei bacteria species. A set of primer-probe targeting orf2 gene within the putative type III secretion system (T3SS) cluster genes was generated, and then the parameters for the LFD-RPA assay were optimized. At the same time, we validated the LFD-RPA assay for detecting B. pseudomallei with 120 clinical B. pseudomallei isolates identified by 16S rRNA gene sequencing. The results showed that the detection sensitivity and specificity are 100%. These results present the developed LFD-RPA assay as a new simple, specific, sensitive, rapid and convenient method for the detection of B. pseudomallei infection in hospital, and it has great application potential for detecting B. pseudomallei and other non-B. pseudomallei bacteria species.

PU-0926

陕西地区他汀类药物代谢相关基因多态性研究

文少佳、张维、李永霞、梁建萍、张强、朱亚荣
西安金域医学检验所有限公司

目的 通过对陕西地区多名检测者的他汀类药物代谢相关基因 SL-CO1B1 和 APOE 的基因多态性进行研究，从而对不同个体进行精准用药指导，提高用药的有效性和安全性；
方法 利用实时荧光定量 PCR 技术检测陕西省 2018 年 4 月至 2021 年 4 月在本单位进行检测的共 289 例患者的外周血中基因组的 SL-CO1B1 基因的 rs2306283(388A＞G) ，rs4149056 (T＞C)位点和 APOE 基因的 rs429358(388T＞C)，rs7412(526c＞T)位点的基因多态性分布特点，并与已报道的中国其他地区检测者的数据进行比较，分析不同地区间的基因型分布差异；
结果 检测到陕西地区检测者中 SL-CO1B1 基因型共有 6 种，分别为*1a/*1b 型（27.3%），*1b/*1b 型（50%），*15/*15 型（9%），*1b/*15 型（4.5%），*1a/15 型（4.5%），*1a/*1a 型（4.5%）；APOE 基因共有 5 种表型，分别为 E2/E3 型（13.6%），E2/E4 型（4.5%），E3/E3 型（59.1%），E3/E4 型（18.1%），E4/E4 型（4.5%）。本研究人群中携带 SL-CO1B1 正常肌病风险型的比例最高，约占 75％ ；SL-CO1B1 中度肌病风险型和高度肌病风险型的人群比例较低，分别为 16.7％ 和 8.3％。APOE 大众类基因型比例最高，约占 63.6％ ；APOE 保护类基因型及风险类基因型的人群比例分别为 13.6％ 和 22.6％。
结论 陕西地区 289 例检测者 SL-CO1B1 和 APOE 基因型分别以他汀药物剂量耐受性较高的正常肌病风险型和对他汀药物敏感的大众类基因型为主；且两种基因的多态性分布均不受性别的影响。因此，检测 SL-CO1B1 和 APOE 基因多态性对于临床评估效益/风险比有重要的指导意义，可实现“个性化用药”的目标。

PU-0927

FISH 检测 IGH/CCND1 联合免疫表型 CyclinD1 在诊断一例伴有浆细胞分化的套细胞淋巴瘤中的应用及文献复习

黄林林、高菲、谭鸿文、敬敏、陈虹、左梅琳、徐之裕、杨友谊、唐梅
四川金域医学检验中心

目的 探讨联合荧光原位杂交（FISH）检测 IGH/CCND1 及免疫表型 CyclinD1 在伴有浆细胞分化的套细胞淋巴瘤的诊断及鉴别诊断中的应用。
方法 回顾研究本中心一例 79 岁男性患者，左锁骨淋巴结肿大，大小约 1.2cm，切除肿大淋巴结送实验室检查，通过病理组织形态、免疫表型及 FISH 多平台检测综合诊断及鉴别诊断并复习文献。
结果 淋巴结结构基本破坏，深染和浅染区交替分布，深染区为中等偏小淋巴细胞浸润，核分裂可

见，浅染区为浆样细胞，深染区细胞免疫表型 CD20、CD5、CyclinD1 阳性,浅染区浆样细胞 CD20 部分阳性，CD138 阳性，cyclinD1 阴性，CD3、CD5、lambda 阴性，kappa 阳性，显示为克隆性浆细胞，轻链限制性表达，Ki-67 约 20%阳性，FISH 检测：IGH/CCND1 融合基因深染区细胞和浅染区浆样细胞均阳性。结合病理组织形态、免疫表型及 FISH 检测，综合诊断为：伴有浆细胞分化的套细胞淋巴瘤。

结论 套细胞淋巴瘤是相对少见的 B 细胞淋巴瘤，预后较差，检索文献，发现伴有浆细胞分化的形态学特征非常罕见，容易误诊为其它伴有浆样细胞分化的小 B 细胞淋巴瘤。细胞周期素蛋白 D1（CyclinD1）尽管是套细胞淋巴瘤相对特异的诊断指标，但是在浆细胞瘤、毛细胞白血病、弥漫性大 B 细胞淋巴瘤、恶性黑色素瘤等肿瘤中也可有部分细胞弱-中等强度阳性，这在鉴别诊断中要特别注意，本例 FISH 检测浆样分化细胞 IGH/CCND1 阳性，提示克隆性浆细胞分化也可见于套细胞淋巴瘤，而联合 IGH/CCND1 的 FISH 检测和 CyclinD1 的免疫表达并结合组织形态，基本上可以准确诊断套细胞淋巴瘤，即使罕见的伴有浆细胞分化，也能避免误诊，从而为临床精准治疗提供了保障。

PU-0928

陕西地区 9765 例女性叶酸代谢相关基因多态性分布研究

文少佳、朱亚荣、张强、梁建萍、张维、李永霞
西安金域医学检验所有限公司

目的 通过对陕西地区多名女性亚甲基四氢叶酸还原酶（MTHFR）和甲硫氨酸合成酶还原酶（MTRR）基因多态性分布情况进行研究，旨在为临床医师指导育龄妇女个体化的叶酸补服方案提供科学依据。

方法 以陕西省 9 765 例育龄期妇女为研究对象，利用单碱基延伸方法检测 MTHFR C677T、A1298C 位点和 MTRR A66G 位点的基因型，统计分析基因多态性的分布特征，根据基因型结果评估叶酸代谢能力强弱，从而得出陕西省育龄女性是否有叶酸补充风险及风险级别。

结果 统计全部样本中的 MTHFR C677T 位点，其中野生型（CC）、杂合突变型（CT）及纯合突变型（TT）基因型频率分别占 24.4%、46.9%和 28.7%；MTHFR A1298C 位点野生型（AA）、杂合突变型（AC）及纯合突变型（CC）基因型频率分别为 71.7%、25%和 3.3%；MTRR A66G 位点野生型（AA）、杂合突变型（AG）及纯合突变型（GG）基因型频率分别为 48.6%、44.6%和 6.8%。MTHFR C677T、A1298C 和 MTRR A66G 位点基因型分布与中国人群差异均具有统计学意义（$P<0.05$）。育龄女性存在叶酸代谢障碍者高达 60%以上。

结论 陕西省育龄女性 MTHFR C677T、A1298C 和 MTRR A66G 基因多态性的分布具有地域特异性，超过 60.00%的育龄女性携带高风险基因，需根据叶酸代谢基因检测结果，给予补充相应剂量的叶酸，以降低出生缺陷。

PU-0929

Comprehensive Analysis of regulatory factors and immune-associated patterns to decipher common and BRCA1/2-mutation type-specific critical regulation in breast cancer

Yue Li
The Second Affiliated Hospital of Xi'an Jiaotong University

Background BRCA1/2 mutations are currently proven to be closely related to high lifetime risks of breast cancer. The objective of this study is to identify the genes and associated regulators and

immune-associated patterns underlying disease pathology in BRCA mutations and its association with clinical traits.
Results Consensus network analysis identified 13 modules, including 8 upregulated modules and 3 downregulated modules, in the BRCA1-mutant compared with wild-type cohorts; and 13 modules including 9 upregulated modules and 2 downregulated modules in the BRCA2-mutant breast cancer. Among them, some modules showed significantly positive correlations with tumor stage, number of positive lymph nodes and margin status, without any significance in wild-type patients. Function enrichment suggested the potential mechanisms by which BRCA1/2 carriers could regulate cell cycle, immune response, cellular metabolic processes and cell migration, and thus influence the metastasis and prognosis of BRCA1/2-mutant breast cancer, via enriched pathways including p53, JAK-STAT signaling and so on associated with its multi-genes from these modules. Therefore, consensus network helped identify the specificity and commonality of carcinogenic mechanism of BRCA mutations, relative to wild-type breast cancer. Intermodular network of transcription factors showed some transcription factors and miRNAs enriched, notably, significantly enriched E2F transcription factor family associated cell cycle regulation, and IRF family associated with immune response regulation. The validation of multi-gene using other TCGA and GEO databases, could screen the hub genes including ISG15, MX1, IF1T1, ITGAX and so on, and indicate the close relationships between BRCA1/2 mutations and TNBC at molecular levels. Furthermore, on this basis, we could identify BRCA1/2-mutation type-specific immune-associated patterns and imply that BRCA1 mutation could regulate multi-gene and multi-pathway and thus influence the tumor immune microenvironment (TIME), manifested as the recruitment of T cells, neutrophils, dendritic cells, T-regulatory cells (Tregs) infiltration and T cell exhaustion.
Conclusions In our study, we identify a BRCA1/2-mutation type-specific co-expressed gene network with associated transcription factors, and its immune-associated patterns, accordingly, to reflect the common and specific regulation patterns of tumor metastasis and TIME, which provides novel insights into the pathological process of this disease and corresponding BRCA mutations.

PU-0930

茎环引物辅助的新型等温扩增技术实现高特异性和高灵敏性核酸检测

罗光成
川北医学院附属医院

目的 建立特异性高、灵敏度好的新型等温扩增技术和可视化核酸检测方案。
方法 本研究采用全新的引物设计原则，开发了一种名为茎环引物辅助的新型等温扩增技术 (Stem-loop-primer assisted isothermal amplification, SPA)。SPA 的引物设计非常简单，只需针对模板的 2 区域，设计 1 对普通引物（正向引物 FP 和反向引物 BP)。然后再基于普通引物构建 1 对茎环引物（正向茎环引物 SFP 和反向茎环引物 SBP)。SFP 和 SBP 是在 FP 和 BP 的 5’端增加一段茎环序列。通过将普通引物和茎环引物按一定比例混合就构成了 SPA 的扩增引物，并能在 Bst DNA 聚合酶的催化下对待测核酸进行恒温扩增。
结果 SPA 的确可以快速。灵敏、特异地扩增靶核酸。本研究以扩增 ALDH2 基因为模型，充分验证了 SPA 的扩增机理和检测性能。SPA 的特异性好且灵敏度高，其非特异性扩增比目前广泛使用的 LAMP 等温扩增技术更低，且灵敏度与之相当。另外，本研究通过对临床样本中 16、18、52 和 58 型 HPV DNA 的检测，充分验证了 SPA 的临床实用性。最后，本研究建立了基于 pH 指示剂的可视化 SPA 检测方案（即通过反应前后扩增液的颜色变化来判断扩增结果的阴阳性），并将其成功地应用于 16 型 HPV 的检测之中。

结论 本研究建立了一种名为茎环引物辅助的新型等温扩增技术（SPA），并基于 SPA 技术进一步建立可视化核酸检测方案。可视化 SPA 展现出了良好的临床实用性，为实现便携式核酸检测提供了思路和方案。

PU-0931

两例 FGB 基因 c.1115 T>A 杂合突变导致的遗传性异常纤维蛋白原血症家系的表型及遗传学分析

王晓欧、姚雅婷、林素珍 、王锦乐、舒旷怡、艾心怡、江明华（通讯作者）
温州医科大学附属第二医院、育英儿童医院

目的 对 2 例遗传性异常纤维蛋白原血症家系进行临床表型和基因型分析，初步探讨其发病机制。
方法 用 STA-R 全自动血凝仪检测先证者及其家系成员血浆凝血酶原时间（PT）、部分活化凝血活酶（APTT）、凝血酶时间（TT）、纤维蛋（原）降解产物（FDPs）、D 二聚体（D-D）及 TT 的硫酸鱼精蛋白纠正实验；分别用 Clauss 法和免疫散射比浊法分别检测血浆纤维蛋白原活性（Fg:A）和纤维蛋白原抗原（Fg:Ag）；用 PCR 扩增纤维蛋白原 FGA、FGB 和 FGG 基因的所有外显子及其侧翼序列，扩增产物纯化后直接测序分析，寻找基因突变位点并排除基因多态性；用 4 个生物信息学预测软件（PolyPhen-2、SIFT、PROVEAN 和 Mutation Taster）对突变进行功能预测；采用 PyMol 软件对突变蛋白进行结构分析；用 Clustal X 软件分析突变氨基酸的保守性。
结果 2 例先证者 PT、APTT、FDPs、D-D 正常，而 TT 延长且不能被硫酸鱼精蛋白校正，Fg 活性明显降低，分别为（1.25 和 1.17g/L），但 Fg 抗原含量正常，分别为（3.50g/L 和 3.81g/L）。基因分析显示 2 例先证者均为 FGB 第 7 号外显子 c.1115 T>A（p.Val372Glu）杂合错义突变，突变均来源于父亲。四个生物信息学软件预测结果均表示此突变可影响蛋白质功能，且为有害突变。Clustal X 软件保守性分析结果表明 Val372 在同源物种间高度保守；PyMol 显示 p.Val372Glu 突变使 Fg 蛋白二级结构和三维结构改变，导致活性降低。
结论 2 例先证者是 FGB c.1115 T>A 所致的遗传性异常纤维蛋白原血症，该位点为尚未见报道的新变异。

PU-0932

新型冠状病毒的检测方法概述

王丽娟、许宏涛
北京医院

新型冠状病毒(SARS-CoV-2)最先在武汉爆发，随后蔓延至全国各地。这种新型冠状病毒感染成为国际关注的突发性公共卫生事件，其主要传播途径为呼吸道飞沫及密切接触，具有高传染性、高致病性。快速、准确检测病毒感染对防控疫情非常重要，SARS-CoV-2 的检测方法主要包括核酸检测、高通量测序、血清学检测等。核酸检测和抗原检测是诊断新型冠状病毒肺炎（Corona Virus Disease, COVID-19）的直接证据，IgM 和 IgG 抗体检测可以辅助诊断 COVID-19 和评价疫苗接种是否有效。核酸检测联合抗体检测有助于提高临床诊断 COVID-19 的特异性和敏感性。本文主要对 SARS-CoV-2 的检测方法进行概述。

PU-0933

Prognostic value of the baseline circulating T cell receptor β chain diversity in advanced lung cancer

Yujie Zhu[2]、Jiaqi Wang[1]
1. National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College
2. Xuanwu Hospital, Capital Medical University

Purpose An indicator for systemic evaluation of the adaptive immune status is lacking. Peripheral blood is important in antitumour immunity, and the T-cell receptor (TCR) repertoire diversity is key for effective immunity. This study aimed to investigate changes in the circulating T cell receptor β chain (TCRB) diversity during the first few (1~4) treatment cycles and its clinical value in patients with advanced lung cancer.
Experimental Design TCRB-enriched sequencing data combined with transcriptomic RNA sequencing data of peripheral blood leukocytes was obtained from 72 patients with advanced lung cancer before and after targeted therapy or chemotherapy. Changes in the circulating TCRB diversity during treatment and relationship of the baseline circulating TCRB diversity with prognosis and therapeutic effect were evaluated.
Results We found that targeted therapy or chemotherapy did not significantly affect the T lymphocyte composition or circulating TCRB diversity (3.83 vs 3.74, T-test, p=0.16) in patients with advanced lung adenocarcinoma (LUAD) during the first few treatment cycles. The circulating TCRB diversity links to improved therapeutic effects (T-test, p=0.00083) in LUAD patients receiving targeted therapy. Higher baseline circulating TCRB diversity was associated with better prognosis. In addition, a five-factor prognostic risk score model was built for more accurate prognosis prediction for LUAD patients.
Conclusions The chemotherapeutic agents for advanced lung cancer does not significantly affect adaptive immune function over the first few treatment cycles. The circulating TCRB diversity reflects the adaptive immunological repertoire and it might be a convenient indicator for evaluating the adaptive immune status and prognosis.

PU-0934

HMBOX1 与非小细胞肺癌预后及免疫浸润的相关性分析

于运亮[1]、李婷[2]、封建凯[1]
1. 滨州医学院烟台附属医院
2. 烟台市烟台山医院

目的 探索 HMBOX1（Homeobox Containing 1）基因在非小细胞肺癌中的表达及与患者预后及肿瘤免疫细胞浸润的相关关系，为非小细胞肺癌免疫治疗提供新的靶点。
方法 利用 qRT-PCR 技术和免疫组化技术检测 HMBOX1 在非小细胞肺癌与正常肺组织中的表达差异；利用 Kaplan-Meier Plotter 数据库分析 HMBOX1 与非小细胞肺癌患者预后相关关系；使用 FunRich 软件、MetaScape 等生物在线数据库进行 GO 和 KEGG 富集分析；利用 TIMER、TSIDB 等数据库综合分析 HMBOX1 与肿瘤微环境中免疫细胞浸润程度、肿瘤突变负荷（TMB）、肿瘤微卫星不稳定性（MSI）、新抗原等相关关系。
结果 肺鳞癌和肺腺癌组织中 HMBOX1 的表达水平明显低于正常肺组织。肺癌患者尤其是肺腺癌患者 HMBOX1 高表达的其总生存时间较长（P=0.0014）。肺癌分期 1 期患者中 HMBOX1 高表达的患者其总生存期较长（P=0.0084）；男性肺癌中 HMBOX1 高表达的患者其总生存期较长（P=0.00083）；未经过化疗的肺癌患者 HMBOX1 高表达的其总生存期较长（P=0.033）。HMBOX1 与 DSCC1（DNA replication and sister chromatid cohesion 1）高度相关，两者可能在调控肿瘤细胞 DNA 复制过程中发挥相互拮抗作用。HMBOX1 与多种肿瘤微环境中 T 细胞的活化有

关，且与肺腺癌患者 TMB 和 MSI 呈负相关关系。HMBOX1 很可能通过激活 JAK2/STAT3 信号通路调控机体免疫细胞。
结论 HMBOX1 基因在非小细胞肺癌患者中低表达，且 HMBOX1 的表达水平与非小细胞肺癌尤其是肺腺癌患者的预后及免疫细胞浸润有关。

PU-0935

SENP1 在 HIV 抗 I 型干扰素固有免疫通路中的作用研究

宋艳辉
苏州大学附属第一医院

目的 确定 HIV 感染过程中去 SUMO（Small ubiquitin-like modifier）化酶 SENP1（Sentrin-specific protease 1）对底物 PTP1B 的 SUMO 化及功能影响，以及 PTP1B 对 STAT1 磷酸化的调控，探讨 SENP1 在 HIV 抗 I 型干扰素固有免疫通路中的作用。
方法 我们在细胞中感染 HIV 并检测 SENP1 的表达变化；同时我们在细胞中用 siRNA 下调 SENP1，检测 HIV 的复制。在 293T 细胞中过表达 SENP1 的质粒，然后用 phos-tag 沉淀细胞内磷酸化的蛋白，检测其 STAT1 和 STAT2 的磷酸化水平。用 Co-IP，MS 的方法在 293T 过表达 Flag-SENP1, 然后用 HIV-luc 病毒感染细胞，质谱鉴定与蛋白磷酸化相关的重要蛋白。
结果 下调 SENP1，可以显著地增加 I 型干扰素信号通路中 ISRE 控制下的 luciferase 的表达。在 HIV 感染过程中，SENP1 表达水平增加；通过 siRNA 下调 SENP1，HIV-1 病毒的复制减少。过表达 SENP1 可以明显降低胞内 STAT1 的磷酸化水平。质谱鉴定与蛋白磷酸化检测结果表明 PTP1B 和 SENP1 有相互的直接作用。
结论 在 HIV 感染过程中，SENP1 表达得到上调，进而可能通过 PTP1B 磷酸化酶，减少 STAT1 磷酸化水平，抑制 I 型 IFN 干扰素信号通路中抗病毒基因的表达，帮助病毒复制。

PU-0936

长链非编码 RNA 在脓毒症相关器官损伤中致病机制的研究进展

胡元慧
武汉大学人民医院

脓毒症是一种由感染、创伤等多因素引起机体炎症反应紊乱的综合症，常并发肾损伤、心肌损伤、肺损伤和肝损伤等相关器官损伤，临床致死率极高预后不理想。现有的实验室生物标志物如降钙素原、C 反应蛋白等，对脓毒症早期诊断、治疗效果评估和预后判断提供了一定的帮助，但仍存在特异性和敏感性差的不足。近期长链非编码 RNA（long non-coding RNA，lncRNA）功能的研究被重视，在炎症反应、器官功能障碍等过程中，lncRNA 主要通过参与各种信号通路发挥重要作用。本文就目前 lncRNA 在脓毒症引起的常见器官功能损伤中可能的作用机制进行综述。

PU-0937

淋巴细胞 Pole2 增龄性表达变化及在老年病患者中初步观察

张弛、侯玉丽、王培昌
首都医科大学宣武医院

目的 探讨北京市健康人群外周血淋巴细胞 Pole2 表达水平的增龄性变化，分析部分老年病患者外周血淋巴细胞 Pole2 表达水平的变化。

方法 以 RT-PCR、 Western blot 方法检测不同年龄组健康人群外周血淋巴细胞 Pole2 的 mRNA 及蛋白表达水平，绘制增龄相关曲线；检测糖尿病（DM）、冠心病（CHD）、阿尔茨海默病（AD）、脑动脉粥样硬化（CVD）外周血淋巴细胞 Pole2 的 mRNA 及蛋白表达水平，分析其与同龄健康人群的差异。
结果 北京健康人群 Pole2 的 mRNA 及蛋白表达水平在 20～50y 年龄区间随龄上升，60y 以后随龄下降（P<0.001）；CHD、AD、DM、CVD 患者外周血淋巴细胞 Pole2 的 mRNA 及蛋白表达水平明显高于同年龄健康人群，其中 AD 患者组 Pole2 蛋白表达水平明显高于其他疾病组（P<0.001）。
结论 外周血淋巴细胞 Pole2 表达水平随龄及在老年病中变化显著，其具有成为衰老及上述老年病标志物的较大潜能。

PU-0938

HBsAg 和 HBV DNA 定量水平在慢性 HBV 感染自然史中的关系

薛占成、庞伟
武警特色医学中心

目的 探讨慢性乙型肝炎（chronic hepatitis B, CHB）患者 HBsAg 和 HBV DNA 定量的变化及两者的相关性。
方法 纳入慢性 HBV 感染患者 144 例，其中根据自然史分为免疫耐受期（immune tolerance phase，IT）（n=46）、免疫清除期（ immune clearance phase，IC）（n=28）、低复制期（ low-replication phase，LR）（n=24）、再活动期（reactivation phase），RA）（n=46）。采用化学发光定量法和实时荧光 PCR 定量法检测患者血清 HBsAg 和 HBV DNA。
结果 CHB 患者不同时期 HBsAg 和 HBV DNA 定量水平差异均具有统计学意义（P<0.05），HBsAg 和 HBV DNA 在 IT 期显著高于其他 3 期，LR 期最低（P<0.05）。HBsAg 和 HBV DNA 定量在 IC 期（r=0.3873,P<0.05）和 RA 期（r=0.7401,P<0.05）具有相关性。ROC 曲线分析显示: HBsAg>3.455 log10 IU/ml 的截断值（2852 IU/mL），用于预测 IC 期敏感度为 78.60%，特异度为 79.10%；HBsAg>3.505 log10 IU/ml 的截断值（3200 IU/mL），用于预测 RA 期敏感度为 74.31%，特异度为 80.21%。
结论 CHB 自然史不同阶段 HBsAg 和 HBV DNA 水平有明显差异,但仅在 IC 期和 RA 期 HBsAg 与 HBV DNA 相关。这些发现表明 HBsAg（3200 IU/mL）作为预测 HBV 再激活有重要价值。

PU-0939

亚甲基四氢叶酸还原酶基因 677 位多态性与 H 型高血压相关性研究

迟忠雨
光谷大街 1977 号金域检验

目的 叶酸（folate acid）也称为蝶酰谷氨酸或者维生素 B9，是由蝶啶、对氨基苯甲酸和 L-谷氨酸组成。在 DNA 和 RNA 合成中起重要作用，为核苷酸的合成提供一碳单位。在氨基酸的甲基化循环中参与甲基转运，在同型半胱氨酸（Hcy）的转化中起重要作用，而 H 型高血压患者血液中的同型半胱氨酸（Hcy）水平高于正常。H 型高血压患者更易发生脑卒中风险。本实验的目的是探讨亚甲基四氢叶酸还原酶基因 677 位多态性与高同型半胱氨酸血症及 H 型高血压之间的关系。判断叶酸对 H 型高血压治疗是否有效，为临床应用提供参考。
方法 收集高血压患者 300 例,根据测得的同型半胱氨酸水平被分为 H 型高血压组（H 组）（n=159）、原发性高血压组（HT 组）（n=141）,收集其一般临床资料，并利用 PCR 方法检测其亚甲基四氢叶酸还原酶基因（MTHFR）多态性 677 位点的三种基因型,应用统计学软件分析结果。

结果 H 组与 HT 组同型半胱氨酸（Hcy）水平比较（18.89±9.43 vs 8.09±1.53,P<0.01）;H 组与 HT 组 TT 型基因频率比较（41.73% vs 17.86%,P<0.01）。亚甲基四氢叶酸还原酶基因（MTHFR）C-T 的突变与 H 型高血压密切相关,300 例研究对象中携带 TT 基因型的高血压患者同型半胱氨酸（Hcy）水平比 CC 和 CT 基因型显著增高。
结论 亚甲基四氢叶酸还原酶基因（MTHFR）TT 型与高同型半胱氨酸血症及 H 型高血压有关；叶酸可用于治疗高同型半胱氨酸血症且有助于改善 H 型高血压。

PU-0940

The kynurenine derivative 3-HAA sensitizes hepatocellular carcinoma to sorafenib by upregulating phosphatases

Guifang Gan[1]、Zhaopeng Shi[2]、Fuxiang Chen[1]、Jun Mi[2]
1. Ninth People's Hospital, Shanghai Jiao Tong University School of Medicine
2. 上海交通大学医学院

Objectives Sorafenib is the FDA-approved first-line target drug for HCC patients. However, sorafenib merely confers 3-5 months of survival benefit with less than 30% of HCC patients sensitive to sorafenib therapy. Thus, it's necessary to develop a sensitizer for hepatocellular carcinoma (HCC) to sorafenib.
Methods The principal component analysis, gene ontology, and KEGG analysis are utilized following RNA-sequencing. The mass spectrometry analysis following immunoprecipitation is performed to discover the phosphatase targets. Most importantly, both the cell line-derived xenograft (CDX) and the patient-derived xenograft (PDX) mouse model are used to determine the effect of 3-HAA on sorafenib-resistant HCC in vivo.
Results In nude mice carrying HCC xenograft, tumor growth is inhibited by sorafenib or 3-HAA alone. When used in combination, the treatment particularly prevents the xenograft from growing. Combined treatment also suppresses the growth of sorafenib-resistant (≥30mg/kg) PDXs. In a set of mechanistic experiments, we find enhanced AKT activation and decreased apoptotic cells in de novo and acquired sorafenib-resistant HCC cells and tissues. 3-HAA decreases AKT phosphorylation and increases the apoptosis of HCC in both cultured cells and mouse xenografts by upregulation of phosphatases PPP1R15A/DUSP6. PPP1R15A/PPP1α directly reduces Akt phosphorylation while DUSP6 decreases Akt activity through inhibiting PDK1. The AKT activator abolishes 3-HAA inhibition of HCC growth in vitro and in mice.
Conclusion This study demonstrates that 3-HAA sensitizes HCC cells to sorafenib by upregulation of phosphatases, suggesting it as a promising molecule for HCC therapy.

PU-0941

TREM2 水平升高与神经退行性疾病患者和阿尔茨海默病模型小鼠的认知水平相关

张晓敏、刘静、曹敏、王培昌
首都医科大学宣武医院

背景 髓样细胞表达的触发受体 2（Triggering receptor expressed on myeloid cells 2， TREM2）主要表达于小胶质细胞，在神经退行性疾病特别是阿尔茨海默病（Alzheimer's disease, AD）中起重要作用。本研究旨在阐明 TREM2 作为阿尔茨海默病诊断生物标志物的潜在价值。
方法 采用 ELISA 法检测人和小鼠血清 TREM2 水平，采用实时荧光定量 PCR（RT-qPCR）和 Western Blot 方法检测小鼠淋巴细胞和脑组织中 TREM2 的 mRNA 和蛋白表达情况。采用 MMSE/MoCA 评分法测定患者的认知能力。采用 Morris 水迷宫（MWM）实验评价小鼠的认知能力。

结果 研究结果发现神经退行性变疾病患者与 AD 模型小鼠的血清 TREM2 浓度和淋巴细胞的蛋白表达水平均升高，且 TREM2 的表达水平与 AD 患者、APP/PS1 小鼠的认知能力有相关性。
结论 TREM2 作为一种新的 AD 诊断标志物具有潜在的临床价值。

PU-0942

APP/PS1 转基因小鼠基因型与蛋白水平鉴定及认知水平分析

张晓敏、曹敏、刘静、王培昌
首都医科大学宣武医院

目的 对 APP/PS1 转基因小鼠与野生型（WT）小鼠进行基因型鉴定，并比较二者的认知行为能力和脑内 APP 蛋白的表达量。
方法 利用聚合酶链式反应（PCR）与琼脂糖凝胶电泳技术鉴定不同年龄组 APP/PS1 双转基因小鼠与 WT 小鼠基因型；行水迷宫实验检测 2 月，5 月，10 月龄小鼠的认知水平；取不同组小鼠的海马组织进行匀浆，利用 Western blot 检测海马组织 APP 蛋白含量。
结果 正确鉴定了 APP/PS1 转基因小鼠与 WT 小鼠；10 月龄 APP/PS1 转基因小鼠的学习记忆能力比同月龄对照组 WT 小鼠明显下降，而 2 月龄、5 月龄的两组小鼠之间学习记忆能力差异不显著；同月龄的 APP/PS1 转基因小鼠海马组织 APP 蛋白表达量显著高于 WT 小鼠。
结论 正确鉴定了 APP/PS1 转基因小鼠，10 月龄的 APP/PS1 转基因小鼠比 WT 小鼠认知水平明显降低，该转基因小鼠可作为研究阿尔茨海默病等衰老疾病的动物模型。

PU-0943

血清 PLCG2 作为生物标志物对阿尔茨海默病早期诊断的价值

曹敏、刘静、张晓敏、王培昌
首都医科大学宣武医院

根据全基因组关联分析发现 PLCG2 基因突变是迟发性 AD 的危险因素，本研究的目的是探索 PLCG2 基因在 APP/PS1 小鼠中的作用，并验证血清中 PLCG2 能否作为 AD 的潜在生物标志物。
方法 取 2 月龄、5 月龄及 9 月龄 APP/PS1 小鼠及 WT 小鼠海马及皮层组织，WB，RT-PCR 检测组织中 PLCG2 的表达水平，同时收集轻度认知障碍患者（25 例），阿尔茨海默病痴呆患者（71 例），帕金森病患者（48 例），血管性痴呆患者（39 例）及健康对照患者（60 例）血清样本，通过 ELISA 方法检测血清中 PLCG2 在不同疾病中含量有无差异，并验证血清中 PLCG2 含量与认知功能 MMSE 评分、MOCA 评分的相关性，同时制作受试者工作曲线，计算曲线下面积，判断血清 PLCG2 对 AD 的诊断价值。
结果 与同龄 WT 小鼠相比，在 9 月龄 APP/PS1 小鼠皮层组织中，PLCG2 蛋白表达水平增高，而在 RNA 水平上，与同龄 WT 小鼠相比，在 9 月龄 APP/PS1 小鼠海马组织中 PLCG2 表达水平增高。与健康对照组相比，AD 患者血清中 PLCG2 含量明显下降（$P<0.01$），且在 AD 轻度认知障碍期，血清 PLCG2 含量低于重度痴呆期（$P<0.01$），我们发现血清 PLCG2 含量帕金森病患者低于重度痴呆期（$P<0.05$）,而血管性痴呆患者血清 PLCG2 含量低于帕金森患者（$P<0.005$），同时我们发现血清中 PLCG2 含量与 MMSE、MOCA 评分有显著的相关性。通过受试者工作曲线计算曲线下面积，发现血清 PLCG2 在鉴别 AD 与 PD 时，曲线下面积为 0.812。鉴别 AD 与 VaD 时，曲线下面积为 0.815，表明血清中 PLCG2 含量能够鉴定 AD 型痴呆与非 AD 型痴呆。
结论 我们的结果表明 PLCG2 基因在 AD 模型鼠中的作用，同时验证了血清 PLCG2 能够早期诊断 AD，为 AD 提供了一个潜在血液生物标志物

PU-0944

衰老细胞染色质开放变化的初步分析

宋乔、王亚琦、侯玉丽、刘静、张晓敏、曹敏、王培昌
首都医科大学宣武医院

为研究复制性衰老中表观遗传学的变化，以年轻代龄(PD26)和年老代龄(PD55)的人胚肺二倍体成纤维细胞(2BS)为材料，进行 ATAC-seq 测序，并使用 Bowtie2、FastQC、MACS、deepTools、phastCons、R 语言、HOMER 以及基因本体论(Gene Ontology，GO)对测序结果进行深入分析和挖掘。结果显示，2BS 细胞染色质开放区域的保守性较强，其主要集中于启动子(promoter)区至转录起始位点(transcription start site，TSS)，且年轻细胞与年老细胞的启动子区至转录起始位点的开放程度不同，细胞随着衰老在启动子区至转录起始位点的开放程度逐渐下降。进一步对年轻和年老细胞之间存在显著差异的靶基因进行 GO 分析发现，这些差异基因主要与细胞进程、代谢、生物性调节、结合功能、催化功能相关。本次研究发现衰老过程中染色质开放区减少、转录调控水平下降，提示复制性衰老与转录调控关系密切。

PU-0945

MicroRNA-135a in ABCA1 Labeled Exosome is a Candidate Biomarker for Alzheimer's Disease in Serum

Chengeng Liu、Yao Lu、Yue Zhao、Peichang Wang
Xuanwu Hospital,Capital Medical University

In the present study, ABCA1 protein was used as a specific exosome label to capture specific exosomes, and evaluate the value of ABCA1 labeled exosomal microRNA-135a (miR-135a) in the diagnosis of AD, especially in the early diagnosis of AD.

Methods This study conducted preliminary research on the levels of ABCA1 in white blood cell (WBC), red blood cell (RBC), HT-22 cells, and neuronal cells. The diagnostic value of ABCA1 labeled exosomal miR-135a in cerebrospinal fluid (CSF) and serum in APP/PS1 double transgenic mice and 152 SCD, 131 MCI, 198 DAT and 30 control subjects.

Results The ABCA1 levels of exosome harvested from HT-22 cells and neurons medium was significantly higher than that of RBC and WBC ($P < 0.05$). The ABCA1 labeled exosomal miR-135a were increased in the CSF of MCI and DAT patients compared with control group ($P < 0.05$). The ABCA1 labeled exosomal miR-135a were slightly increased ($P > 0.05$) in the serum of SCD and significantly increased in MCI and DAT patients compared with control group ($P < 0.05$).

Conclusion In summary, this study provides a method to capture specific exosomes and detect them using immunological methods, which is more efficient for early diagnosis of AD.

PU-0946

Severely High Lactic Acid in Severe Pneumonia Patient: a Case Report

Chengeng Liu、Yiming Chu、Yao Lu、Peichang Wang
Xuanwu Hospital,Capital Medical University

Background Severe pneumonia (SP) is a clinically critical acute disease which has a higher mortality rate in infectious diseases. In this report, a rare case of severe pneumonia with severely high lactic acid (up to 24 mmol/L) and relatively normal pH was analyzed.

Methods The case was discussed from different angles including acid-base balance disorder, the using of extracorporeal membrane oxygenation (ECMO), dialysis treatment, circulatory disturbance, and inspection methodology.
Results Hypoxia and dissolution of muscles caused by circulatory disorders may be the cause of the abnormal increase of lactate in this case; while the relatively normal pH may be caused by the dialysis treatment.
Conclusions Such a high blood gas lactic acid value is extremely rare, and this increase is not due to the limitations of the test method; high lactic acid may not result in the significant decrease of pH when the patient receives continuous systemic treatment.

PU-0947

ABCA1 Labeled Exosome Contain Higher MicroRNA-193b in the Serum of Alzheimer's Disease

Chengeng Liu、Yao Lu、Yue Zhao、Peichang Wang
Xuanwu Hospital,Capital Medical University

This study used immunocapture to isolate serum exosomes labeled with ABCA1 for diagnosis of Alzheimer's disease dementia and differential diagnosis of vascular dementia.
Methods This study conducted preliminary research on the levels of ABCA1 labeled exosomal miR-193b in white blood cell (WBC), red blood cell (RBC), HT-22 cells, and neuronal cells. The ABCA1 labeled exosomal miR-193b in cerebrospinal fluid (CSF) and serum of APP/PS1 double transgenic mice and 89 subjective cognitive decline (SCD), 92 stage and mild cognitive impairment SCD (MCI), 92 dementia of the Alzheimer type (DAT), 60 vascular dementia (VaD) and 60 control subjects.
Results The ABCA1 levels of exosome harvested from HT-22 cells and neurons medium was significantly higher than that of RBC and WBC ($P < 0.05$). The ABCA1 labeled exosomal miR-193b were increased in the CSF of MCI and DAT patients compared with control group ($P < 0.05$). The ABCA1 labeled exosomal miR-193b were slightly increased ($P > 0.05$) in the serum of SCD and significantly increased in MCI and DAT patients compared with control group ($P < 0.05$).
Conclusion In summary, this study provides a method to capture specific exosomes and detect them using immunological methods, which is more efficient for early diagnosis of AD.

PU-0948

脊髓小脑共济失调及强直性肌营养不良症易感基因突变位点的研究进展

兰贺、刘辰庚、王培昌
首都医科大学宣武医院

脊髓小脑共济失调(spinocerebellar ataxia, SCA)以及强直性肌营养不良症（myotonic dystrophy，DM）均为临床上较常见的常染色体显性遗传病，其主要基因突变类型为动态突变。SCA 常见突变亚型为 SCA1、SCA2 和 SCA3，其动态突变类型均为核苷酸（CAG）序列拷贝数异常。强直性肌营养不良症 I 型（DM1）突变位点多位于 19q13.3，主要为蛋白激酶 K（dystrophia myotonic protein kinase，DMPK）基因 3′端非翻译区核苷酸（CTG）拷贝数异常；强直性肌营养不良症 II 型（DM2）主要突变类型为 3 号染色体长臂（3q21.3）锌指蛋白 ZNF-9（zinc finger protein 9）第一内含子中重复序列（CCTG）拷贝数异常，(CCTG)n 的重复序列在健康人群中是间断的，而在基因突变人群中 CCTG 是连续出现的。Sanger 测序以及多重 DNA 聚合酶链反应是目前 SCA、DM 动态突变基因检测的重要方法。

PU-0949

转录因子 CTCF 在衰老过程中对 POLD1 转录调控机制的研究

侯玉丽、宋乔、高世超、张晓敏、王亚琦、刘静、付静轩、曹敏、王培昌
首都医科大学宣武医院

衰老是细胞、组织、器官等结构及功能随龄渐进性退行性变，最终走向不可逆的死亡过程。是多种老年病的发病基础，因此研究衰老的机制对于老年病的预防和治疗具有重要意义。POLD1 是 DNA 聚合酶 δ 的催化亚基，在 DNA 合成和 DNA 修复过程中起关键作用。已有研究表明 POLD1 表达的增龄性下调通过降低 DNA 合成率以及 DNA 损伤修复能力加速细胞衰老。但是对于 POLD1 增龄性下调的具体机制尚未清晰，本文从转录调控的水平研究 POLD1 的增龄性下调机制。本研究首先发现 CTCF 与 POLD1 启动子区的两个位点进行结合，并对 POLD1 启动子活性起激活作用。此外，在衰老细胞系、SAMP8 小鼠组织和人外周血淋巴细胞中发现 CTCF 和 POLD1 表达均随龄下降并具有正相关性，并且这种表达趋势与 CTCF 和 POLD1 启动子的结合水平相关，表明 CTCF 有可能是通过影响与 POLD1 启动子的结合而调控 POLD1 的表达。更深入的机制研究表明，在衰老细胞中进行 CTCF 敲除后 POLD1 表达下降，细胞增殖能力下降、DNA 合成率下降、DNA 损伤修复能力下降及细胞衰老染色加深，而当 CTCF 过表达后具有相反的结果。当在 CTCF 敲除后进行 POLD1 过表达后发现 POLD1 表达增高，并且 CTCF 对细胞衰老的作用被回复。在 CTCF 过表达后进行 POLD1 敲除也出现同样的回复作用，表明 CTCF 是通过靶向调控 POLD1 的表达而调控衰老的进展。总之，以上结果表明衰老过程中转录因子 CTCF 的增龄性下调导致了 CTCF 与 POLD1 启动子结合水平的下降而调控细胞衰老。该研究为衰老的分子机制提供了新的思路，进而可能为延缓衰老提供了新的靶点。

PU-0950

阿尔茨海默病中 β 淀粉样蛋白的生成及清除的调节

崔雨婷、王亚琦、王培昌
首都医科大学宣武医院

阿尔茨海默病（Alzheimer's disease， AD）是一种慢性退行性神经系统疾病，临床主要表现为进行性认知能力下降、记忆力衰退、人格改变等。AD 的标志性病理特征包括脑细胞外 β 淀粉样蛋白（β-amyloid protein，Aβ）沉积形成老年斑、细胞内神经纤维缠结（neurofibrillary tangles，NFT）、神经炎症增加以及神经元凋亡。β 淀粉样蛋白主要在神经元产生，是淀粉样前体蛋白经过一系列酶解反应生成的由 39～42 个氨基酸组成的多肽，调节 Aβ 的生成和清除能够有效延缓甚至逆转阿尔茨海默病的进程，因而具有重大的研究价值。β-分泌酶（β-site APP cleaving enzyme 1，BACE1）为 Aβ 产生过程中的关键酶，其含量及活性的改变均能影响 Aβ 产生，在阿尔茨海默病的发生发展中发挥至关重要的作用；老年斑周围炎性细胞的聚集提示，AD 与神经炎症高度相关，神经炎症相关细胞能够参与 Aβ 的清除，多种炎性因子也能调节 Aβ 的生成；非编码 RNA 虽很少直接参与 Aβ 的产生、沉积和清除，但其可以通过多种途径调节 Aβ 的产生。本文从 β 淀粉样蛋白生成及清除的机制着手，重点阐述了 BACE1、神经炎症、非编码 RNA 对 Aβ 调控的重要作用，以期为 AD 发病机制的进一步研究提供思路，并对阿尔茨海默病早期干预及治疗提供理论参考。

PU-0951

A Case Report on Delayed Diagnosis of COVID-19 Infection: On the Critical Role of Specimen Type and Quality, Limit of Detection of Test Kits, and IgM and IgG Antibodies Test

Dequan Tian、jing Liu、Jingrong Cao、Diandian Chen、Yidan Wang、Wenshuo Yang、Leiming Wang、Ying Li、Chengeng Liu、Peichang Wang
Department of Clinical Laboratory Xuanwu Hospital, Capital Medical University

Background The outbreak of COVID-19 caused by SARS-CoV-2 has spread globally and has become a public health emergency of international concern. Molecular diagnostic reverse-transcription RT-PCR assay is regarded as the gold standard for the etiological diagnosis of COVID-19. However, the sensitivity and specificity of RT-PCR were questioned because of the presence of negative results in some patients who were highly suspected of the disease based on clinical manifestations.
Methods In the case of negative nucleic acid result of SARS-CoV-2 in throat swabs, we chose a more sensitive SARS-CoV-2 Molecular Diagnostic Assays and sputum samples with higher viral load. In addition, the detection of IgG and Ig M against SARS-CoV-2 played an indicative role in this process.
Results The detection of IgG against SARS-CoV-2 and the nucleic acid of sputum samples were positive, eventually, the patient were diagnosed novel coronavirus pneumonia.
Conclusion Sputum specimens are most suitable for the detection of SARS-CoV-2 in middle-late-stage patients with the lower LOD of molecular diagnostic assays. Antibody detection may play an important role in the diagnosis of COVID-19 as a complementary approach for viral nucleic acid assays.

PU-0952

Homer1 基因重组质粒的构建与其在 HT22 细胞中的表达

曹敏、张晓敏、王培昌、刘静
首都医科大学宣武医院

目的 构建鼠 Homer1 基因真核表达重组质粒并在 HT22 细胞中表达。
方法 提取小鼠海马组织的 RNA，经逆转录获得 cDNA，以 cDNA 为模板，扩增得到长为 1064bp 的 Homer1 基因编码序列，经双酶切、连接、转化得到重组质粒 p3XFLAG-CMV-10-Homer1，双酶切反应鉴定后送公司测序。将构建成功的重组质粒转染到 HT22 细胞中，利用蛋白免疫印迹（Western Blot）检测 Homer1 基因的表达情况。
结果 测序结果显示重组序列与目的基因完全一致，质粒构建成功。Western Blot 结果显示 Homer1 在 HT22 细胞中成功表达。
结论 成功构建了 p3XFLAG-CMV-10-Homer1 真核表达载体并在 HT22 细胞中得到表达，为研究 Homer1 对 Ca2+调控及抑郁症、创伤性脑损伤等神经系统疾病奠定基础。

PU-0953

The Predictive Model of key Molecules in Liquid Biopsy for Prognosis of Bladder Cancer

xin dong、Baojun Wei、Wei Cui
Department of Laboratory, National Cancer Center/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Purpose The aim of present study was to explore the expressive status of overexpressed in lung cancer-1 (OLC1) gene in bladder urothelial carcinoma, and analyzed the correlation between the aberrant expression of OLC1 and the clinicopathological features. On the basis of clarifying the expression of OLC1 gene in the tumor tissue of bladder cancer patients, explore the relationship between OLC1 expression and the prognosis of bladder cancer patients. Determine the expression of OLC1 in blood and urine before operation, and evaluate the possibility of OLC1 as a biopsy marker for predicting the prognosis of bladder cancer.
Methods The mRNA expression of OLC1 was examined in 70 bladder cancer tissues and 38 corresponding normal urothelial samples by reverse real-time quantitative polymerase chain reaction (qRT-PCR); and OLC1 protein expression was examined in 114 bladder cancer specimens by immunohistochemical staining，OLC1 protein expression was examined in 52 bladder cancer patient serum by ELISA. Kaplan-Meier analyses were performed to determine the association between OLC1 expression and progression-free survival (PFS) and overall survival (OS) of the patients.
Results The mRNA and protein expression of OLC1 was markedly up-regulated in the tumor tissues($p<0.05$) and serum($p<0.05$) of the bladder cancer patients, especially in those with the muscle invasive bladder cancer (stage T2-T4, $p<0.001$), and of the smoker patients ($p<0.05$). The 5-year OS rate for the patients with high level OLC1 in the tumor was considerably lower than those with low level OLC1 ($p=0.04$). Additionally the 5-year OS rate for the smoking patients with high level OLC1 protein was significantly lower than those of non-smoking patients with low level OLC1 ($p=0.01$).
Conclusions OLC1 was overexpressed in bladder urothelial carcinoma which correlated with the tumor invasion, overall survival, and smoking history of the patients, suggesting that OLC1 is a potential biopsy prognosis biomarker for bladder cancer.

PU-0954

高通量分子测序在男性新生儿 G6PD 缺乏症筛查中的应用研究

杨金玲、陈大宇、黄丽华、韦江艳、蔡稔
柳州市妇幼保健院

目的 探讨高通量分子测序（NGS）在男性新生儿葡萄糖-6-磷酸脱氢酶（G6PD）缺乏症筛查中的应用，研究本地男性新生儿 G6PD 基因多态性及 G6PD 酶活性筛查截断值。
方法 随机收集男性新生儿足跟干滤纸血片 1092 例，采用 G6PD 酶活性分析和 NGS 技术进行筛查，多色探针荧光 PCR 熔解曲线法进行验证。
结果 共检测 1092 例男性新生儿，121 例检出 G6PD 基因突变，本地区男性新生儿 G6PD 活性缺乏发生率为 11.08%；G6PD 酶缺乏的男性新生儿酶活性为 1.2±0.72U/gHb，正常男性新生儿 G6PD 酶活性为 6.66±0.91U/gHb。酶活性分析检出 G6PD 酶活性缺乏 114 例，假阴性 7 例；NGS 检出 G6PD 基因变异 115 例，假阴性 6 例。高通量测序的灵敏度、特异性、阳性预测值和阴性预测值分别为 95.04%、100%、100%和 99.39%。酶活性分析灵敏度、特异性、阳性预测值和阴性预测值分别为 94.21%、100%、100%和 99.28%，两种检测无差异（P＞0.05）。共检测到 7 种 G6PD 突变，c.1376G>T、c.95A>G、c.1388G>A、c.1024C>T 突变为本地区男性新生儿 G6PD

基因常见突变类型，酶活性依次升高；常见突变类型分属于Ⅱ、Ⅲ类，以Ⅱ类为主。4 种变异位点酶活性比较差异有统计学意义（F=16.2，P<0.05）。本地男性新生儿 G6PD 活性以 II 型为主和 III 型为主，II 型占其中 85.12%（103/121）。男性新生儿 G6PD 酶活性检测截断值＜4.24U/gHb，敏感度为 99.28%，特异度为 100%，AUC 面积为 0.999。
结论 NGS 是男性新生儿 G6PD 缺乏症筛查的可靠方法，设置合理 G6PD 酶活性检测截断值，两种检测可以互为补充，为遗传咨询及临床指导用药提供参考依据。

PU-0955

Efficacy of Circulating miR-130b and Blood Routine Parameters in Early Diagnosing Gastric Cancer

Jianlin Chen、Yifan Sun
Affiliated Liutie Central Hospital of Guangxi Medical University

Background Gastric cancer (GC) is a common malignant cancer worldwide, with its poor prognosis. which is mainly due to lack of early diagnosis. Circulating biomarkers with diagnostic and prognostic value remain to be found. This study aimed to evaluate whether circulating miR-130b and blood routine parameters are useful markers to diagnostic GC, early-stage GC(EGC) and precancerous lesions (Pres), and to find more effective diagnostic models by combining circulating blood markers.
Methods 90 GCs, 90 Pres and 45 normal controls (NCs) were enrolled in this study. Plasma miRNA-130b was measured using quantitative real-time polymerase chain reaction (qRT-PCR) and retrospective analysis of selected blood parameters were performed. Receiver operating characteristic (ROC) curves were performed to evaluate the diagnostic value of markers for GCs, EGCs and Pres.
Results Circulating levels of M#, M%, RDW-CV, MPV, PDW, MLR and NLR were significantly higher and Hb, L% were significantly lower in patients with GC and Pre than that in NCs (all P<0.05). The levels of N#, N% and PLR in patients with GC were significantly higher and Hct was significantly lower than that in NCs (all P <0.05). Values of MPV/PC were significantly higher in Pre cohort versus healthy controls. The area under the ROC curve (AUC) of potential biomarkers in the diagnosis of GC was 0.634-0.887 individually, and increased to 0.978 in the combination of miR-130b-PDW-MLR-Hb. Moreover, the expression of RDW-CV, PLR, NLR, N#, N% were positively correlated and MPV, L#, L%, Hb, Hct were negatively correlated with cancer stage; Furthermore, the circulating levels of miRNA-130b, NLR, RDW-CV, PDW, M%, Red blood cell count (R#), Hct, Hb and MLR differed significantly between the EGCs and NCs. The AUCs of these biomarkers was 0.6491-0.911 individually in the diagnosis of EGC, and increased to 0.960 in combination; In addition, the AUC values of miR-130b, RDW-CV, MPV/PC ratio, MLR, NLR, PDW, L %, M%, M# and Hb in the diagnosis of Pre was 0.638-0.811 individually. The dual-model of miR-130b-PDW manifested a significantly largest AUC 0.896 in the diagnosis of Pre, and the sensitivity and accuracy increased when miR-130b and PDW were combined.
Conclusions Circulating miR-130b and blood routine parameters maybe novel biomarkers in early diagnosing gastric cancer, and combined biomarkers assay could improve diagnostic accuracy up to a point.

PU-0956

Remarkable inhibition effects of afatinib alone or combining with paclitaxel in esophageal squamous cell carcinoma

Liyan Yang[1]、Zhijian Cheng[2]、Jiajie Hao[3]、Mingrong Wang[3]、Yu Zhang[3]
1. National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College
2. The People's Hospital of Huangshan
3. National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Background and Aim Chemotherapy drugs do not work well in esophageal squamous cell carcinoma (ESCC), and none of the targeted drugs have been applied in clinic. This study aims to identify effective targeted drugs and related biomarkers for the treatment of ESCC.
Methods The effect of of 40 FDA approved small-molecule inhibitors were first tested in five ESCC cell lines. CCK8 assays and xenografts derived from ESCC cell lines were performed to evaluate the anti-ESCC effects of inhibitors or chemotherapeutic agents in vitro and in vivo, respectively. Immunohistochemistry was utilized to analyze the p-EGFR expression in tissues. Western blot combining with gray analysis was conducted to detect the expression of interest protein. Flow cytometry and immunofluorescence assay were used to analyze apoptosis, cell cycle, and mitotic changes after drug treatment.
Results Afatinib showed remarkable effects on inhibiting ESCC cells with higher expression of p-EGFR. Results from combinatorial screening in ESCC cells expressing lower phosphorylation level of EGFR showed that paclitaxel and afatinib presented a significant synergistic inhibitory effect ($P < 0.001$). Molecular analysis revealed that paclitaxel sentisized afatinib by activating EGFR, and afatinib in combination with paclitaxel effectively blocked MAPK pathway, induced G2/M cell arrest and apoptosis which is an indicator of mitotic catastrophe.
Conclusions Our data demonstrate that afatinib is an effective drug for patients with ESCC expressing higher phosphorylation level of EGFR. And for patients with lower p-EGFR in tumors, paclitaxel in combination with afatinib might be a promising therapeutic strategy in ESCC.

PU-0957

Expression levels of miR-192-5p in colon cancer serum and their relationships with clinicopathological features

Xu Chen、Jun Qiu
First Affiliated Hospital of Soochow University

Background Colon cancer has a poor prognosis due to a lack of biomarkers for early diagnosis and prognosis. The present study analyzed serum miR-192-5p expression levels in colon cancer patients and their correlations with clinicopathological features.
Methods Relative mRNA expression was assessed by real-time fluorescence-based quantitative PCR in the serum of 164 colon cancer patients and 60 healthy controls. Patients were enrolled in the high or low miR-192-5p group according to the cutoff value determined by ROC curve analysis. The Kaplan-Meier method and univariate and multivariate Cox regression models were applied to analyze the risk factors influencing the postoperative survival of colon cancer patients.
Results miR-192-5p mRNA expression in the colon cancer group was significantly reduced compared with the control group ($P<0.01$). Low miR-192-5p expression was significantly associated with a poor differentiation degree, lymphatic metastasis, vascular invasion and high TNM stage ($P=0.027$, 0.001, 0.010, and <0.001, respectively). Colon cancer patients in the low miR-192-5p group exhibited a low survival rate ($P<0.001$). The independent risk factors for

postoperative survival included lymphatic metastasis, a high TNM stage and miR-192-5p<1.16 (P=0.017, 0.025, and 0.008, respectively).
Conclusions miR-192-5p may represent a promising biomarker for early diagnosis and prognosis prediction in colon cancer patients.

PU-0958

miR-612 对前列腺癌能量代谢及增殖凋亡的影响

张强、卢凯
东南大学附属中大医院

目的 探讨 miR-612 在调控前列腺癌能量代谢转变、增殖及凋亡中的作用。
方法 用 miRNA 芯片筛选前列腺能量代谢转变相关 microRNA，定量 PCR 方法进行验证，通过测定葡萄糖摄取率、乳酸产生水平、MTT、Western blotting 及 FACS 来研究 miR-612 对于前列腺癌细胞能量代谢及增殖、凋亡的影响。
结果 增加 miR-612 在前列腺癌中的表达，可抑制细胞糖酵解及增殖，并增加其凋亡。
结论 miR-612 参与前列腺癌糖酵解，并行使癌基因作用，与前列腺癌的增殖及凋亡相关。

PU-0959

MS-HRM 定量检测乳房外 Paget 病 MSH2 启动子甲基化的研究

董柳、关明
复旦大学附属华山医院

研究背景及目的 乳房外 Paget 病（EMPD）是一种罕见的皮肤肿瘤，DNA 错配修复（MMR）基因 MSH2 基因启动子甲基化在 EMPD 具有较高的检出率，由 MSH2 甲基化引起的蛋白表达下降可能在 EMPD 发病中发挥重要作用。本研究拟建立基于甲基化敏感性高分辨率熔解曲线（MS_x0002_-HRM）检测 MSH2 启动子甲基化的分析策略。
材料和方法 1. 材料：收集华山医院收治的 EMPD 患者，共计 57 例组织样本
2. 样本 DNA 的提取和重亚硫酸盐修饰
3. 甲基化标准品制备
4. 构建 MS-HRM 检测 MSH2 启动子甲基化水平的分析方法
5. 甲基化阳性的 EMPD 样本 DNA，采用焦磷酸测序对阳性样本进行验证
结果 1. 构建基于 MS-HRM 的 MSH2 基因启动子甲基化的水平检测方法
按甲基化阳性对照 DNA 比例为 100%，50%，30%，10%，5%，1%，0%的系列浓度梯度，构建标准曲线。利用该 MS-HRM 检测方法，将亚硫氢酸盐修饰后的 EMPD 样本与标准曲线同时扩增，以浓度梯度的标准曲线确定 EMPD 样本中的 MSH2 甲基化水平，96.5%（55/57）的样本存在不同程度的甲基化。此后对 19 例阳性样本进行焦磷酸测序验证，均检测出一定甲基化阳性，与 MS-HRM 检测结果吻合。
讨论 MS-HRM 是一种快速的甲基化水平分析方法，本研究建立基于 MS-HRM 的 MSH2 启动子甲基化水平分析策略，以期证实 MSH2 甲基化作为 EMPD 分子标志物的可行性。此外，若将 MMR 蛋白表达状态与其基因启动子甲基化水平检测结合起来，并探索 2 者之间及其与 EMPD 的关联，可能有利于揭示 EMPD 发病的分子机制，对 EMPD 的诊断和对疾病分级的分子病理标志物具有积极意义。

PU-0960

A Bioorthogonal Time-Resolved Luminogenic Probe for Metabolic Labelling and Imaging of Glycans

judun zheng[1,4]、Qiuqiang Zhan[2]、Lijun Jiang[3]、Da Xing[4]、Tao Zhang[4]、Ka-Leung Wong[3]
1. Dermatology Hospital, Southern Medical University, Guangzhou 510091, P. R. China.
2. Centre for Optical and Electromagnetic Research, South China Academy of Advanced Optoelectronics, South China Normal University, Guangzhou, 510006, P.R. China
3. Department of Chemistry, Hong Kong Baptist University, Kowloon Tong, Hong Kong SAR, P.R. China
4. College of Biophotonics, South China Normal University, Guangzhou 510631, P. R. China

Bioorthogonal fluorogenic probes are superior to the labelling and imaging of biomolecules in live cells and organisms, while how to overcome the limitation of the autofluorescence is still a challenge for current probes to achieve high illumination resolution of the target of interest. We herein demonstrate a functionalized terbium complex Tb-1 that is stable and biocompatible to enable bioorthogonal ligation with engineered cell-surface glycans for providing responsive luminescence. A luminescence resonance energy transfer (LRET) quencher with bioorthogonal properties is strategically incorporated in a tripodal terbium complex with low toxicity, which can undergo a click-cycloaddition reaction with a cyclooctene to completely change the electronic structure of the quencher, resulting in much less efficient LRET but a 5-fold enhancement in the long-lived terbium emission intensity. This work therefore establishes a time-resolved platform that enables labeling and imaging of biomolecules of interest.

PU-0961

Establishment of a Scalable Nanoliter Digital LAMP Platform for Rapid, Accurate and Quantitative Detection of Multiple Myeloproliferative Neoplasm Molecular Markers

Guojun Cao[1]、Jinze li[2]、Lianqun Zhou[2]、Ming Guan[3]
1. Huashan Hospital North, Shanghai Medical College, Fudan University
2. 中科院苏州医工所
3. 复旦大学附属华山医院

Objective Philadelphia chromosome-negative myeloproliferative neoplasms (MPNs) are a series of unique blood disorders characterized by the continuous clonal proliferation of relatively mature bone marrow hematopoietic stem cells in one or more lines, including essential thrombocytosis (ET), polycythemia vera (PV), and primary myelofibrosis (PMF) lines. Compared with myeloid neoplasms, MPNs were characterized by benign myeloproliferation with a natural history and supportive care alone, measured in decades rather than years in most cases. However, MPNs was associated with a risk of bone marrow failure or acute leukemia transformation, the frequencies of which varied between disorders. In addition, each type of MPNs had phenotypic mimicry and was capable of evolving into another type, which makes clinical diagnosis, risk assessment, and treatment prescription tricky. Host genetic variation plays an important role in the mutational landscape of MPNs, including in the presence of a shared disease allele. The quantitative detection of molecular markers is one of the important criteria for MPNs diagnosis. So it is necessary to detect the molecular markers early, fast and multi index. Therefore, a nanodigital LAMP platform (nano-dLAMP) was established in this study.
Methods Chips with four physical partitions were fabricated for the simultaneous detection of CALR-1, CALR-2 and JAK2 V617F mutations and internal reference genes. PCR additives and nanoparticles were used to make traditional LAMP suitable for amplification of nanoliter samples. The performance of this dLAMP system was verified with simulated samples. A total of 281

clinical samples were examined synchronously by nano-dLAMP and the commercial Quantstudio 3D system to preliminarily evaluate the new platform.
Results Nanoparticles improved the amplification performance of the nanoliter LAMP. Quantitative detection of the main MPNs molecular markers could be performed simultaneously in one four-partition chip within 1 hour. The detection sensitivity of CALR-1 was 0.5% mutation burden, that of CALR-2 was 0.1%, and that of JAK2 V617F was 0.5%. The agreement between the self-built platform and Quantstudio 3D was as high as 99.64% (280/281).
Conclusions A nano-dLAMP platform with good sensitivity and specificity and fast detection was established for the detection of MPNs markers. As a general platform, it could also be used for the detection of other nucleic acid markers, and the chip throughput could be adjusted flexibly according to each experiment.

PU-0962

2019 新型冠状病毒（2019-nCoV）核酸检测体系性能验证

吴剑、龚纯全、傅后榜、龚虹、张恒超、支林俊、徐媛、刘宇
邵武市立医院

目的 评估 2019 新型冠状病毒（2019-nCoV）核酸检测体系在质量上是否能满足临床需求。
方法 对本实验室采用的新冠核酸采样管、提取试剂、两种扩增试剂及相应仪器在配套使用时的阴阳性符合率、批内精密度、批间精密度及最低检测限、交叉反应等项目进行性能验证。
结果 本实验室的新冠核酸检测体系阴阳性符合率 100 %；ORF1ab、N 与 E 各基因批内精密度、批间精密度 CV 均≤5 %；新冠标准物质稀释至厂家声明的最低检测限浓度 500 copies/ml 时，ORF1ab、N 与 E 每个基因重复提取扩增 10 次，每次均出现了扩增曲线，Ct 值均<37，检出率 100 %，利用本核酸检测体系对人类冠状病毒（HKU1，OC43，NL63 和 229E）、MERS 冠状病毒、甲型流感病毒、乙型流感病毒、人副流感病毒 I 型、腺病毒 I 型、EB 病毒，人巨细胞病毒，肺炎支原体及人基因组 DNA 进行提取扩增，结果为阴性。
结论 本实验室的新冠核酸检测体系阴阳性符合率一致，重复性好，最低检测限与厂家声明一致，与能引起相同或相似临床症状的其它病原体及人基因组 DNA 不产生交叉反应，特异性好，能够在质量上保证临床新冠核酸检测的需要,可为其他实验室选择配套检测体系提供参考依据。

PU-0963

Breakpoints Identification of a Balanced Complex Chromosome Rearrangement Case: 46,XX, t(6;15;10;9)(q13;q15;p11.2;q34.3) ins(9;8)(q22.33;q21.1q21.3)

Bohong Li[1,2]、Suli Li[2]、Fuwei Luo[2]、Chuanchun Yang[3]、Jiansheng Xie[2]
1. Southern Medical University
2. 南方医科大学附属深圳妇幼保健院
3. 深圳市乐土精准医疗科技有限公司

Background Balanced complex chromosome rearrangement (CCR) carriers are phenotypically normal but at high risk of reproductive failure, recurrent miscarriages, and affected offspring, so that cytogenetic characterizations of CCR carriers are crucial.
Methods We report a case of CCR: 46,XX, t(6;15;10;9)(q13;q15;p11.2;q34.3) ins(9;8)(q22.33;q21.1q21.3). The peripheral blood was collected for karyotyping, single nucleotide polymorphism array (SNP-array) analysis, and whole genome mate-pair sequencing.
Results The patient's karyotype is detected and identified as 46,XX, t(6;15;10;9)(q13;q15;p11.2;q34.3) ins(9;8) (q22.33;q21.1q21.3), with no significant duplication

and deletion found by SNP-array analysis. There are 16 break-points among chromosomes 6, 8, 9, 10, and 15 identified by whole genome sequencing.
Conclusions With a variety of detection techniques, we can deeply study the genetic characteristics of CCRs, thus providing a basis for genetic counseling and choice of fertility.

PU-0964

人 MTHFR C677T 基因多态性检测试剂盒的性能验证评价

张强、文少佳
西安金域医学检验所有限公司

目的 对苏州旷远和西安金磁两个厂家的人 MTHFR C677T 基因多态性检测试剂盒的性能进行分析评价，并探讨其临床应用价值。
方法 选取 50 例临床样本进行验证，分别使用苏州旷远和西安金磁的人 MTHFR C677T 基因多态性检测试剂盒进行检测，比较两种试剂盒检测结果的准确度、重复性、检测限等性能指标。
结果 使用两种试剂盒对 50 例临床样本 MTHFR C677T 基因多态性的检测结果完全符合，3 次重复试验的结果均保持一致，稀释到检测限以下均可以准确分型。
结论 苏州旷远采用 PCR-荧光探针法，检测快速用时较短；西安金磁采用 PCR-胶体金法，结果判读简单方便。上述两种试剂盒的准确度高、重复性好、灵敏度高，能满足临床检测的要求。并且其操作快速方便、结果可靠，特别适用于叶酸代谢的风险评估，可以进一步推广使用。

PU-0965

2016～2019 年长治市手足口病病原学研究

王亚飞
长治医学院附属和平医院

目的 了解长治市 2016～2019 年手足口病病原学分布情况及流行特征，为预防控制手足口病提供科学依据。
方法 采集手足口病患儿咽拭子标本，通过荧光定量 PCR 方法进行肠道病毒核酸检测，采用 SPSS21.0 软件对资料进行统计分析。
结果 2016～2019 年共检测手足口病样本 1424 例，肠道病毒核酸阳性 1122 例，阳性率为 78.79%（1122/1424），其中有 246 例检出两种病毒，共检出 1368 株病毒，肠道病毒 71 型（EV-A71）、柯萨奇病毒 A16 型（CV-A16）、通用型肠道病毒构成比分别为 7.09%（97/1368）、15.79%(216/1368)、77.12%(1055/1368)。男女阳性比例为 1.43:1，1～4 岁龄阳性构成比为 86.03%(965/1122)，5 年中 6、7、8 月阳性标本构成比分别为 16.13%(181/1122)、36.15%(405/1122)、24.51%(275/1122)。
结论 长治市 2016～2019 年手足口病以 1～4 岁幼儿为主，发病风险与性别无关，7～8 月为发病高峰期，病原以通用型肠道病毒为主，CV-A16 次之，EV-A71 最低。

PU-0966

11 个基因突变、PD-L1 表达及临床病理特征在非小细胞肺癌病人中的分析

刘艳清、吴爱华、王姗姗、房树玉、莫翼军
宁波市第一医院

目的 探讨程序性细胞死亡配体 1 (PD-L1)、11 个突变基因的表达与 273 例非小细胞肺癌(NSCLC)临床病理特征的关系。
方法 采用 SP263 抗体检测的免疫组化方法，回顾性检测 247 例手术切除的原发性和 26 例晚期 NSCLC 患者的肿瘤 PD-L1 表达。NGS 序列检测 EGFR、TP53、KRAS、PIK3CA、ERBB2、MET、RET、ALK、BRAF、ROS1、APC 基因突变情况。数据分析采用 SPSS 22.0 进行。通过单因素和多因素分析评估 PD-L1 表达、11 个突变基因和临床病理特征之间的关系。
结果 273 例患者中，PD-L1 表达阳性 68 例(24.9%)。数据显示，EGFR 基因的突变率最高，为 63.0%(172/273)，其次为 TP53(11.7%， 32/273)和 KRAS(5.5%， 15/273)。女性、非吸烟者和腺癌患者更可能有 EGFR 突变。多因素 logistic 回归显示 PD-L1 表达与非腺癌、淋巴浸润、EGFR 野生型和 TP53 突变显著相关(p 分别为 0.041、< 0.001、0.004 和 0.014)。此外，PD-L1 在腺癌中的表达与淋巴浸润、TP53 和 KRAS 基因突变有关(p 分别为 0.012、< 0.025 和 0.041)。
结论 临床应常规检测 EGFR、KRAS 和 TP53 的突变，以更好地指导 NSCLC 患者的免疫治疗。未来的研究需要阐明驱动基因突变和 PD-L1 表达在指导 NSCLC 患者免疫治疗中的潜在机制。

PU-0967

The Effect of Methotrexate on Serum Levels of Trace/Mineral Elements in Patients with Psoriatic Arthritis

Yue Gao、Zheng Liu
Guilin Medical University

Psoriatic arthritis is a type of inflammatory arthritis that occurs in some patients with psoriasis. Clinically, low-dose methotrexatewas used to treat psoriatic arthritis as a first-line agent. However, the pathogenesis of psoriatic arthritis and the mechanism ofmethotrexate treating psoriatic arthritis remained unclear. In recent years, a variety of side effects associated with methotrexatehave been reported. In order to illuminate the role of trace/mineral elements in the pathogenesis of psoriatic arthritis and the sideeffect of low-dose methotrexate on blood cells and trace/mineral elements in patients with psoriatic arthritis, 37 psoriatic arthritispatients and healthy 50 people with similar age and gender were enrolled in this study. The blood cells, serum trace/mineralelements, liver function, and kidney function were determined. The results revealed that the level of serum zinc was significantlylower and copper was significantly higher in psoriatic arthritis patients in comparison with healthy control. After giving patientsmethotrexate intravenously (15 mg weekly), their serum zinc was significantly increased, and copper was significantly decreasedwith symptoms relieved. Our study provided the evidence that low zinc and high copper might be associated with the patho_x0002_genesis of psoriatic arthritis, and the possible mechanism of methotrexate treating psoriatic arthritis was through elevating zincand reducing copper in serum. Moreover, we demonstrated that low-dose methotrexate could induce liver damage to psoriaticarthritis patients.

PU-0968

浙江地区 120245 例检测新型冠状病毒血清抗体阳性率分析

王欢[1]、刘军权[1]、张幸[2]、陈信[3]
1. 杭州金域医检验所有限公司
2. 台州市第二人民医院
3. 天台县人民医院检验科

目的 了解浙江地区新型冠状病毒血清抗体阳性率概况，以期找到后续抗体监测重点。
方法 回顾性分析我中心实验室检测的 120245 例新型冠状病毒血清抗体结果，依照样本来源、年龄、性别分组探究浙江地区人群 IgG 血清抗体单阳性率、IgM 血清抗体单阳性率和 IgG 与 IgM 血清抗体双阳性率。
结果 在 120245 例研究对象中，发热门诊、新住院及陪护人员占比最多，年龄以 30-50 岁为主，IgG 抗体单阳性率为 0.11%，IgM 抗体单阳性率为 0.15%，IgG、IgM 抗体双阳性率为 0.13%。依照样本来源分组，发热门诊新住院及陪护人员 IgG、IgM 血清抗体单阳性率最高，隔离点人员 IgG 和 IgM 血清抗体双阳性率最高(0.16%)；依照年龄性别分组，男性组 IgG 单阳性率与 IgG、IgM 双阳率高于女性组，且差异有统计学意义；与>50 岁组相比，其他各组 IgG 单阳性率、IgM 单阳性率、IgG 和 IgM 双阳性率均更低，且差异有统计学意义。
结论 浙江地区新型冠状病毒血清抗体阳性率较低，应继续做好对隔离点人员和发热门诊新住院及陪护人员的检测工作，尤其是年龄在 50 岁以上的人群。

PU-0969

多评价指标分析浙江天台地区新型冠状病毒肺炎确诊病例

陈信[3]、刘军权 Liu[1,2,3]、张幸[3]
1. 杭州金域医检验所有限公司
2. 台州市第二人民医院，
3. 天台县人民医院检验科

目的 采用临床症状、疾病转归、理化检查、病原学检测等多种评价指标来分析浙江省天台地区新型冠状病毒肺炎确诊病例，以了解天台地区疫情的防治概况，为后续临床工作和新型传染病的防治提供理论指导。
方法 选取我院于 2020 年 1 月 17 日以来初诊收治的 8 例新型冠状病毒肺炎确诊住院患者和 20 例疑似病人为研究对象，并追踪到密切接触者 38 人（其中医务人员 14 人）。运用发热、咳嗽等呼吸系统临床症状，住院时间、痊愈等疾病转归，实验室检测指标、影像学检查等理化检查，病毒核酸检测、病毒抗体检测等病原学检测的多种评价指标对其进行分析。
结果 确诊患者共 8 例，男 5 例，女 3 例，年龄 37～55 岁，平均年龄(48.0±7.27)岁；7 例从武汉归来，2 例为与确诊患者有接触史，属家庭聚集性发病；1 例有高血压基础疾病；1 例为甲流患者；7 例有武汉接触史(91.37%)，1 例家族聚集性发病。主要症状为发热和干咳，8 例中仅有一例乏力且胸闷，一例头晕头痛，均无呼吸困难、畏寒、鼻塞流涕、腹痛腹泻、恶心呕吐、结膜充血等症状。8 例确诊患者现已全部治愈出院，住院治疗时间 15～29d，平均住院时间 21.88d，行肺部 CT 检查渗出均已吸收。送检疾控中心标本中除 8 例确诊患者阳性外，其余均为新型冠状病毒核酸检测阴性。出院 2-4 周后，确诊患者新型冠状病毒抗体 IgM 转阴，而 IgG 阳性。
结论 采用临床症状、疾病转归、理化检查、病原学检测等的多种评价指标来分析新型冠状病毒肺炎确诊病例可提升我们对疾病的认识，更好的指导临床诊疗。

PU-0970

Pathogenesis of COVID-19 and the quality control of nucleic acid detection

Kangsheng Liu
Department of Clinical Laboratory, Women's Hospital of Nanjing Medical University，Nanjing Maternity and Child Health Care Hospital, Nanjing, Jiangsu 210029, China.

The new coronavirus pneumonia (COVID-19) epidemic spread rapidly throughout the world. Considering the strong infectivity and clustering of COVID-19, early detection of infectious cases is of great significance to control the epidemic. Nucleic acid testing (NAT) plays an important role in rapid laboratory diagnosis, treatment assessment, epidemic prevention and control of COVID-19. However, since COVID-19 is caused by a new emerging virus and NAT for COVID-19 has not been clinically applied before, false negative results inconsistent with clinical diagnosis have appeared in clinical practice. Therefore, it is urgent to improve the sensitivity of NAT for COVID-19. This study aimed to summarize the current situation and prospect of NAT based on the latest findings on COVID-19 infection. Also, the quality control of sample collection was discussed. Hopefully, this study could help to improve the effectiveness of NAT for COVID-19.

PU-0971

IL-17B/IL-17RB signaling cascade contributes to self-renewal and tumorigenesis of cancer stem cells by regulating Beclin-1 ubiquitination

Qingli Bie、Haixin Dong、Bin Zhang
Department of Laboratory Medicine, Affiliated Hospital of Jining Medical University, Jining, Shandong, P. R. China

Cancer stem cells (CSCs) are characterized by robust self-renewal and tumorigenesis and are responsible for metastasis, drugresistance, and angiogenesis. However, the molecular mechanisms for the regulation of CSC homeostasis are incompletelyunderstood. This study demonstrated that the interleukin-17 (IL-17)B/IL-17RB signaling cascade promotes the self-renewaland tumorigenesis of CSCs by inducing Beclin-1 ubiquitination. We found that IL-17RB expression was significantlyupregulated in spheroid cells and Lgr5-positive cells from the same tumor tissues of patients with gastric cancer (GC), whichwas closely correlated with the degree of cancer cell differentiation. Recombinant IL-17B (rIL-17B) promoted the sphere_x0002_formation ability of CSCs in vitro and enhanced tumor growth and metastasis in vivo. Interestingly, IL-17B inducedautophagosome formation and cleavage-mediated transformation of LC3 in CSCs and 293T cells. Furthermore, inhibition ofautophagy activation by ATG7 knockdown reversed rIL-17B-induced self-renewal of GC cells. In addition, we showed thatIL-17B also promoted K63-mediated ubiquitination of Beclin-1 by mediating the binding of tumor necrosis factor receptor- associated factor 6 to Beclin-1. Silencing IL-17RB expression abrogated the effects of IL-17B on Beclin-1 ubiquitinationand autophagy activation in GC cells. Finally, we showed that IL-17B level in the serum of GC patients was positivelycorrelated with IL-17RB expression in GC tissues, and IL-17B could induce IL-17RB expression in GC cells. Overall, theresults elucidate the novel functions of IL-17B for CSCs and suggest that the intervention of the IL-17B/IL-17RBsignalingpathway may provide new therapeutic targets for the treatment of cancer.

PU-0972

Delivery of mRNA for cancer immunotherapy

Lang Yi
Xiangya hospital central south university

mRNA vaccines have enormous potential to fight against cancer due to superiorities in safety, efficacy and industrial production. Promising preclinical works have begun using mRNA vaccines for cancer immunotherapy. However, safe and effective delivery of mRNA in vivo is still a critical challenge for their clinical applications. In this review, we summarized the delivery of mRNA vaccines systems by physical methods, viral vectors and non-viral vectors for cancer immunotherapy, and discuss their relative merits. In addition, the prospects for the development of different ways for delivery of mRNA are reviewed, and promising advances in cancer treatment using mRNA vaccines are discussed.

PU-0973

Expression, clinical significance and function of long non-coding RNA CTC-425O23.2 in gastric adenocarcinoma

KAI WANG[2]、XIAOJUAN OUYANG[3]、YUAN DANG[1]、ZHIHUA WANG[4]、MIAO ZHENG[5]、QIAOJIA HUANG[1]
1. Fuzhou General Hospital of Nanjing Military Command
2. Affiliated Hospital of Shaanxi University of traditional Chinese Medicine
3. Fuzhou General Hospital of Nanjing Military Command
4. No.92 Hospital of Chinese people's Liberation Army
5. Fujian Provincial Maternity and Children's Hospital

Objectives Long-noncoding RNAs (LncRNAs) play important roles in gastric cancer (GC). However, the expression and effect of many LncRNAs remain largely unknown. Long non-coding RNA CTC-425O23.2 (lncRNA CTC-425O23.2) related to gastric adenocarcinoma (GA) is unreported yet. The present study was aimed to assess the significance and potential function of lncRNA CTC-425O23.2 levels in GA.
Methods According to our previous lncRNA expression chips data, LncRNA CTC-425O23.2 levels in the 131 tissues collected from surgically resected primary GA and in BGC-823, SGC-7901 and MGC-803 GA cell lines were further analyzed by the real-time quantitative reverse transcription–PCR (qRT-PCR), and the associations between its levels and clinical significance were then analyzed. The potential function and mechanisms of LncRNA CTC-425O23.2 were explored by the MTT, scratch damage, Transwell, Flow cytometry and bioinformatics analysis.
Results The expression of CTC-425O23.2 in GA tissues was significantly higher than that in the adjacent tissues in 79 out of 131 cases (over-expressed rate: 60.3% and over-expressed folds: 10.58 times, $p<0.05$), and its levels in BGC-823, SGC-7901 and MGC-803 GA cells was also significantly higher than that in normal gastric cell GES-1 ($p<0.05$, respectively). CTC-425O23.2 expression was associated with tumor size ($p=0.0280$), T staging ($p=0.0185$), venous invasion ($p= 0.0467$), and peripheral nerve invasion ($p=0.0115$) as well as with the expression levels of ribonucleotide reductase subunit M1 (RRM1) ($p=0.0275$) and Ki67 antigen (Ki67) ($p=0.0283$) in GA tissues. CTC-425O23.2 expression level was higher in patients with tumor size ＜5cm, not venous invasion or not perineural invasion than those patients with tumor size≥5cm, appearing venous invasion or appearing perineural invasion. Silencing of CTC-425O23.2 by transfecting siRNA decreased SGC-7901 and BGC-823 cell's proliferation ($P < 0.001$), inhibited SGC-7901 migration ($P < 0.0001$) and reduced SGC-7901 invasion ($P < 0.0001$). But compared with untreated control group, knockdown of CTC-425O23.2 in SGC-7901 exhibited no significantly affecting on the apoptosis of GA cells. The qRT-PCR results revealed that the CTC-425O23.2's expression levels were positively correlated with AKT2's (the parent gene of CTC-425O23.2) mRNA expression levels($R =0.5873$, $P < 0.0001$),

and had a certain interaction between them. The expression levels of lncRNAGK-IT1, lncRNATRAF4-AS1 and lncRNA CTC-425O23.2 exhibited no statistical correlation between each other.

Conclusion The results of this investigation indicated that the aberrant expression of lncRNA CTC was associated with GA. Detection the expression levels of lncRNA CTC in GA tissues may predict disease progression and prognosis in patients with GA. LncRNA CTC could be used as one of molecular markers of GA.The independent expression of different LncRNAs may suggest that the expression of different LncRNA may have biological independence.

PU-0974

Natch CS2 - ABI 7500 全自动核酸提取与定量检测系统 HCV-RNA 性能验证及评价

王凯、冯飞雪、肇玉博、周嘉迪、梁伟伟、宫伟、马艳侠*
陕西中医药大学附属医院

目的 对基于 Natch CS2 全自动核酸提取仪和 ABI 7500 实时荧光定量 PCR 的丙型肝炎病毒核糖核酸（HCV RNA）定量检测系统进行性能验证。

方法 依据中国合格评定国家认可委员会（CNAS）-GL039《分子诊断检验程序性能验证指南》的方案，使用临床样本及标准物质，对检测系统的精密度、正确度、线性范围、检出限、抗干扰能力进行验证，并与制造商声明比较。

结果 精密度验证结果显示，高、低浓度水平样本的重复性精密度变异系数（CV）值分别为 2.09%、2.54%，中间精密度 CV 值分别为 2.14%、4.72%，均小于厂家声明的 5%。正确度：与本实验室参考方法进行样本比对，20 个样本，Bias 均小于 7.5%。线性范围：经拟合分析，证实在 50～1.51E+07IU/mL 呈良好线性（R2=0.997>0.97）。抗干扰能力验证：含 28 mg/dL 的胆红素（TBIL），3.0g/dL 的甘油三酯（TG），2g/dL 的血红蛋白（Hb）的干扰物质对样本检测结果无影响。检出限 25 IU/mL，与制造商声明一致。

结论 HCV-RNA 定量检测系统精密度、正确度、线性范围、抗干扰能力、检出限各项性能指标与制造商声明一致，满足 CNAS 以及 ISO15189 要求，可用于临床检测。

PU-0975

NUCB-2/Nesfatin-1 Promotes the Proliferation of Nasopharyngeal Carcinoma Cells

Yunlai Liang、yating ma、kangkang huang、kun wang、manlin xiang、bin yi
Xiangya Hospital of Central South University

Recent studies indicate that a high level of nucleobindin-2 (NUCB-2)/nesfatin-1 promotes cell migration in breast, prostate and colon cancers and is a risk factor for poor outcome of the disease. However, the role of NUCB-2 remains poorly understood in nasopharyngeal carcinoma (NPC). In this study, NUCB-2 level in NPC tissue was higher than that in rhinitis tissue. Suppression of NUCB-2 in the NPC cell line CNE2 inhibited proliferation and clone formation of the cells; on the contrary, improvement of NUCB-2 in the NPC cell line CNE1 promoted cell propagation and clone development. An elevated serum level of NUCB-2 in NPC patients was detected, compared to that in patients with other head and neck tumors, rhinitis or healthy donors. Determination of nesfatin-1 combined with EA-IgA, VCA-IgA and Rta-IgG in serum samples for NPC diagnosis reached a sensitivity of 93.6% and a specificity of 94.5%, while the positive and negative predictive value of this diagnostic model was 89.8% and 96.6%, and the accuracy yielded 94.2%. In summary, our results proved that NUCB-2 could enhance proliferation of NPC

cells and NUCB-2/nesfatin has the potential to be a serological marker to aid early diagnosis of nasopharyngeal carcinoma.

PU-0976

Therapeutic effect of imidazole group-substituted arylaminopyrimidines (IAAPs) as potent BTK inhibitors against B-cell lymphoma and AML cells

Si Li[1]、Hong Yuan[2]
1. The First Affiliated Hospital of Dalian Medical University
2. 大连医科大学附属中心医院

Objective We aimed to identify the inhibitory effect of new imidazolyl-substituted arylaminopyrimidines (IAAPs) on Bruton's tyrosine kinase（BTK) and its effect on B-cell lymphoma and acute myeloid leukemia (AML), preliminarily explore the anti-tumor mechanism of the compounds in B-cell lymphoma and AML cell lines, and provide new targets and new ideas for the treatment of B-cell lymphoma and AML.
Methods The inhibitory activity of IAAPs against BTK was evaluated using the ADP-Glo™ Kinase Assay. The CCK8 assay was used to detect the proliferation inhibitory ability of the compounds and clinical reference drugs on the lymphoma cells Ramos NAMALWA, Raji and acute myeloid leukemia (AML) cells HL60, U937. AO/EB staining was used to observe the changes in cell number and apoptotic morphology after treatment with compounds, and to evaluate the toxicity of the drug to human normal peripheral blood PBMC. Annexin V-FITC/PI staining and flow cytometry was used to detect the early and late apoptosis of B-cell lymphoma and AML cells after the compound treatment. The effects of compounds on the cell-cycle progression of AML and B-cell lymphoma cells were detected by PI staining and flow cytometry. Western Blot was used to detect the activation of BTK in cells and the changes of Akt and ERK protein levels in downstream pathways after compound treatment.
Results Here, a series of IAAPs were synthesized and characterized as potent BTK inhibitors. Among them, most of the target compounds displayed inhibitory activity against BTK with an IC50 lower than 42.40 nM. In particular, 11a markedly inhibited the proliferation of HL60 and U937 cells with an IC50 value of 108.57 and 38.02 nM, respectively. Besides, 11b exhibited strong antiproliferative activity against Raji, Namalwa and Ramos cells with an IC50 value of 4.37, 4.95 and 9.25 μM, respectively. The results of AO/EB staining showed that the number of cells decreased after drug treatment and there was obvious nuclear pyknosis, that is, early apoptosis. Moreover, normal PBMCs were not sensitive to 11a and 11b, indicating their low toxicity towards normal cells. The results of Annexin V-FITC/PI showed that 11a and 11b significantly induced apoptosis of B-cell lymphoma and AML cells. Compared with the control group, with the increase of the drug concentration, the proportion of early and late apoptosis of HL-60 had both increased.11a and 11b can also block cells in G2/M phase and affect cell cycle progression. Furthermore, the analysis of the mechanism of action of these compounds revealed that 11a and 11b induce the activation of BTK and its downstream pathways in these cells.
Conclusion IAAPs compounds can be used as new BTK targeted drugs, which have a strong inhibitory effect on AML and B-cell lymphoma cells. The representative compounds significantly induce cell apoptosis and cause cycle arrest in AML and B-cell lymphoma cells and have low cell cytotoxicity. 11a and 11b can inhibit BTK phosphorylation and inhibit the activation of downstream ERK and Akt pathways. 11a and 11b may act as a potential new therapeutic drug against B-cell lymphoma and AML and provide a new perspective to conduct further research on the development of BTK inhibitors for the treatment of B-cell lymphoma and AML.

PU-0977

PCR-荧光探针法检测对 G6PD 酶活性临界女性临床诊断价值的探讨

熊君
南方医科大学珠江医院

目的 分析酶速率法对 G6PD 缺乏合并地贫患者的检测率，并分析 PCR-荧光探针法检测该类型患者的基因突变型,初步探讨 PCR-荧光探针法检测对 G6PD 酶活性临界女性的临床诊断价值。
方法 收集酶速率法检测 G6PD 酶活性水平的样本 323 例；从中筛出用 GAP－PCR 法检测 α 地贫基因和反向斑点杂交(RDB) 法检测 β 地贫基因的标本 190 例；并对收集的 323 例的标本一致采用 Taqman 探针荧光定量 PCR 检测 16 种中国人群中常见的 G6PD 基因突变型（c.1376G>T, c.1388G>A, c.95A>G, c.392G>T, c.871G>A, c.1024C>T, c.487G>A, c.1004C>A, c.202G>A, c.383T>C, c.473G>A, c.493A>G, c.1339G>A, c.1360G>A, c.1381C>T, c.1387C>T）。
结果 1.在 G6PD 缺乏患者（活性<1300 U/L）中,男女性别比为 103:35；而在 G6PD 酶活性偏低（1300-1800 U/L）人群中，男女性别比为 4:17；两组间的差异有统计学意义。2. 在 130 例单纯一种突变型中分析，其中前四位的基因突变类型分别是 c.1388G>A（60 例，46.15%)，c.1376G>T（40 例，30.77%)，c.95A>G（12 例，9.23%)，c.871G>A（10 例，7.69%)。3.在 G6PD 缺乏合并地贫的基因检测中，2 例酶活性临界值的女性均检测突变基因型。

PU-0978

Regulatory Role and clinical significance of circular RNAs in Spinocerebellar ataxia type 3

Minjin Wang
West China Hospital

Backgrounds Spinocerebellar ataxia type 3/Machado-Joseph disease (SCA3/MJD) is the most common autosomal dominant spinocerebellar ataxia and one of many inherited polyglutamine (polyQ) neurodegenerative diseases. Nevertheless, the exact mechanism of the disease still remains ambiguous. At present, circular RNAs (circRNAs) have been attracting extensive research interest in different human diseases, which emerged as new key regulators via different biological functions in genetic and epigenetic processes, but it remains largely unknown if they are correlated with SCA3/MJD pathogenesis. Therefore, the objuective of this work was to investigate the significance and potential role of circRNAs in SCA3/MJD.
Methods Here, we adopted next-generation sequencing（NGS）to examine the expression profile of circRNAs and mRNAs in cerebrospinal fluid（CSF）samples and peripheral blood samples from 11 SCA3/MJD patients and 10 healthy controls. Next, quantitative real-time reverse transcription polymerase chain reaction(qRT-PCR) was performed to validate NGS data. ROC analysis was also used to evaluate the predictive power of candidate circRNAs. In order to elucidate potential functions and signaling pathways involved in the pathogenesis of SCA3/MJD, we applied Gene ontology(GO) and Kyoto Encyclopedia of Genes and Genomes(KEGG) pathway analysis of the differentially expressed mRNAs and parental genes of circRNAs. Furthermore， after the knockdown or overexpression of candidate circRNA, MTT assay along with flow cytometric assays were used to assess changes in cell viability as well as apoptosis , and Western blot was performed to analyze the disease protein—polyQ-ataxin3 expression in SY-SH5Y/SCA3 cell models.
Results Our results showed that circRNAs and mRNAs profiles presented a total of 262 circRNAs and 1001 mRNAs commonly expressed in both CSF samples and peripheral blood samples of SCA/MJD patients. Among them, 14 circRNAs as well as 429 mRNAs were

upregulated and 42 circRNAs as well as 549 mRNAs were downregulated in SCA3/MJD group. The expression level changes of 5 differentially expressed circRNAs estimated by qRT-PCR were in accord with NGS data. Moreover, hsa_circ_0019149 (AUC:0.953; 95% CI: 0.911–1.005) were the most upregulated and significantly associated with SCA3/MJD, which could be identified as novel candidate diagnostic biomarker for the disease. Significantly enriched signaling pathways were involved in apoptosis, protein degradation, etc. The viability of cells increased markedly and polyQ-ataxin3 expression decreased following the knockdown of hsa_circ_0019149, whereas over expression of hsa_circ_0019149 had the opposite effects on cells.

Discussions These findings were the first report of differentially expressed circRNAs in SCA3/MJD, indicating a possible role for circRNAs as potential dynamic monitoring progress biomarkers and possibly original diagnostic or therapeutic targets of the disease. Also, our results provide novel insights into the mechanisms of the pathological process as well as important cues for further functional studies of the disease.

PU-0979

Development and validation of a LASSO prediction model for better identifying ischemic stroke: A case- control study in China

Minjin Wang
West China Hospital

Objective The diagnosis of ischemic stroke in the acute phase is a key clinical problem. We are committed to developing a Diagnosis Aid APP based on commonly used laboratory findings and electronic health records to provide more effective information for the early diagnosis.

Methods We retrospectively enrolled 931 subjects with proven ischemic stroke and other cerebrovascular diseases from March, 2017 to December, 2018 in the derivation cohort to establish identification model. The Least Absolute Shrinkage and Selection Operator algorithm was used for feature selection and construct laboratory panel. Combined with Electronic Health Record information, multivariate logistic regression was used for a identification model and was encapsulated as a visual and operable APP. It was internally evaluated by AUC calibration plot and DCA curve and was verified by an independent validation cohort containing 64 patients enrolled prospectively from January to March, 2019.

Results The Stroke Diagnosis Aid APP consisted of 14 laboratory-associated features and four Electronic Health Record factors (smoking, hypertension, diabetes, and hyperlipidemia) were established. User can get the recognition result by inputting index values in the graphical user interface (GUI) of the APP. It showed good discrimination (AUC=0.916, cutoff=0.577), calibration, and clinical availability, which were reconfirmed in independent verification cohort (positive predictive value=90.32%, negative predictive value=87.88%, sensitivity=87.50% specificity=90.62%).

Conclusion The Stroke Diagnosis Aid APP could facilitate the early identification of ischemic stroke, which is friendly, convenient, accurate and easy to use.

PU-0980

高通量测序揭示中国西南地区肺癌循环肿瘤 DNA 靶向药物相关基因突变特征

白玲、周娟、翟建昭、宋佳佳、应斌武
四川大学华西医院

目的 肺癌靶向药物的广泛应用使得分子基因检测逐步成为临床精准治疗的常规检测，本研究旨在分析中国西南地区肺癌病人血浆中循环肿瘤 DNA（Circulating tumor DNA, ctDNA）变异情况。
方法 项目纳入 2017 年至 2019 年间到我院就诊的肺癌病人共 672 例，对其外周血血浆 ctDNA 靶向测序结果及临床特征进行了回顾性分析。
结果 (1) 73.36%的患者 ctDNA 中至少检测到一个分子异常，主要类型为基因突变；(2) 突变频率前 10 位基因依次为 EGFR (42.41%)、ROS1 (8.04%)、HER2 (7.59%)、ALK (6.99%)、FGFR1 (5.51%)、RET (5.51%)、PIK3CA (4.46%)、TSC1 (4.46%)、KRAS (3.87%)、SMO (3.72 %)，无吸烟史患者的 EGFR、HER2 基因突变频率显著高于吸烟患者；(3) EGFR 基因突变类型主要是 19DEL（28%），其次是 T790M 和 L858R，T790M 几乎都是伴随 19DEL 或 L858R 出现的；(4) 与未服用过靶向药物的患者相比，接受过靶向治疗的患者 EGFR 基因与其他基因（HER2、ROS1、PIK3CA）的共突变更加常见，但其 PTEN 基因突变频率更低（1%）；(5) 晚期肺癌在肝、骨、脑、肾上腺等不同转移部位阳性检出率不同，尤其是脑转移阳性率只有 52%，而肾上腺转移阳性率为 100%；另外肾上腺转移患者 HER2 突变频率较高，脑转移患者无 AKT1 基因变异检出，骨转移患者与多部位转移患者的 ctDNA 突变图谱类似。
结论 ctDNA 高通量测序在无创性鉴定肺癌靶向药物相关分子标志中发挥重要作用，几乎一半的受检者能够从中获益，ctDNA 突变谱在检测前是否接受过靶向药物治疗的患者中明显不同，同时也受到肺癌晚期转移部位的影响。

PU-0981

Cancer Genomic Alterations: Potential Biomarkers for Early Recurrence Prediction after Surgery of Hepatocellular Carcinoma

Juan Zhou、Zhaodan Xin、Liting You、Yi Zhou、Xingbo Song、Xiaojun Lu、Binwu Ying
West China Hospital, Sichuan University

Objective In this study, we aimed to detect the genomic variations of HCC and evaluated the potential value of mutant genes in predicting Early Recurrence of HCC patients after hepatectomy.
Methods 52 patients with initially suspected HCC who were undergoing hepatectomy at West China Hospital of Sichuan University in 2019 were prospectively recruited. Preoperatively peripheral blood samples and fresh surgical tumor tissues were obtained. Those who relapse within one year (≤12 months) after operation are regarded as early recurrence. High-throughput targeted sequencing using a 1021-gene panel was performed for tumor tissues and circulating tumor DNA (ctDNA).
Results 50 individuals were detected mutations in tissue samples (50/52, 96.2%) and 26 plasma samples were detected mutations (26/33, 78.8%). The gene mutation rate of TP53 (84.62% vs 40.54%), KEAP1 (23.08% vs 0%) and CTNNB1 (46.15% vs 13.51%) was significantly higher in the recurrence group than the non-recurrence group in tumor tissue analysis ($P<0.05$); the gene mutation rate of both ATM and TSC2 (27.27% vs 0%) was significantly higher than the non-recurrence group in ctDNA analysis ($P<0.05$). CtDNA variant allele frequency (VAF) were further

compared between recurrence and non-recurrence groups, both the median and maximal VAF of ctDNA were higher in the recurrence group though did not reach the statistically significant difference (P＞0.05).
Conclusion We demonstrated that those genes with higher mutation rate in the recurrence group might be potential biomarkers for prognosis of HCC. The application of specific genomic mutations for predicting early recurrence of HCC can assist timely intervention and treatment after operation, and ultimately achieve better clinical outcomes.

PU-0982

机器学习方法构建抗结核药物导致结核病人肝损伤的治疗风险预测模型研究

周易、周娟、宋兴勃、应斌武
四川大学华西医院

目的 抗结核药物在结核病患者中引起的药物不良反应以肝损伤（Anti-tuberculosis drugs-induced liver injury，AT-DILI）最为常见，大量研究证明药物导致肝损伤与个体的多因素异质性有关，危险因素包括年龄、性别、相关病症、生活方式及遗传变异等。综合考虑识别遗传位点并结合人口学特征等的风险因素，构建抗结核药物患者肝损伤的风险模型，可能更有效的用于临床抗结核药物个体化风险预测。
方法 纳入四川大学华西医院一线抗结核药物治疗患者 280 例，其中共 59 例发生 AT-DILI，221 例耐受，收集电子病历（EHRs）和前期课题组 GWAS 筛选出的差异 SNPs。（1）EHRs：主要包括了患者的人口统计学指标和实验室检查数据。实验室指标来源于患者未使用抗结核药物前的基线指标数据；（2）SNPs：经由第一部分 GWAS 研究筛选出耐受或发生 AT-DILI 患者的差异 SNPs 位点(P<1×10-4)。用特征变量筛选算法，通过机器学习算法构建联合 SNPs 及电子病历的 AT-DILI 预测模型，评估模型的预测效能和临床适用性。
结果 联合差异 SNPs 与 EHR 用机器学习方法建模：“EHR+SNPs”模型的效果优于“SNPs”模型与“EHR”模型。“EHR+SNPs”模型的三种不同建模方法中，敏感性方面 SVM 模型较低（0.44），逻辑回归和随机森林模型能够达到中等性能（分别为 0.72 和 0.74）。而在特异性方面，逻辑回归、SVM 和随机森林三种模型具有极好的性能（分别为 0.95、0.97 和 1.00）。
结论 研究结果进一步提示采用机器学习算法整合 SNPs 和电子病历信息构建预测模型是优化 AT-DILI 治疗风险预测的可行方法。但是本研究结果需要在更大的群体中进行扩大验证。

PU-0983

A preliminary study of circRNA encoded by EBV as a serum molecular marker of malignant tumors

Yali Song、Juan Liao、Tingting Zeng*
Department of Laboratory Medicine, West China Hospital, Sichuan University

Objective With the rapid development of life science, more and more studies have confirmed that non-coding RNA plays an important role in the development of malignant tumors. It has been reported that the Epstein-Barr virus has 3 genes that can encode 6 kinds of circular RNA molecules, among which the BART gene transcription product can be spliced and processed into four circular forms of circBART1.1, circBART1.2, circBART2.1 and circBART2.2, given circRNA’s key role in malignant tumors, we are looking for effective from circRNA tumor molecular markers, hoping to find a malignant tumor related gene targets.The potential molecular markers of malignant tumor in blood have high clinical value, so we take the molecular markers of malignant

tumor serum as the breakthrough point to explore the highly specific molecular markers of malignant tumor serum.
METHODS The expression of these four circBARTs was detected by qRT-PCR in gastric cancer tissues and cell lines. qRT-PCR was used to detect circBARTs encoded by EBV in 6 cases of EBV-positive gastric cancer clinical tissue samples and EBV-infected gastric cancer cell line AGS-EBV. The EBV protein encoding genes LMP1 and Beta-actin were used as internal controls. We evaluated the expression levels of 4 circBARTs in malignant tumors.
RESULTS Among the four circRNAs, we found that the possibility of exon II participating in loop formation was first detected by primers across the splicing site, and circBART1.1 and circBART1.2 were found to be looped by exons II, IIIa, IIIb and IV. It is not detected in the serum of patients with gastric cancer. Through the expansion of the full-length primers, it was found that circBART2.1 and circBART2.2 were significantly up-regulated in the serum of gastric cancer patients. Therefore, circBART2.1 and circBART2.2 may be used as serum molecular markers of gastric cancer.
CONCLUSIONS The expressions of circBART2.1 and circBART2.2 are significantly up-regulated in serum of gastric cancer patients, which may be used as serum molecular markers of gastric cancer.

PU-0984

寨卡病毒的研究进展

曹震
南方医科大学珠江医院

近年来，寨卡病毒在全球多地爆发大规模疫情，因其可致新生儿小头畸形和成年人吉兰巴雷综合症等严重并发症，引起全球广泛关注，寨卡病毒感染的诊断和防治尤为重要。本文简要介绍寨卡病毒的结构、流行历史，并主要对当前病毒检测方法和疫苗研究进展进行综述与应用展望。

PU-0985

Development and validation of a predictive model for severe COVID-19: A case-control study in China

Minjin Wang
West China Hospital

Background Comprehensively understanding and early predicting the risk of progression to severe COVID-19 can facilitate personalized diagnosis and treatment options, optimizing utilization of medical resource.
Methods In this prospective study, 206 COVID-19 patients were enrolled from regional medical institutions between 20th December 2019 and 10th April 2020. Demographics, clinical characteristics, laboratory findings and cytokine levels were adequately described and analyzed for deriving and validating a predictive model. Variation analysis, lasso and boruta algorithm were used for modeling. Performances of models were evaluated by specificity, sensitivity, AUC, AIC, calibration plot, Decision Curve Analysis e and Hosmer-Lemeshow test.
Results Predictive model including ALT, IL6, Expectoration, Fatigue, LYMR, AST and CREA established by using LASSO algorithm and logistic regression can predict the progression risk of severe COVID-19 accurately. It yielded satisfactory predictive performance with an AUC of 0.9104 and 0.8792 in derivation and validation cohort, respectively. This model finally was visualized in the form of a nomogram plot and packaged into an open-source and free predictive calculator for clinical use easily and is available online at https://severeconid 19predction.shinyapps.io/SHINY/.

Conclusion The model combining demographics, clinical characteristics, laboratory findings and cytokine levels can effectively predict the progression to severe COVID 19, promoting early personalized management and the allocation of appropriate medical resources.

PU-0986

在肝细胞癌中联合检测 TERT 及 TP53 基因突变的临床意义研究

李晋、周娟
四川大学华西医院

目的 端粒酶逆转录酶（Telomerase reverse transcriptase, TERT）是一种能够维持端粒长度及稳定性的逆转录酶，于正常体细胞中处于沉默或失活状态。TERT 基因突变主要涉及启动子 C228T 和 C250T 两种类型，已在肝细胞癌（hepatocellular carcinoma, HCC）中广泛报道，被认为是 HCC 癌变的早期标志。细胞肿瘤抗原 p53（Cellular tumor antigen p53, TP53）是一种抑癌基因，在细胞周期阻滞、细胞衰老和凋亡等过程中发挥重要调节作用。TP53 是肝癌、肺癌等肿瘤中最常见的突变基因。虽然 TERT 和 TP53 在肝癌中均有较高的突变率，但二者在 HCC 发生、发展及预后等过程中的联合应用价值尚不清楚。本研究旨在探索二者联合检测在 HCC 中的临床意义。
方法 利用高通量测序技术检测 50 例 HCC 患者肿瘤组织中基因信息，进一步分析基因突变与患者临床特征之间的相关性。
结果 50 例样本中分别有 24 例（48%）和 16 例（32%）检测到 TP53 突变和 TERT 突变，其中 TERT 均为启动子 C228T 突变。分析结果表明，男性（P = 0.002）或肝炎症程度较高（P = 0.044）的 HCC 患者中更易发生 TPMs；有 TP53 突变的患者术后更易复发（P = 0.039），而 TERT 启动子突变和 TP53 突变同时存在时，患者的复发率显著升高（P = 0.009）。
结论 TERT 启动子突变和 TP53 基因突变在 HCC 中高频发生，提示二者在肝癌发生发展过程中可能发挥着重要作用。此外，TERT 启动子突变和 TP53 基因突变作为联合检测指标，有望成为临床评估 HCC 患者术后复发风险的重要依据。

PU-0987

CYP2C8 基因多态性与中国西部结核病患者抗结核药物性肝损伤的相关性研究

陈小娟[1,2]、赵珍珍[2]、周易[2]、杨阳[1]、应斌武[2]
1. 乐山市人民医院
2. 四川大学华西医院

目的 探讨细胞色素 P450 2C8(CYP2C8)基因多态性与中国西部结核病患者应用一线抗结核药物致肝损伤（anti-tuberculosis drug-induced liver injury，ATDILI）的相关性。
方法 本研究共纳入结核病患者 746 例，收集临床资料及相关实验室指标，根据肝功能指标将其分为 ATDILI 组和非 ATDILI 组，采用 QIAamp® DNA Blood Mini Kit 提取 DNA，利用高通量基因分型技术对 CYP2C8 基因 4 个单核苷酸多态性（single nucleotide polymorphism，SNP）分型。利用 Plink 软件分析不同遗传模型下两组间等位基因及基因型分布的差异。
结果 ATDILI 组 118 例，非 ATDILI 组 628 例。CYP2C8 基因 rs1058932、rs1113129、rs11572126、rs2275622 位点的等位基因、基因型及遗传模型（加性模型、显性模型与隐性模型）分布在 ATDILI 组与非 ATDILI 组中差异均无统计学意义（P＞0.05）。rs1113129、rs11572126、rs2275622 存在连锁不平衡，构成的 4 种单倍型模型在 ATDILI 组与非 ATDILI 组间分布差异无统计学意义（P＞0.05）。

结论 CYP2C8 基因 rs1058932、rs1113129、rs11572126、rs2275622 位点 SNP 可能与中国西部结核病患者应用一线抗结核药物致肝损伤无关，需进一步扩大样本量进行验证。

PU-0988

跨膜蛋白 40 在膀胱癌中作用的初步研究

张振飞
南方医科大学珠江医院

目的 跨膜蛋白 40（TMEM40）是一个大小为 34 kDa，由 233 个氨基酸构成且含有两个结构域的跨膜蛋白。在我们前期的研究中发现，TMEM40 在膀胱肿瘤中表达上调，预测它可能是一个潜在的促癌基因。
方法 在当前的研究中我们通过 qRT-PCR 及 WB 检测了膀胱癌细胞及组织中 TMEM40 在 mRNA 及蛋白水平的表达，结果表明 TMEM40 在膀胱癌细胞与组织中表达均上调；其次，通过组织芯片的免疫组化实验，探究 TMEM40 表达水平高低与膀胱癌患者临床病理参数间的关系。
结果 在 115 例膀胱癌患者中，TMEM40 的表达与患者的临床分期、pT 分期、组织病理学分级具有明显的相关性，而与患者的年龄、性别等无显著相关。接下来，我们选取两株人膀胱癌细胞系（5637、EJ），采用不同浓度梯度的 G418 筛选 TMEM40 过表达及敲减的膀胱癌细胞，扩大培养来得到稳定表达的细胞株。最后，通过 CCK-8、EdU、Transwell、细胞周期、凋亡及裸鼠皮下成瘤等一系列功能实验，来进一步验证 TMEM40 对膀胱癌恶性表型的影响。细胞增殖实验结果表明，TMEM40 表达上调促进细胞的增殖，而 TMEM40 下调则在一定程度上抑制了细胞的增殖；Transwell 实验表明，TMEM40 表达上调促进细胞迁移、侵袭，而 TMEM40 敲减则抑制细胞迁移、侵袭；流式细胞仪检测结果表明，过表达 TMEM40 对细胞的凋亡具有一定的抑制作用，而敲减 TMEM40 则促进了细胞的凋亡；过表达 TMEM40 加快 G1/S 期变，而敲减 TMEM40 则细胞周期阻滞在 G1 期。因此，TMEM40 在膀胱癌的发生发展过程中发挥着重要的作用，有可能成为膀胱癌患者临床治疗的基因靶点及分子标志物。

PU-0989

A case-control study on the correlation between the single nucleotide polymorphism of CLEC4E and the susceptibility to tuberculosis among Han people in Western China

Wenjing Zhou、Wu Lijuan、Jiajia Song、Lin Jiao、Zhou Zhou、Juan Zhou、Binwu Ying
West China Hospital

Background Tuberculosis (TB) is one of the leading causes of morbidity and mortality in West China. Preclinical studies have suggested the protective effect of the C-type lectin receptor of family 4 member E (CLEC4E) from TB. Herein, we investigated the association between CLEC4E gene variants and TB susceptibility in a western Chinese Han population.
Methods We genotyped four single-nucleotide polymorphisms (SNPs) rs10841856, rs10770847, rs10770855 and rs4480590 in the CLEC4E gene using the improved multiplex ligation detection reaction (iMLDR) assay in 900 TB cases and 1534 healthy controls.
Results After stratifying the whole data by sex, it was found that males exhibited mutant allele G of rs10841856 that was more strongly associated with increased TB risk after Bonferroni correction (OR = 1.334, 95% CI: 1.142–1.560; P<0.001 after adjusting for age; p=0.001 after Bonferroni correction). The genetic model analysis found that rs10184856 was associated with the increased risk of TB among males under the dominant model (OR = 1.557, 95% CI = 1.228-1.984, P<0.001 after adjusting for age, P<0.001 after Bonferroni correction). Bioinformatics

analysis suggested that rs10841856 might fall in putative functional regions and might be the expression quantitative trait loci (eQTL) for CLEC4E and long noncoding RNA RP11-561P12.5.
Conclusions Our study revealed that rs10841856 in the CLEC4E gene might be related to increased TB risk, especially the dominant genetic model among male Han individuals from Western China.

PU-0990

不同类型 miRNA 在类风湿关节炎中的病理生理学意义

周韶松
南方医科大学珠江医院

小 RNA（miRNA）是小分子非编码 RNA，负调控基因表达后的转录水平。目前，有 939 成熟的人类小 RNA 序列 Sanger 小 RNA 的注册表更新。预计人类基因组可能有大约 1500 的小 RNA 在控制我们三分之一基因的表达。在细胞中通过控制合成目标蛋白的，这些调控 RNA 分子，参与多种生理网络和主要职能，他们的管制已经牵连严重的人类疾病的发病机制，如癌症和感染。这暗示了最近出现基于小 RNA 的治疗方法在这些小 RNA 在免疫介导的疾病，如类风湿关节炎（RA）中的潜力。在这里，我们提供了在类风湿关节炎中一个小 RNA 的状态，集中讨论全身和局部病理特征。

PU-0991

Multiplex detection of Meningitis and Encephalitis pathogens: A study from Laboratory to the Clinical

Shuo Guo、yanbing zhou、minjin wang、zirui meng、tingna wu、binwu ying
West China Hospital, Sichuan University

Background Infectious Meningitis and Encephalitis(ME) as potentially life-threatening conditions are caused by various pathogens of which less sensitive and specific conventional laboratory testing projects cannot meet the demand for early diagnosis. Multiplex PCR is newly applied to the assistance in rapid and early diagnosis. Therefore, a retrospective study using the Multiplex PCR detection for Meningitis and Encephalitis panel of 18 pathogens (MME-18) was conducted to investigate the epidemiology characteristics of ME patients among the Chinese population in southwestern China while to help physicians achieve rapid and accurate diagnosis in ME.
Methods The hospitalized patients with suspected intracranial infection were analyzed retrospectively between May and July in 2019 in West China Hospital of Sichuan University. MME-18 was designed to detect 18 pathogens in cerebrospinal fluid (CSF) of enrolled patients. Conventional experiments including cryptococcal capsular antigen detection, GeneXpert, real-time PCR, and clinical feedback were used to verify the result of MME-18.
Results 146 eligible individuals were enrolled in the study in a total of 581 tested patients. Among 139 final diagnosis of infectious meningitis or encephalitis, M.tuberculosis, was the most common causative agents in mono-infection, viruses and C.neoformans were also frequently detected. There are 10 patients infected by more than one pathogen. Of 139 infected patients, 12 cases were diagnosed by MME-18 only, 57 patients by conventional testing only, 70 cases by both comparator tests and MME-18.
Conclusion MME-18 was designed with its rapid detection and wider range of pathogenic spectrum and may help clinicians with early identification of pathogens with comprehensive evaluation combined with conventional testing and clinical suspicion.

PU-0992

The association of polymorphisms in MAPK signaling pathway with antituberculosis drug-induced hepatotoxicity （ATDH）

Tangyuheng Liu
Department of Laboratory Medicine, West China Hospital, Sichuan University, Sichuan Province, P. R. China

Introduction Tuberculosis (Tuberculosis,TB) is an infectious disease seriously harmful to human health caused by Mycobacterium tuberculosis (Mycobacterium tuberculosis,MTB) infection. But at the same time, it is also accompanied by a very serious adverse drug reaction-drug-induced liver injury, which is the main reason for the interruption of anti-tuberculosis treatment. Oxidative stress is one of the important mechanisms of anti-tuberculosis drug-induced hepatotoxicity (Antituberculosis drug-inducedhepatotoxicity,ATDH), and its role in ATDH has been paid more and more attention in recent years, in which mitogen-activated protein kinase ((mitogen activated protein kinase,MAPK) signal pathway participates in the occurrence and development of ATDH by regulating the process of oxidative stress. In order to prevent and reduce the occurrence and development of clinical ATDH, there is an urgent need to further understand the relevant risk factors of ATDH and its mechanism, and to screen out effective markers for predicting the risk of ATDH, which can be used to predict the risk of ATDH and guide clinical medication.
Methods In this study, 746 tuberculosis patients in western China were randomly enrolled. Peripheral blood samples were collected and DNA was extracted. Combined with literature reports and bioinformatics database system, key genes and SNPs in MAPK signaling pathway were screened. A total of 18 SNPs were genotyped by imLDRTM multiplex SNP typing. SPSS22.0, Plink 1.90, Haploview and GMDR software were used to analyze the unit point, haplotype and gene interaction of target SNPs to explore the relationship between SNPs and the risk of ATDH and clinical characteristics. The Boruta algorithm is used to select the forecasting factors, and the R software is used to establish the line chart model.
Results There were significant differences in rs7160912 and rs11626707 loci of MAP3K9 gene, allele frequency and genotype frequency of rs882348 and rs57813199 loci of PPARGC1A gene, and allele frequency of rs4792246 of MAP2K4 gene between ATDH group and non-ATDH group. The An allele of rs7160912, rs11626707 and rs882348, and the C allele of rs57813199 may reduce the risk of ATDH. The values of OR and 95%CI are 0.68,0.66, 0.59 and 0.61, respectively. On the other hand, the G allele carriers of rs4792246 have an increased risk of ATDH (OR = 1.31Magazine 95% CIRC 1.00-1.72Power0.046). The sensitivity and specificity of the model are 0.14 and 0.67 respectively, suggesting that there is a moderate coincidence in predicting the risk value of ATDH, but the predictive ability of SNPs as a predictor of tuberculosis risk remains to be verified.
Conclusions It was found that six SNPs sites in MAPK signal pathway: MAP3K9 (rs7160912, rs11626707), MAP2K4 (rs4792246), PPARGC1A (rs882348, rs57813199, rs17885261) were associated with ATDH susceptibility, suggesting that the above SNPs may be a potential marker to predict the risk of ATDH. The haplotypes composed of rs7160912 and rs11626707 loci of MAP3K9 gene are associated with ATDH susceptibility, and the risk of ATDH of [AA] haplotype is reduced. The genetic variation of PPARGC1A gene (rs882348, rs57813199) may affect the changes of blood system (white blood cell count, low percentage of neutrophils, percentage of lymphocytes), and it is also related to (ALT), an index related to liver injury.

PU-0993

CMV DNA 和 CMV 抗体在器官移植病人巨细胞病毒

谭伟清
南方医科大学珠江医院

目的 探讨巨细胞病毒（Cytomegalovirus， CMV） DNA 和 CMV-IgM 抗体在诊断器官移植病人巨细胞病毒感染中的作用。
方法 以实时荧光定量聚合酶链反应（PCR）检测 52 例器官移植患者共 56 份尿和外周血单个核细胞 （PBMC） CMV-DNA，同时以酶联免疫吸附分析（ELISA）方法检测血清 CMV-IgM 抗体。
结果 56 份血清标本中 CMV-IgM 抗体阳性 8 例 （14.3%），而尿和 PBMC 的荧光定量 PCR 检测 CMV-DNA 阳性例数分别为 17 例（30.4%）和 21 例（37.5%）。
结论 对于器官移植患者，CMV-IgM 抗体作为 CMV 现症感染的血清学标志物阳性率偏低，检测尿中 CMV-DNA 可以提高阳性率，但依然存在部分漏检的情况，而 PBMC 的 CMV-DNA 则具有较高的阳性率，应该作为器官移植术后患者 CMV 现症感染的首选指标。

PU-0994

Distribution characteristics of CYP2D6 and ADRB1 genetic polymorphisms in Han Chinese hypertensive patients

李颖、陈克平
东南大学附属中大医院

Objective To investigate the allele and genotype frequencies of CYP2D6 and ADRB1 genetic polymorphisms and explore the potential role of these polymorphisms in guiding the selection of antihypertensive beta-receptor blockers for Han Chinese hypertensive patients.
Methods Totally 2419 Han Chinese hypertensive patients and 126 normotensive controls were recruited into the study in Zhongda Hospital. Venous blood samples were collected for each patient. The genetic polymorphisms of CYP2D6 and ADRB1 were determined using a gene chip platform. The allele and genotype frequency for each gene, as well as the combined genotypes among the subjects were analyzed respectively.
Results The gene chip analysis identified an allelic frequency of 39.29% for *1 and 60.71% for *10 allele of CYP2D6 in the cohort of Han hypertensive patients. Statistical analysis showed that the frequency of *1/*1 wild-type homozygous for CYP2D6 was 9.71%, while the frequency of *1/*10 heterozygous or *10/*10 mutant homozygous was 59.16% or 31.13%. In the meantime, we detected allelic frequencies of 32.78%, 67.22% for the G and C allele frequency of ADRB1. While the genotype frequency of GG wild-type homozygous was 10.29%, the frequency of GC heterozygous, or CC mutant homozygous was 44.98%, or 44.73%, respectively. Notably, the results showed *1/*10 + CC (25.88%) and *1/*10 + CG (27.78%) were the two combined genotypes with highest frequencies. Importantly, no significant differences in CYP2D6 and ADRB1 polymorphism distributions were revealed between normotensive control and hypertensive patients, or among all three grades of hypertensive patients.
Conclusion These data showed the CYP2D6 and ADRB1 polymorphisms characteristics in Han Chinese hypertensive patients. The present results would provide valuable information for antihypertensive effect of beta-receptor blockers in Han Chinese hypertensive patients in prospective clinical studies in the future.

PU-0995

Utilizing Machine Learning for Prediction of the Diagnostic Model of Microvascular Invasion Risk in Hepatocellular Carcinoma

Weiwei Liu[1]、Juan Zhou[2]、Binwu Ying[1]
1. West China Hospital of Sichuan University
2. 四川大学华西医

Background and objectives Microvascular invasion (MVI) has been proved to be an important independent risk factor for poor outcome in hepatocellular carcinoma (HCC), however, MVI can only be diagnosed by postoperative pathology and its pre-operative assessment remains largely challenge. The studies aimed to develop a machine learning model with valid prediction performance and clinical interpretability for MVI before surgical therapies.
Methods A total of 2375 patients with HCC were included, including 215 patients with macrovascular invasion, and 2160 patients without macrovascular invasion. Of the patients without macrovascular invasion, 575 patients suffered microvascular invasion (MVI), and 1585 patients didn't (non-MVI). In the model construction stage, the ratio of training set to test set was 8: 2. Three models were constructed using several machine learning algorithms: the "full indicators" model (model 1), the "preoperative prediction" model (model 2), and the "objective indicators only" model (model 3).
Results Three models were constructed using several machine learning algorithms: the "full indicators" model (model 1), the "preoperative prediction" model (model 2), and the "objective indicators only" model (model 3). Model 1 had the highest performance, with a sensitivity of 72.90%, a specificity of 67.06%, and an AUC of 0.74 in the test set, followed by model 2 with a sensitivity of 66.67%, a specificity of 65.11%, an AUC of 0.717, and model 3 with a sensitivity of 69.16%, a specificity of 62.91% and an AUC of 0.703, which were better than using only AFP or PIVKA-II. The most important features for MVI prediction were determined during modeling, including satellite lesions, tumor diameter, PIVKA-II, AFP, degree of differentiation, AST / ALT, PLT, etc. Although taking full advantage of EHR information to build a clinical MVI prediction model based on machine learning algorithms could improve prediction performance compared to a single indicator, the final AUC of the three models could only reach 0.7-0.8, considering the applicability of the models.
Conclusion Through a retrospective study of 2375 HCC electronic health records (EHR) in the past 5 years, based on a variety of machine learning algorithms, three MVI prediction models were constructed and optimized: "full index" model (model 1), "preoperative prediction" model (model 2), and "objective index only" model (model 3), the models performance were better than single index prediction, which reflects the advantages of the prediction model based on machine learning and provides new ideas for MVI prediction.

PU-0996

基于血清游离 microRNAs 的肌层浸润性膀胱癌预测 panel 的建立

蒋秀梅
山东大学齐鲁医院

目的 检测肌层浸润性膀胱癌血清游离 miRNAs 表达谱，建立肌层浸润性膀胱血清游离 miRNA 预测 panel。

方法 选取 6 例肌层浸润性膀胱癌患者、6 例非肌层浸润性膀胱癌患者和 6 例对照者血清，通过 miSeq 测序技术分别进行血清游离 miRNAs 表达谱检测，采用 RT-qPCR 在 111 例肌层浸润性膀胱癌患者、111 例非肌层浸润性膀胱癌患者和 187 例对照者血清中验证候选 miRNAs，确立肌层浸润性膀胱癌差异表达的 miRNAs，采用多元 logistic 回归分析建立预测肌层浸润性膀胱癌的血清 4-miRNA panel。在 90 例肌层浸润性膀胱癌患者和 168 例非肌层浸润性膀胱癌患者血清中对 4-miRNA panel 的肌层浸润预测效能进行验证。
结果 miSeq 高通量测序分析筛选出可作为肌层浸润性膀胱癌差异表达的 23 个候选 miRNAs 同时纳入课题组前期研究中发现的可用于膀胱癌诊断的 6 个 miRNAs。RT-qPCR 验证显示，miR-422a-3p，miR-486-3p，miR-103a-3p 和 miR-27a-3p 在三组间呈现差异表达（p 均<0.05）。构建血清 4-miRNA panel。血清 4-miRNA panel 预测肌层浸润性膀胱癌的 AUC 为 0.894。在另一人群中分析 4-miRNA panel 对肌层浸润性膀胱的预测价值。结果显示，4-miRNA panel 正确预测 121 例非肌层浸润性膀胱癌患者，特异度达 70.06%（95%CI，79.1~90.1）；正确预测 79 例肌层浸润性膀胱癌患者，灵敏度达 90.00%（95%CI, 81.9~95.3）。4-miRNA panel 预测肌层浸润性膀胱癌的 AUC 为 0.880。
结论 研究构建的血清 4-miRNA panel 对膀胱癌分期预测具有较高的临床价值。

PU-0997

MiR-27a-3p 在膀胱癌组织中的表达及功能研究

蒋秀梅
山东大学齐鲁医院

目的 通过 miR-27a-3p 在膀胱癌细胞系中的表达水平进行细胞功能试验。
方法 1. 选取在肌层浸润性膀胱癌血清中差异表达的 miRNAs，RT-qPCR 检测其在膀胱癌组织中的表达。
2. 检测差异表达 miR-27a-3p 在 40 对肌层浸润性膀胱癌及癌旁对照组织中的表达。
3. 采用 RT-qPCR 检测 miR-27a-3p 在膀胱癌细胞（T24）及永生化正常上皮细胞（SV-HUC-1）中的表达。
4. 通过 CCK8 细胞增殖实验、划痕实验及 Transwell 迁移和侵袭实验等分析 miR-27a-3p 对 T24 细胞的增殖、迁移及侵袭活性变化影响。
结果 1．miR-27a-3p 在肌层浸润性膀胱癌组织中的表达显著低于非肌层浸润性膀胱癌，且在 70%的肌层浸润性膀胱癌患者组织中较癌旁对照组织显著降低。
2．RT-qPCR 检测显示，miR-27a-3p 在 T24 细胞中的表达量显著低于 SV-HUC-1 细胞。
3.划痕实验中，miR-27a-3p mimic 转染组膀胱癌细胞伤口愈合率明显低于 miR-NC 组和 mock 组。miR-27a-3p inhibitor 转染组膀胱癌细胞伤口愈合率明显高于 miR-NC 组和 mock 组。
4. Transwell 迁移实验中，T24 膀胱癌细胞 miR-27a-3p mimic 组在转染 24h 后穿膜细胞数显著低于 miR-NC 组和 mock 组。T24 膀胱癌细胞 miR-27a-3p inhibitor 组在转染 24h 后穿膜细胞数显著高于 miR-NC 组和 mock 组。
5. Transwell 侵袭实验中，T24 膀胱癌细胞 miR-27a-3p mimic 组在转染 24h 后穿膜细胞数显著低于 miR-NC 组和 mock 组。T24 膀胱癌细胞 miR-27a-3p inhibitor 组在转染 24h 后穿膜细胞数显著高于 miR-NC 组和 mock 组。
结论 低表达的 miR-27a-3p 可显著增强膀胱癌细胞的增殖、迁移和侵袭能力。

PU-0998

CD47 在非小细胞肺癌中促进肿瘤侵袭和转移

刘元斌
山东大学齐鲁医院

CD47 在许多人类癌症中过表达，其水平与肿瘤的侵袭和转移呈正相关。然而，在非小细胞肺癌(NSCLC)中，CD47 过表达是否驱动转移以及 CD47 如何导致肿瘤转移仍是一个很大程度上未知的问题。在本研究中，我们分析了 NSCLC 标本和细胞株，发现 CD47 的表达水平高于无瘤对照标本。此外，CD47 表达增加与临床分期、淋巴结转移相关。为了理解其分子机制，我们在细胞系中将其功能增加和功能丧失观察其现象和结果。siRNA 介导的 CD47 下调抑制了体外细胞的侵袭和转移，而质粒转染 CD47 过表达则产生相反的作用。在体内，CD47 特异性 shRNA 显著降低了肿瘤的生长和转移。在分子水平上，无论是细胞系还是 NSCLC 标本中，CD47 的表达都与 Cdc42 的表达相关。抑制 Cdc42 可减轻 CD47 过表达细胞的侵袭和转移。这些结果表明 Cdc42 是 cd47 促进转移的下游介质。我们的发现首次证明 CD47 是疾病进展和转移的不良预后因素，也是 NSCLC 有希望的治疗靶点。

PU-0999

快检病理组织 EGFR 基因突变的方法

刘元斌
山东大学齐鲁医院

目的 寻找一种新的，高效快速检测 EGFR 基因突变的方法。
方法 这项研究描述了利用多种分子诊断学技术相结合的方式快速检测 EGFR 基因突变的新方法。相比 DNA 测序的检测方法，该方法是基于等位基因特异性扩增（ASA），重组酶聚合酶扩增（RPA），肽核酸（PNA），和 SYBR Green I，我们称之为 AS-RPA-PNA-SYBR （ARPS）系统。
结果 使用这种方法，在细胞系水平 5 分钟内即检测出了 EGFR 19Del（2）突变，同样在 10 分钟内检测出了 EGFR L858R 点突变；利用优化的 ARPS 系统检测临床标本，15 分钟即可很好的得到检测结果，并与临床信息和测序结果相一致。
结论 在这项研究中，使用 ARPS 系统检测 EGFR 基因突变的结果数据与由聚合酶链式反应（PCR）和 DNA 测序方法相一致，并且更快速，过程简单，方便使用。因此，利用该 ARPS 系统新方法检测基因突变，用以评估临床样品中 EGFR 基因突变有着可靠和实用的优势，并可在桥式 PCR 技术基础上更进一步检测循环肿瘤 DNA（ctDNA），在未来的床旁检测（POCT）和体液检测研究和应用中有很大的前景。

PU-1000

宫颈液基细胞学技术联合高危型人乳头瘤病毒 mRNA 检测技术在宫颈癌前病变中的应用价值

苗微微
吉林大学第一医院

目的 探讨宫颈液基薄层细胞学（TCT）联合高危型人乳头状瘤病毒 mRNA 检测在早期宫颈病变诊断中的价值。
方法 对 2019 年 10 月～2020 年 12 月在吉林大学第一附属医院妇产科就诊的 2456 例宫颈病变的患者行 TCT 检查联合 HPV mRNA 检测，并对一项或两项异常者行阴道镜下取活检，以病理组织学

结果为金标准。比较宫颈液基细胞学、HPVmRNA 检测以及两者联合检查与组织学结果的符合率。
结果 TCT 检测阳性者 180 例,敏感度为 83.9% ，HPV mRNA 检测阳性 161 例,敏感度 84.4% ,与 TCT 检测的敏感度相比差异无统计学意义(P＞ 0.05)，两种方法联合应用敏感度达到 92.4%，与单独应用 TCT 技术或 HC2 技术差异有统计学意义（P＜0.05）。
结论 可将 TCT 与 HPV mRNA 检测联合应用，可提高宫颈癌前病变筛查及早期诊断的检出率，有效降低假阴性率，弥补各自的不足。

PU-1001

The dominant model analysis of Sirt3 genetic variants is associated with susceptibility to tuberculosis in a Chinese Han population

Tao Wu[1,2]、Lin Jiao[1]、Hao Bai[1]、Xuejiao Hu[1,3]、Minjin Wang[1]、Zhenzhen Zhao[1]、Hui Xue[1]、Binwu Ying[1]
1. West China Hospital, Sichuan University
2. 宁夏回族自治区人民医院
3. 广东省人民医院

Background Tuberculosis (TB) is a complex infectious disease caused by the pathogen Mycobacterium tuberculosis (Mtb) which has coexisted with humanity since the Neolithic. Recent research indicated that SIRT3 plays a pivotal role in promoting the antimycobacterial response of mitochondria and autophagy during Mtb infection.
Materials/Methods A case-control study comprised 900 TB patients and 1534 heathy controls were retrospectively enrolled to assess the association between Sirt3 gene polymorphisms and TB susceptibility. In total of five single-nucleotide polymorphisms (SNPs) (rs511744, rs3782118, rs7104764, rs536715, and rs28365927) which were selected through database 1000 Genomes Project and offline software Haploview V4.2, and genotyped by a customized 2×48-Plex SNPscanTM Kit.
Results Our results suggested that the minor allele genotypes (A carriers) of rs3782118 confers the decreased risk of TB susceptibility (p Bonferroni = 0.032), and a similar but more significant effect was observed under the dominant model analysis (OR = 0.787, 95% CI = 0.666-0.931, p Bonferroni = 0.026). Haplotypes analysis showed that haplotype AGAAG (rs511744 / rs3782118 / rs7104764 / rs536715 / rs28365927) was associated with an increased risk of TB (p = 0.023, OR = 1.159, 95% CI = 1.019-1.317). In stratification analysis, we found that rs3782118 was associated with decreased risk of TB in female subgroup under the dominant model analysis (p Bonferroni = 0.016, OR = 0.678, 95% CI = 0.523-0.878). Moreover, functional annotations for three loci (rs7930823, rs3782116, and rs3782115) which are strongly linked to rs3782118 indicated that they may be responsible for the changes in some motifs.
Conclusions Our study suggested that the SNP rs3782118 was associated with a lower susceptibility to TB, especially under the dominant model analysis, and that the haplotype AGAAG (contains the major allele G of rs3782118) was associated with an increased risk of TB. Further independent cohort studies are necessary to validate the protective effect of Sirt3 genetic variants on the risk of TB.

PU-1002

结核分枝杆菌微滴式数字 PCR 检测方法的建立及临床应用评价

赵珍珍、应斌武
四川大学华西医院

目的 结核病（Tuberculosis，TB）是由结核分枝杆菌（Mycobacterium tuberculosis, MTB）感染引起的重大全球性疾病。传统的 MTB 检测方法对低菌含量样本检出率低，导致漏诊或延迟诊断。微滴式数字 PCR（droplet digital PCR，ddPCR）能准确定量痕量核酸靶标，基于 ddPCR，建立快速灵敏的 MTB 检测方法。
方法 以 MTB 插入序列（insert sequence, IS）6110 为靶标，构建 IS6110-ddPCR 检测方法。应用 IS6110-ddPCR 检测多类型临床样本，ROC 曲线分析评价 IS6110-ddPCR 对结核病的诊断价值，统计分析 IS6110-ddPCR 与常规结核检测试验效能，评估其对结核病的临床诊断效能。
结果 本研究建立的 IS6110-ddPCR 检测 MTB 的方法具有高特异性，与常见的非结核分枝杆菌和呼吸道感染细菌均无交叉反应。对 1012 例临床疑似结核病患者的各类型标本的检测，以临床最终诊断为结局指标（结核患者 432 例，非结核患者 580 例），IS6110-ddPCR ROC 曲线下面积（AUC）为 0.82（95%CI，0.79-0.85）。IS6110-ddPCR 诊断结核病的灵敏度、特异性、阳性预测值分别为 54.63%（95%CI，49.91-59.26%）、95.69%（95%CI，93.71-97.06%）、90.42%（95%CI，86.24-93.43%）。与传统 MTB 相关检测试验比较，IS6110-ddPCR 诊断结核病的灵敏度最佳[qPCR：29.86%，Xpert MTB/RIF ：36.43%，抗酸染色：13.95% ，分枝杆菌培养：30.66%]。
结论 IS6110-ddPCR 灵敏度优于常规结核检测试验，有助于低菌负荷的结核患者的早期诊断，对结核病疫情防控具有重要意义。

PU-1003

Identification of an exosomal long non-coding RNAs panel for predicting recurrence risk in patients with colorectal cancer

Xin Zhang
Qilu Hospital of Shandong University

Background Recurrence is a major cause of cancer-related deaths in colorectal cancer (CRC) patients, but the current strategies are limited to predict this clinical behavior. Our aim is to develop a recurrence prediction model based on long non-coding RNAs (lncRNAs) in exosomes of serum to improve the prediction accuracy.
Methods High-throughput lncRNAs microarray and reverse transcription quantitative real-time PCR were used to identify the recurrence-associated lncRNAs in 30 matched CRC tissues and sera. The recurrence prediction model was built with multivariable Cox analysis in 150-patient training set, and evaluated in an independent 203-patient test set using ROC, Kaplan–Meier, and COX analysis.
Results In discovery phase, 11 lncRNAs were found to be associated with CRC recurrence in tissues, and 9 of them were correlated with their expression levels of serum exosomes. In training phase, a model based on 5-exosomal lncRNAs (exolncRNAs) panel was constructed, and showed high distinguish capability for recurrent CRC patients. ROC showed the panel was superior to serum CEA and CA19-9 in prediction of CRC recurrence. In both training and test sets, high-risk patients defined by the 5-exolncRNAs panel had poor recurrence free and overall survival. And, COX model showed it was an independent factor for CRC prognosis.
Conclusions The 5-exolncRNAs panel robustly stratifies CRC patients' risk of recurrence, enabling more accurate prediction of prognosis.

PU-1004

ctDNA 突变丰度和分布与酪氨酸激酶抑制剂对非小细胞肺癌治疗效果相关性的研究

宋佳佳、周娟、白玲、应斌武
四川大学华西医院

背景 循环肿瘤 DNA（circular tumor DNA，ctDNA）检测对于组织量不足的患者或无法进行活检的患者十分重要。ctDNA 的突变丰度和分布可以反映患者整体肿瘤负担程度和肿瘤的已执行，目前关于突变的丰度和突变的分布与酪氨酸激酶抑制剂治疗效果的关系尚无最终结论。
方法 本研究回顾性纳入了 2017 年 12 月 18 日至 2019 年 12 月 31 日在华西医院收治的 100 例携带 EGFR 酪氨酸激酶抑制剂敏感突变（外显子 19 缺失，L858R 和 T790M 突变）的非小细胞肺癌患者。本研究通过二代测序技术和数字 PCR 技术检测患者外周血中 ctDNA 的突变及其丰度。
结果 EGFR 敏感突变丰度低于 3%的患者比 EGFR 敏感突变丰度更高的患者具有更长的无进展生存时间（progression free survival，PFS）（15 个月 vs. 10 个月，P = 0.028）。在 T790M 亚组分析中，T790M 突变丰度/最大突变丰度（T790M / MSAF）低于 30%的患者的 PFS 延长（7 个月）对比 15 个月，P = 0.013）。
结论 本研究结果表明，EGFR 敏感突变丰度较低或 T790M / MSAF 较高的患者预后更好。ctCNA 中 EGFR 敏感突变丰度和分布可能是酪氨酸激酶抑制剂治疗效果的重要预测因素。

PU-1005

SELEX 技术及核酸适体在感染性病原体检测中的研究进展及挑战

徐一心、王旻晋、应斌武
四川大学华西医院

Infectious diseases are considered as a pressing challenge to global public health. Accurate and rapid diagnostics tools for early recognition of the pathogen are essential for controlling the spread of infectious diseases. Aptamers, which screened by systematic evolution of ligands by exponential enrichment (SELEX), can bind to targets with high affinity and specificity so that have exciting potential in diagnosis of infectious diseases. In this review, we provide a comprehensive overview of the latest development of SELEX technology and focus on the applications of aptamer-based biosensor strategies for detecting of various infectious pathogens. The challenges and the future development in this field of clinical application will also be discussed.

PU-1006

ddPCR 检测 PML-RARa 融合基因的建立及其在中枢侵润诊断中的评价

叶远馨、周汶静、王念、周燕虹、陆小军、应斌武
四川大学华西医院

目的 PML-RARα 融合基因相互易位是诊断 APL 的分子基础。尽管实时定量 PCR (qPCR)已广泛应用 PML-RARa 的检测，但随着对微小残留（MRD）检测要求的提高，特别是中枢神经系统侵润时脑脊液检测的增多，已无法满足要求。微滴式数字 PCR (ddPCR)可以提供直接定量，具有更高敏

感度，受到广泛关注。本课题旨在设计 PML-RARa 的 ddPCR 检测体系，并探讨其在脑脊液 PML-RARa 检测中的应用价值，以提高早幼粒细胞白血病的 MRD 检测水平。
方法 本研究采用两步法 ddPCR 建立了 PML-RARa 的 ddPCR 检测体系，进行了灵敏度及特异性评价，采用 110 临床样本（96 例骨髓或外周血，14 例脑脊液）比较了 ddPCR 和 qPCR 在 PML-RARα 定量方面的差异，以评估 ddPCR 的诊断潜力，并验证 ddPCR 在脑脊液 PML-RARa 检测中的应用价值。
结果 建立了 PML-RARα 的 ddPCR 检测体系，敏感性实验提示 PML-RARα 的 ddPCR 检测 LOD 达到 0.002%。ddPCR 与 qPCR 检测结果的总符合率为 93.4%，在 68 例较高拷贝数（qPCR 检测>100copies/ml）PML-RARα 样本中，ddPCR 检测结果与 qPCR 检测定性结果完全符合，且两种方法定量结果具有良好的相关性（R2>0.97）。在另 42 例 qPCR 阴性样本中（含 14 例脑脊液样本），7 例 ddPCR 结果提示阳性（其中 2 例为脑脊液样本），但定量结果均<5copis/20ul。所有结果表明，ddPCR 与 qPCR 在临床样本 PML-RARα 的检测方面具有显著的一致性，但在精度、检测限(LOD)等基本性能参数上均优于 qPCR。
结论 ddPCR 被认为有可能成为一种可靠的 PML-RARα 定量替代技术，它将为 PML-RARα 水平在 qPCR LOD 上下波动的患者提供准确的结果，这可能与 ddPCR 比 qPCR 对抑制的耐受性更强有关。

PU-1007

Nacl 对大鼠肠道菌群构成改变的影响

董召刚
山东大学齐鲁医院

目的 高盐饮食被认为参与某些慢性疾病的发生发展，最近研究显示慢性疾病与肠道菌群密切相关，然而，对于高盐饮食对肠道菌群构成的影响尚不清楚。本研究的目的是探讨 Wistar 大鼠摄取高盐后肠道菌群构成的改变。
方法 4 周龄雄性 Wistar 大鼠按标准流程喂养后分为高盐组和对照组。高盐组大鼠通过灌胃方式给予 1 ml 10％NaCl 溶液，每周 3 次，共 4 周。收集粪便，提取 DNA 后，利用靶向 V4 区的 16S rRNA 基因测序技术分析粪便菌群表达谱。利用贝叶斯分类器对 OTUs 进行了分类分析，观察菌群多样性。LEfSe 分析比较微生物种群的相对丰度，并利用 PCA 和 LDA 分析来寻找两个或多个组之间差异表达菌群。使用微生物群落的系统发育研究，通过 PICRUSt 生物信息学软件预测微生物基因组的功能。
结果 结果表明高盐组和对照组粪便微生物 α 多样性无显着差异，而主成分分析（PCA）表明两组之间的菌群结构不同。在门水平，高盐组含量最丰富的是 Bacteroidetes（58.4％），而对照组为 Firmicutes（48.0％）。根据 LDA≥4 的标准使用 LEfSe 进一步分析显示，高盐摄入后 wistar 大鼠粪便中 Lactobacillus 和 Prevotella NK3B31 显着降低，而 Alloprevotella 和 Prevotella 9 在高盐组大鼠中增加。但是两组间的体重、肠道形态变化和血压、生化指标等参数均无明显差异。
结论 作为一项探索研究，高盐摄入与肠道微生物菌群构成变化有关，本研究为提高微生物菌群在高盐相关疾病发病机制中作用的认识提供了理论基础。

PU-1008

LncRNA-HOXA11-AS 结合 miR-124-3p 调控整合素 β3 表达在胃癌侵袭转移中的机制研究

宋兴勃、吴茜、钟慧钰、温阳、应斌武
四川大学华西医院

目的 通过细胞功能实验验证目标 lncRNA 及 miR-124-3p 和 ITGB3 的关系，以及三者的表达对胃癌细胞的增殖、侵袭迁移是否有影响。
方法 构建 pcDNA3.1-HOXA11-AS 重组质粒及 HOXA11-AS 干扰序列，通过 qPCR 检测了不同细胞中过表达或者敲降 HOXA11-AS 后 miR-124-3p，ITGB3 的表达。Western blot 检测 HOXA11-AS 对整合素 β3 表达水平的影响。采用划痕试验和 Transwell 迁移实验检测细胞的迁移能力，Transwell 侵袭实验检测细胞侵袭能力，CCK8 增殖实验检测细胞增殖能力。
结果 MKN45 细胞系中过表达 HOXA11-AS 后 miR-124-3p 的水平明显降低，ITGB3 表达明显升高，整合素 β3 表达明显上调；MGC-803 细胞中敲降 HOXA11-AS 后 miR-124-3p 的水平明显升高，ITGB3 表达明显下降，整合素 β3 表达明显下调。细胞功能试验显示，胃癌细胞过表达 HOXA11-AS 组的增殖，侵袭和迁移能力较对照组均有明显增强，而在 HOXA11-AS 敲降后，敲降组细胞的增殖，侵袭，迁移能力较对照组明显减弱。挽救实验显示，敲降 HOXA11-AS 的基础上沉默 miR-124-3p 可挽救由敲降 HOXA11-AS 导致的 miR-124-3p mRNA 水平的升高，ITGB3 表达的降低，整合素 β3 表达的降低。过表达 HOXA11-AS 的基础上过表达 miR-124-3p 可挽救由过表达 HOXA11-AS 导致的 miR-124-3p mRNA 水平的降低，ITGB3 表达的升高，整合素 β3 表达的升高。
结论 HOXA11-AS/miR-124-3p/ITGB3 参与了胃癌的增殖、侵袭和转移。HOXA11-AS 充当 miR-124-3p 的分子海绵，与 miR-124-3p 竞争性结合，上调了 ITGB3 蛋白整合素 β3 的表达，进而参与胃癌的发生发展。

PU-1009

Prognostic and predictive value of a hypoxia-related microRNA signature in patients with colorectal cancer

Ailin Qu
Qilu Hospital, Shandong University

Purpose Hypoxic is considered a critical microenvironment feature determining tumor behavior. Therefore, we sought to develop a hypoxia-related microRNA signature that could identify high-risk colorectal cancer patients.
Methods HT-29 cells cultured in hypoxia and normoxia were subjected to miRNA sequencing to identify differentially expressed miRNAs. These hypoxia-induced miRNAs were further used to construct microRNA-based signature for the prediction of overall survival of CRC patients using cox regression model, which was subsequently determined for its prognostic value in testing and independent validation cohorts.
Results We identified 52 hypoxia-induced miRNAs by analyzing sequencing data from HT-29 cells under normoxia and hypoxia conditions. Then using univariable and step multivariable cox regression model, we trained a four-microRNA signature in the training cohort (n=381) which could distinguish patients in high-risk group from those in low-risk group (AUC at 3 year: 0.711, 95%CI: 0.630-0.791; AUC at 5 year: 0.737, 95%CI: 0.627-0.845). Patients in high-risk group had poor overall survivals compared to those in low-risk group (log-rank test, $P < 0.001$ in training cohort). This microRNA signature was further confirmed in the testing cohort ($P=0.042$) and an independent validation cohort ($P < 0.001$). Multivariate Cox regression and stratified survival analysis revealed that the prognostic value of this signature was independent of

clinicopathological risk factors. ROC analysis indicated that the AUC of this signature was significantly larger than that of any other clinical risk factors or single miRNA alone (all $P < 0.05$). A nomogram was constructed for clinical use, which incorporated both miRNA signature and clinical risk factors (CEA, age and clinical stage) and did well in the calibration plots.
Conclusions This novel hypoxia-related miRNA signature was an independent prognostic factor of, and possessed stronger predictive power than, currently used clinicopathological features for identifying high-risk CRC patients. It may be a useful tool for patient counselling and personalize management for patients with CRC.

PU-1010

Development of a preoperative prediction nomogram for lymph node metastasis in colorectal cancer based on a novel serum miRNA signature and CT scans

Ailin Qu
Qilu Hospital, Shandong University

Purpose Preoperative prediction of lymph node (LN) status is of crucial importance for appropriate treatment planning in patients with colorectal cancer (CRC). In this study, we sought to develop and validate a non-invasive nomogram model to preoperatively predict LN metastasis in CRC.
Methods Development of the nomogram entailed 3 subsequent stages with specific patient sets. In the discovery set (n=20), LN-status-related miRNAs were screened from high-throughput sequencing data of human CRC serum samples. In the training set (n=218), a miRNA panel-clinicopathologic nomogram was developed by logistic regression analysis for preoperative prediction of LN metastasis. In the validation set (n=198), we validated the above nomogram with respect to its discrimination, calibration and clinical application.
Results Four differently expressed miRNAs (miR-122-5p, miR-146b-5p, miR-186-5p and miR-193a-5p) were identified in the serum samples from CRC patients with and without LN metastasis, which also had regulatory effects on CRC cell migration. The combined miRNA panel could provide higher LN prediction capability compared with computed tomography (CT) scans ($P<0.0001$ in both the training and validation sets). Furthermore, a nomogram integrating the miRNA-based panel and CT-reported LN status was constructed in the training set, which performed well in both the training and validation sets (AUC: 0.913 and 0.883, respectively). Decision curve analysis demonstrated the clinical usefulness of the nomogram.
Conclusion Our nomogram is a reliable prediction model that can be conveniently and efficiently used to improve the accuracy of preoperative prediction of LN metastasis in patients with CRC.

PU-1011

A serum piRNA signature as promising non-invasive diagnostic and prognostic biomarkers for colorectal cancer

Ailin Qu
Qilu Hospital, Shandong University

Purpose Piwi-interacting RNAs (piRNAs) are a novel class of small non-coding RNAs, which are not easily degraded but detectable in human body fluids. Recent studies have shown that aberrant piRNA expression is a signature feature across multiple tumor types. However, the expressions of piRNAs in serum of tumor patients and their potential clinical values remain largely unclear.

Methods High-throughput sequencing was performed to investigate the serum piRNA profiles, followed by evaluations in serum samples of 220 colorectal cancer (CRC) patients and 220 healthy controls using reverse transcription quantitative real-time PCR (RT-qPCR). Biomarker panels including piRNA-based Panel I and carcinoembryonic antigen (CEA)-based Panel II, were developed by logistic regression model, and their diagnostic potentials were compared. Fagan's nomogram was plotted to promote clinical application.
Results We identified five differently expressed serum piRNAs (piR-001311, piR-004153, piR-017723, piR-017724 and piR-020365), which, when combined in the piRNA-based Panel I, outperformed the CEA-based Panel II ($P < 0.001$) and could detect CRC with an area under the receiver operating characteristic curve of 0.867. In addition, Kaplan-Meier analysis showed that patients with low serum piR-017724 level had worse overall survival (OS) and progression-free survival (PFS). In multivariate Cox regression analysis, serum piR-017724 was an independent prognostic factor for OS and PFS ($P < 0.05$).
Conclusion Our findings suggest serum piRNA expression signatures have potential for use as biomarkers for CRC detection and to predict prognosis at the time of diagnosis.

PU-1012

RNA interference reveals tumor-promoting roles of Integrin alpha 6 (ITGA6) in Hepatocellular Carcinoma

Guixi Zheng
Qilu Hospital of Shandong University

Hepatocellular carcinoma (HCC) is the sixth most common malignancy worldwide and the third leading cause of cancer related mortality. The incidence and mortality rates of HCC are two times higher in Latinos than in the general population in the US and are the highest in Latinos from the South Texas region. The genetic and epigenetic events associated with the increased incidence of HCC in this population are still unclear. Increasing evidence suggests that integrins are one of the most important receptors for cell metastasisincluding integrin α6β1 and α6β4. However, few studies have focused on the function of integrin alpha 6 (ITGA6)in the tumorigenesis and progression of HCC.We aim to investigate the expression and potential roles ofITGA6 in HCC.
Materials and Methods Paired HCC tissues and adjacent non-tumor tissues were collected for RNA sequencing. ITGA6 RNA and protein expression levels were evaluated by RNA sequencing, RT-qPCR, Western blot and immunohistochemistry.HCC cell lines (SNU398 and Huh7) were transiently transfected with two ITGA6siRNAs and stably transfected with an ITGA6 shRNA lentivector. These cell lines were used for assays testing the effects of ITGA6 knockdown on HCC cellproliferation, migration and anchorage independent growth.
Results Analysis of RNA sequencing data indicatedthat the expression of ITGA6 increased 4-fold in HCC tumor tissues compared to adjacent non-tumor tissues, which was validated by RT-qPCR. Western blotting also confirmed increased expression of ITGA6 in the tumor tissues. The knockdown of ITGA6 by siRNAs and shRNAwasconfirmedwith Western blot and qRT-PCR. ITGA6 knockdownsignificantly decreased proliferation, migration and anchorage independent growth of HCC cell lines.
Conclusions ITGA6 is upregulated in HCC tumors in Latinos patients. ITGA6 may play a malignant-promoting role in HCC cells. Our studies provided new insights into the molecular mechanisms that drive HCC progression and potential therapeutic targets for treating patients with HCC including South Texas Latino patients.

PU-1013

DNA methylation analysis reveals the potential cancer-related lncRNAs in colon cancer

Guixi Zheng
Qilu Hospital of Shandong University

Purpose In the present study, we aimed to systemically characterize the profile of DNA methylation in colon cancer (CC), especially the methylation of aberrant lncRNAs genes, and identify the potential cancer-related long non-coding RNAs (lncRNAs) in CC.
Methods The genome-wide DNA methylation profile of CC was constructed using MethylRAD technology. The differentially methylated sites (DMSs) and differentially methylated genes (DMGs) were identified by EdgeR. LncRNA DMGs were identified after annotation by GENCODE v25. The RNA sequencing data were downloaded and analyzed from The Cancer Genome Atlas (TCGA) database. The aberrant lncRNA DMGs and dysregulated lncRNAs were co-analyzed by Venny 2.1. The lncRNAs, which were hypermethylated and down-regulated or hypomethylated and up-regulated, were identified as CC-related lncRNAs and screened to perform further functional analysis.
Results A total of 132,999 CCGG/8,487 CCWGG sites were identified as DMSs, which were mainly located on the introns and intergenic elements. Moreover, 1,359 CCGG DMGs and 1,052 CCWGG DMGs were screened respectively. Our results demonstrated that lncRNAs occurred frequently in DMGs, including 510 lncRNA genes (37.5%) in CCGG DMGs and 466 lncRNA genes (44.3%) in CCWGG DMGs. As a result, we totally obtained 963 lncRNA DMGs, including 387 hypermethylated and 576 hypomethylated genes. In addition, 1,328 differentially expressed lncRNAs, including 1,311 up-regulated and 16 down-regulated lncRNAs, were identified from TCGA data. Finally, we identified that 15 lncRNAs might be CC-related lncRNAs. ZNF667-AS1 and MAFA-AS1 were down-regulated in CC, which might be silenced by hypermethylation. Besides, 13 lncRNAs (A008781.2, HULC, AC100839.1, CRAT37, LINC01198, LINC01482, SMAD1-AS2, TH2CLCRR, DISC1-IT1, ABCC5-AS1, NFIA-AS1, AC007431.1 and AC012494.1) were hypomethylated and up-regulated in CC.
Conclusions We performed a genome-wide DNA methylation analysis by MethylRAD to acquire both CCGG and CCWGG DMSs and DMGs in CC. This study provided lncRNA DMSs and DMGs as potential biomarkers, novel therapy targets and valuable insights into molecular mechanism in tumorigenesis and development of CC.

PU-1014

Islet1 在女性肿瘤中有差异表达

耿燕、郑刚、郑刚、曹建林、曹建林、师伟、师伟、杨志宁、杨志宁
山西省人民医院

目的 胰岛素基因增强子结合蛋白-1 (isl1)是 LIM/homeodomain 家族的转录因子。ISL1 的异常表达已被证实与癌症的发展和进展密切相关。我们评估了 ISL1 在女性肿瘤中的表达及其与临床病理参数的关系。
方法 对 20 例宫颈癌、20 例卵巢癌、20 例子宫内膜癌和 30 例乳腺癌患者进行观察研究，免疫组织化学染色检测 ISL1 表达。
结果 ISL1 在不同女性肿瘤组织中的表达差异有统计学意义:宫颈癌、卵巢癌、子宫内膜癌均呈低表达($p < 0.05$）与癌旁组织中相比。同时，ISL1 在乳腺癌(组织分类为腔内 A、B，甚至三阴性乳腺癌(TNBC))中均未出现差异表达。此外，在乳腺的良性疾乳腺增生和乳腺纤维腺瘤中，ISL1 与正常乳腺组织表达无差异。

结论 与以往研究的其他肿瘤中 ISL 促肿瘤作用，ISL1 在女性肿瘤中一反常态的异常低表达。我们推测 ISL1 在抑制或促进癌症进展方面具有双重功能。其机制可能与 ISL1 甲基化或与雌激素相互作用有关。虽然 isl1 是否可以作为女性肿瘤的生物标志物或治疗靶点还需要进一步的研究。

PU-1015

RNF14 介导的 ORF45 单泛素化调控卡波氏肉瘤相关病毒（KSHV）定位于自噬体进行组装

王鑫、张义
山东大学齐鲁医院

目的 卡波氏肉瘤相关疱疹病毒（KSHV）是人类七种致瘤病毒之一，可致淋巴和皮肤粘膜等系统肿瘤。阻断 KSHV 组装将有效的抑制子代病毒的产生，抑制 KSHV 的持续感染。前期研究发现 KSHV 结构蛋白在宿主细胞内组装释放的过程中需要泛素化修饰指导病毒蛋白的组装，本研究试图揭示泛素化修饰调控 KSHV 组装释放的机制。
方法 免疫沉淀加蛋白质谱技术筛选与 KSHV 的被膜蛋白 ORF45 相互作用的蛋白质，并通过免疫共沉淀验证二者的相互作用。应用免疫印迹和激光共聚焦等技术检测泛素连接酶 RNF14 对 ORF45 蛋白的影响，包括 ORF45 蛋白的稳定性，泛素化修饰，细胞定位。最后运用免疫荧光和 qPCR 技术比较 RNF14 介导的泛素化修饰在 KSHV 组装和释放过程中的作用。
结果 通过筛选和鉴定我们发现一个与 ORF45 相互作用的 E3 泛素连接酶——RNF14。用 siRNA knockdown RNF14 后，用 anti-ORF45 沉淀 ORF45，再用泛素抗体 anti-Ub 检测 ORF45 的泛素化，发现 RNF14 knockdown 后，有一条泛素化的 ORF45 条带明显消失，提示 RNF14 介导了 ORF45 的泛素化，并且是 ORF45 的单泛素化。由于泛素化修饰常见的作用是介导蛋白质经蛋白酶体途径降解。因此，我们进一步检测 RNF14 对 ORF45 的稳定性的影响。敲除 RNF14 后，ORF45 的蛋白水平明显降低，由此，我们推测 RNF14 介导的泛素化非但没有降解 ORF45，反而稳定 ORF45。由于我们前期研究发现 ORF45 可以定位于自噬体，我们就进一步检测了 RNF14 对 ORF45 定位的影响。在病毒基因组 BAC16 稳定转染的细胞系中，用 siRNF14 敲低 RNF14 的表达后，ORF45 和 ORF65 不能与 LC3 共定位，并且 KSHV 病毒颗粒的产量明显低于对照组。表明 RNF14 介导了 ORF45 定位于自噬体，并且指导病毒在自噬体内组装。
结论 ① E3 泛素连接酶 RNF14 介导了 KSHV 被膜蛋白 ORF45 的单泛素化，以及；② RNF14 介导了 ORF45 定位于自噬体，并且将自噬体作为病毒组装释放的平台。

PU-1016

Analysis of protocols for SARS-CoV-2 nucleic acid extraction from pharyngeal swab samples

Lijuan Wu、Nian Wang、Wenjing Zhou、Juan Zhou、Huiyu Zhong、Jiajia Song、Tangyuheng Liu、Xingbo Song、Yuanxin Ye、Xiaojun Lu、Yi Zhou、Binwu Ying
West China Hospital of Sichuan University

We aimed to provide data toward optimizing detection **Methods** for COVID-19 in order to improve diagnostic protocols, focusing on swab type, viral inactivation protocol, RNA extraction methods, and extraction reagents. We found that the quality of viral materials was very important, with nylon flocked swabs performing better than dry cotton swabs in obtaining pharyngeal samples. Q-PCR results indicated that the virus at not inactivated, 56 °C for 30 min, and 65 °C for 30 min all yielded similar Ct values, suggesting that RNA was not significant degradation after inactivated virus was more suitable from the perspective of biosafety. There was no difference in

RNA extraction efficiency between NucliSENS easyMAG and Concert Bio C1016 magnetic-based protocols, and the magnetic-based protocols and a centrifugation-based protocol (QIAamp Viral RNA Mini Kit) for RNA extraction was no significant difference too. We suggested that SARS-CoV-2 RNA extraction in different laboratories should proceed based on a comparison of differences extraction methods, and use protocols that are most suitable according to the facilities of each laboratory.

PU-1017

The influence of HLA polymorphism and haplotype frequency on susceptibility to uremia in southwest China

Lijuan Wu[1]、juan zhou[1]、turun song[1]、jing li[2]、jie zhuang[1]、xiaojun lu[1]、tao lin[1]、binwu ying[1]
1. West China Hospital of Sichuan University
2. 攀枝花市中心医院

Kidney transplantation is the most effective and appropriate treatment for uremia, and HLA matching is an important factor affecting the success of organ transplantation and long-term survival. At present, many genome-wide association studies reveal a possible association between HLA and uremia, so this paper begins with the frequency distribution of HLA and analyzes the impact of HLA polymorphism on susceptibility to uremia in the population in southwest China. In this study, PCR-SSO (polymerase chain reaction and sequence specificoligonucleotide probe hybridization) typing technology was used to detect the genotypes of the HLA-A, -B, -DRB1 and -DQB1 loci in 8252 patients with uremia and 6193 donors in southwest China. To compare the frequency distribution of these HLA alleles and the influence of HLA polymorphisms on susceptibility between patients and donors. We detected 17 HLA-A, 44 HLA-B, 13 HLA-DRB1 and 7 HLA-DQB1 alleles. The major alleles of the HLA-A、-B、-DRB1 and -DQB1 loci of the patients were similar to those in the donors group. The five most common alleles in the HLA-A、-B、-DRB1 and -DQB1 loci accounted for 89.9%, 48.0%, 66.2% and 85.8% of the patients, while the five most common alleles in the donors group accounted for 89.4%, 49.4%, 64.2% and 86.0%, respectively. Four of the HLA-DQB1 alleles had significantly different distribution of patients and controls, while three of the -DRB1 alleles, two of the HLA-B alleles, and the HLA-A locus was zero. These HLA-B、-DRB1、-DQB1 alleles may be closely related to uremia. The haplotypes (combinations of HLA-A, -B, -DRB1 and-DQB1) with significantly different frequency between patients and controls, which mostly account for more than 1% have 27 haplotypes, of which 18 are risk factors for uremia and 9 are protective. This study sheds new light on HLA composition and differences, uremia patients and healthy people in southwest China of HLA genotype and can be used as a guide and renal transplantation HLA match HLA classification research resources. At the same time, the discovery of susceptibility genes and protective genes provides a theoretical basis for the clinical treatment, prognosis and preventive measures of uremia.

PU-1018

Hsa-miR-4484 调控整合素 α6 表达影响 VEGF 信号通路在胃癌侵袭转移中的机制研究

钟慧钰、周娟、由丽婷、温阳、周汶静、王军、宋兴勃
四川大学华西医院

目的 本研究筛选出位于整合素 α6 基因（ITGA6）3'UTR 内的位点 rs17664，进一步预测与之结合的 miRNA，通过组织实验及细胞实验揭示在胃癌侵袭与转移过程中 miRNA 调控整合素 α6 表达、影响 VEGF 信号通路的可能作用机制。
方法 利用生物信息学方法对可与 ITGA6 的 3'UTR 区相结合的 miRNA 进行预测，并采用双荧光素酶报告基因检测验证靶点。在 30 对配对胃癌组织和远端正常组织中采用荧光定量 PCR (RT-PCR) 及荧光探针原位杂交（FISH）检测 miRNA 和 ITGA6 的组织定位及表达水平，并采用免疫荧光组织化学（IFHC）和蛋白免疫印迹（WB）方法检测胃组织中整合素 α6 及 VEGF 信号通路相关蛋白的表达水平。进一步在胃癌细胞系中采用 RT-PCR 及 WB 检测相应目标分子的表达水平，并采用 CCK-8 增殖实验、Transwell 侵袭与迁移实验、小管形成实验观察胃癌细胞的增殖、迁移、侵袭及血管形成能力。统计学分析采用 GraphPad Prism 6.0 和 SPSS 22.0 软件。
结果 生物信息学预测结果显示 ITGA6 的 3'UTR 区内存在 hsa-miR-4484 的结合位点，双荧光素酶报告基因实验显示 ITGA6 是 hsa-miR-4484 的直接靶基因，hsa-miR-4484 可与 ITGA6 的 3'UTR 区结合并下调后者的表达。ITGA6 和整合素 α6 在胃癌组织表达水平显著高于配对的远端组织（P=0.015；P<0.001），hsa-miR-4484 表达水平则低于配对的远端组织（P=0.029）。分层分析显示 ITGA6 及 hsa-miR-4484 的表达水平与胃癌患者的临床病理特征具有相关性。在胃癌细胞系中分别对 ITGA6 进行过表达及干扰后，VEGF 信号通路相关蛋白表达水平以及胃癌细胞增殖、迁移侵袭、血管形成能力分别显著升高及降低；对 hsa-miR-4484 进行过表达及封闭后，ITGA6、整合素 α6、VEGF 信号通路相关蛋白的表达水平以及胃癌细胞增殖、迁移侵袭、血管形成能力分别显著降低及升高。
结论 本研究结果提示整合素 α6 基因（ITGA6）是 hsa-miR-4484 的直接靶基因，后者可结合并下调 ITGA6 及整合素 α6 的表达。miR-4484 在胃癌的发展过程中通过调控 ITGA6 和整合素 α6 的表达发挥抑制 VEGF 信号通路及胃癌侵袭转移、血管形成的功能。

PU-1019

基薄层细胞学技术联合 HPV DNA 检测在诊断高级别宫颈病变中的临床价值

魏爱婷
河南省漯河医学高等专科学校第三附属医院

目的 探讨液基薄层细胞学、HPV DNA 检测在诊断高级别宫颈病变中的临床价值。
方法 收集 439 例样本进行常规细胞学、HPV DNA 及组织学检测的患者为研究对象，分别采用液基薄层细胞学技术及 2001 版 Bethesda 分类系统对病人进行细胞学诊断，采用第二代杂交捕获法（hybrid captureⅡ，HC2）检测 HPV DNA。其中正常/慢性炎症组 194 例，CIN1 组 97 例，CIN2 组 56 例，CIN3 组 73 例，SCC 组 19 例。
结果 正常/慢性炎症组、CIN1、CIN2、CIN3 和 SCC 组细胞学阳性率和 HPV DNA 阳性率分别为 39.2%、70.1%、87.5%、87.7%、100%和 57.7%、73.2%、94.6%、90.4%、100%。HPV DNA 检测和细胞学诊断级别间、细胞学检测和组织学检测、HPV DNA 检测和组织学检测的关联系数 r 分别为 0.348、0.625 和 0.333（P 均<0.001）。以组织学为金标准，检测 CIN2+，细胞学检测、

HPV DNA 检测和两者联合检测间相比，仅细胞学和 HPV DNA 检测的特异性间，及联合检测与细胞学检测的敏感性、特异性间差异具有统计学意义（P 均<0.05）。
结论 液基细胞学和高危 HPV DNA 检测方法可互为补充，两者联合检测可以提高女性宫颈癌筛查筛查准确性。

PU-1020

柳州地区新生儿高胆红素血症 G6PD 基因结果分析

陈大宇、谭建强、杨金玲、黄丽华
柳州市妇幼保健院

目的 通过回顾性分析本地区不同程度新生儿高胆红素血症患儿葡萄糖-6-磷酸脱氢酶活性及基因突变位点，分析其不同突变蛋白功能改变情况，了解不同 G6PD 基因突变类型在高胆红素血症患儿诊疗价值，为新生儿高胆红素血症患儿的临床诊断及治疗提供科学依据。
方法 回顾性选取 2018 年 6 月-2020 年 6 月本院新生儿科确诊为高胆红素血症患儿 353 例为研究对象，运用生化分析仪分析总胆红素（BILIT）、G6PD 酶活性，利用多色探针熔解曲线分析法（Multicolor melting curve analysis， MMCA）检测 G6PD 基因 16 个热点突变位点。通过综合评估，分析不同类型 G6PD 突变位点及活性变化在高胆红素诊疗中的价值。
结果 在 353 例检测结果中，共有 114 例 127 频次的基因突变，发生率为 32.29%，其中男性半合子患者 70 例，女性纯合患者 4 例，女性复合杂合患者 9 例，女性杂合患者 31 例。高发突变位点为 c.1388G>A（33.07%），其次为 c.1376G>T（24.41%），c.95A>G（19.68%）。采用 PROVEAN 分析软件对这几种氨基酸改变导致的蛋白功能改变情况进行预测，结果显示高发的这三种突变的 PROVEAN 得分均低于阈值，被判定为有害影响。同时不同程度的高胆红素血症患儿的总胆红素与酶活性水平变化呈现负相关，具统计学意义（P<0.05）。
结论 通过研究本地区新生儿高胆红素血症患儿 G6PD 基因突变与酶活性变化的关系，根据基因突变引起的表达差异，从蛋白功能改变上分析导致酶活性降低的可能原因。同时本地区新生儿高胆红素血症患儿 G6PD 缺乏症发生率较高，高发突变位点有一定的地域性，在诊疗疾病的过程中，临床应同时综合分析胆红素水平、G6PD 活性水平变化及基因突变类型。在新生儿高胆红素血症 G6PD 功能影响的研究上，部分已知的突变位点的蛋白结构仍然未被解析，还有待未来研究人员进一步探索。高胆红素患儿的 G6PD 酶活性降低程度是否与不同突变位点存在关联，是否存在少数民族地域性，也还有待一步研论证。

PU-1021

Epoxide hydrolase gene(EPHX2)Arg287Gln is a promising hypertension-susceptibility locus in Han Chinese

Liang Ma、yongwei jiang、Yi Liu、Meimei Zhao、Xiaomu Kong、Peng Gao、Yongtong Cao
China-Japan Friendship Hospital

Backgrounds and Objectives Experimental studies indicate that the gene EPHX2 coding for epoxide hydrolase (sEH) is a potential candidate in the pathogenesis of hypertension. We genotyped a missense mutation at exon 8, R287Q (rs751141), in EPHX2 gene, aiming to assess its association with protein activity of soluble epoxide hydrolase and the risk of primary hypertension in Han Chinese and we also study the sEH activity of R287Qvariantby plasmid construction and transduction in vitro .
Methods This is a hospital-based case-control association study involving 1240 participants, including 782 patients with primary hypertension and 458 healthy controls. Genotyping was done using TaqMan technique and confirmed using direct sequencing. WT and R287Qvariant plasmids

were constructed using pcDNA3.1/V5-His A vector, and activity of sEH fusion proteins was evaluated by the conversion of 11,12-EET to corresponding 11,12-DHET using ELISA kit.
Results The genotypes of R287Q variant in EPHX2 gene were in the Hardy-Weinberg equilibrium. Only marginal significance was noticed for the genotype and allele distributions of this variant between patients and controls (P=0.032 and 0.023, respectively). After taking carriers of GG genotype of R287Q variant as a reference group, those with GA genotype had a significantly reduced risk of hypertension (adjusted odds ratio: 0.72, 95% confidence interval: 0.56 to 0.93, P=0.013). Five significant risk factors were identified using Forward logistic regression analysis, including age, body mass index, total cholesterol, homocysteine and R287Q variant. These five risk factors for hypertension were represented in a nomogram graph, with a descent prediction accuracy (C-index: 0.833, P<0.001). The enzyme activity of soluble epoxide hydrolase was significantly lower in the R287Q group than in the wild type group
Conclusions We provide genetic evidence that the mutation of R287Q variant in EPHX2 gene was associated with low enzyme activity of soluble epoxide hydrolase and reduced risk of having primary hypertension.

PU-1022

Neoadjuvant Chemotherapy Modulates the Tumor Microenvironment in High-Grade Serous Ovarian Cancer

Zhongling Zhuo、Fei Xiao
Beijing Hospital

Background While surgical reduction with adjuvant chemotherapy is the traditional treatment for high-grade serous ovarian cancer (HGSOC), neoadjuvant chemotherapy (NACT) has increasingly been applied. This work aims to investigate the expression profiles before and after NACT, explore changes in the tumor microenvironment, expand current treatments, and design a combination of treatment options for patients.
Methods We downloaded 326 pre-NACT RNA sequencing data and 37 matched pre- and post-NACT samples from The Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO) databases. Differentially expressed genes (DEGs) were determined with EdgeR, and Gene Ontology analysis was performed to identify the clusters responsible for the biological processes and pathways of HGSOC. Immune infiltration was analyzed using Single-sample Gene Set Enrichment Analysis (ssGSEA) and CIBERSORT. Kaplan-Meier (KM) survival analysis was performed to assess prognosis, and the potential correlations between modules and phenotypes were explored using weighted gene co-expression network analysis (WGCNA).
Results After NACT, a total of 352 genes showed significant changes in RNA expression, among which 180 genes were up-regulated and 172 down-regulated. The most influential pathway was the positive regulation of mitogen-activated protein kinase (MAPK) cascade. Correlation analysis and KM survival analysis showed that overexpression of MAPK cascade genes correlated with shorter survival time in HGSOC patients. ssGSEA results showed that the expressions of anti-tumor cells (central memory CD4+ T cell and central memory CD8+ T cell) and pro-tumor cells (neutrophil and dendritic cells) were significantly increased after NACT. CIBERSORT showed that the abundances of memory B cells, NK cells, and monocytes were increased and the abundance of plasma cells was decreased after NACT. WGCNA and KM survival analysis showed that a lower abundance of Regulatory T cells (Tregs) was correlated with a better prognosis.
Conclusions Gene expression of the MAPK pathway is up-regulated and the abundance of CD4+ T regulation cell decreases after NACT. Thus, the MAPK pathway may promote the differentiation of CD4+ T cells into Th17 cells while inhibiting Tregs development. The inhibited Tregs' development can lead to a better prognosis. Therefore, it is speculated that Tregs inhibitors combined with platinum-based NACT are potential treatment options for HGSOC.

PU-1023

Long non-coding RNA ZFAS1 promotes the invasion and proliferation of gastric cancer cells by regulating LIN28 and CAPRIN1 and has the potential value of tumor marker

Zhongling Zhuo[1]、Xiaotao Zhao[2]
1. Beijing Hospital
2. 北京大学人民医院（北京大学第二临床医学院）

Object LncRNA ZNFX1-AS1 (ZFAS1) is a newly discovered long non-coding RNA (LncRNA), but its value in the diagnosis of gastric cancer is unclear. The aim of this study was to investigate the potential role of ZFAS1 in gastric cancer and to evaluate the clinical significance of ZFAS1 as a biomarker for gastric cancer screening.
Methods Quantitative real-time polymerase chain reaction (qRT-PCR) was used to screen for gastric cancer-associated LncRNAs in gastric cancer patients, gastric stromal tumor patients, gastritis or gastric ulcer patients, and healthy controls. The correlation between ZFAS1 expression and clinicopathological features was analyzed. The biological effects of ZFAS1 on proliferation, migration and invasion of gastric cancer cells were studied by MTT assay, colony formation assay and transwell migration assay. The potential mechanism of ZFAS1 was demonstrated using ELISA and qRT-PCR. The relationship between ZFAS1 and tumorigenesis was demonstrated using in vivo tumor formation assays.
Results The expression of LncRNA ZFAS1 in plasma of preoperative patients with gastric cancer was significantly higher than that of the other 4 groups. Increased expression of ZFAS1 was significantly associated with lymph node metastasis, TNM staging, and poor prognosis. ZFAS1 knockdown inhibited the proliferation, migration and invasion of gastric cancer cells. In contrast, ZFAS1 overexpression promoted proliferation, migration and invasion of gastric cancer cells. LIN28 and CAPRIN1 are key downstream mediators of ZFAS1 in gastric cancer cells. ZFAS1 overexpression promoted the growth of gastric cancer cells in vivo. Meanwhile, ZFAS1 knockdown expression inhibited the growth of gastric cancer cells in vivo.
Conclusion LncRNA ZFAS1 promoted invasion and proliferation of gastric cancer cells by modulating LIN28 and CAPRIN1, suggesting that ZFAS1 can be used as a potential biomarker for the diagnosis and prognosis of gastric cancer.

PU-1024

Four novel BRCA variants found in Chinese hereditary breast cancer patients by next-generation sequencing

Zhongling Zhuo[1]、Pengfei Liu[2]、Xiaotao Zhao[2]
1. Beijing Hospital
2. 北京大学人民医院（北京大学第二临床医学院）

Object Breast cancer is the most frequent cancer among women worldwide. Patients carrying mutations in breast cancer susceptibility genes like BRCA1 and BRCA2 (BRCA1/2) account for 5%-10% of all breast cancer patients. Therefore, screening for breast cancer susceptibility genes may reduce the incidence of breast cancer and improve prognosis.
Methods To provide evidence for mutation interpretation and targeted drug use in breast cancer patients, gene mutations were screened in 78 women diagnosed with sporadic breast cancer using a next-generation sequencing (NGS) panel, confirmed by Sanger sequencing. Then the pathogenicity of the identified novel mutations was explored using in vitro experiments including western blotting, co-immunoprecipitation and cell-migration assays.

Results Four novel mutations (BRCA2 L1390T, BRCA2 G432F, BRCA1 P659L, and BRCA1 C835F) were identified. BRCA2 G432F decreased the expression of BRCA2 protein, enhanced cell migration and invasion ability, and prevented the protein from interacting with RAD51, resulting in a defect in the homologous recombination pathway.
Conclusions The identification of these four novel BRCA mutations and the confirmation of their pathogenicity have enriched the genetic database of breast cancer, especially in the Chinese population. Moreover, the mutations are the genetic risk factors for hereditary breast cancer. Therefore, BRCA mutation detection and genetic counseling for breast cancer patients are meaningful and important.

PU-1025

Transfer of microRNA-216a-5p from exosomes secreted by human urine-derived stem cells reduces renal ischemia reperfusion injury

Shuo Yang、Yinmei Zhang、Boxin Yang、Rui Qiao、Liyan Cui
Peking University Third Hospital

Objective Human urine-derived stem cells (USCs) protect rats against kidney ischemia/reperfusion (I/R) injury. Here we investigated the role of USCs exosomes in protecting tubular endothelial cells and miRNA transfer in the kidney.
Methods Urine samples were collected from 7 healthy adult male donors ranging in age from 22 to 28 years. USCs were collected, cultured and identified. The total RNA of USCs, USCs-Exos and MPs was used to prepare the template library. Two independent small RNA libraries were generated from USCs-Exos and MPs compared with the USCs library.HK-2 cells were treated with hypoxia for 1 h and reoxygenation for 24 h in vitro to establish H/R model. A CCK8 assay was used for the cell proliferation assay.PTEN, Akt, pAkt and β-actin were measured by Western blot.A dual-luciferase reported gene assay was employed to further assess whether PTEN was indeed a direct target gene of miR-216a-5p. Caspase-3 activity was measured using the Caspase 3 Activity Assay Kit.Rat renal I/R model was performed on adult male SD rats,and the renal Tissue specimens were embedded in paraffin and sliced into 4μm-thick sections, stained with hematoxylin and eosin (H&E).Immunohistochemical staining for PTEN in the renal cortex was detected using commercial assay kits,while apoptosis was assessed by the TUNEL assay.Serum creatinine and urea nitrogen levels were measured by AU5800 Analyzer.
Results Human USCs and exosomes from urine-derived stem cells (USCs-Exos) were isolated and verified by morphology and specific biomarkers. USC-Exos played a protective role in HK-2 cells exposed to H/R. USCs-Exos were rich in miR-216a-5p, which targeted phosphatase and tensin homolog (PTEN) and regulated cell apoptosis through the Akt pathway. In HK-2 cells exposed to H/R, incubation with USC-Exos increased miR-216-5p, decreased PTEN levels and stimulated Akt phosphorylation. Exposure of hypoxic HK-2 cells to exosomes of USCs pretreated with anti-miR-216a-5p can prevent the increase of miR-216-5p and Akt phosphorylation levels, restore PTEN expression and promote apoptosis. The dual-luciferase reported gene assay in HK-2 cells confirmed that miR-216a-5p targeted PTEN. In rats with I/R injury, intravenous infusion of USCs exosomes can effectively induce apoptosis suppression and functional protection, which is associated with decreased PTEN. Infusion of exosomes from anti-miR-216a-5p transfected USCs weaken the protective effect in the I/R model.
Conclusion Therefore, USCs exosomes can reduce renal I/R injury by transferring miR-216a-5p targeting PTEN. Potentially, USCs exosomes rich in miR-216a-5p can serve as a promising therapeutic for AKI.

PU-1026

COX-2 基因多态性与大肠癌易感性的关系

邢培祥、阚士锋、杨发林
山东大学齐鲁医院

目的 探讨环氧合酶-2（COX-2）基因多态性（SNP）与大肠癌发生发展的关系。
方法 采用聚合酶链反应限制性片段长度多态性（PCR-RFLP）检测 COX-2-3618A/G 及 COX-2-765 G/C SNP，免疫组化检测 COX-2 表达，通过病例-对照研究分析大肠癌与 COX-2-(3618,765)SNP 的关系；以 χ2 检验行相关指标的比较，以比值比(OR)及 95％可信区间(95％CI)估计相对风险。
结果 （1）大肠癌组 COX-2-3618AG 频率显著高于对照组（χ2 =7.41，P<0.05），-3618 AA 及其 A 频率均显著低于对照组（χ2 =6.98，P<0.05 及 χ2 =5.49，P<0.05）；COX-2-765 SNP 频率与对照组比较无统计学意义（P 值均>0.05）。（2）在结、直肠癌、管状腺癌、高、中分化管状腺癌亚组中 COX-2-3618AG 频率显著高于对照组，而相应 AA 频率显著低于对照组（P <0.05）。（3）低分化管状腺癌亚组中 COX-2-765C 频率显著高于对照组（χ2=10.7，P<0.05，OR=1.7，95%CI=1.24～2.34）。（5）大肠癌组、-3618G 及 AA， -765C 及 G 携带者大肠癌中 COX -2 表达阳性率均显著高于对照组（P < 0.01）。
结论 COX -2-3618 及-765 SNP 可能与大肠癌易感性相关。

PU-1027

Polymorphic Variation of NFKB1 and Risk of Tuberculosis for Tibetan Population in China

Wu Peng
Department of Laboratory Medicine, West China Hospital, Sichuan University

Objective Polymorphic Variation of NFKB1 has been conformed associated with numerous immune-related diseases. This study aims to find out the association between three SNPs--rs2836491, rs72696119, and rs1585215--in NFKB1 gene and TB risk in Chinese Tibetan population.
Methods The SNPs were genotyped using MassARRAY mass spectrometry in 305 Chinese Tibetan TB patients and 333 health controls. A comprehensive analysis of single loci (including the genotype and allele distributions, the genetic models of target SNPs) and haplotype between case and control groups were conducted by SPSS17.0, Plink, and Editplus software.
Results There were no significant differences between TB patients and healthy controls with regard to gender or age (p>0.05). Genotype distributions of three SNPs in cases and controls were all in agreement with Hardy-Weinberg equilibrium (p>0.05). For rs2836491, rs72696119, and rs1585215, we found a p value greater than 0.05 of genotype or allele comparison between cases and controls. Further considering of the inheritance models (recessive model or dominant model) also found non significantly different between two groups. Linkage analysis of the three tested SNPs showed strong linkage disequilibrium, but these haplotypes were not associated with TB in Chinese Tibetan population.
Conclusions We first evaluated the association between rs2836491, rs72696119, and rs1585215 in NFKB1 and TB in Chinese Tibetan population. Although there were numerous evidence indicated that NFKB1 gene was a key target for TB risk, we found no significant association between tested SNPs and TB in our study, further studies are still needed.

PU-1028

血清 TNF-γ、TGF-β1、IL-6 与乳腺癌患者临床分期及淋巴结转移的关系研究

李琳瑄
黄河三门峡医院

研究血清 TNF-γ、TGF-β1、IL-6 与乳腺癌患者临床分期及淋巴结转移的关系。可作为临床诊断乳腺癌的重要依据。

转化生长因子 β1(TGF-β1)、肿瘤坏死因子 γ(TNF-γ)以及白细胞介素-6(IL-6)可通过对乳腺癌的导管上皮细胞的早期浸润作用以及细胞周期的调控作用，进而促进乳腺癌肿瘤细胞的进展[7]。本研究主要通过血清 TNF-γ、TGF-β1、IL-6 与乳腺癌患者临床分期及淋巴结转移的关系研究，为临床诊断提供科学依据。

PU-1029

一例 47，XN，+der（13）t（7；13）（q35；q12）胎儿染色体的微阵列鉴定及遗传学研究

王玉萍、武其文、付夏、李琴、洪云、江峰
皖南医学院弋矶山医院

目的 明确一胎儿罕见异常染色体的来源、断裂点、临床意义，探讨微阵列芯片分析的临床诊断价值。

方法 常规抽取孕妇羊水行细胞培养染色体核型分析，进一步 cy750K 微阵列（chromosome microarray analysis，CMA）鉴定；对胎儿行 B 超检查；对夫妻双方及其表型正常孩子行外周血染色体核型分析。

结果 羊水染色体核型分析发现多一染色体片段，结果拟报告为 47，XN，+mar，该片段经 CMA 鉴定为 arr[hg19]7q35q36.3（144，913，870-159，119，707）×3 重复 14.2Mb；arr[hg19]13q11q12.13（19，436，286-27，584，302）×3 重复 8.1Mb；孕妇外周血染色体结果为 46，XX，t（7；13）（q35；q12），孕妇丈夫及其表型正常孩子外周血染色体正常；B 超显示胎儿室间隔缺损，三尖瓣后瓣回声增强，三尖瓣轻度反流，心轴略偏移。

结论 胎儿染色体核型为 47，XN，+der（13）t（7；13）（q35；q12）mat，此染色体片段来源于孕妇，是由孕妇平衡易位染色体重组后形成的衍生染色体。对于罕见的异常染色体片段，一定要进一步明确诊断，为临床后续产前诊断提供有效的诊断依据。微阵列分析用于衍生染色体片段、微重复检测具明显的优势，可以作为细胞遗传技术的有效补充手段。

PU-1030

Genetic Polymorphisms of Delta-Like 1 Homolog Influence the Susceptibility to Antituberculosis Drug-Induced Hepatotoxicity

Tangyuheng Liu、Yang Fu
Department of Laboratory Medicine, West China Hospital, Sichuan University, Sichuan Province, P. R. China

This study was designed to investigate the relationship between Delta-like 1 homolog (DLK1) polymorphisms and the occurrence of antituberculosis drug-induced hepatotoxicity (ATDH) in the

Western Chinese Han population. A total of 746 tuberculosis patients including 118 ATDH cases and 628 non-ATDH cases were enrolled from West China Hospital of Sichuan University during 2016–2018. Ten single nucleotide polymorphisms (rs11160604, rs7149242, rs7141210, rs7155375, rs876374, rs57098752, rs2400940, rs12431758, rs4900472, and rs6575802) within DLK1 were studied by the improved multiplex ligation detection reaction method genotyping technology assay. It was found that G allele of rs11160604 was associated with an increased risk for ATDH (p = 0.001) and G allele of rs4900472 showed a protective effect for ATDH (p = 0.030). Recessive model and dominant model of rs11160604 were observed as a risk factor for ATDH predisposition, whereas the recessive model of rs4900472 was a protective one. Moreover, the interaction genetic model composed of rs11160604, rs57098752, and rs12431758 showed a combined effect for the occurrence of ATDH. Our finding was a novel one indicating that the G allele of DLK1 rs11160604 might serve as a hazard for the development of ATDH in the Western Chinese Han population.

PU-1031

血浆 SEPT9 基因甲基化联合血清 CEA 和 CA724 检测在结直肠癌诊断中的临床应用

高海锋
陕西省宝鸡市中心医院

目的 探讨血浆 SEPT9 基因甲基化联合血清 CEA 和 CA724 检测在结直肠癌诊断中的临床应用，为结直肠癌的诊断提供实验室依据。
方法 选取 2018 年 5 月至 2020 年 10 月云南省新昆华医院收治的 219 例结直肠病变患者为研究对象，后经病理确诊为结直肠癌患者 149 例，结直肠息肉患者 70 例，同时选择同期体检健康者 100 例作为对照组。采用实时荧光 PCR 测定 SEPT9 基因甲基化的情况，电化学发光法测定 CEA 和 CA724 的水平，并对结果进行统计学分析。
结果 CRC 组 SEPT9 基因甲基化阳性率显著高于结直肠息肉组和对照组（P＜0.05），结直肠息肉组 SEPT9 阳性率亦高于对照组（P＜0.05）；SEPT9 基因甲基化诊断 CRC 的敏感度为 90.3%，阳性预测值为 84.68%，ROC 曲线下面积为 0.823，均显著高于血清 CEA 和 CA724，但 CEA 诊断 CRC 的特异度和阴性预测值最高；三项指标联合检测的敏感度、阳性预测值和 ROC 曲线下面积较单项指标高（P＜0.05）。
结论 SEPT9 基因甲基化、CEA 和 CA724 检测 CRC 具有快速、准确、敏感度高、患者依存性好及适于普查等优点，三项联合检测可以做到优势互补，提高诊断效率，对于 CRC 的诊断具有高的临床诊断价值，并对结直肠良恶性疾病的鉴别具有一定的辅助诊断价值，值得在临床上推广。

PU-1032

P16 蛋白和 HPV 分型联合检测在宫颈上皮内瘤变诊断中的临床研究

高海锋
陕西省宝鸡市中心医院

目的 了解宝鸡地区女性 HPV 感染现状，探讨 P16 蛋白和 HPV 分型联合检测在宫颈上皮内瘤变（CIN）检测中的应用价值。
方法 选择 2019 年 2 月至 2020 年 2 月来宝鸡市中心医院妇科门诊就诊的患者共计 8346 例为研究对象，后经阴道镜活组织病理检查确诊存在 CIN 患者共计 5282 例。按照年龄段分组，对本地区各

年龄段 HPV 感染现状进行调查分析，再以活组织病理检查为金标准，按照病理分级结果，分别研究 P16、HPV 分型的检出率及其单项及联合检测对 CIN 的诊断效能，对结果进行统计学分析。

结果 以年龄为分组依据，对 P16 和 HPV 结果的人群进行分类，结果表明阳性率最高的年龄组为 31~40 岁，其次为 41~50 岁年龄组，各年龄组间感染阳性率比较差异具有统计学意义（P<0.05）。以 P16 检查为依据，筛查出阳性病例 2584 例，其中炎症 22 例、CINⅠ 1105 例、CINⅡ 761 例、CINⅢ 548 例和 SCC 147 例。以 HPV 为依据，筛查出阳性病例共计 2169 例，其中炎症 35 例、CINⅠ 904 例、CINⅡ 651 例、CINⅢ 447 例和 SCC 122 例。随着 CIN 的持续进展，逐渐以 HPV16/18 型感染为主，P16 检出率也逐渐增高。HPV 单项检测 CIN 的敏感度为 75.26%，特异度为 81.13%，阳性预测值为 67.78%，阴性预测值为 86.14%；P16 单项检测 CIN 的敏感度为 89.66%，特异度为 84.52%，阳性预测值为 75.34%，阴性预测值为 83.94%，显著高于 HPV 检测，差异均具有统计学意义（P<0.05）；二者联合检测的敏感度为 94.10%，特异度为 91.33%，阳性预测值为 85.12%，阴性预测值为 96.71%，显著高于 HPV 检测，差异均具有统计学意义（P<0.05）。

结论 宝鸡地区 HPV 感染以 31~40 岁年龄段为主，41~50 岁次之，且有年轻化感染的趋势。P16 阳性率及 HPV 型别与 CIN 严重程度相关。二者联合检测可提高检测的敏感度和特异度，减少漏诊率，对 CIN 的早期诊断和治疗有重要的临床价值。

PU-1033

Association Between Levels of Serum Vitamin D Components and the Risk of CKD in RA Patients: a Case-Control Study

Jie Tang[1,2]、Yuwei Yang[1]、Jiafu Feng[1]、Bei Xu[1]、Lin Yu[1]、Wenqiang Jiang[1]、Binwu Ying[2]
1. Mianyang Central Hospital, School of Medicine,University of Electronic Science and Technology of China
2. 四川大学华西医院

Objective Determination of 25-hydroxyvitamin D[25(OH)D] based on liquid chromatography-tandem mass spectrometry (LC-MS/MS) can accurately evaluate the vitamin D reserve in human body and simultaneously detect its components 25(OH)D2, 25(OH)D3 which helping guide the clinical selection of vitamin D supplements. The aim of this research is to explore the relation of 25(OH)D and its components [25(OH)D2, 25(OH)D3, and Free 25(OH)D] levels to the risk of concurrent chronic kidney disease (CKD) in patients with rheumatoid arthritis (RA).

Methods A total of 883 RA patients were enrolled based on inclusion and exclusion standard, and were classified into low risk , medium risk and high risk CKD group according to the CKD risk classification criteria recommended by the "Kidney Disease: Improving Global Outcome (KDIGO) 2012" guideline, which classing the CKD risk on the basis of glomerular filtration rate and albuminuria. The differences and change trends of vitamin D components measured by LC-MS/MS were compared and analyzed among different CKD risk groups. Then analyze the association between vitamin D components levels and the risk of CKD in RA patients after adjusting gender, age, inflammatory factors (hsCRP), and specific antibody (RF) titers.

Results 25(OH)D, 25(OH)D3, and Free 25(OH)D[F-25(OH)D] in the medium-risk group and high-risk group were lower than the low-risk group (Median=21.57 and 18.77 vs. 24.40 ng/ml), (Median=16.63 and 12.97 vs. 19.09 ng/ml) and (Median=5.96 and 4.89 vs. 6.30 pg/ml) (all P<0.05) respectively, while 25(OH)D2 levels showed no statistically significant in three groups (P=0.328). When the risk of CKD increased from low to medium, the degree of reduction in 25(OH)D, 25(OH)D3, and F-25(OH)D had statistically significant difference (all Padj. <0.05); but from medium to high risk, only the degree of reduction in 25(OH)D3 had statistically significant difference (Padj.=0.014). Multiple logistic regression analysis showed that 25(OH)D3 and F-25(OH)D were significant risk factors for CKD in RA patients (all P<0.01).

Conclusion Serum 25(OH)D3 and F-25(OH)D levels of RA patients should be routinely monitored to understand the risk of CKD progression and perform timely intervention.

PU-1034

检验科带教学生特点及教育管理方法

王裔雄、肖传宇、陶锋、谢强、邱枫
枣阳市第一人民医院

医院检验科作为各级、各类医学检验类学生毕业前实践演练及理论联系实际的培养基地，已成为检验相关医学院校培养合格检验人才的最重要一环。现如今，医院检验科每年都会安排各级各类高校检验专业学生进行毕业前的带教实习，针对其自身特点及毕业后的发展方向，科室应形成不同培养机制，让带教学生在自主理论学习和基础实践操作上都能有所收获，对学生因材施教，促进各类学生共同成长。

PU-1035

革兰阳性菌的耐药性

朱时帅
哈尔滨医科大学第一附属医院

目的 了解哈尔滨医科大学附属第一医院医院 2020 年常见革兰阳性菌的耐药情况及耐药迁徙率分析。
方法 收集哈尔滨医科大学附属第一医院消化科革兰氏阳性细菌 100 菌种鉴定的体外药物敏感性试验。
结果 100 株革兰氏阳性细菌中，金黄色葡萄球菌 134 株（30%），屎肠球菌 84 株（19%），表皮葡萄球菌 61 株（14%），粪肠球菌 45 株（10%），这四种主要细菌占所检出的革兰阳性菌的 73%。在细菌的科室分布中，医学重症科内科（15%）和泌尿科（13.5%）是检出革兰氏阳性细菌最多的科室，而标本来源可知尿液（31.2%）和痰液（18.5%）检出率最高的标本。检出的最主要的四种细菌中，金黄色葡萄球菌、表皮葡萄球菌、粪肠球菌和屎肠球菌对抗生素的耐药种类及相应的耐药率表现出不同的特点。检测的四种主要细菌中，有三种对青霉素有高度耐药性，分别是屎肠球菌（95.2%）、金黄色葡萄球菌（92.5%）和表皮葡萄球菌（90.2%），并且细菌对红霉素耐药性也较高，但耐药率不如青霉素，分别是金黄色葡萄球菌（64.9%）、表皮葡萄球菌（73.8%）粪肠球菌（71.1%）和屎肠球菌（85.7%）。粪肠球菌、金黄色葡萄球菌和表皮葡萄球菌对万古霉素，替考拉宁百分之百敏感。值得注意的是，屎肠球菌对万古霉素（94%）和替考拉宁（94%）敏感率较以前有所下降，疑似出现耐药菌株，需引起关注。金黄色葡萄球菌和表皮葡萄球菌对达福普汀百分之百敏感，屎肠球菌和粪肠球菌对替加环素百分之百敏感。
结论 四种细菌对青霉素类和大环内酯类抗生素的耐药性强，对多肽类抗生素敏感。应进行长期动态耐药性检测，为临床用药的合理化和个体化提供参考依据，避免药物滥用的等现象的出现。

PU-1036

校企合一创新“六融合”育人机制---以医学检验技术专业建设改革为例

叶耘峰
江苏护理职业学院

江苏护理职业学院积极构建职业教育创新体系，坚持战略导向，将办学体制机制改革与健康中国建设、卫生职业教育服务社会、行业发展有机融合，自 1990 年起，与企业共同组建集“卫生行业、医学检验产业、医学检验企事业、医学检验技术专业、学生就业、创业”六融合的产教集群---“医学检验职业教育与产业发展联盟”。以产业集群理论、共生理论为指导，构建具有理论创新和实践解释力的协同、合作、共生的“职业教育+产业+科技创新”的组织结构和理事会管理体制，科学合理确定校企合一发展战略的逻辑起点，坚持产业与专业无缝对接、协同发展、双向反哺，使医学检验技术专业厚植企业承担职业教育责任的社会环境，凸显专业根植于产业的先天优势，实现了课程内容与职业标准的有效对接、教学过程与生产过程的相互衔接、教学资源与企业实境的紧密链接、操作习得与职业特质养成的至深嵌接、人才规格与岗位执业要求的精确铆接，提高了卫生职业教育服务社会的贡献度、人才培养目标达成度、人才供给侧与产业人才需求侧吻合度、办学条件支撑度、教学质量保障有效度、用人单位满意度，提升了办学质效。

“六融合”使医学检验技术专业建设由学科导向转向产业导向、专业分割转向产业专业的交叉融合、人才供给的单一支撑服务转向办学体制改革的创新引领，丰富了专业生态，避免了专业设置同质化倾向，延展了卫生职业教育开放、跨界、无区域性优势，提升了职业教育对经济社会发展的贡献度、开放度和职业教育市场辨识度。

PU-1037

健康中国战略背景下医学检验技术专业人才培养

石玉荣、 李玉云、梅传忠、耿建、武文娟、周继红、黄桦
蚌埠医学院

目的 探讨 “健康中国”战略背景下，医学检验技术人才培养面临新的路径，提升医学检验技术人才培养质量。

方法 调研我校医学检验技术专业学生的专业认知和职业认同情况调研影响我校医学检验技术专业学生专业认知和职业认同的影响因素；着力贯彻本科生全程导师制；健全医学检验技术专业认知及认同教育；对医学检验技术专业学生进行人文素养教育，着力研究医学检验技术专业岗位胜任力培养路径。

结果 在对我校医学检验技术专业学生的问卷调查的结果显示，我校医学检验技术专业学生对所学专业有比较认同的仅占，就业前景、社会因素和个人兴趣是影响学生专业认知的前三位因素。全程导师制的实施注重对学生的全程培养，有助于提升学生职业认知和专业认同，牢固树立社会主义核心价值观，做好学业设计和人生规划，有利于学生专业学习和综合素质的提高。提升医学检验技术专业的社会影响力，有助于学生专业认同。 医学检验技术专业人才人文素养的提升可利于医学各界以及医学与其他专业之间的交流、联系与合作，对健康促进、理顺医患关系具有促进作用。培养学生的岗位胜任力，是提升人才培养质量的关键。批判性思维能力培养、学生专业素质专业技能培养和学生的职业精神的塑造有助于提升学生的人才培养质量。

结论 多渠道、多方位培养有助于提升医学检验技术专业人才培养质量。

PU-1038

坚持四个回归，实现三全育人，强化内涵建设，做好高水平医学检验本科教育

李玉云[1]、耿建[1]、张英杰[1]、曹蕴[1]、王珏[2]
1. 蚌埠医学院
2. 蚌埠医学院第一附属医院检验科

2018 年 6 月 21 日，教育部在四川成都召开新时代全国高等学校本科教育工作会议。会议强调，要坚持“以本为本”，推进“四个回归”，加快建设高水平本科教育、全面提高人才培养能力，造就堪当民族复兴大任的时代新人。 2018 年 10 月 8 日教高〔2018〕2 号“教育部关于加快建设高水平本科教育全面提高人才培养能力的意见”。

一是回归常识。要围绕学生刻苦读书来办教育，引导学生求真学问、练真本领。对大学生要合理“增负”，真正把内涵建设、质量提升体现在每一个学生的学习成果上。二是回归本分。要引导教师热爱教学、倾心教学、研究教学，潜心教书育人。三是回归初心。要坚持正确政治方向，促进专业知识教育与思想政治教育相结合，用知识体系教、价值体系育、创新体系做，倾心培养建设者和接班人。四是回归梦想。要推动办学理念创新、组织创新、管理创新和制度创新，倾力实现教育报国、教育强国梦。医学检验教育怎么做，我们从以下几个方面进行全员育人、全程育人、全方位育人，全面培养学生的技能、知识、价值观、自我定位、驱动力、人格特征、岗位胜任力，培养德智体美劳全面发展的社会主义建设者和接班人。

PU-1039

The relationship between atherosclerosis and bone mineral density in patients with type 2 diabetes depends on vascular calcifications and sex

Ni Zhong[2]、Ran Cui[1]、Hui Sheng[1]
1. 同济大学附属上海市第十人民医院内分泌科
2. 同济大学附属上海市东方医院检验科

It is unknown whether a relationship exists between bone mineral density (BMD) and atherosclerosis with or without vascular calcification. In our study, a negative correlation between carotid atherosclerosis and BMD was found in female T2DM patients with vascular calcification, but not in those without calcification and males.

Introduction: Atherosclerosis is considered associated with low bone mineral density (BMD). However, most previous studies focus on patients with arterial atherosclerosis with vascular calcification. It is still unknown whether a relationship exists between atherosclerosis and BMD in patients without calcification. It is also unknown if sex plays a role in this relationship.

Methods We performed a retrospective cross-sectional study, which included 1459 type 2 diabetes mellitus (T2DM) patients (648 males ≥ 50 years old, and 811 postmenopausal females). They were assigned to three groups: group 1 (patients without carotid plaques and without carotid calcification), group 2 (patients with carotid plaques but without carotid calcification), and group 3 (patients with carotid plaques and with carotid calcification). Clinical characteristics and BMD were compared. The relationship between atherosclerosis and BMD was determined by binary logistic regression analysis. Statistical analysis was performed using SPSS 25.0.

Results Significant differences were only observed in women. The percentage of osteoporosis was higher in group 3 (43.64%) than in groups 1 (34.82%) and 2 (32.14%) ($P = 0.016$). Low BMD was found in the lumbar ($P = 0.032$), hip ($P < 0.001$), and femoral neck ($P < 0.001$). The odds ratio for osteoporosis increased significantly in a score-dependent manner in postmenopausal

female patients with calcified atherosclerosis, but not in uncalcified patients. In men, no differences or relationships were identified.
Conclusion A negative correlation between carotid atherosclerosis and BMD was found in female T2DM patients with vascular calcification, but not in those without calcification. A similar relationship was not observed in male patients with or without calcification. Thus, the relationship between atherosclerosis and bone mineral density in patients with type 2 diabetes depends on vascular calcifications and sex.

PU-1040

医学检验专业实习生教学思考

徐会涛、周颖
连云港市第一人民医院

临床实习是学生走上工作岗位的过渡阶段，是培养专业人才的关键期。因此，实习教育显得尤为重要。如何实现学生专业能力的有效提升，达到优质的实习效果，需要多管齐下。其一，专责的实习管理者是不可或缺的。无规矩不成方圆，好的管理是见成效的重要保障。其二，优良且有责任心的师资是必不可少的，让更多高学历的青年教师积极地参与实习教学，能够对实习同学做出更加科学合理的引导，从而提高实习同学的专业能力和综合素养，教学相长。实习实践性特别强，因此我们要舍得放手，给学生更多的动手机会，要给他们更多的容错机会。多些鼓励，少些批评与斥责。其三，调动实习主体的积极性、主动性，发挥其主观能动性。了解更多的相关知识，并将理论知识付诸于实际操作中，在运用的过程中不断发现问题、解决问题，周而复始，不断地更新知识，提高自己。其四，制定详实的实习计划和规章制度，狠抓落实，做到理论和实践的统一。如何评价计划落实的好与坏，我们需要引入严格的评判机制，适当的奖惩制度。不仅考核学生，同时也对实习带教老师进行考核。其五，以人为本，安全教育，多元化的教育，不仅学习专业知识，也要学习人文、哲学等其他学科知识。促进学生身心健康，全面发展。总而言之，实习是一个系统化的工程，每个环节都需要配合好，落实好。学习是终身教育，需要不断的学习。

PU-1041

2 型糖尿病肾病和 ANA 阳性的 2 型糖尿病肾病与肝肾功能和补体关系的研究

丁世锐
襄阳市第一人民医院

目的 对 2 型糖尿病肾病和 ANA 阳性的 2 型糖尿病肾病患者的肝肾功能、血糖和补体 C3 和 C4 指标进行检查分析，为临床动态监测和预防糖尿病肾病的恶化提供有价值的参考。
方法 选择襄阳市第一人民医院肾病内科住院和门诊糖尿病患者 29 例，平均（49±10）岁；糖尿病肾病患者 142 例，平均（51±12）岁；健康人群 29 名，平均（46±15）岁。肝肾功能和补体由全自动生化分析仪 ARCHITCET C16000 检测。
结果 肝功能指标 ALT 和 AST 在健康组、2 型糖尿病组和 2 型糖尿病肾病组间的比较，差异无统计学意义（FALT = 1.61；FAST = 1.76，$p > 0.05$）；肾功能指标和血糖在健康组、2 型糖尿病组和 2 型糖尿病肾病组间比较，差异有统计学意义（FUrea = 26.44；FCr = 59.40；Fβ2-M = 51.20；FUA = 3.43，F 血糖 = 5.62，$p < 0.05$）；补体 C3 和 C4 在健康组、2 型糖尿病组和 2 型糖尿病肾病组间比较，差异具有统计学意义（F 补体 C3 = 3.14；F 补体 C4 = 3.20，$p < 0.05$）；肾功能指标 β2-M 在 ANA--T2DN-CKD4 期和 ANA+- T2DN-CKD4 期组间比较，差异有统计学意义（tβ2-M = 2.52，$p < 0.05$）；肾功能指标 Cr 和补体指标在 ANA--T2DN-CKD5 期和 ANA+-T2DN-CKD5

组间比较，差异有统计学意义（tCr = 2.74，t 补体 C3 =2.87；t 补体 C4 =3.63，p < 0.05）；肾功能指标和补体指标在 ANA+-T2DN-CKD3 组，ANA+-T2DN-CKD4 组和 ANA+-T2DN-CKD5 组间比较，差异有统计学意义（FUrea = 8.07，FCr = 25.78，Fβ2-M = 18.49，F 补体 C3 =8.06；F 补体 C4 =4.41，p < 0.05）。

结论 肾功能和补体水平和 DN 分期和抗核抗体具有一定关系，可作为 DN 患者，尤其 ANA 阳性的 DN 患者疾病进展的动态检测指标，可为临床治疗和预防疾病提供有价值理论依据。

PU-1042

异常早幼粒细胞与正常早幼粒细胞的鉴别诊断及一例报道

杨发林
山东大学齐鲁医院

前言：1 例女性脑胶质瘤患者术后服用替莫唑胺后继发了急性早幼粒细胞白血病。同第一代烷化剂相比，替莫唑胺的致白血病副作用明显较低，经国内外文献检索，本例治疗相关性急性早幼粒细胞白血病系首次报道。

病历描述：33 岁中国妇女经手术证实为左额叶脑胶质瘤，术后行同步放化疗，在完成替莫唑胺首次周期化疗时，外周血发现异常早幼粒细胞轻度增多，其特点是细胞形态不规则，核不规则，呈双叶核或蝴蝶核，染色质颗粒密集粗大，棒状小体多见，可与细胞集落刺激因子等因素导致的外周血正常形态早幼粒细胞轻度增多进行鉴别。本例化疗时间短，总剂量小，且病人异常血象发生在刚使用了细胞集落刺激因子之后，这在临床极为少见。

结论 近二十年来，通常认为替莫唑胺是治疗脑胶质瘤的安全而高效的化疗药物，但其致恶性血液病变的风险仍值得密切监测和预防，明确的鉴别诊断和危急值管理程序有助于及时与临床肿瘤医师沟通，病人可得到及时的救治，意义重大。

PU-1043

带有二维码信息的样本载玻片示教片在教学中的应用

张玲
阿克苏地区第一人民医院

背景 在临床或医学教学时，载玻片是医学实验中重要的材料。通常将包含细菌、真菌、细胞或组织切片等的样本放在载玻片上，然后将其放置在显微镜下对样本的病理、形态学进行观察与分析。而用于临床检验、病理病例资料及教学的示教载玻片保存时需要对其进行标记。由于载玻片的尺寸小，那么可用于标记的内容也就极其有限。目前载玻片上标记的信息一般包括样本编号或类别及名称，具体的病理及形态学还需要根据标签上的编号或类别、名称通过电脑或其他的途径另作查询。这给实验人员尤其医学教学人员造成了极大的不便。基于上述原因，对现有载玻片标记方式进行改进。提供一种带有样本信息二维码贴在载玻片上，只需通过扫描二维码即可调取储存在载玻片上的与样本有关的各种形式（文档、图谱、PPT 甚至视频）的信息。方便了病历资料整理及保存，也为教学人员的教学提供了便利。

方法 根据载玻片上样本包含的内容制作需要展示的文档、图谱、PPT 甚至视频；信息化解码；生成二维码；扫码提取信息。选取 2020 年我院检验科学员及新进员工 16 人随机分组，A 组 8 人采用传统培训模式，集中授课、现场演示练习等；B 组 8 人，在传统培训模式的基础上，加用二维码示教片进行自主学习。两组干预周期均为两个月，干预后比较两组人员学习的效果，指标包括形态学理论知识与实践操作考核、培训的满意度。

结果 传统培训的基础上，加用二维码示教片进行自主学习后理论考试(91.8±6.50 vs.83.2±5.1，P=0.003)、操作考试(90.3±5.80 vs.82.90±5.2，P=0.007)均高于 A 单纯的传统培训模式；并且培训的满意度也比单纯的传统培训模式高 (98.2±2.30 vs.93.40±5.3，P=0.02)，且差异具有统计学意义。
结论 带有二维码信息的教学载玻片示教片是将现代信息技术与临床技能教学结合，有效激发了学员、新进员工及工作人员的学习兴趣，可提高对形态学教学的培训效果。让现代化信息技术为临床技能教学添彩加翼。

PU-1044

红细胞冷凝集现象与肺炎支原体感染相关性的研究

李晓娟
新疆生产建设兵团第五师医院

目的 探究出现红细胞冷凝集现象后肺炎支原体感染阳性率。
方法 采用前瞻性研究，统计 2020 年 10 月 1 日至 2021 年 3 月 31 日在第五师医院就诊，使用帝迈 DH76 五分类血液细胞分析仪及血细胞涂片镜检确诊为红细胞冷凝集阳性的患者 30 例。患者平均年龄为（15±6.58）岁。与患者主管医生联系后，用无抗凝剂的真空采血管采集静脉血 4ml，用胶体金法检测患者肺炎支原体抗体。
结果 红细胞冷凝集阳性的患者 30 例中发现肺炎支原体抗体阳性者 21 例，阳性率为 70%。
结论 在红细胞冷凝集现象青年患者中出现肺炎支原体感染阳性率较高，为临床提供了一定的诊断意义。

PU-1045

虚拟仿真实验平台在细胞培养实验教学培养无菌观念中的尝试和探讨

张梦莹
江苏省人民医院（南京医科大学第一附属医院）

细胞培养技术现已广泛应用于生物学、医学各个领域，是细胞与组织研究的重要技术之一，防止污染是细胞培养成败的关键条件，但是传统的教学方式在该教学过程中体现出了一系列的弊端。虚拟仿真技术依托网络科技，通过虚拟的视听触觉和三维空间环境等方式提供形象生动的场景和良好的人机互动，更好地调动学生自主探索的学习热情和学习兴趣，并弥补了传统线下教学的不足。本文对于如何依托虚拟仿真技术在有限的实验教学课时内培养学生严格的无菌意识，使学生掌握无菌操作和细胞培养实验技能，启发学生科研思维进行了初步尝试和探索。

PU-1046

医学检验技术专业主干课程《临床检验仪器与技术》教学组织模式现状及展望

谢而付、王芳、黄蕾
江苏省人民医院（南京医科大学第一附属医院）

《临床检验仪器与技术》是医学检验技术专业的主干课程之一，该学科是基础医学、工程学与仪器学之间的一门交叉学科，也是检验医学其它主干课程的基础课程，在本科生专业能力的培养中

发挥重要作用。规划教材在授课的过程中起到重要作用，为了适应专业培养目标的变化，该课程的规划教材也经历了多次改版。因本学科实践性强，每个学校该专业的组织形式不同，教学组织模式也存在差异。本文列举了现有常见教学组织模式以及本校使用的教学组织模式，以供同行之间交流借鉴并调研，为提高该课程的教学效果提供理论依据。

PU-1047

医学检验教育整合多媒体信息化教学

姜贝贝
牟平区中医医院

随着我国信息技术的不断发展与进步，信息化教学在教育领域得到了广泛的应用，信息技术可以使教学手段呈现出多样化，在医学检验教学当中，可以通过信息化教学，利用模拟仿真软件、VR 演示系统等手段有效帮助学生理解医学知识，可见信息技术已经成为了目前教学当中必不可少的手段，为了更好地帮助学生完成理论与实践有效结合的教学目的，文章主要针对信息化教学在医学检验教学当中的应用策略展开探究。

PU-1048

浅谈医学检验实习带教的教学技巧与实践

冯倚帆、李世宝
徐州医科大学附属医院

临床实习是医学检验专业学生将理论转化成技能的重要阶段，而提高实习带教质量是当前检验医学专业的学生更好发展的必然要求。在实习带教过程中，坚持以学生为主体的教学理念，在教学内容的输出过程中综合优化理论与实践，促进思政、教学、科研的融合，培养学生的主动思考、联系临床病例的实践能力，通过一些有效的措施提高了实习带教的教学质量，收获了良好的教学效果。

PU-1049

临床分离大肠埃希菌与肺炎克雷伯菌的对比性分析

郑港森
厦门大学附属第一医院

目的 对比性分析临床分离大肠埃希菌和肺炎克雷伯菌之间差异性，包括敏感性、标本类型分离和科室分布情况等，及时充分了解当前这两种主要病原菌耐药情况。
方法 回顾性分析 2020 年临床分离大肠埃希菌和肺炎克雷伯菌，采用法国 BioMerieux VITEK2 Compact 全自动细菌鉴定及药敏分析系统对菌株进行细菌鉴定和药物敏感性检测，并用 Excel 软件进行数据分析。
结果 2020 年临床分离的大肠埃希菌 1614 株，肺炎克雷伯菌 579 株；两者尿液分离菌株最多，大肠埃希菌尿液分离占一半以上（947 株/1614 株)，而肺炎克雷伯菌不同标本分离相差不大；另外，呼吸道标本分离数量肺炎克雷伯菌远多于大肠埃希菌(108 株/37 株）；ICU 中两者分离菌株差不多，而其它科室分离相差较大；两者产 ESBLs 菌株，检出率有显著性差异（$P<0.05$)，ESBLs（-）菌株没有差异性（$P>0.1$)，非 ESBLs（无法确定 ESBLs（+）和 ESBLs（-））检出率有显著性差异（$P<0.05$)；大肠埃希菌对亚胺培南敏感率在 98.9%，而肺炎克雷伯菌只有 82.4%，尤其在 ICU 其敏感率更低至 59.5%，痰液分离肺炎克雷伯菌敏感率也只有 64.8%；大肠埃希菌对头孢噻肟和头孢他啶敏感率分别是 56.4%和 79.2%，而肺炎克雷伯菌对两者敏感率相差不明显（52.0%和 62.9%），

在 ICU 中，对两者敏感率耕地且基本一致（37.4%和 38.2%）；两者对三种酶抑制剂组合敏感性，哌拉西林/他唑巴坦最好（92.3%和 67.7%）；对左氧氟沙星的敏感性，肺炎克雷伯菌反而比大肠埃希菌好（64.9%/46.3%)，在门急诊分离菌株中，其敏感率达 80.7%；两者对阿米卡星敏感性是 96.5%和 83.2%，对氨曲南敏感率分别是 72.8%和 61.3%；另外，102 株耐亚胺培南肺炎克雷伯菌只有 4 株对氨曲南敏感，而 17 株耐亚胺培南大肠埃希菌对氨曲南敏感有 10 株。
结论 大肠埃希菌和肺炎克雷伯菌均出现对碳青霉烯类抗菌药物耐药菌株，尤其是肺炎克雷伯菌上升明显，而且两者产碳青霉烯酶的类型有所区别。肺炎克雷伯菌对大多数抗菌药物敏感性比大肠埃希菌较差，除了左氧氟沙星相对比较好；另外，ICU 耐药问题尤其严重，全血分离菌株敏感性较好，而痰液最差尤其是肺炎克雷伯菌更差。

PU-1050

一例伴有 MYC 和 BCL2 重排的高级别 B 淋巴瘤的诊疗经过经验分享

周宇[1]、曾彦[2]、王方[2]
1. 四川金域医学检验中心有限公司
2. 成都市第二人民医院

目的 探讨一例伴有 MYC 和 BCL2 重排的高级别 B 淋巴瘤的实验室检查及治疗。
方法 对一例伴有 MYC 和 BCL2 重排的高级别 B 淋巴瘤的临床资料、MICM 检查结果分析诊断，对应治疗和疗效评估。
结果 骨髓细胞形态学分析提示淋巴细胞异常增生，原始及幼稚淋巴细胞占 67.5%，疑为淋巴瘤细胞白血病。骨髓流式检测到 90.63%单克隆 B 淋巴细胞，符合 CD5 阴性 CD10 阳性成熟 B 细胞淋巴瘤/白血病免疫表型。细胞遗传学检测到 BCL2 和 MYC 基因分离重排，未检到 BCL6 基因分离重排。分子生物学检测到具有临床意义的 3 个基因突变：EZH2 基因、KMT2D 基因和 MYC 基因。结合临床表现及 MICM 相关检查结果，综合诊断为伴有 MYC 和 BCL2 重排的高级别 B 淋巴瘤（IV期，高中危）。给予患者 R+Hyper-CVAD 方案、REDCH 方案、R-DHAP 方案化疗后评估治疗有效，疾病缓解。继而行自体周血干细胞移植和 CAR-T 治疗，患者获得较好疗效。
结论 临床表现、形态学、免疫表型、细胞遗传学、分子生物学及相关实验室检查有助于高级别 B 淋巴瘤的诊断。经过几期对症化疗方案调整，获得缓解，进而行自体周血干细胞移植和 CAR-T 治疗，患者获得较好疗效。

PU-1051

超敏 C 反应蛋白和纤维蛋白原对缺血性脑卒中的临床应用价值

叶涛、李琴
重庆市人民医院

目的 探讨缺血性脑卒中患者血超敏 C 反应蛋白（hs-CRP）和纤维蛋白原（Fib）的临床应用价值。
方法 选择 2020 年 6 月-2021 年 5 月我院 27 例缺血性脑卒中患者作为研究组，及同期于我院进行体检的健康人群 54 例作为对照组， 检测和比较两组静脉血中 hs-CRP 和 Fib 水平的差异，并进行统计分析。
结果 缺血性脑卒中患者的超敏 hs-CRP 和 Fib 与健康对照组比较，差异有统计学意义。
结论 缺血性脑卒中患者静脉血中超敏 C-反应蛋白和纤维蛋白原会明显上升，具有一定的临床价值。

PU-1052

高质量检验医学高等教育体系的思考与实践

李博
南方医科大学南方医院

构建高质量检验医学高等教育体系，培养高质量的检验医学人才，是新时代医药卫生事业发展的迫切需求。南方医科大学医学检验技术专业在建设国家一流专业过程中秉持高质量高等教育理念，通过构建全程式德育体系、多模态培养模式、国际化师资队伍、智能化教学技术的教学改革实践，提高检验医学人才培养水平。本文对高质量检验医学高等教育体系的内涵进行深入分析，并对建设经验进行总结，以期在增加院校间交流与沟通的同时，为 2035 年建成教育强国的国家战略目标做出本专业应有的贡献。

PU-1053

医学检验教育的现状及未来发展

庄明慧
武城县人民医院

目的 为了培养更多更优秀的动手能力强的医学检验技术型人才，许多高等医学院对本科医学检验教育进行了改革。
方法 为了更好的适应现代检验医学快速发展的要求及对新型实用型医学检验人才的需求。自 2018 年起，由原来的五年制医学检验改为四年制医学检验技术。授予理学学位。
结果 改变了原来基础与临床明显分离加之知识结构偏重检验而缺乏足够的临床医学知识等问题，集中力量加强对学生技术，操作和动手能力的培养，以更好的适应社会对技术型人才的需求。弊端是 2018 年以前入学的五年制医学检验是可以考执业医师的，但四年制不可以，这就意味着四年制本科毕业生不能考执业医师，也就不能考检验医师。五年制医学检验授予医学学位，而四年制医学检验技术则只授予理学学位。
结论 大胆改革创新，小心探索求证。
自医学检验专业“五改四”以来，尝试了一系列改革措施，事实证明，取得了较为理想的效果。四年制检验技师培养内容的重点之一是将理论与实践有机结合。这不仅使学生对所学的知识通过见习有更深入的理解，而且有利于他们更快的熟悉实验室的工作性质和岗位要求。
中国检验医学的未来将会是实验室自动信息化系统和实验室信息化系统的进一步完善，绝大部分常规操作都将会被机器取代。人员分工也将向细分化方向发展，独立实验室也将成为重要的发展方向。社会也将需要更多的技术型人才。

PU-1054

PDCA 循环法在提高血培养标本质量中的应用

何天娇
西安医学院第一附属医院

目的 血培养是采集患者血液标本并接种到培养瓶中,用以发现、识别引起菌血症或真菌血症。血培养是诊断血流感染的重要手段之一。资料显示,血流感染是临床上严重危及患者生命的感染性疾病,病情进展迅速,病死率高如何在提高血培养的阳性率时同时规范些培养的送检,血培养标本采集的质量控制至关重。为进一步改善患者血培养标本的送检质量,为临床提供快速准确的检测结果,我科再用 PDCA 循环管理法探讨 PDCA 循环管理法对提高住院患者血培养标本送检质量的应用效果。

方法 在发现问题阶段调查 2019 年 1—12 月(PDCA 实施前)住院患者血培养标本送检情况,统计血培养的送检结构，阳性率及分析不合格原因。于是成立了 CQI 小组（持续质量改进理论），运用头脑风暴，运用鱼骨图和柏拉图针对问题和原因，运用甘特图对 2020 年 1—12 月(PDCA 实施后)进行任务分解，在实施阶段运用更换仪器和血培养瓶，加强临床培训以及实验室内部整改的实施，运用 PDCA 循环法进行管理,比较 PDCA 循环实施前后血培养送检套数、阳性率以及不规范标本送检情况等各项评价指标。

结果 在检查阶段，实施 PDCA 循环后,血培养标本双套送检率从 31.7%上升至 68.4%,单套送检率从 68.3 下降至 31.6%,血培养标本阳性率从 8.62 上升至至 10.24%,血培养标本不规范情况在实施前和实施后发生明显改变，差异均有统计学意义(P<0.05)在处理阶段对取得的成绩形成常态化的严格监管，对出现的问题提出进一步的整改方案。

结论 应用 PDCA 循环管理法对血培养标本送检进行质量控制,可以有效提高血培养标本送检质量,为临床提供准确可靠的检验结果。

PU-1055

一例 Rh 血型结果与历史不符的病例分析

周祺淇
南方医科大学珠江医院

患者女性，年龄 21 岁，为血液内科病区病人，临床诊断为急性淋巴细胞白血病。于 10 月某天早晨送来一份血型标本做检测，经过常规操作流程离心上机检测，第一次检测结果为：正定型 Anti-A 柱 4+，Anti-B 柱阴性；Anti-D 柱报 MF 警；Ctrl 阴性；反定型 A1-Cells 柱阴性，B-Cells 柱 4+。点开仪器的标本血型卡快照，显示 Anti-D 柱中有两群细胞，离心后沉下去的细胞数量较少。查看病人送检血型的结果历史，发现病人最近一次检测为同年 3 月份，Rh 血型结果为阴性。此时出现了 Rh 血型结果与历史不符的情况，在等待与联系临床医生的时间里，与同事几番讨论，提出输血、移植等几种可能性。后经与医生沟通了解到，该病人早前往当地血站送过血型鉴定，结果为 Rh 阳性（DEL 阳性），谜底逐渐揭开。

PU-1056

检验技术创新应用型人才培养思路的探讨

宋志纯
丽水市人民医院

为响应国务院实施健康中国的战略新任务，提升检验专业本科教育阶段及初入职人员医学检验技术水平，使之能更好的适应未来的检验工作，本文初步提出了各类医学院校医学检验专业创新应用型人才培养的方向及思考，初步提出了大学附属医院在开展临床、科研，实践教学等方面培养高层次创新应用型人才的几点建议。

PU-1057

浅谈临床医学检验技术的提升

周美玲
东南大学医学院

目的 随着科技的飞速发展，医学技术水平的不断提升，医学检验作为临床医生诊疗的重要信息来源，检验技术逐步要求自动化、智能化。同时，检验科室对检验人员的要求也越来越严苛。本文旨在探讨在我国现有医疗水平下，该如何提升临床检验医学技术。
方法 本文从临床检验技术的现状及发展方向入手，查阅专业期刊文献，考察了我国近年来高等医学院校对临床检验医学生的教育理念的改革、授课模式的创新，临床医学检验科室的管理改革及医疗检验仪器设备研发与生产状况，并对其进行归纳总结。
结果 通过查阅文献，发现临床检验医学技术的提升的根本在于高校对优秀人才的培养。医学院校应改变对临床检验医学生的教育理念，从传统“灌输式”授课方式教学转变为多元化授课方式，重视实践教学；师生相互考核评价，相互学习进步；另外，医院应加强实验室日常管理及检验人员安全知识意识、质控意识，重视对检验人员的考核。此外，政府应战略性成立区域检验中心，为乡镇、社区级别小医院提供医学检验服务，弥补因资金、设备、人员不足所致的医疗限制，应激励医疗检验仪器设备厂商研发生产先进仪器，不断提高仪器检验结果的高效与准确性，为临床医师提供可靠的诊疗依据。
讨论 与世界先进国家相比，我国的医疗卫生事业还有很大不足，医学检验作为其中独立的一门学科，还具有相当大的发展空间。而检验技术发展的根本，是要从检验人员的基本素质抓起。我国医学院校正在积极借鉴世界优秀的教育、管理理念，总结、创新、发展一套适合我国国情的临床检验技术教育及管理系统，培养出基本理论扎实、实际操作能力强、具有创新思维、人文意识强的优秀医学检验人才，使他们能够参与临床治疗讨论，助力临床医师的诊疗工作，成为我国医学事业的新鲜血液。

PU-1058

抗 CD38 干扰相容性检测

侯希亮
东南大学附属中大医院

抗 CD38（达雷妥尤）是近年来治疗多发性骨髓瘤的一个靶向药，2015 年获 FDA 批准，2019 年才在中国上市，我们医院血液科现在也在使用。抗 CD38 可结合高表达 CD38 抗原的骨髓瘤细胞，然后通过多种机制杀死瘤细胞。但红细胞上也少量表达 CD38 抗原，所以使用抗 CD38 会对我们输血相容性检测带来一些干扰。

PU-1059

COVID-19 疫情期间相关国际组织对血制品供应安全的建议

侯希亮
东南大学附属中大医院

新型冠状病毒疫情给全球的血液采集和血制品管理等工作带来的严峻挑战。对此，近期世界卫生组织（WHO）等相关机构陆续发布或更新了关于新冠疫情期间血液采集和血制品输注的建议，以帮助采供血机构采取有效措施落实血制品安全、充足供应保障工作。

PU-1060

医学检验学生生物安全防护知识调查及教育效果研究

苏云福、李文静
和田地区人民医院

目的 分析医学检验学生生物安全防护知识调查及教育效果。
方法 研究共抽取 161 名学生，来源时间 2020 年，上学期末针对 161 名实习生全部开展生物安全防护教育，下学期开展生物安全防护教育，对上下学期末 161 名实习生生物安全防护情况以及生物安全防护知识认知状况通过问卷调查方式进行分析。
结果 干预后 161 名实习生生物安全防护认知情况高于干预前，干预后 161 名实习生物安全防护情况高于干预前（P＜0.05）。
结论 将生物安全防护教育应用在医学检验科实习生中至关重要，能够显著增强学生生物安全防护及相关知识认知程度，值得临床广泛推行。

PU-1061

“翻转课堂”教学模式在 MBBS《实验诊断学》教学中的实践分析

黄松苓、赵滢
昆明医科大学第一附属医院

目的 探讨“翻转课堂”教学模式在 MBBS《实验诊断学》教学中的应用效果。
方法 选取昆明医科大学 2015 级临床专业 MBBS 留学生为实验研究对象,分为实验组和对照组。在进行《实验诊断学》教学时,对照组采用课堂讲授法教学,实验组授课时充分使用 MBBS 教学模式,以期末考试成绩和教学满意度,比较两种教学模式的教学效果。
结果 完成《实验诊断学》教学工作后,实验组学生期末考试成绩明显高于对照组,差异有统计学意义(P<0.05)。实验组学生对教学方法与教学效果的评价明显高于对照组,差异有统计学意义(P<0.05)。
结论 “翻转课堂”教学方法应用于 MBBS《实验诊断学》课程教学，可调动学生的学习积极性并且显著提升学生学习效果,值得在 MBBS《实验诊断学》教学中加以推广。

PU-1062

浅谈检验医师教育

王新慧
山东大学第二医院

检验工作不只是简单地接收标本发出报告这么简单，随着检测技术的不断提高，检测项目不断出现，现代医学检验实验室不再是单纯的化验室，而是与临床科室一样，是集教学培训、医疗服务和科学研究于一体的综合科室。长期以来，大多数医院都是由检验技师承担实验室检测和临床沟通，但是在相关疾病的诊断、鉴别诊断等方面缺乏临床医学知识。因此，推行检验医师规范化培训势在必行。检验医师不仅要具备检验基础知识还需要扎实的临床知识，同时具备执业医师和检验技师双重资格，才能够胜任标本检测、质控分析、临床沟通和解释等工作，2003 年中国医师协会检验医师分会在北京成立，但是经过十几年的发展，检验医师仍然是个“新鲜名词”，认知度和接受度都非常低，这与检验医师制度不成熟密不可分。政府主管部门也出台了相关的制度和办法。一、通过招收临床医学专业-医学检验方向学位连读生培养检验医师，在欧美发达国家, 检验医师并不是一个新的职 业名称。在英国、美国称其为“laboratory physician”,在完成临床医学 5 年教育之后，进行检验学相关知识学习，并进入到生化科、免疫科、血液科进行轮转后，撰写毕业论文通过答辩后方可毕

业。这样的方式是可行的，但是由于有些学校对此专业的重要性和特点宣传得不够，很多学生对“检验医师”这一职业不够了解，导致这方面报考的考生比较少。二、建议完善的专科医师培训与培养制度。作为专业培养，应采取完整性、连贯性的教育模式，分别指定技师、主管技师及研究学者不同层次的老师分别负责不同层次的教学，同时定期举办小范围的学术交流会，提高学习的兴趣。

PU-1063

地市级区域医学检验中心的功能定位

张晓梦
潍坊医学院附属医院

为深化医药卫生体制改革，充分发挥医学检验中心人才、技术、设备和管理优势，有效整合检验资源和人才队伍，现阶段各地区都主张建立区域医学检验中心独立实验室。充分利用这一服务平台，努力开展检测项目满足临床需要，力争做到项目全覆盖，同时深入开展技术合作，带动各医院实验室提高检测能力，做大做强医学检验行业，为医学的发展提供技术支撑。

PU-1064

CBL、PBL 教学法结合在线课程在实验诊断学教学中的探讨

陈蓉艳
福建中医药大学附属人民医院

为适应“疫情”特殊时期的线上教学模式，提升学生自主学习的能力，将 CBL、PBL 教学法引入到福建中医药大学《实验诊断学》线上教学课程中。本文就 CBL、PBL 教学法的具体实施、教学效果评价、教学经验总结及应用中存在的难点，探讨 CBL、PBL 教学法结合在线课程在实验诊断学教学中的可行性。

PU-1065

检验教育中生物安全防护教育的探究

白兰
成都市双流区第一人民医院

目的 当代生物安全教育极为重要，尤其是在时时刻刻接触具有潜在生物危险标本的检验专业，生物安全教育的作用就更加突出。加强检验教育中的生物安全防护教育有利于完善检验学教育，更好地促进公共生物安全管理，同时有效防范生物危害，促进社会安全的稳定，在一定程度上能防止实验意外发生，有效降低医者在职业生涯中暴露的风险。
方法 对某大学医学检验专业大四学生进行调研，随机选取该校大四医学检验专业学生 100 人，随机分为两组，一组称为实验组，一组称为对照组，每组 50 人。对两组进行同一问卷调查，根据其对生物安全知识的了解程度从高到低分为 A、B、C、D 四等。初步了解之后，再对实验组 50 名大学生进行为期 5 天的生物安全知识的培训及实验训练，其后对两组同时进行相同的生物安全知识的考核，根据其对生物安全知识的了解程度同样分为 A、B、C、D 四等，记录结果。
结果 结果显示在进行系统的培训和实践教育之前，实验组 A 等学生有 14 人，B 等 16 人，C 等 15 人，D 等 5 人；对照组 A 等 12 人，B 等 14 人，C 等 17 人，D 等 7 人；在进行生物安全教育培训和实践教育之后，实验组 A 等级 32 人，B 等 16 人，C 等 2 人，D 等 0 人；对照组 A 等 12 人，B 等 16 人，C 等 17 人，D 等 5 人。

结论 根据实践结果，可见生物安全防护教育的重要性与有效性。首先应加强检验医学背景下的生物安全理论体系建设，只有对于生物安全理论研究的完善和进步，才能更好地指导现代化的、甚至是超前时代的生物安全防护，才能指导更系统、更完善、更有效的在检验实践中的生物安全防护教育。其次，加强检验学教育中的生物安全防护教育必须有坚实的医学理论、检验学理论和生物安全理论知识，故加强基础知识的教育也是生物安全防护教育不可或缺的一部分。加强检验的实践培训和生物安全的岗前培训同样能够加强生物安全防护教育，丰富的理论知识只有运用到实践中才能收到成效，故模拟生物安全的实验课程开设和进入工作前的生物安全防护教育实践也就显得尤为必要。最后，从宏观上看，需要加强对于生物安全防护的管理，制定行之有效的政策、规范，从政策的层面发展检验教育中的生物安全防护教育。

PU-1066

对于检验教育中生物安全防护教育的探究

白兰
成都市双流区第一人民医院

目的 当代生物安全教育极为重要，尤其是在时时刻刻接触具有潜在生物危险标本的检验专业，生物安全教育的作用就更加突出。加强检验教育中的生物安全防护教育有利于完善检验学教育，更好地促进公共生物安全管理，同时有效防范生物危害，促进社会安全的稳定，在一定程度上不仅能防止实验意外发生，有效降低医者在职业生涯中暴露的风险。
方法 对某大学医学检验专业大四学生进行调研，随机选取该校大四医学检验专业学生 100 例，随机分为两组，一组称为实验组，一组称为对照组，每组 50 人。对两组进行同一问卷调查，根据其对生物安全知识的了解程度从高到低分为 A、B、C、D 四等。初步了解之后，再对实验组 50 名大学生进行为期 5 天的生物安全知识的培训及实验训练，其后对两组同时进行相同的生物安全知识的考核，根据其对生物安全知识的了解程度同样分为 A、B、C、D 四等，记录结果。
结果 结果显示在进行系统的培训和实践教育之前，实验组 A 等学生有 14 人，B 等 16 人，C 等 15 人，D 等 5 人；对照组 A 等 12 人，B 等 14 人，C 等 17 人，D 等 7 人；在进行生物安全教育培训和实践教育之后，实验组 A 等级 32 人，B 等 16 人，C 等 2 人，D 等 0 人；对照组 A 等 12 人，B 等 16 人，C 等 17 人，D 等 5 人。
结论 根据实践结果，可见对于生物安全防护教育的重要性与有效性。首先应加强检验医学背景下的生物安全理论体系建设，只有对于生物安全理论研究的完善和进步，才能更好地指导现代化的、甚至是超前时代的生物安全防护，才能指导更系统、更完善、更有效的在检验实践中的生物安全防护教育。其次，加强检验学教育中的生物安全防护教育必须有坚实的医学理论、检验学理论和生物安全理论知识，故加强基础知识的教育也是生物安全防护教育不可或缺的一部分。加强检验的实践培训和生物安全的岗前培训同样能够加强生物安全防护教育，丰富的理论知识只有运用到实践中才能收到成效，故模拟生物安全的实验课程开设和进入工作前的生物安全防护教育实践也就显得尤为必要。最后，从宏观上看，需要加强对于生物安全防护的管理，制定行之有效的政策、规范，从政策的层面发展检验教育中的生物安全防护教育。

PU-1067

浅谈网络教育在医学检验继续教育中的优势作用

赵雪粉、杨勇、张宏磊
甘肃金域医学检验所有限公司

随着经济的发展，当今的医学也在快速发展，传统的继续教育模式已不满足知识和科技日新月异，网络教育在医学检验继续教育的中发挥至关重要的作用，随着信息技术的逐渐发展，以网络为

渠道的医学教育模式可以比传统的教育模式获得更多的信息，时间及地点等具有更大的灵活性、内容更具有开放性，从而促进检验人员继续教育的公平性及可及性。网络教育在医学检验继续教育中发挥着种种优势：良好的资源共享、节约成本、扩展学习平台，增强临床知识学习、打破空间交流上的界限、学习行为自主化。网络教育的形式能够弥补传统继续教育模式中的不足之处，通过快速检索信息资源，掌握最新的检验技术及临床知识; 丰富继续教育形式，真正实现个性化教育教学以及拓展交流互动平台; 共享与传播临床工作经验等方式，构建灵活、开放以及互动的继续教育模式，创设一个良好的继续教育平台。

PU-1068

骨髓细胞形态学临床实践教学经验分享

张凤
福建医科大学附属协和医院

目的及方法 血液细胞形态是本科检验及检验实习的重点学科，是优秀检验医师成长的必经之路，也是许多检验工作者进修的常选科室之一。骨髓细胞形态室工作性质要求工作者无论是技师还是医师均需具备检验医师的临床思维，优秀的骨髓细胞形态室从业人员应具备较高的人文修养,善于处理检验科室与临床科室关系;能了解血液科、风湿科、感染科疾病的相关基础知识熟练掌握骨髓涂片、染色的基本操作,能够准确出具血液科常见病及多发病的骨髓象报告;具有良好的逻辑思维与发散思维,将理论知识与临床实践相结合。故本文以临床医师从事骨髓细胞形态检验工作带教的经历对骨髓血液细胞形态室实习生、规培医师及进修医师的重要性、人文修养、阅片能力、临床思维的培养和考核等方面进行总结反思。
结论 骨髓细胞形态学教学是检验医学实习、进修、住院医师规范化培训带教中的重点及难点，在教学中注重动手操作，利用多媒体资源及现代通讯网络学习平台，提升学生阅片能力和临床思维，注重人文修养，培养出符合当前教学及医疗环境要求的骨髓细胞形态室检验员。

PU-1069

基于病例对照研究的血脂与乳腺癌关系的 Meta 分析

何建伟[1]、曹薇薇[2]、于子恒[1]
1. 石河子大学医学院第一附属医院
2. 石河子大学医学院

目的 乳腺癌已经成为我国女性发病的首位恶性肿瘤。国内外的研究均表明：女性的血脂水平与乳腺癌的发生和进展以及预后显著相关。但是国内外学者对血脂与乳腺癌的关系持有不同的，甚至是相悖的观点。该研究通过用 Meta 分析对近些年来乳腺癌血脂相关因素研究文献进行综合定量分析，探讨总胆固醇、甘油三酯、高密度脂蛋白、低密度脂蛋白与乳腺癌发病之间的关系
方法 计算机检索整理大量乳腺癌与血脂研究的相关文献，文献检索范围为 2020 年 10 月前发表的相关文献。根据文献纳入与排除标准并采用参照纽卡斯尔渥太华量表（newcastle-ottawascale, NOS）设立质量评价体系，采用 Stata 15.0 软件进行 Meta 分析。
结果 该研究共纳入 9 篇文献，不同研究中研究对象最少 114 人，最多 1261 人。最终 8 个研究汇总 TC 的 SMD 为 0.223，95%置信区间为 0.153-0.293，且具有统计学意义，Z=2.37,P<0.05；6 个研究汇总 TG 的 SMD 为 0.078，95%置信区间为 0.014-0.143，且具有统计学意义，Z=6.25,P=0.018<0.05；7 个研究汇总 LDL-C 的 SMD 为 0.271，95%置信区间为 0.199-0.344，且具有统计学意义，Z=7.32,P=0.00<0.05；5 个研究汇总 HDL-C 的 SMD 为-0.018，95%置信区间为-0.086-0.051，无统计学意义，Z=0.51,P=0.609>0.05。 **结论** 高总胆固醇（TC）、甘油三脂（TG）、低密度脂蛋白胆固醇（LDL-C）是乳腺癌发生的危险因素，而高密度脂蛋白胆固醇

（HDL-C）不是乳腺癌发生的危险因素。然而，因为受纳入研究数量及研究质量的限制，上述结论仍需更高质量及更大样本的试验研究进一步验证。

PU-1070

中西医结合与检验医学

卢晴晴、谢小兵
湖南中医药大学第一附属医院

中医是我国人民不断实践与积累的产物，是中国传统文化的重要组成部分，然而近代以来受到西方思想的冲击，中医不被大众信任，直到新中国成立后才重新登上医学舞台。中西医结合是中医现代化的必经之路，结合不是简单的相加或配合，而检验医学则是两者之间沟通与结合的重要桥梁，帮助从西医的角度解释中医所认为的外邪和七情致病。中医药利用现代细胞生物学、分子生物学等现代技术，在许多中医领域都取得了重大突破，然而中西医结合医院还存在认识不清、人才缺乏、比例不协调等问题，中西医结合检验专业的同学中医理论知识匮乏、临床工作经验缺乏、西医理论知识也不够扎实，因此需要不断学习，并对未来努力的方向进行规划。

PU-1071

自然辩证法维度下的医学实践思考

卢晴晴、谢小兵
湖南中医药大学第一附属医院

自然辩证法思想是唯物辩证法理论的重要组成部分，它有着深厚的理论基础与渊源，系统地阐述了自然科学的产生、发展、壮大，这一理论实现了唯物辩证的自然观的突破，对当代社会的发展具有重要借鉴意义，对于指导具体科学的进步也有具有重要意义。自然辩证法维度下，作为医学生应该用联系的观点和综合思维看问题、具体问题具体分析，用自然辩证法指导医学实践过程。本文从自然观演变的轨迹及其当代价值与意义出发，探讨自然辩证法在世界观与方法论方面为医学的发展提供的指导，以期促进医学的良性运行与协调发展。

PU-1072

EGFR 抑制剂治疗非小细胞肺癌研究新进展

刘博
天津医科大学朱宪彝纪念医院

非小细胞肺癌（NSCLC），占肺癌总数的 80%，是最为常见的肺癌。表皮生长因子受体（EGFR）抑制剂在 NSCLC 的治疗中具有极大潜力。然而随着时间的推移，EGFR 抑制剂靶向治疗出现了耐药现象。本文将选取各代中的典型药物，通过对其作用机制. 药理作用. 临床疗效. 耐药性及不良反应出发，综述其研究进展。

PU-1073

临床分子生物学检验教学模式反思与探索

林艳凤、林东红、林梨平、吴娟、薛龑、林旎
福建医科大学

当前，临床医学已经进入了以分子诊断为代表之一的精准医学时代，提高医学生临床分子生物学检验及其相关技术的理论功底、实践技能，积极提升教学质量，将有助于医学创新型高层次人才培养。本文基于目前的课程教学模式和培养现状，针对性地提出了优化课程体系、多渠道强化实践能力、增设多元化考核指标等解决方法和举措，以期为该课程教学模式改革提供借鉴。

PU-1074

临床检验教学实习中 PBL 教学模式初步探讨

杨亚平
陆军军医大学第一附属医院（西南医院）

目的 为了解决国内医学检验专业本科的专业实习教学安时间短、学生的临床知识比较有限，对现代临床检验和疾病的关系掌握不扎实等问题，特对近三届来我院实习带教的本科生进行了问题导向学习法(problem-based learning PBL 教学法)的应用探讨，以期培养学生主动学习和思考能力。
方法 在临床检验教学实习中，以临床检验学为实验模块，进行 PBL 教学法和传统教学法对比研究，考核评价教学效果，通过调查问卷评价学生的学习态度和满意度。
结果 PBL 教学组的专业测试平均成绩明显高于传统教学组($P<0.05$)，三年学生教学满意度为 91.8%，较之前有显著提高。
结论 PBL 教学法能较为显著地提高临床检验实习教学效果，从教学体验的实际参与中促进教学质量提高。

PU-1075

心跳骤停外周血骨髓小粒 1 例报道

金晓娟
联勤保障部队第九〇三医院

目的 心跳骤停外周血骨髓小粒 1 例报道。
方法 对患者血液标本进行临床血液检查。
结果 外周血出现骨髓小粒和巨核细胞。
结论 当机体无生命体征后，各屏障功能随之紊乱，各类造血细胞逐步移向髓窦，基膜退变，穿过内皮细胞，进入外周血循环中，故该患者外周血中可见原始幼稚细胞、巨核细胞、骨髓小粒、有核红细胞。

PU-1076

香兰素抗氧化作用机制研究进展

孔蓓蓓
联勤保障部队第九〇三医院

目的 氧化应激和 ROS 的生成经证明与肿瘤进展有关。香兰素作为一种重要的香料和芳香成分，常用于加工食品。其具有抗氧化性和抗肿瘤潜力。现对香兰素在氧化还原状态中的作用及抗癌作用进行探讨。
结论 本文揭示了香兰素的抗氧化活性，抗癌作用以及在肿瘤治疗和预防中的潜力。因此食用富含香兰素的蔬菜水果可能会抑制促进肿瘤发展的自由基。本综述所展示数据也符合“通过健康食品以及天然生物活性产品的有益作用可以提高生活质量、延长寿命”这一理念。

PU-1077

医学模拟教学联合 PBL 教学方法在医学检验实习生带教中的应用

刘丽莎、李松涛、高岭
南京市儿童医院（南京医科大学附属儿童医院）

目的 研究医学模拟教学（simulation based medical education, SBME）联合问题为基础的教学法（problem-based learning，PBL）在医学检验实习生带教中的应用效果，以期寻求新的实习生带教模式。
方法 以在本院检验科实习的学生群体为分析对象，随机抽取 40 名同学分别设为对照组和实验组，对照组同学采用传统实习带教方式，实验组同学采用 SBME+PBL 的带教方式，分别对两组同学进行理论知识、技能操作和应变能力考核并收集两组同学教学满意度调查表。
结果 实验组同学各项考核指标均高于对照组同学，且实验组同学对教学质量认同度高于对照组同学（$P<0.05$）。
结论 采取 SBME 联合 PBL 的教学方法可以提高医学检验专业实习生的学习效率和学习质量，是一项优于传统带教模式的教学方法。

PU-1078

科研成果融入临床检验实习教学的探索与实践

廖林、向立群、林发全
广西医科大学第一附属医院

临床实习是医学检验教育的重要环节，激发学生学习热情和科研兴趣、培养学生临床思维与科研能力是临床检验实习教学的基本任务。本文阐明了将科研成果融入临床检验实习教学的必要性，通过血细胞分析的科研成果融入实习教学实践，取得了较好的教学效果。

PU-1079

异基因造血干细胞移植研究现状

吕长坤、马菲菲、万雪莲、张卫斌、杨颖、周健
商丘医学高等专科学校

目的 造血干细胞移植可重建患者的造血系统和免疫功能，从而达到治疗某些重大的疾病的功能，详解异基因造血干细胞移植研究现状。
方法 本文总结异基因骨髓造血干细胞捐献的发展历程，分析了造血干细胞移植的现状，移植流程，临床应用，以及未来前景。
结果 我们认为异基因造血干细胞捐献需要更细致和精准的标准化操作流程，熟练的操作技术人员，优化检索和便捷供受者干细胞程序。
结论 希望通过异基因造血干细胞捐献知识的普及，让更多加入成为中华骨髓库志愿者，进一步推进造血干细胞捐献事业的发展，拯救或延长更多适应症相符的患者的生命。

PU-1080

以专业组为主导的多医疗区医学检验实习生带教模式构建和实践

滕文友、刘蓉
郴州市第一人民医院

目的 通过构建以专业组为主导的多医疗区实习生带教模式，提高医学检验实习生的培训质量。
方法 将实习生随机分为两组，对照组按医疗区轮转模式带教，实验组按以专业组为主导的模式带教，实习结束，比较两组实习生理论、操作和综合成绩。
结果 实验组实习生理论、操作和综合成绩分别为 83.25、91.13 和 87.19，均高于按医疗区轮转的对照组（80.17、86.96 和 83.56），且差异有统计学意义(P<0.05)。
结论 以专业组为主导的模式比按医疗区轮转模式更适合多医疗区大型三甲综合医院的检验专业实习生带教。

PU-1081

自身抗体与先兆早产的相关性研究及预测价值分析

方伟[1]、冯安妮[2]
1. 广东省人民医院（广东省医学科学院）
2. 广东医科大学

目的 探讨患者血清中 APS、LA、ds-DNA、ANA 的水平与先兆早产的相关性，同时结合年龄、孕周、生产史、流产史等对先兆早产进行预测分析。
方法 回顾性收集 2018 年 6 月至 2020 年 12 月在广东省人民医院就诊的诊断为先兆早产的孕妇资料，共收集 43 例，纳入病例组；对照组为同一时期孕龄相近的健康孕妇，共 47 例。采用酶联免疫吸附法（ELISA）、间接免疫荧光法检测两组孕妇血清中 APS、LA、ds-DNA、ANA 水平，结合年龄、孕周、生产史、流产史，寻找先兆早产相关独立影响因素，采用受试者工作特征曲线（ROC 曲线）对先兆早产进行预测价值分析。
结果 在本研究中，病例组 APS 中的 β2-GPⅠ-IgM 水平明显高于对照组，差异有统计学意义（P<0.05），且 β2-GPⅠ-IgM 是先兆早产的独立影响因素；LA、ds-DNA、ANA 与先兆早产无相关性；年龄、孕周、生产史、流产史均不能作为先兆早产的独立影响因素。

结论 β2-GPⅠ-IgM 可作为先兆早产的预测指标。

PU-1082

肿瘤标志物的电化学发光分析研究进展

李宏柱
呼和浩特金域检验所有限公司

目的 随着医学技术的发展，许多疾病正慢慢被人们所熟知，在这些疾病中最令老百姓们害怕的莫过于肿瘤。肿瘤（Tumor）是机体在各种致癌因素作用下，局部组织的某一个细胞在基因水平上失去对其生长的正常调控，导致其克隆性异常增生而形成的新生物。近年来，肿瘤的发病率一直居高不下，并且大多发现自己得了肿瘤的患者病程已经到达了晚期，彻底治愈的概率极低。因此，早发现早治疗是治疗肿瘤的关键。但早期的肿瘤患者无特异性临床表现，再加上检查的流程非常的繁琐，这导致许多患者面对检查也就不了了之，延误了治疗。因此，亟需开发更加准确、高效的诊断方法。电化学发光(ECL)由于其灵敏度高、准确度高等优点，在肿瘤标志物检测的领域有着迅速的发展。本文对电化学发光分析在检测 CEA 、AFP 、CA199、CA125、等肿瘤标志物的诊断价值及其研究进展进行了评述，并展望了电化学发光法在未来的发展趋势。
方法 本文采用了文献研究法对这些年来 ECL 在肿瘤标志物检验的领悟对其研究的发展进行了评述。
结果 ECL 分析在肿瘤标志物中的研究主要体现在构建多功能传感界面、制备新型纳米复合物和反应装置设计等方面，其目的是为了使 ECL 的检出限更低，灵敏度和分析速度进一步提升。
结论 所以可以预测到，随着新型肿瘤标志物的不断发现，新型分子识别材料、功能纳米材料和高通量微型装置的持续发展，将为高灵敏度诊断肿瘤提供更方便快捷的方法。所以，通量微型检测装置的设计和多功能生物传感界面的构建将是未来研究的重点方向之一。

PU-1083

医学检验专业本科生学习压力情况的调查与分析

黄奔、王洁、张祥、徐艳、赵鸿
南京医科大学第一附属医院（江苏省人民医院）

目的 为了解新形势下医学检验专业本科生学习压力的情况，使用问卷调查法进行调查分析。
方法 采用分层整群的抽样方法，调查江苏省某医学院校医学检验学专业三个年级的在校本科生，发放问卷 336 份，回收有效问卷 269 份，有效率为 80.59%。采用 Epidata3.1 软件建立数据库，双人双录入的方式来确保数据输入的准确性。采用 IBM SPSS Statistics 25.0 统计软件进行一般性统计学分析。
结果 此次调查分析中，共有男生 78 名，女生 191 名；大一学生 93 名，大二学生 95 名，大三学生 81 名。在感受学习压力很大、压力较大、压力较小和无压力的分析中，仅有 5（1.85%）名学生认为学习压力很大，135（50.19%）学生认为学习压力加大，129（47.96%）学生认为学习压力较小；0 人认为无学习压力。在性别方面，男女生在学习压力感受上无明显差异（P<0.05）。在不同年级上，学生在学习压力感受上存在着显著性差异（P<0.01），其中感受学习压力很大和学习压力较大以大三学生人数最多 155 人（57.62%），其次是大二学生 88 人（32.71%），大一年级人数最少 26 人（9.67%）。
结论 此次调研显示，约半数（52.04%）的在校学生存在着程度不一的学习压力，学习压力随着年级而增长。表明医学检验本科生学习压力情况较为严重，亟待重视。

PU-1084

探讨 PBL 教学方法在临床免疫检验中的应用效果

于建英
山东第一医科大学第一附属医院

目的 探究 PBL 教学方法在临床免疫检验中的应用效果。
方法 选取 2019 年 7 月～2020 年 1 月在院实习的 36 名临床免疫专业实习生为研究对象，将其随机分为观察组和对照组，各 18 人。观察组在教学中采用 PBL 教学，对照组采用传统带教法。
结果 观察组的实习成绩以及对本组教学模式的效果评价均优于对照组（P<0.05）。
结论 采用 PBL 教学模式在临床免疫带教中的效果显著，有利于教学效率的提高，有利于提高学生临床免疫理论和操作水平。

PU-1085

风湿性关节炎患者的外周血 C 反应蛋白 、血小板/淋巴细胞比率和红细胞体积分布宽度对疾病诊断价值的探讨

战伟
大连大学门诊部

选 105 例门诊健康体检者和 105 例风湿性关节炎患者，用对照法将上述人员分为健康对照组和患者组。根据风湿关节炎的的病情轻重 DAS28 评分法，将患者组又分为重度炎症组和轻度炎症组。分别对患者组（重度炎症组和轻度炎症组）与健康对照组的 C 反应蛋白（CRP） 、血小板/淋巴细胞比率（PLR）和红细胞体积分布宽度（RDW）的水平进行测定，用 t 检验比较两组间的测定水平，通过各受检者的工作特征（ROC）曲线，探讨患者体内 CRP、PLR 和 RDW 的特异性和灵敏度。患者组外周血 CRP 水平高于健康对照组，重度炎症组外周血 CRP 水平明显高于轻度炎症组，前后两组有明显相关性（P＜0.05）。患者组与健康对照组、重度炎症组与轻度炎症组的外周血 RDW 水平对比，无相关性（P＞0.05）。CRP、PLR、RDW 对风湿关节炎患者的特异性和灵敏度依次为 96.21% 和 26.47%，19.65%和 89.25%，83.40%和 29.31%，有明显相关性（P＜0.05）。CRP、PLR 和 RDW 与风湿性关节炎的严重程度有相关性，对该病良好的特异性和灵敏度，对风湿性关节炎有一定的诊断价值。

PU-1086

医学检验技术专业临床输血学教学与实践应用研究

王世波
云南商务职业学院

目的 针对医学检验技术专业临床输血学教学与实践应用效果进行探讨。
方法 观察期：2019 年 1 月-2020 年 1 月，纳入医学检验技术专业 40 名学生作为观察对象，按照教学方案的不同分为两组，观察组（n=20）与对照组（n=20），前组予以成果导向式教学，后组予以常规模式教学，比较不同方案的教学效果。
结果 观察组学生平均护理理论知识考核得分与实践操作考核得分均明显高于对照组学生，（P＜0.05）。
结论 在医学检验技术专业临床输血学教学中，应用成果导向式教学模式，可有效提升学生对临床输血的理论知识掌握程度，实践操作能力熟练程度，为其今后更好地胜任临床工作奠定基础，方案值得推荐。

PU-1087

急诊患者人性化护理应用效果分析

张燕
昆明市中医医院

为观察人性化护理在急诊患者护理工作中的应用效果，选择昆明市中医医院 2019 年 1－6 月入院接受急诊治疗的患者 60 例，平均分为两组。常规组以常规护理模式进行临床护理工作，实验组采用人性化护理模式。人性化组患者干预后，SAS 及 SDS 评分较对照组患者降低显著，本次对比分析结果有效。说明人性化护理工作在急诊患者临床护理工作中有着良好的应用优势，能够充分提高患者对医院各项工作的满意度，值得临床推广应用。

PU-1088

成果为导向教育模式下临床微生物检验技术教学改革探索

宋为娟
江苏省人民医院（南京医科大学第一附属医院）

“OBE”理念教学模式以成果为导向，通过课程改革有利于提升医学生临床实际操作能力。临床微生物学检验技术是医学检验专业重要的基础课程之一，本文以成果导向教育理念为指导，通过分析目前教学现状，对教学内容和方法改革提出改进措施，以期达到更好的教学效果。实践表明，成果为导向教育模式下临床微生物检验技术教学改革提高了学生的专业认可度、课堂参与度和解决实际问题的能力，符合检验医学的行业需求，为微生物检验技术教学改革提供了新思路。

PU-1089

临床检验技术教学中应用“岗位融入式”教学模式的作用

王琴、王世波
云南商务职业学院

目的 分析临床检验技术教学中应用"岗位融入式"教学模式的作用。
方法 2020 年 2 月至 2021 年 2 月于我院实习的 52 例医学检验技术专业学生为研究对象，抽签分组法分组，对照组实施常规教学模式，实验组实施岗位融入式教学模式，分析作用。
结果 教学实施前，两组学生成绩对比无统计学意义（P＞0.05）。教学后，实验组学生考核成绩较对照组高，P＜0.05。实验组学生对教学模式满意度较对照组高，P＜0.05。
结论 临床检验技术教学中应用"岗位融入式"教学模式可提高学生考核成绩，提高学生满意度。

PU-1090

疫情下的医学检验网络教学

朱琼
江苏省人民医院（南京医科大学第一附属医院）

新冠肺炎疫情背景下,各学校都选择进行线上网络教学与考核，医学检验是一门集理论与实践相结合的学科，充分利用网络进行教学，以及互联网微信、企业微信、云班课等 app 进行考核与互动，开展多元化的线上教学活动，激发学生的积极性与互动性，督促学习进展，与注重学习成果考核，提高医学检验网络教育质量。

PU-1091

临床生物化学检验的课程思政教学实践

黄桦[2]、梅传忠[1]、武文娟[1]、耿建[1]、周继红[1]、石玉荣[1]
1. 蚌埠医学院检验医学院
2. 蚌埠医学院检验医学院

在医学类专业课程的教学过程中要注重加强医风医德、医者仁心教育，在培养精湛医术的同时，提升综合素养和人文修养。临床生物化学检验是医学检验技术专业的专业课之一，在学习专业知识培养科学精神的同时，也要将价值引导有机融入，贯穿到课程教学的全过程中，于潜移默化之中达到综合育人的效果。

PU-1092

实验诊断学

张翔
空军军医大学第一附属医院

实验诊断学是临床医学专业的一门必修专业课程。是运用医学基本理论和基本知识对疾病进行诊断的一门学科，是诊断学中重要的一部分，也是重要的医学“桥梁”课程。教学对象是五年、八年制临床、航医、心理、预防、口腔专业。

通过“实验诊断学”课程的学习，学生能够掌握和应用实验诊断学的基本理论、知识和技能；学会充分利用、科学分析临床检验所提供的信息和数据，结合其它辅助手段，对疾病进行初步和鉴别诊断、观察疗效、判断预后；重要的是通过理论、线上和实验课教学以及教员与学生的双边互动，培养自主学习的意识，掌握独立思考、分析概括和创新能力，为继续学习其他课程和长远发展打下坚实的基础。

PU-1093

高浓度非结核胆红素对血红蛋白测定的影响初探

贾文祥[1]、曲菲[2]
1. 山东省千佛山医院
2. 山东省耳鼻喉医院（山东省立医院西院）

目的本人自工作以来，发觉高胆红素血症的病患，其血常规结果几乎都有所异常，经过文献查询发现业界有对高胆红素血症影响血常规内测定白细胞、红细胞、血小板的较深入研究，但对研究其影响血红蛋白测定较浅，故尝试从试验方面对高胆红素血症常出现的人群—新生儿入手，探究高胆红素血症对血常规测定血红蛋白的影响，且新生儿高胆红素血症以非结合胆红素升高为主，故特研究非结合胆红素对血红蛋白测定的影响。

PU-1094

对临检细胞形态学进修自学互教模式的探讨与实践

巩中华
山东省千佛山医院

目的 在临检细胞形态学学习过程中，对进修学生自学互教模式的一些探讨和实践。
方法 带教老师在日常工作中对临床细胞学要不断学习，不断更新自己的知识，和学生参与实验教学的"导学导思-自学自练-合作探究-展示共享-评价总结"互教模式,培养学生综合运用理论知识和细胞鉴别识别能力的同时,注重学生在合作交流 、自我学习及探索新知识 、新技能等方面能力的提升,制定相关的学习制度，对现有的学习资料进行有效地优化，
结果 在学生进修结束时，对其考核，考核结果与前几届相比，结果显示现有的自学互教模式更加有利于进修学生的学习，更加有效的提高进修学生对细胞形态鉴别识别能力。
结论 细胞形态学在临检专业占的位置是相当重要，地位是毋庸置疑的，所以从而培养符合当今社会需求的 、专业知识全面的 、具有一定创新精神和科研能力 、善于交流和合作的高素质医学检验专业人才。

PU-1095

《临床血液学检验技术》实习带教体会

李英
川北医学院附属医院

《临床血液学检验技术》是一门与临床血液学疾病的诊断及预后判断相关的学科，在临床主要应用于骨髓涂片细胞形态学检查，由于其专业的特殊性无法实现自动化与智能化，且与临床结合非常紧密，故实习要求与实习特点有别于其他专业。本人多年从事本专业的理论及实践教学与实习生带教工作，现就带教多年的体会作一小结，希望加强实习同学对本专业的正确深入认识、提早做好实习规划及规避在实习中一些意识上的误区，更好利用短暂的实习时间达到最优的学习效果，培养形态检验接班人。带教体会主要包括以下五个方面：一、合理安排实习时间及做好实习规划。二、看懂血常规报告、明确骨髓检验目的。三、培养学生自主学习与思考问题的能力。四、培养学生独立处理报告的能力。五、实习过程中的思政教育。

PU-1096

结合疫情时事提升《分子诊断学》教学效果的探索

刘湘
湖北中医药大学

2020 年上半年突如其来的新型冠状肺炎疫情给高校医学专业课程教学带来了挑战，也带来了新的关注点和教学契机。《分子诊断学》是一门理论性和应用性很强的医学检验技术专业核心课程，本文通过具体教学实践，从制定教学方案、优化教学内容、开展课程思政、引导学生科研思维四个方面，探索在疫情期间紧密结合热点时事开展课程教学的方法，同时对教学效果进行了评价和思考，为后续教学实施中提升《分子诊断学》的教学效果提供了思路和参考。

PU-1097

系统性红斑狼疮（SLE）患者血浆细胞因子水平分析及其临床意义

曾聪[1]、王启广[1]、程振波[2]
1. 湖南省人民医院
2. 湖南师范大学

目的 对六项细胞因子[白细胞介素 IL-4、IL-6、IL-10、IL-17、干扰素-γ(IFN-γ)、肿瘤坏死因子-α(TNF-α)]在系统性红斑狼疮患者血浆中的水平变化进行统计学研究并探讨其临床意义，以期辅助临床检测治疗，帮助药物研发。

方法 湖南省人民医院 2020 年 1 月至 2021 年 4 月收治的系统性红斑狼疮患者中选择 30 例初次发病或患病后初次进行治疗病人作为观察组，选择同时间段内 30 例（排除肿瘤免疫系统等疾病的外科患者）检测者作为对照组。比较两组血浆细胞因子水平，进行统计学独立 t 检验分析；并将观察组与检测试剂盒厂家提供的医学正常值范围进行比较讨论。对观察组中进行了复查的 3 例患者的六项细胞因子检测结果分为治疗前与治疗后两配对组进行配对 t 检验分析，分析治疗前后 IL-4、IL-6、IL-10、IL-17、IFN-γ、TNF-α 水平有无显著性差异。

结果 观察组患者血浆 IL-6、IFN-γ 水平均高于对照组（P<0.05），IL-4、IL-10、IL-17、TNF-α 变化无显著差异（P>0.05）。观察组 SLE 患者仅 IL-6 血浆浓度升高占 SLE 患者总数 46.66%；IL-6 和干扰素 IFN-γ 升高占 16.66%；仅干扰素 IFN-γ 升高占 10.00%；仅 IL-10 升高占 3.34%；六项细胞因子结果均正常占 23.34%。同一患者血浆中 IL-4、IL-6、IL-10、IL-17、IFN-γ、TNF-α 水平结果在治疗前与治疗后均无显著性差异（P>0.05），治疗后三位复查患者异常血浆 IL-6 水平均回归正常参考值范围。

结论 系统性红斑狼疮患者血浆中细胞因子存在活性水平紊乱，重点体现为 IL-6、INF-γ 在 SLE 患者外周血血浆中表达增加，在 SLE 的发生中产生关键作用，为 SLE 疾病的预防以及诊疗建立理论基础，可以作为病情监测以及判断疗效指标，帮助疾病早期发现。

PU-1098

冷球蛋白导致的血小板假性增高病例分析

朱颖珊、陈卓曦
广东省人民医院

目的 血小板假性增高的原因很多，这里着重讨论冷球蛋白引起的血细胞分析仪阻抗法通道测定血小板假性增多。

方法 一次审核结果时偶然发现的血小板计数与历史结果不符，触发复检规则，用 PLT-F 通道复查，血小板减少，推片染色观察血小板计数与 PLT-F 通道符合，同时发现细胞间存在片状淡蓝色不定形物质存在，怀疑是该物质是冷球蛋白。通知病房重新采血立即送检，用该标本于室温放置 0、30、60、90、120 min 后分别同时用电阻法通道和 PLT-F 通道检测，记录各项指标结果，对比血小板直方图曲线，同时手工涂片评估各阶段标本血小板计数，并观察血涂片细胞形态。联系病房做冷球蛋白血症相关检测。

结果 该标本电阻法通道血小板计数随着放置时间越长结果越高，PLT-F 通道则无差别，直方图曲线无异常，未触发血球仪报警信息，血片未见小红细胞及红细胞碎片等可能引起血小板计数假性增高的常见因素。血常规标本室温放置 60 min 后推片，可见不定形物及不规则形红细胞；标本 37 ℃温浴 30 min 后涂片，不定形物消失，不规则形红细胞明显减少。

结论 该患者血小板计数历史结果正常，这次检测血小板计数减少，是因之前采血后样本放置时间过长才检测，冷球蛋白形成引起阻抗法测定血小板计数假性增高。目前全自动血球分析仪阻抗法仍

是最常用的检测血小板的方法，因为直方图正常、结果正常、无报警信息导致冷球蛋白患者的血小板计数很假性增高不容易被发现，值得警惕。建议多和临床沟通，冷球蛋白血症患者血常规应做相应标识，同时日常工作时看到冷球蛋白血症诊断时，注意手工推片复检，用 PLT-F 通道检测血小板。

PU-1099

“需求引领、能力驱动”中高职一体化人才培养模式的探索与实践

李珍珠[1]、钟楠楠[2]
1. 陕西能源职业技术学院
2. 西安市卫生学校

《国家职业教育改革实施方案》和教育部《国家中长期教育改革和发展规划纲要（2010—2020 年）》都明确提出了中高职教育衔接，构建人才培养“立交桥”的重要性，良好有效的中高职衔接是现代职教体系建设中的重要步骤。

自 2015 年陕西省实行高职分类考试招生以来，西安市卫生学校成为陕西能源职业技术学院优质生源基地，医学检验技术专业每年有 80%以上的毕业生进入陕西能源职业技术学院学习。自 2016 年西安市卫生学校专门成立“能源基地班”，两校联合开始实施“需求引领、能力驱动”中高职一体化人才培养，在中高职人才培养有效衔接方面做了有益尝试，通过 5 年多的探索与实践，为近 400 名中职学生架设中高职一体化立交桥，铺就人才技能提升之路。本文以这两所中、高职院校医学检验技术专业五年来的实践为依据，通过分析中、高职不同阶段学生及岗位需求变化，厘清中高职人才培养目标和任务，对中高职一体化人才培养过程中，在人才培养模式构建、课程体系建设、教学资源开发、课证融合、校企合作、学生管理、技能竞赛等方面对“需求引领、能力驱动”中高职一体化人才培养模式进行的探索和实践进行了阐述。简要介绍了方案实施以来，两校在专业建设内涵、教育教学、学生培养等方面取得的成绩。

PU-1100

网络教学平台在检验科继续教育中的应用与研究

周琰、张春燕、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 随着网络平台的普及和线上教学软件的推广，探讨其在检验科员工继续教育工作中的应用情况。
方法 应用网络教学平台在专业理论和技能培训、对分课堂教学方案应用、三基培训考核和生物安全等质量体系培训，以及人员管理中均取得了较好的效果，有效增强了“教”与“学”的双方沟通，提高了教学的时效性，提高了参与者的学习兴趣和主观能动性。
结果 基于检验科继续教育模式的现状，网络教学平台在教学工作安排、人才规划和培养、实验操作教学、科教成果评定和在其他培训考核中的应用发挥积极作用。
结论 基于网络通讯平台的教学模式可以作为现有检验医学继续教学方式的有效扩充。

PU-1101

CD85K、CD85J 在流式细胞术中评价单核细胞及急性单核细胞白血病中的应用

楚玉兰
天津金域医学检验实验室有限公司

目的 未成熟单核细胞缺乏特异性和敏感性的早期谱系标记，流式诊断急性单核细胞白血病受到限制。探讨 CD85K、CD85J 在鉴别单核细胞及其在临床诊断中的价值。CD85K、CD85J 是免疫球蛋白样转录本（ILT）的成员，是一种免疫抑制受体，CD85K 又称 ILT3，CD85J，又称 ILT2，两者均在单核细胞中表达。
方法 采用多色流式细胞术（FMC），分析了 49 例 AML 患者中，主要检测未成熟单核细胞（尤其对无单核细胞系成熟相关抗原，如 CD14，CD11b，CD15，CD64）CD85K、CD85J 表达情况。
结果 我们发现 CD85K、CD85J 在检测未成熟单核细胞分化方面优于 CD36、CD64 及 CD14。白血病母细胞或幼稚单核细胞 CD85k、CD85J 表达一般比正常单核细胞表达强度会减弱，同时 CD85K 表达敏感性优于 CD85J。CD85K、CD85J 在所有显示单核细胞分化的 AML 病例中均有表达(FAB M4/M5;n=29)；而在 M1、M2 和 M3 无表达 (n= 20;P <0.0001)
结论 CD85K、CD85J 两着联合是区分具有单核细胞分化的 AML 与其他类型 AML 的高敏感性和特异性标志物。CD85K、CD85J 表达检测可以纳入 AML 患者的初始诊断和监测。

PU-1102

医学检验专业妇幼检验科临检组实习教学改进的探讨

丁红梅
江苏省人民医院（南京医科大学第一附属医院）

对医学检验技术专业学生在妇幼检验科的实习带教中存在的理论知识欠缺、重视程度不够等问题进行分析，应用“导师制”教学法，设立阶段式“一对一”带教老师，利用现代化多媒体教学等措施，开展针对妇幼特色的带教。通过实习考核成绩比较和学生问卷调查两种形式，反馈带教效果，发现此些改进措施后可获得更好的带教效果。使学生能够了解妇幼检验工作的重要性，为其以后步入工作岗位打好基础。

PU-1103

杭州地区乙肝患者 HBV 核苷类似物耐药位点分析

许生样
杭州迪安医学检验中心有限公司

目的 检测杭州地区乙型肝炎患者体内 HBV 逆转录酶基因的耐药突变情况，为临床制定合理的治疗方案提供依据。
方法 通过聚合酶链反应（PCR）及 DNA 测序将 2020 年 1 月至 9 月送检杭州迪安医学检验中心的 746 例乙型肝炎患者进行 HBV 耐药突变位点和基因耐药情况检测，并对结果进行统计分析。
结果 在 746 例血清标本中有耐药突变位点产生的有 324 例，检出率是 43.43%（324/746），其中 M204I、L180M+M204V、L180M+S202G/C+M204V 和 L180M+T184L/A/F+M204V 检出率较高。患者对替比夫定（L-dT）、拉米夫定（LMV）、恩曲他滨（FTC）、恩替卡韦(ETV)、阿德福伟（ADV）、替诺福韦(TDF)耐药比例分别是 95.37%（309/324）、87.04%（282/324）、87.04%（282/324）、38.27%（124/324）、31.17%（101/324）、0.31%（1/324）。单药耐药比例为

4.63%（15/324），多药耐药比例为 95.37%（309/324）。27 例患者对 L-dT 和 ADV 耐药，比例为 8.33%（27/324）。129 例患者对 LAM、FTC 和 L-dT 耐药，比例为 39.81%（129/324）。47 例患者 LAM、FTC、L-dT 和 ADV 耐药，比例为 14.51%（47/324）。93 例患者对 LAM、FTC、L-dT 和 ETV 耐药，比例为 28.70%（93/324）。13 例患者对 LAM、FTC、L-dT、ETV 和 ADV 耐药，比例为 4.01%（13/324）。发生耐药突变与患者的性别无关（P＞0.05）。

结 论 在杭州地区乙肝患者中，常见的突变模式为 M204I 、L180M+M204V 、L180M+S202G/C+M204V 和 L180M+T184L/A/F+M204V；耐药情况主要以多药耐药为主。

PU-1104

肺癌晚期患者 CD8+T 细胞细胞毒活性

朱时帅
哈尔滨医科大学第一附属医院

探索服用扶正抗癌方后非小细胞肺癌（NSCLC）晚期患者 CD8+T 细胞细胞毒活性的变化。

方法 NSCLC 晚期患者共 31 例，根据不同的临床因素进行分组（服用扶正抗癌方前后、病理类型、TNM 分期和性别），流式细胞术检测外周血 CD4+T、CD8+T 细胞绝对值以及 CD8+T 细胞表达 CD107a、颗粒酶 B 和 IFN-γ 百分比的变化。

结果 Ⅲ期患者 CD8+T 细胞表达 CD107a、颗粒酶 B 和 IFN-γ 百分比都显著高于Ⅳ期。服用扶正抗癌方后 IFN-γ+CD8+T 细胞的百分比较治疗前显著升高，大部分患者的生存质量稳中有升。CD8+T 细胞表达 CD107a、颗粒酶 B 和 IFN-γ 的百分比在鳞癌和腺癌无差异，也无男、女性差别。

结论 服用扶正抗癌方后 NSCLC 晚期患者分泌 IFN-γ 的 CD8+T 细胞的百分比明显提升，有助于改善患者的生存质量和预后。

PU-1105

地贫的产前诊断概述

韦骁元[1]、胡销[2]
1. 柳州市妇幼保健院
2. 柳州书妇幼保健院

地中海贫血(thalassemia,简称地贫)是一组全球最常见的、对人类健康影响极大的单基因遗传病,在我国广东、广西、云南、四川等省份发病率高，广西 α 地贫 携带率为 17.55%，β 地地贫携带率为 6,43% ，重型 α 地中海贫血是致死性遗传病,患病胎儿高度水肿、畸形,在出生前窒息死亡或出生后不久死亡。重型 β 地中海贫血患儿则需每月输血和去铁治疗来维持生命,骨髓或脐血移植是惟一的根治方法,但目前成功率不高,而且合适的配型也较难找到。患者严重贫血时,只能依赖长期输血维持生命。

因此,控制该病最有效的办法是通过产前筛查和对高风险夫妇采取产前基因诊断来防止重型患儿的出生。

目的 探讨目前可开展的地贫诊断方法的优劣。

方法 查阅最新文献。

结果 目前检测地贫的手段多样，能满足各级实验室的要求。

结论 血液学检测和家系分析可以为血红蛋白病的 DNA 诊断提供必要的线索, 是开展基因诊断的基础;基于 DNA 检测的方法是用于 a- 和 β-地贫临床基因分型和产前诊断确诊的重要手段; 为保证质量,一个好的 DNA 诊断实验室应具备至少二种检测各种 a- 和 β-地贫突变的可选择的技术。就技术而言，高通量、高敏感性、高准确性、自动化和标准化是方法学研究的目标与方向，二代测序技术以其独特的技术优势将成为主流技术平台。

PU-1106

消失的球蛋白

卢洁仪
南方医科大学珠江医院

遇到一例 IgG、IgM 等球蛋白明显减少的病例，尝试从分析前（样本留取、样本状态等）、分析中（试剂状态、仪器状态、当天质控、方法学比对等）、分析后（患者临床资料、其他辅助检测等）等分析其中原因。后来分析发现该病人 CD19 淋巴细胞明显减少，未排除免疫缺陷症的可能，及时提醒临床完善基因检测，确定病因。

PU-1107

病例分析：双虫混合感染（粪类圆线虫+肝吸虫）

兰萌
南方医科大学珠江医院

佛山市南海区的李阿伯（化名）因全身浮肿一个月，发热 10 天在当地医院治疗无缓解后被家人送往我院就医。初进院时李阿伯情况危急，精神差，食欲差，睡眠差，小便少，全身浮肿加重，面色苍白，重度贫血貌，并出现发热，不喜言语，还有现感染性休克。初进院的第 1 天，李阿伯的抽血检测项目肿瘤指标高，呼吸科邓教授查房指示不排除胃肠道及肺部肿瘤的可能，并于床边在局麻下行右锁骨下深静脉穿刺置管术，手术顺利。第 2 天李阿伯全身水肿减轻，但仍有发热，精神很差，睡眠差。第 3 天李阿伯留取粪便送检，粪便涂片于显微镜观察发现有活动的虫体，虫体细长，大小约为 0.6-0.7mm，咽管呈柱状，尾端尖而分叉。于当天粪检结果报查见粪类圆线虫，又查见了肝吸虫卵。这一检查结果让呼吸科的医务人员振奋人心，夏教授查房听取病史汇报后，认为这是一例较少见的两种寄生虫同时感染。 增加抗寄生虫药物，继续肠虫清治疗，余治疗继续营养支持，纠正贫血处理。一直到了第 13 天，李阿伯无水肿，无发热，意识清楚，小便正常，感染休克已纠正。抽血检测结果大部分正常。面色较前红润，中度贫血貌。且粪便检查结果均未查见圆线虫和肝吸虫卵。李阿伯经历了两周的住院治疗症状好转后，家属满意签字出院。

PU-1108

面向未来的检验医学教育

何穗芬
南方医科大学珠江医院

一直以来，检验医学的教学重在把检验学子培养成“懂规矩”的检验人，因而，大多数学生都缺乏主动学习、独立思考的意识。现实的检验工作中，检验工作者普遍进化为与仪器紧密相连的半机器人，每天都在遵照检验相关的法律法规、行业准则、科室流程和 SOP 完成一套套规定性动作，日复一日，锁定在大大小小的检验流水线上，成为相同或相似功能的“工具人”。然而，面对异常复杂的临床工作，未来的“专业”检验人，除了必须“懂规矩”，还需要在临床疑难病例诊疗方面及实施科学合理的质量管理方面都能适应检验医学与时俱进的专业要求。目前，国内外有部分顶尖的检验实验室会主动挑战检验领域的高难度技术问题和/或创造能应对特殊临床检测任务的临床实验室运作新模式。他们的发展预示着未来的检验必将更重视协助临床鉴别诊断疑难病例和给出更具指导意义的报告解读、开发更具鉴别意义的实验技术和新项目，以及建立能高效应对临床特殊要求的组织形式。随着检验学科的快速发展，检验医学的未来注定充满各种不确定性。对于检验医学方向的学生们依靠记忆力、动手能力和执行力已不足以帮助他们适应未来检验高速发展的专业要求，因此，

他们迫切需要医学院校和教学医院的老师们能全方位地激发他们主动学习、自主思考及创造性劳动的主观能动性，进而强化他们观察能力、分析能力、决策能力及应变能力。

PU-1109

医学检验专业教育中通识教育满意度情况调查

王霞、何訸、张玫
四川大学华西医院

目的 调查在医学检验专业教育中学生对通识教育的满意度了解情况，以促进本专业通识教育的持续性改进。
方法 结合文献及学生访谈对问卷进行设计，采用“问卷星”进行线上匿名问卷调查。李克特五点量表分析学生对通识教育的满意度和了解情况，卡方检验进行不同专业组间的比较，SPSSAU.(Version 20.0)对数据进行统计分析及可视化。
结果 本次调查共回收有效问卷 209 份，研究数据信度质量高且具有效度。90%的学生表示喜欢通识类课程，检验专业学生喜欢的通识类课程为“科学探索与生命教育”与非检验专业学生喜欢的通识类课程有差异。学生对通识类课程的接受度较高，喜欢通识类课程的学习。但对通识教育的不了解仍然是影响满意度的主要原因，同时，由于医学类专业本身课业的繁重，对专业知识无帮助成为影响学生不喜欢通识类课程的主要原因。
结论 现阶段，我校所开设通识类课程已获得学生的普遍认可。增强学生对通识教育的了解程度，增设融合专业课程体系的通识类课程可提高通识教育的满意度。

PU-1110

一种新型快速全血心梗三项免疫检测方法的性能评估

于金星、崔凯、蔺亚晖、周洲
中国医学科学院阜外医院

目的 心梗三项检测在急性冠脉综合征的诊断中具有重要价值。大型检验化学发光设备结果准确，但通常只能使用血清或血浆样本，报告时间长。全血检测速度快，但通常检测准确性不足。本研究旨在评估一种基于探针的新型心梗三项检测应用于全血、血浆和血清三种样本类型的分析性能。
方法 根据 EP 文件，用全血、血浆和血清三种类型的样本评价 Pylon 平台循环增强免疫荧光发光法（CEFA）心梗三项（肌红蛋白 MYO、肌酸激酶同工酶 CK-MB、高敏肌钙蛋白 I hs-cTnI）检测的分析性能，包括精密度、线性范围、可报告范围、正常参考区间、方法学比对和样本类型比对。
结果 基于 Pylon CEFA 的心梗三项检测重复性和实验室内总不精密度均小于 10%，其中包括 hs-cTnI 第 99 百分位上限附近及以下的中低浓度水平。三项的线性范围和正常参考区间验证均满足要求。可报告范围实验表明，Pylon CEFA 方法 MYO、CK-MB 和 hs-cTnI 的可报告范围分别可达 10-40000 ng/mL、1-3000 ng/mL 以及 0.5-30000 ng/L。方法学比对显示，血清（n=100）和血浆样本（n=100）的 Pylon CEFA 法与 Architect i2000 化学发光法结果相关性好（相关性系数 R^2>0.95）。样本类型比对中，全血和血浆样本（n=100）的 Pylon CEFA 心梗三项检测结果相关性系数（R^2）均超过 0.95，且 Passing-Bablok 线性拟合斜率在 0.94-1.01 之间，表明两种样本类型可相互替代。Pylon CEFA 检测采用全血标本原管上机，心梗三项报告时间仅 15 分钟。
结论 Pylon CEFA 心梗三项检测的分析性能与大型化学发光设备相似，检测结果与化学发光相关性好。同时，其通过探针表面的特殊化学处理和分析系统的自动实时血细胞校正功能，实现准确的全血检测，简化实验室操作流程，减少周转时间和人力。

PU-1111

降钙素原及 C 反应蛋白联合检测在新生儿败血症诊断中的价值分析

黄瑶楠
空军军医大学西京医院

目的 探究降钙素原（PCT）及 C 反应蛋白（CRP）联合检测在新生儿败血症中的诊断价值。
方法 选择我院 2019 年 2 月-2020 年 10 月我院收治 80 例新生儿败血症患儿纳入败血症组，另选取同期于我院产科分娩的健康新生儿 78 例作为对照组。比较两组 PCT 及 CRP 水平；以血培养结果作为诊断“金标准”，分析 PCT、CRP 单独及联合检测的诊断价值，另分析 PCT、CRP 单独及联合检测与血培养结果的一致性。
结果 败血症组 PCT 及 CRP 水平均高于对照组，有统计学差异（P＜0.05）；PCT 及 CRP 联合检测在新生儿败血症中灵敏度、特异度及准确度均高于单项检测，有统计学差异（P＜0.05）。kappa 检验显示：PCT 与血培养结果的一致性尚可（kappa 值=0.708，P＜0.001）；CRP 与血培养结果的一致性尚可（kappa 值=0.557，P＜0.001）；联合检测与血培养结果的一致性良好（kappa 值=0.899，P＜0.001）。
结论 PCT 及 CRP 联合检测在新生儿败血症诊断中具有较高的应用价值，为临床鉴别诊断提供参考依据，大大降低误诊率及漏诊率，值得推广应用。

PU-1112

脑出血患者血清 SBDP145 与格拉斯哥昏迷、mRS 评分的相关性分析

王虹霏、史清海
新疆军区总医院

目的 探讨 SBDP145 作为诊断高血压性脑出血疾病及评估患者病情和预后的价值。
方法 对 55 例经头颅 CT 确诊的高血压性脑出血患者进行临床资料收集，在脑出血发病后 12 小时内和入院后 10 天内及出院时连续采集静脉血作为待检测样本，采用酶联免疫吸附法进行分析血清中 SBDP145 的浓度。用格拉斯哥昏迷评分对患者临床状况进行评估，用 mRS 评分（改良 Rankin 评分量表）评估存活患者出院后两个月的恢复情况。
结果 SBDP145 诊断脑出血的最佳截止值是 1.54ng/ml[ROC 分析曲线下面积 0.98(95% CI,(0.826 - 1),p＜0.001],入院时精神表现正常患者（格拉斯哥昏迷评分 15 分）与健康体检者相比,血清中 SBDP145 升高,平均血清 SBDP145 水平为 0.45ng/ml，健康体检者平均血清 SBDP145 水平为 0.23ng/ml。与格拉斯哥昏迷评分相比，患者发病 12h 内血清中 SBDP145 的水平与其成显著相关性（相关系数 0.78，p＜0.001），患者出院前血清中 SBDP145 的水平与 mRS 评分也有相关性（相关系数 0.568，p＜0.05）。
结论 SBDP145 可作为诊断脑出血疾病的特异性的生物标志物，并可作为初始评估患者病情的客观指标协助临床医生评估入院患者的病情。

PU-1113

甲亢性肝病患者血清检验指标改变的临床价值及检出率分析

周毅君
资阳市乐至县人民医院

目的 探讨甲亢性肝病患者血清检验指标改变的临床价值及检出率。
方法 抽取 50 例甲亢性肝病患者，作为观察组，均在 2019 年 10 月至 2020 年 10 月期间到我院接受治疗。并选择同期 50 例甲亢患者作为对照组，均进行血清指标检测。将两组患者的检查结果和并发症情况进行比较分析。
结果 在观察期间，观察组的并发症发生情况与对照组相比，呈现出更高的趋势（P<0.05）；在血清指标的比较中，观察组患者的 TT3、TT4、FT3、FT4、TSH 的数值较对照组，均有着明显的差异（P<0.05）。
结论 在甲亢性肝炎患者的检查中，血清指标的变化较明显，可通过此种方式对病情进行早期的诊断，更好对疾病进行控制，防止病情的进一步恶化，可在临床进行应用推广。

PU-1114

STAT5b 及其磷酸化与胃癌的相关性研究

孙涛
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 信号转导和转录激活蛋白 5(signal transduction and transcriptional activation protein 5，STAT5)，被认为在多种肿瘤的发生发展中起重要作用，本研究旨在检测胃癌组织 STAT5b、pSTAT5b 的表达，并分析二者与胃癌临床参数及胃癌预后的关系。
方法 选取 92 例初诊的原发性胃癌患者作为研究对象, 免疫组化法检测患者胃癌组织中 STAT5b、pSTAT5b 的表达，并分析二者与胃癌患者临床病理参数的相关性。
结果 STAT5b 及 pSTAT5b 表达与胃癌 TMN 分期、T 值、N 值、临床分期和淋巴结是否转移均有相关性。
结论 STAT5b 可能通过其活性形式 pSTAT5b，影响胃癌的发生发展。

PU-1115

血清抗 p53 与抗 PTEN 自身抗体联合检测在原发性肝癌诊断中的研究

孙晓彤
大连市中心医院

目的 探讨 p53 及 PTEN 两种肿瘤相关抗原是否可作为 HCC 诊断的生物标志物，以及二者联合 AFP 检测在 HCC 中的诊断价值。
方法 采用原核表达技术获取 PTEN 蛋白，用镍柱层析法纯化 PTEN 蛋白；通过 SDS-PAGE（sodium dodecyl sulfate-polyacrylamide gel electrophoresis，十二烷基硫酸钠聚丙烯酰胺）凝胶电泳鉴定 p53 蛋白和 PTEN 蛋白；采用间接酶联免疫吸附实验（enzyme linked immunosorbent assay，ELISA）检测实验组和对照组血清标本中抗 p53 及抗 PTEN 自身抗体；采用电化学发光免疫测定（electrochemiluminescence immunoassay，ECLIA）检测各组血清标本中 AFP 浓度；通过 ROC 曲线计算 和对照组特征曲线下的面积（AUC），运用灵敏度和特异度来评估单个抗 TAA 自身抗体、抗 p53 和抗 PTEN 自身抗体及 AFP 联合检测对 HCC 的诊断价值。

结果 抗 p53 和抗 PTEN 自身抗体单独检测，阳性率很低；抗 p53 和抗 PTEN 自身抗体联合检测，阳性率由抗 p53 自身抗体 14.8%、抗 PTEN 自身抗体 21.3%升高至抗 p53 联合抗 PTEN 自身抗体 24.6%，灵敏度升高至 24.6%。特异度由 97.9%降低至 96.9%；二者与 AFP 三者联合检测时，阳性率由 24.6%升高至 69.3%，灵敏度由 24.6%升高至 69.3%，特异度由 96.9%降低至 62.5%。
结论 单个抗 TAA 自身抗体检测在 HCC 中的阳性率较低，p53 联合 PTEN 两种肿瘤相 关抗原的自身抗体检测能够提高 HCC 检测的阳性率；二者再联合 AFP 检测 HCC，HCC 检测的阳性率较高，对 HCC 具有一定的免疫学诊断价值。

PU-1116

血清 KL-6，PIVKA-Ⅱ表达水平在胰腺癌诊断中的应用价值研究

邢瑞青、彭道荣、刘杨
空军军医大学西京医院

目的 探讨血清异常凝血酶原（PIVKA-Ⅱ）,涎液化糖链抗原（KL-6）对胰腺癌的诊断价值。
方法 纳入 2020 年 1 月---2020 年 5 月来空军军医大学第一附属医院就诊的胰腺癌患者 49 例，胰腺炎患者 44 例，健康对照者 42 例。分别比较三组血清 CA199，PIVKA-Ⅱ，KL-6 表达水平。绘制 ROC 曲线评价 CA199，PIVKA-Ⅱ，KL-6 对胰腺癌的诊断价值。计算分析单一指标与联合检测对于胰腺癌的诊断价值。
结果 胰腺癌组血清 CA199，PIVKA-Ⅱ，KL-6 水平均显著高于健康对照组、胰腺炎组，差异具有统计学意义（U=263.000，Z=-6.098，P=0.000; U=1006.500，Z=-5.010，，P=0.004; U=299.500，Z=-5.808，，P=0.000; U=482.000，Z=-4.587，P=0.000；U=1972.000，Z=-2.540, P=0.003；U=667.500，Z=-3.159，P=0.002）。胰腺炎组与健康对照组之间无统计学差异(U=693.000，Z=-1.996，P=0.460；U=576.000，Z=-3.090，P=0.650; U=482.500，Z=-3.815，P=0.320)。

PU-1117

抑郁症患者免疫功能紊乱的相关研究

席倩
四川省医学科学院·四川省人民医院

目的 探讨血清免疫球蛋白（IgA、IgM、IgG）、补体（C3、C4）以及外周血 T 淋巴细胞亚群（CD3+、CD4+、CD8+、CD4/CD8）水平与抑郁症的相关关系。
方法 测定血清免疫球蛋白、C3、C4 以及外周血 T 淋巴细胞亚群的水平，分析并比较病例组与健康对照组以及不同性别、临床症状抑郁症患者之间免疫相关成分的水平。
结果 ①与健康对照组相比，抑郁症患者的血清 IgM 水平及外周血 CD4+细胞数和 CD4/CD8 比值明显升高，而血清 C3 水平降低；②男性抑郁症患者与正常男性相比，其血清 IgM 和外周血 CD4+细胞数升高，血清 IgG、C3 降低；女性抑郁症患者与正常女性相比，其血清 IgM 和外周血 CD4+细胞数升高；不同临床症状的抑郁症患者间无明显差异；③Logistic 多因素分析显示血清 C3、外周血 CD4+细胞数的改变与抑郁症关系密切，血清 IgM 水平改变可能与抑郁症相关。
结论 血清 C3 和外周血 CD4+细胞数是抑郁症的独立影响因素，他们可能作为抑郁症的监测指标。抑郁症患者血清免疫球蛋白 IgM、IgG、C3 和外周血 T 淋巴细胞亚群 CD4+水平的改变，提示抑郁症患者存在体液免疫异常和细胞免疫激活，同时抑郁症患者可能存在慢性免疫炎性损伤，进一步证实了抑郁症与免疫功能紊乱密切相关。

PU-1118

肝素结合蛋白对急性胆囊炎的诊断价值研究

郭斌[1]、何仁栋[2]
1. 川北医学院附属医院
2. 川北医学院

目的 评估肝素结合蛋白（HBP）在局部炎症疾病急性胆囊炎中的诊断价值。
方法 选取 58 例局部炎症疾病急性胆囊炎患者作为实验组，并以同期 29 例健康体检者为对照组。采用免疫荧光干式定量法测定 HBP 水平，并通过全自动化学发光免疫分析仪和全自动血细胞分析仪分别测定 PCT 和中性粒细胞水平。正态分布的定量资料采用 T 检验，非正态分布定量资料采用 Mann-Whitney U 检验，定性资料采用 χ2 检验，两变量间相关性采用 Spearman 相关分析，建立受试者工作特征(ROC) 曲线评估各指标诊断效能。
结果 局部炎症疾病急性胆囊炎患者和健康体检者 HBP 水平分别为(16.28±20.74)ng/ml、(6.48±1.39) ng/ml，PCT 水平分别为(0.11±0.28) ng/ml、(0.05±0.01) ng/ml，中性粒细胞绝对值分别为(4.62±2.83) ×109/L、(3.83±0.98) ×109/L。局部炎症急性胆囊炎 HBP 升高率明显高于 PCT 升高率（χ2=16.06，p=0.000）。同时急性胆囊炎患者 HBP 与中性粒细胞水平呈正相关（p=0.042，r=0.267），与 PCT 无明显相关性。HBP 用于急性胆囊炎诊断时 AUC 为 0.750。
结论 HBP 可用于辅助诊断急性胆囊炎，在一定程度上弥补传统指标的不足。

PU-1119

济南地区中老年人群 HP 抗体分型分析

耿丽丽
山东第一医科大学附属省立医院

目的 了解山东地区中老年人群 HP 抗体分型的感染情况。
方法 收集 2019 年 1 月至 2020 年 2 月在山东大学附属省立医院门诊就诊和查体患者 632 例。用免疫印印记方法进行血清细胞毒（CagA-116KD）、空泡毒(VacA-91KD)、空泡毒(VacA-95KD)、尿素酶（UreB-66KD）、尿素酶（UreB-30KD）五项指标检测。用 SPSS21.0 软件分析中老年人群 HP 抗体分型感染情况。
结果 632 例血清标本中，CagA-116KD 阳性率为 43.64%，VacA-91KD 阳性率为 27.18%，VacA-95KD 阳性率为 29.18%，UreB-66KD 阳性率为 69.76%，UreB-30KD 阳性率为：30.24%。男性 CagA-116KD、VacA-91KD、VacA-95KD、UreB-66KD、UreB-30KD 阳性率分别为 26.56%、16.41%、16.41%、50.78%、21.09%，均明显低于女性的 28.46%、17.82%、19.95%、51.33%、22.87%（P 均<0.05）。CagA-116KD、VacA-91KD、VacA-95KD、UreB-66KD、UreB-30KD 阳性率以 90 以上为最低：0、0、0、40%、0；40~49 岁开始升高阳性率为：24.63%、16.04%、17.16%、48.88%、18.66%；50~59 岁持续升高阳性率为：29.53%、19.29%、20.47%、53.15%、26.38%；60~69 岁阳性率最高为：33.33%、19.05%、19.05%、53.97%、25.4%。70~79 岁开始逐渐降低阳性率为：32%、8%、12%、56%、12%没；80~89 岁人群略微降低阳性率为：29.41%、17.65%、23.53%、41.2%、17.65%。（P 均<0.05）。CagA-116KD、VacA-91KD、VacA-95KD、UreB-66KD、UreB-30KD 阳性率 I 型和 II 型阳性率分别为 63.45%和 73.26%，II 型明显高于 I 型（P 均<0.05）。
结论 山东济南地区中老年人群 HP 抗体分型检测阳性率存在性别、年龄差异，HP 抗体分型以 II 型阳性为主。血清分型抗体检测对 HP 感染的判断具有重要的价值。

PU-1120

七种肿瘤相关抗原自身抗体在非小细胞肺癌诊断中的应用

刘京萍
江苏省人民医院

目的 探讨七种肿瘤相关抗原自身抗体在非小细胞肺癌（ NSCLC）辅助诊断中的临床价值。
方法 收集 2019 年 7 月至 2019 年 12 月在南京医科大学第一附属医院就诊的 155 例 NSCLC 初诊患者作为疾病组，同时选择 79 例肺部良性疾病患者（BLD）及 95 例健康体检者（HC）作为对照。采用 ELISA 法检测各组血清中七种肿瘤相关抗原自身抗体的水平，同时 ELICA 法检测癌胚抗原（CEA）、细胞角蛋白片段 19（CYFRA21-1）和神经元特异性烯醇化酶（NSE）水平，绘制 ROC 曲线分析并比较不同标志物对 NSCLC 的诊断效能。
结果 肺癌组 7 种自身抗体中有 6 项（p53、SOX2、GAGE7、GBU4-5 和 CAGE）的血清水平在 NSCLC 组均分别高于 BLD 组（p53：P=0.000；SOX2：P=0.000；GAGE7：P=0.000；GBU4-5：P=0.000；CAGE：P=0.000）和 HC 组（p53：P=0.000；SOX2：P=0.000；GAGE7：P=0.018；GBU4-5：P=0.000；CAGE：P=0.000），差异有统计学意义，MAGE A1 项在 NSCLC 组与 BLD 组间的差异有统计学意义（P=0.000）、与 HC 组无差异（P=0.102）。七种肿瘤相关抗原自身抗体联合检测诊断初诊 NSCLC 患者敏感性为 71.61%，特异性为 87.36%，AUC 为 0.795，其敏感性和 AUC 均高于传统肿瘤标志物。七种自身抗体联合检测在 NSCLC 组的阳性率明显高于 BLD 组($\chi2 = 7.293$，P=0.007) 和 HC 组($\chi2 = 8.411$，P=0.004)。
结论 七种肿瘤相关抗原自身抗体联合检测可作为 NSCLC 患者辅助诊断的指标，并且联合 CEA、NSE 和 CYFRA21-1 可以提高 NSCLC 患者的诊断敏感度。

PU-1121

血浆外泌体糖蛋白作为结直肠癌诊断标志物的应用价值

孙祖俊、李冬
上海市同济医院(同济大学附属同济医院)

目的 通过糖蛋白组学研究初步筛查正常对照组和结直肠癌患者血浆外泌体中差异表达的糖蛋白，并探讨其在结直肠癌诊断中的临床应用价值。
方法 提取并鉴定 3 例正常对照和 3 例肠癌患者组织中外泌体，用 O18 标记 N-糖基化位点 PNG F，用 LTQ-Orbitrap Elite mass spectrometer 对蛋白 N-糖基化位点进行筛选，然后进行生信分析并鉴定出表达差异显著的糖蛋白，最后用酶联免疫吸附实验（ELISA）进行验证。
结果 我们发现结直肠癌患者组织外泌体中包含更多的糖蛋白和脂质，初步鉴定纤维蛋白原 β 链（Fibrinogen beta chain，FGB）和 β2 糖蛋白 1（Beta-2-glycoprotein 1，β2-GP1）在结直肠癌患者的表达水平显著高于正常对照组；ELISA 验证结果发现，30 例结直肠癌患者血浆外泌体中 FG-β 和 β2-GP1 表达也显著高于正常对照组；FGB 和 β2-GP1 对结直肠癌具有较高的诊断效能，且优于血清学标志物癌胚抗原 CEA 或糖类抗原 CA19-9。
结论 血浆外泌体 FGB 和 β2-GP1 可能成为结直肠癌患者早期诊断、治疗监测及预后判断的潜在生物标志物，具有重要的临床应用价值。

PU-1122

外周血细胞因子检测与高血压脑出血疾病的相关性研究

邓中华[1]、孟雨婷[1]、张冉[2]、黎村艳[1]、谭超超[1]、曹友德[1]
1. 湖南省人民医院（湖南师范大学附属第一医院）
2. 湖南师范大学医学院

目的 分析外周血细胞因子含量与高血压脑出血疾病的相关性，为高血压脑出血疾病的发生发展机制研究及临床诊治提供研究基础和依据。
方法 收集 2020 年 1 月-2021 年期间湖南省人民医院由高血压引起的急性脑出血患者 91 例为高血压脑出血组，患有高血压疾病但无脑出血的患者 50 例为对照组。所有患者空腹采集外周血分离血浆，采用直接夹心法原理，以荧光发光微球作为固相偶联的细胞因子抗体与生物素标记的细胞因子配对抗体和样本中的细胞因子结合形成三明治复合物，再与加入藻红蛋白标记的链霉亲和素（SA-PE），利用免疫学分析方法与流式细胞荧光强度分析相结合，测定外周血中的 IL-6、IL-10、IL-4、IL-17、IFN-γ 和 TNF-α 六项细胞因子含量。比较高血压脑出血组和单纯高血压组患者之间各细胞因子含量的差异；对高血压脑出血组患者进一步按照 GCS 昏迷评分分为三组，比较各不同 GCS 评分组之间各细胞因子含量的差异。
结果 高血压脑出血患者外周血中 IL-6、IL-10、IL-4、IL-17、IFN-γ 和 TNF-α 的浓度高于对照组浓度，P＜0.05 差异有统计学意义。不同 GCS 昏迷评分组之间细胞因子 IL-6、IL-10、IL-4、IL-17、IFN-γ 和 TNF-α 的差异不具有统计学意义，P>0.05。
结论 高血压性脑出血患者血清中的细胞因子 IL-6、IL-10、IL-4、IL-17、IFN-γ 和 TNF-α 浓度发生显著变化，细胞因子可以辅助高血压疾病的进展诊断。血清中的细胞因子 IL-6、IL-10、IL-4、IL-17、IFN-γ 和 TNF-α 浓度与住院 GCS 评分，病人年龄没有相关性。

PU-1123

Prediction model based on the combination of cytokines and lymphocyte subsets for prognosis of SARS-CoV-2 infection

Ying Luo、Feng Wang、Ziyong Sun
Department of Laboratory Medicine, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Background There are currently rare satisfactory markers for predicting the death of patients with coronavirus disease 2019 (COVID-19). The aim of this study is to establish a model based on the combination of serum cytokines and lymphocyte subsets for predicting the prognosis of the disease.
Methods A total of 739 participants with COVID-19 were enrolled at Tongji hospital from February to April 2020 and classified into the fatal (n=51) and survived (n=688) group according to the patient's outcome. Cytokine profile and lymphocyte subset analysis was performed simultaneously.
Results The fatal patients exhibited a significant lower number of lymphocytes including B cells, CD4+ T cells, CD8+ T cells and NK cells and remarkably higher concentrations of cytokines including interleukin-2 receptor, interleukin-6, interleukin-8 and tumor necrosis factor-α on admission compared to the survived subjects. A model based on the combination of interleukin-8 and the numbers of CD4+ T cells and NK cells showed good performance in predicting the death of patients with COVID-19. When the threshold of 0.075 was used, the sensitivity and specificity of the prediction model were 90.20% and 90.26%, respectively. Meanwhile, interleukin-8 was found to have potential value in predicting the length of hospital stay until death.

Conclusions Significant increase of cytokines and decrease of lymphocyte subsets are found positively correlated with in-hospital death. A model based on combination of three markers provides an attractive approach to predict the prognosis of COVID-19.

PU-1124

壳多糖酶 3 样蛋白 1 在乙肝相关肝脏疾病的鉴别诊断价值

黎村艳[1]、夏婷婷[2]
1. 湖南省人民医院
2. 湖南师范大学医学院

目的 探讨 CHI3L1 蛋白在乙肝相关疾病中表达浓度差异及其辅助乙肝相关肝脏疾病鉴别诊断价值。
方法 本研究纳入 2020 年 11 月——2021 年 3 月在湖南师范大学附属第一医院就诊的慢性乙型肝炎患者 42 例、乙肝相关肝硬化患者 59 例、乙肝相关肝癌患者 72 例及同期入院体检的健康人 52 例作为健康对照组，用 ELISA 检测血清 CHI3L1 蛋白浓度。正态分布数据多组间比较采用方差分析，两两比较采用独立样本 t 检验。
结果 CHI3L1 蛋白浓度随着乙肝相关肝脏疾病进展而升高，与健康对照组相比，慢性乙型肝炎组、乙肝相关肝硬化组和乙肝相关肝癌组的血清 CHI3L1 蛋白浓度升高（P 值均＜0.01）。与慢性乙型肝炎组相比，乙肝相关肝硬化组和乙肝相关肝癌组的血清 CHI3L1 蛋白浓度升高（P 值均＜0.01）。与乙肝相关肝硬化组相比，乙肝相关肝癌组的血清 CHI3L1 蛋白浓度升高(Z=-4.023；P 值均＜0.01）。将乙肝相关肝癌组按是否伴肝硬化分为乙肝相关肝癌伴肝硬化组（45 例）及乙肝相关肝癌不伴肝硬化组（27 例），前者血清 CHI3L1 蛋白浓度为 278.74（119.14，429.90）（ng/mL），后者血清 CHI3L1 蛋白浓度为 268.22（132.81，567.16）（ng/mL）。乙肝相关肝癌伴肝硬化组的血清 CHI3L1 蛋白浓度高于乙肝相关肝硬化组（Z=-3.461；P＜0.01）。CHI3L1 蛋白鉴别诊断乙肝相关肝癌与乙肝相关非肝癌肝脏疾病的 cut off 值为 208.67ng/mL，AUC 为 0.829，95%置信区间为[0.768，0.890]，P＜0.01，敏感度为 0.639，特异性为 0.895。
结论 CHI3L1 蛋白浓度随着乙肝肝脏疾病进展而升高，提示 CHI3L1 蛋白可以作为乙肝相关肝脏疾病患者病情监测、进展、预后生物标志物。CHI3L1 蛋白可作为乙肝相关肝癌潜在鉴别诊断生物标志物。

PU-1125

循环肿瘤细胞(CTCs)检测在肺癌诊断中的研究进展

冯宇欣
沈阳金域医学检验所有限公司

目的 目前临床常用于肺癌检查的方法存在创伤性大、影响诊断价值因素多、不利于反复活检等弊端。因此, 对肺癌患者采用无创、快捷、便宜、有效的检测手段进行检查是非常重要的。
方法 收集沈阳某医院 48 例肺癌患者、31 例肺部良性疾病患者和 19 例健康对照者作为研究对象，利用改良之后的流式细胞检测技术检测外周血循环肿瘤细胞水平，通过荧光标记单抗流式细胞术建立饱和曲线法，确定最适荧光抗体使用浓度；受试者工作特征曲线确定其诊断临界值。电化学发光法同步检测血清癌胚抗原和角质蛋白 19 片段水平，并比较这些肿瘤标志物的阳性率。并比较这些肿瘤标志物的阳性率。受试者工作特征曲线初步分析外周血循环肿瘤细胞的检测在肺癌早期诊断、治疗指导、疗效评估及预后的应用价值。
结果 饱和曲线法确定了荧光抗体最适使用浓度为 79 ng/μL。受试者工作特征曲线分析显示，外周血循环肿瘤细胞最佳诊断临界值为 209 个/mL，对应的敏感度为 52.60%，特异度为 79.88%。肺癌患者外周血循环肿瘤细胞阳性率为 59.40%，显著高于血清癌胚抗原和角质蛋白 19 片段（37.46%和 54.21%）；外周血循环肿瘤细胞水平在肺癌早期即较肺部良性疾病患者和健康体检者明显升高

（P<0.04），且在特异度保持优势的情况下，灵敏度较癌胚抗原和角质蛋白 19 片段单个指标高 56%左右；48 例肺癌患者血清癌胚抗原和角质蛋白 19 片段水平为双阴性，但外周血循环肿瘤细胞检测灵敏度和特异度仍分别达 75.32%和 87.33%。
结论 循环肿瘤细胞检测对肺癌诊断具有较高的灵敏度和准确度，存在重要的临床应用价值，理论上可以使用基于肿瘤细胞大小的分离法 (isolation by size of epithelial tumor cells, ISET) 对循环肿瘤细胞进行富集，这将使未来对高危患者早期筛查协助诊治成为可能。

PU-1126

糖尿病视网膜病变患者 HCY 与炎性因子水平的分析

刘辉
中日友好医院

目的 探讨 2 型糖尿病（Type 2 Diabetes Mellitus，T2DM）患者血清同型半胱氨酸 (Homocysteine，HCY)及炎性因子水平与糖尿病视网膜病变(Diabetic Retinopathy，DR)的发生发展的相关性。
方法 选取 2019 年 2 月至 2020 年 4 月中日友好医院内分泌科和眼科 2 型 DM（T2DM）住院患者 272 例，其中单纯 T2DM 组 146 例，DR 组 126 例 。采用化学发光法检测血清炎性因子：肿瘤坏死因子 α（Tumor Necrosis Factor -α,TNF-α）、白介素 6（Interleukin 6,IL-6）水平，两组间比较使用 Mann- Whitney U 检验。采用循环酶法检测 HCY 水平，两组间比较使用独立样本 t 检验。采用 Logistic 回归分析探讨 DR 患者发病的风险因素 。
结果 DR 组 HCY、TNF-α、IL-6 水平明显高于 T2DM 组（P<0.05）。HCY 是发生 DR 的独立危险因素。
结论 DR 患者血清 HCY、TNF-α、IL-6 水平与 DR 的发生存在相关性，提示 HCY、TNF-α、IL-6 对于评估 DR 的发病风险具有重要意义。

PU-1127

基质金属蛋白酶（MMPs）与动脉粥样硬化的新进展

俞晓晨[1]、孙妍[2]
1. 哈尔滨医科大学附属第一医院
2. 黑龙江省哈尔滨市医科大学附属第一医院

目的 了解基质金属蛋白酶的性能，为其在临床上的应用提供可能。
方法 基质金属蛋白酶（Matrix metalloproteinases, MMPs）是一组具有相似结构和功能的蛋白水解酶。MMPs 通常以无活性的酶原形式分泌，在激活因子的作用下被激活。MMPs 的活性由总蛋白酶抑制剂，组织抑制因子（TIMPs）加以调节。
结果 不同 MMPs 对动脉粥样硬化的作用不同。
结论 使用 MMP 特异的抑制剂来抑制 MMP 的有害作用，这也是将来治疗动脉粥样硬化的一个新靶点。

PU-1128

肺纤维化与衰老的相关机制及如何减缓肺纤维化的最新进展

张俭[1]、李锋[2]
1. 宁夏医科大学临床学院
2. 宁夏医科大学附属医院

肺纤维化是致命性的肺部疾病，与衰老密切相关，预后较差。目前，还没有有效的治疗策略来预防和治疗这一疾病过程在这里，我们研究了近五年来的相关文献，在 PUBMED 上利用 pulmonary fibrosis、aging、treatment 等关键词，搜索 2015-2021 年期间的所有文献，共计检索出 326 篇相关及类似文件，用关键词进一步进行整理，将不必要文献进行进一步的筛选，最后，定性为 42 篇文献，现将所归类的文献进行综述

PU-1129

凝血四项指标及肿瘤标志物诊断乙型肝炎相关肝癌的检验分析

兰隆琴
资阳市雁江区中医医院

目的 探讨凝血四项结合肿瘤标志物指标检测对乙型肝炎相关肝癌的诊断价值。
方法 纳入本院 2018 年 6 月至 2019 年 6 月收治 50 例乙型肝炎相关肝癌患者建立研究组，同期纳入 50 例良性肝病患者建立对照组。两组患者均进行凝血四项结合肿瘤标志物指标检测，对比分析检测结果。
结果 研究组患者 APTT、PT 以及 TT 指标水平相比对照组明显更高（P<0.05）；研究组 Fib 水平相比对照组明显更低（P<0.05）；研究组患者 VEGF、AFP 以及 AFU 指标相比对照组明显更高（P<0.05）。
结论 临床当中检测凝血四项以及肿瘤标志物对于乙型肝炎相关性肝癌的诊断具有积极意义。

PU-1130

Peritoneal resident macrophages in mice with MLL-AF9-induced acute myeloid leukemia show an M2-like phenotype

Chong Chen
Tianjin Medical University Cancer Institute and Hospital

Background Acute myeloid leukemia (AML) is a devastating disease with a poor prognosis. Innate and adaptive immunity is closely related to the progression of leukemia. Macrophages within the leukemic microenvironment have a tendency toward a leukemia-permissive phenotype. However, the characteristics of macrophages in leukemia, including their kinetics, gene expression, and functional roles have not been fully illuminated.
Methods In the current study, the characteristics of peritoneal resident macrophages, whichwere large peritoneal macrophages (LPM), from mice with mixed lineage leukemia (MLL)-AF9-induced AML were investigated. AML-associated large macrophages (AML-LPM) were gated as F4/80high MHC-II- by flow cytometry. To further investigate the relationship between the leukemic microenvironment and macrophage characteristics, RNA sequencing was performed. Meanwhile, apoptosis, killing ability, and phagocytic function of peritoneal resident macrophages in MLL-AF9-induced AML were assessed..

Result The results suggested that AML microenvironment was found to affect the kinetics and morphology of peritoneal resident macrophages. The results of RNA sequencing suggested that the gene expression of AML-LPMs differed significantly from that of normal LPMs. The AML microenvironment also had effects on the apoptosis, killing ability, and phagocytic function of peritoneal resident macrophages.
Conclusions These data suggest that peritoneal resident macrophages in mice with AML induced by MLL-AF9 show an M2-like phenotype. The reversal of macrophage polarization in the leukemic microenvironment may potentially enhance the immunotherapeutic effect in AML.

PU-1131

肺泡灌洗液肝素结合蛋白在细菌性肺炎诊断与鉴别诊断中的临床价值

毕惠娟[1]、沈继录[2]、方文浩[2]、吴珊[3]、尹丽娜[2]、徐倩[2]、薛莹[2]
1. 安徽医科大学第四附属医院检验科
2. 安徽医科大学第四附属医院检验科
3. 安徽医科大学第四附属医院肿瘤科

目的 探讨支气管肺泡灌洗液（Bronchoalveolar lavage fluid, BALF）中肝素结合蛋白（Heparin binding protein, HBP）在细菌性肺炎诊断与鉴别诊断中的临床价值。
方法 选取 2019 年 1 月至 2021 年 1 月安徽医科大学第四附属医院呼吸科收治的 88 例肺炎患者，其中细菌性肺炎 48 例，非细菌性肺炎 40 例，另选取同期 40 例非感染性肺部疾病患者为对照组，检测并比较 3 组患者 BALF 中 HBP、降钙素原和 IL-6 水平，采用受试者工作特征（ROC）曲线分析上述各指标对细菌性肺炎的诊断和鉴别诊断效能。
结果 细菌性肺炎患者 BALFHBP、IL-6 水平均较非细菌性肺炎及对照组明显升高，差异有统计学意义（P<0.05）。ROC 曲线结果显示 HBP 及 IL-6 在细菌性肺炎早期诊断中 AUC 分别为 0.930、0.893，灵敏度分别为 88.5%、82.7%，特异度分别为 92.5%、92.5%，二者联合检测 AUC 为 0.942，灵敏度为 94.2%，特异度为 95.0%。ROC 曲线结果显示 HBP、IL-6 在鉴别细菌性肺炎与非细菌性肺炎时 AUC 分别为 0.890、0.777，灵敏度分别为 80.8%、71.2%，特异度分别为 91.7%、75.0%，二者联合检测 AUC 为 0.902，灵敏度为 96.2%，特异度为 79.2%。
结论 肺泡灌洗液 HBP 及 IL-6 在细菌性肺炎的早期诊断及鉴别诊断中，具有很好的临床价值，二者联合检测价值更优。

PU-1132

血清 CCL1 在肺癌患者外周血的表达及意义

程娟、陈礼文、唐伟、姚杰、周强
安徽医科大学第二附属医院

目的 探讨血清趋化因子 1（Chemokine C-C motif ligand 1，CCL1）在肺癌早期诊断的临床应用价值。
方法 采用酶联免疫吸附法（ELISA）检测 60 例肺癌初诊患者和 36 例健康体检人群血清中 CCL1 的表达水平并分析两组的差异，并采用电化学发光法检测两组肺癌肿瘤标志物（CEA、NSE、SCC、CYFRA211、Pro-GRP）水平。收集肺癌组所有患者的临床资料，包括年龄、病理类型、分期、转移情况。流式细胞术检测肺癌组和对照组 PBMC 中 CCR8+FoxP3+T 细胞占 CD4+T 细胞的比例。
结果 CCL1 和 CEA、NSE、SCC、CYFRA211、Pro-GRP 在肺癌患者的表达水平明显高于健康对照组（P<0.05）；受试者工作曲线显示 CCL1 表达水平检测肺癌的曲线下面积是 0.63，灵敏度是

0.59，特异度是 0.61；CCL1 的表达与肺癌患者的年龄、病理类型等无明显关系（P＞0.05）,但与 TNM 分期、有无转移有关（P<0.05）；肺癌组 PBMC 中 CCR8+FoxP3+T 细胞占 CD4+T 细胞的比例明显高于对照组（P<0.05）。

结论 CCL1 在肺癌患者血清中显著高表达，CCL1 的检测对肺癌的诊断及转移有潜在的临床价值。肺癌患者 CCL1 表达升高，可能与 CCL1 促进 T 细胞向抑制性 T 细胞的转化，免疫监视下降从而导致肺癌的发生和转移有关。

PU-1133

内蒙某三甲医院 2015-2020 年 HIV 检测情况分析

薄晋魏
内蒙古科技大学包头医学院第一附属医院

目的 根据 2015-2020 年艾滋病病毒（ＨＩＶ）检测结果，分析 ＨＩＶ 检测结果的判断和艾滋病的流行趋势。

方法 用化学发光法对临床样本血清进行 ＨＩＶ 抗原抗体联合测定，按检测规范对有反应的样本进行复检和患者基本信息采集，由疾病预防控制中心（ＣＤＣ）进行ＨＩＶ抗体确证试验。

结果 2015-2020 年该院累计进行 ＨＩＶ 检测２４５２２６例，初筛有反应性６６３例（初筛有反应性率２．７０‰），确证阳性４４９例（确证阳性率１．８３‰），确证阴性１３６例（初筛假阳性率０．５５‰），确证不确定报告７８例（可疑阳性率０．３２‰）。五年内确证阳性病例主要为来源于皮肤（１８４例）、急诊（５８例）、呼吸（５３例）及消化内科（２６例），年龄在２０～４０岁的男男性行为者（ＭＳＭ）２０９例。

结论 ２０～４０岁的 ＭＳＭ 是本地区艾滋病防控干预的主要人群；假阳性病例主要来源于消化内科，提示消化道类疾病可能对此检测造成干扰。

PU-1134

神经梅毒对糖尿病和高血压及高血脂的相关性

张惠林
厦门大学附属中山医院

目的 探讨神经梅毒对糖尿病、高血压及高血脂之间的相关性。

方法 采用快速血浆反应素试验和梅毒螺旋体明胶颗粒凝集试验进行梅毒血清学检测。测定脑脊液白细胞计数并检测患者脑脊液蛋白质、血液糖化血红蛋白、空腹血糖、甘油三酯、总胆固醇、脂蛋白(a)、高密度脂蛋白、低密度脂蛋白、载脂蛋白 A1 及载脂蛋白 B 等生化指标。比较神经梅毒患者和非感染性中枢神经系统疾病患者的糖尿病、高血压及高血脂相关指标。

结果 神经梅毒的糖尿病患病率、空腹血糖及糖化血红蛋白水平与非感染性中枢神经系统疾病差异无统计学意义;神经梅毒的高血压患病率、收缩压及 3 级高血压患者比例分别为 45.00%(36/80) 138(117,150)mmHg 和 17.50%(14/ 80),均高于非感染性中枢神经系统疾病(P<0.05);神经梅毒高脂血症患病率、总胆固醇、低密度脂蛋白和载脂蛋白 B 分别为 20.00%(16/80)、4.32(3.77,5.26)mmol/L、3.03(2.48,3.81)mmol/L 和 0.87(0.75,1.08)mmol/L,均高于非感染性中枢神经系统疾病患者(P<0.05)。

结论 神经梅毒可能导致代谢紊乱,对于神经梅毒患者,应及时关注未来可能发生的代谢紊乱,进行及早干预,以免延误治疗。

PU-1135

梅毒螺旋体特异性 IgM 抗体在梅毒患者血清治愈判断中的应用

童曼莉
厦门大学附属中山医院

目的 探讨梅毒螺旋体特异性 IgM（Tp-IgM）抗体在患者血清治愈判断中的应用价值。
方法 厦门大学附属中山医院诊治的 1035 例梅毒确诊患者，经治疗后每 3 个月复查甲苯胺红不加热血清反应素试验（TRUST），首次 TRUST 转阴时，采用荧光密螺旋体抗体吸收试验（FTA-ABS）检测血清治愈患者 Tp-IgM 抗体，阳性者采用胶体金法 和梅毒螺旋体颗粒凝集试验（TPPA）验证，并结合其临床资料进行分析。
结果 在 2 年的血清学随访过程中，共入组 126 例梅毒血清治愈患者，其中 4 例 FTA-ABS-IgM 抗体阳性，经胶体金法和 TPPA 验证后有 3 例 Tp-IgM 阳性。
结论 部分临床血清治愈的梅毒患者可能有传染性，在临床血清治愈判断中除了快速血浆反应素试验外，有必要加入 Tp-IgM 指标。

PU-1136

Treponema pallidum Dysregulates Monocytes and Promotes the Expression of IL-1b and Migration in Monocytes Through the mTOR Signaling Pathway

Lili Liu
Zhongshan Hospital, School of Medicine, Xiamen University

Objective This study aims to analyze the distribution of monocyte subsets in syphilis patients and the effect of Tp on monocyte functions to explore the pathogenesis of syphilis.
Methods Flow cytometry was employed to detect monocyte subsets.
Results Tp infection led to an increase in the proportion of CD14++CD16+ monocytes and a decrease in the proportion of CD14++CD16- monocytes. In addition, Tp promoted monocyte (THP-1) CD14 and CD16 expression in vitro, induced the expression of IL-1b and TNF-a in a dose-dependent manner and promoted the migration and autophagy of monocytes.
Conclusion Tp abnormally regulates monocyte subsets and promotes migration, autophagy, and the expression of IL-1b and TNF-a in THP-1 cells. Meanwhile, the mTOR affected the expression of IL-1b and migration in Tp-exposed THP-1 cells. This study is important as it sheds light on the mechanism by which monocytes interact with Tp during infection.

PU-1137

Immunization with nontreponemal antigen alters the course of experimental syphilis in the rabbit model

kun gao、kun gao
厦门大学附属中山医院

Objective The role of nontreponemal antibodies in the Treponema pallidum infection course is unclear.
Methods We investigated the effect of immunization with nontreponemal antigen on T. pallidum-challenged rabbits.

Results Nontreponemal antigen was injected intravenously into rabbits in the nontreponemal group (n = 12) to elicit antibodies (≥1:64), and normal saline-injected rabbits were used as control (n = 12).
Then, rabbits were challenged with 106 T. pallidum per site along their back. Lesion development was observed, and the injection sites were biopsied for mRNA analysis every week. Six rabbits from both groups were euthanized at 14 d and 28 d.
IL-2 and IFN-γ mRNA expression in the nontreponemal group was significantly higher than that in the control group at 7 d and 14 d post-challenge.
ConclusionImmunization with nontreponemal antigen altered the syphilis course in rabbits, resulting in delayed maximal lesion diameter and ulcer development, but it could not inhibit the spread of T. pallidum from primary lesion sites to viscera.

PU-1138

应用 ROC 曲线分析降钙素原在急性下呼吸道感染中的诊断价值

贾蔚、尹利民
昆明市第一人民医院

目的 探讨降钙素原在急性下呼吸道感染中的诊断价值。
方法 分别测定 126 例急性下呼吸道感染患者和 135 例健康志愿者的降钙素原水平，应用 ROC 曲线分析降钙素原诊断急性下呼吸道感染的最佳阈值、灵敏度、特异度。
结果 急性下呼吸道感染组降钙素原水平明显高于对照组，差异有统计学意义(Mann-Whitney U =1590.00，P=0.000)。ROC 曲线分析降钙素原诊断急性下呼吸道感染的曲线下面积为 0.907，灵敏度 86.5%，特异度 81.5%。**结论** 降钙素原在急性下呼吸道感染的诊断中具有较高的灵敏度和特异度，是可以有效指导临床治疗的细菌感染生物标志物。

PU-1139

探讨 ANA 与抗 ENA 抗体联合检测对诊断自身免疫病的应用价值

徐细兰
景德镇市第一人民医院

目的 探讨抗核抗体（ANA）与抗可提取性核抗原抗体（抗 ENA 抗体）联合检测对诊断自身免疫病的应用价值。
方法 选取 2018 年 1 月至 2020 年 9 月本院接收的 63 例自身免疫病患者和 60 例健康体检者为研究对象，自身免疫病设为研究组，健康体检者设为对照组，对两组实施 ANA、抗 ENA 抗体检测，对比分析其检测结果。
结果 经测定，研究组的 ANA 阳性率显著高于对照组，比较差异存在统计学意义（P<0.05）；在 ANA、抗 ENA 抗体检测中，研究组患者均出现了不同程度的阳性率，且 ANA、抗 ENA 抗体检测对 SLE 的敏感性最高；对照组的检测结果均为阴性。
结论 从 ANA 与抗 ENA 抗体联合检测来看，在本次研究中，ANA 在 SLE、SS 和 RA 方面有着较高的阳性率，且大部分患者的 ANA 在 SLE、SS 和 RA 方面有着较高的阳性率，ANA 滴度都在 1:320 以上。抗 ENA 抗体方面，抗 Sm 抗体为 SLE 的标志性抗体，抗 SS-A 抗体为 SS 的标志性抗体，Scl-70 则为 PSS 的标志性抗体。通过分析这方面的标志性抗体，能在 ANA 筛查的基础上进一步明确患者的自身免疫病类型。这对指导临床制定针对性治疗方案具有重要意义。此外，在自身免疫病患者的诊治过程中，ANA 与抗 ENA 抗体联合检测也能作为监测其诊治效果的方法，以实时掌握患者的病情变化情况，使其在临床中能获得最佳的治疗。虽然本次研究在结果方面获得了良好的应用

效果，但由于样本量少、研究周期短等因素，导致研究依旧存在一定的不足，对此，后续仍需进行进一步深入研究，以进一步明确 ANA 与抗 ENA 抗体联合检测的具有作用机制、诊断效果，从而为临床提供更为准确的数据。同时，建议出现自身免疫病特异症状的患者，应及时就诊，使临床进行早期诊断，并及时采用有效的治疗控制措施。在治疗过程中，自身免疫病患者应养成良好的饮食习惯，避免食用引起自身免疫反应的食物，以避免病情加重。综上所述，在自身免疫病的临床诊断中，ANA 与抗 ENA 抗体联合检测能发挥互补作用，使不同类型的自身免疫病阳性检出率提升，从而为临床制定治疗方案提供准确的指导依据，以快速控制患者的病情，减轻自身免疫病对其身心健康的影响。

PU-1140

病毒性肝炎诊断时行血常规和生化检验项目的临床价值分析

毕婧
丹东市第一医院

目的 分析病毒性肝炎诊断时行血常规和生化检验项目的临床价值。
方法 本实验开展时间确定在 2018 年 1 月到 2019 年 12 月之间，抽取该阶段临床确诊病毒性肝炎患者 80 例设为观察组，以肝活检作为金标准，选择同时期期间检查为健康的人员 80 人作为对照组，两组均开展血常规和生化检验项目，分析检测准确率、血常规检查结果以及生化检验结果。
结果 观察组检验准确率为 97.50%，对照组检验准确率为 100.00%，观察组与对照组检验准确率均较高，数据对比无统计学意义（P>0.05）。观察组淋巴细胞（39.21±6.22）%、中性粒细胞（67.89±12.34）%、白细胞计数（7.86±1.76）*109、血小板计数（103.23±60.23）*109，对照组淋巴细胞（30.87±4.56）%、中性粒细胞（53.76±10.77）%、白细胞计数（5.11±1.53）*109、血小板计数（176.34±72.34）*109，观察组淋巴细胞、中性粒细胞、白细胞计数高于对照组，血小板计数低于对照组，数据对比具有统计学意义（P<0.05）。观察组白蛋白（40.76±2.13）g/L、谷丙氨酸转氨酶（30.21±17.33）U/L、总胆红素（25.68±8.25）μmol/L、血清白蛋白/球蛋白（1.06±0.12）%，对照组白蛋白（46.77±4.32）g/L、谷丙氨酸转氨酶（112.33±54.33）U/L、总胆红素（14.11±6.12）μmol/L、血清白蛋白/球蛋白（1.69±0.23）%，观察组白蛋白、谷丙氨酸转氨酶、血清白蛋白/球蛋白低于对照组，总胆红素高于对照组，数据对比具有统计学意义（P<0.05）。
结论 病毒性肝炎诊断时行血常规和生化检验项目准确率较高，可以及时发现感染的情况，对疾病进行有效干预，可以作为疾病诊断的重要检查方式，为临床疾病诊断提供依据，并且检查操作简单便捷，在临床具有较高的普及价值。

PU-1141

健康体检中联合检测肿瘤标志物的临床价值分析

王海雪
德州市陵城区人民医院检验科

目的 探讨血清癌胚抗原（CEA）、甲胎蛋白（AFP）、总前列腺特异性抗原（t-PSA）单检和联检在肿瘤筛查中的诊断价值。
方法 采用胶乳免疫比浊法检测 358 例男性血清的 AFP、CEA、t-PSA 的含量，441 例女性血清的 AFP、CEA 的含量，分析三种肿瘤标志物在健康体检中阳性指标分布情况以及在不同性别中血清水平的差异性。
结果 799 例健康体检人群中，阳性指标 8 例（阳性率 1.00%），男性 3 例（阳性率 0.84%），女性 5 例（阳性率 1.13%）。两个指标组合阳性 2 例，其中男性 1 例经病理确诊为前列腺炎，女性 1

例经病理确诊为早期肝癌，肿瘤检出率为 0.13%（1/799）。单一肿瘤标志物来说，男性组 CEA 水平明显高于女性，组间比较有显著统计学差异（P<0.001），AFP 水平组间比较无统计学差异。
结论 对健康体检者进行多项肿瘤标志物联合检测，可弥补单项肿瘤标志物检测的不足，为肿瘤的早期诊断和治疗提供了重要的科学依据，临床应用价值高，值得广泛推广。

PU-1142

血清 PSA、CEA 和 ALP 联合检测诊断前列腺癌骨转移的临床价值

冯琳
德州市陵城区人民医院检验科

目的 分析血清总前列腺特异性抗原（PSA）、血清癌胚抗原（CEA）和血清碱性磷酸酶（ALP）水平对列腺癌骨转移的诊断价值。
方法 选取我院 215 例 2018 年 11 月至 2019 年 5 月确诊为前列腺癌患者，进行骨显像和血清 PSA、CEA 和 ALP 水平检测。
结果 前列腺癌骨转移患者血清 PSA、CEA 和 ALP 水平显著高于非前列腺癌骨转移组（P＜0.05）。血清 PSA、CEA 和 ALP 联合检测的敏感度和诊断符合度分别为 89.6%和 94.1%，高于单独检测和二联检测。
结论 血清 PSA、CEA 和 ALP 联合检测，可以提高前列腺癌骨转移的敏感度和检测准确度，对前列腺癌骨转移诊断有重要参考价值。

PU-1143

昆明地区 3472 例九项呼吸道病原体 IgM 检测结果分析

邹映东、张兴宗、李亚波、林云
云南省中医医院（云南中医药大学第一附属医院）

目的 了解九项呼吸道病原体在昆明地区的感染状况以及与年龄、季节的相关性。
方法 回顾性统计分析本院 2014 年 12 月至 2016 年 11 月期间 3472 例呼吸道感染者九项病原体血清 IgM 检测结果。
结果 九项呼吸道病原体血清 IgM 检测，总阳性率为 41.24％，其中，肺炎支原体阳性率最高为 28.40%，嗜肺军团菌和乙型流感病毒次之占 5.50%和 4.35%；不同年龄分组的检测，嗜肺军团菌、肺炎支原体、甲型流感病毒、乙型流感病毒存在统计学差异， Q 热立克次体、肺炎衣原体 、腺病毒、 呼吸道合胞病毒、副流感病毒 1、2 和 3 型差异无统计学意义；不同季节分组的检测，嗜肺军团菌、肺炎支原体、呼吸道合胞病毒、腺病毒、甲型流感病毒、乙型流感病毒、副流感病毒 1、2 和 3 型差异有统计学意义，Q 热立克次体、肺炎衣原体差异无统计学意义。
结论 昆明地区的呼吸道感染，病原体以肺炎支原体为主，嗜肺军团菌和乙型流感病毒次之，感染人群以儿童和青少年为主；在发病季节上，集中于春季和冬季。

PU-1144

抗 Ro60 和抗 Ro52 抗体在自身免疫性疾病中的应用价值探讨

周晖[1]、江楚文[2]、招晓彤[3]、陆子焕[1]
1. 广东省人民医院检验科
2. 广东省人民医院省临床检验控制中心
3. 中山大学南方学院

目的 探讨抗 Ro60 和抗 Ro52 抗体在自身免疫性疾病（AID）中的应用价值。
方法 回顾分析 2017 年 12 月～2018 年 12 月在广东省人民医院同时检测了抗核抗体（ANA）、抗核抗体谱（ANAs）14 项、抗双链 DNA（ds-DNA）抗体的 4561 例住院患者的临床资料、实验室结果，研究抗 Ro52 抗体和抗 Ro60 抗体与 AID 的相关性。
结果 4561 例患者中 1125 例诊断为 AID。女性患者的抗 Ro60 抗体和/或抗 Ro52 抗体阳性率均显著高于男性患者（P<0.05）。332 例 $Ro52^{+}Ro60^{+}$、353 例 $Ro52^{+}Ro60^{-}$、3753 例 $Ro52^{-}Ro60^{-}$患者中 AID、非 AID 所占百分比的差异均有统计学意义（P<0.05），123 例 Ro52-Ro60+患者 AID、非 AID 所占百分比的差异无统计学意义（P>0.05）。在 $Ro52^{+}Ro60^{-}$、$Ro52^{-}Ro60^{+}$、$Ro52^{+}Ro60^{+}$组中，ANA 阳性的 AID 患者均多于 ANA 阴性组（均 P<0.05）。抗 Ro52 抗体和/或抗 Ro60 抗体阳性合并其他 13 种特异性自身抗体阳性时，AID 所占百分比也增加。SS、SLE、DM/PM 是在抗 Ro52 抗体和/或抗 Ro60 抗体阳性组中占比较高的 3 种 AID。256 例 SLE 患者中各组所占百分比由低到高依次为：$Ro52^{+}Ro60^{+}$（43.36%）> $Ro52^{-}Ro60^{-}$(37.50%)> $Ro52^{-}Ro60^{+}$（9.77%）> $Ro52^{+}Ro60^{-}$(9.38%)。114 例 SS 患者依次为：$Ro52^{+}Ro60^{+}$（56.14%）> $Ro52^{+}Ro60^{-}$（21.93%）> $Ro52^{-}Ro60^{-}$（13.16%）> $Ro52^{-}Ro60^{+}$(8.77%)。48 例 DM/PM 患者依次为：$Ro52^{+}Ro60^{-}$（45.83%）> $Ro52^{-}Ro60^{-}$（43.75%）> $Ro52^{-}Ro60^{+}$（6.25%）> $Ro52^{+}Ro60^{+}$（4.17%）。29 例抗 Jo-1 抗体阳性的 AID 患者中，10 例 $Ro52^{+}Ro60^{-}$。$Ro52^{+}Ro60^{-}$的 22 例 DM/PM 患者中，18 例抗 Jo-1 抗体阴性，其中 61.11%（11/18）ANA 阳性。胞浆型是 $Ro52^{+}Ro60^{-}$组中占比最高的 ANA 荧光模型（30.26%）。
结论 抗 Ro60 抗体和抗 Ro52 抗体出现在多种 AID 中，结合 ANA、其他特异性自身抗体可提高诊断的敏感性。相比抗 Ro60 抗体，抗 Ro52 抗体更多出现在 PM/DM、SS 中，当结合 ANA 时对 PM/DM 具有较大的诊断价值。抗 Ro60 抗体和抗 Ro52 抗体分开检测对 AID 的诊断具有一定的临床应用价值。

PU-1145

白细胞介素-6 在原发性肝细胞癌组织中的表达及其对肝癌细胞增殖、侵袭作用

李慧洋
湖南省第二人民医院

目的 探讨白细胞介素-6（IL-6）在原发性肝细胞癌组织中表达的变化,并通过体外实验探讨其对原发性肝细胞癌细胞增殖、侵袭的作用。
方法 收集 2020 年 1 月—2021 年 5 月在湖南省第二人民医院手术切除的原发性肝细胞癌组织及对应的癌旁组织,检测其 IL-6 的表达量;培养肝癌 hepG2 细胞,随机分为对照组、空白质粒组、转染表达 IL-6 的重组质粒组,MTS 检测 3 组肝癌 hepG2 细胞的增殖能力,Transwell 实验检测细胞的侵袭能力,qRT-PCR 检测细胞周期蛋白 D1（CyclinD1）、B 淋巴细胞瘤-2（Bcl-2）、基质金属蛋白酶 2（MMP-2）、基质金属蛋白酶 9（MMP-9）mRNA 相对表达量,Western blotting 法检测 IL-6、蛋白相对表达量。
结果 肝癌组织中 IL-6 的蛋白相对表达量高于癌旁组织（P <0.05）;3 组细胞增殖及侵袭能力,CyclinD1、Bcl-2、MMP-2、MMP-9 mRNA 相对表达量,p-STAT3、p-Akt 的蛋白相对表达量比

较,差异有统计学意义（P <0.05）,IL-6 质粒组的细胞增殖及侵袭能力,CyclinD1、Bcl-2、MMP-2、MMP-9 mRNA 相对表达量,p-STAT3、p-AKT 的蛋白相对表达量均高于对照组、空白质粒组。
结论 IL-6 在原发性肝细胞癌组织中表达增加,下调 IL-6 的表达能够抑制肝癌细胞的增殖、侵袭。

PU-1146

自身免疫性疾病的研究进展

王芳
大理大学第一附属医院检验科
无

自身免疫性疾病被列为继心血管疾病、癌症后危害人类健康的第三大杀手疾病。不同病种危害程度不同，如系统性红斑狼疮可致肾衰竭而引起死亡，类风湿性关节炎可导致关节强直畸形，miRNAs 参与了这两种自身免疫性疾病的发生和发展，因此可通过对 miRNAs 的检测，再结合相应的临床症状和体征，来对这两种疾病进行诊断。另外，肠道菌群失衡，也会引起此类疾病的发生。其治疗方法包括物理治疗法、免疫抑制剂治疗法和中药治疗法等。其中，物理疗法是一种辅助手段，中药具有良好免疫调节效果，且不良反应少。

PU-1147

广州地区健康成人淋巴细胞亚群参考区间初探

蓝名伟、周茂华、李文敏、冼璐桦
广东省人民医院检验科

目的 检测广州地区健康成人外周血淋巴细胞亚群，初步建立其参考区间。
方法 收集广东省人民医院体检中心 176 例健康成人（18-59 岁）的外周血标本，其中男性 87 例，女性 89 例。采用 BD Multitest™ 6-Color TBNK 六色试剂盒进行标记，使用 BD FACSCantoplus 流式细胞仪检测淋巴细胞亚群绝对计数。根据 CLSI C28-A3 文件建立淋巴细胞亚群参考区间。
结果 176 例健康成人外周血淋巴细胞绝对值计数(个/μL）为 2029（998,3736），CD3+T 细胞绝对值(个/μL）和百分比（%）分别为 1430（821,2656）、67.53±8.52，其中 CD3+CD4+细胞绝对值(个/μL）和百分比（%）分别为 774（454,1393）、36.44±7.21，CD3+CD8+细胞绝对值(个/μL）和百分比（%）分别为 551（292,1164）、25.26±6.31，CD4+/CD8+比值为 1.4（0.64,2.80），NK 细胞（CD3-CD16+56+）绝对值(个/μL）和百分比（%）分别为 412（144,1062）、19.39±7.55，B 细胞（CD3-CD19+）绝对值(个/μL）和百分比（%）分别为 230（113,528）、11.52±3.49。
结论 初步建立广州地区健康成人外周血的淋巴细胞亚群参考区间，为今后广州地区人群的疾病诊断、治疗和疗效的评价提供有效依据。

PU-1148

N 末端 B 型利钠肽原与心力衰竭相关性研究进展

刘瑞清
中国人民解放军陆军特色医学中心

N 末端 B 型利钠肽原（NT-proBNP）为心衰诊疗中应用广泛的生物标志物，有助于急慢性心衰的诊断和鉴别诊断、疗效监测及预后评估等。当患者发生心力衰竭时，心肌细胞受到压力和牵拉刺激，可分泌 B 型利钠肽原前体（pre-proBNP），经蛋白酶剪切后成为 B 型利钠肽原（proBNP），

随后裂解为 NT-proBNP 与 B 型利钠肽（BNP），并释放入血。与 BNP 相比，NT-proBNP 半衰期长达 120min，可在常温下稳定 72h，目前常用的检测方法为快速荧光法，操作简便，报告及时，故其作为心力衰竭标志物有其特有的优势，且可作为 POCT 检测项目。早期心力衰竭患者临床症状多不明显，NT-proBNP 的及时检测有助于发现早期心衰患者、筛查心衰高危人群，在治疗心衰期间，可与超声心动图联合评价心功能变化，调整心衰治疗，改善心衰预后。此外，NT-proBNP 还具有辅助诊断急性冠状动脉综合征（ACS）危险分层与心功能分级的潜力。本文对近年来 NT-proBNP 与心力衰竭的相关性研究进展进行综述，分析其在心力衰竭发生中的变化情况与检测节点，以及对心脏相关疾病的诊断与鉴别诊断，进一步体现其临床价值，为实现临床推广归纳提供系统性证据与支持。

PU-1149

乙肝病毒性肝炎患者两对半结果分析

杨彩婷
大理大学第一附属医院检验科

目的 研究乙肝病毒性肝炎患者两对半检验结果和运用效果。
方法 选取 2020 年 7 月至 2021 年 3 月在云南省第四人民医院治疗的 500 例乙肝病毒性肝炎患者为研究对象，对患者进行乙肝两对半的检查，同时对检验结果进行研讨。
结果 大三阳患者 96 例，占总人数的 19.2%,小三阳患者 327 例，占总人数的 65.4%，其他类型患者 77 例，占总人数的 15.4%。对这些数据进行分析和统计，数据差异比较显著，符合统计学意义（p〈0.05）。
结论 在乙肝病毒性肝炎患者的临床检验中，对患者进行乙肝两对半检验，可准确对患者病症进行预判，此外，按时进行两对半的检验，能有效预防乙肝病毒性肝炎的发生，在临床上可以广泛推广。

PU-1150

慢性乙型肝炎患者基因型和核苷酸类似物治疗及耐药突变的临床研究

张仁宁、李娅
昆明医科大学第一附属医院

目的 探究云南地区慢性乙型肝炎患者 HBV 基因型分布特征和核苷酸类似物耐药位点突变情况，分析其临床意义和药物治疗策略，为临床治疗提供指导。
方法 收集昆明医科大学第一附属医院 2018 年 5 月到 2018 年 9 月收治的慢性乙型肝炎患者血清 90 例进行高通量测序检测其基因型和核苷酸类似物耐药突变位点，结合基因型和突变位点、治疗时间分析其各类血清学指标差异变化。
结果 B 基因型患者 54 人，突变率 8.33%，以 M204I 突变为主。C 基因型患者 36 人，突变率 12.96%，以 M/V207I 突变为主，LAM、LdT 耐药患者多于 ADV、ETV，差异具有统计学意义（P<0.05）。治疗后 HBcAb、TBIL、DBIL、ALT、AST、FIB、GGT、GLU 明显上升，而 AST、ALT、TBIL、DBIL、GGT、FIB 随治疗时间延长又出现明显下降；而 PT、APTT 治疗后下降，差异有统计学意义（P<0.05）。B 基因型患者治疗后 BUN 下降，而 ALT、AFP 明显升高；差异有统计学意义（P<0.05）。未经治疗的 C 基因型 HBcAb 值高于 B 基因型，治疗后 C 基因型 TBIL、DBIL、PT、FIB 大于 B 基因型，而 FIB 小于 B 基因型，差异有统计学意义（P<0.05）；随着治疗时间延长，C 基因型 DBIL、ALT、TBIL 高于 B 基因型，同时突变患者 C 基因型 ALB、PT、CREA 值高于 B 基因型，差异有统计学意义（P<0.05）。

结论 云南地区 HBV 基因型以 B 型和 C 型为主，C 型占优势；产生的耐药突变均以 LAM、LdT 突变为主。C 基因型患者肝脏损伤程度较 B 基因型严重，且治疗后血清学改善的比例更低。B 基因型突变患者发生肾功能损伤的比例更大，但 C 基因型突变患者病情更严重。持续较长时间的 NAs 类治疗可以使患者肝功能血清学指标趋于改善，病情缓解；其中凝血功能改善最为显著；故需对患者耐药突变和血清学指标进行及时检测和监测，以指导患者后续治疗。

PU-1151

自身抗体在肺癌早期诊断中的研究进展

王甲甲、铁丹丹、谭太昌
四川省医学科学院·四川省人民医院

肺癌是全世界最常见的恶性肿瘤之一。肺癌高发病率、高死亡率是全球共同面临的问题。肺癌患者早期多无明显症状，多数患者一经发现即处于肺癌晚期，肺癌晚期患者 5 年生存率很低，所以肺癌的早期筛查尤为重要。肺癌自身抗体(Autoantibodies, AABs)，包括 P53、黑色素瘤抗原 (MAGE)-A1、G 抗原 (GAGE)7、肿瘤相关基因(CAGE)、ATP 结合 RNA 解旋酶 (GBU4-5)、性别决定基因家族 2 (SOX2)和蛋白基因产物 9.5 (PGP9.5)的检测在早期肺癌检测中越来越受到重视。P53 基因作为肿瘤抑制基因，在多种恶性肿瘤患者体内发生突变，针对 P53 基因的自身抗体可于肺癌早期出现。MAGE-A1、GAGE7、 CAGE、GBU4-5 均属于肿瘤-睾丸抗原，在多种恶性肿瘤中表 达，可在肺癌患者体内出现，而不表达于人体正常组织。SOX2 自身抗体主要 存在于小细胞肺癌(Small cell lung carcinoma, SCLC)患者血清中，而 PGP9.5 在 非小细胞肺癌(Non-small cell lung carcinoma, NSCLC)患者中表达增加。本文主要对自身抗体在早期肺癌临床诊断中的研究进展进行综述。

PU-1152

IL-6 及 RDW 相关多个参数在慢性阻塞性肺病老年患者急性加重中的风险预测分析

程玉洁、侯彦强
上海市松江区中心医院

目的 慢性阻塞性肺病（COPD）是老年人最常见的呼吸道慢性病之一，感染是引发慢性阻塞性肺病急性加重（AECOPD）最常见的危险因素之一。本研究意在能否通过血免疫和血常规检测来预警 COPD 老年患者的急性加重，探讨相关常规指标和联合因子应用与 AECOPD 发生风险的预测性分析。

方法 本研究分析了 2019 年 10 月至 2021 年 2 月间在上海市松江区中心医院呼吸内科与急诊接受治疗的 COPD 患者。经过 GOLD 标准的筛选，共有 135 名老年患者纳入分析。收集所有样本血清通过化学发光法、免疫比浊法和 WPC 全血细胞计数分别检测 PCT,IL-6，CRP 和全血细胞分析结果 PLT,EOS,NEU,LYM,RDW,MPV，并对这些结果进行二元 logistics 分析，同时对显著影响急性加重的风险因素进行 ROC 模型建立，应用 ROC 曲线获得总体病人的临界值以及各危险因素分组病人的临界值，通过比较灵敏度、特异度、阳性预测值及阴性预测值，判断分组临界值是否更有助于 AECOPD 的诊断或排除。

结果 共有 50 名患者发生 AECOPD，COPD 急性加重发生率 37%，logistic 回归分析显示，CRP，PCT,RDW,IL-6 对 COPD 急性加重变化有显著性影响（P<0.05），其中 CRP（OR,1.045；95% CI,1.023-1.067 ）， RDW （ OR, 1.459 ； 95% CI,1.028-2.068 ）， PCT （ OR, 2.994 ； 95% CI,1.257-7.132），IL-6（OR, 1.005； 95% CI,1.000-1.010）。联合因子 ROC 下面积 93.00%，CRP，PCT,IL-6 和 RDW 的联合使用对 COPD 急性加重有较好的预测价值。

结论 CRP，PCT,IL-6 和 RDW 的联合使用对预测 AECOPD 的发生具有明显价值。对于老年人 COPD 的急性加重风险具有预测作用。对于炎症反应不明显的患者具有一定的诊断意义。同时对于低于临界值的患者可应用于排除诊断。

PU-1153

TNFα、IL-10 基因多态性与肝细胞癌易感性的相关研究

王甲甲、王智斌、谭太昌
四川省医学科学院·四川省人民医院

目的 分析 TNFα、IL-10 基因多态性与肝细胞癌（HCC）易感性之间的相关性。
方法 选取于 2014 年 9 月至 2016 年 8 月就诊于四川省人民医院的 277 例 HCC 患者及 306 例健康对照者作为研究对象，所有研究对象均为汉族人。抽提全血基因组 DNA，PCR 扩增后直接测序法检测 TNFα（-238G/A，-308G/ A）、IL-10（-592 C/A， -819 C/T）基因多态性的分布；ELISA 法检测血清、细胞培养上清中 TNFα、IL-10、IL-2、IL-4、TGF-β 的水平；体外淋巴细胞增殖实验和细胞毒实验检测携带不同基因型的外周血单个核细胞（PBMCs）的增殖能力及细胞毒活性。
结果 TNFα -238AA、-238A 与 HCC 的风险降低明显相关，IL-10 -592CA、 -819CT/TT 和-819T 与 HCC 的风险增加有关（$p<0.05$）。携带 TNFα AA 基因型的 PBMCs 仅与 IL-2、IL-4 水平降低有关。相反，携带 IL-10 -819 CC 基因型的 PBMCs 增殖能力明显降低，分泌 TGF-β、IL-10 水平明显减少，细胞毒活性显著增加（$p<0.05$）；同时，IL-10 -819T/C 与 HCC 的分级有明显的相关性。
结论 IL-10 -819 CT/TT 能够促进 HCC 的发生、发展，这可能与下调 Th1/Th2 型细胞因子，上调 Th3 型细胞因子有关。

PU-1154

炎症指标的研究

常谦
郑州大学第一附属医院

SII、PLR、NLR、LMR、MLR 等炎症指标的研究正逐渐丰富，这些指标被越来越多研究证实与多种类型的疾病进展及预后相关。由于其具有简便易获取且成本低廉的特点，应用前景广泛。尽管如此，仍有一些问题亟待解决。首先，针对健康人群的研究有限，大多数研究都只分析疾病治疗前后（手术或用药等）的 SII、PLR、NLR、LMR、MLR 水平，尤其缺少这些指标在健康人群的参考区间，缺少统一的定量标准，这使得连续监测的意义大打折扣。此外，缺少这些指标在不同疾病中的横向比较，使其临床应用受到限制。再者，缺少连续动态变化的数据，此类研究多以某个疾病状态下患者的检测指标为准，更进一步的研究中需要连续动态监测的数据，以更好的判断疾病进展趋势。最后，SII、PLR、NLR、LMR、MLR 等炎症指标均是基于血液学指标计算得出，血液学指标本身受多种因素影响，其采集和保存过程中也许多不定因素

PU-1155

2018-2019 年快速流感病毒抗原检测筛查结果分析

周庆丰、刘军
上海市松江区中心医院

目的 分析流感病毒抗原检测试剂盒（胶体金法）检测的有效性，评价流感病毒抗原检测试剂盒在临床中的应用。

方法 选择 2018 年—2019 年（1 月、2 月）同期在上海市松江区中心医院就诊的体温＞38℃，且具有流感样症状的患者，采集鼻拭子标本，用甲型/乙型流感病毒抗原检测试剂盒检测筛查，并对结果进行统计分析。
结果 5877 例流感样病例中，共检出 1915 例流感病例，阳性率为 32.5%；其中甲型流感病毒感染 1505 例，阳性率为 78.6%；乙型流感病毒感染 358 例，阳性率为 18.7%；甲、乙型流感病毒混合感染 52 例，阳性率为 2.7%；其中，2018 年与 2019 年同期的甲型流感病毒阳性率差异较大（P<0.05），2019 年 1 月乙型流感病毒阳性率与 2018 年同期相比差异较大（P<0.05）；而甲、乙型流感病毒混合感染阳性率无显著差异（P>0.05）。2018-2019 年（1 月、2 月）流感病毒主要分布于 0-12 岁的婴幼儿及儿童患者，以甲型流感病毒为主，阳性率在 78.0%左右，乙型流感病毒次之，约为 20.0%，甲、乙型流感病毒混合感染较为稳定，为 3.0%左右。
结论 在流感爆发时期，由于流感样本量大，流感病毒快速抗原检测方法可以在数十分钟时间内显示结果，而且具有操作简便，快速、易判读，故可用于流感早期筛查。

PU-1156

成都地区过敏原特异性 IgE 抗体检测结果分析

王甲甲、周佳祥
四川省医学科学院·四川省人民医院

目的 本研究旨在分析成都地区过敏性疾病患者血清特异性过敏原的分布特点及规律，为过敏性疾病的防治提供流行病学资料和诊断依据。
方法 选择 2018 年 9 月至 2021 年 4 月期间在四川省人民医院就诊并进行过敏原特异性 IgE（Immunoglobulin E,IgE）抗体筛查检测的 19744 名患者，采用酶联免疫法（Enzyme Linked Immunosorbent Assay，ELISA）快速试纸条技术检测血清中的总 IgE 和过敏原特异性 IgE 抗体，按照不同年龄段、不同性别、不同季节、不同疾病分组统计过敏原检测结果阳性率，分析过敏原分布特点与规律。
结果 19744 例过敏性疾病患者中，共 8406 例过敏原特异性 IgE 检测结果为阳性，阳性率为 42.57%；吸入性过敏原检测结果阳性率前三名为屋尘螨（15.17 %）、屋尘（10.86 %）、猫毛皮屑（4.04 %）；食入性过敏原检测结果阳性率前三名为牛奶（2.26 %）、牛肉（1.68 %）、蛋清（0.86 %）。通过分组统计分析显示，吸入性过敏原阳性率高于食入性过敏原阳性率；男性阳性率高于女性；0~10 岁、10~18 岁、18~60 岁、＞60 岁患者最主要的过敏原分别为屋尘螨和屋尘；秋季阳性率最高，其次为春季、冬季，夏季最低；以疾病的类型进行分类，阳性率从高到低依次为：过敏性鼻炎、哮喘、皮炎湿疹、过敏性紫癜、荨麻疹。
结论 上述结果在一定程度上反映了成都地区过敏原分布特点及规律，为本地区过敏性疾病的防治提供参考依据。

PU-1157

丽水地区新生儿与婴幼儿 TORCH 感染情况结果分析

张强
丽水市人民医院

目的 了解丽水地区新生儿与婴幼儿 TORCH 的感染情况。
方法 采用 ELISA 法检测 2059 例新生儿与婴幼儿血清中的 TORCH 特异性抗体，并进行结果分析。
结果 2059 例 TORCH 检测结果， TORCH-IgM 总感染率是 2.03%，CMV-IgM、Rv-IgM、TOX-IgM、HSV-IgM 的阳性率分别是 1.89%、0.05%、0.05%、0.05%，CMV-IgM 阳性率最高； CMV-IgG、Rv-IgG、TOX-IgG 的阳性率分别是 98.39%、85.23%、1.02%。不同年龄组 IgM 与 IgG 抗体

检测结果中 CMV-IgM、Rv-IgM、CMV-IgG、Rv-IgG 比较，差异有统计学意义（P<0.05）。不同性别的 IgM 与 IgG 抗体检测结果比较，差异无统计学意义（P>0.05）。
结论 丽水地区的新生儿与婴幼儿的 TORCH 的感染最高是 CMV。

PU-1158

血清胃蛋白酶原联合胃泌素-17 检测对萎缩性胃炎诊断价值的评估

张航烽
四川省医学科学院·四川省人民医院

目的 探讨血清Ⅰ型胃蛋白酶原(PGⅠ)、Ⅱ型胃蛋白酶原(PGⅡ)、PGR(PGⅠ/PGⅡ)和胃泌素-17(G-17)与萎缩性胃炎(AG)发生的关系及其诊断价值。
方法 采用酶联免疫吸附试验(ELISA) 法检测 195 例 AG 患者及 170 例健康对照者的血清 PGI、PGⅡ、PGR 和 G-17 表达水平，采用受试者工作特征(ROC)曲线评估各指标在萎缩性胃炎诊断中的效能。
结果 萎缩性胃炎组血清 PGⅠ、PGⅡ和 G-17 水平低于健康对照组，差异有统计学意义（P<0.05），根据 ROC 曲线，PGⅠ、PGⅡ及 G-17 诊断萎缩性胃炎的最佳临界值分别是 70.1μg/ml（敏感度 96%、特异性 82%、曲线下面积 0.887±0.040）、4.94μg/ml（敏感度 78%、特异性 64%、曲线下面积 0.725±0.051）和 1.65pmol/ml（敏感度 88%、特异性 76%、曲线下面积 0.848±0.04）。
结论 联合检测血清 PGⅠ、G-17 在萎缩性胃炎中有一定的诊断价值，可作为一种无创的筛查萎缩性胃炎的方法。

PU-1159

丽水地区流式细胞术检测白细胞抗原 B27 阳性率分析

张强
丽水市人民医院

目的 了解丽水地区不同年龄段白细胞抗原 B27（HLA-B27）分布情况。
方法 选择 2017 年 1 月-2019 年 1 月在丽水市人民医院风湿免疫门诊就诊的 1795 名患者作为研究对象，通过流式细胞术检测外周血 T 淋巴细胞 HLA-B27 抗原表达，并对结果进行统计分析。
结果 1795 名患者中 HLA-B27 阳性病例数是 251，阳性率为 13.98 %，其中男性、女性阳性表达率分别是 17.21 %、10.90 %。按年龄组分成≤20 岁、21 岁～30 岁、31 岁～40 岁、41 岁～50 岁、51 岁～60 岁、>60 岁，阳性率分别为 11.76 %、26.21 %、 20.25 % 、14.55 %、 9.96 % 和 8.74 %，阳性患者中主要是 21 岁～30 岁最高。
结论 HLA-B27 阳性表达率男性高于女性，主要集中于 21 岁～30 岁，流式细胞术检测 HLA-B27 为强直性脊柱炎的诊断提供重要依据。

PU-1160

间接法建立亚高原地区成年人血清甲状腺激素生物参考区间

鲁彦[2]、梁勤[1]、邢福军[1]
1. 甘肃省中医院检验科
2. 甘肃省中医院检验科

目的 通过“间接法”建立西门子 CP 化学发光仪亚高原地区成年人血清甲状腺激素水平生物参考区间。
方法 收集该院 2014 年 1 月 4 日至 2017 年 6 月 30 日实验室信息系统（LIS）内体检中心体检人员甲状腺资料 15 293 例。采用偏度-峰度值（Skewness-Kurtosis）对数据进行正态性检验。依据设备检测限度、四分位间距法剔除异常数据，采用 Hoffman 法获取参考区间，并与说明书和指南生物参考区间进行比较。
结果 “间接法”建立的生物参考区间为三碘甲状原氨酸（T3）：0.67～1.7 ng/mL；游离三碘甲腺原氨酸（FT3）：2.3～3.6 pg/mL；甲状腺素（T4）：5.5～10.9 μg/mL；游离甲状腺素（FT4）：0.89～1.75 ng/dL。T3、FT3、T4、FT4 与指南生物参考区间相对偏差分别为（﹣9.57%，﹣14.10%）、（2.56%，69.12%）、（﹣8.86%，11.34%）、（﹣9.33%，27.14%）；与说明书相对偏差分别为：（﹣5.85%，8.97%）、（﹣17.09%，0.00%）、（0.00%，20.24%）、（﹣0.52%，0.00%）。
结论 “间接法”建立的亚高原地区成人健康人群生物参考区间与指南和说明书提供的生物参考区间有较大的偏差，应根据不同人群建立实验室参考区间。

PU-1161

胃蛋白酶原影响因素分析以及德阳地区参考区间的建立

曹维维
德阳市人民医院

目的 分析探讨性别、年龄以及幽门螺旋杆菌（Hp）对胃蛋白酶原水平的影响,以及分层建立德阳地区体检人群酶联免疫吸附法血清 PGI、PGII 和 PGR 的参考区间。
方法 收集 2019 年 1 月到 2019 年 8 月来德阳市人民医院进行健康体检者的基本信息，用 ELASA 方法定量检测血清样本中 PGI、PGII 并计算 PGR 值，同时对各体检者进行碳 13 呼气试验。并用统计学方法参考年龄、性别、HP 感染等影响因素进行分层分析，建立血清胃蛋白酶原水平的参考区间。
结果 调查 1403 人的血清 PGⅠ，PGⅡ及 PGR 的值，得出 PGⅠ，PGⅡ和 PGR 呈偏态分布。PG 与年龄有相关性，其中 PGⅠ（r=0.107）、PGⅡ（r=0.249）与年龄正相关，年龄越大，值也相对增大。PGR（r=-0.201）与年龄负相关。男性ＰＧⅠ、ＰＧⅡ及 PGR 水平显著高于女性，差异有统计学意义（P<0.05）。HP 阳性组的 PGⅠ，PG2 水平显著高于 HP 阴性组 差异有有统计学意义(P<0.05)。HP 阳性组的 PGR 显著低于 HP 阴性组，差异具有统计学意义。男性的 HP 感染率为 62.8 高于女性为 37.2，差异具有统计学意义（P<0.05）。
结论 血清 PGⅠ、PGⅡ水平与性别、年龄、HP 感染均相关，将 HP 与血清 PGⅠ PGⅡ水联合检测对胃部疾病的早期筛查有重要意义

PU-1162

骨代谢标志物各项之间及与 IGF-1 的相关性研究

邱洪
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 对骨代谢相关标志物 β-胶原特殊序列(β-CrossLaps)、总 I 型前胶原氨基端延长肽(total procollagen type 1 amino-terminal propeptide, tP1NP)、人 N 端中段骨钙素(N-MID Osteocalcin, N-MID OC)、25 羟维生素 D(25-(OH)D)各项之间及各项与胰岛素样生长因子（Insulin-like growth factor，IGF-1）之间的相关性进行研究。
方法 将于我院进行常规男、女体检者 22 岁至 60 岁共计 194 名作为研究对象，对骨代谢标志物生物各项之间及各项与 IGF-1 之间的相关性进行研究。
结果 性别因素对骨代谢标志物有显著影响，男性组均大于女性组（P<0.05）。tP1NP 及 N-MID OC 水平随年龄的升高而降低，呈现负相关，推测与性激素的减少有直接关系。25-(OH)D 与各骨代谢标志物均无相关性（P>0.05）。IGF-1 水平与 β-CrossLaps、N-MID OC 呈正相关关系，再次证实了 IGF-1 参与调节骨形成、骨吸收的过程。
结论 性别、年龄为骨代谢标志物的独立影响因素，故应设立相应的参考区间。VD 缺乏广泛存在，但与骨代谢标志物无相关性。IGF-1 通过正向调节 β-CrossLaps、N-MID OC 参与机体的骨形成与骨吸收过程。

PU-1163

不同免疫学方法检测自身免疫性肝病患者血清 AMA-M2 的对比研究

王春玲
东南大学附属中大医院

目的 比较不同免疫学检测方法对抗线粒体 2 型抗体（AMA-M2）的检测性能。
方法 收集 2020 年 8 月至 2021 年 4 月间就诊本院的 21 例自身免疫性肝病患者、13 例乙型病毒性肝炎和 20 例健康体检人群对照血清样本，应用多重流式免疫分析法和线性免疫印迹法平行检测 AMA-M2。不同方法之间检测结果的一致性采用 Kappa 检验。
结果 多重流式免疫分析法与线性免疫印迹法检测 AMA-M2 时，阳性符合率为 61.5%，阴性符合率为 100%，总体符合率为 92.5%（Kappa=0.708；P<0.01)。
结论 应用多重流式免疫分析法和线性免疫印迹法检测 AMA-M2 时，两种方法具有良好的符合率和一致性。

PU-1164

Evaluation of the clinic value of serum Anti-rings and rods antibodies detection

Chengjie Xu
Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China

it was reported that Anti-rings and rods (Anti-RR) antibodies are most commonly detected in HCV patients,especially who have undergone treatment with ribavirin or interferon alpha (IFN-α),and which have been associated to a poorer prognosis. Despite the recent availability of more effective and less toxic therapeutic options for the HCV patients,Anti-RR antibodies are still

frequently detected in serum samples from patients with multiple diseases. The aim of this context was to investigate the appearance of Anti-RR antibodies in different patients.Anti-RR antibodies were detected by indirect immunofluorescence (IIF) on HEp-2 cells. this study retrospectively examined the samples received from 2017 to 2019 for antinuclear antibody (ANA) testing. 106 out of 52964 patient samples exhibited the anti-RR antibodies, Among the 106 Anti-RR positive cases,there are 20 diseases involved,51 patients(48.11%) had renal dysfunction ,48 patients(45.28%) had high blood pressure while only 8 patients (7.55%) were infected with HCV, the rest of disease account for a small proportion,but none of the Anti-RR positive patients received ribavirin or IFN-α treatment and there is no evidence to link the use of certain drugs with the emergence of anti-RR antibodies ; further studies showed that RR pattern could not be directly related to disease prognosis,Whether in renal dysfunction or hepatitis C positive patients.in conclusion, these observations led to the hypothesis that the anti-RR antibodies are not significantly for HCV patients with ribavirin or IFN-α treatment and the value of anti-RR antibodies in the disease diagnosis and prognosis need to be futher studied.

PU-1165

TB-IGRA 检测在肾脏疾病患者中关于潜伏性结核的辅助诊断和预防性治疗后效果评价的应用

任亚文、张甲龙
铜川市人民医院

目的 肾脏疾病患者是潜伏性结核感染（Latent tuberculosis infection，LTBI）的重要人群之一。对此类人群进行结核病的筛查是进行预防性治疗的前提。
方法 通过对肾脏疾病患者中潜伏性结核感染者预防性治疗前后 γ 干扰素释放试验结果的比较,判断预防性治疗的效果。
结果 γ 干扰素释放试验在肾脏疾病患者中辅助诊断潜伏性结核和预防性治疗后效果评价具有方便、快速、易于统计等优点。
结论 对筛查试验阳性的 LTBI 者进行预防性治疗可以降低发生活动性结核病地风险。

PU-1166

HIV-1 广谱中和抗体的亲和力成熟、特征及运用

万鑫蕊[2]、李娅[1]
1. 昆明医科大学第一附属医院医学检验科
2. 昆明医科大学第一附属医院医学检验科

人类免疫缺陷病毒（human immunodeficiency virus，HIV-1）感染的长期不进展者（long-term nonprogression, LTNP）中，分离到的广谱中和抗体（broadly neutralizing antibodies，bNAbs）已被证明可以预防 HIV-1 感染并降低感染者体内的病毒载量。成为了指导 HIV-1 疫苗设计和被动免疫治疗的突破口。中和抗体的功能除了与表位有关，其亲和力也极大的影响了抗体的活性。HIV-1 bNAbs 通过体内的多轮亲和力成熟(affinity maturation)获得了较高亲和力，从而实现了广谱度和中和活性的增加。高亲和力 HIV-1 bNAbs 在治疗过程中能更好的辅助机体免疫系统清除病原体，并且使用剂量更少，毒副作用较低。在亲和力成熟的同时，HIV-1 bNAbs 表现出了高水平的体细胞超突变（somatic hypermutation，SHM）、插入缺失、较长的重链第三互补决定区等不寻常的特征。HIV-1 bNAbs 仅在少数长期不进展者中产生以及其异常特征表明，bNAbs 亲和力成熟受到多种复杂因素的调控，这些特征导致通过有效疫苗诱导 HIV-1 bNAbs 的难度增加。因此了解抗体亲和力成熟的过程有助于我们理解中和抗体的活性与特征的关系，并为设计潜在有效的 HIV-1 免

疫原提供参考。目前 HIV-1 疫苗的设计策略更趋向于抗体胚系特异性抗原的设计，即使用能与 bNAbs 前体 B 细胞结合的 HIV-1 免疫原，并采用共进化过程中关键位点突变的免疫原多次免疫以实现亲和力和广谱度的成熟，从而诱导广谱活性抗体产生，基于对 HIV-1 bNAbs 发育过程中亲和力成熟的理解，基于抗体与病毒共进化的研究，将极大的促进我们设计新型 HIV-1 疫苗诱导理想的 bNAbs，为突破 HIV-1 的有效预防提供新的突破口。对 HIV-1 bNAbs 发育过程中亲和力成熟的研究，有利于我们理解疫苗诱导 bNAbs 的机制及突破口。

PU-1167

clinic value of serum Anti-rings and rods antibodies detection

许程洁
电子科技大学附属医院•四川省人民医院

The aim of this context was to investigate the appearance of Anti-RR antibodies in different patients.Anti-RR antibodies were detected by indirect immunofluorescence (IIF) on HEp-2 cells. this study retrospectively examined the samples received from 2017 to 2019 for antinuclear antibody (ANA) testing. 106 out of 52964 patient samples exhibited the anti-RR antibodies, Among the 106 Anti-RR positive cases,there are 20 diseases involved,51 patients(48.11%) had renal dysfunction ,48 patients(45.28%) had high blood pressure while only 8 patients (7.55%) were infected with HCV, the rest of disease account for a small proportion,but none of the Anti-RR positive patients received ribavirin or IFN-α treatment and there is no evidence to link the use of certain drugs with the emergence of anti-RR antibodies ; in conclusion, these observations led to the hypothesis that the anti-RR antibodies are not significantly for HCV patients with ribavirin or IFN-α treatment and the value of anti-RR antibodies in the disease diagnosis and prognosis need to be futher studied.

PU-1168

迈瑞 CL-2000i 化学发光分析系统检测 PCT 的性能评价

王萍
亳州市人民医院

目的 探讨迈瑞 CL-2000i 化学发光分析系统检测 PCT（降钙素原）的临床适应性。
方法 根据美国临床实验室标准化协会（CLSI）的 EP9-A2 文件的规定，以罗氏 cobas® 6000 电化学发光分析系统作为参比系统，以迈瑞 CL-2000i 化学发光分析系统作为实验系统，通过对 PCT 进行检测，并对 2020 年 12 月 7 日～17 日 98 例我院就诊的患者 PCT 测定结果进行比对分析和偏倚评估，评价迈瑞 CL-2000i 化学发光分析系统检测 PCT 的临床适应性。
结果 两套检测系统对 PCT 检测结果的相关系数 r＞0.95，具有良好的相关性。高、中、低等 3 个水平的检测结果均具有较好的一致性。
结论 迈瑞 CL-2000i 全自动化学发光免疫分析系统检测 PCT 能够满足临床，可以应用于临床。

PU-1169

亚精胺调节巨噬细胞及炎症性疾病的研究进展

吴思弦、袁浩、周毅峰、龙贞义、彭亚梦、彭芳
湖南省人民医院

亚精胺是一种天然多胺，可抑制巨噬细胞活化，通过下调炎症介质释放及抗氧化应激水平，诱导自噬，抑制炎症相关信号通路等调节炎症反应。文章就亚精胺在调控巨噬细胞和炎症性疾病中的作用和机制作一综述，以期为炎症性疾病的预防和治疗提供参考。

PU-1170

N 末端脑钠肽前体(NT-proBNP)对心力衰竭的诊断研究

朱薇、何玲鸽 、李耀妮
宝鸡市中心医院

目的 探讨 N-末端脑钠肽前体(NT-pro BNP) 在心力衰竭（HF）患者病变程度及心功能评估中的应用价值。

方法 选择心力衰竭患者 60 例作为试验组，按照美国纽约心脏病学会（NYHA） 分级分为Ⅱ～Ⅳ级，选择健康体检者 60 例作为对照组，采用电化学发光法（夹心法）测定血清 NT-proBNP 浓度。进行统计分析。

结果 与对照组相比，心力衰竭病人血清 NT-proBNP 检测值升高，且随心力衰竭的程度加重而增加，差异具有统计学意义(P＜0．05)。心力衰竭（NYHA 分级）
各组间血清 NT-proBNP 浓度的测定结果存在显著性差异(P<0.01)，具有统计学意义。

结论 在心力衰竭的早期筛查中，不仅可以通过检测血清 NT-proBNP 浓度水平作出初步诊断，而且随着心力衰竭程度的加重，心功能的进一步恶化，血清 NT-proBNP 水平逐渐升高，能有效提示疾病的发展进程和预后情况。

PU-1171

HIV-1-型长期不进展者 B 细胞谱系相关研究进展

李明玉、李娅
昆明医科大学第一附属医院

HIV-1 感染是危害全世界人类健康的公共卫生问题，虽然抗反转录病毒治疗在治疗 HIV-1 感染上取得了显著成效，但目前艾滋病仍然无法治愈，研发出能够诱导中和多种 HIV-1 毒株能力的广谱中和抗体 （Broadly neutralizing antibodies, bNAbs）的 HIV-1 疫苗，成为防治 HIV-1 感染的重要目标。HIV-1 长期不进展者（Long-term nonprogression, LTNP）是 bNAbs 的主要提供者，大量学者对 LTNP 展开了研究，阐释 HIV-1 长期不进展者 B 细胞谱系的特征，将为广谱中和抗体成熟的相关研究奠定重要基础。得益于单个 B 细胞分选、抗体克隆技术的成熟，以及高通量测序在抗体库中的应用，HIV-1 长期不进展者 B 细胞谱系的相关研究取得了一定成效，这些研究为 HIV-1 疫苗研发提供了新思路和新的实践指导。由于靶向 HIV-1 包膜不同位点的 bNAbs 在 HIV-1 长期不进展者中存在特定的 B 细胞谱系，本文就 HIV-1 长期不进展者的特定 B 细胞谱系相关研究进展进行综述。

PU-1172

四川地区不孕患者血清抗缪勒管激素水平的影响因素分析

许程洁
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 通过分析四川地区不同年龄组不孕患者血清中抗缪勒氏管激素(AMH)水平变化及其病因，探讨影响女性不孕患者血清中 AMH 水平变化的影响因素,为评估本地不孕女性卵巢功能水平和寻找不孕病因提供参考。
方法 选择来四川省人民医院就诊的 2350 例 20-50 岁不孕女性作为研究对象，按照年龄分成 5 组，＜25 岁组，26-30 岁组，31-35 岁组，36-40 岁组，＞40 岁组，ELISA 法检测血清 AHM 水平。
结果 血清 AMH 水平与年龄呈现负相关，以 20-25 岁年龄段最高。其中，多囊卵巢综合症和输卵管不通的患者的血清 AMH 水平显著高于平均水平。
结论 年龄、病因是不孕症女性 AMH 水平的主要影响因素。

PU-1173

联合检测血清 CA125、SA 和 SOD 在卵巢癌诊断中的价值

曹修娥、栾芳
山东第一医科大学附属省立医院

目的 探讨血清糖类抗原 125（CA125）、唾液酸（SA）及超氧化物歧化酶（SOD）在卵巢癌诊断中的临床应用价值。
方法 回顾性研究。选择山东大学附属省立医院妇科住院的 180 例卵巢癌患者作为卵巢癌组（所有病例均经病理组织学检查确诊）、105 例卵巢良性疾病患者及 115 名健康对照者（正常对照组），血清 SA 和 SOD 的含量采用酶法在 Beckman 全自动生化流水线上检测，电化学发光法在罗氏 Cobas 8000 全自动化学发光分析仪上检测 CA125 的含量。采用统计软件 SPSS 20.0 对数据进行统计分析，多组比较采用秩和检验，组间比较采用卡方检验。
结果 卵巢癌组血清 SA、SOD、CA125 水平分别为（710.81±182.82）mg/L、（149.22±39.09）U/ml、（766.53±1115.86）U/ml，卵巢良性疾病组血清水平分别为（556.49±70.83）mg/L、（187.22±25.41）U/ml、（15.89±8.49）U/ml，正常对照组血清水平分别为（556.85±57.55）mg/L、（173.68±14.50）U/ml、（11.56±5.50）U/ml，不同组间的血清 SA、SOD、CA125 水平比较，差异均有统计学意义，进一步经 Mann-Whitney 秩和检验两两比较可知，血清 SA 和 CA125 在卵巢癌组中明显高于卵巢良性疾病组和正常对照组（Z 值分别为-8.11、、-11.829、-8.305、-13.145，P<0.001），卵巢癌组中的血清 SOD 含量显著低于卵巢良性疾病组及正常对照组（Z 值分别为-10.265、-8.731，P<0.001）。在单项检测中 CA125 的灵敏度（86.67%）高于 SA、SOD（分别为 63.89%、65.56%）。CA125 与 SOD 联合检测诊断卵巢癌的特异度、准确度最高，分别为 91.3%、91.19%；CA125、SA、SOD 联合检测诊断卵巢癌的灵敏度最高为 92.22% 。
结论 CA125 仍是目前诊断卵巢癌的重要指标。血清 SA、SOD、CA125 联合应用能弥补单项血清标志物检测的不足，对提高卵巢癌的诊断具有重要的临床价值。

PU-1174

外周血淋巴细胞亚群与肺癌患者的预后关系

张璐璐
山东第一医科大学附属省立医院

目的 探讨外周血细胞亚群与肺癌预后的关系。
方法 选取 2013 年 1 月到 12 月来山东省立医院首诊的病例资料完整肺癌患者共 233 例，其中非小细胞癌 203 例，小细胞癌 30 例。另选取 60 例年龄和性别匹配的健康体检患者作为正常对照，同时检测其外周血 T 淋巴细胞亚群、NK cells、CD19+ B cells，结合临床病理特征回顾性分析 NSCLC 患者外周血淋巴细胞亚群与其预后的关系。
结果 肺癌患者外周血 CD3+T cells、CD4+ T cells、CD4/CD8 ratio、CD19+ B cells 明显低于正常对照组（P<0.05），而 CD8+ T cells、明显高于正常对照组（P<0.05），差异均有统计学意义。单因素和多因素变量 Logistic 回归分析结果显示，CD8+T cells 水平降低时与肺癌预后的风险比分别是（HR=3.84、p<0.0001, HR =1.78、P=0.0048）,是影响肺癌预后的因素。
结论 外周血 CD8+T cells 的增高的患者可获得较长时间的生存期。

PU-1175

肥大细胞活化分子及其抗体在鼻息肉中的表达及机制探讨

丁爽
徐州医科大学附属医院

目的 通过分析肥大细胞（Mast Cell, MC）活化分子及其抗体水平在鼻息肉患者血清、组织中的表达，探讨 MC 与鼻息肉发生的关系及其发病机制。
方法 选取 2020 年 1 月至 2020 年 12 月就诊于我院患者作为研究对象，且所有患者均经过术前鼻内窥镜及鼻窦 CT 检查。实验分为两组：30 例鼻息肉（NP 组）作为实验组；30 例行单纯下鼻甲部分切除术的鼻中隔矫正术者作为对照组（N 组）。收集患者的临床资料和外周血及鼻粘膜组织。全自动血细胞分析仪检测外周血中嗜酸性粒细胞百分比，速率散射比浊法检测血清 IgE 水平，酶联免疫吸附试验检测血清中抗 IgE 抗体、FcεRIα 和抗 FcεRIα 抗体水平。鼻息肉组，随机收取自手术中双侧鼻息肉组织，且术后送病理确诊为息肉；对照组，取下鼻甲黏膜组织。HE 观察两组组织病理改变，免疫组织化学方法分析类胰蛋白酶和 FcεRIα 在实验组和对照组的表达。
结果 鼻息肉组中嗜酸性粒细胞百分比、FcεRIα、抗 FcεRIα 抗体水平均明显高于对照组（P < 0.05），IgE 和抗 IgE 抗体与对照组相比，差异不显著（P > 0.05）；HE 染色和免疫组织化学结果提示，鼻息肉组中，嗜酸性粒细胞浸润；鼻黏膜下层和黏膜间质中发现棕色的类胰蛋白酶阳性、膜表面 FcεRIα 阳性的 MC。
结论 鼻息肉患者血清中高表达 FcεRIα 及其抗体，提示此抗体系统参与了鼻息肉的发生发展，MC 影响着鼻息肉形成的可能作用及具体机制值得进一步探讨。

PU-1176

1 例妊娠患者合并干燥综合征及腹中胎儿系统性红斑狼疮确诊的病例报道

李颖
东南大学附属中大医院

目的 报道东南大学附属中大医院产科 1 例妊娠患者合并干燥综合征及腹中胎儿系统性红斑狼疮确诊病例。结合患者该病的既往史、临床表现、实验室检查等，明确该病是一种经胎盘传导的获得性自身免疫性疾病，该自身抗体可存在于母亲羊水和胎儿脐带血中。
方法（1）诊断依据：1.（2021-04-17）患者李某，女，35 岁，因“停经 23 周 1 天，发现胎心偏慢 3 周，加重 1 天”入院。产检：宫高：22cm,腹围：79cm,内检未行。2.常规（2021-04-13,中大医院）胎位 ROP,双顶径 5.66cm,头围 20.88 cm,腹围 18.58 cm,股骨 3.79cm,颅骨可见，四腔心可见，腹壁脐带插入处未见异常膨出，胃泡可见，膀胱可见，双肾可见，颈部未见明显压迹。胎盘位于子宫宫底及前后壁，成熟度 0 度，厚度 1.96cm,位置正常。3.实验室检查（2021-04-13,中大医院）血细胞分析（五分类仪器检测法）：血红蛋白量：81g/L↓;急诊纤溶功能检查：D-二聚体：520μg/L↑;红细胞沉降率测定（ESR)(仪器法）：86mm/h↑,体液免疫特定蛋白检测：免疫球蛋白 G:22.9g/L↑KAP 轻链：5.9g/L↑ LAM 轻链：2.53g/L↑抗 β2-糖蛋白 1 抗体测定：抗 β2 糖蛋白 1 抗体：71.872RU/mL↑;ACA^ANCA:抗核抗体主要核型：细胞核一斑点型；抗核抗体主要核型滴度：1:320 阳性；抗 SSA 抗体 Ro60:阳性；抗 SSA 抗体 Ro52:阳性；抗 SSB 抗体：阳性（＋）。（2）目前诊断：1.妊娠合并干燥综合征；2.胎儿系统性红斑狼疮；3.产科抗磷脂综合征；4.胎儿心包积液；5.胎儿心律失常等；（3）采集患者外周血、羊水及胎儿脐带血进行抗核抗体系列检测,分别对该三种类型的样本进行 1:320 及 1:100 稀释,得出的结果为:患者外周血抗核抗体 1:320 核斑点型阳性；抗 SSA 抗体 Ro60 阳性；抗 SSA 抗体 Ro52 阳性；抗 SSB 抗体阳性。羊水和脐带血抗核抗体 1:100 核斑点型阳性；抗 SSA 抗体 Ro60 阳性；抗 SSA 抗体 Ro52 阳性；抗 SSB 抗体阳性。
结论 (1)临床上对于患有自身免疫性疾病的孕妇进行产前的相关筛查是十分有必要的。(2)该病例直接反应出高滴度自身抗体可通过胎盘进入羊水和胎儿脐带血,造成胎儿系统性红斑狼疮，应引起广泛重视。

PU-1177

结核性脑膜炎的诊断研究进展

黄鑫
襄阳市第一人民医院

结核性脑膜炎是指由于致病菌结核分支杆菌感染颅内脑膜或脑实质的一类非化脓性炎症，其为中枢神经系统常见的一种感染性疾病。该病的诊断主要依赖于对致病菌的检测，近年来关于结核性脑膜炎结核分枝杆菌检测方法的研究越来越多，治疗手段也有了大量的变化。因此，本研究对相关研究资料进行整理分析，对相关诊断结果和治疗方案进行综述，以期为结核性脑膜炎的诊断及治疗做出科学指导，提升诊断准确性，提高治疗的针对性，改善患者的预后。

PU-1178

LncRNA039932 对 RAW264.7 细胞因子分泌谱影响的研究

邵琦
徐州医科大学附属医院

目的 探讨 LncRNA039932 对 RAW264.7 细胞因子分泌谱的影响。
方法 (1)首先采用基因芯片技术筛选出不同极化状态 RAW264.7 中差异表达的 LncRNAs。并运用 qRT-PCR 技术验证了其中的 LncRNA039932。(2)利用小干扰 SiRNA 下调 RAW264.7 中 LncRNA039932,运用 ELISA 技术检测转染组与对照组上清中 IL-1β、TNF-α、IL-10 的含量，同时以流式细胞术检测转染后 RAW264.7 细胞表面抗原递呈分子 CD80、CD86 的表达。
结果 (1)M2 型极化状态下，LncRNA039932 高表达。(2)与对照组相比，SiRNA 组 IL-1β、TNF-α 表达增高；IL-10 含量显著下降.且差异有统计学意义。而转染前后 CD80、CD86 的表达均无明显变化。
结论 LncRNA039932 参与调控 RAW264.7 细胞因子分泌谱。同时我们猜想应该还存在其他差异表达 LncRNA 参与调控巨噬细胞表型及抗原递呈功能。

PU-1179

唐氏综合征实验筛查进展及问题

王丽娜、曹永彤
中日友好医院

目的 如何选择高效价比的筛查方案，更好地对高龄孕妇进行产前筛查和诊断，既可以检出染色体异常的胎儿，又尽量减少有创检查，提高产前筛查和诊断效率
方法 临床常见的多采用孕中期三联联合筛查。
结果 目前北京地区对 35 岁以上的初次怀孕的孕妇直接进行产前诊断，而生育过健康胎儿的 35 岁以上孕妇则在征求孕妇同意的原则下可以先行无创 DNA 筛查，而后根据筛查结果再决定是否进行产前诊断。对 35 岁以下未有不良孕史的孕妇先进行常规血生化筛查，筛查灰区孕妇，再根据后续无创 DNA 筛查结果来决定是否进行产前诊断。而筛查高危的孕妇则直接进行产前诊断。北京地区的产前筛查和产前诊断已经考虑到不同年龄及孕妇的实际情况，也算是在孕妇个体化产前筛查和诊断策略上一个极大的进步。
结论 孕妇血清学标志物筛查已被证实可在孕期有效检出 DS 患儿，便于大规模筛查，又为高危孕妇进一步做羊膜腔穿刺进行细胞染色体检查提供了必要依据，从而减少了盲目性，又降低了漏检率，是预防 DS 患儿出生的重要途径。因此为减少出生缺陷有必要推广产前筛查，使之成为每一个孕妇产前常规检查项目。在此基础上，再结合具体情况，选择最佳筛查方案，以提高检出率，降低假阳性率，减少有创检查，则是今后着重研究的方向。

PU-1180

四川某三甲医院体检人群甲状腺抗过氧化物酶抗体和甲状腺球蛋白抗体与甲状腺功能相关性分析

段笑生[2]、廖凤慧[1]
1. 电子科技大学附属医院 四川省人民医院临床医学检验中心
2. 电子科技大学附属医院 四川省人民医院临床医学检验中心

目的 分析体检人群甲状腺抗过氧化物酶抗体和甲状腺球蛋白抗体的检出率，并分析其与甲状腺功能的相关性。
方法 收集 2020 年 1 月 1 日至 2020 年 12 月 31 日于四川省人民医院体检中心均进行甲状腺抗过氧化物酶抗体（TPOAb）、甲状腺球蛋白抗体（TGAb）、游离三碘甲状腺原氨酸（FT3）、游离四碘甲状腺原氨酸（FT4）、促甲状腺素（TSH）检测的体检者共 14366 名的资料，其中女 6568 名，男 7798 名，平均年龄为 42.96 岁。
结果 14366 名体检者中，TPOAb 的总阳性率为 10.85%，女性阳性率明显高于男性（16.08%比 7.49%, P<0.01），女性阳性率高峰出现在 30~<40 岁人群，为 17.88%，男性阳性率高峰出现在≥70 岁人群，为 9.53%。 TGAb 的总阳性率为 9.72%，女性阳性率明显高于男性（14.37%比 5.28%，P<0.01），女性阳性率高峰出现在 50~＜60 岁人群，为 15.31%，男性阳性率高峰出现在≥70 岁人群，为 6.24%。 临床甲亢、亚临床甲亢、临床甲减、亚临床甲减人群中，TPOAb、TGAb 均阳性者分别占 30.11%、10.56%、53.36%、20.67%，显著高于非甲状腺功能异常人群的 5.36%；TPOAb 阳性者分别占 46.32%、21.79%、54.98%、33.55%，显著高于非甲状腺功能异常人群的 10.55%；TGAb 分别占 39.87%、18.42%、66.77%、24.33%，显著高于非甲状腺功能异常人群的 7.74%。
结论 体检筛查中，甲状腺抗过氧化物酶抗体和甲状腺球蛋白抗体具有重要意义，对于女性体检者，更应及早进行甲状腺抗过氧化物酶抗体和甲状腺球蛋白抗体的筛查，应重视、加强甲状腺自身抗体阳性者的随访，尤其是双抗体阳性者，以利于甲状腺功能异常疾病的预防和临床早诊治期。

PU-1181

三种新型冠状病毒总抗体检测试验的临床应用价值比较

罗风、李晓非
昆明市第三人民医院

目的 比较三种新型冠状病毒（2019-nCoV）总抗体检测方法（胶体金法、酶联免疫法和化学发光法）的临床应用价值。
方法 纳入 2020 年 2 月至 2020 年 3 月我院门诊及住院新冠肺炎（NCP）患者 39 例为病例组，195 例非 NCP 患者为对照组。收集所有入组对象不同发病时间的空腹静脉血，分别采用三种方法检测样本，并对试验数据进行统计分析。
结果 胶体金法、酶联免疫法和化学发光法的灵敏度分别为 85.71％、86.81％、81.32％，特异度分别为 99.21％、95.24％、97.22％，受试者工作特征曲线（ROC curve）下面积（AUC）分别为 0.925、0.938、0.965。此三种方法在机体发病不同时间对 2019-nCoV 抗体检出率差异没有统计学意义；随着发病时间延长，三种方法对 2019-nCoV 抗体的检出率呈先升高后下降的趋势（检出率在第 15~21 天达峰）。
结论 化学发光法诊断 NCP 的准确性最高，此三种方法的诊断性能均能满足临床需求。

PU-1182

人乳头瘤病毒与血清肿瘤标志物 CEA、CA125、CA199 联合检测在宫颈癌诊断中的价值

渠滕
山东第一医科大学附属省立医院临床医学检验部

目的 探讨人乳头瘤病毒（HPV）与血清肿瘤标志物癌胚抗原(CEA), 糖类抗原 125 (CA125), 糖类抗原 199(CA199)检测在宫颈癌诊断中的价值。
方法 选取 2019 年 1 月到 2020 年 12 月来本院就诊的 100 例经病理确诊为宫颈癌患者作为宫颈癌组，同时选取同期宫颈良性肿瘤 100 例为良性肿瘤组，另选取同期健康体检者 100 例作为健康组，所有患者均用上海之江配套试剂检测其 HPV,罗氏 Cobas 8000 全自动化化学发光免疫分析仪及配套试剂检测血清肿瘤标志物 CEA、CA125、CA199，探讨三组间 HPV 阳性检出率、血清 CEA、CA125、CA199 的表达水平，比较 HPV 及 CEA、CA125、CA199 单独检测与联合检测在宫颈癌诊断中的价值。
结果 研究数据显示, 宫颈癌组血清 CEA、CA125、CA199 水平明显高于良性肿瘤组和对照组，差异有统计学意义（P<0.05）；宫颈癌组 HPV16、HPV18 单独检测与联合检测阳性率均高于良性肿瘤组和对照组，差异有统计学意义（P<0.05）； HPV 与血清 CEA、CA125、CA199 联合检测的灵敏度、准确度均高于任一指标单独检测，组间比较差异有统计学意义（P<0.05）。
结论 宫颈癌患者 HPV 与血清 CA125、CA153、CA199 联合检测可明显提高宫颈癌诊断的准确度和灵敏度,值得临床推广应用。

PU-1183

尿 sCD163 在肾小球炎症疾病中的研究进展

宋佳、孙淑艳
吉林大学第一医院

目的 肾小球肾炎（glomerulonephritis，GN）约占慢性肾脏病的 20%，常见于青年，是青年终末期肾病的最常见原因。肾小球肾炎诊断的金标准是肾活检，是一种有创性检查，必须在满足适应症且排除禁忌症的情况下才能开展。因此，非侵入性的生物标志物检测对肾小球肾炎的早期诊断及病情监测则显得尤为有意义。sCD163 是一种与多种疾病相关的炎性标志物，尿液中 sCD163 水平被证实与肾脏炎症水平直接相关，可作为活动性肾小球肾炎的早期识别和监测的生物标志物，尤其在 ANCA 相关血管炎(AAV)合并肾脏病变的患者和活动期狼疮性肾炎患者的尿液中 sCD163 浓度会明显升高。
方法 通过计算机在 PubMed、Google Scholar 等数据库中进行文献检索，输入相应关键词，年限在 2000 年至 2020 年之间，对纳入文献进行人工审查，识别参考文献进行综述。
结果 尿液中 sCD163 作为一种独立的、理想的前瞻性验证指标，可用于鉴别活动性肾血管炎。相比缓解期的 AAV 患者、急性肾衰竭或脓毒症患者以及无肾受累的 AAV 患者，87%伴有肾受累的活跃 AAV 患者的尿液中 sCD163 水平显著升高；而在狼疮性肾炎（LN）发生发展过程中，sCD163 在尿液中的浓度能够反映 LN 的病理损伤，可作为 LN 新的生物标志物；尿 sCD163 被证实还可应用于其他形式的新月体肾小球肾炎的诊断及辅助识别复发，在一些肾脏疾病如 IgA 肾病、糖尿病肾病、膜性肾病和急性肾损伤中也具有巨大的潜力。
结论 尿液中 sCD163 水平的测定有助于在肾脏发生不可逆损害之前尽早发现累及肾脏的 AAV 复发；与经典的肾脏参数相比，尿 sCD163 的敏感性和特异性更好。sCD163 可作为一种非侵入性的生物标志物，直接反映巨噬细胞介导的肾小球炎症；尿 sCD163 可辅助复发性蛋白尿的 LN 的病理分型。

尿可溶性 CD163 作为非侵入性检测新指标，可参与评估多种肾脏疾病活动性、辅助病理分型及判断肾脏疾病复发预后，通过临床对该指标的不断研究，尿 sCD163 可为肾脏疾病患者带来新的希望。

PU-1184

探讨免疫球蛋白测定和免疫电泳在多发性骨髓瘤的诊断中的临床应用

杨奇[1]、刘旻[2]、张丽翠[1]
1. 石河子大学医学院第一附属医院检验科
2. 石河子大学医学院第一附属医院生殖医学科

目的 探讨免疫球蛋白定量检测、免疫蛋白电泳和免疫固定电泳在多发性骨髓瘤（MM）诊断中的应用与价值。
方法 收集在 2020 年 6 月-2021 年 6 月间就诊于我院确诊为 MM 患者 58 例血清，检测血清免疫球蛋白定量(IgG，IgA，IgM，κ 轻链(kappa light chain)和 λ 轻链(lambda light chain))，并进行血清蛋白电泳及免疫固定电泳，评价上述检测指标在 MM 诊断中的应用价值。
结果 58 例 MM 患者中 51 人经蛋白电泳检测发现存在 M 蛋白，检出阳性率为 87.9%，其中 IgG、IgM 型单克隆条带多出现在 γ 区域，IgA 型多出现在 β 区域；经免疫固定电泳检测后；54 例检测阳性，阳性率 93.1%，其中 IgG 型 32 例（55.2%）、IgA 型 8 例（13.8%）、IgM 型 3 例（5.1%）、轻链型 8 例（13.8%），7 例经蛋白电泳检测未发现 M 蛋白条带，后经固定电泳分析后：3 例均为微量双克隆蛋白分泌型，余 4 例为不分泌型。同时相应类型的免疫球蛋白和轻链增高并伴其它组分免疫球蛋白及轻链降低。
结论 免疫球蛋白及轻链检测、免疫蛋白电泳是临床初筛多发性骨髓瘤的重要方法，而基于毛细管电泳技术的免疫固定电泳则是 MM 快速诊断及分型的重要途径，可为临床提供重要的实验室依据。

PU-1185

拉曼光谱分析推动流式细胞术新发展

华木星[1,2]、段勇[1]
1. 昆明医科大学第一附属医院
2. 云南省阜外心血管病医院

流式细胞术目前在临床和科研领域都有着广泛的应用，通过制备细胞或实体颗粒的悬液从而测量细胞大小、细胞颗粒度以及细胞表面和细胞内分子的表达，能对生物过程进行系统性观察。甚至还能通过特定参数的设置对细胞进行分选，以及辅助实现分选样本的后续附加分析，例如 DNA/RNA 测序、克隆和定向分化。但是，传统的流式细胞术主要依靠荧光进行标记间接反应目的细胞的理化性质，这会对细胞的活性有一定的影响，同时受可用荧光种类限制和荧光间相互干扰的影响，无法同时对细胞内所有复杂成分进行分析。为了克服这些困难，一种基于拉曼光谱直接测量细胞特性的流式细胞术应运而生，简称“拉曼流式细胞术”。“拉曼散射”是指一定频率的激光照射到物质时，物质中的分子与光子发生能量转移，振动态发生不同方式和程度的改变，然后散射出不同频率的光。不同种类的原子团振动的方式是独一的，因此可以产生与入射光频率有特定差值的散射光，其光谱就称为“指纹光谱”。通过对指纹光谱的鉴定分析细胞内外的各个组分并不会对目的细胞产生损伤和破坏。因不需要对细胞进行标签，甚至有望在体内进行流式细胞检测。但是，拉曼散射的光分子相互作用很弱，信号采集缓慢，近年来随着信号转换及放大系统的进一步研究，激光科学、光子学、微流体学、计算机科学、分子工程和生物医学的合作愈加紧密，基于不同类型的受激拉曼散射(SRS)和相干反斯托克斯拉曼散射(CARS)的原理，如 CARS、多路 CARS、傅立叶变换 CARS、SRS、SRS 成像流式细胞术和 RIACS 发展迅速，实现了高灵敏度和高通量并存，并与液

滴微流体集成，利用机器学习技术，实现活体流式细胞术检测，尤其在微生物筛选、细胞分化跟踪、肿瘤检测和细胞治疗等领域的应用将迎来新机遇、新挑战和新发展。

PU-1186

Cyfra21-1、CEA 和 CA15-3 与乳腺癌早期诊断及病理特征的相关性研究

熊文祺、李清祥、仇丽娟、张小艳
南昌市第三医院

目的 基于血液的生物标记物对乳腺癌的早期检测都不够敏感，本研究通过对乳腺癌患者血清细胞角蛋白 19 片段抗原 21-1(Cyfra21-1)、糖类抗原 153(CA15-3)、癌胚抗原(CEA)水平变化检测，以探究这三个生物指标对乳腺癌的单独和联合诊断价值，旨在提高乳腺癌诊断率。
方法 选取 2020 年 1 月至 2021 年 12 月南昌市第三医院乳腺癌患者 84 例，乳腺良性肿瘤患者 60 例以及健康体检者 60 例。电化学发光法测定血清 Cyfra21-1 水平，化学发光法测定血清 CEA、CA15-3 以及实验室常规肿瘤标志物 AFP、CA242、CA50 和 CA125 水平。分析比较各组患者肿瘤指标水平，进一步分析肿瘤分期、淋巴结转移以及 ER、PR、HER-2 和 Ki-67 指数与研究指标的关系；绘制受试者工作曲线(ROC)，通过曲线下面积(AUC)评价 Cyfra21-1、CEA 和 CA15-3 对乳腺癌的诊断价值。
结果 乳腺癌组 Cyfra21-1、CEA 和 CA15-3 水平显著高于良性肿瘤组和健康对照组($P<0.05$)；Cyfra21-1、CEA 与肿瘤分期有关，CEA 与淋巴结转移有关；Cyfra21-1、CEA 和 CA15-3 诊断乳腺癌的 AUC 分别 0.753、0.690 和 0.683，三个指标联合诊断 AUC 最大，为 0.829，Cyfra21-1 诊断特异度最高，为 88.89%；CA15-3 灵敏度最高，为 96.43%。
结论 Cyfra21-1、CEA 和 CA15-3 与乳腺癌病理特征相关且对乳腺癌具有较高的诊断价值，联合诊断价值更高。

PU-1187

357 例抗磷脂抗体谱阳性病例的分析

潘晶晶
郑州大学第一附属医院

目的 探讨抗磷脂抗体谱检测结果中抗心磷脂抗体（aCL）和抗 β2 糖蛋白 I 抗体（aβ2GPI）的阳性率及分布特征。
方法 选取 2018 年 1 月至 2021 年 1 月在我院就诊并通过化学发光法进行 aCL 和/或 aβ2GPI 检测的 6977 例患者作为研究队象。
结果 至少一项 aCL 或 aβ2GPI 阳性的患者 357 例，占 5.12%，年龄范围为 9-85 岁（中位数 37 岁），其中女性 223 例，男性 134 例，男女比例为 1:1.66。仅 aCL 阳性（aβ2GPI 阴性）127 例，占 35.58%，仅 aβ2GPI 阳性（aCL 阴性）113 例，占 31.65%，aCL 和 aβ2GPI 同时阳性的 117 例，占 32.77%。aCL 亚型的阳性率分别为：aCL-IgA 为 20.31%，aCL-IgG 为 44.62%，aCL-IgM 为 28.21%,阳性率 aCL-IgG>aCL-IgM>aCL-IgA。aβ2GPI 亚型阳性率分别为：aβ2GPI-IgA 为 19.79%，aβ2GPI-IgG 为 58.18%，aβ2GPI-IgM 为 15.34%，阳性率 aβ2GPI-IgG>aβ2GPI-IgM> aβ2GPI-IgA。阳性病例中系统性红斑狼疮患者数量最多，共 48 例，占 13.45%，其次为抗磷脂综合征患者 36 例，占 10.08%，血栓形成、脑梗塞和血液系统疾病分别是 23 例、22 例和 22 例，占 6.4%、5.6%和 5.6%。
结论 对系统性红斑狼疮和抗磷脂综合征病患者定期检测抗磷脂抗体谱，协助临床疗效监测和判断预后。

PU-1188

肿瘤标志物 SP70 在宣威肺癌中的临床应用研究

洪源、段勇
昆明医科大学第一附属医院

目的 肺癌是目前世界上最常见的恶性肿瘤之一,在中国,云南省宣威地区人群以肺癌高发、恶性程度高、预后极差等特点引起了广泛的关注和研究。在对于宣威肺癌的研究中,一直缺乏特异性高、与病情变化相关性高、检测方法简便快速的肿瘤标志物。肿瘤特异性蛋白 70（tumor specific protein 70,SP70）是单克隆抗体 NJ001 识别的特异性抗原,在非小细胞肺癌组织上的表达率为 80%～90%,在肿瘤细胞的恶性增殖和侵袭转移中发挥着极其重要的作用。探索肿瘤标志物 SP70 与宣威肺癌相关性,有助于此类癌症的早期诊断、动态监测以辅助判断病情进展或治疗效果。因此本文就肿瘤标志物 SP70 在宣威肺癌诊断中的应用现状,对其特点进行分析,从宣威肺癌的疾病背景、肿瘤标志物 SP70 与宣威肺癌的相关性及检测方法等方面出发,探究肿瘤标志物 SP70 在宣威肺癌诊断和治疗中的应用,以期为宣威肺癌的早期诊断和预后判断提供新的思路。

PU-1189

了解恶性肿瘤患者血清自身抗体的临床意义

司文
山东省立医院

目的 了解恶性肿瘤患者血清自身抗体的临床意义。
方法 对 48 例原发性肝癌、46 例原发性肺癌,36 例胃瘤,28 例结直肠癌,67 例慢性肝炎、38 例肝硬化、36 例 自身免疫疾病和 50 例健康人血清，应用间接免疫荧光法检测自身抗体，蛋白印迹法检测 ENA 抗体谱，间接 ELISA 法检测,dsDNA 抗体,以及检测 ANA 抗体谱。
结果 原发性肝癌，原发性肺癌、胃癌、结直肠癌、慢性肝炎及肝硬化患者血清自身抗体检出率高于健康人(P< 0. 05)，低于自身免疫疾病患者(P < 0.05),原发性肝癌、原发性肺癌、胃癌、结直肠癌、慢性肝炎、肝硬化和自身免疫疾病患者均具有多种自身抗体荧光模式及较宽的自身抗体谱，健康人荧光模式少且自身抗体谱很窄，与其他疾病比较，癌症患者的自身抗体不具有特征性分布。大部分间接免疫荧光法自身抗体阳性的癌症患者，蛋白印迹法未检出 ENA 抗体。
结论 自身抗体有助于鉴别诊断健康人与癌症患者，但无独立诊断价值。癌症患者体内尚有许多自身靶抗原有待于进一步鉴定。

PU-1190

化学发光法检测新型冠状病毒总抗体假阳性结果的临床特征分析

黄宇、洪国斧
厦门大学附属第一医院

目的 探讨化学发光法检测新冠总抗体的假阳性结果与性别、年龄、疾病、炎症性指标以及肿瘤标志物的关系。
方法 对我院 2020 年 5 月至 2021 年 1 月门诊及住院患者的新冠总抗体检测结果进行统计分析。采用电化学发光法检测 PCT、免疫比浊法检测 CRP、流式细胞法检测 IL-6、化学发光法检测 CEA、AFP、CA125 等。对性别、年龄、疾病种类等进行描述性分析，组间采用卡方分析相关性。
结果（1）149 例假阳性样本中，女性浓度中位数为 2.655S/CO 高于男性，男女 2019-nCoVAb 假阳性率差异无统计学意义（P=0.120）；（2）149 例假阳性样本中，21~40 这组的浓度中位数最

高，为 2.250；（3）149 例假阳性样本结果≤5 S/CO 占比 85.91%，主要集中在低浓度水平；（4）149 例假阳性样本中，自身存在恶性肿瘤或炎症的占比较高，分别是 27.52%和 20.13%；（5）炎症性指标的阳性率较高，PCT、CRP、IL-6、WBC 的阳性率分别是 57.14%、18.06%、75%、15.56%。

结论 化学发光法检测新冠总抗体存在一定假阳性，与肿瘤、炎症疾病存在一定相关性，本研究为疫情防控与临床决策提供依据。

PU-1191

IL-6 在托珠单抗和恢复期血浆治疗 COVID-19 中的应用

武剑、夏欣一
中国人民解放军东部战区总医院

目的 重症 COVID-19 患者的体内有细胞因子风暴综合征 (CSS)，研究白细胞介素 6（IL-6）水平的动态变化对监测和治疗重症患者的指导意义，本文旨在评价 IL-6 在托珠单抗和恢复期血浆 2 种新疗法治疗 COVID-19 中的应用。

方法 纳入 1472 例经临床诊断和实验室确诊为 COVID-19 感染的住院患者(2020 年 2 月 4 日至 2020 年 3 月 30 日在火神山医院收治)，统计相关临床特征和实验室检测指标，分析 IL-6 水平与患者的基础疾病、治疗方式以及预后之间的相关性。

结果 1.IL-6 水平随年龄增长而升高，男性高于女性，体温高于 37.3°C 的患者 IL-6 水平更高，IL-6 水平与 SpO2 的水平呈负相关；2.患有糖尿病和高血压等基础疾病的患者，IL-6 水平高，疾病进展较快；3.用与 IL-6 正相关系数最高的 IL-10，绘制 ROC 曲线，两种细胞因子的曲线下面积 (AUC) 为：IL-6，0.686、IL-10，0.701，基于此，IL-6 可以作为生物标志物来直观反映机体炎症水平；4.新冠 IgG 抗体水平随着疾病严重程度的增加而增加，重症和危重症 COVID-19 患者体内的 IgG 水平随着 IL-6 水平的升高而降低，这可能是由于中和抗体耗尽所致；5.基于六类量表评分（SCSS）评估托珠单抗治疗患者的状况，发现托珠单抗治疗可以改善患者的炎症状况，但对于疾病的转归未发现改善，尤其是死亡病例数；6.接受 CPT 治疗的患者疾病持续时间缩短，炎症程度降低。

结论 IL-6 可作为一个稳定的检测指标，其水平的动态变化可以监测病毒感染期间的机体炎症状况。IL-6 水平高于正常水平 30 倍的患者，与 IL-6 水平较低的患者相比，预后较差。使用托珠单抗和恢复期血浆疗法 (CPT)，可降低 IL-6 水平，缓解患者全身炎症状况。（本文部分内容已发表于 Front Immunol, IF=5.085）

PU-1192

双阴性 T 细胞在耐药性肺结核中的表达及意义研究

梁骑、郭晓兰、刘文、杨尚瑜
四川省南充市川北医学院附属医院

目的 探究 CD3＋CD4-CD8-(double negative T，DNT)细胞在耐药性肺结核中的表达及意义。

方法 选取 2017 年 6 月-2018 年 1 月期间我院收治的 50 例耐药性肺结核患者为耐药肺结核组，并选取同期 50 例肺结核患者为结核组，同期来我院进行健康检查的 30 例健康志愿者为对照组。分析并比较三组对象的 DNT 细胞水平及白细胞介素 10(IL-10)和干扰素 γ（IFN-γ）水平，检测并比较三组对象的外周血 T 淋巴细胞亚群水平及 DNT 细胞、IL-10 和 IFN-γ 细胞的凋亡情况，并分析 DNT 细胞凋亡与 IL-10 和 IFN-γ 水平的相关性。

结果 耐药肺结核组与肺结核组患者的各项外周血 T 淋巴细胞水平均低于对照组，且耐药肺结核组低于肺结核组；耐药肺结核组与肺结核组患者的 DNT 细胞、IFN-γ 水平均低于对照组，且耐药肺结核组低于肺结核组，IL-10 水平均高于对照组，且耐药肺结核组高于肺结核组；耐药肺结核组与肺

结核组患者的 DNT 细胞、IFN-γ 细胞凋亡率均高于对照组，且耐药肺结核组高于肺结核组，IL-10 细胞凋亡率低于对照组，且耐药肺结核组低于肺结核组，差异有意义（p＜0.05）。DNT 细胞凋亡与 IL-10 水平呈现相关（r=0.644，p=0.010），DNT 细胞凋亡与 IFN-γ 水平呈现负相关（r=-0.230，p=0.016）。

结论 耐药性肺结核的出现可能与细胞免疫功能紊乱相关，耐药性肺结核患者 DNT 细胞凋亡率显著增加导致 DNT 细胞数减少，DNT 细胞凋亡与 IL-10 水平呈现相关，与 IFN-γ 水平呈现负相关。

PU-1193

ALCAM 在 HIV-1 感染者中的表达及意义

李明玉、李娅
昆明医科大学第一附属医院

目的 探讨 HIV-1 感染长期不进展者血清中活化白细胞黏附分子（activated leukocyte cell adhesion molecule，ALCAM）的水平及长期不进展者的产生机制。

方法 选取确诊的 HIV-1 感染者中的 10 例 HIV-1 长期不进展者为病例组 A，10 例 HIV-1 典型进展者作为病例组 B，10 例未感染 HIV-1 同时未患有其他疾病的健康志愿者作为对照组，采用双抗体夹心酶联免疫吸附实验（ELISA）法检测血清中 ALCAM 水平，使用 SNK（q）法进行组间两两比较。

结果 HIV-1 典型进展者血清 ALCAM 水平要高于 HIV-1 长期不进展者组和对照组，但是 P<0.05 差异具有统计学意义。而 HIV-1 长期不进展者血清 ALCAM 水平与对照组相比，P>0.05 差异不具有统计学意义。

结论 ALCAM 在 HIV-1 感染长期不进展者血清中水平与健康人无差异，在 HIV-1 感染典型进展者血清中升高，ALCAM 与 HIV-1 感染的疾病进展有关，有望成为 AIDS 治疗的潜在靶点。

PU-1194

Serum C1q concentration positively correlates with erythrocyte sedimentation rate in polymyositis/dermatomyositis

Liubing Li[1]、Li Yongzhe[2]
1. Peking Union Medical College Hospital, Chinese Academy of Medical Sciences
2. 北京市东城区北京协和医院东院检验科

C1q is an important component of the classical complement pathway. This study aimed to investigate C1q concentrations in the sera of PM/DM patients.

C1q concentrations were measured in the sera of 87 PM/DM patients and 100 healthy subjects. In addition, the association between C1q concentration and laboratory indexes such as CK, AST, ALT, LDH, hsCRP, and ESR were also evaluated.

Our data indicated no significant difference in the serum C1q concentration between PM/DM patients and healthy subjects. However, serum C1q concentrations were observed to be significantly higher in PM/DM patients in patients group with elevated ESR than in those with normal ESR (207.55 ± 37.54 mg/L and 180.69 ± 38.90 mg/L, respectively; P=0.008). Furthermore, there was a positive correlation between serum C1q concentration and ESR (P=0.002), but no association was observed with CK, AST, ALT, LDH, and hsCRP levels.

This study demonstrated C1q levels were elevated in PM/DM patients with higher ESR, and revealed significant positive correlation. However, the exact role of the classical complement pathway in PM/DM needs further elucidation.

PU-1195

Analysis of myositis auto-antibodies in Chinese patients with cancer-associated myositis

Liubing Li[1]、Li Yongzhe[2]
1. Peking Union Medical College Hospital, Chinese Academy of Medical Sciences
2. 北京市东城区北京协和医院东院检验科

Background Cancer-associated myositis (CAM) has poor prognosis and causes higher mortality. In general, myositis-specific auto-antibodies (MSAs) and myositis-associated auto-antibodies (MAAs) have been shown to be useful biomarkers for its diagnosis.
Methods In the present study, focus was given in assessing the presence, prevalence and diagnostic values of myositis auto-antibodies in Chinese patients diagnosed with CAM. The sera collected from 49 CAM patients, 108 dermatomyositis/polymyositis (DM/PM) patients without cancer, 105 disease controls and 60 healthy controls were detected for the presence of 16 auto-antigens (Jo-1, OJ, EJ, PL-7, PL-12, MDA5, TIF1γ, Mi-2α, Mi-2β, SAE1, NXP2, SRP, Ku, PM-Scl75, PM-Scl100, Ro-52) using a commercial Euroline assay.
Results The frequency of anti-TIF1γ was significantly higher in CAM patients than in DM/PM patients without cancer (46.9% vs. 14.8%, P<0.001). Importantly, the sensitivity and specificity for this MSA was 46.9% and 85.2%, respectively. These helped to differentiate CAM patients from DM/PM patients without cancer. However, there was no difference in other MSAs and MAAs between CAM and DM/PM patients without cancer.
Conclusion The present study indicates that anti-TIF1γ levels can serve as important biomarkers for CAM diagnosis, and help in distinguishing between CAM and DM/PM patients without cancer.

PU-1196

生长刺激表达基因 2 蛋白和肝素结合蛋白在川崎病中的应用价值

胡文霞
连云港市第一人民医院

目的 探讨生长刺激表达基因 2 蛋白(growth stimulation expressed gene 2，ST2)和肝素结合蛋白(Heparin-Binding Protein，HBP)在川崎病中的临床应用价值。
方法 选取 60 例川崎病患儿为研究对象，根据有无并发冠状动脉损伤（coronary artery lesion，CAL） 将入选患儿分为 CAL 组（21 例）和 NCAL 组（39 例），选取该院同期伴有发热并排除心肌损害的呼吸道感染患儿 30 例纳入对照组。检测所有患儿 ST2 和 HBP 水平，结果川崎病患儿 ST2 和 HBP 水平均显著高于对照组（均 P ＜ 0.05）； CAL 组患儿 ST2 和 HBP 水平显著高于 NCAL 组（均 P ＜ 0.05）。
结论 ST2 和 HBP 与川崎病患儿冠状动脉损伤密切相关，则作为预测是否发生冠状动脉损伤的指标。

PU-1197

Myositis-specific autoantibodies in dermatomyositis/polymyositis with interstitial lung disease

Liubing Li[1]、Li Yongzhe[2]
1. Peking Union Medical College Hospital, Chinese Academy of Medical Sciences
2. 北京市东城区北京协和医院东院检验科

Aim The prevalence and diagnostic values of myositis-specific autoantibodies (MSAs) and myositis-associated autoantibodies (MAAs) in dermatomyositis/polymyositis (DM/PM) were studied.
Method A commercial immunoblot assay with 16 autoantigens was used to detect MSAs and MAAs in serum samples from 130 DM/PM patients, 100 disease controls, and 50 healthy subjects.
Results The prevalence of anti-Jo-1, anti-MDA5, anti-TIF1γ, anti-Mi-2α, and anti-Mi-2β was significantly higher in DM/PM than in other connective-tissue diseases (CTDs). Moreover, anti-MDA5 and anti-Ro-52 were significantly higher in DM/PM with interstitial lung disease (ILD) than in DM/PM without ILD, while that of anti-TIF1γ and anti-NXP2 were significantly lower in DM/PM with ILD than in DM/PM without ILD. For distinguishing DM/PM from other CTDs, the sensitivity, specificity, and positive predictive value (PPV) for anti-MDA5 were 28.46, 99.00, and 97.37%, respectively, with a positive likelihood ratio (LR+) of 28.46; they were 46.15, 58.00, and 58.82%, respectively, for anti-Ro-52 with an LR+ of 1.10. For distinguishing DM/PM with ILD from DM/PM without ILD, the sensitivity, specificity, and PPV for anti-MDA5 were 45.57, 100.00, and 100.00%, respectively, and for anti-Ro-52 were 60.76, 73.91, and 80.00%, respectively.
Conclusion MSAs and MAAs serve as biomarkers for differentiating DM/PM from other CTDs as well as distinguishing DM/PM with ILD from DM/PM without ILD.

PU-1198

Associations between anti-NXP2 antibody and demographics, clinical characteristics and laboratory results of patients with dermatomyositis: A systematic meta-analysis

Liubing Li[1]、Li Yongzhe[2]
1. Peking Union Medical College Hospital, Chinese Academy of Medical Sciences
2. 北京市东城区北京协和医院东院检验科

Objective Anti-nuclear matrix protein 2 (NXP2) is a specific biomarker in patients with dermatomyositis (DM). Results from several studies that examined the relationship between anti-NXP2 antibody and the demographics, clinical characteristics, and laboratory results of DM patients have been conflicting. The purpose of this study was to identify the relationship, if any, of anti-NXP2 antibody with demographics, clinical characteristics, and laboratory results of DM patients.
Methods PubMed, Web of Science, Embase, and the Cochrane Library databases were searched for studies without language restrictions conducted before January 31, 2019. Stata 12.0 software was used to calculate pooled odds ratios (ORs) or weighted mean differences (WMDs) and corresponding 95% confidence intervals (CIs) to determine the relationship between anti-NXP2 antibody and patient characteristics.
Results Eleven studies comprising 2,047 cases were included in this meta-analysis. Anti-NXP2 antibody was associated with the following characteristics of patients: edema (OR = 3.90, 95% CI = 2.01–7.55, P < 0.001), muscle weakness (OR = 10.69, 95% CI = 4.67–24.47, P < 0.001), myalgia/myodynia (OR = 2.97, 95% CI = 1.97–4.46, P < 0.001), ILD (OR = 0.25, 95% CI = 0.15–

0.40, P < 0.001), dysphagia (OR = 4.00, 95% CI = 2.71–5.90, P < 0.001), calcinosis (OR = 3.74, 95% CI = 1.91–7.30, P < 0.001).
Conclusions Our meta-analysis indicated anti-NXP2 antibody is related to edema, muscle weakness, myalgia/myodynia, ILD, calcinosis in patients with DM.

PU-1199

Whole Exome Sequencing Identifies Rare Protein-Coding Variants in Dermatomyositis

Liubing Li[1]、Li Yongzhe[2]
1. Peking Union Medical College Hospital, Chinese Academy of Medical Sciences
2. 北京市东城区北京协和医院东院检验科

Objective Dermatomyositis (DM) is an idiopathic inflammatory myopathy characterized by chronic skeletal muscle and skin inflammation. Despite the identification of multiple common genetic variants associated with DM, rare genetic variants have been less explored. This study aimed to investigate the rare variants in juvenile DM (JDM) and adult DM (ADM) of Han Chinese using whole exome sequencing (WES).
Methods WES was conducted in a discovery set comprising 20 patients with JDM, 20 patients with ADM and 20 healthy controls of Han Chinese. WES data were generated for the cases and controls. Variants were annotated and filtered by quality, minor allele frequency, and deleteriousness on gene function. Candidate variants were identified in patients compared to healthy controls as well as controls from China National GeneBank. For validation, Multiplex polymerase chain reaction (PCR) was performed in an additional independent set of 34 JDM, 262 ADM and 241 healthy controls of Han Chinese.
Results In discovery stage, nine rare variants with predicted protein-damaging effects in DM were identified in cases but not in controls, harboured in FCRL1, DMBT1, COL1A1, KIAA1033, DDX58, DYSF, IL31RA, JAK2 and WDFY4. These variants were subsequently subject to multiplex PCR. A novel variant in WDFY4 (chr10: 50154140 C>T) was validated to be associated with JDM. Another novel variant in DDX58 (chr 9: 32487565 T>C) was validated to be associated with ADM.
Conclusion Our findings are helpful for providing new ideas for understanding the pathogenesis of DM by detecting and analyzing gene mutations at the whole-exome level. Rare putative protein-damaging genetic variants in WDFY4 and in DDX58 may be new susceptibility loci for DM, but their roles in the pathogenesis of DM are worthy of further study.

PU-1200

Heat inactivation of serum interferes with the immunoanalysis of antibodies to SARS-CoV-2

Xiumei Hu
Nanfang Hospital, Southern Medical University

Background The detection of serum antibodies to the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is emerging as a new tool for the coronavi_x0002_rus disease 2019 (COVID-19) diagnosis. Since many coronaviruses are sensitive to heat, heating inactivation of samples at 56°C prior to testing is considered a possible method to reduce the risk of transmission, but the effect of heating on the measurement of SARS-CoV-2 antibodies is still unclear.
Methods By comparing the levels of SARS-CoV-2 antibodies before and after heat inactivation of serum at 56°C for 30 minutes using a quantitative fluorescence immunochromatographic assay

Results We showed that heat inactivation significantly interferes with the levels of antibodies to SARS-CoV-2. The IgM levels of all the 34 serum samples (100%) from COVID-19 patients decreased by an average level of 53.56%. The IgG levels were decreased in 22 of 34 samples (64.71%) by an average level of 49.54%. Similar changes can also be observed in the non–COVID-19 disease group (n = 9). Of note, 44.12% of the detected IgM levels were dropped below the cutoff value after heating, suggesting heat inactivation can lead to false-negative results of these samples.
Conclusion Our results indicate that heat inactivation of serum at 56°C for 30 minutes interferes with the immunoanalysis of antibodies to SARS-CoV-2. Heat inactivation prior to immunoanalysis is not recommended, and the possibility of false-negative results should be considered if the sample was pre-inactivated by heating.

PU-1201

Genome-wide Association Study Identifies rs7770370 and rs35953215 within HLA-DPB1 loci as Major Genetic Factors for Polymyositis/Dermatomyositis

Liubing Li
Peking Union Medical College Hospital, Chinese Academy of Medical Sciences

Objective The polymyositis/dermatomyositis (PM/DM) are a spectrum of heterogeneous autoimmune diseases, characterized by skeletal muscle weakness and muscle inflammation. PM/DM are thought to be complex genetic diseases, arising from an interaction between environmental and genetic factors. This study aimed to identify genetic risk factors in patients with PM/DM of Han Chinese.
Methods We conducted a genome-wide association study (GWAS) of 576 PM/DM, which included 232 polymyositis (PM), 344 dermatomyositis (DM), 266 PM/DM-interstitial lung disease (PM/DM-ILD) and 97 PM/DM with anti-Jo-1 autoantibodies, and compared them with 1455 healthy controls. A total of 642832 single nucleotide polymorphisms (SNPs) were genotyped using the Affymetrix Axiom Genome-Wide CHB 1 Array Plate.
Results We found two SNPs, rs7770370 and rs35953215 within HLA-DPB1 loci, which were significantly associated with PM/DM. Rs7770370 was identified as a novel genetic risk factor for PM/DM [P = 1.69×10-8, odds ratio (OR) = 1.52], and rs35953215 was defined as a novel genetic protective factor for PM/DM (P = 1.17×10-8, OR = 0.63).
Conclusion Two novel susceptibility loci in HLA-DPB1 were identified to be associated with PM/DM of Han Chinese. Additional studies will be needed to determine the role of these findings in the genetic etiopathogenesis of PM/DM.

PU-1202

综合性医院首诊 HIV 患者中 HBV HCV 和梅毒混合感染状况及临床特征

王万海、孟宪春、明亮
郑州大学第一附属医院

目的 了解综合性医院首诊人类免疫缺陷病毒(HIV)患者中合并乙型肝炎病毒(HBV)、丙型肝炎病毒(HCV)和梅毒螺旋体(TP)的混合感染情况及临床特点，为艾滋病(AIDS)的防控和治疗提供科学依据。
方法 2013 年 1 月至 2017 年 12 月，以非艾滋病首诊于某综合性医院而确证为 HIV 患者，收集其人

口学资料和临床资料，并进行乙型肝炎病毒表面抗原(HBsAg)、丙型肝炎病毒抗体(HCV-Ab)和梅毒特异性抗体(TP-Ab)检测。
结果 359 例 HIV 患者年龄中位数为 45 岁(2~86 岁)，男性 251 人(69.92%)，女 108 人(30.08%)。4.18%的 HIV 患者通过母婴途径感染，33.98%通过性途径感染和 61.84%通过血液途径 (单采血浆)感染。混合感染 HBV 为 9.75%，HCV 为 17.55%和 TP 为 15.88%。HIV 感染的不同途径中，HBV、HCV 和 TP 的混合感染率存在差异。HIV 患者首诊科室共涉及 26 个，其中内科相关科室达到 58.22%，外科为 13.65%，其它科室占到 28.13%。涉及疾病谱 18 类，主见呼吸系统疾病、感染性疾病、神经系统疾病、消化系统疾病、血液系统疾病。
结论 首诊综合性医院的 HIV 患者中合并 HBV、HCV 和 TP 感染率相对较高，涉及就诊科室多，疾病谱广。

PU-1203

人免疫缺陷病毒检测的质量控制

周蓉
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 探所讨论人免疫缺陷病毒初筛检测的质量控制影响因素，提高人免疫缺陷病毒化学发光微粒法检测水平，快速为临床提供参考结果。
方法 用化学发光微粒法对人免疫缺陷病毒抗原抗体进行检测，初步检测阳性反应者用人免疫缺陷病毒 HIV(1+2)抗体胶体金法进行复检。
结果 影响人免疫缺陷病毒初筛检测质量的因素包括：标本采集是否正确，运输是否合理，试剂、试管的使用、人员操作过程、环境温湿度、仪器维护、质控设置等很多方面的原因。
结论 在日常工作检测中，除开客观不可抗力因素影响外，需要检测人员拥有高度的责任心，从标本采集到标本上机整个过程都要用心，保证标本的质量。在从仪器维护、试剂准备到质控完成，都要细心做到正确。对各种影响检测结果的因素，积极采取全面有效的质量控制措施，减少或想办法消除误差，才能有效预防假阴性或者假阳性结果的出现，从而避免或者预防医院感染及交叉感染，降低职业暴露的危险，加强医护人员的自我保护，为临床提供可靠准确的检测结果。

PU-1204

血清热灭活对胶体金法检测 2019-nCoV 抗体的影响

胡秀梅
南方医科大学南方医院

目的 评估热灭活对胶体金法检测新型冠状病毒（2019 novel Coronavirus, 2019-nCoV）特异性抗体 IgM 和 IgG 的影响。
方法 收集新型冠状病毒肺炎确诊住院患者血清 106 份及健康医护人员血清标本 52 份，采用商品化 2019-nCoV 抗体检测试剂盒（胶体金法）分别对 56℃ 30 min 热灭活前后的血清标本特异性 IgM 和 IgG 抗体进行检测，分析灭活前后抗体检出率的差异及一致性。根据患者发病时间分析热灭活对不同发病阶段抗体检出率的影响。
结果 健康对照组标本灭活前后测试均为阴性。56℃ 30min 灭活后降低 2019-nCoV 特异性抗体 IgM 和 IgG 的检出率，106 例确诊患者 IgM 抗体总检出率由 66.04%（70/106）降至 43.40%（46/106），差异有统计学意义（$\chi2=22.042$，$P=0.000$）；IgG 抗体阳性率由 81.13%（86/106）降至 76.42%（81/106），差异无统计学意义（$\chi2=0.800$，$P=0.063$）。在发病第 3 周、第 5 周和第 6 周热灭活可显著降低 IgM 抗体检出率。不同发病时段，血清热灭活前后 IgG 抗体检出率差异无统计学意义。

结论 56℃ 30 min 热灭活降低胶体金法 2019-nCoV 特异性 IgM 抗体检出率，易导致假阴性结果。

PU-1205

550 例儿童食入物过敏原 IgG 检测结果分析

郭争艳
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 通过分析特异性过敏 IgG 的检测结果，对儿童食入物过敏性疾病预防和治疗提供理论支持。
方法 采用酶联免疫吸附法对我科 2020 年 1 月～2020 年 12 月 550 例儿童保健门诊、儿科门诊和住院患儿食入物过敏原特异性 IgG，进行统计分析。
结果 在 550 例患儿中检出总阳性率 87.3%蛋清/蛋黄阳性率最高 50.5%，牛奶次之 41.6%，一份血清标本可出现多种食入物过敏原存在。
结论 食物过敏原中蛋清/蛋黄和牛奶是最主要食入性过敏原，采取有效的预防措施，可以有效降低食入物导致过敏疾病的发生。

PU-1206

健康体检人群抗核抗体与抗核抗体谱检测结果相关分析

刘芳、司元全
山东省立医院东院

目的 通过对本实验室健康人群抗核抗体与抗核抗体谱定量检测结果的分析，揭示健康人群 ANA 分布情况及规律，进一步探讨人群筛查的意义，为临床疾病的诊断提供有用的价值。
方法 采用间接免疫荧光法(IIF)检测血清 ANA,流式荧光发光法检测 15 项 ANAS 特异性抗体。
结果 在 18240 例体检人群中，ANA 滴度阴性为 15482 例，ANAS 特异性抗体阳性率为 2.6%，流式荧光发光法检测 15 项 ANAS 特异性抗体按顺序阳性率排前三的为抗补体 C1q 抗体、SSA-52、抗双链 DNA 抗体（dsDNA）；ANA 滴度>1:100 阳性为 2758 例，阳性率为 15.12%，男性阳性率为 9.27%，女性阳性率为 21.23%，ANA 滴度>1:320 阳性率为 10.12%，男性阳性率为 6.60%，女性阳性率为 13.80%，不同性别阳性率差异有统计学意义。其中 ANA 滴度>1:320 时，男性阳性率随年龄增长出现平缓上升趋势，女性在青春期及更年期出现两个高峰；ANA 滴度>1:320 阳性人群中 15 项特异性抗体阳性率为 69.99%，按顺序阳性率排前三的为抗 SSA-52：14.84%、M2：13.00%、SSA60：9.97%。
结论 体检人群中 ANA 滴度阴性者中也存在一定的 ANAS 特异性抗体阳性者；ANA 滴度>1:100 各年龄段均存在阳性者，且其 ANA 滴度>1:320 分布随性别、年龄不同存在明显差异；对于健康人群尤其是处于青春期及更年期的女性筛查 ANA 是极其必要的，对于筛查中 ANAS 特异性抗体阳性人群进行定期的 ANA 及 ANAS 联合检测，可以有效防止漏诊和误诊，ANA 滴度阳性人群应做好自身免疫性疾病防御知识的宣传及追踪随访工作，为疾病诊断治疗及预后提供重要的临床价值。

PU-1207

白塞病患者外周血 T/B/NK 淋巴细胞亚群分析

王斐
中国医学科学院北京协和医院

目的 研究白塞病（Behcet’s disease，BD）患者外周血 T/B/NK 淋巴细胞亚群分布情况。

方法 回顾性分析就诊于北京协和医院的白塞病患者（114 例）的外周血淋巴细胞亚群分布情况，所有患者均根据国际白塞病研究组于 1989 年制定的诊断标准进行诊断和分类，并选用 75 例表观正常、无系统性炎性疾病和其他疾病的健康人群作为对照。统计分析采用 Graphpad Prism5 软件进行处理，P<0.05 差异有统计学意义。Kolomogorov-Simirnov 检验用于评价数据的正态性，其中正态分布资料采用（±S ）表示，两组间比较采用非配对 t 检验，非正态分布资料采用中位数[M(P25~P75)]表示，组间比较采用 Kruskal-Wallis 检验。
结果 白塞病患者外周血中淋巴细胞绝对计数（1.74±0.83）与健康对照组（2.21±0.47）相比明显降低（p<0.0001）；其中 CD3+T 细胞所占比例（77.08%±10.00%）与健康对照组（73.25%±5.23%）相比明显升高（p=0.0026）；CD3+CD4+T 细胞所占比例（35.33%±11.85%）与健康对照组（39.57%±4.66%）相比明显降低（p=0.0036）；CD3+CD8+T 细胞所占比例（32.85%±12.71%）与健康对照组（28.01%±4.69%）相比明显升高（p=0.0026）；CD3+CD4-CD8-双阴性 T 细胞所占比例（8.90%±10.60%）与健康对照组（5.63%±2.79%）相比明显升高（p=0.0097）；NK 细胞所占比例（12.69%±8.60%）与健康对照组（14.43%±4.69%）相比没有明显差异（p=0.1125）；B 细胞所占比例（9.66%±5.53%）与健康对照组（11.69%±2.70%）相比明显降低（p=0.0037）。
结论 在白塞病发病过程中，除 NK 细胞外，外周血淋巴细胞亚群各群占比发生了明显变化，值得注意的是白塞病患者 CD3+CD4-CD8-双阴性 T 细胞明显升高，但该群细胞在白塞病中的发病机制还需要进一步研究来证实。

PU-1208

肿瘤专科医院患者梅毒抗体检测分析

竺明晨
江苏省肿瘤医院

目的 分析肿瘤患者梅毒感染情况，为肿瘤患者的梅毒防治工作提供科学依据。
方法 收集我院 2011 年-2020 年共 119875 例肿瘤住院患者，梅毒螺旋体明胶颗粒凝集试验(TPPA)检测结果，统计分析阳性患者性别、年龄和肿瘤类型等分布情况。
结果 经 TPPA 检测结果梅毒抗体呈阳性的患者共 3128 例，阳性率 2.61%，其中男性 1714 例，女性 1414 例，阳性患者年龄 15 岁-95 岁，中位年龄 60 岁。男性患者阳性率 2.92%，女性患者阳性率 2.31%，男性阳性率高于女性患者。统计分析各年龄段梅毒抗体阳性情况，发现随着年龄增加阳性率也逐渐增加。从小于 20 岁的 0.24%阳性逐渐增加到大于 91 岁患者的 7.14%阳性。按年度统计分析梅毒螺旋体抗体检测阳性情况，抗体阳性率介于 2.57%~2.82%之间，各年度之间阳性率无显著差异。选择 119875 例肿瘤患者中 103299 例常见肿瘤，分别统计分析梅毒螺旋体抗体阳性率，结果发现梅毒抗体阳性率在 1.43%-10.00%之间，其中排名前五的肿瘤类型分别是阴囊肿瘤(10.00%)、宫颈肿瘤(4.77%)、阴道恶性肿瘤(3.59%)、膀胱恶性肿瘤(3.38%)和头颈肿瘤(3.12%)。
结论 部分肿瘤患者的梅毒阳性率较高，需要引起足够的关注 。

PU-1209

血清 CYFRA21-1、NSE、ProGRP 检测在非小细胞肺癌筛查中的应用

何成禄、段勇
昆明医科大学第一附属医院

目的 探讨细胞角蛋白 19 片段（CYFRA21-1）,神经元特异性烯醇化（NSE）,胃泌素释（ProGRP）在非小细胞肺癌（NSCLC）中诊断的临床诊断价值。

方法 选取经病理确证的 NSCLC 的病例组 720 例 ，肺部良性疾病组 240 例和同期健康体检者 550 名 (健康对照组) 作为研究对象, 运用微粒子化学发光法检测静脉血血清中 CYFRA21-1、NSE 和 ProGRP 浓度，计算各指标的敏感度、特异性、阳性预测值和阴性预测值，运用卡方检验及 ROC 曲线，单独比较各指标在 NSCLC 中的阳性率，并与两两或多重指标的并联做模式比较，构建 NSCLC 筛查的最佳组合模式。
结果 三组不同受检者的 CYFRA21-1,NSE 和 ProGRP 阳性率分别为（50%，29.2%，31%）、（16.7%，8.3%，8.3%）和（1.8%，0.2%，1.8%），组间比较结果显示 NSCLC 组大于良肺部良性疾病组和健康对照组,差异有统计学意义（P<0.05），不同肿瘤标志物间阳性率比较， 结果显示 NSCLC 组中的 CYFRA21-1 显著高于 NSE 和 ProGRP，而对照组 CYFRA21-1 和 ProGRP 均高于 NSE，差异均有统计学意义（P<0.05）；联合检测结果显示，两两联合的和三项联合的四项检测指标均高于单项检测，其中 CYFRA21-1+NSE、CYFRA21-1+ProGRP、NSE+ProGRP 两两联合比较差异无统计学意义（P>0.05），CYFRA21-1+NSE+ProGRP 联合检测比单项检测和两两联合检测的四项诊断指标均明显提高，差异有统计学意义(P<0.05)；单项检测指标 CYFRA21-1 的 ROC 曲线下面积最大为 0.721。
结论 对于单一指标的筛查，应首选 CYFRA21-1。三种肿瘤标志物联合检测的血清诊断学诊断有利于非小细胞肺癌的有效筛查，在临床具有很大应用价值。

PU-1210

溶血对新生儿静脉血丙肝抗原（HCV-Ag）检测的影响

李晓菲
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 探讨溶血对新生儿静脉采血标本丙肝抗原（HCV-Ag）检测结果的影响，避免因溶血原因导致的 HCV 检测窗口期的错误判断。
方法 收集 2018.1-2018.12 在山东省千佛山医院检验科进行丙肝抗原(HCV-Ag)检测的新生儿静脉血标本 160 例，应用双抗体夹心法化学免疫分析原理在 CLIA500 板式化学发光免疫分析仪进行 HCV-Ag 检测。按照标本是否溶血进行分组检测，共分为两组，非溶血标本组(80 例)和溶血标本组(80 例)。对所有纳入研究的标本均进行离心分离血清，然后进行 HCV-Ag 即时检测和静止 24 小时后重新离心再检测。以 HCV-Ag 检测结果 S/CO>1 作为结果阳性的标准，计算 HCV-Ag 检测阳性率，观察溶血是否影响 HCV-Ag 检测阳性率，以及静置 24h 小时后能否降低阳性率。
结果 对非溶血标本，HCV-Ag 即时检测阳性率为 1.25 % (1/80)，静止 24 小时后重新离心再检测阳性率为 0% (0/80)。而对溶血标本，HCV-Ag 检测阳性率为 30% (24/80),静止 24 小时后离心重新检测阳性率 2.5 %(2/80),显著低于即时检测阳性率。
结论 溶血增加了新生儿静脉血标本 HCV-Ag 检测的假阳性率，静止 24 小时后离心重新检测假阳性率能够显著降低。

PU-1211

山东济南地区中年人 25-羟维生素 D 水平分析

张平
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 了解山东济南地区中年人 25-羟维生素 D［25-(OH)D］的水平。
方法 选取 2020 年 1 月至 2020 年 12 月，在山东省千佛山医院内科门诊，中年人 850 例，年龄 45-59 岁，平均（51±4.50）岁。采用高效液相色谱串联质谱法检测 25-(OH)D 水平。

结果 850 例中年人 25-(OH)D 的平均水平（56.33±8.26）ng/ml。其中缺乏状态（＜25ng/ml）356 例，占 41.9%；不足状态（25～75ng/ml）170 例，占 20%；正常状态（75～250ng/ml）324 例，占 38.1%。按照年龄分组中，>55 岁水平最低（22.50±8.17）ng/ml，45-50 岁水平最高（88.92±8.25）ng/ml。按照月份分组，3 月份水平最低（19.73±6.34）ng/ml，9 月份水平最高（96.09±8.60）ng/ml，差异无统计学意义（P＞0.05）。各月 25-(OH)D 水平与平均气温具有相关性（r=0.846，P＜0.05）；与日照时数不具有相关性（r=0.231，P＞0.05）。
结论 山东济南地区中年人 25-(OH)D 总体水平偏低，存在缺乏和不足的占 61.9%；年龄分组中 >55 岁的水平最低；各月分组中 3 月份水平最低。临床应引起高度重视，采取预防措施；同时加强健康宣教，提高中年人对维生素 D 不足现状的认识。

PU-1212

Performance Characteristics of Light Initiated Chemiluminescence Assay for the Quantitative Determination of High Sensitivity Cardiac Troponin I

Jing Wang[3]、Yanv Ren[1]、Haifang Kong[1]、Luyun Peng[2]
1. Tianjin Medical University General Hospital
2. West China Second Hospital of Sichuan University
3. Tianjin Medical University

Objectives High sensitivity cardiac troponin I (hs-cTnI) assays have been used clinically throughout the world. How to select healthy reference subjects in deriving 99th percentiles for cardiac troponin I assays still needs to be clarified. In order to help the early diagnosis of myocardial infarction (MI) in chest pain patients, we evaluate the analytical performance of the newly developed hs-cTnI on light initiated chemiluminescence assay (LiCA) system.
Methods Evaluation of the sensitivity, imprecision, linearity, method comparison and 99th percentile sex-specific upper reference limit (URL) of hs-cTnI on the LiCA system. Comparison studies were performed vs Abbott ARCHITECT hs-cTnI assay. The 99th percentile sex-specific URL studies were established in 320 healthy males and 307 healthy females respectively.
Results The limit of blank, limit of detection and limit of quantitation at 20% coefficient of variation (CV) were 1.23pg/mL, 1.79pg/mL and 1.84pg/mL respectively. The intermediate imprecision ranged from 2.16% to 5.07%. Linearity was observed up to 5000pg/mL. The method comparison between LiCA and Abbott demonstrated a correlation coefficient of 0.975 with a slope of 1.09. The 99th percentile URL of healthy males and females were 13.23pg/mL and 10.59pg/mL respectively.
Conclusion The LiCA hs-cTnI immunoassay demonstrates excellent analytical performance with good sensitivity and precision, which can be an aid in the early diagnosis of acute myocardial infarction.

PU-1213

从中性粒细胞胞外捕获网角度探讨系统性红斑狼疮患者易于感染细菌的原因

穆丹妮、刘昱东
北京大学人民医院检验科

目的 包括中性粒细胞胞外捕获网(neutrophil extracellular traps, NETs)在内的人体先天免疫系统是机体对抗入侵病原体的重要防御屏障。针对系统性红斑狼疮(systemic lupus erythematosus, SLE)

患者 NETs 水平升高但更易于感染细菌这个现象，我们从 NETs 的角度探讨了 SLE 患者易于细菌感染的影响因素。

方法 收集 SLE 确诊病例 50 例（疾病活动期 23 例，稳定期 27 例），健康对照 27 例。分离受试者中性粒细胞，体外刺激 NETs 形成，与肺炎克雷伯菌(Klebsiella pneumoniae, KPN) 菌株 ATCC 43816 和一株分离自临床的 KPN 18219 分别共孵育 90 分钟，计算 NETs 介导的杀菌百分率。分析患者各项临床指标，包括疾病活动度、补体水平、血红蛋白浓度和病程等与 NETs 杀菌能力的关系。

结果 （1）狼疮活动组 NETs 对 KPN 43816 的杀菌率显著低于稳定组和健康对照（p=0.0162，p=0.0238），而稳定组和健康对照的杀菌百分率无显著性差异（p>0.05）。各组 NETs 对 KPN 18219 的杀菌率也呈现类似的现象。（2）SLE 患者的 NETs 对 KPN 43816 和 KPN 18219 的杀菌百分率与 SLEDAI 评分呈负相关关系（r=-0.3108，p=0.04；r=-0.2686，p=0.0679），而与患者病程、补体水平和用药情况无关。（3）用 ROC 曲线确定 NETs 杀菌率降低的临界值，NETs 杀菌率受损的 SLE 患者与杀菌率正常的 SLE 患者相比，SLEDAI 评分显著升高（p=0.0022），补体 C3、C4 水平显著降低（p=0.0244；p=0.0034），而病程、血红蛋白浓度、血小板和中性粒细胞/淋巴细胞比值都无显著性差异（p>0.05）。

结论 NETs 杀菌能力的降低可能与 SLE 易于细菌感染有关，活动期狼疮患者 NETs 介导的杀菌能力相比于稳定期和健康对照显著降低，与疾病活动度有关，而与病程和药物的使用无关。

PU-1214

流式细胞术测 12 项细胞因子性能验证及评价

陈学飞、李汉华、吴亚洲、翁文浩
上海市杨浦区中心医院（同济大学附属杨浦医院）

目的 对流式细胞术同时测 12 项细胞因子[白细胞介素 1β（IL-1β）、白细胞介素 2（IL-2）、白细胞介素 4（IL -4）、白细胞介素 5（IL -5）、白细胞介素 6（IL-6）、白细胞介素 8（IL-8）、白细胞介素 10（IL-10）、白细胞介素 12P70（IL-12P70）、白细胞介素 17（IL-17）、干扰素 α（IFN-α）、干扰素 γ（IFN-γ）、肿瘤坏死因子 α（TNF-））]的性能进行验证及评价。

方法 参照 WS/T492-2016《临床检验定量测定项目精度和正确度性能验证》、WS/T 402—2012《临床实验室检验项目参考区间的制定》，使用 BD FACS Canto II 流式细胞仪对青岛瑞斯凯尔生物科技有限公司 12 项细胞因子检测试剂盒进行线性及范围、精密度、准确性、参考区间进行验证。

结果 IL-1β、IL-2、IL-4、IL-5、IL-6、IL-8、IL-10、IL-12P70、IL-17、IFN-α、IFN-γ、TNF-α 在 BD Canto Ⅱ流式细胞仪上检测结果在 2.44 pg/mL—10000pg/ml 范围内呈线性。最低检测限浓度 2.44pg/ml 下能良好检出，变异系数符合要求；批内精密度和批间精密度变异系数均≤15%；准确性验证相对偏差均在±15%以内，参考区间可直接使用。

结论 12 细胞因子检测试剂盒（多重微球流式免疫荧光发光法）在 BD CantoⅡ流式细胞仪的线性及范围、最低检测限、精密度、准确性及参考范围通过验证，可以满足临床检测需求。

PU-1215

结直肠癌患者粪便钙卫蛋白和外周血可溶性 IL-2 受体、IL-6 水平变化与患者生活质量和临床预后之间的关系

邢继成
解放军第八一医院

目的 探讨结直肠癌患者粪便钙卫蛋白和外周血可溶性白细胞介素-2 受体(sIL-2R)、白细胞介素-6(IL-6)水平变化与患者生活质量和临床预后的关系。
方法 选择结直肠癌患者 186 例为观察组，另选择同期健康体检者 55 例为对照组，采用胶体金免疫层析法测定粪便钙卫蛋白，酶联免疫吸附法测定 sIL-2R 和 IL-6 水平，分析粪便钙卫蛋白、sIL-2R 和 IL-6 水平与结直肠癌患者临床资料、术后生活质量及临床预后的关系。
结果 观察组粪便钙卫蛋白、外周血 sIL-2R 和 IL-6 水平显著高于对照组 (P<0.05)；有淋巴结转移者 sIL-2R 和 IL-6 水平显著高于无淋巴结转移者(P<0.05)，粪便钙卫蛋白无显著意义(P>0.05)；TNF 分期Ⅲ一Ⅳ期者粪便钙卫蛋白和 sIL-2R、IL-6 水平显著高于 I～Ⅱ期者 (P<0.05)；粪便钙卫蛋白和 sIL-2R、IL-6 高水平组健康状况调查问卷(SF-36) 评分、终点事件发生率与粪便钙卫蛋白和 sIL-2R、IL-6 低水平组比较有显著性差异(P<0.05)。
结论 粪便钙卫蛋白和 sIL-2R、IL-6 在结直肠癌患者中呈高水平表达，其表达水平与淋巴结转移情况和临床分期有关，高水平粪便钙卫蛋白和 sIL-2R、IL-6 者术后生活质量较低，临床预后较差。

PU-1216

南京市秦淮区杨公井 34 标 34 号

杨帆
南京八一医院

目的分析评价雅培 Alinity i 全自动化学发光免疫分析仪检测乙肝表面抗原（HBsAg）及乙肝表面抗体（HBsAb）的性能。
方法 收集 HBsAg、HBsAb 的阳性及阴性血清各 25 例，健康体检标本 20 例，极高浓度 HBsAg 及 HBsAb 血清各一例，用 Alinity i 全自动化学发光免疫分析仪分别检测 HBsAg 及 HBsAb，分析其精密度、线性检测范围、检出限、携带污染率及正常生物参考区间，以雅培 Architect i2000 全自动化学分析仪的结果为对照，评价 Alinity i 与 Architect i2000 结果的相关性，通过检测 2021 年度卫生部临检中心室间质评样本来判定与其他实验室结果的一致性。
结果 Alinity i 全自动化学发光免疫分析仪 HBsAg 低高浓度的批内精密度为 3.76%和 1.16%，批间精密度为 6.72%和 3.89%；HBsAb 低高浓度的批内精密度为 3.81%和 3.28%，批间精密度为 6.42%和 3.78%。HBsAg 及 HBsAb 检测范围内的线性方程相关系数 r2 分别为 0.9958 和 0.995，回归方程斜率 a 分别为 0.9881 及 1.0244。HBsAg 及 HBsAb 的定值质控品稀释到定量限浓度后检测的均值分别为 0.053 及 2.0755，CV 分别为 8.87%和 7.89%。HBsAg 与 HBsAb 的携带污染率皆为 0.0%，健康人群 HBsAg 及 HBsAb 的结果均落在正常参考范围内。Alinity i 与 Architect i2000 比对检测 HBsAg 及 HBsAb 的线性相关方程相关系数 r2 分别为 0.9982 及 0.9939，回归方程斜率 a 分别为 0.9568 及 1.0355，Alinity i 检测卫生部室间质评结果与预期结果一致。
结论 雅培 Alinity i 全自动化学发光免疫分析仪检测 HBsAg 及 HBsAb 的稳定性、重复性和精确性完全符合临床应用要求。

PU-1217

乙型肝炎病人的血清免疫球蛋白检验价值探讨

常蕊
黄河水利委员会黄河中心医院

目的 探究乙型肝炎病人的血清免疫球蛋白检验价值探讨。
方法 将乙型肝炎患者 105 例作为此次研究观察组，105 例根据病情严重程度分为轻度组、重度组，再选取 105 例健康体检者作为对照组，收取时间为 2019 年 12 月 2021 年 1 月,对所有受检者均进行血清免疫球蛋白检验，并分析检验结果。
结果 重度组患者 IgG（17.12±2.15)g/L、IgM（2.45±0.16)g/L、IgA 水平（2.65±0.12)g/L 均高于轻度组 IgG（14.35±3.15)g/L、IgM（2.15±0.26)g/L、IgA 水平（2.26±0.65)g/L 和对照组 IgG（11.52±2.01)g/L、IgM（1.40±0.25)g/L、IgA 水平（1.50±0.35)g/L；而轻度组患者 IgG（14.35±3.15)g/L、IgM（2.15±0.26)g/L、IgA 水平（2.26±0.65)g/L 均高于对照组健康体检者，三组受检者各项指标具有显著差异（P＜0.05）。
结论 通过对乙型肝炎患者实施血清免疫球蛋白检验，取得显著的检验价值，不仅能够对患者病情程度进行判断，还能根据诊断结果制定针对性的治疗方案，从而提高治疗效果，并且改善患者疾病预后，促进疾病的转归。

PU-1218

涎液化糖链抗原-6 在类风湿性关节炎相关间质性肺疾病诊疗中的应用价值

王恩运[1,2]、豆小文[1]、胡纪文[1,2]
1. 深圳市罗湖医院集团医学检验实验室
2. 深圳市罗湖区中医院

目的 结缔组织病相关间质性肺疾病（CTD-ILD）多继发于类风湿关节炎（RA），国内外分别报道 22.5%和 47% RA 患者合并 ILD，RA-ILD 患者的中位生存期为 3 年，5 年生存率为 38.8%。研究已证实，涎液化糖链抗原-6（Krebs von den Lungen-6，KL-6）是 ILD 病变的敏感指标，可早期识别 CTD-ILD 改善预后。本研究拟探讨 RA 患者的血清 KL-6 水平升高是否有助于将 CTD-ILD 诊断窗口前移，预警其在 RA 继发 ILD 的诊疗价值。
方法 以临床诊断为金标准，纳入来我院就诊的类风湿性关节炎患者 29 例作为疾病组（32~64 岁，平均年龄 49 岁）；体检人员 27 例作为对照组（33~78 岁，平均年龄 53 岁）。收集血清，采用 AXCEED260 化学发光试剂，双抗体夹心法分别检测疾病组和对照组患者血清中 KL-6 水平。采用 MedCalc 19.0.4 统计学分析对照组与疾病组 KL-6 水平差异。
结果 KL-6 试剂 cutoff＞500U/mL（99%置信区间），可辅助诊断为间质性肺炎可知，对照组无阳性，疾病组检测出阳性 1 例（546 U/mL），经临床诊断 RA-ILD；KL-6 试剂可定量血清中 KL-6 含量，对照组和疾病组血清 KL-6 含量中位数分别为 170 U/mL（95%CI 111~189 U/mL）和 205 U/mL（95%CI 150~283 U/mL），疾病组相比对照组 KL-6 水平升高，经 Mann-Whitney U 检验两组水平无显著性差异（P＞0.05）。
结论 KL-6 试剂相比有创穿刺，该血清指标仅需简单采血可进行辅助诊断间质性肺炎；CTD-ILD 疾病早期 RA 疾病相比健康人群 KL-6 水平升高不显著，可能还需联合其他指标辅助鉴别 RA 继发的 ILD，实现 CTD-ILD 诊断窗口前移。

PU-1219

郑州市某大型医院近三年 HIV 抗体确证试验结果分析

张磊
郑州大学第一附属医院

目的 分析我院近三年经 HIV 抗体初筛阳性患者的 HIV 抗体确证结果。
方法 收集我院 2019 年-2021 年 HIV 抗体初筛（电化学发光法）阳性的标本，采用电化学发光法及胶体金法复检，复检结果双阳性或一阳一阴的标本，进一步用免疫印迹法进行确证，分析确证阳性患者的带型特点。
结果 704 例复检呈阳性（含一阴一阳及双阳结果）的患者，因知情同意受限 8 例未进行 WB 确证，696 例经免疫印迹试验证实，HIV-1 型抗体阳性患者 476 例，确证阳性率 68.39%，不确定 113 例，阴性 107 例。476 例确证试验阳性标本经流行病学调查 95．8％(456／476)是性行为（同性/异性性行为）传播。113 例 WB 不确定样本中要集中在孕产妇占 89．4％(101／113)，经随访及结合其它检查综合判断，89 例最终排除 HIV 感染。在 WB 结果为阴性的 107 例样本中，采用电化学发光法复检，其 COI 值介于 0.9～33.85 之间。
结论 性接触传播尤其是男男性接触者(MSM)是我实验室报告 HIV／AIDS 的主要传播途径；不确定样品主要集中在孕产妇人群，多是非特异性免疫反应，在低流行人群尤其孕产妇 HIV 抗体不确定样本最终以阴性转归为主。

PU-1220

20 例阿尔茨海默病患者自身抗体结果追踪分析

吴晓琪、陈婧、何亭亭、肖琼、董瀚淳、苏义恒
杭州迪安医学检验中心有限公司

目的 探讨自身抗体与阿尔茨海默病的关系。
方法 回顾性分析 20 例阿尔茨海默病患者 2017-2020 年自身抗体持续多次检测情况。
结果 20 例中有 7 例抗核抗体（ANA）持续检测均为阴性，ANA 检测有阳性的 13 例，10 例持续结果≤1：320，有 3 例检出中有 1：1000 高滴度，共检测 514 次 ANA，阴性检出率为 59.7%，阳性检出率为 40.3%，波形蛋白、纺锤体、肌动蛋白、Jo-1、SCL-70、Sm、U1nRNP、抗核糖体、AMA、抗着丝点均检测为阴性。SS-A，SS-B、ACA、抗组蛋白、c-ANCA、ds-DNA、p-ANCA 阳性检出率分别为 12.3%，8.4%、7.2%、6.6%、3.5%、1.4%和 0.4%。
结论 自身免疫疾病或许和阿尔茨海默病风险增加直接相关。

PU-1221

肾功能对肿瘤标志物 CA125 和 HE4 血清水平的影响初探

刘玲[2]、苗强[1]、张君龙[1]、蔡蓓[1]、牛倩[1]
1. 四川大学华西医院
2. 四川大学华西临床医学院

目的 探讨肾功能对糖类抗原 125（Carbohydrate antigen，CA125 ）和 人附睾蛋白 4（human epididymis protein4，HE4）血清水平的影响，并尝试建立适用于慢性肾脏病人群的 CA125 和 HE4 血清参考范围。

方法 纳入 CKD 患者 729 例，同时纳入性别匹配的健康体检者 94 例，采用罗氏电化学发光免疫分析仪检测血清 CA125 和 HE4 的水平，采用罗氏全自动生化分析仪检测血清尿素、肌酐和胱抑素 C 的水平。
结果 与健康对照组相比，CKD 组患者的尿素、肌酐、胱抑素 C、CA125、HE4 水平均明显升高，在校正年龄因素后差异仍具有统计学意义（P<0.001）。CKD 2-5 期患者的 CA125、HE4 表达水平均不一致，CKD4 期患者 CA125 表达水平最高，CKD2-5 期患者的 HE4 表达逐渐升高。Spearman 分析结果显示，CA125 与年龄、尿素、肌酐、胱抑素 C、eGFR 相关性较弱， HE4 水平与 eGFR 呈很强的负相关，与尿素、肌酐、胱抑素 C 呈很强正相关（P<0.001）。建立 CKD 女性人群特定的 CA125 和 HE4 参考范围，女性 CKD 人群 CA125 的参考范围为<213.9 pmol/L；HE4 的参考范围：CKD3 期人群为<564.5 pmol/L，CKD4 期人群为<1713.5 pmol/L，CKD5 期人群为<5022.6 pmol/L。
结论 肾功能下降可导致血清 CA125 和 HE4 水平明显升高；建立 CKD 女性人群特定的血清 CA125 水平参考范围为：<213.9 pmol/L；血清 HE4 水平参考范围为：CKD3 期： <564.5 pmol/L, CKD4 期 <1713.5 pmol/L, CKD5 期 <5022.6 pmol/L。

PU-1222

PI3K/Akt 信号通路在 SLE 患者中性粒细胞胞外诱捕网形成中的作用

蒋瑶[1,2,3]、祝静[1,2,3]、邢艳[1,2,3]
1. 川北医学院附属医院
2. 川北医学院医学检验系
3. 川北医学院转化医学研究中心

目的 系统性红斑狼疮（systemic lupus erythematosus，SLE）是一种经典的全身性自身免疫性疾病，近年来新发现的中性粒细胞死亡形式-中性粒细胞胞外诱捕网（neutrophil extracellular traps，NETs），因其形成过程释放大量自身抗原而参与 SLE 发病，但参与其形成的分子机制仍不明确。本文旨在探究 PI3K/Akt 信号通路在 SLE 患者 NETs 形成中的作用，从而为 SLE 的治疗提供新思路。
方法 密度梯度离心法分离 6 例健康体检者外周血中性粒细胞（PMN）后，瑞士染色及台盼蓝拒染实验检测 PMN 的纯度及活性；在加入或不加入 PI3K/Akt 特异性抑制剂 LY294002 或 MK2206 的情况下，荧光光度法检测经佛波酯（PMA）及 SLE 患者混合血清分别处理 PMN 90min 和 120min 后 NETs 形成水平，并分析 NETs 形成量的差异。
结果 分离得到的 PMN 纯度及活性均>95%，满足体外细胞实验要求；在 PMA 及 SLE 混合血清刺激 PMN 形成 NETs 过程中，加入 PI3K 抑制剂 LY294002 后，NETs 生成水平明显降低[（310±182.77）VS（840.20±334.54），P=0.005]、[（419.33±196.83）VS（703±266.71），P=0.004]；同样地，在加入 Akt 抑制剂 MK2206 后,NETs 生成明显减少[（593±224.93）VS（842.60±307.04），P=0.007]、[（500.67±271.53）VS（784.50±348.28），P=0.009]，组间均有统计学差异，表明 LY294002、MK2206 能通过抑制 PI3K/Akt 活化而减少 PMA 及 SLE 血清刺激 NETs 形成。在 PMN 自发形成 NETs 的过程中，Akt 抑制剂 MK2206 能抑制 NETs 形成[（138.67±52.11）VS（210.33±80.66），P=0.03]，但 PI3K 抑制剂 LY294002 无此作用[（168±78.08）VS（220.60±87.03），P=0.15]，表明在 PMN 自发形成 NETs 的过程中，有 Akt 的参与，但其上游调控蛋白可能不是 PI3K。
结论 PMA 及 SLE 混合血清可能通过 PI3K/Akt 信号通路启动了 NETs 的形成，提示对 PI3K/Akt 信号分子的调控可能抑制 NETs 的产生，继而控制 SLE 的病理进程。

PU-1223

上海市杨浦区人群 3 年间主要过敏原的分布和变迁

陈燚琼、赵迪、任方、钱朵朵、李智、翁文浩
同济大学附属杨浦医院

目的 分析上海市杨浦区人群的主要过敏原在 2016～2018 年的分布及变迁情况，为该地区过敏性疾病的预防和管理提供依据。
方法 对 2016 年 1 月～2018 年 12 月在本院就诊的疑似过敏性疾病的患者，应用 Immuno CAP100 过敏原检测系统检测过敏原特异性 IgE（sIgE），统计每种 sIgE 的检测量、阳性检出量和阳性率，并对阳性检出率进行排序分析。
结果 三年间 1010 例患者中，主要的食物性过敏原为虾和蟹，致敏阳性率分别为 9.51%和 7.33%；主要吸入性过敏原为粉尘螨和户尘螨，致敏阳性率分别为 24.17%和 21.94%；6 种混合性过敏原中阳性率最高的是户尘/户尘螨/粉尘螨/德国小蠊（hx2），阳性率为 25.27%。不同性别阳性率比较，男女虾 sIgE 阳性率分别为 12.09%和 6.05%，男女蟹 sIgE 阳性率分别为 9.69%和 4.18%，男女蟑螂 sIgE 阳性率分别为 13.49%和 5.95%，差异均有统计学意义（P<0.01）。鸡蛋白、粉尘螨和户尘螨阳性率在 0～18 岁组最高，并随年龄增大逐渐降低，3 个年龄组间差异有统计学意义（P<0.01）。
结论 上海市杨浦区过敏患者食物性过敏原以虾和蟹为主，吸入性过敏原以粉尘螨和户尘螨为主；且不同性别和年龄过敏原结构存在差异。3 年间粉尘螨和户尘螨阳性率出现年间波动，其他过敏原变化相对稳定。

PU-1224

抗核抗体、抗双链 DNA 抗体和抗中性粒细胞胞浆抗体检测的性能验证

邹麟
重庆医科大学附属第一医院

目的 对实验室间接免疫荧光法检测抗核抗体（ANA）、抗双链 DNA 抗体（dsDNA）、抗中性粒细胞胞浆抗体（ANCA）以及免疫印迹法检测可提取性核抗原抗体（ENA）进行性能评价，确保检测方法性能满足实验室及临床诊疗的质量要求。
方法 参考 WS/T 505-2017《定性测定性能评价指南》及 CNAS-GL038：2019《免疫定性检验程序性能验证指南》，对精密度、方法学符合率、检出限、携带污染率、人员比对五个方面进行验证。
结果 ANA 两个不同水平的批内精密度和批间精密度均为 100%；ANA、抗 dsDNA、ANCA 以及 ENA 室间质评阴阳性符合率均为 100%；ANA、抗 dsDNA 以及 ANCA 的检出限阳性率分别为 100%、100%和 95%；ANA 及 ANCA 携带污染率验证中样本 L1、L2、L3 结果均为阴性；ANA、抗 dsDNA 及 ANCA 人员比对结果一致率均为 100%。
结论 ANA、抗 dsDNA、ANCA 以及 ENA 的精密度、方法学符合率、检出限、携带污染率、人员比对验证均全部通过。本室 ANA、抗 dsDNA、ANCA 和 ENA 的检测方法性能验证结果能够满足 ISO 15189 对临床免疫学定性检验的性能评价要求，可为临床实验室检测方法评价提供参考。

PU-1225

CA199、NSE、CA153、CEA 联合检测用于脑胶质瘤的诊断

巨桓宇
江苏省人民医院

目的 本次实验简要的探讨在脑胶质瘤的诊断中，糖类抗原（CA）199、神经元特异性烯醇化酶（NSE）、CA153、癌胚抗原（CEA）价值。
方法 收集 2018 年 6 月—2019 年 6 月医院患者的数据，按照随机性的原则，选取 68 例脑胶质瘤患者和 67 例脑外伤颅内压手术患者。使用传统的分组实验对比的方法，将患者分为两组，68 例脑胶质瘤患者为实验组，67 例脑外伤颅内压手术患者作为对照组。检测两组患者的 CA199、NSE、CA153、CEA 水平，使用酶联免疫吸附试验法进行检测；使用曲线表示的形式进行评估，采用受试者工作特征曲线，评估两组患者的 CA199、NSE、ＣＡ153、CEA 对脑胶质瘤的诊断价值，对比 4 项指标联合检测与单项检测的诊断效能。
结果 实验结束后，可以看出各组患者的各项数据都是不相同的，脑胶质瘤组患者血清 CA199、NSE、CA153、CEA 水平较高，明显高于对照组；差异有统计学意义（Ｐ＜ 0.05）；低级别脑胶质瘤患者与高级别脑胶质瘤患者又有着明显使的差异，尤其是血清的数值，高级别脑胶质瘤患者的血清 CA199、NSE、ＣＡ153、CEA 水平较高差异有统计学意义（Ｐ＜0.05）。CA199、NSE、ＣＡ153、CEA 联合检测诊断脑胶质瘤具有较好的灵敏度，灵敏度为 88.46％，因此诊断的效果较好，准确度为 86.34％，即使诊断的灵敏度很高，但是仍然不会影响诊断的准确性，诊断的准确性较高，高于单项检测，差异有统计学意义（Ｐ＜0.05）。
讨论 根据实验的结果显示，CA199、NSE、ＣＡ153、CEA 对脑胶质瘤的诊断效果较好，联合诊断的效果优于一次性诊断。

PU-1226

降钙素原在辅助诊断血流感染中的价值研究

黄瑜
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 近年来，随着临床创伤性治疗手段的应用以及广谱抗生素的使用，血流感染的发病率有逐年增高的趋势。血流感染早期诊断甚至疗效评估显得尤为重要。本文将系统论述降钙素原在辅助诊断血流感染中的价值。
方法 查阅近 10 年的文献，归纳和总结降钙素原在辅助诊断血流感染中的价值。
结果 降钙素原（PCT）是一种无激素活性的降钙素前肽物质。正常代谢状态下，PCT 在健康个体血浆中的浓度极低(< 0.1ng /ml)，一旦出现严重的细菌、真菌、寄生虫感染，降钙素原在内毒素等细胞因子诱导下其血浆水平会升高。降钙素原血清浓度在提示临床病原体感染方面有较高的诊断价值，且能够根据 PCT 血浆水平的不同早期判断病原菌的类型：有脓毒血症的患者血浆 PCT 水平明显高于非脓毒症患者，细菌性脓毒症患者的 PCT 水平显著高于非细菌性脓毒症，与 IL-2，IL-6，IL-8，CRP 和 TNF-α 相比，PCT 对脓毒症患者的全身炎症反应综合征（SIRS）患者的敏感性最高（85％）和特异性（91％）最高，因此可以作为诊断脓毒症和鉴别严重细菌感染的生物标志物，而目前来讲，菌血症的患者体内 PCT 的浓度一般大于 0.5ng/ml，其血浆浓度随着患者感染的严重程度浮动变化，若血浆浓度达到 10ng/ml，一般提示存在严重革兰阴性细菌的感染，可在微生物血培养结果尚未出来之前，建议临床进行早期治疗。
结论 血流感染发病迅猛，后果严重，因此能够早期对血流感染进行筛检极为重要。临床医生能够通过降钙素原的血浆浓度，在患者出现血流感染症状后，经验治疗（PCT<0.51μg/L,但存在血流感染症状时，使用抗生素无效，反之 PCT 水平短时间内升高，可能提示存在细菌感染，建议使用抗生素治疗）以挽救患者生命。

PU-1227

Comprehensive review the roles of autoantibodies in diseases

Gongjun Tan
zhuhai center for maternal and children healthcare

Antibodies are an essential immune component mediating both clearance and control of infections. autoantibodies, which recognize the host's own molecules and tissues, play a crucial role in the pathology of autoimmune disorders. Autoantibodies are most commonly associated with autoimmune diseases, but a large body of evidence indicates that they are also present in numerous other diseases. Surprisingly, with the increase of autoantibody research **Methods** and the change of research technology, the incidence and prevalence of autoantibodies in the disease is large and underestimated. Increasing number of autoantibodies being reported suggests that currently "idiopathic" diseases may someday be explained by neutralizing or agonizing autoantibodies. In this review, we comprehensive overview of autoantibodies in human diseases, the production mechanism of autoantibodies, the method of identification of autoantibodies as well as the application potential of autoantibodies.

PU-1228

急性胆囊炎严重程度与血清肌钙蛋白升高的临床研究

巨桓宇
江苏省人民医院

目的 探究分析血清肌钙蛋白 I(Tn I)水平与急性胆囊炎严重程度之间的关系，分析其对保守治疗无效的预测价值研究。
方法 收集 2018 年 6 月—2019 年 6 月医院患者的数据，选取 68 例急性胆囊炎患者作为研究对象，按照患者病情的严重程度，将患者分为三组，即重度组、中度组、轻度组。每一组患者接受不同的治疗措施，比较各组一般资料及血清 C-反应蛋白(CRP)、降钙素原(PCT)及 Tn I 水平，分析血清 Tn I 水平对保守治疗无效的预测效能，探究治疗的实际效果。
结果 实验结束后，可以看出三组患者的各项数据都是不相同的，重度组、中度组和轻度组患者的血清水平有着明显的差异，血清 Tn I 水平上差异具有统计学意义(P＜0.05)；血清 CRP、PCT 和 Tn I 水平会发生变化，在患者病情严重的时候，血清 CRP、PCT 和 Tn I 水平会升高。在 68 例急性胆囊炎患者中，保守治疗并非对每一位患者都有效，其中无效的共有 24 例。使用 Logistic 回归分析，患者保守治疗无效的原因有很多，胆囊长径、血清 Tn I、PCT 等都是独立预测因素。
结论 急性胆囊炎是临床上较为常见的一种疾病，但是患者对其了解的程度并不高，急性胆囊炎越严重，对患者造成的身体危害越大。本次实验简要的探究血清肌钙蛋白 I(Tn I)水平与急性胆囊炎严重程度之间的关系。根据实验的结果显示，血清 Tn I 水平与急性胆囊炎严重程度有关系，二者呈正相关，在患者病情严重的时候，血清 CRP、PCT 和 Tn I 水平会升高。这为患者早期分类诊治提供了重要的依据。

PU-1229

HBP 和 IL-6 在脓毒症中的临床应用

王然
第一人民医院

目的 观察 HBP 和 IL-6 检测在脓毒症中的临床价值。
方法 比较不同组别脓毒症患者的血浆 HBP 和血清 IL-6 水平，并进行相关性分析。 方法选取 120 例脓毒症病人,免疫荧光法测血浆 HBP、流式细胞仪测血清 IL-6 的水平,按照危重评分（ PCIS）将其分成非危重组（ PCIS 评分＞ 80 分， n = 46 例）、危重组（ PCIS 评分为 71 ～ 80 分， n = 40 例）以及极危重组（ PCIS 评分≤ 70 分， n =34 例）。并按照患者的临床结局分成死亡组（ n = 30 例）以及存活组（ n = 90 例）。
结果 非危重组、危重组以及极危重组的 HBP 和 IL-6 具有明显的差异（ P ＜ 0.05)，两两相比均具有明显的差异（ P ＜ 0.05），其中非危重组最低，危重组次之，极危重组最高。脓毒症患者的 PCIS 评分与 HBP，IL-6 水平均呈负相关（ P ＜ 0.01）
结论 HBP 和 IL-6 与脓毒症患者的病情危重程度紧密相关，可作为评估病情和预后情况的指标。

PU-1230

ELISA 技术与 Luminex 多因子检测技术在免疫学指标检测中的应用及比较

张娟、徐守久、刘迪、石春雨、程宇、刘建勇、梁超、陈忠
北京海思特医学检验实验室有限公司

研究目的 本文分析了 ELISA 试剂盒验证中易出现的问题和解决方案，并将 ELISA 技术与 Luminex 多因子检测技术相比较，为应用 Luminex 多因子检测技术开展免疫学检测提供参考。
研究**方法** ELISA 技术和 Luminex 多因子检测技术。
研究结果 酶联免疫吸附技术（enzyme-linked immunosorbent assay, ELISA）是临床免疫学检测中常用方法。以往研究发现应用新试剂盒前必须对试剂盒严格验证，本文对验证实验中常遇到的问题和解决方案进行讨论，同时与 Luminex 多因子检测技术进行比较。
ELISA 验证实验：（1）制定定标合格标准。定标时不仅要考察标曲的 R^2 值，同时关注斜率（K 值）。避免出现 R^2 值合格（R^2>0.95），但斜率差异较大（K 值偏离 1±10%）而造成结果不准确的情况。（2）准确度验证。优先选用可溯源的标准物质进行准确度验证，如果没有商用标准物质，则需要选用低、中、高值标准品进行回收实验验证。（3）精密度验证。可以将多样本混合成低、中、高 3 个浓度后，每个浓度每天重复检测 3 次，重复 5 天进行批内和批间精密度验证。临床样本可以通过复孔检测和留样待测来确定孔间和批次间的稳定性。（4）确定定量下限。实验室要根据试剂盒说明书的检测范围建立定量下限，一般会将高值标准品稀释到原浓度的 20-25%，重复测定 20 次，如果 CV 值在 20%以内为合格，否则需要重新调整稀释比例。（5）样本保存期限。常规样本 2-8 度保存，一周内完成检测。长期保存样本，建议在冻融≤3 次，超低温（-80 度）情况下保存不超过 1 年。
ELISA 技术具有数据结果准确、操作简便、仪器造价低等优点。但进行多指标检测时费时、费力。为了应对这种情况，我们尝试了 Luminex 多因子检测技术。此技术是基于 Luminex 仪器系统的高通量蛋白定量技术。
此技术优势：（1）单一样本同时进行多指标检测，减少由于操作不同 ELISA 试剂盒，各因子检测条件无法平行而造成的系统误差。（2）节省样本量和操作时间。每孔最低标本量 50μl，单孔最多可同时检测 100 种指标。即使检测指标增多，标本量和实验用时也不需要显著增加。（3）panel 灵活。可以根据检测需要自由组合检测指标。

此技术不足：（1）检测项目不全。由于是新兴技术，目前开发出的检测指标只局限于临床需求量较大的指标。（2）要求使用 luminex200 或 FLEXMAP3D 等仪器，仪器造价高。（3）仪器的使用、校准、验证、维护和保养复杂，需要专门培训。
因而，严格把控 ELISA 验证流程，做好实验质控，积极尝试新技术，才能使检测结果更具有临床指导意义。

PU-1231

补体系统在先兆子痫中的研究进展

唐娜、周玉球
珠海市妇幼保健院

先兆子痫（Preeclampsia, PE）是一种常见的威胁孕妇生命的妊娠高血压疾病。补体活化在维持健康的怀孕起着至关重要的作用，但补体系统的过度激活或不适当监管可能会导致 PE 的发生。本文就补体系统在 PE 发病中的活化和作用进行简要概述，为补体成分作为 PE 临床诊断的生物标志物和预防靶点提供参考依据。

PU-1232

2019 年湖北省 4966 例九项呼吸道感染病原体检测结果分析

周梅英、胡庆、冯园、徐能、申建维
武汉千麦医学检验实验室有限公司

目的 对 2019 年 1 月至 2019 年 12 月湖北地区共 4966 例呼吸道感染患者血清九项病原体 IgM 抗体检测结果进行回顾分析，为呼吸道疾病的临床诊断和预防提供辅助依据。
方法 采用间接免疫荧光法（呼吸道九联检试剂）检测 4966 例呼吸道感染患者血清标本中的九项常见病原体的 IgM 抗体，包括嗜肺军团菌(LP1)、肺炎支原体(MP)、Q 热立克次体(COX)、肺炎衣原体(CP)、腺病毒(ADV)、呼吸道合胞病毒(RSV)、甲型流感病毒(INFA)、乙型流感病毒(INFB)及副流感病毒(PIV)1、2、3 型。
结果 在 4966 例呼吸道感染患者中共检测出 IgM 抗体阳性 1653 例（33.29％），其中 MP 感染率最高（15.85%），其次 LP1（13.95%），最低为 RSV（0.12%）。不同季度感染率也不相同，其中第四季度感染率最高（53.07%）。
结论 MP、LP1 是湖北地区 2019 年呼吸道感染主要病原体，其中冬季为呼吸道病毒感染的高发期，在季节更替时需要加强对呼吸道感染疾病的预防和控制。

PU-1233

CNPY2 与肿瘤发生发展关系的研究进展

段文冰
山东第一医科大学附属省立医院临床医学检验部

CNPY2（Canopy FGF Signaling Regulator 2，CNPY2）作为一种新型的分泌蛋白，在心脏、肝脏、胰腺等机体各器官和组织上都广泛表达，CNPY2 是未折叠蛋白质反应（UPR）相关疾病（如代谢紊乱、炎症、癌症）潜在的新型治疗靶点，多个研究证明其与多种肿瘤的发生与发展密切相关。近年来，癌症的发病率迅速增长，已经严重威胁人类的身体健康和生活质量，CNPY2 可能通过促血管生成作用参与肿瘤的发生发展，且可通过激活 NF-κB 增强抗凋亡信号通路提高化疗敏

感性，因而深入研究 CNPY2 在癌症中的作用机制及临床应用价值，对癌症的发生、发展、治疗及预后都有着深远的意义。

PU-1234

壳多糖酶 3 样蛋白 1 在丙肝性肝硬化中的检测及临床意义

谢婉莹、黄霞
湖南省人民医院

目的 探讨血清壳多糖酶 3 样蛋白 1（CHI3L1）对丙型肝炎性肝硬化的诊断价值。
方法 选取 2018 年 10 月至 2021 年 1 月由湖南省人民医院诊治的 35 例慢性丙型肝炎患者、65 例丙型肝炎合并肝硬化患者作为研究对象，选取同期在该院体检的 100 例健康体检者作为对照组。采用酶联免疫双抗体夹心法测定血清 CHI3L1 水平，Pearson 线性相关分析血清 CHI3L1 水平与肝功能指标白蛋白（ALB）、谷丙转氨酶（ALT）、谷草转氨酶（AST）、γ-谷氨酰转移酶（γ-GGT）及碱性磷酸酶（ALP）之间的相关性。
结果 丙型肝炎合并肝硬化组 CHI3L1 水平明显高于慢性丙型肝炎组（P<0.05）和健康体检组（P<0.001），有统计学意义。CHI3L1 鉴别诊断丙型肝炎有肝纤维化和无肝纤维化的 ROC 曲线下面积为 0.806，最佳临界值为 119.4ng/ml，敏感度为 93.8%，特异度为 56.0%。CHI3L1 与 ALB 呈显著负相关（r＝-0.526，P<0.01），CHI3L1 与 AST、γ-GGT 均呈显著正相关（AST：r=0.507，P<0.01；γ-GGT：r=0.474，P<0.01），CHI3L1 与 ALT、ALP 无显著相关性（P>0.05）。
结论 血清 CHI3L1 对丙型肝炎合并肝硬化的诊断具有一定应用价值，有望成为判断肝硬化严重程度的指标。

PU-1235

肾移植排斥非侵入性生物标志物的研究进展

毛静秋
昆明市第一人民医院

肾移植已成为治疗终末期肾病的有效方法，但移植后的排斥反应仍是目前影响患者生存质量的关键因素。目前肾病患病率逐年上升，但较为成熟的肾移植技术给患者带来生存的希望，研究显示目前移植物的短期存活率可达 95%，我们现在面临的难题是如何提高患者移植后的生存质量及长期生存率。移植后发生的排斥反应是影响移植物的关键因素，选择合适的生物标志物检测有利于移植前排斥反应的预测并对其进行干预以及对移植后排斥的监测，以此改善患者的生存预期。目前，临床上移植物活检是诊断排斥反应的金标准。活检属于侵入性操作，对病人有一定伤害。非侵入性生物标记物可以减少移植物活检对患者和临床医生的负担。理想的非侵入性生物标志物可以区分排斥与其他肾脏疾病或短暂的变化，预测患者和移植物的预后，为患者提供个体化的治疗。本文描述了现在临床上常用及新提出的生物标志物，如 HLA 抗体已成为预测抗体介导的排斥反应的重要生物标志物。抗体介导的排斥反应是肾移植后移植物丢失的主要原因，部分移植患者由于输血，妊娠等情况致使机体处于致敏状态或自身存在针对供体的抗体，移植后 HLA 抗体针对移植物发生免疫应答，导致组织损伤。文中还描述了补体、免疫细胞、外泌体等。本综述总结的生物标志物对监测移植患者排斥方面都具有一定的有效性和局限性，选择合适的单个标志物及组合有利于对患者状态有更好的了解，随着各种技术的发展，相信更多更好的生物标记物被开用于临床，更好的为提高患者生存质量服务。

PU-1236

Diagnostic Value of PCT, IL-6 and CRP in the solid tumor patients with infections

Jia Gao
National Cancer Center/Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing

Fever is a common symptom in the course of cancer patients. It is very important to identify bacterial infection in time to guide the use of antibiotics. In this study, we evaluated the diagnostic value of procalcitonin (PCT), interleukin-6 (IL-6) and C-reactive protein (CRP) for bacterial infections in tumor patients. Firstly, we recruited 100 non-fever tumor patients, and determined the reference of PCT and IL-6 in tumor patients. After that, 334 patients were retrospectively categorized into the bloodstream infection (n=100), localized bacterial infection (n=100), tumor-relate fever (n=34) and the non-fever cancer (n=100) groups. Serum PCT, IL-6 and CRP were detected to assess their diagnostic value for fever. The results are summarized as follows: Firstly, the normal reference range of serum PCT and IL-6 in tumor patients is 0~0.14ng/ml and 0~29.42pg/ml, respectively, slightly higher than that of the healthy controls. In the bloodstream infection group, PCT yields a remarkably higher median concentration (Median=0.46, IQR=0.99) comparing with that of the localized bacterial infection group (Median=0.19; IQR=0.48, P=0.02) and tumor-relate fever group (Median=0.13; IQR=0.17, P<0.001). When using 0.195ng/ml as the cutoff value, PCT yielded the best diagnostic valve (sensitivity:72%; specificity:59%). No differences were observed for IL-6 and CRP among the three groups (P=0.118). In conclusion, PCT is feasible as an infection marker in diagnosing bloodstream infection in cancer patients.

PU-1237

肝素结合蛋白在感染早期中的作用

华春兰
郑州大学第一附属医院

Aim Infectious diseases remain a major health problem for patients, they lead to organ dysfunction and finally cause morbidity and mortality. Heparin-binding protein (HBP) has several biological functions. In this study, we found that HBP levels on admission are associated with the development of infection, so it can be regard as an early indicator of infection, which may be a potential biological marker and a new target for infection treatment.
Methods A total of 262 patients with a suspected infection from the ICU were included and HBP concentration on plasma samples from admission to the ICU was analyzed. Statistical analysis was performed by Student's t-test, the data shown were expressed as the mean ± SD.
Results The levels of plasma HBP, PCT, WBC, NEU were elevated in patients in ICU, however, HBP displayed a high level than other three biomarkers in 24 hours.
Conclusion Altogether, we proved that HBP may be a promising infection related biomarker with a potential for predicting serious infection. It is suggested that further studies either on plasma HBP are warranted.

PU-1238

乙肝两对半检测方法学及其临床应用差异对比

侯家旭
大理大学第一附属医院（云南省第四人民医院）

目的 研究不同检测法在检测乙肝两对半的各方面及其临床应用。现今临床常用的乙肝两对半的血清学检测方法主要有化学发光免疫分析法、酶联免疫法、免疫胶体金法。但在真正临床应用中各种方法有各自具有其不同的优缺点，可能受不同因素的影响其各自的敏感性和特异性不同。所以就乙肝两对半的不同检测方法及其临床应用的差异对比进行进一步研究。
方法 免疫胶体金法、酶联免疫吸附法、电化学发光法、统计学处理采用 SPSS22.0 进行统计分析，计数资料 n(%)表示，行 X^2检验比较，差异具有统计学意义（P＜0.05）
结果 灵敏度差异为电化学发光法的灵敏度最高；酶联免疫吸附法的灵敏度次之；免疫胶体金法最低
特异性的差异为为电化学发光法的灵敏度最高；酶联免疫吸附法的灵敏度次之；免疫胶体金法最低
结论 对于乙肝血清学标志物的检测方法在临床上的应用各有各的优点各有各的好处，但同时也各自存在一定的局限性和缺点。总的对比来说，电化学发光法在乙肝两对半的检测中较免疫胶体金法和酶联免疫吸附法灵敏度更好，特异性更好。其结果对于临床诊断的准确性以及对乙肝患者的整个感染、恢复过程的监测都具有重要意义。但是该方法成本高，还未能大量投入使用。而免疫胶体金法则因其灵敏度以及特异性的局限性，且只可做定性检测，但因其价格廉价，检测速度快，操作简单，所以大多只用于乙肝大面积筛查。酶联免疫吸附法则是现在应用比较广泛的方法，其成本价格低，技术较为成熟,所以现在大部分医院都在开展。但是其影响因素较多，其在今后的发展过程中也将会逐步被新的技术方法所替代。在如今这个科技快速发展的时代，对于乙肝的诊断治疗技术方法也将会逐步发展，所以我相信，将来一定会有对于乙肝诊断治疗更精确方便慧民的方法出现，人们将再也无惧乙肝病毒所给人们带来的健康困扰。

PU-1239

血清磷脂酶 A2 受体抗体检测在特发性膜性肾病中应用及患者临床特点分析

万青
东南大学附属中大医院

目的 探讨磷脂酶 A2 受体（PLA2R）抗体在成人特发性膜性肾病（IMN）中的诊断作用和病情活动监测价值，及特发性膜性肾病 PLA2R 阳性患者与阴性患者的临床指标差异及特点。
方法 对 2016 年 3 月至 2018 年 4 月期间东南大学附属中大医院 PLA2R 检测 602 例标本进行回顾性分析，其中肾脏活检明确诊断的 IMN 患者 60 例，肾脏活检确诊为其他类型的肾脏病患者 135 例为对照组，包括有 45 例糖尿病肾病、24 例高血压肾病、27 例 IgA 肾炎、24 例系膜增生性肾炎、15 例狼疮性肾炎的患者为阴性对照。分析 ELISA 法检测血清 PLA2R 的敏感性及特异性。此外将 IMN 患者 PLA2R 抗体浓度与 24 小时尿蛋白量、血清 IgG、IgA、IgM、补体 C3、补体 C4、IgG4、血清肌酐、血清白蛋白等临床指标进行相关性分析，探讨血清 PLA2R 检测的临床价值。根据 PLA2R 结果，将患者分组为 PLA2R 阳性组和 PLA2R 阴性组，对两组患者上述临床指标进行比较，分析特发性膜性肾病 PLA2R 阳性与阴性患者的临床相关指标特点。
结果（1）60 个确诊的 IMN 患者中有 39 个血清 PLA2R 阳性，阳性率为 65%，135 个对照组阳性患者只有 2 个阳性，其余 PLA2R 均为阴性，特异性达到 98.52%。（2）血清 PLA2R 与 24 小时尿蛋白量成正相关，P = 0.001，相关系数 rp = 0.523，两者相关性密切。（3）与膜性肾病 PLA2R

阴性组比较，PLA2R 阳性组患者 24 小时尿蛋白量显著增加（P=0.003），血清 IgG4 水平显著降低（P = 0.038），但其他指标没有统计学意义。
结论 血清 PLA2R 检测特异性高，可作为 IMN 的诊断指标。动态监测血清 PLA2R 与 24 小时尿蛋白量可以反应病情变化及评估临床疗效。

PU-1240

肺癌七项自身抗体在肺部结节中的诊断价值

万青
东南大学附属中大医院

目的 分析七项血清自身抗体在肺部结节患者中的诊断价值和临床意义。
方法 选择本院从 2020 年 1 月到 2021 年 4 月期间 298 例标本，其中分为 17 例确诊肺癌患者、221 例肺部良性结节患者和 57 例体检者三组，选用 ELISA 法检测血清中抑癌基因 53(p53)、蛋白基因产物 9.5(PGP9.5)、干细胞转录因子(SOX2)、G 抗原 7(GAGE7)、肿瘤抗原 4-5(GBU4-5)、黑色素瘤抗原 A1(MAGEA1)、人癌抗原(CAGE)共七项自身抗体的表达水平，进行统计学分析。
结果 p53、SOX2、GBU4 -5 和 MAGEA1 在肺癌组中的表达水平显著增高，表达水平均明显高于肺良性结节组和体检组，差异均有统计学意义（P<0.05）。使用 ROC 曲线进行统计分析结果显示：p53 (AUC =0.675，P<0.05)对肺癌组和其他组的鉴别诊断有意义；GBU4-5(AUC =0.632，P<0.05)及七项联合检测(AUC =0.624，P<0.05)对鉴别良性肺结节和肿瘤组具有一定的诊断价值。
结论 七项自身抗体及其联合检测对肺癌和良性肺结节的鉴别诊断均具有一定的价值，为肺部结节诊断提供了一种新的方法。

PU-1241

补体 C3 在成人 still 病和脓毒症中的鉴别诊断价值

李洁
江苏省人民医院（南京医科大学第一附属医院）

目的 评价血清补体 C3 在成人 still 病（AOSD）和脓毒症中的鉴别诊断价值。
方法 收集江苏省人民医院 2016 年至 2019 年 AOSD 患者 58 例、脓毒症患者 50 例，并选取 50 名江苏省人民医院体检中心健康体检者作为健康对照。检测三组血清中补体 C3 水平，并比较 AOSD 患者和脓毒症患者的其他实验室指标有无差异性，运用单因素和多因素分析各变量与 AOSD 鉴别诊断的关系，并采用 ROC 曲线探讨补体 C3 与血清铁蛋白水平对 AOSD 和脓毒症的诊断效能。
结果 AOSD 组补体 C3 水平（1.49±0.24）显著高于脓毒症组 C3（1.00±0.37），两组数据中高密度脂蛋白、铁蛋白、补体 C3 差异具有统计学意义。多因素分析显示铁蛋白≥472.20ng/ml（OR 56.968，95%CI 2.218~1463.439，P＜0.05），补体 C3 ≥1.20g/L（OR 27.801，95%CI 3.217~240.277,P ＜ 0.01 ），高密度脂蛋白 ≥0.82mmol/L （ OR 13.335 ，95%CI 1.009~176.293,P＜0.05）与 AOSD 发生的可能性独立相关。血清 C3 鉴别诊断 AOSD 和脓毒症患者的曲线下面积（AUC）为 0.81（95%CI 0.63~1.00），当 C3 临界值为 1.21 时，诊断灵敏度为 0.90，特异度为 0.73，此时可达最大的诊断效能，然而当 C3 联合铁蛋白鉴别诊断时，AUC 则为 0.86（95%CI 0.75~0.96）。
结论 血清 C3 可作为 AOSD 和脓毒症的鉴别诊断指标，对 AOSD 的诊断具有临床价值。

PU-1242

高敏肌钙蛋白 T 分析性能的评价及参考范围的建立

朱琳
中国人民解放军总医院第一医学中心检验科

目的 评价电化学发光法检测高敏肌钙蛋白 T（hs-cTNT）的分析性能，并建立本实验室的参考范围。
方法 按 2019 年发布的《临床化学定量检验程序性能验证指南》的具体操作方法评价 hs-cTNT 检测的正确度、精密度、线性范围、可报告范围，并收集 493 名表面健康人群的血清，检测其 hs-cTNT 浓度，建立本实验室参考范围。
结果 卫生部室间质评质控样本的检测结果均值与靶值之间的偏倚绝对值均小于 12.5%，全部通过；两个水平的批内标准差（低值 0.001ng/ml，高值 0.03ng/ml）和实验室内标准差（低值 0.001ng/ml，高值 0.027ng/ml）均小于厂家声称的重复精密度（低值 0.004ng/ml，高值 0.188ng/ml）和期间精密度（低值 0.005ng/ml，高值 0.339ng/ml）；线性分析 R2=0.9991；可报告范围为 0.017-100ng/ml；Spearman 相关分析评估 hs-cTNT 浓度与年龄的相关系数为 0.325，p<0.01；与性别的相关系数为 0.330，p<0.01；本实验室 hs-cTNT 的表面健康人群第 99 百分位值为：男性≤60 岁为 0.028ng/ml，>60 岁为 0.078ng/ml；女性≤60 岁为 0.026ng/ml，>60 岁为 0.024ng/ml。
结论 电化学发光法检测 hs-cTNT 的检测性能良好，符合实验室要求；本实验室建立的表面健康人群的 hs-cTNT 水平明显高于厂商声明的第 99 百分位值，建立一个适合于本实验室表面健康人群的参考范围有重要的临床意义。

PU-1243

通过尿素解离减少自身免疫性疾病患者新型冠状病毒抗体的假阳性及其临床评价

李小凤
重庆市公共卫生医疗救治中心

目的 探讨新型冠状病毒(SARS-CoV-2）IgM/IgG 胶体金免疫层析法在自身免疫性疾病中的假阳性情况及解决方法，同时探讨解决方法是否影响新型冠状病毒肺炎（COVID-19）患者 SARS-CoV-2 IgM/IgG 的检测。
方法 应用胶体金免疫法检测 396 份血清标本中 SARS-CoV-2 IgM/IgG，其中系统性红斑狼疮（SLE）、干燥综合征（SS）、混合性结缔组织病（MCTD）、自身免疫性肝炎（HIA）患者各 50 例、健康体检人员 50 例和确诊 COVID-19 患者 146 例，采用尿素解离试验以最佳解离浓度对 SARS-CoV-2 IgM/IgG 阳性血清进行解离。
结果 200 例自身免疫性疾病患者 SARS-CoV-2 IgM 抗体均为阴性，6 例 SARS-CoV-2 IgG 为阳性，其中 3 例 SLE 患者 IgG 阳性，SS、MCTD 和 AIH 患者各 1 例 IgG 阳性。6mol/L 尿素处理自身免疫性疾病患者 SARS-CoV-2 IgG 阳性标本后，5 例转为阴性。100 例（早、中、后期）COVID-19 患者 IgG 抗体阳性率 77%（77/100）；IgM 抗体的阳性率为 56%，IgM/IgG 总阳性率为 85%。用尿素(6mol/L)解离后，中期 1 例 IgG 阳性转为阴性；38 例弱阳性 SARS-CoV-2 IgM 中 1 例转为阴性；36 例弱阳性 SARS-CoV-2 IgG 中 1 例转为阴性。在 50 名健康体检人员中 SARS-CoV-2 IgM/IgG 抗体均阴性,经尿素解离后仍为阴性。
结论 尿素解离试验有助于减少自身免疫性疾病患者 SARS-CoV-2 IgG 假阳性，尿素解离使 COVID-19 患者 SARS-CoV-2 IgM/IgG 抗体转为阴性可能与抗体的亲和力有关，但需进一步研究。

PU-1244

血清多指标联合检测对肺癌的诊断价值

李丹、陈燕
福建省肿瘤医院

目的 探讨血清中癌胚抗原（CEA）、特异性烯醇化酶(NSE)、胃泌素释放肽前体(Pro-GRP)、细胞角蛋白 19 片段(CYFRA21-1)、鳞状细胞癌抗原（SCC）和胱抑素 C(Cys C)联合检测对肺癌诊断的价值。
方法 将研究对象分为健康对照组（医院体检者）和肺癌患者组（初次确诊肺癌患者），分别收集他们的 CEA、NSE、CYFRA21-1、Pro-GRP、SCC 及 Cys C 数据，进行比较；进而分析 CEA、NSE、CYFRA21-1、Pro-GRP、SCC 及 Cys C 单独检测和联合检测的检验效能，从不同类型的患者和疾病的不同阶段分析它们在肺癌中的诊断价值，结合 ROC 曲线，从而选出最优的肿瘤标志物组合，提高临床对肺癌的检出率。
结果 CEA、NSE、CYFRA21-1、Pro-GRP、SCC 及 Cys C 在年龄、性别表达上无显著差异。通过单因素方差分析，得出 CEA、CYFRA21-1、NSE、Pro-GRP 在 T1 期到 T4 期间，表达水平依次递增；CYFRA21-1 与 NSE 在 TNM 期中Ⅰ期到Ⅳ期，表达水平递增；CYFRA21-1 在鳞癌中，表达水平高于另外两种癌症；Pro-GRP 在小细胞癌的表达水平最高；SCC 随着肿瘤增大和淋巴转移其表达水平上升；Cys C 随着肿瘤增大表达水平上升，随着肿瘤多处转移减小。通过对数据进行相应 t 检验和卡方检验，得出正常组和健康对照组的差异是有统计学意义的。通过绘制 ROC 曲线，得出联合检测是可以提高诊断率的。其中两两联合检测中 Pro-GRP+SCC 高达 0.905，CEA+NSE 高达 0.976，明显比单独检测敏感度高。通过相关性分析，得出 CEA 与 CYFRA21-1、NSE 之间有相关性，Pro-GRP 与 NSE 之间有相关性，其余各项之间是可以起互补的作用。
结论 CEA、NSE、CYFRA21-1、Pro-GRP、SCC 及 Cys C 在肿瘤不同分期、癌症种类、肿瘤大小和肿瘤转移中表达水平存在差异；并且这些指标的联合检测是可以提高肺癌早期的辅助诊断率；肺癌表达 Cys C 水平和正常人表达的水平具有一定差异。

PU-1245

血清 ANCA 检测阳性患者的结果分析

侯彬、刘阳、杨平、王芳、袁丹、方堃
四川省科学城医院

目的 分析中性粒细胞胞浆抗体（ANCA)在临床应用。
方法 选取本院 2018 年 4 月至 2020 年 12 月期间进行了 ANCA 项目检测的患者的临床资料。
结果 共 922 患者检测 ANCA，其中阳性 39 例，占 4.2%。P-ANCA33 例，其中 11 例靶抗原 MPO 阳性。C-ANCA33 例，其中 1 例靶抗原 PR3 阳性。其中 6 例诊断为未分化结缔组织病，3 例诊断为系统性红斑狼疮，7 例 ANCA 相关性血管炎诊断明确，1 例诊断为类风湿关节炎，3 例无任何表现，考虑为假阳性，其余病例需进一步检查。
结论 1.在存在自身免疫性疾病时，应加查 ANCA 检测，以免漏检。2.ANCA 阳性不一定为血管炎，需根据临床症状对每个病例分析，防止误诊。3.ANCA 相关性血管炎早期临床表现复杂多样，故实验室开展 ANCA 检测，及实验室检测结果的准确性对临床在该病的诊断上具有重要意义。

PU-1246

抗髓过氧化物酶抗体及抗蛋白酶 3 抗体双阳性的 ANCA 相关性血管炎 1 例

宁明哲、臧福宇、朱文波、陶月
南京大学医学院附属鼓楼医院

目的 抗髓过氧化物酶（myeloperoxidase, MPO）抗体和抗蛋白酶 3（proteinase 3，PR3）抗体双阳性的病例，临床和实验室工作中罕见，我院检出 1 例抗 MPO 抗体、抗 PR3 抗体双阳性的患者标本，为临床实验室人员提供学习资料。
方法 2019 年 7 月，患者男，54 岁，因“反复发热 20 余天，伴有咳嗽、咯痰”入院，拟诊“肺部感染”；抗生素治疗效果欠佳，在完善相关实验室检查后发现抗 MPO 抗体、抗 PR3 抗体双阳性， pANCA 阳性, cANCA 阳性，肾功能受损，修改诊断为“ANCA 相关性血管炎”，转入风湿科，予以激素治疗，患者症状好转，出院随诊。后因患者擅自停药，造成症状反复，继续服药后症状好转。MPO、PR3 检测结果恢复至参考范围内。
结果 患者因 pANCA 阳性，MPO 阳性，出现肾脏相关症状；因 cANCA 阳性，PR3 阳性，亦出现上呼吸道相关症状。
结论 近年来，临床对 ANCA 和 AAV 的认识普遍提高，国际公认 ANCA 是 AAV 敏感性、特异性均较高的血清学指标，并将其作为诊断和分类 AAV 的重要参考 ，因此需要临床实验室提高 ANCA 检测报告的准确性，为临床诊治提供可靠依据。

PU-1247

肌钙蛋白 T 和 N 端 B 型脑利钠肽前体对乳腺癌患者蒽环类药物序贯曲妥珠单抗治疗致心脏毒性的预测价

陈岩松、陈燕
福建肿瘤医院

目的 探讨 cTnT 与 NT-ProBNPHER2 阳性乳腺癌患者接受蒽环类药物序贯曲妥珠单抗治疗所致的心脏毒性的预测价值。
方法 选取 2018 年 1 月-2021 年 3 月福建省肿瘤医院治疗的 70 例乳腺癌患者，按照发生心脏毒性和未发生心脏毒性分为两组，比较两组在基线期临床病理参数的差异；比较两组 cTnT 与 NT-proBNP 水平在基线和终点的动态变化，ROC 曲线分析 cTnT 与 NT-proBNP 对心脏毒性的诊断价值；将 cTnT 与 NT-proBNP 纳入 COX 回归分析，评估两生物标志物对心脏毒性的预测价值。
结果 两组在基线时期高血压、高血脂发生率、ER、PR 阳性率无明显统计学差异（P>0.05）,心脏毒性组基线高尿酸血症发生率高于非心脏毒性组，差异有统计学意义（P<0.05）；在基线时两组 cTnT 与 NT-proBNP 差异均无统计学意义（P>0.05）。然而在终点时间时，发生心脏毒性组 cTnT 与 NT-proBNP 水平明显高于未发生心脏毒性组，差异具有显著统计学差异（P<0.01）；ROX 曲线分析 cTnT 与 NT-ProBNP 诊断心脏毒性的曲线下面积分别为 0.883 和 0.892，最佳诊断阈值分别为 8.66 和 194.30； COX 回归分析提示患者 cTnT 与 NT-proBNP 对心脏毒性具有一定的预测价值，cTnT 与 NT-proBNP 任一指标高于阈值者发生心脏毒性的风险是两指标均正常者的其发生心脏毒性的可能性是 cTnT 和（或）NT-ProBNP 没有超过阈值者的 17.94 倍（HR=17.94）。
结论 cTnT 与 NT-proBNP 可以做为 HER2 阳性乳腺癌患者接受蒽环类药物序贯曲妥珠单抗治疗致心脏毒性的预测指标。

PU-1248

白细胞介素 6 在结直肠癌患者中的表达及与肿瘤疗效关系

陈岩松、陈燕
福建肿瘤医院

目的 探讨人白细胞介素 6（Interleukin-6，IL-6）在结直肠癌患者中的表达及意义。
方法 收集 132 例首诊结直肠癌患者（CRC）、34 例肠道良性疾病患者(CBD)及 84 例表观健康体检者(HC)血清,采用电化学发光双抗体夹心免疫分析法（ECLIA）检测血清中白细胞介素 6（IL-6）及癌胚抗原（CEA）含量，分析 IL-6 水平与结直肠癌患者临床病理特征的相关性；应用受试者工作特性曲线（ROC）和二元 Logistic 法回归分析 IL-6 和 CEA 两指标对结直肠癌的诊断价值；对随访资料完整的 120 例结直肠癌患者动态观察治疗前后血清 IL-6 和 CEA 水平，分析两指标与肿瘤疗效的关系。
结果 结直肠癌患者血清 IL-6 水平显著高于肠道良性疾病组(P<0.01)和健康对照组(P<0.01)，结直肠癌患者血清 CEA 水平显著高于肠道良性疾病组(P<0.05)和健康对照组(P<0.01),差异均有统计学意义。CRC 患者血清 IL-6 水平与肿瘤直径、分化程度、组织类型、淋巴结转移、远处转移、TNM 分期均显著相关(P<0.05)，而与年龄、性别及肿瘤发生部位无明显相关。IL-6 诊断结直肠癌的灵敏度（72.7%）和准确性（78.6%）均高于 CEA(分别为 68.2%和 77.9%，特异性（85.2%）低于 CEA（88.9%），两指标联合检测能够提高灵敏度（97.2%）和准确性（85.6%）。结直肠癌肿瘤控制组(CR+PR+SD)治疗后两指标均较治疗前有显著下降(P<0.05)，差异有统计学意义，而肿瘤进展组(PD)治疗后两指标均未显著下降(P>0.05)。
结论 IL-6 和 CEA 两指标联合检测有助于结直肠癌的诊断和疗效观察。

PU-1249

PIVKA-II 对肝癌患者疗效评价和预后评估的价值

叶倩、陈燕
福建肿瘤医院

目的 探讨异常凝血酶原（PIVKA-II）在肝癌患者疗效评价和预后评估中的应用价值。
方法 采集治疗前 163 例肝癌患者的血清，检测患者异常凝血酶原（PIVKA-II）和甲胎蛋白（AFP）浓度, 探讨其对肝癌患者疗效评估的价值，采用卡方检验分析患者临床病理特征与 PIVKA-II 浓度的关系，采用 Kaplan-Meier 法计算总生存率及无进展生存率，单因素分析采用 Log-rank 法，多因素分析采用 Cox 回归模型。
结果 肝癌进展组 PIVKA-Ⅱ、AFP 浓度显著高于缓解组，差异具有统计学意义（P<0.05）。PIVKA-II 高表达与 AFP、AST、ALT 有统计学意义（c2=13.664，P＜0.001；c2=4.013，P=0.045；c2=5.504，P=0.019）。随访 1-55 个月，163 例肝癌患者的 1 年总生存率为 57.67%，平均 OS 为 33.66 个月（95% CI：28.55~38.77）。3 年总生存率为 34.36%，平均 OS 为 23.76 个月（95% CI：19.24~28.28），中位 OS 为 16 个月（95% CI：9.39~22.61）。1 年无进展生存率为 38.04%，平均 PFS 为 26.61 个月（95%CI：21.93~31.3），中位 PFS 为 25 个月（95%CI：16.01~33.99）。单因素生存分析显示：肿瘤转移、血管侵犯、门脉癌栓、PIVKA-II、AFP、AST、ALT、ALB、TBIL、PT 对患者预后具有统计学意义（P 均<0.01）。Cox 回归模型多因素分析结果显示：PIVKA-II（P=0.003；HR =1.975，95%CI:1.269~3.073）、AFP（P=0.028；HR=1.663，95%CI:1.057~2.616）、TBIL（P=0.042；HR=1.530，95%CI:1.016~2.304）、血管侵犯（P=0.002；HR=2.523，95%CI:1.387~4.588）、肿瘤转移（P=0.022；HR=2.008，95%CI:1.107~3.642）、门脉癌栓（P=0.003；HR=1.970，95%CI: 1.256~3.092）、PT（P=0.030；HR=1.636，95%CI: 1.050~2.551）对患者预后具有统计学意义。

结论 PIVKA-Ⅱ、AFP 在肝癌中的表达水平，可成为预测肝癌患者发生发展及预后的分子标记物，对肝癌患者疗效评价和预后评估具有一定价值。

PU-1250

HSP90α、EBVCA-IgA、EBV DNA 在鼻咽癌诊断及预后相关性研究

叶倩、陈燕
福建肿瘤医院

目的 探讨热休克蛋白 90α（HSP90α）、EB 病毒衣壳抗原 IgA 抗体（EBVCA-IgA）、EBV DNA 对鼻咽癌(NPC)诊断及预后的价值。
方法 选取福建医科大学附属肿瘤医院 113 例鼻咽癌患者和 40 例健康体检者,采用 ELISA 法检测 HSP90α 和 EBVCA-IgA、采用实时定量 PCR 法检测 EBV DNA, 分析 HSP90α、EBVCA-IgA、EBV DNA 水平并进行统计分析和临床评价。
结 果 NPC 组 HSP90α 、EBVCA-IgA 、EBV DNA 水平均显著高于健康对照组(t/Z=15.317,11.459,24.261, P <0．05)，在 NPC 不同分期的患者中，III 和 IV 期患者的 HSP90α、EBVCA-IgA、EBV DNA 的表达水平均高于 I 和 II 期，IV 期 HSP90α、EBVCA-IgA、EBV DNA 表达水平均明显高于 III 期，差异有统计学意义(Z=5.347,4.768,6.418,P<0.05)。采用 ROC 曲线分析 HSP90α、EBVCA-IgA、EBV DNA 水平对 NPC 的预测价值,曲线下面积分别为 0.884 (95% CI 0.832～0.935)、0.841(95% CI0.781～0.901)、0.934(95% CI 0.897～0.970),最佳截断值分别为 121.70 ng/ml, 1.84 S/CO, 2.7×103 copies/ml,联合检测 ROC 曲线下面积最大为 0.954，灵敏度为 92.5%，特异性为 86.0%。预后不良组患者 HSP90α、EBVCA-IgA、EBV DNA 水平均显著高于预后良好组(P<0.05), Pearson 相关分析显示,NPC 患者 HSP90α 与 EBVCA-IgA、EBV DNA，呈正相关(r =0.768,0.873,P<0.05),随访 3 年患者总体生存率,经绘制生存曲线,低 HSP90α、EBV DNA 组患者 3 年总体生存率高于高 HSP90α、EBV DNA 组,差异有统计学意义(χ2 =9.715,12.805,P<0. 001)。
结论 HSP90α、EBV DNA 对 NPC 具有较高的诊断价值和预后预测价值, EBV DNA 诊断价值优于 HSP90α、EBVCA-IgA，联合检测诊断价值最高, HSP90α 可作为临床治疗监测指标之一,具有较好临床应用价值。

PU-1251

Transient positive Hepatitis B Surface Antigen due to recent vaccination in neonate.

Qiaodi Zhang、erfu xie
the First Affiliated Hospital of Nanjing Medical University

Background Recently, transient positive HBsAg was observed in the serum of neonates. The aim of this study was to investigate whether the transient positive HBsAg was due to a recent hepatitis B vaccination.
Methods Neonates with hepatitis B vaccination who were treated at our hospital between March 2013 to December 2017 were recruited. Newborns whose mothers were HBsAg-positive or chronic hepatitis B were excluded. HBsAg in the serum of the neonate was measured. In some neonates who were HBsAg-positive, HBsAg was redetected at 1–14 days of follow-up. The vaccine was diluted to various degrees and directly measured for HBsAg. Moreover, rabbit serum HBsAg was measured before vaccination and at days 3 and 7 after vaccination.

Results In the present study, 124 neonates among all 2223 newborns after vaccination were HBsAg positive, a 5.5% (124/2223) percentage. The range of neonate age was from 1 to 7 days. The children aged three days reached a peak of 8.09% percentage. The part of positive neonates was retested for HBsAg at 1–14 days of follow-up, showing their negative conversion ratio was 79.5% (35/44). Moreover, the hepatitis B vaccine was HBsAg positive without dilution and was positive even at a 1:32000 dilution. Animal tests showed that HBsAg could increase by day 3 and decrease by 7 days after vaccination.
Conclusion We have revealed that serum transient HBsAg, which has been observed in neonates, is due to hepatitis B vaccination. Subsequently, HBsAg gradually turns negative. Moreover, animal experiments have also confirmed that HBsAg increased after vaccination.

PU-1252

“冰火两重灸”对 HIV/AIDS 患者 IL23 及 IL10 影响的研究

唐亚娟
昆明市中医医院

目的 连续监测“冰火两重灸”疗法在不同淋巴细胞计数值的 AIDS 免疫重建不良患者的 IL23 及 IL10 影响差异研究。
方法 选取云南中医学院第三附属医院的 AIDS 免疫重建不良患者 30 例，按淋巴细胞计数值分为两组，运用冰火两重灸联合 HAART 治疗，观察 0，3，6,9,12 月的 IL23 及 IL10 的数值变化。
结果 两组实验组，其不同测定时间的 IL-10 及 IL-23（对数值）均数的差异均有统计学意义（P＜0.05），且都有随时间推移而下降的趋势（P＜0.05）。
结论 在不同免疫重建不良的 AIDS 患者中，因淋巴细胞数值的不同，在同一联合治疗方案下，均呈现有效治疗趋势，中医治疗联合国家推荐的一线方案治疗值得长期观察。

PU-1253

治疗前异常凝血酶原血清水平与原发性肝癌预后相关性研究

林莺莺、陈燕
福建省肿瘤医院

目的 探讨治疗前异常凝血酶原（PIVKA-Ⅱ）血清水平在原发性肝癌预后中的临床应用价值。
方法 收集 2013 年 12 月至 2014 年 3 月福建省肿瘤医院连续收治的 100 例未经治疗的肝细胞癌患者入院时血清样本，用化学发光免疫技术检测 PIVKA-Ⅱ血清水平。收集患者临床资料，同时对患者每隔三个月至半年进行随访，对随访结果结合临床资料，运用 X-tile 软件确立 PIVKA-Ⅱ对总生存期的最佳截断值，并用 SPSS16.0 软件包进行生存分析。
结果 截止 2017 年 3 月，100 例患者中位生存时间为 4.1 个月，3 年生存率为 20%。X-tile 软件确立 PIVKA-Ⅱ对总生存期的最佳截断值为 55859mAU/ml，PIVKA-Ⅱ>55859 mAU/ml 的患者 17 例（占总人数的 17%），中位生存期为 2.0 个月，与 PIVKA-Ⅱ≤55859 mAU/ml 组相比（中位生存期为 5.6 个月），差异有统计学意义（P=0.000）。PIVKA-Ⅱ的表达与总胆红素、腹水、肿瘤直径和门脉癌栓成正相关。单因素分析显示治疗前 PIVKA-Ⅱ表达、发现肿瘤途径、肝功能生化指标、腹水、CH 分级、侵犯肝被膜、肿瘤大小、肿瘤数量、临床分期、门脉癌栓、下腔静脉癌栓、远处转移以及治疗方式是患者总体生存率的影响因素。多因素分析显示治疗前 PIVKA-Ⅱ高表达（OR=5.405；95%CI： 0.219-0.879， P=0.020），下腔静脉癌栓和远处转移是患者预后较差的独立预测因素。

结论 治疗前血清 PIVKA-II 水平可作为肝癌预后标志物，治疗前 PIVKA-II 高表达提示不良预后。

PU-1254

成都市某综合医院 2020 年 HIV 抗体检测结果的分析

罗才会、王智斌、许程洁、唐义斌
电子科技大学附属医院·四川省人民医院

目的 了解综合医院就诊患者人类免疫缺陷病毒（HIV）的感染状况，为艾滋病的防治工作提供科学的依据。
方法 对 2020 年 1-12 月我院各科室送检检验科的血浆样本进行 HIV 抗体的初筛试验（酶联免疫吸附试验、化学发光试验和胶体金快速试验），初筛试验有反应的血浆样本进行确证试验（线性免疫印迹试验），对 2020 年我院 HIV 抗体初筛和确证试验的结果进行分析。
结果 共有 151284 例血浆样本进行初筛试验，初筛试验有反应的共 480 例，其中 HIV 抗体确证阳性 414 例，阴性 52 例，不确定 14 例。414 例 HIV 抗体确证阳性中男性 317 例（76.57%），女性 97 例（23.43%），男:女为 3.27:1；年龄最小 17 岁，最大 89 岁，17-19 岁 4 例（0.97%），20-29 岁 71 例（17.15%），30-39 岁 88 例（21.25%），40-49 岁 72 例（17.39%），50-59 岁 89 例（21.50%），60 岁以上 90 例（21.74%）。HIV 抗体确证阳性中门诊患者 238 例（57.49%），住院患者 171 列（41.30%），体检 5 例（1.21%），其中科室分布在内科（43.96%），皮肤科（22.71%），外科（12.08%），感染科（11.59%），急诊科（6.52%），五官及口腔科（1.93%），体检中心（1.21%）。
结论 本次研究中检出的 HIV 抗体阳性以男性为主，主要分布在 30-39 岁和 50 岁以上年龄段，可见青年和中老年人群为该地区 HIV 感染的主要高危人群，应重点关注这两个年龄段人群。但是也要加强对其他年龄段人群的监测及检测，特别是青少年，他们有着对社会极大的好奇心，但又缺乏性教育知识，从而导致青少年感染 HIV 的人数越来越多，年龄越来越小，因此应该引起社会的重视。

PU-1255

梅毒血清学试验生物学假阳性与自身免疫疾病相关性分析

陈斌[1]、吕敏红[2]、陈林强[1]
1. 广州市第一人民医院
2. 广东医科大学检验系

目的 分析可能造成梅毒非密螺旋体抗体检测生物学假阳性（biological false-positive，BFP）反应的相关因素，旨在分析其与自身免疫疾病的相关性，降低临床误诊率。
方法 回顾 2016 年 1 月至 2020 年 12 月在广州市第一人民医院进行梅毒筛查的 31846 名住院、门诊患者和体检人群，根据假阳性患者标准纳入 BFP 患者，分析 BFP 患者年龄、性别、基础疾病等特点。将 1570 例进行自身抗体系列检测和梅毒筛查的患者根据梅毒筛查结果分为假阳性组、阴性组和梅毒组，分析组间自身抗体系列检测结果差异。
结果 201 例发生梅毒非密螺旋体抗体检测 BFP 反应，假阳性率为 0.63%;在不同年龄分组的比较中，BFP 反应的差异存在统计学意义（P<0.05）;假阳性组与阴性组间自身抗体系列中抗双链 DNA 抗体（ds-DNA）、抗核糖体抗体（rRNP）、可溶性物质 A （SSA）、抗 Sm 抗体（Sm）、抗核糖核酸蛋白抗体（nRNP）、抗核抗体（ANA）、抗核小体抗体（AauA）、着丝点抗体（CENP B）、组蛋白阳性率存在统计学差异（P<0.05）。
结论 多种疾病可能引起梅毒非密螺旋体抗体检测 BFP 反应，其中自身免疫疾病患者体内 ds-DNA、rRNP、SSA、Sm、nRNP、ANA、AauA、CENP B、组蛋白阳性可能与 BFP 反应相关。

PU-1256

血清 sFlt-1、PLGF 及 sFlt-1/PLGF 与子痫前期发病的相关性研究

钟志敏[1]、霍心燕[2]、陈斌[1]
1. 广州市第一人民医院
2. 广州医科大学金域检验学院

目的 研究血清可溶性血管内皮生长因子 1（sFlt-1）、胎盘生长因子（PLGF）水平及其比值与子痫前期的相关性及预测价值。
方法 选择在广州市第一人民医院总院区妇科和产科就诊的住院孕产妇为研究对象，其中选取正常对照组 38 例，高血压对照组 38 例，病例组 15 例。应用全自动电化学发光免疫分析仪检测病例组和对照组中血清标本中 sFlt-1 和 PLGF 水平并计算 sFlt-1/PLGF 的比值，最后应用 SPSS16.0 软件统计分析，分别对病例组、高血压组和正常对照组的 sFlt-1、PLGF 和 sFlt-1/PLGF 的比值进行两两比较，从而得出 sFlt-1、PLGF 和 sFlt-1/PLGF 的比值与子痫前期的相关性及预测价值。
结果 1.病例组和高血压组 PLGF 测定值的 P 值为 0.039（P<0.05），存在差异性；病例组和正常组 PLGF 的 P 值为 0.750（P>0.05），不存在差异性；高血压组和正常组 PLGF 的 P 值为 0.02（P<0.05），存在差异性；病例组和高血压组 sFlt-1 测定值的 P 值为 0.019（P<0.05），存在差异性；病例组和正常组 sFlt-1 的 P 值为 0.000（P<0.001），存在显著差异性；高血压组和正常组 sFlt-1 值为 0.038（P<0.05），存在差异性；病例组和高血压组 sFlt-1/PLGF 值的 P 值为 0.000（P<0.001），存在显著差异性；病例组和正常组 sFlt-1/PLGF 的 P 值为 0.000（P<0.001），存在显著差异性；高血压组和正常组 sFlt-1/PLGF 值为 0.817（P>0.05），不存在差异性。2.当选取 PLGF 的 Cutoff 值为 18.9150pg/ml 时，对应的灵敏度和特异度分别为 93.3%和 21.05%，曲线下面积（AUC）=0.447;当选取的 sFlt-1 的 Cut off 值为 2890.00pg/ml 时，对应的灵敏度和特异度分别为 73.3%和 65.79%，AUC=0.673;当选取的 sFlt-1/PLGF 的 Cutoff 值为 53.5244pg/ml 时，对应的灵敏度和特异度分别为 60.0%和 90.79%，AUC=0.783。
结论 PE 孕妇血清中 sFlt-1、sFlt-1/PLGF 比正常妊娠孕妇高，PLGF 水平比正常妊娠孕妇低；而且 sFlt-1/PLGF 比值可用于预测和评估子痫前期,而且 sFlt-1/PLGF 的比值比 sFlt-1 和 PLGF 单因子更具检测价值。

PU-1257

Comparative analysis of serum CA125 and SCCA expression between pulmonary tuberculosis and lung cancer patients

Xingtian Liu
Taian City Centrol Hospital

Objective To investigate the changes of serum CA125 and SCCA expression in pulmonary tuberculosis and lung cancer patients，and to provide theoretical basis for clinical differential diagnosis of pulmonary tuberculosis and lung cancer.
Methods From June 2019 to December 2019， 87 cases of tuberculosis patients diagnosed in the department of infectious diseases of our hospital and 79 cases of lung cancer patients diagnosed in the cancer research center were selected， and 50 cases of healthy patients were collected. The contents of CA125 and SCCA in serum of three groups were determined by electrochemical luminescence.

Results The serum CA125 content of the pulmonary tuberculosis group (75.54±26.23) U/ml was significantly higher than that of the lung cancer group (46.08±13.76) U/ml，and that of the lung cancer group (11.25±5.92) U/ml was significantly higher than that of the control group (P<0.05)。The SCCA content of lung cancer group (2.68±1.30) ng/ml was significantly higher than that of pulmonary tuberculosis group (1.07±0.68) ng/ml and control group (1.03±0.45) ng/ml，the difference was statistically significant (P<0.05)。There was no significant difference in serum SCCA content between pulmonary tuberculosis group and control group (P>0.05)。The Ⅳ period lung cancer of serum CA125 levels (50.96±14.52) U/ml、SCCA levels (3.18±1.18) ng/ml are significantly higher than Ⅲ stage of CA125 (40.54±10.54) U/ml、SCCA (2.11±1.20) ng/ml，the differences were statistically significant (P < 0.05)；The serum CA125 content (50.00±14.58) U/ml in adenocarcinoma was significantly higher than that in squamous cell carcinoma (42.79±12.27) U/ml，and the serum SCCA content in squamous cell carcinoma (3.08±1.18) ng/ml was significantly higher than that in adenocarcinoma (2.20±1.30) ng/ml，the differences were statistically significant differences (P<0.05).

Conclusion The combined detection of serum CA125 and SCCA has certain clinical diagnostic value for the auxiliary differential diagnosis of pulmonary tuberculosis and lung cancer， and has certain reference value for the staging and classification of lung cancer.

PU-1258

乙肝表明抗原通过上调 IDO 抑制 T 细胞增殖

王森
南京大学医学院附属鼓楼医院

T 细胞的增殖分化失衡是乙肝病毒建立和维持免疫耐受的重要机制之一，乙肝病毒表面抗原（HBsAg）在逃逸机体的天然免疫和适应性免疫中发挥重要的作用。本课题研究发现 HBsAg 可显著抑制 CD4+T 细胞及 CD8+T 细胞的增殖，并以剂量依赖性的方式抑制 T 细胞的 IFN-γ 及 TNF-α 的产生能力。为了对 HBsAg 抑制 T 细胞的机制进行进一步的研究，我们使用基因芯片的方法筛选 HBsAg 诱导上调的基因，发现 HBsAg 可以显著上调 T 细胞抑制分子吲哚胺 2,3 双加氧酶(IDO)的表达，流式细胞仪检测 IDO 的表达证实 HBsAg 可上调 PBMC 及单核细胞中 IDO 的蛋白表达水平。IDO 的特异性抑制剂 1-MT 可以逆转 HBsAg 对 CD4+及 CD8+ T 细胞增殖的抑制作用，IDO 的代谢产物犬尿氨酸可发挥 HBsAg 的类似作用。表明 HBsAg 通过 IDO 抑制了 CD4 及 CD8 T 细胞的增殖。另外，我们在慢性乙肝患者外周血中也发现了 IDO 表达水平的上升。本项目有助于加深对 HBsAg 免疫调节功能及 HBV 感染慢性化机制的认识，同时为开发逆转 HBV 免疫耐受的策略提供理论基础。

PU-1259

吉林地区 2020 年幽门螺旋杆菌结果分析

谭宇鹏
吉林金域医学检验所有限公司

目的 幽门螺旋杆菌 (Helicobacter Pylori HP)作为人类最常见的慢性感染源之一，日渐被人们所关注。许多研究表明，HP 是消化性溃疡、慢性胃炎的重要病因，并与胃癌密切相关，时刻威胁人类健康。本文就 2020 年长春地区幽门螺旋杆菌检测结果进行分析，了解感染幽门螺旋杆菌在人群中比例，为临床提供参考依据。

方法 选取 2020 年 1 月至 2020 年 2 月送我公司检测幽门螺旋杆菌的 2000 例标本。采用免疫印迹法，（0.1ml 样本稀释液+10ul 血清）摇半小时，清洗液洗 3 次，每次一分钟；（0.05ml 样本稀释液+10ul 酶）摇半小时，清洗液洗 3 次，每次一分钟；（500ul 底物）摇 6 分钟，然后清洗。
结果 2000 例检测幽门螺旋杆菌的标本中，阳性的有 700 例，阳性率为 35%。
结论 实验表明，幽门螺旋杆菌的阳性率高达 35%，世界卫生组织癌症研究会已将 HP 定为Ⅰ级或明确的人类致癌因子。而幽门螺旋杆菌的传播途径广泛，可通过口-口传播、粪-口传染还有医源性传播，既通过接吻、就餐都可以传染，通过大便排出水的污染也可以传播，再就是患者进行胃镜检查时，幽门螺旋杆菌会寄附在胃镜检查仪器上，倘若仪器清理不彻底，医生手套没有及时更换，都可能造成感染。因此，健康人群感染 HP 的风险也很大，健康人群进行 HP 感染检测，可减少慢性胃炎、消化性溃疡的发生，降低胃癌等重大疾病的发生风险。所以，提高卫生意识，关注健康人群的幽门螺旋杆菌检测，做到早发现，早诊断，早治疗，提高人们的生活质量。

PU-1260

Increased CD4+CD8+ double positive T cell in patients with Primary Sjögren's Syndrome correlated with disease activity

Sen Wang
Nanjing Drum Tower Hospital

Primary Sjogren’s syndrome (pSS) is an autoimmune disease that invades lacrimal glands, salivary glands and other exocrine glands, but its pathogenic mechanism is still unclear. CD4+CD8+ double positive T (DPT) cells have been discovered in recent years to play an important role in autoimmune diseases and viral infections, but the frequency and significance of DPT in primary Sjogren’s syndrome are still unclear. This study detected the frequency of DPT in the peripheral blood of patients with pSS, and detected the clinical indicators and cytokines in patients. We then analyzed the correlation between DPT and clinical indicators, cytokines, and disease activity scores. The results showed that the peripheral DPT frequency of pSS patients was significantly higher than that of healthy controls. The peripheral DPT frequency was negatively correlated with ESR, IgA and IgG, and peripheral DPT frequency was positively correlated with anti-inflammatory cytokine IL-10. Analysis of DPT and pSS disease activity scores found that DPT frequency had a negative correlation with ESSDAI and SSDAI. This study suggests that peripheral DPT may play a protective role in pSS. The frequency of peripheral DPT cells can be used as an indicator for disease activity. Regulating the expression of peripheral DPT cells is expected to become a new strategy for treatment of pSS.

PU-1261

狼疮抗凝物（LA）检测的临床诊断分析

梁津
吉林大学第一医院

目的 探讨狼疮抗凝物检测对临床症状及诊断的实际意义。
方法 回顾性分析狼疮抗凝物阳性患者 43 例的具体病例和临床病症，均为自身免疫性疾病患者。以 LA 标准化比值 1.2 为标准，大于则判定为阳性。选 50 例低于标准化值的狼疮抗凝物阴性患者，并选择 30 例健康者作为对照，比较分析。

结果 阳性患者的标准化比值高于阴性组，远高于对照组。阴、阳性组中具有血栓及有关临床病症的患者标准化值远高于其他病症；同一组别中性别间比值几乎无差异；阴、阳组中女性在妊娠丢失表现明显。同一组内具有复合病症患者的标准化比值明显高于单一病症。
结论 狼疮抗凝物检测在临床病症判定时，与性别无显著学意义；与血栓相关病症具有极显著意义；与妊娠丢失具有显著学意义；对于狼疮抗凝物的检测不能仅作为单一病症的确诊分析，要结合临床判定复合病症的发生。

PU-1262

促甲状腺激素受体刺激性抗体检测的临床应用

王春玲
东南大学附属中大医院

目的 研究促甲状腺激素受体刺激性抗体（TSI）对甲亢诊断的临床作用。
方法 利用重组的人促甲状腺激素受体蛋白采用化学发光法对确诊为临床甲亢的 46 例患者的血清样本进行促甲状腺激素受体抗体（TRAb）中的 TSI 的检测，同时检测同一样本中 TRAb 的含量，比较 TSI 和 TRAb 在甲亢辅助诊断中的敏感性差异。
结果 在 46 例样本中，TSI 阳性 42 例（cutoff 值 0.55 IU/L），阴性 4 例，阳性率 91.3%；TRAb 阳性为 38 例（cutoff 值 1.75IU/L），阴性为 8 例，阳性率 82.6%；比较两组间阳性率无显著统计学差异（P=0.33）。
结论 血清 TSI 检测对甲状腺功能亢进诊断具有和 TRAb 相似的敏感性，可用于临床甲亢的辅助诊断。

PU-1263

Clinical Significance of the detection of HBV-DNA by the Real-time Fluorescence PCR

Yongsheng Shi、yingyu jin
The first affiliated hospital of Harbin medical university

Objective To analyze the correlation of hepatitis B virus (HBV) DNA with hepatitis M, and to uinvestigate their clinical significance in HBV diagnosis and prognosis.
Methods 200 cases of Clinical specimens were detected by enzyme linked immunosorbent assay (ELISA）and fluorescent quantitative PCR assay detected HBV- DNA of blood samples and the results were divided groups.
Results There were 48 positive in group that the HBsAg(+), HBeAg(+) and HBcAb(+) were positive and positive rate was 92%(48/52). There were 30 positive in group that the HBsAg(+), HBeAb(+) and HBcAb(+) were positive and positive rate was 43%(30/70). There was 1 positive in group that the HBsAb(+), HBeAb(+) and HBcAb(+) were positive and positive rate was 33%(1/3). There were 6 positive in group that the HBsAg(+), HBcAb(+) were positive and positive rate was 27%(6/22). There were 8 positive in group that the HBeAg(+), HBcAb(+) were positive and positive rate was 44%(8/18). 3 were negative in group of HBsAb(+). 12 were negative in group of HBsAb(+) and HBcAb(+). There was 1 positive in group that the HBsAb(+) were positive and positive rate was 30%(1/3). 2 were negative in group of HBeAb(+).There was a positive HBV-DNA in 3 total negative samples, and the positive rate was 33%.
Conclusion HBV DNA levels and HBV e antigen significant correlation, HBV DNA quantification and HBV M detection for clinical hepatitis B virus infection, replication and clinical diagnosis and treatment is important.

PU-1264

不同检测方法对肺结核早期诊断的应用

史永胜、金英玉
哈尔滨医科大学附属第一医院

目的 分析建立一种对结核分枝杆菌检出简便、快速、特异的方法。
方法 对 68 例研究对象根据医院肺结核诊断标准包括典型症状，典型体征，或痰菌阳性，PPD 皮试阳性或抗结核治疗的结果进行分析分为 2 组：结核病组 50 例，非结核病组 18 例；对这 68 例研究对象进行痰涂片结核分枝杆菌检查，痰液聚合酶链反应（Polyerase Chain Reaction PCR），结核菌素纯蛋白衍生物(purified protein derivative PPD)检测，并对其检出率进行比较。
结果 结核病组的痰涂片检测阳性 11 例，阳性率为 22%，非结核病组均为阴性。痰标本 PCR 检测结核病组阳性率 54％，非结核组阳性率 5.6%。PPD 皮试结果阳性 18 例，阳性率为 36％，非结核组为 3 例，阳性率 16.7％。痰标本经 PCR 的检出阳性率明显高出其余两种检测方法。
结论 PCR 技术对于痰液结核分枝杆菌的检出阳性率较其他两种方法而言具有更高的检出率，该技术发挥了重要的作用，检测结果具有方便、快速的特点，对临床上结核病的确诊有很大的意义。

PU-1265

血清 CK18、OPN 水平与原发性喉癌患者临床分期的相关性

屈慧
空军军医大学第一附属医院西京医院

目的 分析血清细胞角蛋白 18（CK18）、骨桥蛋白（OPN）水平与原发性喉癌患者临床分期的关系。
方法 前瞻选择 2019 年 1 月-2019 年 12 月医院 93 例原发性喉癌患者作为研究对象，入院时检测患者的 CK18、细胞角蛋白 19（CK19）、OPN、肿瘤标志物水平[糖类抗原 50（CA50）、糖类抗原 199（CAl99）、癌胚抗原（CEA）、糖脂类抗原 72-4（CA72-4）]，均接受纤维喉镜和病理活检，并根据检查结果分为晚期[国际抗癌联盟制定的肿瘤（TNM）分期Ⅲ期、Ⅳ期]和早中期（TNM 分期Ⅰ期、Ⅱ期），比较不同临床分期患者的 CK18、CK19、OPN、肿瘤标志物水平，重点分析入院时血清 CK18、OPN 水平与原发性喉癌患者临床分期的关系。
结果 晚期组 CK18、CK19、OPN、CA50、CA199、CEA、CA72-4 高于早中期组，差异有统计学意义（P＜0.05）；经 Logistic 回归分析检验结果显示，入院时血清 CK18、CK19、OPN、CA50、CA199、CEA、CA72-4 水平与原发性喉癌患者临床分期有关，CK18、CK19、OPN、CA50、CA199、CEA、CA72-4 高表达可能是原发性喉癌患者进展至晚期的风险因子（OR＞1，P＜0.05）；绘制 ROC 曲线图，结果显示，入院时血清 CK18、OPN 单独及联合评估原发性喉癌患者预后不良的 AUC 分别为 0.886、0.832、0.899，均有一定评估价值；经 Spearman 相关性分析检验，原发性喉癌患者血清 CK18、OPN 呈正相关（r＞0，P＜0.05）。
结论 血清 CK18、OPN 水平与原发性喉癌患者临床分期相关。可用于原发性喉癌患者临床分期的评估。

PU-1266

实时荧光定量 PCR 检测 乙肝病毒 DNA 的分析与临床意义

史永胜、金英玉
哈尔滨医科大学附属第一医院

目的 探讨乙型肝炎病毒 DNA 含量与血清标志物的关系及其临床意义。
方法 用酶联免疫吸附实验（ELISA）和实时荧光定量聚合酶链法（RTFQ-PCR）两种方法分别对 200 例疑似乙肝患者进行乙肝病毒血清学检测和 HBV-DNA 含量检测。然后分组进行分析。
结果 52 份 HBsAg(+)、HBeAg(+)、HBcAb(+)标本中有 48 份 HBV-DNA 为阳性，阳性率为 92%；70 份 HBsAg(+)、HBeAb(+)、HBcAb(+)标本中有 30 份 HBV-DNA 为阳性，阳性率为 43%；3 份 HBsAb(+)、HBeAb(+)、HBcAb(+)标本中有 1 份 HBV-DNA 为阳性，阳性率为 33%；22 份 HBsAg(+)、HBcAb(+)标本中有 6 份 HBV-DNA 为阳性，阳性率为 27%；18 份 HBeAg(+)、HBcAb(+)标本中有 8 份 HBV-DNA 为阳性，阳性率为 44%；3 份 HBsAg(+)、HBcAb(+)标本中 HBV-DNA 均为阴性；12 份 HBsAb(+)、HBcAb(+)标本中 HBV-DNA 均为阴性； HBsAb(+)的三份标本中 HBV-DNA 为阳性的有一份，其阳性率为 30%；2 份 HBeAb(+)标本中 HBV-DNA 均为阴性；全阴性的三份标本中 HBV-DNA 为阳性的有一例，阳性率为 33%。
结论 乙肝病毒 DNA 含量与 HBeAg 有明显的关联，乙型肝炎病毒 DNA 定量和乙型肝炎病毒血清学标志物检测对于临床乙型肝炎病毒感染、复制及临床诊断与治疗都有其重要的意义。

PU-1267

免疫功能检测在儿童肺炎支原体感染中的应用价值探讨

史永胜、金英玉
哈尔滨医科大学附属第一医院

目的 探讨免疫功能检测在儿童肺炎支原体感染中的应用价值。
方法 选取同期肺炎支原体感染患儿和体检健康的小儿来进行观察，检测两组儿童的血清免疫球蛋白 （IgA、 IgM、IgG）和补体 C3、C4，外周血的 T 淋巴细胞亚群水平。
结果 患儿急性期各项指标均低于对照组，且恢复期仍有差异。
结论 小儿受到肺炎支原体感染后免疫功能低下，若着手于儿童免疫功能的治疗，对于疾病的改善和治疗有很好的作用。

PU-1268

纳米金棒应用于血吸虫病敏感性检测的基础研究

杨毅梅[1]、马顺高[2]、李倩[1]、李家萌[1]、钟国梁[2]
1. 大理大学
2. 大理州医院

目的 本研究对纳米金棒的制备条件进行了优化，成功聚合最具有所需光学性质的纳米金棒，并将其功能化，制备了实验室条件下可针对日本血吸虫病检测的高敏感性纳米金生物探针。
方法 通过种子介导生长法合成纳米金棒，通过系统的研究纳米金棒最佳的合成条件，最大程度提高单个纳米颗粒的生物功能，聚合具有所需的形貌和波长可控的纳米金棒。制备日本血吸虫尾蚴和成虫可溶性抗原，通过抗原与纳米金棒结合，构建功能化 NanoSPR 生物探针，检测不同浓度梯度的感染日本血吸虫阳性血清抗体，并与 ELISA 检测结果做对照分析研究，探索日本血吸虫 NanoSPR 生物芯片的高敏感性。

结果 通过对 GNRs 在制备过程中还原剂、活性剂、温度等条件的优化，系统的研究了 GNRs 的最佳实验制备条件，成功制备 NanoSPR-SCA 生物探针，通过纳米金标记对抗原抗体反应产生的放大作用，使 NanoSPR-AWA 生物探针对血清中血吸虫抗体的检测更具有灵敏性，最低检测限可达到稀释倍数的 80 倍。相比于传统的 ELISA 检测法，NanoSPR 生物探针针对日本血吸虫感染早期的血清体现出了更强的识别能力。
结论 成功聚合了功能化纳米金棒。制备了纳米金标记的免疫传感器 NanoSPR 生物探针，研究证实纳米金标记的传感器是一种可以针对日本血吸虫病具有更灵敏的检测方法，为提高日本血吸虫感染敏感检测方法提供了新的技术，为纳米金生物技术应用于临床寄生虫检测提供了实验基础及科学依据。

PU-1269

血清 CEA、CA199、CA724 肿瘤标志物联合检验在胃癌诊断中的应用研究

渠滕
山东第一医科大学附属省立医院临床医学检验部

目的 分析血清癌胚抗原(CEA)及糖类相关抗原(CA199、CA724)的联合检测在胃癌诊断中的价值。
方法 选取 2019 年 1 月到 2020 年 12 月来本院治疗的 168 例胃癌患者作为胃癌组，同时选取同期良性胃病患者 159 为良性胃病组，另选取同期健康体检者 160 例作为健康组，用罗
氏 Cobas 8000 全自动化化学发光免疫分析仪及配套试剂进行检测，比较三组间 CEA、CA199、CA724 的表达水平以及单项、联合肿瘤标志物的阳性检出率，分析 CEA、CA199、CA724 的单一诊断和联合诊断在胃癌诊断中的价值。
结果 胃癌组血清 CEA、CA199、CA724 表达水平明显高于良性胃病组和健康组，差异均有统计学意义（P<0.05）；胃癌组血清 CEA、CA199、CA724 单独检测与联合检测阳性率均高于良性胃病组和健康组，差异均有统计学意义（P<0.05）；血清 CEA、CA199、CA724 三项联合检测的灵敏度均高于单独检测和任意两项检测，差异具有统计学意义（P<0.05）。
结论 胃癌患者血清 CEA、CA199、CA724 水平高于正常人，应用血清 CEA、CA199、CA724 联合检测能够有效提高胃癌的阳性检出率，有利于辅助早期胃癌的诊断，减少漏诊与误诊的发生。

PU-1270

ER、PR、CerbB-2 在甲状腺乳头状癌中的表达和临床意义

史永胜、金英玉
哈尔滨医科大学附属第一医院

目的 研究 ER、PR 和 CerbB-2 在甲状腺乳头状癌中的所起作用及其与甲状腺乳头状癌生理性行为存在的联系。
方法 以免疫组化法检测法为主电子显微镜检测为辅，随机抽取 89 例典型甲状腺乳头状癌标本、13 例典型结节性甲状腺肿标本中 ER、PR 和 CerbB-2 在癌变中所起的作用。
结果 ER、PR 和 CerbB-2 在甲状腺乳头状癌中的表达率分别为 50.48%、44.36%、17.98%，在结节性甲状腺肿中的表达率分别为 15.38%、7.69%、0%，俩组实验数据对比（P<0.01）。所以在甲状腺乳头状癌的表达中，ER 基因的影响与病人的年龄存在反比例关系；PR 基因的作用在无淋巴结转移的患者中表达更强。
结论 ER、PR、CerbB-2 基因在甲状腺乳头状癌癌变过程中的所起的作用明显增高，所以通过对 ER、PR、CerbB-2 检测可以起到对甲状腺乳头状癌的预防和治愈。

PU-1271

ELISA 检测梅毒螺旋体抗体的最佳临界值和可疑区间的建立

黄涛涛
联勤保障部队第九〇〇医院

目的 探讨酶联免疫法（enzyme-linked immunosorbentassay,ELISA）检测梅毒螺旋体抗体（TP-Ab）诊断阳性的最佳临界值（Cut-off 值）和可疑区间，降低本实验室的假阳性率和假阴性率。
方法 选取在联勤保障部队第九〇〇医院就诊共 26 例经 ELISA 初筛 TP-Ab 结果为阳性和试剂盒规定的 Cut-off 值（0.15）附近（阴性）的患者血清标本（OD＝0.1～0.6），分为 3 组，[0.1－0.3）共 12 例，[0.3－0.45）共 2 例，[0.45－0.6）共 12 例；并采用梅毒螺旋体特异性抗体明胶凝集试验（Treponema Pallidum Particle Agglunation Test,TPPA）检测确定其阴、阳性。通过软件 SPSS22.0 绘制受试者工作特征(receiver operating characteristic，ROC)曲线，取约登(Youden)指数最大时（0.737）的吸光度值为最佳 Cut-off 值，并进一步确定可疑区间。
结果 ELISA 检测 TP-Ab 诊断阳性的最佳 Cut-off 值为 0.3055，确定最佳 Cut-off 值后 ELISA 与 TPPA 一致性 kappa 值为 0.75，可疑区间为[0.168,0.351]。
结论 确定适合本实验室 ELISA 检测 TP-Ab 最佳 Cut-off 值和可疑区间能够有效降低假阳性率和假阴性率，减少临床的漏诊率和误诊率，为临床诊断工作提供有力依据。

PU-1272

服用螺旋藻致 CA72-4 异常升高一案例分析

肖雅[1]、渠文涛[2]、史小芹[1]
1. 郑州安图生物工程股份有限公司
2. 郑州安图生物工程股份有限公司

目的 笔者发现，患者在服用含有螺旋藻的保健品后，血清中 CA72-4 检测结果异常升高，停服一段时间后，CA72-4 检测结果又降低到原来的正常水平，现报道如下。
方法 患者在健康体检时发现，CA72-4 单项结果异常高，＞300.0 U/ml，而前一年的体检结果还是正常的。随后笔者查看了其胃镜、CT 等检查结果，均显示正常，且未发现肿瘤迹象。曾有文献报道服用灵芝孢子粉、虫草等后会导致 CA72-4 异常升高的案例，经仔细询问患者体检前的饮食史和病史发现，患者近半年来一直在规律服用螺旋藻片。于是，建议患者停服该保健品一段时间后再来复查 CA72-4。
结果 患者停服螺旋藻片 7 天后，CA72-4 由原来的＞300U/ml 降到了 80.96 U/ml；停服螺旋藻片 15 天后，CA72-4 已经降低到 5.17 U/ml。考虑到螺旋藻片中可能含有 CA72-4 的交叉物，笔者将螺旋藻片溶解到纯化水中，CA72-4 检测结果仅仅 0.15U/ml，可以排除检查干扰的可能。
结论 CA72-4 是一种消化道相关的肿瘤标志物。本例中的患者在服用螺旋藻后 CA72-4 检测结果异常升高，停服之后，CA72-4 检测结果逐渐降低，两周后已降到原来的正常水平。排除螺旋藻片本身可能含有 CA72-4 检测干扰物的影响，笔者推测，摄入螺旋藻之后，其在人体内的某种代谢产物可能与 CA72-4 抗原结构类似，或者螺旋藻或其代谢产物与体内细胞相互作用后可能会促进细胞过多表达 CA72-4 抗原。因此，临床上发现 CA72-4 异常升高时，应仔细询问患者饮食或用药史，确认是否是因为服用药物或保健品引起 CA72-4 异常升高的情况。

PU-1273

Ultrasensitive immunochromatographic assay based on graphene oxide-fluorescent nanoprobe for rapid and multiplexed detection of respiratory bacteria

Xiaodan Cheng、Chongwen Wang、Shengqi Wang
Beijing Institute of Radiation Medicine, Beijing 100850, PR China

Background Respiratory pathogens including a variety of bacteria and viruses are highly infectious to human, cause similar clinical symptoms, and pose serious threats to public health globally. Early and accurate identification of respiratory bacteria from other pathogens is crucial for guiding the rational use of antibiotics and controlling the epidemic spread.
Methods Here, we developed a multiplexed fluorescent immunochromatographic assay (ICA) for ultrasensitive qualification of respiratory bacteria in biological samples with high accuracy. A novel two-dimensional graphene oxide (GO)-based quantum dot (QD) nanoflake was designed as film-like immunoprobe to efficiently and closely stick onto the bacteria surface, which not only provide superior fluorescence signal but also ensure the liquidity of the captured bacteria for ICA detection. GO-QD nanoflakes were fabricated via the PEI-mediated electrostatic adsorption of numerous CdSe@ZnS-MPA QDs onto both sides of GO nanosheet. The conjugation of GO-QD and anti-bacteria antibodies was conducted via the carbodiimide chemistry, the antibody-conjugated GO-QD nanoflakes were directly mixed with the bacteria sample and dropped onto the sample pad of ICA. The formed GO-QD/bacteria complex migrated along the strip toward the absorbent pad by capillary forces and then captured by pre-coated monoclonal antibodies on the T lines. Sensitive and quantitative detection of two target bacteria was easily realized by reading the fluorescence intensity values of the two T lines.
Results By optimization of the assay conditions, our proposed method enables simultaneous and sensitive detection of two common respiratory bacteria, namely Streptococcus pneumoniae (S. pneumoniae) and Staphylococcus aureus (S. aureus) in one test within 20 min. The detection limit of the proposed method reached 13 and 20 cells/mL for S. pneumoniae and S. aureus, respectively, and was approximately 500 times more sensitive than traditional colloidal gold-based ICA. The GO-QD-ICA also exhibited the advantages of good stability, reproducibility (RSD < 4.1%), and specificity in sputum, suggesting its great potential for detection of real respiratory tract samples.
Conclusions Our results have demonstrated the incorporation of immuno-GO-QD into ICA system could improve the detection sensitivity and increase the testing throughput, leading to rapid, simple, accurate, and ultrasensitive POCT detection of respiratory pathogens.

PU-1274

2 型糖尿病患者中颈动脉斑块风险模型的建立及验证

姜繁明
中国医科大学附属第一医院

目的 使用列线图建立并验证 2 型糖尿病患者中颈动脉斑块的风险模型。
方法 选取在中国医科大学附属第一医院进行过劲动脉超声检查的 2 型糖尿病患者共 236 例，根据颈动脉超声结果，将任意一侧颈动脉有斑块的患者纳入颈动脉斑块组，将 2 侧颈动脉均无斑块的患者纳入无颈动脉斑块组，并收集 26 项临床常规检测项目。在 236 例患者中随机选取 168 例（70%）作为建模人群，用来构建列线图，其余 68 例患者（30%）用来验证建立的模型。以是否有颈动脉斑块作为因变量，以 26 项临床常规检测项目作为自变量，通过 lasso 回归以及多因素 logistics 回归选取与颈动脉斑块独立相关的自变量并绘制列线图。计算 C-index，绘制校准曲线，并通过验证队列进行校准分析。统计分析采用 R 3.6.1，P 小于 0.05 认为有统计学差异。

结果 建模人群及验证人群在性别、年龄及其他常规检测上均无显著性差异（P>0.05）。通过 lasso 回归进行变量筛选后，原来的 26 个变量缩减为 4 个，将这 4 个变量纳入多因素 logistics 回归分析后发现，年龄（OR=3.45, P<0.001）、红细胞平均血红蛋白浓度（OR=0.95, P=0.021）、血小板分布宽度（OR=1.60 P=0.003）以及高密度脂蛋白胆固醇（OR=0.11，P=0.007）这 4 个变量均为颈动脉斑块的独立风险因素，将上述 4 个变量绘制列线图。回归方程的 C-index 为 0.837（95%可信区间：0.773-0.902）。通过验证队列发现模型预测的结果与验证队列中的结果较为一致，验证队列的 C-index 为 0.774（95%可信区间：0.656-0.893），校准曲线拟合良好。
结论 我们建立并验证了 2 型糖尿病患者中颈动脉斑块的风险模型。

PU-1275

BRD7 通过 PI3K/AKT 信号通路抑制鼻咽癌细胞 PD-L1 的表达

李晓旭[1,2]、李梦娜[3]、陈镁琳[1]、周清[1]、刘影[1]、李夏雨[3]、周鸣[3]、李桂源[3]、张文玲[1]
1. 中南大学湘雅三医院湘雅医学院医学检验系
2. 芜湖市第二人民医院
3. 中南大学肿瘤研究所

Objective To investigate whether BRD7 gene could regulate the expression of PD-L1 in nasopharyngeal carcinoma (NPC) cells through PI3K/Akt pathway and provide more sufficient evidence for BRD7 as a candidate tumor suppressor gene and a promising target for NPC immunotherapy.
Materials and Methods Please refer to the appendix of the abstract.
Results The expression of PI3K-P85α protein in the nucleus in the PI3K/AKT pathway increased and the expression of p-mTOR, p-AKT, PI3K-P85, PI3K-P110α, PI3K-P110β and PD-L1 decreased after overexpression of BRD7, while the result was opposite after BRD7 was interfered. More interestingly, the expression of PI3K-P85α protein remained unchanged after interference with BRD7, but the PI3K-P85α protein increased in cytoplasmic and decreased in the nucleus. The expression of key molecules in PI3K/Akt pathway and PD-L1 were decreased after adding the pathway inhibitor LY294002 into NPC cells.
Conclusion BRD7 inhibited the expression of PD-L1 of NPC cells by inhibiting the activation of the PI3K/AKT signaling pathway.

PU-1276

血清 TK1、CA199 和 CA242 联合检测在结直肠癌中的诊断价值

黄献中、巫仕霞
广州金域医学检验中心有限公司

目的 探讨血清胸苷激酶 1(TK1)、糖类抗原 199(CA199)、糖类抗原 242(CA242) 联合检测对结直肠癌诊断的临床应用价值。
方法 采用化学发光法对 93 例结直肠癌患者、95 例结直肠良性病变患者和 100 例健康体检者（对照组）的血清 CA199、CA242 含量进行检测, 采用酶免疫点印迹化学发光法对各组血清 TK1 含量进行检测。
结果 结直肠癌组的 TK1、CA199 和 CA242 水平显著高于结直肠良性病变组患者和正常对照组,差异有统计学意义(P ＜ 0.05) ，单独检测 TK1 对结直肠癌诊断的敏感度、特异度和准确度分别为 62.4%、75.8%、69.1%, CA199 为 56.0%、82.1%、69.1%, CA242 为 64.5%、80.0%、72.3% ；联合检测 TK1、CA199 和 CA242 为 78.5%、68.4%、73.4%。
结论 血清 TK1、CA199 和 CA242 联合检测可以提高结直肠癌的检出率，对于结直肠癌的早期诊断、疗效监测、判断预后等方面具有重要的临床价值。

PU-1277

重组人型肿瘤坏死因子受体-抗体融合蛋白治疗强直性脊柱患者淋巴细胞亚群和单核细胞 CD36 表达的分析

王倩、王昌敏、李智伟
新疆维吾尔自治区人民医院

目的 观察重组人型肿瘤坏死因子受体-抗体融合蛋白(RhTNFR-Fc）治疗强直性脊柱炎(AS)患者外周血 T 淋巴细胞亚群的变化及 CD36 的表达，探讨 RhTNFR-Fc 治疗对活动性 As 患者淋巴细胞亚群和单核细胞 CD36 的影响。
方法 选取 2017 年 1 月～2019 年 12 月于新疆维吾尔自治区人民医院风湿科首次进行生物制剂治疗的活动性 AS 患者 78 例，随机分为观察组和对照组各 39 例，其中对照组进行非甾体类药物口服治疗，观察组在常规治疗基础上应用 RhTNFR-Fc 治疗，应用流式细胞学检测活动性 AS 患者治疗前后 T 淋巴细胞亚群、CD36 的表达情况。
结果 在活动性 AS 患者中，观察组患者治疗后临床 BASDAI 评分、BASFI 评分、CRP、ESR、Th1 细胞水平、Th17 细胞水平、CD36 荧光强度表达与对照组相比明显降低，存在统计学差异（P<0.05）。两组患者的 BASDAI 评分、BASFI 评分、Th1 细胞水平在治疗前后组间比较有统计学差异（P<0.05）。BASDAI 评分、BASFI 评分、Th17 细胞水平和 CD36 荧光表达强度在组别和时间之间存在交互效应，随时间的延长，观察组和对照组 BASDAI 评分、BASFI 评分、Th17 细胞降低的幅度和 CD36 荧光表达强度升高幅度存在明显差异（P<0.05）。在活动性 AS 患者外周血中 Th1、Th17 细胞水平与骶髂关节 CT 分级、BASDAI 评分和 BASFI 评分呈正相关性（P<0.05，r=0.3~0.5），CD36 荧光强度与 Th1 细胞、Th17 细胞、骶髂关节 CT 分级、BASDAI 评分和 BASFI 评分呈负相关性（P<0.05，r=-0.392、r=-0.368，r=-0.374,r= -0.413,r=-0.427），与 Th2 细胞、Treg 细胞水平成正相关（P<0.05,r=0.330,r=0.306）。
结论 检测外周血 T 淋巴细胞亚群和单个核细胞 CD36 的表达是对活动性 AS 病情变化和治疗监测的较好手段。此外，重组人型肿瘤坏死因子受体-抗体融合蛋白联合非甾体类药物共同治疗 AS 起效快、可有效缓解 AS 临床症状，达到协同用药效果。

PU-1278

非小细胞肺癌患者血清中 14 种可溶性免疫检查点蛋白的检测

彭蓑[1]、陈雨欣[2]、芮志莲[1]、童欣[2]
1. 溧阳市人民医院
2. 南京市鼓楼医院

目的 免疫治疗特别是免疫检查点抑制剂作为一种全新的抗肿瘤疗法，已在包括肺癌在内的多个肿瘤治疗领域取得了突破性的进展。免疫检查点相关的预测性生物标志物对于患者的诊断及预后有重要的价值。然而，免疫检查点蛋白能否作为 NSCLC 血清学标志物的研究仍然较少。本研究探讨了 NSCLC 患者血清中 14 种可溶性免疫检查点蛋白的表达水平，并评估其对非小细胞肺癌的潜在诊断价值。
方法 收集南京鼓楼医院经病理证实的 86 例 NSCLC 患者及 57 例健康体检者的血清。通过 Luminex 液相芯片技术对血清中 14 种免疫检查点蛋白进行定量检测，同时以电化学发光法检测常见肺癌肿瘤标志物 CEA、NSE 和 CYFRA211。组间比较采用 Mann-Whitney U 检验，临床病理参数与蛋白表达之间的相关性采用 Spearman 法。受试者工作特征曲线（ROC）用于评价免疫检查点蛋白在 NSCLC 中的诊断价值。
结果 14 种可溶性免疫检查点蛋白中 9 种在 NSCLC 血清中高表达，分别是 sTIM3、sCD137、sCD27、sLAG3、sIDO、sPDL2、sCD152、sCD80 和 sPD1。其中，sCD27 在肺鳞癌组的表达

（108.48 pg/mL）显著高于肺腺癌组（59.91 pg/mL），P = 0.003。sTIM3、sCD137 和 sCD27 在晚期组的表达（1.28、0.30 和 84.69 pg/mL）显著高于早期组（0.58、0.10 和 61.84 pg/mL），且与 TNM 分期之间呈正相关；而在早期组中 sLAG3 的表达（2.75 pg/mL）显著高于健康组（0.94 pg/mL），P < 0.001。ROC 曲线分析显示 sTIM3 有最高的诊断准确度（75.53%），AUC = 0.761，对应的诊断灵敏度和特异性分别是 60.47%和 98.25%。其次，sLAG3 的准确性为 73.43%，其 AUC 达 0.774。此外，sTIM3 和 sLAG3 的 AUC 与 CEA 接近（AUC=0.794），略高于 NSE（AUC = 0.741）。

结论 sTIM3、sCD137、sCD27、sLAG3、sIDO、sPDL2、sCD152、sCD80 和 sPD1 在 NSCLC 患者血清中高表达。其中，sCD27 在肺鳞癌中高表达将有助于病理类型的判别；sLAG3 在早期组中的高表达，有望在 NSCLC 的早期诊断中发挥作用。sTIM3、sCD137 和 sCD27 与肿瘤的分期正相关，提示其可能与 NSCLC 的发生发展密切相关。sTIM3 和 sLAG3 的 AUC 与肺癌常见肿瘤标志物 CEA 接近，且高于 NSE，提示这两个指标在 NSCLC 中存在较高的诊断价值。

PU-1279

结核分枝杆菌特异性细胞因子(IFN-γ、IL-2)联合检测对活动性结核诊断的真实世界研究

吴迪
广州市胸科医院（广州市结核病防治所、广州市结核病治疗中心）

目的 分析结核分枝杆菌特异性细胞因子(IFN-γ、IL-2)联合检测在真实世界中对活动性结核诊断的价值。

方法 回顾性队列分析法，连续收集广州胸科医院 2020 年 11 月 1 日-2021 年 1 月 25 日入院的患者共 790 例，纳入符合研究入组标准的患者 700 例，其中 542 例结核病、158 例非结核，统计分析两组患者检测结核分枝杆菌特异性细胞因子(IFN-γ、IL-2)的结果。

结果 结核分枝杆菌特异性细胞因子(IFN-γ、IL-2)联合检测的灵敏度为 80.1%（95%CI 76.5%~83.4%），特异性为 82.9%（95%CI 76.1%~88.4%），阳性预测值 94.1%（95%CI 91.6%~96.1%），阴性预测值 54.8%（95%CI 48.3%~61.2%），总符合率 80.7%（95%CI 77.6%~83.6%）。单独分析 IFN-γ 的灵敏度为 79.9%（95%CI 76.2%~83.1%），特异性为 82.9%（95%CI 75.9%~88.2%），阳性预测值为 94.1%（95%CI 91.5%~96.0%），阴性预测值为 54.6%（95%CI 48.1%~61.0%），总符合率 80.6%（95%CI 78.5%~81.4%）。单独分析 IL-2 的灵敏度为 48.2%（95%CI 43.9%~52.5%），特异性为 93.0%（95%CI 87.6%~96.3%），阳性预测值为 96.0%（95%CI 92.7%~97.9%），阴性预测值为 34.3%（95%CI 29.9%~39.0%），总符合率 58.3%（95%CI 56.4%~62.7%）。双因子阳性的灵敏度为 48.0%（95%CI 43.7%~52.3%），特异性为 93.0%（95%CI 87.6%~96.3%），阳性预测值为 95.9%（95%CI 92.6%~97.9%），阴性预测值为 34.27%（95%CI 29.8%~39.0%），总符合率为 58.1%（95%CI 75.2%~79.5%）。

结论 结核分枝杆菌特异性细胞因子联合检测方法在检测 IFN-γ 的基础上增加了 IL-2 的检测，在结核感染检测灵敏度不变的情况下提高了检测的特异性。

PU-1280

2014-2020 年四川省综合医院 HIV 感染者流行病学分析

麦涛
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 探讨综合性医院 HIV 感染者的流行病特征，为医院制定 HIV 的防控措施提供参考依据。

方法 回顾性分析 2014-2020 年四川省人民医院确诊的 5102 例 HIV 感染者人群的流行病学资料。

结果 HIV 感染人群数量呈现上升趋势。男女比例约为 5:1, 以 18-50 岁处于性活跃期的青壮年为主，占比约为 63.88%；而≥51 岁老年 HIV 群体数量逐年增加，从 26.15%升至 30.58%。已婚有配偶者居多(62.91%);异性传播为主要感染途径(78.48%) ,其他途径较少。HIV 感染者就诊临床科室众多，以皮肤科、神内科、呼吸内科、血液内科、简易门诊等为主，合占 34.30%。
讨论 2014-2020 年间我院 HIV 感染者在性别、年龄以及感染途径等方面同其他学者的研究一致。值得关注的是，老年 HIV 患者逐年增加, 调查发现该群体多缺乏 HIV 感染相关防护意识和检测行为。其 HIV 感染多经由入院时期常规感染性疾病筛查发现，表现出隐匿性强的流行病学特点，危害极大。应针对老年人群开展相关宣传工作,积极倡导自愿咨询检测。再者，皮肤科、神内科、呼吸内科、血液内科等是发现 HIV 感染者的重点科室，应加强在重点科室和高危人群中的筛查。

PU-1281

87 例维持性血液透析患者自身免疫性抗体分析

宋颖博、李晓苗、董清清、蒋菲、张艳、张新
新疆生产建设兵团总医院

目的 对 87 例维持性血液透析(maintenance hemodialysis, MHD)患者自身免疫性抗体分布情况进行分析，为 MHD 患者的综合治疗提供参考依据。
方法 选取我院血液净化中心透析龄在 3 个月以上的 87 例 MHD 患者（男性 49 例，女性 38 例），其中原发病为糖尿病肾病 50 例、高血压肾病 10 例、其他类型（多囊肾、慢性肾小球疾病等）27 例。采用间接免疫荧光法（IIF）检测血清抗核抗体（ANA）以及采用线性免疫印迹法（LIA）检测血清抗核抗体谱（ANAs）中抗 U1- nRNP、抗 Sm、抗 SSA、抗 Ro-52 、抗 SSB、抗 Scl-70、抗 PM-Scl、抗 Jo -1、抗 CENP -B、抗 PCNA、抗 dsDNA、抗核小体、抗组蛋白、抗核糖体 P 蛋白、抗 AMA -M2 等 15 种抗体。
结果 87 例 MHD 患者血清 IIF-ANA 阳性 16 例（占 18.4%），其中男性占 37.5%（6/16），女性占 62.5%（10/16），性别间 IIF-ANA 阳性率差异有统计学意义（P<0.05）。糖尿病肾病 MHD 患者 IIF-ANA 阳性率高于高血压肾病和其他类型的 MHD 患者阳性率（均 P<0.05）。87 例 MHD 患者血清 LIA-ANAs 阳性 20 例（占 23.0%），其中男性占 40%（8/20），女性占 60%（12/20），性别间 LIA-ANAs 阳性率差异有统计学意义（P<0.05）。LIA-ANAs 阳性的女性患者抗体谱分布广，主要为抗 Ro-52、抗 SSA、抗 SSB、抗 dsDNA 和抗组蛋白等 10 种抗体，而 LIA-ANAs 阳性的男性患者抗体谱主要以抗 AMA-M2、抗 Jo-1 抗体为主。糖尿病肾病 MHD 患者 LIA-ANAs 阳性率高于高血压肾病和其他类的 MHD 患者的阳性率（均 P<0.05）。
结论 女性 MHD 患者 IIF-ANA 和 LIA-ANAs 阳性率高于男性，且女性 MHD 患者 LIA-ANAs 分布较广；糖尿病肾病 MHD 患者的 IIF-ANA 阳性率和 LIA-ANAs 阳性率较高。因此，临床在 MHD 患者治疗过程中应关注女性 MHD 患者和糖尿病肾病 MHD 患者免疫功能状态。

PU-1282

Clinical utility of CD64 index in diagnosis with pediatric sepsis

Xian Chen 、Ruijing Lu、Xiyou Zhou、Feng Wang
深圳市宝安区妇幼保健院

Backgrounds The early detection and effective treatment of sepsis in the children is difficult due to the lack of representative signs and promising laboratory diagnostic biomarkers in clinical practice. This study aimed to explore the character and clinical application of CD64 index in early diagnosis of pediatric sepsis in comparison with common infection indicators including routine blood tests.

Methods We recruited 37 cases of sepsis, 34 cases of non-sepsis (common infections free of sepsis), and 20 cases of health children as control. We collected laboratory data such as absolute white blood cell (WBC) numbers, ratios of neutrophils and lymphocytes (NLR), neutrophil percentages, and C-reactive protein (CRP), procalcitonin (PCT) and CD64 index from all 91 participants.
Results We found that sepsis cohort had higher CRP and PCT, along with WBC numbers, NLR, neutrophil proportions compared to healthy control cohort, but these parameters could not distinguish non-sepsis cohort and sepsis cohort. However, CD64 index showed statistical significance in sepsis cohort, compared with non-sepsis cohort and control cohort, and could be used for sepsis diagnosis in the clinic.
Conclusion In summary, CD64 index combined with conventional blood parameters might shed light on early diagnosis of sepsis in pediatrics.

PU-1283

基于系列肿瘤标志物对肿瘤进展过程的认证和分子变化的解析

赵鹏飞
丹东市第一医院

目的 目前癌症仍然是威胁人类健康及生命的最主要的疾病，虽然目前有很多的诊断方法，但往往就诊时患者大多已经处于晚期或转移状态，不利于后期治疗和预后。肿瘤标志物检测的优点是对患者没有创伤、操作方法简单、检测时间短，并对于癌症的早期筛查很有效，但如果用某单一的肿瘤标志物进行诊断检测，其结果的灵敏性、特异性都不高，不利于肿瘤的筛查和早期诊断。因此，开发高效的肿瘤标志物联合检测技术对各系统肿瘤的早期诊断和治疗具有重要意义。文章旨在探讨肿瘤标志物在不同肿瘤分化程度中，其浓度的相关性分析以及联合检测肿瘤标志物对肿瘤分期及肿瘤分化程度的辅助诊断意义。
方法 收集 2016 年 2 月至 2019 年 6 月，在丹东市第一医院住院的肿瘤患者共 162 例，同期来院健康查体的正常对照组 55 例，分别记录性别、年龄、肿瘤良恶程度；用化学发光酶免疫分析技术测量静脉血清中 CEA、AFP、CA19-9、CA72-4、NSE、CYF21-1、FER 及 CRP 的浓度，整理入库。用 IBM SPSS 24.0 统计软件，对以上数据进行统计学分析。
结果 1、162 例肿瘤患者血清中 CEA、AFP、CA19-9、CA72-4、NSE、CYF21-1、FER 及 CRP 浓度均高于 55 例正常对照组，差异有统计学意义（$P<0.05$）。其中低分化高恶性和高分化低恶性肿瘤患者 8 种肿瘤标志物浓度均高于良性肿瘤息肉囊肿组和正常对照组。
2、单独检测 8 种肿瘤标志物的 ROC 曲线分析，CRP 曲线下面积最大，AFP 最小，FER 灵敏度最高，CA72-4 最低。
3、8 种肿瘤标志物联合检测的 ROC 曲线下面积、灵敏度及特异性均优于单独一种标志物的检测。
4、随着肿瘤分化程度降低，呈现各类肿瘤标志物阳性，有可能成为判断肿瘤分化程度的分子标志物。
5、在恶性肿瘤的不同分型中，与单项检测相比，8 种肿瘤标志物联合检测的阳性检出率均高于单独一种肿瘤标志物的检测。
结论 1、肿瘤患者的血清肿瘤标志物浓度高于正常体检者，恶性肿瘤患者肿瘤标志物高于良性肿瘤患者；
2、随着肿瘤分化程度降低，呈现各类肿瘤标志物阳性，有可能成为判断肿瘤分化程度的分子标志；
3、肿瘤标志物联合检测可能是肿瘤发展过程中的分子变化标志，并可以作为量化肿瘤分化程度的指标。

PU-1284

粪便潜血定量检测在体检人群中的应用价值分析

程守军
南京大学医学院附属鼓楼医院

目的 通过对体检人群粪便潜血定量检测，统计分析检测结果阳性人群的患大肠癌及相关肠道疾病的风险及其应用价值。
方法 统计分析 2019 年 1 月至 2019 年 12 月在本院体检中心接受体检人员的粪便潜血定量检测的检测结果，并分析其中阳性结果人员的肠镜检查及相关病理检查结果，统计分析粪便潜血定量检测的检测结果阳性结果占比，并且分析阳性结果体检人员与患大肠癌及肠道疾病相关性，得出应用价值相关分析。
结果 体检人群中共 17845 人次做了粪便潜血定量检测，结果为阳性(大于 100ng/ml) 是 787 例，其中 158 例做了肠镜检查及病理检查，检测出大肠癌、低级别上皮肉瘤变、息肉或腺瘤等肿瘤相关病变 82 例，肠炎及其他病患 52 例，无异常发现的 23 例。
结论 粪便潜血定量检测在体检人群中可以无创性提前筛选出无症状大肠癌及其他肠道相关性疾病，说明粪便潜血定量检测在体检人群中可以达到早发现，早治疗，减少疾病进展而引起的治疗延误，很好地诠释了健康体检的作用。

PU-1285

不同方法检测 1 型糖尿病患者胰岛自身抗体结果分析

陈菲
南京大学医学院附属鼓楼医院

目的 探讨三种方法在胰岛自身抗体检测中的应用价值。
方法 收集 94 例 2019 年 6 月-12 月南京鼓楼医院内分泌科的 T1DM 确诊住院患者血清，20 例健康人群血清（正常对照组），酶联免疫吸附法(ELISA)和化学发光法(CLIA)检测谷氨酸脱羧酶抗体（GADA）、酪氨酸磷酸酶抗体(IA2A)结果，免疫荧光法(IFA)和化学发光法(CLIA)检测胰岛细胞抗体(ICA)结果。
结果 ELISA 法、CLIA 法检测 GADA 的阳性率分别为 76.6％、62.8％，检测 IA2A 的阳 28.7%、9.6%，IFA 法、CLIA 法检测 ICA 的阳性率分别为 17％、 48.9％，三种抗体检测均两者有统计学差异（P<0.05）。
结论 三种方法学各有利弊，需联合检测，才能提高胰岛自身抗体检测的准确性。

PU-1286

热灭活后 COVID-19 IgG/IgM 抗体检测的潜在假阳性和假阴性结果分析

戴薇、夏欣一
中国人民解放军东部战区总医院

目的 随着由严重急性呼吸系统综合症冠状病毒 2 （SARS-CoV-2）引起的冠状病毒病 19（COVID-19）)在世界范围内的快速传播，已经开发出多种抗体检测试剂盒用以检测 SARS-CoV-2 IgG、IgM 和总抗体。然而，在各种热灭活条件下使用不同的免疫学检测方法可能会影响 COVID-19 的抗体检测结果。因此，本研究主要分析不同热灭活条件下，使用不同免疫学检测方法对 COVID-19 IgG/IgM 抗体检测的潜在假阳性和假阴性现象。

方法 中国武汉火神山医院共计使用了四家厂商生产的七种不同 SARS-CoV-2 抗体检测试剂盒，用于检测 SARS-CoV-2 IgG、IgM 和总抗体。抗体试剂盒主要采用双抗原夹心法、捕获法和间接免疫法。针对不同的检测方法，本研究分析了多种热灭活条件对 SARS-CoV-2 特异性 IgG、IgM 和总抗体检测结果的影响。
结果 采用间接免疫法，SARS-CoV-2 IgG 抗体值随着热灭活温度的升高或热灭活时间的延长而显著升高，而 IgM 抗体值显著降低。当使用捕获法和双抗原夹心法时，SARS-CoV-2 IgM 和总抗体的值没有明显变化。使用间接免疫法时，IgG 和 IgM 抗体值的变化表明热灭活可以影响 COVID-19 的检测结果。其中，18 个（22.2%）SARS-CoV-2 IgM 阳性样本经 65℃热灭活 30 分钟后检测为阴性结果，1 个（25%）IgG 阴性样本经 56℃热灭活 60 分钟或 60℃热灭活 30 分钟后检测为阳性结果。
结论 样本经热灭活后 SARS-CoV-2 IgG 抗体值升高，IgM 抗体值下降，导致使用间接免疫法检测 COVID-19 抗体时可能出现假阳性或假阴性检测结果。因此，在进行 COVID-19 抗体检测之前，应根据相关要求对检测平台进行评估，以确保准确可靠的 COVID-19 抗体检测结果。

PU-1287

T cell cytotoxicity toward Gastric Cancer via immunotherapy targeting

Xinlin Li
Affiliated Hospital of Xuzhou Medical University

T cells are important effectors in anti-tumor immunity, and aberrant expression of B7 family members may contribute to tumor evasion. In this study, we analyzed expression of costimulatory molecules on human gastric cancer cells and explored whether B7-H3, a member of the B7 superfamily, is an effective target for T cell mediated cytotoxicity toward gastric cancer. We investigated the bispecific antibody anti-CD3 × anti-B7-H3 (B7-H3Bi-Ab) for its ability to redirect T cells to target B7-H3 positive gastric cancer, including mgc, hgc, sgc, mkn cells and a primary culture. The capacity of T cells armed with B7-H3Bi-Ab to kill hematologic tumors was evaluated by lactate dehydrogenase assay, flow cytometry, ELISA, and luciferase quantitative assay at an effector/target ratio of 10:1. Compared with unarmed T cells, B7-H3Bi-Ab-armed T cells exhibited significant cytotoxicity toward gastric cancer cells. Moreover, B7-H3Bi-Ab-armed T cells secreted more IFN-γ, TNF-α, IL-2, and Granzyme B and expressed higher levels of activating marker CD69 compared to unarmed T cells. In conclusion, B7-H3Bi-Ab enhances the ability of T cells to kill gastric cancer cells, and B7-H3 may serve as a novel target for immunotherapy against gastric cancer.

PU-1288

肺癌诊断中血清肿瘤标志物五项联合检测的临床意义

刘瑛
禹城市中医院

目的 肺癌诊断过程中血清肿瘤标志物联合检测的临床价值分析及体会。
方法 分析我院 2017 年 1 月至 2019 年 2 月收治的 127 例患者的临床资料，其中 61 例为肺癌患者，将其分为肺癌组，余者 66 例为肺部良性病变分为良性病变组，另选择同期来我院进行体检的健康人员 51 例为对照组，比较三组研究对象血清中的肿瘤标志物检测五项结果，肿瘤标志物五项血清癌胚抗原(CEA)、细胞角蛋白 19 片段(CYFRA21-1)、神经元特异性烯醇化酶(NSE)、胃泌素释放肽前体（ProGRP)鳞癌相关抗原(SCC-Ag)。

结果 比较三组研究对象的血清肿瘤标志物检测结果可知，肺癌组血清中血清癌胚抗原(CEA)、细胞角蛋白 19 片段(CYFRA21-1)、神经元特异性烯醇化酶(NSE)、糖类抗原 125(CA125)胃泌素释放肽前体（ProGRP)五项指标的水平均显著高于肺部良性病变组及对照组，差异具有统计学意义(P<0.05)；肺部良性病变组与对照组比较差异不显著(P>0.05)。肺癌诊断中联合检测肿瘤标志物五项，以 CEA+ +CA125+CYFRA21-1+NSE+ProGRP 阳性率最高，显著优于 CEA+NSE +CYFRA21，差异具有统计学意义(P<0.05)；五项联合检测的特异性差异无统计学意义(P>0.05)。
结论 在肺癌诊断过程中联合检测血清肿瘤标志物五项可获得较高的阳性率，具有重要的临床应用价值。

PU-1289

T-SPOT 和 NLR 检测在肺结核诊断中的临床应用分析

贵志芳、张腊红、潘峰
杭州师范大学附属医院

目的 探讨和分析肺结核患者外周血结核感染 T 细胞斑点试验（T-SPOT）和中性粒细胞与淋巴细胞比值(neutrophil-lymphocyte rate，NLR)检测在肺结核诊断中的临床应用价值。
方法 回顾性纳入 2019 年 8 月至 2020 年 7 月在我院收治的 115 例肺结核患者（肺结核组），86 例非肺结核者即肺部其他疾病（非肺结核组）和 30 例健康体检者（健康对照组）作为研究对象，均行 T-SPOT 试验与 NLR 检测。采用受试者工作特征曲线（Receiver Operating Characteristic, ROC）分析 T-SPOT 和 NLR 对肺结核的诊断价值，用 Spearman 相关分析 T-SPOT 和 NLR 之间的关系。
结果 肺结核组中 T-SPOT 和 NLR 的水平分别为 120.86（27.45，525.36）pg/ml，3.52（2.18，5.64）均高于非肺结核组中 T-SPOT 和 NLR 的水平 18.06（5.28，132.26）pg/ml，2.58（1.62，4.03）和健康对照组 T-SPOT 和 NLR 的水平 6.08（3.56，11.11）pg/ml，1.62（1.24，2.02），差异有统计学意义（P<0.01）；T-SPOT 和 NLR 的 ROC 曲线下面积（Area Under Curve, AUC）分别为 0.67 和 0.63，T-SPOT+NLR 的 ROC 曲线下面积为 0.71；T-SPOT 和 NLR 的敏感性分别为 72.3%和 58.9%; 特异性分别为 65.8%和 67.1%。Spearman 相关性分析表明，肺结核患者 T-SPOT 和 NLR 之间存在一定的负相关关系(r=-0.269, P<0.01)。
结论 肺结核患者 T-SPOT 和 NLR 水平均升高，对肺结核的早期诊断有较大的应用价值，且 T-SPOT 和 NLR 的联合检测优于每项的单独检测。

PU-1290

血清 AFP、DCP 在乙肝相关原发性肝癌中的应用

邹珍珍
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 探讨血清异常凝血酶原（DCP）、甲胎蛋白（AFP）在乙型肝炎病毒（HBV）感染相关的原发性肝癌（PHC）患者中的临床应用。
方法 收集 83 例乙肝相关原发性肝癌患者、76 例非乙肝相关原发性肝癌患者、54 例乙肝相关肝硬化患者、72 例慢性乙型肝炎患者以及 66 例健康体检者作为对照组，应用化学发光法检测患者的血清 DCP 水平、血清 AFP 水平、乙肝病毒 S 抗原（HBsAg）、乙肝病毒 S 抗体（HBsAb）乙肝病毒 E 抗原（HBeAg）、乙肝病毒 E 抗体（HBeAb）、乙肝病毒 C 抗体（HBcAb）。
结果 乙肝相关 PHC 组患者血清 DCP、AFP 水平高于非乙肝相关 PHC 组、乙肝相关肝硬化组、慢性肝炎组、健康对照组，差异具有统计学意义（P<0.05）。非乙肝相关 PHC 组血清 DCP 水平高于乙肝相关肝硬化组，乙肝相关肝硬化组血清 DCP 水平高于慢性肝炎组，慢性肝炎组血清 DCP 水

平高于健康对照组，差异具有统计学意义（P<0.05）。在乙肝相关 PHC 患者中，大三阳患者（HBsAg、HBeAg、HBcAb 三项同时阳性）组血清 DCP、AFP 水平高于小三阳患者（HBsAg、HBeAb、HBcAb 三项同时阳性），差异均具有统计学意义（P<0.05），两组患者中的血清 DCP 的阳性率高于血清 AFP 阳性率，但未见明显的统计学差异。经受试者工作曲线（ROC）分析，在乙肝相关的 PHC 患者中，血清 DCP、AFP 的曲线下面积为 0.896、0.672，血清 DCP 的敏感度和特异性分别为 70.22%、96.45%，血清 AFP 的敏感度和特异性分别为 60.47%、89.21%。
结论 血清 DCP、AFP 在乙肝相关性 PHC 患者中有较高的诊断价值，其中血清 DCP 诊断价值优于血清 AFP，临床可结合血清 PIVKA-Ⅱ与 HBV 感染模式对乙肝相关原发性肝癌进行早期筛查与疾病评估。

PU-1291

卵白蛋白多克隆抗体制备及其效价检测

林子沛
南方医科大学珠江医院

目的 制备卵白蛋白多克隆抗体及测定小鼠血浆中抗体效价。
方法 利用动物免疫的方法,分别用含弗式完全佐剂、含弗式不完全佐剂以及不含佐剂的卵白蛋白作为抗原，对小鼠进行皮下和三次腹腔注射，每次接种间隔 7 天或 14 天。以眼球采血法采取小鼠全血后离心分离出血浆，用 ELISA 方法测定血浆中的抗体效价。
结果 制得抗体血浆良好，测得抗体血浆中抗体效价为 1:8000。
结论 卵白蛋白抗体制备及其效价测定实验基本成功。

PU-1292

吖啶脂化学发光法检测抗髓过氧化物酶抗体和抗蛋白酶 3 抗体 的性能评价

胡静、高雪丹、杨滨
四川大学华西医院

目的 验证吖啶脂化学发光法检测抗髓过氧化物 酶 (myeloperoxidase，MPO) 抗体和抗蛋白酶 3 (proteinase 3，PR3) 抗体的检测性能，并研究该方法在检测抗 MPO，抗 PR3 的临床应用价值。
方法 参照相关标准结合科室实际情况，对吖啶脂化学发光法检测抗 MPO，抗 PR3 的日内重复性、日间重复性、线性范围、携带污染、参考区间及可报告范围进行验证和评价，并对 1026 例常规申请检测抗中性粒细胞胞浆抗体（antineutrophil cytoplasmic antibodies，ANCA）的样本同时采用间接免疫荧光法（IIF）、吖啶脂化学发光法和 ELISA 法进行检测，分析其结果。
结果 吖啶脂化学发光法检测 MPO 高低值的日内重复性和日间重复性的变异系数均在可接受范围内；MPO，PR3 线性范围回归方程和判定系数分别为 y=1.0067x+3.7417,R2=0.9953,y=0.995x+6.4,R2=0.9985，MPO 和 PR3 的线性范围为分别为 2.5-300 AU/ml，10-300 AU/ml；携带污染在可接受范围内；20 例健康体检者检测结果均在厂家提供的参考区间内；吖啶脂化学发光法和 ELISA 法在检测 MPO 和 PR3 时具有良好的准确性、阳性符合率、阴性符合率、总符合率（P＜0.01）；吖啶脂化学发光法及 ELISA 与 IIF 筛查检测结果亦具有良好的阳性符合率、阴性符合率、总符合率（P＜0.01）。
结论 吖啶脂化学发光法检测 MPO，PR3 的验证指标均达到规定要求，与 ELISA 相比，吖啶脂化学发光法在检测 MPO 和 PR3 时具有良好的准确性和符合率，可用于临床检测。

PU-1293

ERp44 参与动脉粥样硬化的机制研究

胡明晰
复旦大学附属中山医院青浦分院

目的 ERp44（Endoplasmic Reticulum Protein 44，ERp44）是蛋白质二硫键异构酶家族（protein disulfide isomerase，PDI）中的一员, 含有硫氧还蛋白结构域, 在内质网应激时表达上调，常被用作内质网应激的标志蛋白。探讨动脉粥样硬化（AS）的发病机制，内质网应激（endoplasmic reticulum stress，ERS）和 ERp44 在 AS 发生发展过程中的机制进行研究，为寻找动脉粥样硬化的生物标志物和可能的治疗靶点提供依据。
方法 构建动脉粥样硬化小鼠模型，选取动脉粥样斑块形成不同时间点，做免疫组化和免疫细胞荧光染色研究 ERp44 的细胞定位，做 RNA 抽提和 qRT-PCR，蛋白抽提和 Westernblot 研究 ERp44 的表达，取外周血分离血清利用 ELISA 检测 ERp44 水平。
结果 通过 ERp44 在 2 型糖尿病动物模型中的表达以及在 ERp44-/-小鼠中的表达，发现 ERp44 在高血糖、高血脂的条件下，表达降低；ERp44 敲除小鼠除了脂质代谢异常外，作为内分泌器官的脂肪组织也出现异常。
结论 ERp44 的缺失会导致血糖和血脂合成障碍，这些结果表明 ERp44 与糖脂代谢密切相关，而糖代谢和脂代谢又与 AS 的发生密切相关，所以 ERp44 在 AS 中可能起到了重要的作用，它为心血管疾病治疗提供新的理论依据，我们仍需要继续研究 ERp44 参与动脉粥样硬化的机制。

PU-1294

急性心肌梗死中心型脂肪酸结合蛋白与肌钙蛋白、肌红蛋白的诊断性对比

王一多、金英玉
哈尔滨医科大学附属第一医院

心型脂肪酸结合蛋白是一种心肌损伤的早期标志物，其具有分子量低（15KD），水溶性好，在心肌损伤时出现早等特点。在正常的人体中其含量很低，但是当心肌出现损伤时心型脂肪酸结合蛋白能在短时间内出现明显的升高。这一特点就为临床的诊断提供了更加快捷有利的辅助手段，所以研究心型脂肪酸结合蛋白对于指导临床诊断急性心肌梗死方面拥有重要意义。

PU-1295

尿转铁蛋白与冠心病及冠状动脉狭窄程度关系的分析

杨威、关庆柏
哈尔滨医科大学附属第一医院

目的 探讨尿转铁蛋白与冠心病及冠状动脉狭窄程度之间的关系。
方法 选取因冠心病住院的患者 138 例（冠心病组）和健康体检者 108 例（对照组）。调查入选对象存在的心血管疾病危险因素，包括: 性别、年龄、高血压病史、糖尿病病史及吸烟史; 检测受试者血清高密度脂蛋白（HDL）、低密度脂蛋白（LDL）、C 反应蛋白(CRP) 、肌酸激酶同工酶（CK-MB）、心肌肌钙蛋白 I（TnI）及尿转铁蛋白（TRF）。对冠心病的多重危险因素采用非条件 logistic 回归模型进行分析。
结果 冠心病组的血清中 LDL、CRP、CK-MB、TnI 及 TRF 水平明显高于对照组，差异具有统计学意义。冠心病组血清 HDL 水平低于组，差异有统计学意义；Logistic 回归分析显示 TRF 为冠心病

的独立危险因素，回归系数（β）为 0.729，相对危险度(OR) 为 1.36；尿转铁蛋白与冠状动脉狭窄程度之间存在着正相关关系，二者相关系数 r=0.886，P<0.01。
讨论 尿转铁蛋白是冠心病的独立危险因素，尿转铁蛋白水平有助于对冠状动脉狭窄病变程度进行判断。

PU-1296

EB 病毒与细胞因子在鼻咽癌患者中的作用

姜湘湖
武汉大学中南医院

目的 免疫细胞(CD3+ T 细胞、CD3+CD4+ T 细胞、CD3+CD8+ T 细胞、CD19+ B 细胞、CD16+CD56+自然杀伤(NK)细胞)、十二项细胞因子（IL-1β, IL-2, IL-4, IL-5, IL-6, IL-8, IL-10, IL-12, IL-17, IFN-γ, TNF-α, IFN-α）和血常规生化指标与鼻咽癌患者中 EB 病毒的关系。
方法 收集患者血液，从血浆和 PBMC 中分别提取 DNA，进行 EBV 实时定量聚合酶链反应(qPCR)，检测 EBV 载量。采用 BD FACSCalibur 流式细胞术按说明书检测血清细胞因子 IL-1β、IL-2、IL-4、IL-5、IL-6、IL-8、IL-10、IL-12、IL-17、IFN-γ、TNF-α 和 IFN-α。通过流式细胞术(BD)，按照制造商的说明，获得 CD3+ T 细胞、CD3+CD4+ T 细胞、CD3+CD8+ T 细胞、CD19+ B 细胞和 CD16+CD56+自然杀伤(NK)细胞的外周绝对细胞计数和淋巴细胞百分比.
结果 EBV-与 EBV+患者中，A/G, GLB, LYMPH%, MONO%, ALT, IL-10, RBC CD19+Abs, RBC 有明显差异。一些细胞因子与 EBV 载量有很好的相关性。如 EBV 载量与 IFN-α、IL-12 显著相关。在 EBV-组中，细胞因子之间存在令人满意的相关性，然而，这些细胞因子在 EBV +组中并没有很强的相关性。免疫细胞、细胞因子和血常规生化指标中，EBV-组 IL-6 与 AST、IL-8 与 WBC、IL-8 与 NEUT#、TNF-α 与 CD3+CD4-CD8-Abs 的相关系数分别为 0.793、0.749、0.741、0.031。而在 EBV+组，IL-6 与 AST、IL-8 与 WBC、IL-8 与 NEUT#、TNF-α 与 CD3+CD4-CD8-Abs 的相关系数分别为-0.021、0.261、0.314、0.552。TNM 分期 EBV 载量比较，N0-1 期与 N2-3 期肿瘤患者 EBV 载量差异有统计学意义。多变量 logistic 回归分析，T 期的独立危险因素为 ALT、IL-6、CD3+CD4+Abs 和 CD19+%Lym。N 期的独立危险因素包括 CD3+CD8+Abs、IL-8、CD16+CD56+%Lym 和 EO#。N 期的独立危险因素为 CD3+CD4+抗体、CD19+%Lym 和 LYMPH#。
结论 免疫细胞，十二项细胞因子和血常规生化指标中存在鼻咽癌患者 EBV+的预测因子。联合它们能更好的筛选出 EBV+的鼻咽癌患者。

PU-1297

酶联免疫反应加速仪在麻疹病毒 IgM 抗体检测中的应用

杨威、董莉芹
哈尔滨医科大学附属第一医院

目的 探讨酶联免疫反应加速仪在麻疹病毒 IgM 抗体检测中的应用价值。
方法 选取已知麻疹病毒 IgM 抗体阳性血清和临床疑似麻疹病毒感染者的血清分别用常规酶联免疫吸附试验（常规法）和酶联免疫反应加速仪法（加速法）进行麻疹病毒 IgM 抗体的检测，比较两种方法在检测麻疹病毒 IgM 抗体的重复性、精密度及特异性是否符合试剂盒标准。
结果 加速法的变异系数为 2.86%～9.52 %，灵敏度为 97.4%，特异度为 100%，均符合试剂盒标准。相关性分析加速法和传统法定量结果呈显著正相关关系。
结论 酶联免疫反应加速仪在麻疹病毒 IgM 抗体检测中，各项指标均符合试剂盒要求，可应用于临床检测。

PU-1298

Graves 病患者血清 TRAb 水平与甲功五项的相关性研究

闫洪宇
吉林大学第一医院

目的 研究 Graves 病患者血清 TRAb 水平与甲功五项之间相关性关系。
方法 收集本院 2020 年至今的 Graves 病患者共计 300 例，其中 TRAb 采用罗氏电化学发光免疫分析仪，以 1.75IU/L 作为 TRAb 的参考界限。甲功五项分别为 TSH、FT3、FT4、T3、T4，甲功五项采用雅培化学发光免疫分析仪检测。将患者分为 TRAb 阴性组（n=45）和 TRAb 阳性组（n=255）。分析两组患者间甲功五项的差异，采用相关性分析研究血清 TRAb 水平与甲功五项的关系。
结果 TRAb 阴性组 TSH 水平远高于阳性组（p<0.05），FT3、FT4、T3、T4 水平低于阳性组（p<0.05），相关性分析表明 Graves 病患者血清 TRAb 水平与 TSH 呈负相关（p<0.05），而与 FT3、FT4、T3、T4 呈正相关（p<0.05）。
结论 Graves 病患者血清 TRAb 水平与甲功五项有关，具有统计学意义，而与患者年龄和性别等无关。

PU-1299

56℃加热 30min 灭活的血液标对半乳甘露聚糖检测产生影响

黄晓晖[1]、兰圣雨[2]
1. 联勤保障部队第九 00 医院
2. 福建医科大学

目的 探究 56℃加热 30min 灭活的血液标本是否会对半乳甘露聚糖检测产生影响,旨在不影响检测结果的同时保护检验者,降低医源性感染的风险。
方法 收集中国人民解放军联勤保障部队第 900 医院 2021 年 02 月至 2021 年 04 月半乳甘露聚糖检测血清标本共 50 例,对血清标本采取热灭活的标本前处理方法后开展 GM 试验。1.检测 20 例 GM 阴性血清标本灭活后的 GM 抗原水平,将灭活后测得的 OD 值与原始 OD 值比较,分析灭活前后结果是否有统计学差异。2 检测 30 例 GM 阳性血清标本灭活后的 GM 抗原水平,比较灭活前后 OD 值,分析灭活前后结果是否有统计学差异。3.分析 50 例血清标本灭活前后的 GM 定性结果是否有统计学差异。
结果 1.GM 阴性血清标本灭活前 OD 值与灭活后 OD 值存在差异,曼-惠特尼 U 检验 sig 值<0.05,整体 OD 值较灭活前偏低。2.GMB 性血清标本灭活后阳性符合率仅为 0.321,在临界值范围内由阳转阴率为 0.333,灭活前后 OD 值之间具有显著差异性(sig 值<0.05) 。3 灭活前后 GM 检测标本卡方检验的 sig 值为 0.000,灭活前后 GM 检测标本定性结果存在显著差异。
结论 半乳甘露聚糖检测血液标本灭活前后 OD 值存在显著差异,表明了 GM 定性结果是受到热灭活处理影响的,此时 GM 检测结果不具有临床可接受性。因此建议临床实验室工作中开展半乳甘露聚糖检测暂勿使用 56℃加热 30minh 热灭活的标本前处理方法。

PU-1300

网膜素对动脉粥样硬化及相关疾病影响的研究进展

刘月娥、关秀茹
哈尔滨医科大学附属第一医院

网膜素主要是由内脏脂肪组织分泌的一种细胞因子，它具有参与代谢，调控炎症，增强胰岛素敏感性等的生物学活性。网膜素通过 eNOS、AMPK、Akt 等多种信号通路影响血管内皮细胞，巨噬细胞及血管平滑肌细胞的分泌、增殖、转化活动、血脂和血糖的代谢及血管钙化过程，从而参与动脉粥样硬化的形成、冠心病和脑梗死的发生和发展。已有研究表明体内网膜素水平的增加在动脉粥样硬化，冠心病及脑梗死的进展中起到保护作用。

PU-1301

冠心病患者血清 hs-CRP、TnI、CK-MB 测定的临床意义

姜玉玲、蒋丽鑫
哈尔滨医科大学附属第一医院

目的 探讨冠心病患者血清 hs-CRP、TnI、CK-MB 测定的临床意义。
方法 利用乳胶增强免疫比浊法和电化学发光法，对 112 例健康人群和 52 例急性心肌梗死（AMI），64 例不稳定性心绞痛（UA），32 例稳定性心绞痛（SA）患者检测超敏 C 反应蛋白（hs-CRP）、肌钙蛋白 I(TnI)和肌酸激酶（CK-MB）水平。
结果 SA 组、UA 组和 AMI 组 hs-CRP、TnI、CK-MB 水平明显高于健康组（P<0.05）。
结论 hs-CRP 是心血管疾病的独立危险因素，与 TnI、CK-MB 联合检测对冠心病的诊断、治疗及预后判断有重要意义。

PU-1302

An epitope vaccine based on Hepatitis B virus core protein triggers protection against Neisseria meningitidis serogroup B in BALB/c mice

Hui Cao[1]、Sihai Hu[2]、Jun He[1]
1. Institution of affiliated Nanhua Hospital, University of South China
2. 南华大学

Objective The primary objective of present study was to develop an effective epitope vaccine HBc-N144-epitope (1+2) ,which was constructed by fusing the selected peptides of Neisserial surface protein A (NspA) into the HBc-N144 virus like particles , as a promising candidate to prevent the infection of Neisseria meningitidis serogroup B (MenB).
MethodsWe screened the conserved dominant epitopes of N. meningitidis surface protein A (NspA) by bioinformatics analysis, establishing a recombinant prokaryotic expression plasmid, which was termed as pET28a-HBc-N144-epitope (1+2). The steps were recommended as follows: we obtained the NspA gene sequence of MC58 strain in GenBank of NCBI. DNASTAR and IEDB software were used to screen the dominant peptides of NspA, and two selected fragments were inserted into the major immunodominant region (MIR) between 78-79 of HBc-N144 DNA sequences to create recombinant plasmid pET28a-HBc-N144-epitope (1+2). Next, Escherichia coli BL21 DE3 containing the fused plasmid pET-28a-HBc-N144-epitope (1+2) was cultured to induce the expression of target protein. And then the purified protein was identified by Western Blot.The formation of virus-like particles from chimeric protein was observed by negative staining

transmission electron microscopy (TEM).After that, BALB/c mice were vaccinated intramuscularly (i.m.) or intranasally (i.n.), we analyzed the immune response and protective effect.The specific antibody levels of IgG and its subclass in serum were determined by ELISA, IFN-γ, the IL-4 and IL-17A cytokines in the supernatant of splenocytes were detected by ELISA. Meanwhile, flow cytometry (FCM) was used to identify antigen-specific T-Cell responses elicited by splenocytes. Two weeks after the final immunization, we prepared a lethal dose of MC58 bacteria ,and MenB challenge test was performed. Then, the survival was recorded twice-daily until day 14. Finally, SBA(serum bactericidal activity) assay was used to measure the functional antibody titers in immune sera against N. meningitidis, The reciprocal of the maximum serum dilution resulting in more than 50% decrease of the bacteria was defined as positive.
Results Mice immunized with HBc-N144-epitope(i.m. or i.n.) can produce high levels of specific antibodies, and the ratio of IgG1/IgG2a is greater than 1, which means a Th2 biased immune response. The flow cytometry (FCM) result confirmed that the HBc-N144-epitope(1+2) immunization could lead to a Th2 tendentious immunity. The HBc-N144-epitope(1+2) vaccine also induced increased IL-4, IFN-γ and IL-17A cytokines in splenocyte supernatants. Following intraperitoneal infection with N. meningitidis MC58, we found that this epitope vaccine based on HBc can confer an obvious protective efficacy. Furthermore, serum bactericidal activity（SBA） correlated with the i.m. vaccination was up to 1:32 after giving a booster injection. We used pathology analysis to investigate the effects of vlp vaccination on inflammatory response at injection sites. Muscle tissues at the inoculation site of intramuscularly immunized mice and lung tissues from the intranasally immunized mice were collected for pathological sections to assess the inflammatory cell infiltration. The result shows that the muscles collected from mice i.m. immunized with HBc-N144-epitope(1+2) vlp revealed no obvious inflammatory response, while the lung pathological analysis of mice to i.n. vaccination with HBc-N144-epitope(1+2) vlp exhibited a mild scattered inflammatory infiltration compared with the mice i.m. vaccination with HBc-N144-epitope(1+2) vlp.
Conclusion The study proved that i.m. or i.n. immunization with HBc-N144-epitope(1+2) may provide a novel and efficient tactic for the exploration of a vaccine against the MenB infection.

PU-1303

血清抗缪勒氏管激素在多囊卵巢综合征诊断中的临床价值

项国谦
杭州市第一人民医院

目的 探讨多囊卵巢综合征患者（polycystic ovary syndrome, PCOS）血清抗缪勒氏管激素（anti-mullerian hormone, AMH）水平变化及临床诊断价值。
方法 检测实验组 110 例 PCOS 患者、对照组年龄匹配的 70 例健康女性血清 AMH、睾酮（T）、卵泡刺激素（FSH）、黄体生成素（LH）、催乳素（PRL）、雌二醇（E2）、孕酮（P）、性激素结合球蛋白（SHBG）、脱氢表雄酮（DHEAS）、甘油三酯（TG）、总胆固醇（TC）、高密度脂蛋白胆固醇（HDL-C）、低密度脂蛋白胆固醇（LDL-C）、葡萄糖（GLU）和空腹胰岛素（INS）水平；同时通过构建受试者工作特征 (receiver operating characteristic, ROC) 曲线以及分析曲线下的面积 (area under ROC curve, AUC) 来分别评价 AMH 单独及联合其它血清学指标对 PCOS 的诊断效能。
结果 PCOS 患者 AMH 水平与对照组比较，差异有统计学意义（P＜0.05），且 PCOS 组血清 AMH 与 T、LH 呈正相关（P＜0.05）；AMH 的临界值（cutoff）为 3.94ng/mL，诊断 POCS 的 ROC-AUC 为 0.858，灵敏度为 0.861，特异性为 0.776；AMH 联合检测 T、LH 的 ROC-AUC 为 0.873，灵敏度为 0.903，特异性为 0.761。
结论 PCOS 患者 AMH 水平显著升高，且联合 T、LH 检测指标能提高对 PCOS 的诊断效能。

PU-1304

骨髓增生异常综合症患者中的 NOTCH1 基因变异

毕莉、董丽梅
哈尔滨医科大学附属第一医院

背景 Notch1 基因变异出现在半数以上的 T-ALL 患者中，对 T-ALL 的发生发展有着重要的意义。我们希望通过本试验在骨髓增殖异常综合症（MDS）患者中寻找 Notch1 基因变异。对象：20 例骨髓增殖异常综合症（MDS）患者的骨髓细胞。
方法 应用 nested-PCR 法，银染色-SSCP，direct sequencing 法分析。
结果 在患者 1 的白血病细胞中发现，在地 27 号外显子的第 5097 个对偶基因的 G 变异为 A。然而这个变异是在基因库中可查找的 SNP。
结论 在 MDS 患者中没有发现 Notch1 基因的变异。

PU-1305

TCS 通过 RAGE/NF-κB 信号通路调节 MDSCs 从而改善 STZ 诱导的小鼠糖尿病

殳洁、盛慧明
上海交通大学医学院附属同仁医院

Including various immature antigen-presenting cells (APCs), myeloid-derived suppressor cells (MDSCs) are implicated in immune regulation. Trichosanthin (TCS) was shown to induce APC-mediated immune regulation. Here, we investigated that MDSCs were involved in molecular mechanism of the therapeutic effect of TCS on streptozotocin (STZ) induced type 1 diabetes mellitus (T1DM). TCS treatment significantly decreased fasting blood glucose, glycosylated hemoglobin and significantly alleviated islet inflammation with reduced inflammatory factors IL-6 in the peripheral blood. In addition, the proportion of bone marrow MDSCs, and IL-6+ MDSCs decreased, while the proportion of IL-10+ MDSCs increased. Moreover, we found that the mRNA expression of arginase 1 (Arg1), inducible nitric oxide synthase (iNOS), advanced glycation end product receptor (RAGE) and NF-κB in MDSCs was significantly downregulated. These findings demonstrated that TCS treatment alleviated diabetic symptoms in STZ-induced T1DM mice through downregulation of RAGE/NF-κB signaling pathway in MDSCs.

PU-1306

S100B 蛋白的临床意义及研究进展

凌芸、薛丽、杨淑娴、陈蓉
江苏省人民医院（南京医科大学第一附属医院）

目的 S100 蛋白是一类酸性低分子量 Ca2+ 结合蛋白，由 α、β 两种亚基组成。在哺乳动物的中枢神经系统中，S100 蛋白主要由神经胶质细胞合成和分泌，其中 S100B 钙结合蛋白就是最为重要的一种。它在各种体液中的含量被认为是多种疾病的生物标志。因此，检测 S100B 蛋白水平，可协助了解中枢神经系统疾病，特别是累及神经胶质细胞的损伤。
方法 本文根据近几年相关文献对 S100B 蛋白的检查方法、临床意义及研究进展做一个综述。
结果 随着临床和医学界对 S100B 蛋白的重视，S100B 蛋白的检测方法和临床应用也在飞速地发展。
结论 S100B 蛋白的检测将会成为一种有效的工具。而随着不断地研究，未来可能会发现 S100B 蛋

白对更多疾病的意义与作用。这样将有助于临床医师对更多疾病进行早期诊断、病情进展评估及预后判断。

PU-1307

急性肾损伤早期标志物的研究进展

唐凯宏、金英玉
哈尔滨医科大学附属第一医院

急性肾损伤(acute kidney injury,AKI)是重者患者的常见并发症，其延长重症患者住院时间、影响患者预后，增加了重症患者的病死率。早期识别急性肾损伤并进行早期干预至关重要。目前急性肾损伤的诊断标准仍是以血清肌酐和尿量的变化为主。但由于血清肌酐的滞后性及受多种因素影响，使其并非为理想的急性肾损伤早期诊断标志物。目前，已有多种急性肾损伤早期标志物受到广泛研究，包括血清胱抑素 C（CysC）、视黄醇结合蛋白(RBP)、中性粒细胞明胶酶相关脂质运载蛋白(NGAL)、肾损伤因子 1(KIM-1)、可溶性髓样细胞触发受体-1（sTREM-1）、基质金属蛋白酶组织抑制因子-2（TIMP-2）、胰岛素样生长因子结合蛋白 7(IGFBP-7)、微小 RNA(miroRNA)、N-乙酰基 β-氨基葡萄糖苷酶(NAG)、白介素-18（IL-18）、白介素-6（IL-6）IL-6、白介素-5（IL-5）等。这些急性肾损伤的早期标志物有些已经应用于临床，应用于临床的指标中，对患者急性肾损伤的早期诊断仍存在不足，导致目前诊断急性肾损伤主要还是依靠血清肌酐的变化。有些指标尚处于临床前的研究阶段。目前对于急性肾损伤的早期识别和诊断非常急迫，而目前国内外报道多种急性肾损伤指标都只在研究阶段。对于这些指标的继续探索和应用方法需要进一步研究。本文综述目前对急性肾损伤有意义的多种指标。探讨每种指标在诊断急性肾损伤的优势，讨论其联合使用是否有更大意义。

PU-1308

血清抗 CHrom 抗体的检测分析与临床价值探讨

何增品
昆明医科大学第一附属医院

目的 探讨临床应用流式点阵免疫发光法测定的血清抗 chrom 抗体联合其他血清抗体在临床诊断中的意义，为疾病的诊断提供依据。
方法 选择 2019 年 1 月至 2021 年 4 月昆明医科大学第一附属医院就诊的 312 例血清抗 CHrom 抗体阴性（<0.2）的患者作为阴性组，169 例血清抗 CHrom 抗体阳性（≥0.2）的患者作为阳性组。对所有两组患者的一般资料、临床诊断、抗双链 DNA 抗体（ds-DNA）、抗核糖体 p 蛋白抗体（RIB）、抗 SM 抗体、抗 RNP 抗体进行对比分析，总结其临床诊断的意义。
结果 抗 CHrom 抗体阴性组患者男性 120 例，女 192 例，男女比例为 1:1.60；抗 CHrom 抗体阳性组患者男性 65 例，女 104 例，男女比例同样为 1:1.60，两组患者的性别比无显著性差异（P>0.05）。抗 CHrom 抗体阴性组患者年龄范围 28-79 岁，平均为 49±1.19 岁；抗 CHrom 抗体阳性组患者年龄范围 27-68 岁，平均为 48±2.01 岁。两组患者年龄无显著性差异（P>0.05）。与抗 CHrom 抗体阴性患者相比，抗 CHrom 抗体阳性患者的抗 ds-DNA 比例最高，其次是抗 RIB 比例，分别为 49.70%和 33.14%，均与阴性组患者相比具有显著性差异，P 值均为 0.002。而抗 SM 抗体以及抗 RNP 抗体，两组患者间无显著性差异（P>0.05）。与抗 CHrom 抗体阴性患者相比，抗 CHrom 抗体阳性患者的中诊断确诊病例最多的为类风湿关节炎和结缔组织病，均为 36 例，占 21.30%；第二的为系统性红班狼疮，病例 32 例，占 18.93%，两组具有显著性差差异（P<0.05）。

结论 抗 CHrom 阳性患者以中老年女性为主，临床相关诊断主要为类风湿关节炎、结缔组织病以及系统性红斑狼疮，抗 CHrom 抗体阳性患者的抗 ds-DNA 比例最高，其次是抗 RIB。使用流式点阵免疫发光法检测的抗 CHrom 抗体联合抗 ds-DNA 以及抗 RIB 对疾病的诊断与鉴别诊断有重要意义。

PU-1309

Autophagy induced by micheliolide alleviates acute irradiation-induced intestinal injury via inhibition of the NLRP3 inflammasome

jin li
The First Affiliated Hospital of Chengdu Medical College

Purpose Radiation-induced enteropathy (RIE) is one of the most common and fatal complications of abdominal radiotherapy, with no effective interventions available. Pyroptosis, a form of proinflammatory regulated cell death, was recently found to play a vital role in radiation-induced inflammation, and may represent a novel therapeutic target for RIE. Micheliolide (MCL) has shown promising anti-inflammatory, immunomodulatory, and therapeutic efficacy against multiple forms of cancer. Therefore, we postulated that MCL may play a promising role in the treatment of RIE, and investigated the therapeutic effects of MCL in RIE and evaluated the possible mechanisms by which it may be therapeutic.
Materials and Methods We screened a high-throughput pyroptosis drug library with 441 compounds and found that MCL exerted anti-radiation effects and blocked pyroptosis in vitro. Furthermore, we developed a mouse model of RIE by exposing C57BL/6J mice to abdominal irradiation.
Results MCL treatment significantly ameliorated radiation-induced intestinal tissue damage, inflammatory cell infiltration, and pro-inflammatory cytokine release. Moreover, MCL markedly inhibited radiation-induced activation of the nucleotide binding domain leucine-rich repeat-containing receptor - pyrin domain containing 3 (NLRP3) and suppressed pyroptosis in vivo. Furthermore, we observed that MCL treatment induced autophagy, which inhibited activation of the NLRP3 inflammasome and prevented caspase-1-dependent interleukin (IL)-1β and IL-18 secretion. In agreement with these observations, the beneficial effects of MCL treatment in RIE were abolished in Becn1+/- mice. Furthermore, super-resolution microscopy revealed a close association between NLRP3 and lysosome-associated membrane protein/ light chain 3-positive vesicles following MCL treatment, suggesting that MCL facilitates phagocytosis of the NLRP3 inflammasome.
Conclusion MCL-mediated induction of autophagy can ameliorate RIE by NLRP3 degradation, and identify MCL as a novel therapy for RIE.

PU-1310

丙型肝炎病毒亚型的 E1、E2 变异性分析

周海舟、张萱
哈尔滨医科大学附属第一医院

目的 了解丙肝病毒几种亚型（1a、1b、2a、2b、3a、4a、5a 和 6a）包膜基因变异性。
方法 我们用相应的软件分析了丙肝病毒包膜蛋白（E1、E2）的核苷酸和氨基酸序列，计算了这些包膜基因的非同义突变与同义突变的比值(dN/dS)，并预测 E1 和 E2 的糖基化位点。
结果 我们发现在丙肝病毒 1b 亚型内，E1 与 E2 相比变异性更大、dN/dS 值更大、糖基化位点更多。
结论 E1 蛋白可能在 HCV 免疫机制中起到重要作用，尤其是在 1b 亚型内，E1 内基因更大的变异

性、更高的 dN/dS 值和更多的糖基化位点数足以证实这点；因此 E1 区域应该在未来有关 HCV 药物抵抗性和免疫机制的研究中纳为一个重要因素。

PU-1311

TNFAIP3 Gene Polymorphisms Associatied with differential Susceptibility to Juvenile Idiopathic Arthritis, Childhood-Onset Systemic Lupus Erythematosus in the Chinese population

刘新乐、张梦兰、柳晓琴、段义飞、颜灵逸、李文胜、江咏梅
四川大学华西第二医院

We investigated the relationship between polymorphisms in the TNF-a-induced protein 3(TNFAIP3) gene and genetic susceptibility to JIA and cSLE in the west China.The present case-control study included 165 patients with JIA, 151 patients with cSLE and 302 healthy controls. Genotyping for TNFAIP3 gene polymorphisms rs2230926, rs3757173 and rs5029939 in TNFAIP3 gene polymorphisms was performed. Significantly different frequencies of minor alleles in three TNFAIP3 polymorphisms were found in patients with cSLE compared with healthy controls (P= 0.02). Moreover, patients with cSLE showed different frequencies of haplotypes and lower level of TNFAIP3 in the serum compared with healthy controls (P=0.01). However, no association was found between JIA susceptibility and TNFAIP3 polymorphisms (P= 0.54). The results suggest that TNFAIP3 gene polymorphisms are associated with differential susceptibility to cSLE and JIA in the Chinese population.

PU-1312

血清心肌标志物检测的临床意义

杜柏岩、姜玉玲
哈尔滨医科大学附属第一医院

目的 探讨冠心病患者血清 hs-CRP、TnI、CK-MB 测定的临床意义。
方法 利用乳胶增强免疫比浊法和电化学发光法，对 112 例健康人群和 52 例急性心肌梗死（AMI），64 例不稳定性心绞痛（UA），32 例稳定性心绞痛（SA）患者检测超敏 C 反应蛋白（hs-CRP）、肌钙蛋白 I(TnI)和肌酸激酶（CK-MB）水平。
结果 SA 组、UA 组和 AMI 组 hs-CRP、TnI、CK-MB 水平明显高于健康组（P<0.05）。
结论 hs-CRP 是心血管疾病的独立危险因素，与 TnI、CK-MB 联合检测对冠心病的诊断、治疗及预后判断有重要意义。

PU-1313

血浆 BNP 水平检测对于心衰患者的诊断意义

杜柏岩、郭欣
哈尔滨医科大学附属第一医院

目的 探讨血浆 BNP 水平检测对于心衰患者的诊断意义。
方法 对 107 例心衰患者和 50 例健康体检者采用化学发光微粒子法测定血浆脑钠肽（BNP）水平。心衰患者根据美国 NYHA 心功能分级分成 I、II、III、IV 级四组。

结果 正常对照组与心衰组 BNP 水平及阳性率差异极显著，P<0．001。NYHA 心功能分级各级之间均差异显著，有统计学意义（P<0．01）；并且随着分级的增高，BNP 水平也明显升高，除 I 级中有一例阴性外，其他阳性率均为 100%。
结论 血浆 BNP 水平对于心衰的诊断、预后判断及指导治疗等方面具有重要意义。在筛选 LVD 方面具有明显的优越性，是评估心功能的一项重要指标。

PU-1314

异常凝血酶原检测在肝脏疾病中的诊断价值研究

张运丽[1]、黄逸[2]、赵声远[1]
1. 中南大学湘雅医院
2. 中南大学湘雅医学院医学检验系

目的 探讨血清异常凝血酶原（PIVKA-Ⅱ）对肝炎病毒相关性肝脏疾病的临床诊断价值。
方法 选择中南大学湘雅医院于 2020 年 6 月-2021 年 3 月收治的慢性肝炎患者 51 例（慢性肝炎组）、肝炎肝硬化患者 57 例（肝硬化组）、原发性肝细胞癌患者 70 例（原发性肝细胞癌组）以及健康体检人群 105 例（健康对照组）。比较四组人群 PIVKA-Ⅱ、AFP、ALP、γ-GT 水平，分析其在肝炎、肝硬化和原发性肝细胞肝癌等肝脏疾病中 PIVKA-Ⅱ和 AFP 水平的相关性，分析 AFP、PIVKA 单项检测与二者联合检测对于原发性肝细胞癌诊断价值。
结果 原发性肝癌组血清 PIVKA-Ⅱ和 AFP 水平高于肝硬化组，差异具有统计学意义（P < 0.05）。良恶性肝脏疾病中 PIVKA-Ⅱ和 AFP 水平呈现正相关，r=0.56。PIVKA-Ⅱ诊断 HCC 的 AUC 为 0.858，灵敏度为 97.1%，特异度为 61.5%；AFP 诊断 HCC 的 AUC 为 0.717，灵敏度为 71.4%，特异度为 67.3%。
结论 在病毒相关性肝脏良恶性疾病中，对于原发性肝细胞癌的诊断，血清异常凝血酶原具有重要价值，诊断效能优于 AFP，对临床诊断有重要参考作用。

PU-1315

补体 C3、C4 和 LDH 在多发性骨髓瘤中的临床应用

朱萍
资阳市第一人民医院

目的 探讨补体 C3、C4 和 LDH 在多发性骨髓瘤中的应用价值。
方法 选取资阳市第一人民医院 2016 年 8 月至 2021 年 1 月收治的多发性骨髓瘤 80 例，其中Ⅰ期 38 例，Ⅱ期 23 例，Ⅲ期 19 例。同时收集同期健康体检者 50 例作为对照组。检测全部受检者的补体 C3、C4、LDH 含量。
结果 病例组补体 C3、C4 含量均有不同程度的降低，均低于对照组，差异有统计学意义（P<0.05）；Ⅰ期补体 C3、C4 含量低于对照组，差异有统计学意义（P<0.05）；Ⅱ期补体 C3、C4 含量低于Ⅰ期，差异有统计学意义（P<0.05）；Ⅲ期补体 C3、C4 含量低于Ⅱ期，差异有统计学意义（P<0.05）；Ⅰ期、Ⅱ期 LDH 含量与对照组相比无统计学意义，Ⅲ期 LDH 含量明显高于Ⅰ期、Ⅱ期，差异有统计学意义（P<0.05）；骨髓瘤细胞比例、单克隆免疫球蛋白含量与补体 C3、C4 和 LDH 含量具有相关性（P<0.01）。
结论 补体 C3、C4 含量在多发型骨髓瘤中均有不同程度降低，LDH 含量有不同程度升高，可以预测疾病发展，在诊断和疾病分期中发挥重要作用。

PU-1316

高敏肌钙蛋白 T 诊断心肌损伤临界值设定的探讨

凌芸、丁红梅、王敏、张小莉
江苏省人民医院（南京医科大学第一附属医院）

目的 血清高敏肌钙蛋白 T（high sensitivity-cardiac troponin T，hs-cTnT）诊断心肌损伤时是否有必要建立年龄和性别的特异性临界值。建立临界值时如何选择参考人群以及如何正确选用临界值等方面存在着较大的争议。实际工作中临界值的使用参差不齐，不合理的临界值会误导临床决策而产生严重的后果。
方法 本文通过综述相关文献，对以上问题进行了探讨。
结果 我们认为使用年龄特异性临界值不如采用持续监测 hs-cTnT 的变化。hs-cTnT 在诊断新生儿心肌损伤的使用尚待深入研究。临床针对 hs-cTnT 可纳入性别特异性临界值，但需要可靠的方法证明其诊断心肌损伤的改善作用并且建立临界值。建立临界值选择参考人群时每组健康群体至少 300 人，男女均分，同时选择年轻和年长，分布在 20-70 岁之间，筛选时应纳入病史、用药史，排除心肾功能障碍和糖尿病等疾病。
结论 选用临界值时，绝对值可作为预后评估的指标，变化值可鉴别诊断急性心肌损伤，动力学监测和绝对值临界值应当结合使用，并注意要结合其他诊断手段做出全面可靠的评估。

PU-1317

PCT 及超敏 CRP 在新生儿败血症诊断中的应用探讨

罗小庆
资阳市第一人民医院

目的 探讨 PCT、hs-CRP、红细胞沉降率、白细胞计数及中性粒细胞杆状核/分叶核(I/T)比值的测定在新生儿败血症早期诊断中的价值.
方法 选取患有败血症的新生儿(84 例)和同时期在同病区收治的非感染性疾病患儿(84 例,对照组),采集败血症患儿静脉血测定其治疗前的 PCT、hs-CRP、红细胞沉降率、白细胞计数及 I/T 比值,并与对照组进行比较.
结果 败血症组 PCT、hs-CRP 与对照组比较差异有统计学意义(P＜0.05),红细胞沉降率、白细胞计数及 I/T 比值与对照组相比差异无统计学意义(P＞0.05).PCT 诊断新生儿败血症时的临界值为 0.5 ng/ml,此时敏感度为 73.8％,特异度为 80.9％.hs-CRP 诊断新生儿败血症的临界值为 3 mg/dl,此时敏感度为 54.8％,特异度为 76.2％.PCT 联合 hs-CRP 在诊断新生儿败血症时敏感度为 85.7％,特异度为 88.1％.
结论 PCT 及联合检测 PCT、hs-CRP 对新生儿败血症的早期诊断具有一定价值,PCT 是诊断新生儿败血症价值较高的指标.

PU-1318

基于纳米抗体对黄曲霉素 B1 的直接免疫法检测

陈梦园[1]、孙倩[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学中大医院，临床检验医学中心
3. 东南大学江苏省重症重点实验室

食品安全作为全球最重要的问题之一，受到人们的极大关注。而黄曲霉毒素 B_1（AFB_1）是一种毒性最强的真菌毒素，广泛存在于各种食品和农产品中，严重威胁到人类的生命健康，亟待开发

出准确灵敏检测 AFB_1 的简单方法。而 AFB_1 作为小分子因其尺寸小，使得大分子的单抗隆抗体难以对其产生有效的特异性识别，致使传统的传感策略难以产生可检测的信号。为解决上述问题，我们课题组使用分子量更小的纳米抗体（常规抗体的 1/10）与纳米材料结合。具体来说，利用普鲁士蓝作为电化学信号探针，氧化石墨烯/芘四甲酸二酐衍生物（GO/$PTCNH_2$）修饰在玻碳电极上用于信号放大，纳米抗体偶联在 GO 表面，通过目标物与纳米抗体的特异性识别，使得电化学信号与目标物浓度呈线性关系，从而达到对小分子 AFB_1 的准确定量检测。该免疫传感器具有 0.01-100 ng mL^{-1} 的检测范围，同时检测限低至 3.3pg mL^{-1} (S/N=3). 与传统间接免疫分析中使用的单克隆抗体制备的免疫传感器相比，该免疫传感器的线性范围宽了两个数量级，且灵敏度提高了 10 倍。另外，该方法被成功运用到实际样品中 AFB1 的检测。此法为 AFB1 的直接免疫检测提供了一种简单、高灵敏度和高选择性的方法。此传感体系在食品安全领域，将新开发的纳米抗体作为识别单元，为小分子的直接非竞争性免疫分析开辟了一条新的途径。

PU-1319

肿瘤标志物 CA724 在原发性胃癌及胃炎患者中的诊断鉴别价值

丁洁颖、吴紫娴、张晗
上海交通大学医学院附属第九人民医院

目的 探讨肿瘤标志物 CA724 在原发性胃癌及胃炎患者中的诊断鉴别价值及效能 ROC 曲线。
方法 选择 2018 年 1 月-2020 年 12 月原发性胃癌患者 146 例设为观察组；选择同期治疗的胃炎患者 89 例为对照 1 组；选择同期健康体检者 91 例为对照 2 组。采用电化学发光免疫分析法测定各组糖类抗原 CA724 水平；查阅观察组患者病理资料，分析不同病理状态下肿瘤标志物 CA724 表达水平；绘制 ROC 曲线，分析 CA724 在胃癌、胃炎中的诊断鉴别价值。
结果 对照 1 组和对照 2 组肿瘤标志物 CA724 水平无统计意义（P>0.05）；观察组肿瘤标志物 CA724 水平均高于对照 1 组和对照 2 组（P<0.05）；原发性胃癌患者肿瘤标志物 CA724 水平与肿瘤直径、肿瘤分期、分化类型、淋巴结转移具有统计学意义（P<0.05）；以肿瘤标志物 CA724 截断值为 7.94U/mL，绘制 ROC 曲线，结果表明：肿瘤标志物 CA724 用于原发性胃癌患者中 AUC 值为 0.815，诊断灵敏度为 84.68%，特异度为 71.95%。
结论 肿瘤标志物 CA724 在原发性胃癌患者中呈高表达，能实现胃癌及胃炎的诊断鉴别，可获得较高的诊断效能，为临床诊疗提供参考依据。

PU-1320

ELISA 联合荧光定量 PCR 检测丙型肝炎病毒的临床效果

丁燕
武城县人民医院

目的 分析丙型肝炎病毒检测中联合应用酶联免疫吸附法（ELISA）与荧光定量 PCR 法的价值。
方法 选取 2019 年 1 月～2020 年 12 月期间在我院接受检查的疑似丙型肝炎病毒感染患者 92 例，采集血液标本，分别采用 ELISA 法和荧光定量 PCR 进行检测，比较不同方法检测效果。具体为：（1）ELISA 检测，在酶标孔中加入样品稀释液 100μL，在相应孔中加入待测样本 10μL。并另外设置 2 个阳性对照孔和 3 个阴性对照孔，在各对照孔中加入 100μL 的阳性或阴性对照，操作完成后，实施封板，并将样品置于 37℃环境下，温育 1 小时。对其进行 5 次洗涤处理后，在各孔中分别加入酶标记物 100μL，在同样的温度条件下实施半小时的温育，再次洗涤 5 次后，在各孔中加入底物缓冲液和底物液各 50μL。将其充分混匀后，置于 37℃条件下温育半小时后，在各孔中加入终止液 50μL，然后使用酶标仪对其结果进行测定，严格按照说明书进行操作。（2）荧光定量 PCR 检测，使用核酸提取试剂盒，在反应孔中加入样品 200μL，然后加入 10μL 的 Protein-asek 和 4μL 的 Acryl

carrier，上机自动处理，操作完成后，取 20μL 上清液加入到分装好的反应扩增管中，对其进行 PCR 定量扩增检测，所有操作均严格按照使用要求完成。
结果 92 例疑似患者经病理等检查确诊为阳性 42 例，阴性 50 例，将其作为判断标准，ELISA 与 PCR 联合检测的准确度 94.56%，特异度 96.00%，阳性预测值 95.12^%，与单独 ELISA 或单独 PCR 检测结果比较均显著较高，差异有统计学意义（P＜0.05）。
结论 ELISA 与荧光定量 PCR 联合应用，能够显著提升临床对丙型肝炎病毒的阳性检出率及准确率，减少漏诊等情况出现，可推广应用。

PU-1321

抗核抗体谱检测结果应用

李军、许桂荣、程绍民、王倩、李新
禹城市人民医院

目的 分析自身免疫性抗体的分布，探索抗核抗体谱对自身免疫性疾病的诊断价值；
方法 收集 2018 年 6 月—2020 年 12 月我院确诊及待诊的自身免疫性疾病患者共 703 例，均采用欧蒙印迹法进行抗核抗体谱检测；
结果 抗核抗体谱检测阳性为 312 例，阳性率为 44.38%，男性检出率（28.00%）低于女性检出率（53.19%）；50 岁以下患者（32.12%）阳性率低于 50 岁以上患者（53.62%）；在系统性红斑狼疮 SLE、混合型结缔组织病 MCTD、干燥综合征 SS、类风湿性关节炎 RA 中有较高的检出率；
结论 针对特定人群检测抗核抗体谱对自身免疫性疾病的筛查及早期治疗和预防有重要的作用。

PU-1322

尿液结合珠蛋白联合微量白蛋白肌酐检测在筛查糖尿病早期肾损伤中的临床应用

王春玲、时彦、芦慧霞
东南大学附属中大医院检验科

目的 研究尿液中结合珠蛋白联合尿微量白蛋白/肌酐检测在评估糖尿病肾损伤中的临床应用价值。
方法 收集临床明确诊断为 2 型糖尿病（无明显肾损害依据）患者的尿液样本 35 例，分别采用双抗体夹心免疫层析法、散射免疫比浊法、苦味酸法同时进性尿液结合珠蛋白、微量白蛋白、肌酐的定量检测。
结果 35 例样本中，尿微量白蛋白/肌酐比值检测阳性 15 例（95%CI 3.46-12.85,cutoff:3.39mg/mmol)，阳性率 42.9%；尿液结合珠蛋白/肌酐比值检测阳性 15 例（95%CI 8.33-21.03,cutoff:7.0μg/mmol)，阳性率 42.9%。尿液结合珠蛋白联合尿微量白蛋白及肌酐检测阳性 20 例，阳性率 57.1%，较单检尿微量白蛋白/肌酐阳性率提高 14.2%。
结论 尿液结合珠蛋白与微量白蛋白、肌酐联合检测能够提高糖尿病早期肾损伤的阳性检出率，可作为糖尿病早期肾损伤筛查和预测指标。

PU-1323

一种无金属全碳纳米复合物用于甲胎蛋白的超灵敏光电化学检测

陈梦园[1]、杨二利[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学中大医院，临床检验医学中心
3. 东南大学江苏省重症重点实验室

光电化学（PEC）生物传感因同时具备光化学方法和电化学技术的优势，受到研究者的广泛关注。为降低生物环境毒性，提高材料的生物兼容性，寻找新型光活性材料一直是研究热点。C_{60} 作为富勒烯的一种，能够可逆接受 6 个电子且在整个紫外-可见光区拥有良好的吸收性能，为其作为光活性探针提供优势。而其因导电性差、与生物分子的界面连接活性低致使在 PEC 生物传感领域少有报道。为此，我们通过简单的机械研磨将将高电导率的石墨片(Gr)、具有足够含氧官能团的氧化石墨烯(GO)和烷基化的 C_{60}(AC_{60})组装成无金属全碳纳米杂化物(AC_{60}-Gr-GO)。所制备的 AC_{60}-Gr-GO，一方面与原始 AC60 相比，光电流强度提高 35 倍；另一方面为生物分子偶联提供了丰富的活性位点。以甲胎蛋白（AFP）作为目标物，将其作为光活性探针与抗 AFP 连接，使得检测体系中的目标物含量与 PEC 信号的提高成正比，制备出了一种“signal on”型 PEC 传感器。该传感器具有较宽的线性检测范围（1pg·mL^{-1}-100 ng·mL^{-1}）以及检测限达到 0.54pg·mL^{-1}。这项工作展现出了基于富勒烯的纳米杂化物作为高灵敏的 PEC 探针在早期疾病诊断的生物传感方面的巨大潜力。

PU-1324

双抗原夹心 ELISA 检测丙肝抗体与 RIBA 确证阳性的相关性研究

刘义庆[1,2]、张庆[1,2]、邱旸[1,2]、刘春梅[1,2]、鞠瑛[1,2]、卢志明[1,2]
1. 山东第一医科大学附属省立医院
2. 山东省立医院

目的 探讨双抗原夹心 ELISA 检测抗-HCV 与重组免疫印迹试验（RIBA）确证结果的关系。
方法 对 10120 例在山东大学附属省立医院就诊的患者标本采用双抗原夹心 ELISA 法进行抗-HCV 检测，对检测阳性的标本做 RIBA 确证。
结果 双抗原夹心 ELISA 检测抗-HCV 抗体阳性的标本共计 51 份，采用 RIBA 对 51 份阳性标本进行检测，确认阳性 38 份、不确定 13 份，阴性 0 份，确认阳性比例为 74.51%，且确认阳性标本比例与 S/CO 比值相关。
结论 双抗原夹心 ELISA 法特异性高，可根据双抗原夹心 ELISA 法 S/CO 比值预测 RIBA 确证结果。

PU-1325

系统性红斑狼疮血清 tsRNA 标志物研究

张孝山、李智洋
南京市鼓楼医院

系统性红斑狼疮（Systemic lupus erythematosus，SLE）是一种损伤全身器官的自身免疫性疾病，狼疮性肾炎（Lupus nephritis，LN）是其最常见的一种并发症。tsRNA 是 tRNA 在外界压力或酶的作用下断裂形成，前人研究表明 tsRNA 在生物体各个生理和病理时期的丰度变化差异显著。本研究旨在从 SLE 病人血清中筛选 tsRNA 标志物，以期为该病的早期诊断、及时治疗提供科学依据。研究以临床诊断为 SLE 和健康体检病人的血清为材料，通过 RNA 提取、sRNA 高通量测序、

生物信息学分析、实时荧光定量聚合酶链式反应（Real Time Quantitative PCR，RT-qPCR）验证等方法筛选候选 tsRNA。试验表明，SLE 血清中 tsRNA 的表达特征与健康组差异显著，其中 tRF-1:28-His-GTG-1 在 SLE 组中显著高表达（P<0.001），受试者工作曲线（ROC）下面积为 0.6650（P=0.0012）。研究表明，SLE 血清中的 tsRNA 的表达谱相比健康对照组差异显著，提示 tsRNA 可能在 SLE 的发生发展中发挥重大作用；tRF-1:28-His-GTG-1 的表达水平显著上调，可以区分健康人、SLE 患者，具有成为 SLE 早期诊断和疗效检测标志物的潜力。

PU-1326

毛兰素对头颈鳞癌细胞的生长抑制作用及其机理研究

罗清琼、陈福祥
上海交通大学医学院附属第九人民医院

目的 探讨毛兰素对人头颈鳞癌（HNSCC）细胞的生长抑制作用及其机理。
方法 通过 MTT 和克隆形成实验探讨毛兰素对 HNSCC 细胞体外生长的影响；通过流式细胞术分析毛兰素对 HNSCC 细胞周期、凋亡和细胞内活性氧（ROS）生成的影响；分别通过酶联免疫吸附法和终点比色法检测细胞培养上清中白介素 1b（IL-1b）和乳酸脱氢酶（LDH）的量；采用免疫印迹实验探究毛兰素影响 HNSCC 细胞生长的作用机制。
结果 毛兰素能够明显抑制 HNSCC 细胞的活力和克隆形成能力。毛兰素能够下调 CDC25c 和 p-CDC2 的表达而上调 cyclin B1 水平，将 HNSCC 细胞的周期阻滞于 G2/M 期；可以上调促凋亡蛋白 Bax 和 cyto C 的表达，下调抗凋亡蛋白 Bcl-2A1 的表达水平，从而促进细胞内 caspase-9 和 caspase-3 的剪切活化，继而使 PARP 的剪切增加,导致 HNSCC 细胞发生凋亡；能够增加 HNSCC 细胞中的 ROS 水平,可能通过影响线粒体膜的稳定性而促进凋亡的发生；此外,还可引起 GSDME 介导的细胞焦亡。
结论 毛兰素可以抑制 HNSCC 细胞的体外生长，在 HNSCC 的治疗中具有潜在的应用前景。

PU-1327

乙肝患者血清 Pres1-Ag 和 HBsAg 及 HBeAg 相关性分析

刘义庆[1,2]、张庆[1,2]、邱旸[1,2]、刘春梅[1,2]、鞠瑛[1,2]、卢志明[1,2]
1. 山东第一医科大学附属省立医院
2. 山东省立医院

目的 分析乙肝患者血清 Pres1-Ag、HBsAg 和 HBeAg 三者之间的关系。
方法 采用电化学发光免疫分析法对 2015～2019 年 281628 例住院及门诊患者进行乙肝五项定量检测，酶促化学发光法检测 Pres1-Ag，并对结果进行统计学分析。
结果 共检出 HBsAg 阳性 12546 例，HBsAg 阳性率为 4.45％，2015-2019 年 HBsAg 阳性检出率分别为 4.56%、4.56%、4.49%、4.36%、4.34%，呈逐年下降趋势。乙肝患者中 HBeAg 阳性检出率为 24.85%，HBeAg 阳性患者 Pres1-Ag 阳性率为 93.52%，明显高于 HBeAg 阴性者的 75.40%（93.52% vs 75.40%，P<0.05）。乙肝患者 Pres1-Ag 阳性率为 79.91%，且阳性率随着患者 HBsAg S/CO 值增高呈升高趋势。
结论 乙肝患者 Pres1-Ag 与 HBsAg、HBeAg 具有良好的相关性，将 Pres1-Ag 可作为 HBsAg 和 HBeAg 检测的补充，预测乙肝病毒感染和复制。

PU-1328

探讨四代化学发光 HIV 筛查试剂在 AIDS 诊断中的应用

刘文清
资阳市第一人民医院

目的 将第四代人类免疫缺陷病毒（HIV）化学发光免疫分析（CLIA）试剂筛查阳性结果与免疫印迹试验（WB）结果进行比较,评估 CLIA 法 HIV 筛查在艾滋病诊断中的临床价值。
方法 CLIA 法对 2019 年 10 月-2020 年 12 月本院 64987 例患者进行 HIV 抗体初筛检测,复核阳性标本用 WB 法确证,确证阴性或者不确定样本进行核酸检测，记录结果并进行对比分析。
结果 CLIA 法初筛阳性送疾控中心 131 例,WB 确证阳性 120 例。其中不确定 2 例,经继续核酸检测均为高值，CLIA 初筛方法确证阳性率为 93.13%。核酸 9 例未检出，其中包含肿瘤和自身免疫性疾病患者各 1 例，且>50 岁的患者有 4 例，占假阳性的比率为 44.44%，老年患者的假阳性率占比较高，值得引起我们的重视。比较 1<COI≤10、10<COI 两组,WB 法获得的阳性率的差异有统计学意义（P<0.05）。
结论 CLIA 法筛查 HIV 在 COI 值>10 的样本中灵敏度和特异性均较高,但在 COI 值≤10 的样本中存在较高的假阳性率。方法学的更新确实加快了检测的自动化、报告的及时性以及阳性检出率，但如何减少假阳性，避免给患者带来较大的心理负担则是我们现在应该关注的重要内容。

PU-1329

血清 sST2、NT-proBNP 水平与血液透析患者发生心力衰竭的相关性分析

林胜
资阳市第一人民医院

目的 观察血清可溶性 st2（sST2）、N 末端脑钠肽前体（NT-proBNP）表达水平与血液透析患者发生心力衰竭的相关性。
方法 选取在我院血液透析中心行维持性血液透析（MHD）治疗的 100 例慢性肾功能不全尿毒症患者，依据是否发生心力衰竭，分为并发心衰组与未并发心衰组，比较 2 组一般资料、透析前后血清心肌酶[肌酸激酶同工酶-MB（CK-MB）、肌钙蛋白 I（cTn I）]、血肌酐（Scr）、sST2、NT-proBNP、心功能指标[心排出量（CO）、心脏指数（CI）与左室射血分数（LVEF）]，比较并发心衰组不同心功能分级患者血清 sST2、NT-proBNP 水平，分析血清 sST2、NT-proBNP 对心力衰竭的预测价值。
结果 并发心衰组透析后 CO、CI、LVEF 明显低于未并发心衰组（P＜0.05），且 CK-MB、cTn I、sST2 及 NT-proBNP 水平明显高于未并发心衰组（P＜0.05）；心力衰竭患者 sST2、NT-proBNP 水平为：II 级＜III 级＜IV 级，比较差异显著（P＜0.05）；sST2 预测心力衰竭敏感度 77.9%，特异度 68.1%；NT-proBNP 预测敏感度 91.8%，特异度 92.0%。
结论 血液透析并发心衰患者血清 sST2、NT-proBNP 表达水平呈异常升高趋势，心功能越差，升高程度越大，对心力衰竭具有较高预测价值。

PU-1330

山东地区 25-羟维生素 D 水平状况调查

陈瑞丹、刘义庆
山东第一医科大学附属省立医院临床医学检验部

目的 探讨山东省 5 181 例人群血清 25-（OH）维生素 D 水平与年龄、性别、季节之间的关系。
方法 采用整体抽样的方法收集 2014.3-2017.6 期间来我院就诊的血清标本，用电化学发光法检测血清 25-（OH）维生素 D 水平。根据性别、年龄和季节分组。年龄分成 9 组：0-9 岁，10-19 岁，20-29 岁，30-39 岁，40-49 岁，50-59 岁，60-69 岁，70-79 岁和≥80 岁。采用 SPSS17.0 软件对不同年龄、性别和季节的维生素 D 结果进行统计分析。
结果 1.不同性别之间比较：男性维生素 D 水平（17.11±11.75）ng/ml，女性为（15.08±11.73）ng/ml，稍高于女性，且数据具有统计学差异(P＜0.01)。2.不同年龄之间比较：0-9 岁和≥80 岁与其余各组相比具有统计学差异(P＜0.01)，其他各组之间无统计学差异（P＞0.05），0-9 岁维生素 D 水平为（26.99±17.28）ng/ml，明显高于其他各组。3.不同季节之间比较：春和夏，秋和冬之间数据具有统计学意义(P＜0.01)，且夏季维生素 D 水平最高（19.73±11.57）ng/ml，冬季最低（12.78±12.90）ng/ml。
结论 山东省人群维生素 D 营养状况存在性别、年龄和季节的差异，且普遍缺乏维生素 D。

PU-1331

灭活新型冠状病毒疫苗诱导的特异性抗体分析

陶月
南京大学医学院附属鼓楼医院

目的 动态监测灭活新型冠状病毒疫苗诱导的抗体水平。
方法 采用前瞻性队列研究。2021 年 1 月到 2021 年 2 月期间，招募本院 98 位健康受试者，接种新冠疫苗，采集接种前、第一次接种后第 14 天，第二次接种后第 14 天血清，检测血清中新冠病毒特异性 IgM、IgG 和阻断抗体。
结果 受试者接种新冠疫苗后，产生的新冠抗体 IgG 和阻断抗体转阳率均为 99%，新冠 IgG 和阻断抗体水平分别为 89.67（55.59,153.00）IU/mL 和 47.87（25.58, 99.99）IU/mL。另外，年龄和免疫间隔时间对人群新冠疫苗免疫应答有一定影响；而性别对新冠疫苗诱导的抗体免疫反应没有差异。
结论 灭活新冠疫苗诱导的抗体应答较好，年龄和免疫间隔时间对新冠疫苗免疫应答有一定影响。监测新冠疫苗诱导的抗体水平，将为新冠疫苗的免疫原性评价和免疫接种程序的优化提供最新重要参考依据。

PU-1332

成年人 EB 病毒感染者抗体特征分析

刘义庆[1,2]、张庆[1]、邱旸[1,2]、刘春梅[1,2]、鞠瑛[1,2]、卢志明[1,2]
1. 山东省立医院
2. 山东第一医科大学附属省立医院

目的 了解济南地区成年人 EB 病毒（EBV）感染者的抗体特征。
方法 检测 1472 例疑似 EBV 感染的成人血清样本中的 EB 病毒抗体，分析人群 EB 病毒感染情况。
结果 1472 例血清标本中，VCA IgG 阳性率为 95.58%，VCA IgM 阳性率为 5.30%，EA-D IgG 阳性率为 10.39%，EBNA IgG 阳性率为 93.95%。不同性别 EBV 感染者的 VCA IgM、EA-D IgG、

EBNA IgG 阳性率比较，差异无统计学意义（均 P >0.05）；男性 VCA IgG 阳性率为 94.54%，低于女性的阳性率 96.79%（P<0.05）。VCA IgG 阳性率以 18~29 岁最低，70~79 岁年龄组最高；VCA IgM 阳性率以 18~29 岁组最高（11.22%），60~69 岁年龄组最低（0.71%）；EA-D IgG 阳性率以 18~29 岁年龄组最低（6.92%），70~79 岁年龄组最高（16.92%）；EBNA IgG 阳性率以 50~59 岁组最高（97.61%），80 岁以上年龄组最低（90.48%）。VCA IgM 阳性率秋季和冬季分别为 6.40%和 6.35%，略高于春季的 4.62%和夏季的 4.37%（P 均>0.05），但无统计学差异。共检出 12 种 EB 病毒项目组合模式，以 VCA IgG、EBNA IgG 双阳性模式最多见，占 78.67%；EA-D IgG 和 EBNA IgG 双阳性模式最少见，占 0.07%。

结论 济南地区成年人群 EB 病毒抗体阳性率存在性别、年龄差异，季节间差异不明显。EB 病毒抗体组合感染模式以 VCA IgG 和 EBNA IgG 双阳性的既往感染模式为主，其它多种感染模式并存。多项抗体联合检测对 EBV 感染的判断具有重要的价值。济南地区成人中 EB 病毒感染以 18~29 岁年龄组人群感染率最高。

PU-1333

人 β 冠状病毒抗原的捕获抗体制备

武强
潍坊市人民医院

目的 冠状病毒抗原检测较核酸检测具有方便快速和对实验室要求低优势，较抗体检测具有检测无窗口期优势，冠状病毒抗原检测的常用方法为免疫层析法，用于捕获冠状病毒抗原的抗体是配制免疫层析试剂的关键原料，本文将制备同时识别五种人 β 冠状病毒（SARS-CoV-2, SARS-CoV，MERS-CoV，HCoV-HKU1 和 HCoV-OC43）N 蛋白的抗体，以获得一种冠状病毒抗体能够同时适用于所有人 β 冠状病毒抗原检测试剂的配制。

方法 采用 Clustal Omega 和 PyMOL 分析工具比对五种 β 冠状病毒 N 蛋白的氨基酸序列，获得同源序列 PRWYFYY 肽段，并进行不同方式修饰设计，如进行肽段-COOH 端半胱氨酸(C)修饰：PRWYFYY XXC，其中 C 为半胱氨酸提供游离-SH 与载体蛋白偶联，XX 作为肽段与载体蛋白之间的空间臂，X 为 F, G, W, Y, K 中的一种氨基酸，以合成肽段为半抗原再与载体蛋白（如牛血清白蛋白 BSA）偶联即可作为免疫抗原进行新西兰大白兔免疫，经过三次加强免疫后，取兔抗血清并进行纯化获得冠状病毒抗体。

结果 采用酶联免疫法（ELISA）检测免疫兔抗血清的抗体滴度可达 1：32000 以上，采用 Protein A 柱纯化抗体纯度大于 90%，纯化抗体与五种人 β 冠状病毒 N 蛋白均具有良好反应性。

结论 本文制备的冠状病毒抗体能够同时识别五种人 β 冠状病毒 N 蛋白，可用于不同冠状病毒抗原检测试剂（免疫层析法）的配制，大大降低不同种类冠状病毒抗体的研发成本，为冠状病毒疫情防控提供快速、可靠的检测原料；另外，本文列出的同源序列肽段经分析发现具有高度保守性， 说明该肽段是人 β 冠状病毒 N 蛋白的专有肽段序列，因此本文制备的冠状病毒抗体不仅可用于目前发现的人 β 冠状病毒抗原捕获，还极有可能适用于未来新发现人 β 冠状病毒种类的抗原检测，具有很好的技术储备意义。

PU-1334

降钙素原在新生儿非感染性疾病中的临床价值分析

何亮
资阳市第一人民医院

目的 研究在新生儿非感染性疾病中降钙素原的临床意义和影响因素。

方法 在对 300 列非感染性新生儿疾病患者中，在出生后的第一天、第三天、第七天挑选出 PCT 正常和 PCT 异常的部分进行分组，分别对其进行数据分析，其中包括性别、胎龄、体重、早产、剖腹产、抗生素的使用、呼吸机的使用等多种影响因素，通过使用统计学来分析影响 PCT 水平更重要的因素。
结果 有 8.4%第一天升高，31.2%第三天升高，4.3%第七天升高。
结论 在没有细菌感染的新生儿中，PCT 升高与出生时的胎龄、出生后时间、产后抗生素的使用、极低出生体重以及呼吸机的使用显著相关，所以在利用 PCT 对新生儿感染的疾病诊断中，还应多考虑这些非感染性因素。

PU-1335

系统性红斑狼疮中非编码 RNA 的生物学功能及应用

张孝山、李智洋
南京市鼓楼医院

系统性红斑狼疮（Systemic lupus erythematosus，SLE）是一种慢性的、多系统的自身免疫性疾病，它的特征之一是产生自身抗体并在女性人群中高发。非编码 RNA（ncRNA）在人类转录组中丰度较高，根据其来源和功能可分为 microRNA、lncRNA、circRNA、piRNA 和 tsRNA 等。研究表明 SLE 的发病机制复杂，临床治疗方法也具有多样性。NcRNA 如何在 SLE 中发挥作用，其能否作为 SLE 诊断或治疗的生物标志物是当前亟待解决的问题之一。本文综述了 ncRNA 调控人类 SLE 进程相关的研究，从 ncRNA 的分类、生物发生、功能以及其应用潜力等方面进行了总结。研究发现 lncRNA 在 SLE 病人血清、尿液等生物样本中差异表达，并通过外泌体等方式运输到肾脏组织中发挥作用。MiRNA 可以激活 T 细胞大量释放细胞因子（IL-4、IL-10 等）诱导多器官损伤，加重 SLE 的进程。NcRNA 几乎能在所有的生物样本中检测到，但是考虑到个体差异和组织的特异性，不同来源的 ncRNA 在 SLE 中的生物功能可能存在差异。因此，特异性 ncRNA 靶向的策略可能是为 SLE 患者寻找新型诊断性生物分子标志物，或是精确治疗的可靠手段。在这里，我们回顾了 ncRNA 在 SLE 进展中的相关研究，探讨了它们作为新型生物标志物和治疗剂的潜在临床应用价值，以期为 SLE 患者的诊断和治疗提供新的研究方向。

PU-1336

温阳补心汤加减联合常规疗法对慢性心衰患者心功能及血清 H-FABP、cTnI、Ang-2 水平的影响

陈春杰
宁津县人民医院

目的 探析温阳补心汤加减联合常规疗法对慢性心衰患者心功能及血清 H-FABP、cTnI、Ang-2 水平的影响。
方法 抽选本院 2019 年 1 月-2020 年 1 月收治的 120 例慢性心衰患者为研究对象，采用数字随机分组法将其等分为 A 组（n=60）与 B 组（n=60），B 组予以常规治疗（利尿、消肿等），A 组在此基础上加减使用温阳补心汤，每日煎服 150 ml，在治疗两个月后分析比较两组患者的心功能指标、血清 H-FABP、cTnI、Ang-2 水平、血液流变学指标、中医证候积分、中国心血管病人生活质量评定问卷（CQQC）评分。
结果 A 组治疗后的心功能指标、血清 H-FABP、cTnI、Ang-2 水平、中医证候积分和 CQQC 评分显著优于 B 组（P<0.001）；A 组治疗后的血液流变学指标显著优于 B 组（P<0.05）。
结论 温阳补心汤加减联合常规疗法能够改善慢性心衰患者的血清生物标志物水平，增强其心功能，使患者的临床症状得到缓解，生活质量得到提升，该种治疗方式应在实践中使用。

PU-1337

类风湿关节炎患者血清炎症因子 IL-6 和 TNF-α 的水平测定及临床意义

吴琼、易斌
中南大学湘雅医院

目的 检测类风湿性关节炎(RA)患者血清中 IL-6 和 TNF-α 的水平，探讨 RA 患者血清 IL-6 和 TNF-α 的水平变化及临床意义。
方法 采用化学发光法对 195 例 RA 患者和 47 例健康体检者血清中的 IL-6 和 TNF-α 水平进行检测，分析其与抗环瓜氨酸肽(CCP)抗体、血沉(ESR)、类风湿因子(RF)及 C 反应蛋白(CRP)表达的相关性，并对 RA 患者治疗前后血清 IL-6 和 TNF-α 水平进行比较。
结果 RA 患者组血清 IL-6[(29.87±62.41)pg/ml]和 TNF-α[(21.34±29.35)pg/ml]的水平均显著高于正常对照组 IL-6[(2.40±0.77)pg/ml]和 TNF-α[(5.87±1.23)pg/ml]，差异具有统计学意义(P 均＜0.01)。RA 患者血清 IL-6 与 ESR 及 CRP 水平均呈正相关(P 均＜0.01)，与抗 CCP 抗体及 RF 水平无相关性(P 均＞0.05)；TNF-α 与 ESR、CRP 及 RF 水平均呈正相关(P 均＜0.01)，与抗 CCP 抗体无相关性(P＞0.05)。RA 患者治疗后血清 IL-6 水平明显低于治疗前，差异具有统计学意义(P＜0.05),而治疗后血清 TNF-α 水平与治疗前相比，差异无统计学意义(P＞0.05)。通过比较 ROC 曲线下面积大小，血清 IL-6 对 RA 的诊断效能和 TNF-α 接近，敏感性分别为 77.4%、81. 5%，特异性分别为 97.9%、93.6%。
结论 RA 患者血清中的 IL-6 和 TNF-α 水平明显升高，检测 RA 患者血清 IL-6 和 TNF-α 水平，对类风湿关节炎的诊断及病情活动性判断具有重要的临床价值。

PU-1338

SCF 泛素连接酶 E3 指环亚基 RBX1/2 的研究进展

张楠楠
郑州大学第一附属医院

RBX1/2-SCF 泛素连接酶 E3 功能紊乱可导致包括肿瘤在内的一系列疾病。因此检测 RBX1/2 在癌症中的表达情况，并进一步研究了 RBX1/2 作用于肿瘤发生的机制具有重要意义。RBX1/2 也是肿瘤细胞的存活蛋白，提示 RBX1/2 可成为潜在的抗肿瘤靶目标。

泛素-蛋白酶体系统（ubiquitin-proteasome system，UPS）是细胞内降解蛋白质的重要途径，UPS 降解了胞内约 80%以上的底物，本身具有高度的特异性。蛋白降解过程涉及泛素激活酶 E1、泛素结合酶 E2 和泛素连接酶 E3。多聚泛素的底物一般被 26S 的蛋白酶体降解。

SCF 泛素连接酶 E3 是泛素连接酶中最大的家族，在 UPS 中识别底物，500-1000 种泛素连接酶 E3 满足多样性与特异性。泛素连接酶 E3 有 U 盒型、RING 指型、PHD 指型和 HECT-型。SCF-泛素连接酶 E3 是指环型。泛素连接酶 E3 包含: RBX1/ RBX2、Skp1（S 期激酶相关蛋白 1）、Cullins/CDC53、F 盒蛋白。RBX（环盒子蛋白）是最后被发现的泛素连接酶 E3 的亚基。支架蛋白在底物与环盒子蛋白之间起支撑作用。SCF 泛素连接酶 E3 复合体的晶体结构显示支架蛋白一端连接环盒子蛋白，另一端连接 S 期激酶相关蛋白 1-F 盒蛋白复合物。

虽然环盒子蛋白 1/2 的功能对细胞的生长非常重要，但是环盒子蛋白 1/2 以及 SCF-泛素连接酶 E3 组分在肿瘤中表达异常。显示环盒子蛋白 1/2 的过表达对肿瘤细胞生存是必需的。环盒子蛋白 1/2 的过表达对胃癌、肝癌肿瘤细胞的增殖和凋亡起调控作用。敲除环盒子蛋白 1/2 会导致肿瘤细胞的增殖抑制，并造成细胞的衰老与凋亡，可能由于 SCF-泛素连接酶 E3 泛素连接酶降解的底物积累。检测 RBX1/2 在癌症中的表达情况，并进一步研究 RBX1/2 作用于肿瘤发生的机制是具有

十分重要的意义的，而且 RBX1/2 也是肿瘤细胞的存活蛋白，提示 RBX1/2 可成为潜在的抗肿瘤靶目标。

PU-1339

2010-2017 年山东省立医院皮肤科门诊 HIV 抗体检测和感染状况分析

王泽筠
山东第一医科大学附属省立医院

目的 对山东省立医院皮肤科门诊 6335 例艾滋病抗体检测的相关资料进行回顾性分析，旨在有效预防艾滋病病毒的传播。
方法 对 2010 年 1 月~2017 年 12 月于皮肤科门诊进行 HIV 抗体检测人群给予临床回顾性分析，6335 例检测人群均进行艾滋病病毒抗体检测，并对回顾内容给予统计学分析，得出结论。
结果 6335 例在皮肤科门诊进行艾滋病抗体检测人群中，送检数量逐年上升，年龄 21~30 岁和 31~40 岁年龄段人群居多，分别占总数的 52.45%和 28.45%。经艾滋病病毒抗体检测可知结果为阳性人群为 120 例，占检测总人数的 1.89%。男性阳性率明显高于女性（χ^2=6.963，P=0.0083<0.01）。
结论 皮肤科门诊开展艾滋病病毒抗体检测工作的主要目的在于对艾滋病病毒抗体检测阳性患者做到早发现、早治疗，并指导患者采取正确的生活工作方式，从而尽量减少艾滋病对患者自身、家庭以及社会带来的负面影响有效预防艾滋病病毒的传播。

PU-1340

microRNA-149-5p 对宫颈癌细胞生物学功能的影响

刘璐[1]、吕学峰[1]、秦东春[1,2]
1. 郑州大学第一附属医院
2. 河南省医学重点实验室

目的 本研究通过检测 30 例宫颈癌组织及癌旁组织中 miRNA-149-5p 的表达水平，分析 miRNA-149-5p 分子表达水平与患者临床病理特征是否相关。通过构建 miR-149-5p 细胞转染模型，检测 miRNA-149-5p 对宫颈癌细胞（HeLa 和 SiHa）增殖、侵袭、迁移和凋亡的影响，并通过生信探讨 miRNA-149-5p 在 CC 中的作用机制，为 CC 的机制研究提供理论基础。检测 miR-149-5p 在宫颈癌组织中的表达，分析 miR-149-5p 与患者临床病理特征的相关性，进行 miR-149-5p 在宫颈癌（HeLa 和 SiHa）细胞中的功能及潜在作用机制探究。
方法 收集 30 对确诊为 CC 患者的癌组织与癌旁组织，使用 qRT-PCR 检测 miR-149-5p 的表达情况，分析 miR-149-5p 与患者临床信息相关性。通过细胞转染实验，在 CC（HeLa 和 SiHa）细胞中过表达和敲低 miR-149-5p。通过细胞功能实验（CCK-8、Transwell、细胞周期实验、细胞凋亡检测）验证 miR-149-5p 对 CC 细胞的影响。利用生信预测 miR-149-5p 的靶标 FASL，qRT-PCR 和 WB 检测在 SiHa 细胞中敲低 miR-149-5p 表达后 FASL 基因表达的变化。
5.使用 GEPIA2 和 GEO 数据库对 miR-149-5p 的靶基因 PDE1B 进行下游通路分析。
结果 miR-149-5p 在 CC 癌组织中低表达，且与患者淋巴结转移情况呈负相关。.与 mimic NC 组相比，miR-149-5p 在 HeLa 和 SiHa 细胞 miR-149-5p mimic 转染组中表达显著上调，与 inhibitor NC 组相比，miR-149-5p 在 SiHa 细胞 miR-149-5p inhibitor 组中表达显著降低。过表达 miR-149-5p 可抑制细胞增殖、迁移、侵袭和细胞周期，促进 CC 细胞凋亡，敲减 miR-149-5p 可促进细胞增殖、迁移、侵袭和细胞周期，抑制 CC 细胞凋亡。与 inhibitor NC 组相比，FASL 在 miR-149-5p

inhibitor 组中表达显著增高。5.miR-149-5p 靶基因 PDE1B 在 CC 组织中具有表达差异，且 PDE1B 参与调控多个信号转导过程，提示 miR-149-5p 异常表达可能在 CC 进展中发挥重要作用。**结论** miR-149-5p 在宫颈癌中发挥抑癌作用，可能通过靶向 FASL 抑制宫颈癌细胞的增殖、迁移、侵袭和细胞周期，促进细胞凋亡。

PU-1341

miR-100 通过靶向 CXCR7 抑制肝癌细胞的增殖、侵袭和迁移

葛一漫、张朝明、张灵玲、雍江堰
成都中医药大学附属医院

本研究旨在阐明 miR-100 在肝细胞癌进展中的作用，并探讨其机制。采用实时定量 PCR (quantitative real-time PCR, qRT-PCR)检测正常肝癌组织中 miR-100 的表达水平。使用 Transwell、CCK-8 和集落形成法测定转染 mimic-NC 或 mimic-miR-100 的肝癌细胞系的侵袭性和增殖能力。CXCR7 和 miR-100 之间的结合位点使用荧光素酶报告基因测定。通过共转染实验进一步证实 CXCR7 和 miR-100 在肝细胞癌进展中的相关性。我们的结果显示，miR-100 在肝细胞癌组织中表达显著降低，并与 CXCR7 表达呈负相关。细胞功能检测结果发现，miR-100 的上调抑制了肝细胞癌细胞的增殖、侵袭和迁移能力。荧光素酶报告基因检测显示 CXCR7 mRNA 与 miR-100 相互结合。增加 CXCR7 表达逆转了上调 miR-100 在肝细胞癌细胞中的抑制作用。进一步研究表明，miR-100/CXCR7 通过调节金属蛋白酶-2 (MMP2)和血管内皮生长因子(VEGF)在肝癌的进展中发挥作用。总之，miR-100 对肝细胞癌具有抗肿瘤作用。miR-100 的过表达通过靶向 CXCR7 减弱肝细胞癌细胞的侵袭和增殖能力。

PU-1342

PCT.BNP.cTnI 在脓毒症患儿早期诊断中的价值

陈来英
资阳市第一人民医院

目的 探讨血清降钙素原(PCT)、N 端脑钠肽前体(NT–proBNP)、肌钙蛋白 I(cTnI)测定在脓毒症患儿早期诊断中的价值。
方法 选择近两年来我院就诊的脓毒症患儿 88 例,按照患儿病情分为严重脓毒症组 56 例、脓毒症休克组 32 例,并选择没有达到脓毒症诊断标准的相应年龄、性别的普通住院患儿 88 例作为对照组。检测三组患儿血清 PCT、NT–proBNP、cTnI 的水平,并分析三项指标单独检测与联合检测的灵敏度、特异度以及阳性预测值。
结果 与对照组患儿相比较,严重脓毒症组以及脓毒症休克组患儿血清 PCT、NT–proBNP、cTnI 水平均较高,脓毒症休克组患儿均显著高于严重脓毒症组,差异均具有统计学意义(P<0.05)。三项指标联合检测的灵敏度、特异度以及阳性预测值均高于各项指标单独检测,差异均具有统计学意义(P<0.05)。
结论 脓毒症患儿血清 PCT、NT–proBNP、cTnI 水平会显著升高,且与患儿病情密切相关,三项指标联合检测诊断脓毒症的准确度较高。

PU-1343

IL-33 与多囊卵巢综合疾病进展关系的研究

易楠
郑州大学第一附属医院

目的 通过检测 PCOS 患者血清中 IL-33 水平,探讨两者之间的相关性。
方法 选取 2017 年 3 月—2019 年 2 月间 30 例多 PCOS 患者,30 例健康对照者作为研究对象,应用 ELISA 方法检测所有研究对象 PCOS 组和健康对照组血清中 IL-33 水平,并进行统计学分析。
POCS 患者 IL-33 水平与健康对照组相比显著升高,具有统计学差异,且 IL-33 水平与 POCS 疾病的发展呈正相关。
结论 IL-33 水平升高可能通过调节细胞免疫的变化而

PU-1344

重组 HMGB1-A box 蛋白对系统性红斑狼疮肾炎的缓解作用及其机制研究

孙文萍
山东第一医科大学附属省立医院

目的 系统性红斑狼疮是一种慢性自身免疫病，病程长且容易复发，严重威胁人类健康。狼疮肾炎是其中一种典型的并发症，对其治疗方法目前有很多研究。HMGB1-A box 是致炎因子 HMGB1 的特异性拮抗剂，本研究检测重组 HMGB1-A box 蛋白对系统性红斑狼疮肾炎的作用及其可能的机制。
方法 实验室重组 HMGB1-A box 蛋白，鉴定其生物学活性，并且检测其浓度。将造模成功的系统性红斑狼疮 BALB-C 小鼠按照年龄性别分为两组，每组 20 只，实验组注射实验室重组的 HMGB1-A box 蛋白，对照组注射等量的生理盐水。小鼠处死后，对小鼠肾脏进行病理学免疫组化染色，分别检测实验组和对照组肾脏炎症细胞的浸润情况。实验室内重组 HMGB1-A box 蛋白对狼疮肾炎的作用用单核细胞跨血管内皮细胞迁移 Transwell 的方法检测。把微血管内皮细胞株接种在具有通透性的 Transwell 小室的滤膜上，形成一单血管内皮细胞层，将该层血管内皮细胞分为实验组和对照组，实验组用重组 HMGB1-A box 蛋白干预 24 小时，对照组则用等量生理盐水干预相同时间，然后将单核细胞加入到上室中进行跨血管内皮细胞迁移，20 小时后，将迁移至下室的单核细胞收集起来用细胞计数仪计数，并且比较实验组和对照组之间单核细胞跨内皮细胞迁移的差异。
结果 肾脏病理结果显示：与对照组相比，实验组狼疮小鼠肾脏炎症细胞浸润明显减轻；Transwell 结果显示，与对照组相比，实验组单核细胞跨内皮细胞迁移至下室的细胞较对照组明显减少 ($P < 0.05$) 。
结论 重组 HMGB1-A box 蛋白对系统性红斑狼疮小鼠肾炎具有明显的缓解作用，其中一种可能的机制是减少了肾脏炎症细胞的浸润。

PU-1345

近 5 年住院精神病人免疫球蛋白、补体检测结果分析

张明华
资阳市精神病院

目的 在于了解长期住院精神病患者体液免疫状态，以便加强相应的提高免疫机能的治疗及手段，减少精神病人罹患机会感染的机率，相对提高精神病人生活质量，减少精神科工作人员护理难度。
方法 从我院近期(2016 年 5 月-2021 年 05 月)收治的精神症状的患者中,筛选符合入组条件的患者总

计 200 例进行对照研究，对研究结果与正常参考组进行比对分析。采 SPSS17.0 统计软件进行资料整理，用卡方检验及 t 检验进行统计分析，P＜0.05 为有显著性差异，有统计学意义。
结果 长期住院服药精神病人，其免疫球蛋白及补体检测结果明显低于正常对照组。
结论 长期住院精神病人的免疫功能监测，更能反应其免疫状态，有助于精神科医生和护士对病人的治疗，具有较大的社会经济学价值。

PU-1346

多发性骨髓瘤差异基因的生物信息学分析

秦东春[1,2]、吕学峰[1]、刘璐[1]
1. 郑州大学第一附属医院
2. 河南省医学重点实验室

目的 本研通过整合生物信息学分析来探究多发性骨髓瘤（MM）中的关键候选基因和信号通路。
方法 在 GEO 数据库中选择 GSE39754 数据集，通过 GEO2R 平台筛选多发性骨髓瘤（MM）患者相对于健康人的差异基因（DEGs）。然后利用 DAVID 网站对 DEGs 进行 GO 分析，用 REACTOME 网站进行信号通路富集分析，借助 STRING 网站构建 PPI 网络，并用 Cytoscape 软件对网络进行可视化筛选 Hub 基因，利用 PrognoScan 数据库分析 Hub 基因与 MM 患者的生存相关性。
结果 通过 GEO2R 平台共筛选出 302 个 DEGs。其中上调基因 217 个，下调基因 85 个。GO 分析的结果为：DEGs 富集到的 Top5 生物学过程：SRP 依赖的协同翻译蛋白靶向膜、翻译起始、病毒复制、核转录的 mRNA 分解代谢过程，无意义介导的衰变、核糖体 RNA 的加工；富集到的 Top5 生物学组件：细胞外泌体、核糖体、细胞膜、内质网膜、细胞外基质；富集到的 Top5 分子功能：核糖体的结构组成、poly(A)RNA 的结合、碳水化合物结合、蛋白质结合、受体活性。通过 REACTOME 网站分析显示：上调基因富集到的信号通路有 srp 依赖的协同翻译蛋白靶向膜、无义介导衰变(NMD)独立于外显子连接复合体(EJC)、形成一个自由的 40S 亚基池、GTP hydrolysis and joining of the 60S ribosomal subunit、病毒信使核糖核酸的翻译；下调基因富集到的信号通路有中性粒细胞脱颗粒、先天免疫系统、抗菌肽、 免疫系统、白细胞介素-4 和白细胞介素-13 信号。构建 PPI 网络，筛选出 Top10Hub 基因：SEC61A1、UBA52、HSPA5、RPLP0、EPRS、RPL11、RPS23、RPS3、RPL30、RPL18，利用 PrognoScan 数据库分析 Hub 基因与 MM 患者的生存相关性发现 HSPA5、EPRS、RPL30 与 MM 患者的生存情况明显相关。
结论 总共筛选出 302 个多发性骨髓瘤 DEGs，包括 217 个上调基因和 85 个下调基因，从中筛选出 Top10Hub 基因：SEC61A1、UBA52、HSPA5、RPLP0、EPRS、RPL11、RPS23、RPS3、RPL30、RPL18，其中 HSPA5、EPRS、RPL30 与 MM 患者的生存关系最为显著。

PU-1347

血清肿瘤标志物对胃癌诊断和准确率观察

熊杨
资阳市乐至县人民医院

目的 探讨血清肿瘤标志物 CA199、CA125、CA242、CA724 对胃癌诊断和准确率观察。
方法 选取早期胃癌患者 51 例，我院内科 2018 年 1 月至 2019 年 6 月收治，为本次研究的观察组 A。同时选取同期我院收治的良性病变患者 51 例，为本次研究的观察组 B。选取同期于我院进行健康体检者 51 例，为本次研究的对照组。三组均接受多种血清肿瘤标志物的联合检测诊断。对血清肿瘤标志物对胃癌诊断和准确率进行观察研究。

结果 观察组 A 的 CA199、CA125、CA242、CA724 均显著高于观察组 B 和对照组的血清肿瘤标志物水平，差异具有统计学意义（P<0.05）。观察组 B 和对照组的血清肿瘤标志物水平相较，经检测无差异（P>0.05）。观察组 A 组的胃癌患者的胃癌血清肿瘤标志物联合检出率为 74.50%，显著高于各单项的血清肿瘤标志物检出率，差异具有统计学意义（P<0.05）。
结论 血清肿瘤标志物在胃癌患者诊断效果效果显著，而血清肿瘤标志物联合检测效果更加，显著提高患者疾病诊断准确率。

PU-1348

双抗原夹心 ELISA 法检测登革病毒患者血清中的 EDⅢ抗体

丁细霞
南方医科大学珠江医院

目的 建立一种检测登革病毒（dengue virus,DENV）特异性抗体的双抗原夹心 ELISA 方法。
方法 利用毕赤酵母系统表达 4 个血清型登革病毒包膜蛋白Ⅲ区（envelope protein domain Ⅲ,EDⅢ），并采用改良过碘酸钠法对 EDⅢ蛋白标记 HRP，建立一种可同时检测四个血清型登革病毒 EDⅢ蛋白特异性抗体的双抗原夹心 ELISA 法。并对 2014 年广州珠江医院门诊和住院确诊的登革热患者血清标本进行检测，并与澳洲 Panbio MAC ELISA 检测的敏感性进行比较。
结果 本研究成功建立了一种检测登革病毒 EDⅢ蛋白特异性抗体的双抗原夹心 ELISA 法，该方法能同时检测到四个血清型登革病毒 EDⅢ蛋白免疫的小鼠血清和 I 型登革病毒 EDⅢ蛋白免疫的兔血清，而与烟曲霉 AF-MP 蛋白免疫的小鼠血清和兔血清均无交叉反应。对 184 份健康人血清标本检测全为阴性，而对 168 份确诊的登革热患者血清标本检测结果表明，两种诊断方法检测结果无统计学差异，P<0.0001（56.0% vs 58.3%）,联合 NS1 抗原检测方法，其敏感性提高到 95.2%。
结论 双抗原夹心 ELISA 法检测登革病毒 EDIII 特异性抗体具有高度的特异性，但如果能同时联合抗原检测可明显提高登革热的早期诊断率。

PU-1349

抗核抗体系列检测对狼疮性肾炎进行鉴别诊断的临床意义

张娜、郭欣
哈尔滨医科大学附属第一医院

目的 探讨抗核抗体（ANA）系列指标在狼疮性肾炎（LN）患者中的表达情况及临床意义。
方法 对 406 例系统性红斑狼疮（SLE）患者（其中 LN 122 例）和 74 例其他自身免疫病患者及 120 例健康体检者采用间接免疫荧光法测定抗核抗体(ANA)，应用欧蒙印迹法测定抗核抗体系列。
结果 SLE 患者 ANA 阳性率为 94.49％，与其他自身免疫病组间差异显著，(p<0.05)；与对照组比较 P<0.01，差异极显著。LN 组 ANA 系列中，8 个检测项目阳性率均高于不伴肾炎 SLE 组，差异有统计学意义（p<0.05）。抗双链 DNA 抗体+抗 Sm 抗体+抗 nRNP 抗体同时阳性时，LN 组阳性表达显著高于不伴肾炎 SLE 组（p<0.05）。当抗双链 DNA 抗体阳性时，LN 组抗组蛋白抗体、抗核小体抗体和抗核糖体 p 蛋白抗体同时阳性的表达也显著高于不伴肾 SLE 组（p<0.05）。
结论 抗核抗体及抗核抗体系列的联合检测可以相互补充，对提高狼疮性肾炎的诊断率及判断预后、指导治疗等方面具有重要意义。

PU-1350

7 种肿瘤标志物检测对胸腔积液的诊断价值

丁兴龙
徐州矿务集团总医院检验科

目的 探讨胸腔积液 CEA、CA125、 NSE 、CYFRA21-1 、CA50 、SCC、 TSGF 等 7 种肿瘤标志物检测对胸腔积液良恶性的诊断价值。
方法 回顾性分析我院 2019 年 2 月至 2020 年 2 月 195 例胸腔积液住院患者的临床资料，按照胸腔积液性质分良性胸腔积液 109 例为对照组，恶性胸腔积液 96 例为观察组。其中观察组按照脱落细胞类型分为小细胞癌组 10 例，鳞癌组 18 例，腺癌组 68 例。比较 2 组患者及不同病例类型肺癌胸腔积液中 7 种肿瘤标志物的水平差异，同时比较 7 种肿瘤标志物在恶性胸腔积液中的诊断效果。
结果 观察组中 CEA、 NSE、 CYFRA21-1、 CA50 、TSGF 水平明显高于对照组，差异具有统计学意义（P<0.05）。不同病例类型肺癌胸腔积液中小细胞癌 NSE 明显高于其他两组（P<0.05），小细胞癌及腺癌组 CA50 明显高于鳞癌组（P<0.05），鳞癌组 SCC 明显高于腺癌组。CEA 、NSE、CYFRA21-1、 CA50、 SCC、 TSGF 的 ROC 曲线下面积（AUC）分别为 0.992、 0.663、 0.735、0.801、 0.525、 0.680 。所有指标诊断准确度好，CEA 诊断准确度最好，灵敏度和特异性均高于其他指标。诊断率分别 93.54%、39.64%、48.74%、60.38%、25.93%、38.89%。
结论 肿瘤标志物检测对鉴别胸腔积液良恶性及疾病的诊断具有重要价值。

PU-1351

抗心磷脂抗体检测对狼疮性肾炎患者的诊断意义

郭欣、张娜
哈尔滨医科大学附属第一医院

目的 探讨抗心磷脂抗体（ACA）、抗核小体抗体、补体 C3 检测对狼疮性肾炎（LN）患者的诊断意义。
方法 对 406 例系统性红斑狼疮（SLE）患者（其中 LN 122 例）和 120 例健康体检者采用 ELISA 方法测定抗心磷脂抗体，应用欧蒙印迹法测定抗核小体抗体，应用散射比浊法测定补体 C3 水平。
结果 ACA 阳性率在 LN 组和非 LN 组间差异无统计学意义（p>0.05）；与对照组比较 P<0.01，差异显著。抗核小体抗体阳性率和补体 C3 水平在 LN 组和非 LN 组间，差异有统计学意义（p<0.05）；与对照组比较差异显著（P<0.01）。
结论 抗心磷脂抗体、抗核小体抗体、补体 C3 的联合检测可以相互补充，对狼疮性肾炎的诊断及鉴别诊断、预后判断等方面具有重要意义。

PU-1352

急诊胸痛病人超敏 C -反应蛋白检测的诊断价值

姜玉玲、徐兆珍
哈尔滨医科大学附属第一医院

目的 检验超敏 C -反应蛋白（hs-CRP）对急诊室胸痛病人的诊断价值
方法 从 2014 年 1 月至 2014 年 12 月，对急诊接诊主诉为胸痛的病人进行超敏 C 反应蛋白测定，以及心电图检查
结果 各组心血管性疾病患者(112 例)血清 hs - CRP 浓度显著高于对照组(52 例，1.07±0.93mg/L) ，而非心血管性疾病组与对照组相比无显著差别

结论 hs - CRP 的测定可辅助急诊胸痛病人预测心源性疾病的发生，有助于急诊室心源性疾病的诊断。

PU-1353

尿视黄醇结合蛋白及尿微量白蛋白在糖尿病肾病中的早期诊断价值

张娜、徐兆珍
哈尔滨医科大学附属第一医院

目的 探讨 2 型糖尿病(DM)患者尿视黄醇结合蛋白(RBP) 、尿微量白蛋白(ALB) 在糖尿病肾病的早期诊断意义。
方法 选取受检者 24h 尿, 离心去上清液, 运用 ELISA 法测定 RBP、ALB 表现。
结果 2 型 DM 患者尿 RBP、ALB 的阳性率高于尿常规蛋白的阳性率, 尿常规蛋白阳性的尿 RBP、ALB 比尿常规蛋白阴性的阳性率高,不同病程的 DM 患者随着病程的延长尿 RBP、ALB 的阳性率就越高。
结论 检测 DM 患者尿 RBP、ALB 有助于早期诊断糖尿病肾病。

PU-1354

乙肝表面抗原和乙肝表面抗体同时存在的模式分析

姜玉玲、徐兆珍
哈尔滨医科大学附属第一医院

目的 分析乙型肝炎病毒（HBV）感染者乙肝表面抗原（HBsAg）与乙肝表面抗体（HBsAb）同时阳性的模式，与 HBV DNA 的关系，以及其产生的原因及临床意义。
方法 采用化学发光微粒子免疫分析法（CMIA）检测样本的 HBV 血清标志物，从中选出 HBsAg 和 HBsAb 同时阳性的样本，采用荧光定量聚合酶链反应(FQ-PCR)检测其 HBV DNA 定量值。
结果 在选取的 HBsAg 和 HBsAb 同时阳性的 37 例样本中，有 21 例血清 HBV-DNA 检测阳性，阳性率为 57％。
结论 乙型肝炎患者出现 HBsAg 和 HBsAb 同时阳性，原因复杂，不同 HBsAg 亚型双重感染可能是主要原因。HBsAg 和 HBsAb 同时阳性并不代表疾病真正好转，相反其预后较差，应当引起重视。

PU-1355

乙肝血清学标志物检验临床价值研究

凌燕
资阳市乐至县人民医院

目的 探究乙肝血清学标志物两对半检测的临床价值。
方法 选取本院 2018 年 1 月到 2020 年 11 月期间收治的 3186 例在检验科对血标本进行两对半化验的患者进行研究，检测两对半使用 ELISA 法试剂盒，对其结果进行分析，发现其中有 1978 例呈现阳性模式。
结果 两对半检测 3186 例结果中，血清标志物 5 项全部（-）1208 例，出现比率为 37.91%；至少一项成（+）1978 例，出现比率为 62.08%，以 15 组阳性模式出现，其中检测出有 628 例具有保护性的 HBsAb 呈现阳性，出现比率 19.71%。

结论 为了有效的对乙肝病毒进一步的预防和控制，需要对乙肝相关疾病的知识加大宣传的力度，需要接种乙肝疫苗工作更好的开展，需要对广大人民参与检测乙肝两对半的行为进行积极的鼓励。

PU-1356

2007～2012 年哈医大一院艾滋病感染者情况分析

张萱、周海舟
哈尔滨医科大学附属第一医院

目的 中国大多数医院都有可以进行 HIV 检测。然而，这还不是一个面向所有患者的常规试验，许多患者就诊时仍不知道他们感染了艾滋病病毒。目的了解我院艾滋病病毒的感染率和影响感染的因素。
方法 我们收集了从 2007 年到 2012 年这 6 年来就诊于哈尔滨医科大学附属第一医院的 348151 位患者的血液样本，用 ELISA 法进行初筛。阳性结果的标本用不同厂家的试剂盒进行复查，若有一个结果为阳性，就送往疾病预防和控制中心进行确诊实验。
结果 从 2007 年到 2012 年我院 HIV 检测的阳性率有逐渐上升的趋势。并且 HIV 感染与患者的性别、年龄、职业、婚姻状况、教育水平和感染途径相关。艾滋病在男性中更加普遍。超过 80%的 HIV 阳性患者没有接受过高等教育（>12 年）。传播方式主要由为性传播感染，其中由于同性接触而引起的 HIV 感染近年急剧增加，感染率在 36.4%到 65.1%之间。
结论 近年来在医院被诊断为艾滋病毒阳性的患者数量显著增加。提供院内 HIV 常规检测具有可行性并且对艾滋病感染者和患者家属的自身健康有着重要的作用。

PU-1357

降钙素原、C 反应蛋白用于乙肝肝衰竭患者合并感染的诊断意义

宋晓君
乐至县人民医院

目的 探讨降钙素原和 C 反应蛋白用于乙肝肝衰竭患者合并感染的诊断意义。
方法 从我院收治乙肝肝衰竭合并感染患者抽取 50 例作为感染组，另选取乙肝肝衰竭非感染患者 50 例作为非感染组，选取时间在 2019 年 10 月—2020 年 10 月，监测患者的降钙素原和 C 反应蛋白指标，对比两组患者指标变化。
结果 感染组患者相较于非感染组，PCT 和 CRP 指标均较高，P＜0.05。
结论 乙肝肝衰竭患者合并感染患者相较于非感染患者的 PCT 和 CRP 指标均较高，可应用在临床诊断的重要指标。

PU-1358

孕妇产前传染病指标检测结果分析

李文清
山东省千佛山医院

目的 通过对本院孕产妇产前传染病检测项目分析，了解传染病感染状况，为诊断治疗及产科防护提供依据。
方法 对 1653 例孕产妇产前采用化学发光法检测其血清乙型肝炎病毒表面抗原（HBsAg）、梅毒螺旋抗体（TP-Ab）、丙型肝炎抗体（HCV-Ab）、人免疫缺陷病毒抗体（HIVAg-Ab）。

结果 检出 HBsAg 阳性 42 例（2.54%），TP-Ab 阳性 6 例（0.363%），HCV-Ab 0 列，HIVAg-Ab 0 列。
结论 对本院 1653 例孕产妇产前传染病 4 项检测结果表明，HBsAg 阳性率最高，其次是 TP-Ab。在产前检查中应用传染病检测可及时发现孕产妇感染情况，可以减少或阻断母婴传播途径。也对医护人员针对性加强自我防护，减少或防止职业感染具有重要意义。

PU-1359

针对肿瘤标志物碱性磷酸酶（ALP）的 OFF-ON 型近红外荧光探针的设计、合成及临床应用

齐亚军
德州市人民医院

恶性肿瘤已成为威胁人类生命健康的主要疾病之一，在我国这种情况更为严重，能否尽早发现肿瘤和介入治疗对患者生存期的延长起到了重要作用。早期恶性肿瘤可以通过外科手术进行切除，这也是早期患癌病人的最有效和首选的治疗方案。然而，实体肿瘤的切除往往需要富有经验的临床医生负责完成，其往往需要肿瘤的体积达到一定大或出现明显转移灶才能确诊。因此，现代医学急需一种能够帮助临床医生快速诊断肿瘤存在和明确肿瘤大小及边界的检测手段，这也是广大科研工作者急需突破的诊断技术瓶颈。

在动物、植物、微生物中，碱性磷酸酶担任着蛋白质去磷酸化的作用，是调控细胞代谢，参与细胞分裂分化等信号通路上不可或缺的酶，与多种恶性肿瘤的发生发展相关。荧光成像方法是通过聚焦在蛋白质组和活细胞水平上，对 ALP 活性的检测进行了改善。在这其中，小分子荧光探针因具有良好的化学改性、生物兼容性和低成本等优点备受青睐。荧光探针检测法为非入侵性、传感机制简单，操作方法简便，但受到荧光染料的影响，导致其特异性差、不能准确识别，毒性以及存在背景干扰等。传统的荧光染料存在灵敏度低、特异性差、复杂的传感机制以及短的发射和激发波长等弊端，相比传统的荧光染料，近红外荧光染料有更长的激发和发射波长、极好的时空分辨率、更深的组织穿透力以及较低的自发荧光的背景干扰，可以更加完善的检测体内碱性磷酸酶的活性。因此，开发一种灵敏、可靠、简便的生物学和化学方法来检测碱性磷酸酶的表达水平是十分必要的。可以利用磷酸基团为 ALP 的反应位点，DCM 类染料为荧光发色团，合成能特异性检测 ALP 的 OFF-ON 型荧光诊断试剂探针。荧光诊断试剂采用 OFF-ON 型策略设计，基本原理为分子内电荷转移。诊断试剂在 OFF 状态，此时荧光基团处于缺电子状态，整个体系为不发荧光状态。当该体系在体内弱碱性环境下通过碱性磷酸酶的酶促去磷酸化后，磷酸酶去除荧光基团上的磷酸部分，导致分子内电荷转移效应的恢复和荧光的“开启”成为 ON 的状态，此时荧光基团处于给电子状态，该试剂可以发射激发光，并可以被荧光光谱仪检测到。

PU-1360

呼吸系统感染治疗中血清降钙素原检验的作用及准确性分析

易婷
资阳市乐至县人民医院

目的 探索呼吸系统感染治疗中血清降钙素原检验的作用及准确性。
方法 在 2018 年 4 月 21 日至 2019 年 6 月 29 日期间选取对照组 69 例健康体检者、观察组 69 例疑似呼吸系统感染患者为试验对象，均进行血清降钙素原，随后对比两组受检者血清降钙素原，分析降钙素原在疾病判断中准确性。
结果 观察组血清降钙素原（10.53±1.49）ng/mL 高于对照组（P＜0.05）。而血清降钙素原对细菌感染性肺炎准确性为 87.50%，对支气管炎准确性为 94.12%，对细菌感染性哮喘准确性为 96.67%，

且对呼吸系统感染的特异度为 92.86%，敏感度为 94.55%，误诊率为 7.14%，漏诊率为 5.45%。
结论 血清降钙素原在判断呼吸系统感染疾病时，具有较高特异性和敏感性，可鉴别机体感染程度。

PU-1361

化学发光法和 ELISA 法测定乙肝标志物的结果对比分析

李牧
复旦大学附属中山医院青浦分院

目的 研究化学发光法与酶联免疫吸附测定法在乙肝两对半检测中的应用。
方法 选取我院收治的乙肝患者 130 例作为研究对象，分别化学发光法和 ELISA 法检测乙肝 5 项血清标志物，并对乙肝少见模式的病例结果进行数据分析。
结果 ELISA 法和化学发光法检测 HBsAg、HBsAb、HBeAg、HBcAb 的一致性较好，化学发光法测定的检出率高，更灵敏。在少见模式中，ELISA 法测单独 HBeAb 阳性的 22 例标本中用化学发光法测得 22 例 HBeAb 全部阳性，但其中 4 例 HBsAg 弱阳性，2 例 HBsAb 强阳性，2 例 HBsAb 弱阳性，12 例 HBcAb 阳性，说明化学发光法检出率高。用 ELISA 法测得单独 HBeAg 阳性且 DNA 扩增<500 拷贝的 8 例标本用化学发光法测得全部阴性。
结论 化学发光法优于 ELISA 法，但化学发光法 HBeAg 阴性的乙肝感染者还应注意病毒低复制。化学发光法相比 ELISA 能有效防止发生漏诊、误诊。

PU-1362

粪便隐血与肿瘤标志物联合诊断结直肠癌的效果分析

唐昌伟
资阳市乐至县人民医院

目的 讨论粪便隐血与肿瘤标志物联合诊断结直肠痛的效果。
方法 将 50 例于 2018 年 6 月-2020 年 3 月期间本院收治的疑似结直肠癌患者作为研究对象,所入选患者均实施粪便隐血与肿瘤标志物检测,本次研究诊断金标准为病理诊断结果,评判标准:类便隐血与肿瘤标志物联合诊断结直肠癌的准确率。
结果 50 例疑似结直肠癌患者经病理诊断后有 45 例确诊,剩余 3 例为局限性结肠炎、2 例为肠结核。典便隐血联合肿瘤标志物检测下的诊断准确性、敏感性及特异性水平均明显高于单一检测,P<0.05。
结论 与单独性实施粪便隐血检测与肿瘤标志物检测相比,这两种检测方式联合实施下结直肠癌瘸症的诊断准确性、敏感性及特异性更高,值得推广。

PU-1363

ELISA 法在诊断梅毒螺旋体感染中的临床应用对提高检验准确性的价值

陈阳
资阳市乐至县人民医院

目的 分析研究 ELISA 法在诊断梅毒螺旋体感染中的临床应用对提高检验准确性的价值。
方法 纳入 2018 年 04 月至 2019 年 04 月接收的 90 例梅毒螺旋体感染患者，随机平均分为 2 组，对照组 45 例采纳 TRUST 检验，观察组 45 例采纳 ELISA 法，对比特异性、敏感性及准确性。
结果 观察组特异性、敏感性及准确性明显较对照组更高，数据对比差异显著，P＜0.05。

结论 实施 ELISA 法，可提高梅毒螺旋体感染患者诊断率的效果，在临床中值得应用和推广。

PU-1364

超敏 TNI 结果异常增高的原因分析

王连明、鲁平
哈尔滨医科大学附属第一医院

目的 患者症状与超敏 TNI 测定结果不相符，证多个检测系统对同一份样本的测定结果之间差异显著，寻找产生差异的可能原因。
方法 通过动态观察同一患者的超敏 TNI 的测定结果，与同期的临床症状及其他检查、检验结果进行综合分析；在多个品牌、型号的检测系统进行相同样本的检测，观察其差异，并分析原因。
结果 经仔细询问患者,近期未服用生物素制品,核对所服用药物的成分也未发现含有生物素,排除了生物素的干扰; 通过动态观察同一患者的超敏 TNI 的测定结果，与同期的临床症状及其他检查、检验结果进行综合分析发现其临床症状与超敏 TNI 的动态变化不同步。同时在罗氏、强生、西门子、雅培的仪器上测定同一份病人样本得到的结果，其超敏 TNT 或超敏 TNI 升高的倍数差别较大，进一步证实样本中存在干扰测定的物质，且对不同品牌的试剂干扰程度不同。后检测到病人的类风湿因子异常增高，经分析判定病人样本中的类风湿因子是引起超敏 TNI 升高的主要原因。
结论 对于无明显器官/组织功能异常的临床及生物化学指征出现的高超敏 TNI 情况，应怀疑样本中存在影响测定的物质存在，如本病人的类风湿因子异常增高，以保证测定结果对临床的诊断意义。

PU-1365

两种化学发光检测系统对血清降钙素原测定结果的可比性研究

唐万富
安岳县中医医院

目的 探讨迈克 i3000 化学发光仪和罗氏 Cobase e601 电化学发光仪针对人血清中降钙素原(PCT)的检测能力是否等效以及检测结果的可比性。
方法 分别以迈克 i3000 化学发光仪和罗氏 Cobase e601 电化学发光仪为目标系统和待测系统。收集均匀分布于试剂说明书所标注的线性区间(0.02~24ng/mL)内的 120 例血清标本,且排除脂血、溶血及黄疸标本,分别在两个检测系统内检测 PCT 数值。依据 NCCLS EP9-A2 文件并运用 SPSS 20.0 或 EXCEL 软件进行离群点检查,绘制绝对偏倚图和相对偏倚图,计算相关系数和回归方程,统计符合率和 Kappa 值,并进行偏倚分析,综合评估 2 个检测系统检测 PCT 的检验效能和可比性。
结果 纳入的 120 例标本中无离群值;两种设备检测的 PCT 结果高度相关(r=0.987,P〈0.01);回归方程:Y=1.069X-0.021,F 检验显示回归方程差异有统计学意义(P〈0.05);对回归方程的两个系数进行 t 检验显示,截距(b)则反之差异无统计学意义(P=0.768〉0.05),而斜率(a)比较差异有统计学意义(P〈0.05).PCT 在定值 0.23 ng/ml 和 0.50 ng/ml 时的系统误差(SE%)分别为 5.40%和 2.60%.
结论 迈克 i3000 化学发光仪和罗氏 Cobase e601 电化学发光仪检测 PCT 的相关性和线性良好;一致性和符合率均一致,即两者的检验效能一致,均能满足临床检测需求,但两个检测系统检测 PCT 的具体结果数值不具有可比性。

PU-1366

肺部感染患者甲状腺激素的变化及其临床诊断价值

龚代黔
资阳市安岳县中医医院

目的 研究肺部感染患者、正常体检人员的 FT3、FT4 和 TSH 结果，以及肺部感染患者的甲状腺激素与其他可提示感染的指标 HsCPR、PCT 的结果比较。
方法 将 2019 年 1 月-2020 年 5 月我院肺部感染患者 116 例，体检组 116 例，甲状腺激素采用全自动化学发光免疫分析仪 I3000，游离三碘甲状腺原氨酸测定试剂盒、游离甲状腺素测定试剂盒、促甲状腺激素测定试剂盒，检测 FT3、FT4 和 TSH，降钙素原测定试剂盒检测 PCT，超敏 C-反应蛋白测定试剂盒检测 HsCPR。
结果 肺部感染患者与体检组 FT3 和 TSH 的 P<0.05，说明肺部感染患者与体检组的差异具有统计学意义；FT4 的 P>0.05，差异没有统计学意义，且 FT3 对肺部感染的发生的前中期具有一定的指导意义，但没有 PCT、HsCRP 的特异性高，但在对疾病的预后具有高于 PCT、HsCRP 的指导意义。
结论 肺部感染患者的血清 FT3、TSH 浓度低于正常组水平，FT3 可作为肺部感染预后的检测指标。

PU-1367

N 端 B 型脑利钠肽前体与超敏 CRP 联合检测在诊断慢性心力衰竭中的临床意义

唐旭
资阳市安岳县中医医院

目的 慢性心力衰竭（CHF）是各种心血管疾病导致心脏收缩与舒张障碍的一种综合征，主要表现为体液潴留，乏力，呼吸困难等，是心血管疾病的终末阶段。随着人口老龄化加重，CHF 的发病率，病死率也在逐年增加，因此对 CHF 患者进行早诊断，早治疗，促进患者心功能恢复从而延缓病情发展具有重要的临床意义。目前研究表明，心室负荷增加时导致 N 端 B 型脑利钠肽前体(NT-proBNP)释放，超敏 CRP（hsCRP）是在急性炎症期肝脏合成的细胞因子，是心血管疾病的危险因子。此研究旨在联合检测血清 NT-proBNP 和 hsCRP 对诊断 CHF 患者的临床价值。
方法 选取本院收治的慢性心力衰竭患者 88 例作为研究组，根据 NYHA 标准进行分级（Ⅰ级 5 例，Ⅱ级 13 例，Ⅲ级 32 例，Ⅳ级 38 例），同期选择本院健康体检者 30 例作为对照组,通过电化学发光法和透射免疫比浊法对两组研究对象血清 NT-proBNP 和 hsCRP 进行测定并对结果进行比较。
结果 研究组 NT-proBNP 和 hsCRP 水平均明显高于对照组且差异具有统计学意义（P<0.05），研究组中不同心功能分级患者随着心功能下降 NT-proBNP 和 hsCRP 结果逐渐上升，组间两两比较差异有统计学意义（P<0.05）。
结论 CHF 患者血清中 NT-proBNP 和 hs CRP 水平明显升高，且随疾病严重程度呈现一定变化，对 CHF 诊断及病情评估具有重要的临床价值。

PU-1368

心型脂肪酸结合蛋白在急性心肌梗死中的应用

王一多、金英玉
哈尔滨医科大学附属第一医院

心肌梗塞（myocardial infarction）是冠状动脉闭塞，血流中断，使部分心肌因严重的持久性缺血而发生局部坏死。临床上有剧烈而较持久的胸骨后疼痛，发热、白细胞增多、红细胞沉降率加快，血清心肌酶活力增高及进行性心电图变化，可发生心律失常、休克或心力衰竭。患者多发生在冠状动脉粥样硬化狭窄基础上，由于某些诱因致使冠状动脉粥样斑块破裂，血中的血小板在破裂的斑块表面聚集，形成血块(血栓)，突然阻塞冠状动脉管腔，导致心肌缺血坏死，另外，心肌耗氧量剧烈增加或冠状动脉痉挛也可诱发急性心肌梗死。近年来，AMI 的发病率呈逐年上升趋势，是一种常见的心身疾病，每年由急诊科收治诊断的 AMI 患者也日益增多。近几年国内外在 AMI 的诊断中所使用的分子诊断标志物主要以 TnI/T 和 Mb 为主，但其作为主要的诊断依据却缺乏敏感性和特异性。这就导致对该疾病诊断、早期发现和预后评估加大了难度，进而可能延误患者的救治导致死亡。近年的研究发现心型脂肪酸结合蛋白（heart fatty acid-binding protein, HFABP）是心脏中富含的一种新型小胞质蛋白，它具有高度心脏特异性，但在心脏以外的组织中也有低浓度表达。心肌缺血性损伤出现后，hFABP 可以早在胸痛发作后 1-3 小时在血液中被发现，6-8 小时达到峰值而且血浆水平在 24-30 小时内恢复正常。国内外学者及生物制剂公司已经研制出以双抗体夹心法测定 HFABP 的试剂盒。

心型脂肪酸结合蛋白作为心肌细胞中特异性较高的一种蛋白质，其对于急性心肌梗死或者心肌损伤的诊断的意义非常重要，尤其是在心肌梗死的早期对于 AMI 的诊断较传统指标具有更高的灵敏性和特异性，所以研究心型脂肪酸结合蛋白对于指导临床诊断急性心肌梗死方面拥有重要意义。

PU-1369

乙肝病毒性肝炎患者两对半临床医学检验分析

邹航
安岳县人民医院

目的 乙型病毒性肝炎是乙肝病毒感染所致，该疾病的危害性不仅仅在于肝脏本身，乙型病毒性肝炎还会引起其他疾病，例如胆道感染、肾功能衰竭、糖尿病等等，对患者健康存在较大威胁。通过规范性的治疗能够稳定病情，减少传染性，降低肝硬化和肝癌的发生率。本次研究是对乙肝病毒性肝炎患者两对半临床医学检验结果。

方法 对我院 2018 年 11 月至 2019 年 11 月的 184 例乙肝病毒性肝炎患者进行研究。对其进行两对半临床医学检验，观察检查结果。

结果 经检查大三阳检出率 28.26%，小三阳检出率 19.56%，其他类型肝炎检出率 52.17%，组间结果比较差异具有统计学意义，差异明显（P＜0.05）。

结论 乙型病毒性肝炎分为急性、慢性，不同类型的疾病治疗方法不同，为此在乙型病毒性肝炎治疗中需要通过临床诊断鉴别疾病，实施针对性的治疗。两对半临床医学检验在乙肝病毒性肝炎诊断中检出率较高，具有一定临床价值。

PU-1370

小儿肺炎支原体感染临床检验的诊断价值研究

李虹桥
安岳县人民医院

目的 小儿 MP 感染在小儿肺炎中约占 20%以上，学龄期儿童是 MP 感染好发人群。该疾病经呼吸道飞沫、接触等方式传播，幼儿体质较弱，抵抗力不足更容易感染 MP.研究小儿肺炎支原体感染临床检验的诊断价值。
方法 对我院 2019 年 4 月至 2020 年 4 月的 74 例 MP 感染患儿进行研究。患儿均予以实验室痰培养和血清 IgM 抗体检测两种检查方法。比较两种方式的诊断结果。
结果 经诊断实验室培养共检出 31 例阳性，血清 IgM 抗体检测出 61 例阳性，两种诊断方法比较血清 IgM 抗体检测阳性检出率更高，差异明显（P＜0.05）。
结论 MP 感染检查中血清 IgM 抗体检测具有一定临床价值，有利于诊断疾病，具有临床价值可大力推广。

PU-1371

戊型肝炎抗体与血清 ALT 的关系探讨

贺洪军
安岳县人民医院

目的 戊型肝炎病毒（HEV）感染与血清丙氨酸氨基转移酶（ALT）升高的关系进行初步探讨，为了提高对戊型肝炎的认识，以免造成对戊型肝炎的误诊或漏诊。
方法 选择 ALT 异常升高（40-2000U/L）并除外甲、乙、丙、丁肝炎感染者的血清标本 300 例（0-40U/L 参考范围），其中门诊病人 155 例，住院病人 145 例进行抗 HEV-IgG、IgM 检测。
结果 HEV 的感染阳性率有显著性差异（P<0.01）,而 41-100U/L、101-150U/L、151-200U/L 这三组间无显著性差异(P>0.05)。若将此三组合并与≥200U/L 组比较，存在显著性差异（P<0.01）。
结论 HEV 吸引免疫活性细胞的能力可能不强，导致了其感染肝细胞后机体内的免疫活性细胞的损害并不严重。

PU-1372

系统性免疫失调与早期非小细胞肺癌患者临床特征的相关性研究

金胜航、郝志行、杜峰、武当、俞群、伍品
浙江大学医学院附属第二医院

背景 系统性免疫失调与肿瘤进展有关，然而系统性免疫失调在早期非小细胞肺癌中的临床意义并不清楚。
方法 利用 9 个标志物定义的 12 个外周血免疫参数，我们在发现组中探索了早期非小细胞肺癌病人的系统性免疫失调及其特征。然后我们检测了手术治疗对病人系统性免疫状态的影响。最后，我们在验证组中揭示了系统性免疫失调与早期非小细胞肺癌患者临床特征的相关性。
结果 我们发现早期非小细胞肺癌患者外周血出现一种显著的以总淋巴细胞、活化淋巴细胞、T 细胞、静息 T 细胞、CD8+T 细胞、CD4+T 细胞和 NKT 细胞减少及活化 T 细胞、活化 CD8+T 细胞、NK 细胞和 B 细胞增多为特征的系统性免疫失调。进一步研究我们发现，手术治疗可以部分性逆转非小细胞肺癌患者外周血系统性免疫失衡。此外，我们发现系统性免疫失调与肺癌患者多种临床特征，如性别、年龄、吸烟史、体重、病理类型、肿瘤分期、手术方式、肿瘤分化程度及 EGFR 突变等

有关。最后，我们发现系统性免疫失调与早期非小细胞肺癌患者合并症及围术期全身炎症反应综合征发生率相关。
结论 我们的研究发现非小细胞肺癌患者存在显著的系统性免疫失调，并证明了该系统性免疫失调与患者临床特征的相关性。这些研究结果提示系统性免疫失衡参与了肿瘤发展并有可能成为潜在的早期非小细胞肺癌预后预测及干预靶标。

PU-1373

流式细胞术动态监测食管癌患者手术及化疗前后 T 淋巴细胞亚群及 NK 细胞水平变化的意义

龚容
昆明医科大学第一附属医院

目的 探讨利用流式细胞术多时间点监测食管癌患者手术及化疗前后外周血 T 淋巴细胞亚群及 NK 细胞水平变化的价值及临床意义。
方法 采用流式细胞技术检测 39 例食管癌患者在手术及化疗前后外周血 T 淋巴细胞亚群和 NK 细胞的百分率，并与健康对照组比较并进行统计学分析。
结果 食管癌患者 T 淋巴细胞不同的亚群及 NK 细胞水平与正常人群相比均存在明显差异（$P<0.05$）；手术后 T 淋巴细胞各亚群及 NK 细胞水平均较术前明显下降（$P<0.05$），且在术后第 3 天为最低值，随后逐渐升高，但 $CD4^+/CD8^+$未见明显变化；患者化疗后 $CD3^+$、$CD4^+$比例及 $CD4^+/CD8^+$有所升高，而 CD8+比例下降，差异有统计学意义（$P<0.05$），在化疗后 3 周各 T 淋巴细胞亚群比例与化疗前相似，化疗前后 NK 细胞水平虽表现出与 $CD3^+$、$CD4^+$类似的变化趋势，但是并不显著。
结论 利用流式细胞术多时间点监测可发现食管癌患者手术及化疗前后免疫功能的状态及变化。患者的免疫功能处于受抑制的状态，手术后患者免疫功能更是出现一过性降低，化疗能够一定程度上改善这种状态，但长期来看，化疗对 T 淋巴细胞亚群及 NK 细胞水平的影响可能很小，这可能给予化疗与 T 细胞依赖性免疫治疗在同步或序贯方案中有效结合的想法一定的支持。

PU-1374

血清胃蛋白酶原、胃泌素-17 与幽门螺杆菌抗体分型检测临床分析 1

张培莉
山东第一医科大学附属省立医院

目的 检测体检人群幽门螺杆菌（Helicobacter Pylori，HP）感染情况，以及血清中胃蛋白酶原 I(PGI)、胃蛋白酶原 II（PGII）和胃泌素-17(G-17)的含量，探讨其与 HP 感染发生的相关性。
方法 选择 2017 年 2 月至 4 月到本院体检中心体检的 781 例人群，分别用幽门螺杆菌抗体分型试剂盒和酶联免疫吸附试验检测此人群的血清 HP 抗体分型、PGI、PGII、G-17 水平。运用用 SPSS22.0 分析系统，对该人群 HP 感染率，HP 感染者与非感染者间及不同分型感染者间 PGI、PGII、PGI/PGII（PGR）、G-17 水平差异进行分析，并对不同年龄不同性别体检者感染率及各水平差异进行分析。
结果 HP 阳性感染者占 49.81%，不同年龄组间有显著性差异（P<0.05）。HP 阳性与阴性者比较，血清中 PGI、PGII、PGR、G-17 水平有显著性差异（P<0.05）。将感染者按 HPI 型和 HPII 型分组比较，PGII、PGR 水平有显著性差异（P<0.05）。不同性别不同年龄组血清中 PGI、PGII 水平

均有显著性差异（P<0.05），PGI、PGII 水平男性较女性偏高；随年龄升高，PGI、PGII、G-17 有升高趋势，而 PGR 呈下降趋势。
结论 该地区体检人群中，血清 PG 水平与性别、年龄、HP 是否感染有关，且与 HP 感染分型密切相关。将 HP 抗体分型及血清 PG、G-17 水平联合作为胃功能常规检测，对早期胃部疾病的评估和筛查重要的意义。

PU-1375

Logistic 回归和 ROC 曲线评价 EB 病毒抗 VCA-IgM，AST，ALT 对 EB 病毒现症感染的诊断价值

张培莉
山东第一医科大学附属省立医院

目的 应用 Logistic 回归和受试者工作特征 ROC 曲线探讨 EB 病毒衣壳抗原 IgM（EB 抗 VCA-IgM）、AST、ALT 单向检测及联合检测对 EB 病毒现症感染的诊断价值。
方法 回顾性研究。收集 2016 年 1 月至 10 月化学发光法测定 EB 病毒抗 VCA-IgM 阳性的样本，RT-PCR 法检测 EB-DNA，酶速率法检测 AST、ALT,将标本分成 EB-DNA 阳性组和 EB-DNA 阴性组，运用 SPSS22.0 对各指标进行非参数检验，通过 Logistic 回归和 ROC 曲线对各指标进行分析。
结果 EBV DNA 阳性组抗 VCA-IgM、AST、ALT 水平均高于 EBV DNA 阴性组水平，差异有统计学意义（P < 0.05）。抗 VCA-IgM、AST、ALT 三者均与 EBV DNA 呈相关性（P < 0.05）。抗 VCA-IgM、AST、ALT 三者单项检测曲线下面积（AUC）分别为 0.803[95%CI(0.735～0.872)],0.788[95%CI(0.708～0.868)]，0.752[95%CI(0.671～0.832)]，三者联合检测的 AUC 为 0.830[95%CI(0.765～0.896)]，高于各指标单项检测 AUC。
结论 EB 病毒现症感染指标中，抗 VCA-IgM 意义最大，优于 AST、ALT，三者联合检测优于单项检测意义,有助于 EB 病毒感染及其他合并感染的诊断和防治。

PU-1376

解脲支原体感染、细菌性阴道病与女性不孕的相关性分析

岑宜静
四川省人民医院城东院区

目的 研究分析细菌性阴道病（BV）和解脲支原体(UU)感染与女性不孕的相关性。
方法 收集 2018 年 12 月~2020 年 12 月来我院辅助生殖中心就诊的 762 例患者做为此次研究的观察组，选取同期来我院体检的 200 例健康女性作为对照组，检测两组研究对象的细菌性阴道病（BV）和解脲支原体感染情况。将不孕症患者分为原发不孕（N=329）和继发不孕（N=433），对比不同不孕症类型患者的解脲支原感染（UU）和细菌性阴道病(BV)检测结果
结果 观察组患者的解脲支原体（UU）感染和细菌性阴道病(BV)的检出率均显著高于对照组，差异有统计学意义（P<0.05）。继发性不孕症患者的解脲支原体检出率显著高于原发性不孕症患者，差异有统计学意义（P<0.05）。
结论 女性不孕症与解脲支原体感染和 BV 有极为密切的联系，尤其是继发性不孕症患者的解脲支原体感染检出率更高。

PU-1377

三种抗双链 DNA 抗体检测方法在系统性红斑狼疮诊断中的效能评价

毕胜、朱红艳、孙鹭、沈燕迪
云南省第一人民医院

目的 评价间接免疫荧光法(IIFA)、免疫印迹法(LIA)和酶联免疫吸附法（enzyme-linked immunosorbent assay, ELISA）检测抗双链 DNA(dsDNA)抗体的性能。
方法 选取在本院就诊的 93 例系统性红斑狼疮（SLE）患者、84 例其他自身免疫性疾病患者和 50 例健康人作为对照组，采用上述 3 种方法检测血清中的抗 dsDNA 抗体。
结果 在 SLE 患者组中，抗 dsDNA 抗体检测阳性率最高的是 ELISA 法（60.2%），其次为 LIA 法（46.2%），最低的为 IIFA 法（38.7%），均显著高于对照组，差异有统计学意义（P<0.05）。特异度与阳性预测值最高的是 IIFA 法（99.3%、97.3%），灵敏度与阴性预测值最高的是 ELISA 法（60.2%、77.7%），ROC 曲线下面积最大是 ELISA（0.782），其次是 LIA 法（0.724），IIFA 法（0.690）。IIFA 法和 LIA 法(Kappa=0.881，P<0.001)、LIA 方法和 ELISA(Kappa=0.804，P<0.001)诊断结果一致性较好；IIFA 方法和 ELISA 方法诊断结果一致性一般(Kappa=0.693，P<0.001) 。
结论 推荐 ELISA 法联合 IIFA 法检测抗 dsDNA 抗体，对 SLE 诊断和病情活动监测有重要意义。

PU-1378

肾脏病患者血清过敏原检测结果分析研究

朱红艳、毕胜、孙鹭、沈燕迪、余亚玲
云南省第一人民医院

目的 探讨肾脏病患者食入性及吸入性过敏原分布情况。
方法 采用免疫印迹方法对 296 例肾脏病患者和 156 例正常对照的血清进行食入性及吸入性过敏原检测。
结果 肾病患者中食入性与吸入性过敏原阳性者占 70.3%（208/296）；对照组中过敏原阳性者占 31.4%（49/156），两组间差异有统计学意义（p<0.05）；过敏原阳性肾病患者中以肾病综合征（nephrotic syndrome, NS）患者最多，占 27.9%（58/208），其次是慢性肾衰竭（chronic renal failure, CRF）患者和 IgA 肾病患者，分别占 26.4%（55/208）和 11.1%。过敏原阴性肾病患者中 CRF 患者最多，占 40.9%（36/88），其次是 NS 患者，占 14.8%（13/88）,两组病人间差异有统计学意义(p<0.05)。同一种疾病过敏原阳性与阴性病人数量比值最高的是 IgA 肾病和 NS 患者（4.6 VS 4.5）；肾脏病人血清过敏原阳性患者中，最常见的过敏原是户尘螨占 76.4%（159/208）、其次是蟑螂占 58.7%（122/208）及腰果占 38.5%(80/208)。
结论 肾病患者尤其是 IgA 肾病和肾病综合征患者中过敏原阳性情况比较常见，户尘螨和蟑螂是该地区肾病患者中最常见的过敏原。因此，对于肾病患者应常规进行血清过敏原检测筛查。

PU-1379

浙江地区 0-14 岁儿童维生素 D 水平现状分析

柳强
杭州迪安医学检验中心有限公司

目的 了解浙江地区 0-14 岁儿童血清 25-羟维生素 D 水平和现状，为本地区儿童合理补充维生素 D 提供参考依据。
方法 血清 25-羟维生素 D 采用直接化学发光法检测。回顾分析本中心 2019 年 6 月 1 日至 2020 年 5 月 31 日浙江地区 20227 例 0-14 岁儿童健康体检血清 25-羟维生素 D 检测结果，计算 25-羟维生素 D 水平；分析其与年龄、性别以及季节变化之间的关系。
结果 浙江地区 20227 例 0-14 岁儿童血清 25-羟维生素 D 平均水平为（26.45±18.98）ng/ml，其中 25-羟维生素 D 充足(≥20.00ng/ml)占比 73.95%(14958/20227)，25-羟维生素 D 不足（12.00～20ng/ml）占比 23.02%(4657/20227)，25-羟维生素 D 缺乏（＜12.00ng/ml）占比 3.03%(612/20227)；不同性别儿童血清 25-羟维生素 D 水平比较，0-1 岁组和 3-6 岁组男、女童比较差异均无统计学意义[（33.96±19.41）ng/ml 比（33.50±19.47）ng/ml，（25.26±15.48）ng/ml 比（24.93±15.53）ng/ml，均 P＞0.05]，1-3 岁组和 6-14 岁组男童较女童高，比较差异均有统计学意义 [（29.17±19.15）ng/ml 比（28.48±18.21）ng/ml]较女童高[（19.50±13.13）ng/ml 比（18.63±12.69）ng/ml，均 P＜0.05] ；不同季节儿童 25-羟维生素 D 水平不同，秋季儿童血清 25-羟维生素 D 水平[（27.10±18.81）ng/ml]高于其他三季，[春（26.06±19.36）ng/ml、夏（26.57±18.76）ng/ml、冬（25.57±19.11）ng/ml]，其中冬季最低，差异均有统计学意义（均 P＜0.05）；随着年龄增大，儿童血清 25-羟维生素 D 的水平逐渐减低[0-1 岁组、1-3 岁组、3-6 岁组和 6-14 岁组分别为（33.76±19.44）ng/ml、（28.85±18.73）ng/ml、（25.11±15.50）ng/ml、（19.16±12.99）ng/ml]，不同年龄段儿童血清 25-羟维生素 D 的水平差异均有统计学意义（均 P＜0.05）。
结论 浙江地区 0-14 岁儿童维生素 D 营养状况总体良好，仅有小部分维生素 D 含量不足或缺乏。维生素 D 作为儿童生长发育的必要营养元素，其补充应该贯彻儿童发育的不同时期，且还应该根据当地季节变化补充 25-羟维生素 D。

PU-1380

新型冠状病毒防控措施对呼吸道感染谱影响的初步分析

曾家伟、彭梦
绵阳市中心医院

目的 分析新型冠状病毒（Severe acute respiratory syndrome coronavirus 2, SARS-CoV-2）流行后所采取的各种防控措施对甲型流感病毒（Influenza A virus, FluA）、乙型流感病毒（Influenza B virus, FluB）、副流感病毒（Parainfluenza virus, PIV）、腺病毒（Adenovirus, ADV）、嗜肺军团菌（Legionella pneumophila, LP）、肺炎支原体（Mycoplasma pneumoniae, MP）、肺炎衣原体（Chlamydia pneumoniae, CP）和呼吸道合胞病毒（Respiratory syncytial virus, RSV）在呼吸道中感染率的影响。
方法 收集 2019 年 3 月至 2021 年 2 月在绵阳市中心医院门诊和住院进行呼吸道病原体检测的原始数据结果，分析防控前（2019 年 3 月至 2020 年 2 月）和防控后（2020 年 3 月至 2021 年 2 月）8 项呼吸道病原体检出率的变化。
结果 在采取防控措施前 RSV、PIV、MP、LP、FluB、FluA、ADV 和 CP 的阳性率分别为 3.36%、4.62%、21.29%、5.99%、34.78%、36.64%、3.54%和 3.29%，总阳性率为 14.19%；在采取防控措施后，RSV、PIV、MP、LP、FluB、FluA、ADV 和 CP 阳性率分别为 3.21%、7.53%、20.25%、9.74%、27.06%、34.66%、2.57%和 2.29%，总阳性率为 13.41%。前后相比 MP、PIV、

LP、FluB、FluA、ADV 和 CP 阳性率的降低有统计学差异，RSV 阳性率的降低无统计学差异。检出抗体阳性的病例数除 PIV 和 LP 有小幅上升，分别增加了 18.49%和 18.34%外；其余均呈下降趋势，如 RSV（-30.39%）、MP（-30.82%）、FluB（-43.42%）、FluA（-31.21%）、ADV（-47.29%）和 CP（-49.47%），检出阳性的病例数平均下降 24.47%。

结论 针对 SARS-CoV-2 流行所采取的防控措施对降低呼吸道病原体的感染具有重要作用，特别在呼吸道感染性疾病高发季节，做好个人防护，采取有效的措施，能够大大降低感染风险。

PU-1381

核酸适配体在炎症性疾病诊疗中的应用

牛会敏
联勤保障部队第九〇〇医院

炎症是机体组织对损伤和感染的一种保护性生物反应，在病理状态时，促炎与抗炎细胞因子异常释放，选择性诱导受体细胞的特定信号，实现基因调控以影响宿主应答。基于适配体对目标分子高亲和力和特异性，且合成简单、易于修饰、成本低的优势，有望代替抗体用于临床诊断和治疗。本文综述了现有人工筛选的 12 种细胞因子的特异性适配体，包括 IL-1α、IL-6、IL-11、TNF-α、TGF- β、IFN-γ、IL-8、IL-17、IL-32、IL-23、MCP-1 和 IP-10；总结了基于适配体联合纳米材料及信号放大技术的电化学和光学传感器；列举了多种稳定性适配体在有效抑制炎症、减慢肿瘤进程中的免疫治疗应用。随着对疾病标志物的深入研究，需要继续筛选更多特异性适配体。在疾病诊断方面，适配体传感器需要从单一化向组合化发展，从复杂化向简便化发展。在治疗方面，多数适配体在动物测试中有效但还没有被批准用药，需要进一步结构修饰提高稳定性。目前，细胞因子适配体筛选、适配体作用机制分析、适配体相关的即时诊断技术研发及适配体药物的临床试验等方面仍需付出更多努力。

PU-1382

血清抗 Scl-70 抗体的检测分析与临床价值探讨

何增品
昆明医科大学第一附属医院

目的 研究流式点阵免疫发光法测定的抗 Scl-70 抗体联合抗核抗体（ANA）以及实验室检测指标在临床诊断中的意义，为疾病的诊断提供依据。

方法 选取 2019 年-2020 年来院就诊的 115 例抗 Scl-70 抗体阳性（>8.0）ANA（+）患者作为抗 Scl-70 抗体（+）组，以 406 例抗 Scl-70 抗体阴性（<0.2）ANA（+）患者作为抗 Scl-70 抗体（-）组，就两组患者的一般资料、临床诊断、ANA 核型和滴度、ANA 抗体谱及其他实验室指标进行研究，并对结果进行统计学分析。

结果 抗 Scl-70 抗体阳性患者男女比例 1:1.80，且以中老年居多，平均 54（43，67）岁，高于抗 Scl-70（-）组，差异有统计学意义（P<0.05）。抗核抗体 ANA 荧光核型以核仁型为主，其次为核颗粒型、核均质型。ANA 谱中抗 Scl-70 抗体>8.0 合并出现抗 SSA 抗体阳性比例最高，达 41.74%，差异有统计学意义（P<0.05）。临床诊断为系统性硬化症,占 30.43%，其次为结缔组织病，占 13.04%，干燥综合征，占 11.30%，系统性红斑狼疮，占 11.30%。抗 Scl-70 阳性患者血清免疫球蛋白均明显升高，差异有统计学意义（P<0.05）。抗 Scl-70 阳性患者补体 C3、C4 均明显降低，差异有统计学意义（P<0.05）。

结论 抗 Scl-70 阳性患者以中老年女性为主，ANA 荧光核型以核仁型为主，临床相关诊断主要为系统性硬化症，结缔组织病，干燥综合征，系统性红斑狼疮。使用流式点阵免疫发光法检测的抗 Scl-70 抗体联合间接免疫荧光发检测抗核抗体（ANA）对疾病的诊断与鉴别诊断有重要意义。

PU-1383

我院 2019 年-2020 年新生儿乙肝两对半结果分析

罗彩心
资阳市妇幼保健院

目的 为了解我区新生儿乙肝两对半的模式情况，为后期检验结果出具，合理性提供可参考依据。
方法 用化学发光方法检测乙肝五项。
结果 共统计 564 名年龄在 5 天以内的新生儿，四种模式最常见： HBV 五项全阴为 156 人，比率 22.3%；单独抗-HBS 阳性为 117 人，比率 20.74%；HBsAb、HBeAb、HBcAb 阳性为 128 人，比率为 22.69%；HBsAb、HBcAb 阳性人数 146 人，比率为 25.89%。相对少见得模式有三种：HBcAb 阳性人数为 19 人，比率 3.37%；HBeAb、HBcAb 阳性人数为 14 人，比率 2.48%；HBsAb、HBeAg、HBcAb 阳性人数为 9 人，比率为 1.59%。及少见模式四种：HBeAg、HBcAb 阳性人数为 2 人；HBsAg、HBsAb、HBcAb 阳性人数为 1 人；。HBsAg、HBcAb 阳性人数为 1 人；HBsAg、HBsAb、HBeAb、HBcAb 阳性人数为 1 人。
结论 5 天以内的新生儿，五项全阴，表抗体阳性，表抗体、e 抗体、c 抗体阳性，表抗体、c 抗体阳性这四种模式最为常见。

PU-1384

乙型肝炎患者血清免疫球蛋白的临床检验准确性及价值分析

杨利侠
资阳市中医医院

目的 分析乙型肝炎患者血清免疫球蛋白的临床检验准确性及价值。
方法 选取我院 2019 年 1 月至 12 月间收治的乙型肝炎患者 180 例作为此次研究的实验组，再将其按照疾病类型的不同分成各有 90 例的肝硬化组与非肝硬化组，其中肝硬化组再分为各有 45 例的代偿期组以及非代偿期组，此外，在选取同期在我院接受健康体检的人员 90 例作为参照组，对本次研究的所有患者均实施血清免疫球蛋白检测，并对检测结果进行对比分析。
结果 肝硬化组以及非肝硬化组患者的 IgA、IgM 以及 IgG 水平均高于对照组，且肝硬化组高于非肝硬化组，对比均具有统计学差异性（$p<0.05$）；而非代偿期组的 IgA 水平明显高于代偿期组，对比（$p<0.05$），具有统计学意义，但两组的 IgM 以及 IgG 水平对比则无统计学意义（$p>0.05$）。
结论 对乙型肝炎患者实施血清免疫球蛋白检测的价值较高，值得推广。

PU-1385

孕产妇产前检测免疫学检验的临床应用对降低不良分娩发生率的价值分析

兰隆琴
资阳市雁江区中医医院

目的 分析孕产妇产前检测免疫学检验的临床应用及对降低不良分娩发生率的价值。
方法 抽取 2019 年 1 月至 2020 年 8 月间我院收治的孕产妇 168 例作为此次的观察对象，并将其按照抽签法分成各有 84 例常规检验组以及常规检验+免疫学检验组，并对两组的疾病检出率、不良事件发生率、不良分娩发生率进行分析。
结果 从产妇疾病检出率上看，常规检验+免疫学检验组明显较高，与常规检验组相比显著（$p<0.05$），具有统计学意义；从不良事件发生率上看，常规检验+免疫学检验组明显较低，对比

结果（p<0.05），具有统计学差异性；从不良分娩发生率上对比，常规检验+免疫学检验组较低，与常规检验组相比具有统计学差异性（p<0.05）。
结论 孕产妇在产前检测中采取免疫性检验的临床价值较高，值得推广。

PU-1386

TPHA 法与 ELISA 法用于梅毒不同时期患者临床检验的价值分析

杨利侠
资阳市雁江区中医医院

目的 探讨梅毒螺旋体血球凝集试验法（TPHA）与酶联免疫吸附试验法（ELISA）对梅毒不同时期患者临床检验的效果。
方法 选取本院 2018 年 8 月至 2019 年 8 月收治 100 例梅毒患者建立研究组，包括一期梅毒 38 例、二期梅毒 62 例，同期纳入健康体检者 100 例建立对照组。受检者均进行 ELISA 法检测、TPHA 法检测。对比分析两种方法检验情况。
结果 ELISA 法对一期梅毒、二期梅毒阳性检出率相比 TPHA 法明显更高（P<0.05），两种方法检测对照组阳性检出率对比无明显差异（P>0.05）；ELISA 法检测敏感度与准确率相比 TPHA 法检测较高。
结论 临床针对不同时期梅毒疾病患者采用 ELISA 法检验相比采用 TPHA 法检验的敏感度与准确度更高，该方法操便捷，具有临床推广与应用价值。

PU-1387

2020 年吉林地区过敏原检测结果季节性分析

郭亚明
吉林金域医学检验所有限公司

目的 我国过敏性疾病人群发生率很高，是临床常见多发病。本文通过检测和分析吉林地区过敏原检测结果，为临床患者对过敏的预防及治疗提供参考依据。
方法 选取 2020 年 1 月至 2020 年 12 月吉林地区送检我公司的过敏原项目 500 例阳性患者为研究对象。特异性过敏原被吸附于硝酸纤维素膜表面，加入患者血清后孵育，标本中的特异性 IgE 与过敏原发生反应，结合到硝酸纤维素膜上。加入碱性磷酸酶标记的链酶亲和素，与生物素结合。加入 BCIP/NBT 酶作用底物孵育后，发生特定底酶显色反应，试剂条上出现沉底。颜色的深浅与血清中的 sIgE 抗体含量成正比，待试剂条干燥后，用过敏原检测仪器检测，读取定量检测结果。
结果 主要对过敏原阳性高发率当中的其中 2 项进行了统计，豚草在春季的阳性标本 53 例，占比 10.60%，夏季阳性标本 43 例，占比 8.60%，秋季阳性标本 4 例，占比 0.85%，冬季阳性标本 2 例，占比 0.05%。猫毛在春季阳性标本 59 例，占比 11.80%，夏季阳性标本 27 例，占比 5.50%，秋季阳性标本 60 例，占比 12.10%，冬季阳性标本 30 例，占比 6.12%。
结论 实验证明，豚草的发病季节在春季阳性率占比最高。猫毛在春季和秋季阳性率占比较高。目前过敏原最常用的筛查方法是免疫印记法。该方法是检测患者血清特异性 IgE 抗体。过敏原检测对过敏性疾病的诊断，治疗及预后判定均具有重要意义，检测发现过敏原并采取有效措施避免与之接触，是过敏疾病防治的基本原则。因此针对吉林地区，对豚草过敏的人群应远离豚草，远离过敏原就可以避免过敏的发生。对猫毛过敏的人群就不适宜养猫，避免接触猫毛，远离过敏原就可以避免过敏的发生。过敏并不可怕，只要适当远离过敏原就可以减少过敏疾病的发生。

PU-1388

胃癌应用 CA724、CEA、CA242、CA199 肿瘤标志物联合检验的分析

陶贵华、贺爱丽
德州市第二人民医院

目的 分析胃癌应用 CA724、CEA、CA242、CA199 肿瘤标志物联合检验的临床价值。
方法 选择 2018 年 1 月—2019 年 1 月于我院就诊的 30 例胃癌患者为观察组，另选同期 30 例胃良性病变患者为对照组，关于血清 CA724、CEA、CA242、CA199 的检测均给予电化学发光法、放射免疫法与酶联免疫吸附试验，对比分析两组患者的具体情况。
结果 观察组血清肿瘤标志物水平明显高于对照组，且多项检测敏感度随之提高（P＜0.05）。
结论 针对胃癌患者，CA724、CEA、CA242、CA199 肿瘤标志物能够极大的提升临床诊断敏感性，便于早期诊断，在临床上具有很高的应用价值。胃癌是一种恶性肿瘤，在临床上比较常见，关于诊断多采用影像学、胃镜与病理学检查等，会耗费大量的资源，即人力、财力等，并且需要专业人员。近年来，随着我国生活习惯的改变，胃部恶性肿瘤发生率逐年增加，且多出现在胃窦部，病理分型较多，主要是腺癌与鳞状细胞癌，对于胃癌患者而言，早期无典型症状，就诊时多发展到晚期，为此及早诊断能够有效的诊治疾病，取得良好预后效果。随着临床基础医学的逐渐发展，在早期诊断中血清肿瘤标志物的检测成本最低且最为快捷方便，通过特异性指标能够靶向诊断肿瘤，但是肿瘤具有多个形态，一种肿瘤所具有的肿瘤标记物有很多种。关于肿瘤的存在，可经肿瘤标志物及时反映出来，在正常机体中含量较少，在出现癌变时，会提高其浓度，伴随着不断提高的医疗水平，在临床中肿瘤标志物能够更加广泛的诊断恶性肿瘤，且能够将癌症发展进程在一定程度上反映出来，在病变组织与血液中能够检出，待其水平达到一定程度后，便可以提示恶性肿瘤的存在，如 CA724、CEA、CA242、CA199 等已经逐渐成为当下研究的重点。

PU-1389

梅毒抗体三种不同检测方法的检测应用及比较

张敏
合肥金域医学检验实验室有限公司

目的 探讨应用 3 种不同的血清学方法测定梅毒抗体并评价检测结果，建立适合自己实验室的梅毒检测流程。
方法 将 160 例已确诊为梅毒阳性血清标本分别采用酶联免疫吸附测定法（ELISA）、甲苯胺红不加热血清试验（TRUST ）、梅毒螺旋体明胶颗粒凝集试验（TPPA）检测血清梅毒抗体，观察三者的敏感度及特异性。
结果 酶联免疫吸附测定法（ELISA）检测阳性 158 例，阳性率为 98.75%；梅毒螺旋体明胶颗粒凝集试验（TPPA）法检测 154 例，阳性率为 96.25%；TRUST 法检测阳性 105 例，阳性率为 65.62%。而在 120 例非梅毒对照组中，经 TP-ELISA 检测 115 例为阴性，特异性为 95%，TPPA 阴性 118 例，特异性为 98%，TRUST 阴性 108，特异性为 90%。
结论 TP-ELISA 法检测梅毒螺旋体特异性抗体具有操作简便，结果易于保存，敏感度优于 TPPA 及 RPR 法等特点，但也存在一定的假阴性和假阳性为了提高梅毒检出率，对于 TP-ELISA 阳性标本，要做 TRUST 复检和 TPPA 确认实验。

PU-1390

合肥市高新区成人接种新冠疫苗后抗体水平检测结果分析

梅圣学
合肥金域医学检验实验室有限公司

目的 分析研究新冠疫苗接种后新冠抗体的检测结果。
方法 选取 2020 年 10 月份到 2021 年 3 月份送检我中心 103 例接种新冠疫苗 1 月左右的成人抗体水平，对这些人群采用磁微粒化学发光法进行新冠 IgM、IgG 和 IgA 抗体进行检测，并对其检测结果进行总结与分析。
结果 由于个体及新冠 IgM、IgG 和 IgA 抗体在人体中存在时间长短的原因，在我中心送检的 103 例新冠疫苗接种者，其中新冠 IgG 阳性率 90%，新冠 IgM 阳性率 72%，新冠 IgA 阳性率 8%.
结论 随着新冠疫苗接种率的不断提高，抗体检测会逐渐的开展起来，IgG 阳性率对疫苗接种效果监测有一定的辅助指导意义。

PU-1391

强直性脊柱炎发病机制研究进展

彭若玉
郑州大学第一附属医院

强直性脊柱炎（AS）是一种以脊柱及骶髂关节慢性炎症为主的全身性结缔组织疾病，目前 AS 病因和发病机制尚未明确，且疾病也无理想的早期诊断及治疗方法。前期研究发现，AS 的发生与遗传因素相关，且在 AS 发生过程中 miRNA 的改变已经被证实，据此我们可以推测，在此过程中相关的 circRNA 也发生改变，circRNA 与 AS 的生物学行为和临床表现有关，可以作为潜在的分子标志物和治疗靶点。本课题拟通过对 AS 发生相关 circRNA 及其调控 miRNA 的作用进行探讨，以增加我们对 AS 发病机制的了解，并进一步寻找有效的分子诊断标志物和药物治疗的作用靶点，为 AS 发生的早期诊断、有效治疗并改善预后等奠定基础。

PU-1392

异嗜性抗体对血清甲状腺功能免疫检测的干扰及分析处理

钱丹、刘畅、田野
陆军军医大学第二附属医院（新桥医院）

目的 分析和处理异嗜性抗体对血清甲状腺功能免疫检测的干扰。
方法 分别采用倍比稀释法，大分子蛋白干扰排除法，聚乙二醇（PEG）沉淀法及异嗜性抗体阻断剂对血清样本进行异嗜性抗体干扰的分析及处理检测。在排除大分子蛋白干扰的情况下，比较分析倍比稀释，PEG 沉淀，异嗜性抗体阻断剂处理前后的甲状腺功能免疫学血清检测的结果。
结果 使用贝克曼 IMMANGE800 测定干扰血清的免疫球蛋白及类风湿因子，结果均在正常参考范围以内可排除大分子蛋白对检测结果的干扰。使用 ARCHITECT i2000SR 系统检测干扰血清及对照组血清原倍、2 倍、4 倍、8 倍的甲状腺功能检测值，结果提示无干扰对照组倍比稀释检测值成线性，干扰血清倍比稀释检测值不成线性及相关性分析 R 值均小于 90。PEG 沉淀后血清高灵敏血清促甲状腺激素(TSH)，甲状腺球蛋白抗体(TGAB)，甲状腺过氧化物酶抗体(TPOAB)回收率均<40%。使用 ARCHITECT i2000SR 系统检测异嗜性抗体阻断剂处理前后甲状腺功能血清检测结果均在参考范围以内。

讨论 检测血清受到异嗜性抗体的干扰，利用倍比稀释，PEG 沉淀，异嗜性抗体阻断剂可以有效解决此类干扰作用。

PU-1393

感染新冠肺炎病毒康复者体内抗体水平分析

梅圣学
合肥金域医学检验实验室有限公司

目的 分析研究感染新冠病毒康复患者体内抗体的检测结果。
方法 选取 2020 年临床确认感染新型冠状病毒患者送检我中心的 116 例血清新型冠病毒抗体水平，我中心使用化学发光法对这些患者人群进行新冠 IgM、IgG 抗体定量检测，并对其检测结果进行总结与分析。
结果 在送检我中心的 116 例新冠康复者，其中新冠 IgG 阳性率 95%，新冠 IgM 阳性率 24%.
结论 随着新冠疫情的逐渐控制，新冠抗体检测逐渐的开展起来，由于 IgM 人体内存在的时间较短，而 IgG 抗体在人体内存在的时间较长，新冠 IgG、IgM 阳性率对临床监测有一定的辅助意义。

PU-1394

骨折患者纤维蛋白原浓度与骨不连的关系

耿丽丽
山东第一医科大学附属省立医院

背景 骨不连患者的诊断具有挑战性，因此，需要更多地诊断指标加以辅助。已有研究证明纤维蛋白原浓度是骨不连诊断有潜力的诊断指标。本研究的目的就是揭示纤维蛋白原浓度与骨不连的关系。
材料和方法 我们回顾性的研究了 2010 年 1 月-2019 年 5 月山东省立医院就诊的所有锁骨骨折和股骨骨折的患者共 438 例，在这些病例中，确定入排标准后，最终纳入完全愈合的患者 315 例，骨不连患者 23 例，通过曲线拟合、单因素分析、多因素分析的方法探讨血浆纤维蛋白原浓度与骨不连的关系。
结果 在这些所有患者中，骨不连患者大约有 5%。经曲线拟合显示纤维蛋白原浓度增加，骨不连风险越高。多因素分析的结果显示纤维蛋白原在没有调整变量时，纤维蛋白原每增加一个单位，骨不连的风险增加 55%；纤维蛋白原在调整了年龄和性别两个变量时，纤维蛋白原每增加一个单位，骨不连的风险增加 64%；纤维蛋白原在调整了年龄、性别、损伤机制和 ASA 变量时，纤维蛋白原每增加一个单位，骨不连的风险增加 48%。
结论 骨不连与血浆纤维蛋白原呈现独立相关关系。纤维蛋白原浓度增加，骨不连风险越高。

PU-1395

山东地区人群百日咳抗体阳性特征分析

赵万辉
山东第一医科大学附属省立医院

目的 分析山东地区人群中百日咳抗体的阳性特征情况。
方法 收集 2014 年 1 月至 2016 年 12 月在山东省立医院门诊就诊和住院的患者 5 836 例。用酶联免疫分析方法进行血清百日咳 IgG 抗体、百日咳 IgM 抗体两项指标检测。用 SPSS21.0 软件分析人群中百日咳抗体的阳性特征情况。

结果 5 836 例血清标本中，百日咳 IgG 抗体阳性率为 40.42%，百日咳 IgM 抗体阳性率为 35.52%，男性百日咳 IgG 抗体阳性率 37.56%，明显低于女性的 44.36%（P<0.05）；男性百日咳 IgM 抗体阳性率为 29.83%，明显低于女性的阳性率 43.34%（P<0.05）。百日咳 IgG 抗体阳性率以 6 个月~＜12 个月（24.70%）最低，以后逐渐升高，30 岁以上组最高（67.34%）；百日咳 IgM 抗体阳性率以小于 6 个月组最低（2.54%），7 岁~＜15 岁组最高（63.98%）。百日咳 IgM 抗体阳性率秋季最高为 45.79%，明显高于夏季的 34.92%，明显高于春季的 25.23%，冬季最低为 18.82%，四个季节之间阳性率差异均有统计学意义（P 均<0.05）。共检出 4 种百日咳抗体项目组合模式，以百日咳 IgG 抗体、百日咳 IgM 抗体双阴性模式最多见，占 49.43%，其次为百日咳 IgG 抗体、百日咳 IgM 抗体双阳性模式占 25.36%，百日咳 IgG 抗体阴性、百日咳 IgM 抗体阳性模式最少见，占 10.14%。
结论 山东地区人群百日咳抗体的阳性率存在性别、年龄和季节差异，应加强对学龄期儿童百日咳的防控。

PU-1396

抗 CCP 抗体、抗 AKA 抗体、抗 APF 抗体等多种检测对类风湿关节炎的诊断价值

赵万辉
山东第一医科大学附属省立医院

目的 探讨检测抗环瓜氨酸多肽抗体（CCP）、抗角蛋白抗体（AKA）、抗核周因子抗体（APF）、抗 RA33 抗体、抗葡萄糖 6 磷酸异构酶抗体（GPI）、抗突变型瓜氨酸波形蛋白抗体（MCV）、补体 C1q、类风湿因子（RF）、血沉（ESR）在类风湿性关节炎（RA）的临床诊断价值。
方法 选取经临床确诊的类风湿性关节炎患者 120 例，体检健康者 80 例，分别检测其 CCP、AKA、APF、抗 RA33 抗体、抗 GPI 抗体、抗 MCV 抗体、补体 C1q、RF 及 ESR，并对结果进行统计分析。
结果 CCP、AKA、APF、抗 RA33 抗体、抗 GPI 抗体、抗 MCV 抗体、补体 C1q、RF 及 ESR 在 RA 中的灵敏度分别为 86.4%、82%、80%、12%、69.2%、78%、10%、87.3%、82.3%，特异性分别为 94.0%、92.5%、90.3%、97.0%、87.6%、90.8%、90.2%、82.5%、72.20%。
结论 抗 CCP 抗体、抗 AKA 抗体、抗 APF 抗体、与其他抗 RA33 抗体、抗 GPI 抗体、抗 MCV 抗体、补体 C1q、RF 及 ESR 综合检测对 RA 具有一定的诊断价值，有助于 RA 的早期临床诊断。

PU-1397

间接免疫荧光法检测血小板相关抗体新判读标准的建立和评价

杨细媚
江西省儿童医院

目的 通过建立新的判读标准来提高间接免疫荧光法（IIF）检测血小板相关抗体（PAIg）的诊断效能。
方法 收集 2020 年 1 月-12 月的 261 例免疫性血小板减少症（ITP）和 50 例红斑狼疮（SLE）患儿作为实验组，50 例再生障碍性贫血（AA）作为病例对照组，50 例健康体检儿童作为正常对照组进行 PAIg 检测。分析新旧两个判读标准的结果，并与流式细胞仪（FCM）法进行比对，分析两种方法的相关性和符合率。
结果 IIF 法使用新的判读标准后，ITP 组患儿阳性率从 19.54%上升到 62.07%，诊断效率从 45.01%上升为 67.64%。SLE 组患儿阳性率从 16%上升到 38%。IIF 法与 FCM 法在诊断 ITP 和 SLE 中结果具有一致性，kappa 值分别为 0.680 和 0.653。

结论 新的 IIF 法判读标准提高了对临床疾病的诊断效能，与 FCM 法比较更适合儿童 ITP 患儿 PAIg 的筛查实验。

PU-1398

乌鲁木齐某中医三甲医院 2020 年 4 种传染性疾病的感染情况分析

王雪婷[1]、宁萍[1]、李奋荣[1]、赵淑珍[1]、赖长青[2]、王瑾[1]、伏志勇[3]、陈媛[1]、云发超[1]
1. 乌鲁木齐市中医医院
2. 军区总医院北京路医疗区
3. 中国人民解放军 93986 部队医院

目的 了解乌鲁木齐地区患者的乙型肝炎病毒（HBV）、丙型肝炎病毒（HCV）、梅毒螺旋体（TP）和人类免疫缺陷病毒（HIV）的感染情况，分析流行因素，为防止院内感染和我市相关部门制定传染病预防策略提供参考资料。
方法 2020 年共有 8440 名患者在我院进行了以上 4 种疾病的筛查，采用化学发光法定量检测各传染病的血清标志物，对比分析患者的感染情况，用 SPSS 17.0 进行统计学数据处理。
结果 8840 名患者中 HBV、HCV、TP、HIV 的检测者各有 8396 例、7504 例、7554 例、7452 例，感染率为 5.55%（466 例）、1.999%（90 例）、0.40%（30 例）、0.09%（7 例）；比较各传染病上下半年的检测结果，感染率差异均无统计学意义（P>0.05）；HBV、TP 的感染率在男女间无明显差异（P > 0.05），HCV、HIV 的感染率在男性人群中高于女性（P < 0.05）;HBV 感染率在>40 岁年龄组要高于≤40 岁年龄组（P < 0.05），其他 3 种无明显的年龄上的差异。
结论 2020 年本地区 HBV、HCV 感染率较于我国一般人群低，TP、HIV 感染率较高；HCV、HIV 感染在男性中多发，高龄 HBV 感染者较多。需要加强传染病的筛查力度，完善相关预防措施，做好传染病知识宣教工作。

PU-1399

血清 Lp-PLA2 联合 S100β 检测在脑梗死患者的临床应用价值

万青
东南大学附属中大医院

目的 探讨血清脂蛋白相关磷脂酶 A2(Lp-PLA2)和血清 S100 钙结合蛋白 β(S100β)测定在急性脑梗死(Acute cerebral infarct, ACI)患者观察病情严重程度的临床应用价值。
方法 选取 2021 年 2 月-2021 年 5 月在我院收治的 157 例 ACI 患者为观察组，同时选取在我院接受体检的健康人员 70 例作为对照组，将两组血清 Lp-PLA2 和 S100β 水平进行检测分析对比。
结果 患者组血浆 Lp-PLA2 和 S100β 水平均高于对照组，差异具有统计学意义(P< 0.05)；患者神经功能损伤程度越高，血清 Lp-PLA2 和 S100β 水平越高，差异具有统计学意义(P< 0.05)。
结论 ACI 患者的血清 Lp-PLA2 和 S100β 水平与神经功能损伤程度有关，对 ACI 患者进行 Lp-PLA2 和 S100β 水平的相关检测有利于临床病情的观察。

PU-1400

脑特异性蛋白产物 9.5 检测试剂对外源性颅脑损伤患者的检测性能评估

申逸志、姜习新、王锴佳、梁紫薇
岳阳市人民医院

目的 对国产脑特异性蛋白产物 9.5 检测试剂进行检测性能评估。
方法 应用 319 例颅脑损伤患者血清样本（其中具有 CT 诊断结果或格拉斯哥评分的新鲜样本 79 例），分别采用考核试剂盒和对比试剂盒对同一入选患者的血清标本进行检测及结果判定，比较考核试剂的判断结果与临床诊断结论的一致性，以及考核试剂与对比试剂检测结果的相关性和一致性。
结果 本研究共收集 319 例血清样本，用于统计分析，分析结果表明，319 例样本中，考核试剂和对比试剂检测结果之间的阳性符合率为 96.34%，95%可信区间为（92.28%，100%），阴性符合率为 99.16%，95%可信区间为（97.99%，100%），总符合率为 98.43%，95%可信区间为（97.07%，99.80%），Kappa 值=0.9588，考核试剂与对比试剂具有良好的相关性；79 例新鲜样本的考核试剂检测结果与临床诊断结果的阳性符合率为 96.15%，95%置信区间为（90.93%，100%），阴性符合率为 96.30%，95%置信区间为（89.17%，100%）；总符合率为 96.20%，95%置信区间为（91.99%，100%），Kappa 值=0.9163，考核试剂检测结果与临床诊断具有良好的相关性。
结论 考核试剂和对比试剂测定结果之间具有较高的符合程度和较好的一致性，对于临床应用，两者之间具有等效性；此外，考核试剂的检测结果与临床诊断结果同样具有较高的符合程度和较好的一致性，该脑特异性蛋白产物 9.5 检测试剂可用于外源性脑损伤的辅助诊断。

PU-1401

HIV/HCV 共感染和 HCV 感染使用检验指标评估肝纤维化在临床应用的研究

翟秀伟、陈艳芝、李巧清、张思荣、郭霞、杨珅、何丽萍
保山市人民医院

目的 探讨 HIV/HCV 共感染与 HCV 单纯感染对肝纤维进程中的影响进行临床探讨。
方法 选取 299 例研究背景相对一致的患者作为研究对象，且 HCV-RNA 检测均结果>500IU/mL 其中男性 158 例（52.9%），女性 141 例（47.1%），年龄 22～65，平均年龄为（39±11.2）岁，共分为 HIV(CD4+>400 个/ul)与 HCV 共感染、HIV(CD4+<400 个/ul)与 HCV 共感染、HCV 单纯感染三组，通过检测三组研究对象的天门冬氨酸氨基转移酶(AST) 和血小板(PLT)结果计算出 APRI，APRI 值指数是天门冬氨酸氨基转移酶(AST) 与血小板(PLT) 比值，APRI 评分是一种被较多研究者接受的无创诊断模型评价肝病患者肝纤维化程度的方法，本研究使用 APRI 评分作为肝纤维程度指标，并对 HIV/HCV 共感染与 HCV 单纯感染不同患者的肝纤维程度进行比较研究。
结果 ①三组患者的 AST 进行比较（q 0.08，p 0.93）P>0.05,三组差异没有统计学意义②三组患者的 PLT 进行比较（q 0.03，p 0.97）P>0.05,三组差异没有统计学意义③使用 AST 和 PLT 结果计算出 APRI，对三组研究对象的肝纤维程度 APRI 评分比较为（q 0.64，p 0.53）P>0.05。
结论 HIV/HCV 合并感染患者与 HCV 单纯感染者在肝脏纤维化进程的影响没有显著性差异。

PU-1402

实验室自建 B 细胞亚群流式检测方案和商品化试剂盒方案结果的比对

吴伟民
中南大学湘雅二医院检验科

背景/目标 随着流式细胞分析方法和淋巴细胞亚群检测项目的推广，临床医师对流式技术运用于临床检测的需求也高。现有的商品化的 BD 公司的淋巴细胞亚群检测试剂盒包含了 B 细胞、T 细胞和 NK 细胞的比例，而 T 细胞又可以进一步细分为 Th 细胞和 Ts 细胞。但是，一方面高昂的临床收费阻碍了这个项目的广泛开展，另一方面特定的临床专科仅对这一项目的某一个指标感兴趣而不需要其他的结果。所以，针对肾内科的患者进行临床检测，我们实验室自建了一套 B 细胞亚群流式检测方案，并讲其与商品化试剂盒方案结果的比对。
方法 我们实验室自建了一套 B 细胞亚群流式检测试剂由两个部分组成，分别为 BD 公司 3/4/8 检测试剂盒和 CD19-APC 抗体。在自建方法中，全血染色后裂解红细胞，并且使用 PBS 洗涤两次，其中淋巴细胞使用 FSC/SSC 圈门。商品化试剂盒也来自 BD 公司（Multitest CD3/CD8/CD45/CD4 和 CD3/CD16+CD56/CD45/CD19）。商品化试剂盒只裂解红细胞，并不洗涤，其中淋巴细胞使用 SSC/CD45 圈门。选取了 10 个临床标本，分别使用两种方法进行检测，并分析两种方法的结果的差异。
结果和结论 实验室自建方法淋巴细胞圈门清晰，对于外周血比例较高的细胞，如 T、Th 和 Ts，两种方法测得细胞比例的偏倚均小于 15%。B 细胞在外周血中的比例较低，虽然两种方法测得细胞比例的偏倚较大，但是实际比例的差异并不大。因此，对于有特定需求的临床科室，我们实验室自建的实验室自建 B 细胞亚群流式检测方案可以满足要求。

PU-1403

血清 CD146 与血液透析患者腹主动脉钙化的相关性研究

于洋、韩俊岭、徐娟、赵岩、曹婧媛、周成林
泰州市人民医院

目的 血管钙化与血液透析（HD）患者的心血管事件密切相关，是透析患者预后的重要影响因素。本研究旨在评估血清 CD146 水平与 HD 患者腹主动脉钙化（AAC）发生的相关性，为 HD 患者血管钙化风险分层及改善预后提供依据。
方法 选取 2020 年 1 月 1 日至 2020 年 12 月 31 日在南京医科大学泰州临床医学院血液净化中心透析的 HD 患者及同期于我院行健康体检的正常人为研究对象，收集临床、实验室相关资料。采用酶联免疫吸附实验（ELISA）测定血清 CD146 水平。收集 HD 患者腹部 CT 资料，评估有无 AAC 及严重程度。将所有 HD 患者按照是否发生 AAC 分为 AAC 组和非 AAC 组；将 AAC 组按照钙化严重程度分为重度 AAC 组和非重度 AAC 组。数据采用 SPSS 22.0 软件进行统计分析。连续型变量以平均值±标准差或中位数（四分位数）表示，两组间比较采用独立样本 t 检验或秩和检验；分类变量以例数（比例）表示，组间比较采用卡方检验；采用多因素 Logistic 回归分析腹主动脉钙化发生的独立危险因素，使用向前 LR 法来构建最终的模型；构建 ROC 曲线评估不同危险因素预测钙化发生的准确性。
结果 纳入符合标准的 HD 患者 256 例，其中发生 AAC 者 159 例，AAC 发生率为 62.1%。发生 AAC 的 HD 患者中，重度 AAC 者 68 例（42.8%），非重度 AAC 者 91 例（57.2%）。合并 AAC 的 HD 患者血清 CD146 水平明显高于非 AAC 者（123.8-215.3 ng/ml vs 189.2-293.5 ng/ml，$p < 0.001$）；重度 AAC 患者血清 CD146 高于非重度 AAC 组（213.2-301.7 ng/ml vs 142.1-272.3

ng/ml，$p < 0.05$）。多因素 logistic 回归分析显示，PD 患者年龄增长、腹透龄延长、CD146 升高、血磷升高、白蛋白降低时发生 AAC 的风险增加。
结论 发生 AAC 的 HD 患者血清 CD146 水平明显高于非 AAC 患者。PD 患者年龄增长、腹透龄延长、CD146 升高、血磷升高、白蛋白降低与 AAC 的发生风险增加相关。血清 CD146 水平可作为早期预警 HD 患者发生 AAC 的指标。

PU-1404

嗜异性抗体对 CA153 和 HIV 检验结果影响的分析

滕凤猛、顾万建
江苏省中医院

目的 分析干扰物质对 CA153 和 HIV 检测结果的影响，为临川诊断提供有价值的实验数据。
方法 采用倍比稀释法对样本进行稀释，然后进行检测；将检测结果与理论结果进行相关性分析。更换新的检测平台或检测方法对检测结果进行检测。加入嗜异性抗体阻断剂（HBR-1、ALPPool、Poly MAK 和 Mouse IgG）分别进行阻断后检测。
结果 HIV 检测结果原倍为 385.16，2 倍稀释检测结果为 184.35，4 倍稀释检测结果为 41.06，8 倍稀释检测结果为 3.8,16 倍稀释检测结果为<1。糖类抗原 153 检测结果原倍为>800，2 倍稀释检测结果为 367.1，4 倍稀释检测结果为 108.2，8 倍稀释检测结果为 29.1，16 倍稀释检测结果为 8.5。将 HIV 和 CA153 检测结果与理论结果进行相关性分析，发现两者无相关性。利用酶联免疫和金标法对 HIV 进行检测两者结果均阴性，更换新的检测平台发现 CA153 检测结果在正常范围内。嗜异性抗体阻断剂（HBR-1、ALPPool、Poly MAK 和 Mouse IgG）阻断之后 CA153 检测结果 HBR-1 下降-99%、ALPPool 下降 11%、Poly MAK 下降-99%和 Mouse IgG 下降-83%。HIV 检测结果 HBR-1 下降-100%、ALPPool 下降 60%、Poly MAK 下降-100%和 Mouse IgG 下降-91%。
结论 嗜异性抗体 HBR-1 和鼠源性嗜异性抗体 Mouse IgG 以及 ALPPool 均对 HIV 和 CA153 检测结果有干扰。嗜异性抗体干扰，导致临床出现 HIV 和 CA153 假性增高；临床可以利用倍比稀释法或更换新的检测平台以及加入阻断剂的方法消除嗜异性抗体的干扰。

PU-1405

基于双酶扩增信号放大适配体传感器对 IFN-γ 的定量分析

刘畅、蒋栋能、刘琳琳
中国人民解放军陆军军医大学第二附属医院

目的 建立一种用于结核菌感染诊断相关细胞因子 IFN-γ 的电化学适配体传感器。
方法 以石墨烯-纳米金复合材料修饰电极，利用适配体的高特异性，结合核酸外切酶（RecJf）辅助的目标物循环和末端脱氧核苷酸转移酶（TDT）辅助的 DNA 扩增技术建立 IFN-γ 定量检测的电化学传感器新技术，并对该方法进行线性、灵敏度、特异性等性能指标的评估。
结果 以此策略构建的电化学适配体传感器对 IFN-γ 检测的线性范围为 0.01 ng·ml-1～50 ng·ml-1，电流强度的峰值与 IFNγ 浓度的对数值（logC）呈良好的线性关系(r= 0.9915)，其线性方程为：I= 5.38 logC+22.25，传感器显示出良好特异性、稳定性。
结论 本研究建立了基于纳米材料、双酶扩增的无标记、多重信号放大的电化学适配体传感器，该传感器具有操作简单、速度快、抗干扰能力强等优点，可用于细胞因子的定量检测。

PU-1406

诊断 IgG4 相关胆管病的新方法 胆汁中 IgG4 的测定

任雪娇
吉林大学第二医院

目的 IgG4 相关疾病(IgG4-RD)是一种累及多个器官的慢性炎性疾病。常见的表现包括主要唾液和泪腺增大，眼眶疾病，胆道疾病，自身免疫性胰腺炎，肾小管间质肾炎等。血清 IgG4 浓度升高，大量表达 IgG4 的浆细胞浸润是该病的关键特征。IgG4 相关的胆道疾病如今备受关注，但在影像学上，IgG4 相关性胆管炎(IAC)在胆道造影上不能与胆管癌或原发性硬化性胆管炎(PSC)鉴别，诊断困难。血清 IgG4 水平的敏感性虽然较高，但是在区别 PSC 等相关疾病的患者时特异性较低，影响鉴别诊断。由于 IAC 发生在胆管上皮，我们推测胆汁中 IgG4 的测定可能比血清具有更高的敏感性和特异性。
方法 收集 67 例胆道造影患者的胆汁和血清标本，其中 PSC 42 例，胆管癌 35 例，胆总管结石 34 例，IAC 8 例。胆汁和血清中均检测到 IgG4。
结果 IAC 患者胆汁 IgG4 水平明显高于其他胆道疾病患者。血清 IgG4 水平在 PSC 和 IAC 患者中均升高，而胆汁 IgG4 水平仅在 IAC 患者中升高。
结论 本研究表明胆汁 IgG4 测定是可行的，敏感性和特异性高于血清中 IgG4 水平，可能有助于 IAC 与其他疾病的鉴别。

PU-1407

IIF 检测中的影响因素

吴晓玲
西安金域医学检验所

目的 简单总结影响 IIF 的各种影响因素
方法 IIF 法的影响因素较多主要有以下几个方面：
（1）显微镜
（2）试剂盒
（3）标本
（4）实验原理或操作
（5）环境因素
这些因素都会对结果判读产生影响，造成漏检或误检，造成临床诊断的误差。
结果 免疫荧光技术是标记免疫技术中发展最早的一种，它是在免疫学、生物化学和显微镜技术的基础上建立起来的一项技术。具有特异性强、敏感性高、速度快等特点，广泛用于自身抗体筛查等项目。但 IIF 法的影响因素较多，主要有以下几个方面
（1）显微镜：
①光源偏强，导致观察到的细胞荧光强度人为增强选择和调整最合适光源
②光源偏弱，导致观察到的细胞荧光强度人为减弱
③弥散状荧光：荧光显微镜不干净，镜头上可能有划痕
④背景荧光：检查显微镜滤光片/镜头
⑤不均匀荧光：显微镜调节错误，需调节汞灯
⑥荧光偏少或没有：显微镜调节问题
（2）试剂盒：
荧光偏少或没有：①荧光二抗污染失活或载片包被物丢失。②清洗缓冲液的 pH 值发生变化

（3）标本：

①背景荧光：脂血、溶血。

②细胞密度过低：基质被蛋白水解酶水解，需进行灭活血清。

（4）实验原理或操作：

①细胞密度过低：长时间接触去离子水导致细胞裂解或清洗缓冲液直接冲洗反应基质，需严格按照说明书清洗程序进行。

②不均匀荧光：血清没有完全覆盖检测反应区造成或载片用蜡笔标记产生虚影

③背景荧光：实验过程中载片干燥。

（5）环境因素：

①不均匀荧光-反应区中血清干燥，周边荧光更强，需在潮湿环境下进行孵育

这些因素都会对结果判读产生影响，造成漏检或误检，造成临床诊断的误差。

结论 在日常工作中，我们需要总结了解 IIF 法中各种影响因素并加以预防和控制，保证检测结果的准确性，为临床诊断提供可靠依据。

PU-1408

血清可溶性 ST2 水平在原发性脑出血危险分级及预后评估的临床应用价值

曹爽
中国医科大学附属盛京医院

目的 探讨血清可溶性 ST2（sST2）及 D-二聚体在原发性脑出血危险分级及短期预后评估中的临床意义。

方法 选取已确诊为脑出血的患者共 85 例，根据入院时患者状态进行 APACHE-Ⅱ评分将患者分为重症组 45 例，轻症组 40 例，同期检测患者入院时血清 sST2 和 D-二聚体水平。根据出血部位不同分为基底节出血组 65 例，小脑出血组 4 例，脑室出血组 6 例，脑叶出血组 10 例。根据出院报告中病人状态记录依据格拉斯预后评分将患者分为预后较好组 36 例，和预后较差组 49 例。采用 SPSS26.0 软件进行统计学分析，比较不同组间 sST2 和 D-二聚体水平的差异。

结果 重症组 sST2 和 D-二聚体水平显著高于轻症组（P<0.05）；预后较差组 sST2 和 D-二聚体水平显著高于预后较好组（P<0.05）；按照出血部位分组中，不同组间 D-二聚体水平无统计学差异(P>0.05)，而 sST2 水平有统计学差异(P<0.05)，小脑出血组 sST2 水平明显高于其他组；Spearman 分析显示 sST2 与 D-二聚体具有相关性（P<0.05）。

结论 血清 sST2 和 D-二聚体水平对原发性脑出血患者的病情判断和短期预后评估中有重要的临床价值。

PU-1409

血清 NSE、CA-19-9、CEA 检测在肺癌诊断与分期中的临床研究

黄莎莎
山东第一医科大学附属省立医院

目的 研究血清 NSE、CA-19-9、CEA 检测在肺癌诊断与临床分期中的临床意义。

方法 抽取我院 2019 年 1～12 月确诊的肺癌患者 80 例设为观察组,再取同期确诊的肺良性疾病的患者 64 例设为对照组,抽取同期体检健康人员 100 例设为健康组,采用 SPSS17.0 统计学软件,对三组人员的血清 NSE、CA-19-9、CEA 结果进行统计分析,证实检验结果对肺癌诊断及分期的临床价值。
结果 观察组检测神经特异性烯醇化酶(NSE)、糖类抗原 19-9(CA19-9)、癌胚抗原(CEA)的水平均高于健康组,比较差异具有统计学意义(P<0.05);观察组神经特异性烯醇化酶、糖类抗原 19-9、癌胚抗原水平均高于对照组,比较差异具有统计学意义(P<0.05);癌症不同分期测得 NSE、CA19-9、CEA 浓度有着明显差异,(P<0.05)。
结论 通过肿瘤标志物检测对肺癌的诊断与分期具有重要辅助意义,可以作为肺癌临床诊断及评估患者病情严重程度的依据,建议临床推广应用。

PU-1410

系统性红斑狼疮达标治疗与实验室指标关系研究

翟建昭、蔡蓓、武永康
四川大学华西医院

目的 近年来“达标治疗”的概念被引入系统性红斑狼疮（SLE），达标治疗即以病情缓解或尽可能降低疾病活动度作为治疗目标，采取各种积极有效的治疗控制 SLE。本研究旨在寻找可以作为达标治疗的治疗目标的实验室指标，通过关键指标长期规律的监测，控制疾病活动度，减少药物毒性和疾病并发症，最大限度的提高患者的生存时间和生活质量。
方法 纳入 SLE 患者 994 例，通过系统性红斑狼疮疾病活动度评分（SLEDAI-2k）将 SLE 患者分为“达标”（SLEDAI≤4，n=156）和“未达标（SLEDAI>4，n=838）”，对两组患者的实验室数据，包括 PCT，CRP，IL-6，尿素，肌酐，胱抑素 C，eGFR，血小板，白细胞数量、红细胞数量，血红蛋白含量以及尿蛋白进行分析，寻找在两组中有显著差异的指标。
结果 胱抑素 C 在未达标患者中显著升高（1.16 mg/L vs.1.4 mg/L，P<0.001）,蛋白尿也更加常见（阳性率 20.5% vs.42.4%，P<0.001）。红细胞数量在未达标患者中更低（3.81×10^12/L vs.3.59×10^12/L,P=0.009）,血红蛋白含量也更低（109g/L vs.102g/L,P<0.001）。除此之外炎性指标 PCT 也在未达标组中更高(0.06 ng/mL vs.0.08 ng/mL),而 IL-6（10.06 ng/mL vs.7.79 ng/mL）和 CRP（7.51 mg/L vs.5.26 mg/L）则在达标组中更高，但无统计学意义（P>0.05）。
结论 红细胞数量、血红蛋白含量和尿蛋白均可以作为达标治疗效果预测指标，预示疾病的活动程度。未达标的患者肾功能更差，贫血症状也更显著。但实验室指标和临床症状之间不一定完全符合，炎性指标升高的患者不一定具有更活跃的疾病状态。同时，这些物质在体内的代谢过程使得它们不一定能及时准确的反映疾病变化，临床工作中需要结合多个指标并进行长期监测，同时未来需要更多准确、可重复的指标来准确的判断患者的疾病状态。

PU-1411

血清 AFP、CEA、AFU、GGT 联合检测对原发性肝癌的临床诊断

黄莎莎
山东第一医科大学附属省立医院

目的 探讨血清甲胎蛋白、癌胚抗原、α-L-岩藻糖苷酶、γ-谷氨酰转肽酶联合检测在原发性肝癌诊断中的应用价值。
方法 选取 2017 年 1 月至 2021 年 1 月山东省立医院收治的 100 例原发性肝癌患者及 100 例健康体检者作为研究对象，比较各组受检者血清中的甲胎蛋白、癌胚抗原、α-L-岩藻糖苷酶、血清 γ-谷氨酰转肽酶水平, 血清肿瘤标志物检测阳性率,以及单个检测与联合检测的敏感度和特异度。

结果 原发性肝癌组血清甲胎蛋白、癌胚抗原、α-L-岩藻糖苷酶含量与健康对照组比较,差异均有高度统计学意义(均 P ＜ 0.01);血清甲胎蛋白、癌胚抗原、α-L-岩藻糖苷酶、γ-谷氨酰转肽酶各自单项检测的阳性率分别为 65.00%、29.00%、86.00%、75.00%,其中癌胚抗原及 α-L-岩藻糖苷酶及 γ-谷氨酰转肽酶的阳性率均明显升高,与健康对照组比较,差异均有统计学意义(均 P ＜ 0.05);此外血清甲胎蛋白联合癌胚抗原或甲胎蛋白联合 α-L-岩藻糖苷酶或甲胎蛋白联合 γ-谷氨酰转肽酶检测的阳性率分别为 73.00%、84.00%、88.00%,甲胎蛋白、α-L-岩藻糖苷酶联合检测及甲胎蛋白、γ-谷氨酰转肽酶联合检测与甲胎蛋白单项检测相比差异均有统计学意义(均 P ＜ 0.05);此外血清甲胎蛋白同时联合癌胚抗原、α-L-岩藻糖苷酶、γ-谷氨酰转肽酶 4 项检测原发性肝癌的检出阳性率为 95.00%,明显高于甲胎蛋白单项检测的检出阳性率,两者相比差异有高度统计学意义(P ＜ 0.01)。
结论 使用血清甲胎蛋白、癌胚抗原、α-L-岩藻糖苷酶、γ-谷氨酰转肽酶联合检测有助于原发性肝癌的早期诊断,值得在临床工作中推广应用。

PU-1412

罗氏 e801 电化学发光法在 HIV 筛查试验中的假阳性分析

刘丽
临沂市人民医院

目的 分析罗氏 e801 电化学发光法在 HIV 筛查试验中的假阳性的原因。
方法 对本院 2020 年 5 月至 2021 年 5 月期间应用此方法的所有 HIV 筛查样本通过 e801 电化学发光法进行 HIV 筛查试验检测。临沂市疾病控制中心通过免疫印迹法(WB)对初筛 HIV Ab 阳性进行确认，初筛 HIV Ag 阳性患者进行随访。
结果 87795 例病人血清标本中，共筛检出阳性血清 82 例，其中 HIV Ag 阳性 6 例。经临沂市疾病控制中心确认，15 例为阳性，1 例为不确定，66 例为阴性。HIV Ag 初筛阳性样本确认结果均为阴性。
结论 罗氏 e801 电化学发光法 HIV 抗原抗体联合检测假阳性率 0.08％，仍应结合临床资料及确认试验结果综合判断。

PU-1413

r-干扰素释放试验在活动性肺结核诊断中的应用价值

王昌敏、赵进、马晶、李帅
新疆维吾尔自治区人民医院检验科

目的 探讨 γ-干扰素释放试验（SPOTest）在活动性肺结核诊断中的应用价值。
方法 在 2020 年 12 月 1 日-2020 年 12 月 31 日于新疆维吾尔自治区人民医院呼吸内科治疗的 267 例肺结核疑似患者中选择其中 118 例接受过 SPOTest、结核分枝杆菌/利福平耐药实时荧光定量核酸扩增检测技术（Xpert Mtb/RIF）检测及涂片检测的患者，6 例为陈旧性结核患者未纳入研究，112 例肺结核疑似患者中经临床诊断为阴性 80 例，阳性 32 例。以临床诊断为判断依据，计算 SPOTest、Xpert Mtb/RIF 检测、涂片检测诊断 APTB 的敏感度、特异性、准确率，以及与临床诊断结果的一致性。
结果 SPOTest 诊断 APTB 阳性 39 例，阴性 73 例，SPOTest 诊断 APTB 结果与临床诊断结果一致性较高（Kappa 值=0.733）；Xpert Mtb/RIF 检测 APTB 阳性 16 例，阴性 96 例，Xpert Mtb/RIF 检测诊断 APTB 结果与临床诊断结果一致性较高（Kappa 值=0.588）；涂片检测诊断 APTB 阳性 3 例，阴性 109 例，涂片检测诊断 APTB 结果与临床诊断结果一致性差（Kappa 值=0.129）。SPOTest 诊断 APTB 的敏感度 90.63%，高于 Xpert Mtb/RIF 敏感度 50.00%与涂片检测敏感度 9.38%，差异有统计学意义（P＜0.05）；SPOTest 诊断 APTB 的准确率 88.39%高于 Xpert

Mtb/RIF 准确率 85.71%以及涂片检测准确率 74.11%，差异有统计学意义（P＜0.05）；SPOTest 诊断 APTB 的特异性 87.50%，低于 Xpert Mtb/RIF 的特异性 100.00%以及涂片检测的特异性 100.00%，差异有统计学意义（P＜0.05）。
结论 SPOTest 诊断 APTB 敏感度及准确率较高，且 SPOTest 诊断结果与临床诊断结果一致性较高，有助于鉴别诊断 APTB，并指导临床治疗。

PU-1414

调节性 T 细胞、白介素-17、干扰素-γ 在小儿过敏性哮喘的诊断价值探讨

赵莹莹
临沂市人民医院

目的 评估外周血调节性 T 细胞（Treg）、白介素-17（IL-17）、干扰素 γ（IFN-γ）在小儿过敏性哮喘中的诊断价值。
方法 选取 2018 年 3 月至 2021 年 2 月临沂市人民医院收治的过敏性哮喘患儿（符合中华医学会修订的小儿支气管哮喘诊断标准，且经支气管激发试验或运动试验确诊）120 例为观察组，其中男 68 例，女 52 例；年龄 3～13 岁，平均（8.95±1.42）岁，选取同期 75 名健康儿童为对照组，其中男 43 名，女 32 名；年龄 3～14 岁，平均（9.07±1.37）岁。两组儿童基础资料差异无统计学意义（P>0.05）。对比两组外周血调节性 T 细胞（Treg）、白介素-17（IL-17）、干扰素 γ（IFN-γ）水平差异，进行受试者工作特征曲线(ROC 曲线)、曲线下面积(AUC) 分析，得出 3 种指标各诊断小儿过敏性哮喘的灵敏度、特异性，进一步计算 3 种指标联合诊断小儿过敏性哮喘的灵敏度及特异性。
结果 1、观察组的 IL-17 水平高于对照组，Treg、IFN-γ 水平明显低于对照组（P<0.05）。
2、Treg 单独诊断小儿过敏性哮喘的临界值 2.13%，AUC 为 0.894，灵敏度为 79.6%，特异性为 91.2%；IL-17 单独诊断小儿过敏性哮喘临界值 24.13ng/L，AUC 为 0.861，灵敏度为 81.8% ，特异性为 72.9%；IFN-γ 单独诊断小儿过敏性哮喘的临界值为 305.42ng/L，AUC 为 0.836，灵敏度为 82.5%，特异性为 76.6%。
3、Treg、IL-17 及 IFN-γ 三者联合诊断小儿过敏性哮喘的灵敏度及特异性分别为 84.1%，89.3%。
结论 小儿过敏性哮喘诊断灵敏度比较：IFN-γ>IL-17>Treg，诊断特异性比较：
Treg> IFN-γ>IL-17；Treg、IL-17 及 IFN-γ 对小儿过敏性哮喘均有诊断价值，联合检测 Treg、IL-17 及 IFN-γ 可有效提高小儿过敏性哮喘的诊断效能。

PU-1415

雅培 i2000SR 检测梅毒螺旋体特异性抗体效果评价

马梦影
西安医学院第一附属医院

目的 探讨雅培 i2000SR 化学发光微粒子免疫分析法（CMIA）检测梅毒螺旋体特异性抗体的筛查策略。
方法 对本院 2018 年 1 月-2019 年 12 月期间共 46868 例血清样本运用化学发光微粒子免疫分析法（CMIA）检测梅毒螺旋体特异性抗体，并对筛查出的阳性血清样本运用梅毒螺旋体颗粒凝集试验（TPPA）进行确证。
结果 46868 例血清样本中 CMIA 筛查出阳性样本 663 例，运用梅毒螺旋体颗粒凝集试验（TPPA）对阳性样本进行确证，结果显示，真阳性样本 468 例，假阳性样本 195 例。同时，将 CMIA 检测的 S/CO 值分为 1.0～3.0、3.0～6.0、6.0～9.0、>9.0 四组，结果显示，梅毒螺旋体特异性抗体的

真阳性率会随着 S/CO 值的升高而逐渐上升；并且，当 S/CO>9.0 时，真阳性率可达 100%。年龄>60 岁的患者假阳性率为 38.3%，较其他组差异有统计学意义（P<0.05）。
结论 CMIA 检测梅毒螺旋体特异性抗体敏感性较高，可作为筛查实验。但对 S/CO 值在 1.0～9.0 之间的样本需用 TPPA 进行复检，而 S/CO 值>9.0 的样本则无需用 TPPA 进一步确证，可直接发阳性报告。年龄>60 岁的患者因其有较高的假阳性率，故发阳性报告时需更加慎重。

PU-1416

化学发光免疫分析技术相对常规检查技术的优势研究

赵倩雯
山东大学第二医院

目的 研究生化免疫检验中化学发光免疫分析技术的应用价值在甲状腺肿瘤患者生化免疫检验中的应用价值。
方法 将本院某一年内收治的疑似甲状腺肿瘤患者作为研究对象,随机地平均分为两组。对两组患者样本均进行血液生化免疫检验,首先进行少量的空腹采血,取其中一份血液标本进行常规免疫检查（放射免疫测定技术）,另一份血液标本进行化学发光免疫分析技术检查。以术后病理检查为金标准,对比使用两种不同检查方法的甲状腺肿瘤患者的特异度、灵敏度、符合率,球蛋白、游离三碘甲状腺原氨酸及甲状腺球蛋白水平。
结果 根据术后病理检查结果可知,检验结果为恶性的肿瘤略多于检查结果为良性的肿瘤。并且通过数据分析，得出化学发光免疫分析技术检查的特异度、灵敏度、符合率均高于 90%,而常规免疫检查的特异度、灵敏度、符合率最高的一项也仅有 80%,化学发光免疫分析技术相比常规免疫检查技术具有明显优势。此外，化学发光免疫分析技术检查的球蛋白、游离三碘甲状腺原氨酸、甲状腺球蛋白水平也明显高于放射免疫测定技术的球蛋白、游离三碘甲状腺原氨酸、甲状腺球蛋白水平,更加印证了化学发光免疫分析技术的实用性、有效性是更高的。
结论 在临床上，对甲状腺肿瘤患者除了要进行常规的影像学检查，还需要进行生化免疫检验，两者结合后可以较好地降低疑似甲状腺肿瘤患者的误诊率。相比常规免疫检查技术，化学发光免疫测定技术的特异度、灵敏度、符合率较高,球蛋白、游离三碘甲状腺原氨酸、甲状腺球蛋白水平也相对较高。该技术对甲状腺肿瘤的诊断具有指导意义,可以在临床中进行推广。

PU-1417

M 蛋白轻链定量、β2 微球蛋白在不同分期分型的多发性骨髓瘤患者血液和尿液中的变化

霍茜瑜、朱国庆、王艳生 、任彦松、付雪、王守磊
中国医学科学院血液病医院

目的 分析多发性骨髓瘤（multiple myeloma，MM）患者血液和尿液中的 M 蛋白轻链定量和 β2-微球蛋白（beta-2 microglobulin ，β2-MG）在不同的 DS 分期和不同亚型之间的变化，为 MM 患者的病情判断、疗效观察提供依据。
方法 收集 2020 年就诊于中国医学科学院血液病医院（中国医学科学院血液学研究所）MM 患者的血液和尿液中 M 蛋白轻链定量和 β2-MG 检验的结果，分别以患者的临床 DS 分期和 M 蛋白重轻链分型作为分组的依据，对收集的数据进行差异性分析。
结果 排除移植后复发、严重并发症等情况的患者后，共收集患者样本数据 155 例，其中 DS Ⅰ期 19 例、Ⅱ期 38 例、Ⅲ期 98 例。MM 患者血、尿 β2-MG 随分期进展升高，血 β2-MG 升高存在统计学差异（$p<0.05$）。κ 亚型 MM 患者血 κ 轻链定量随分期升高（$p<0.05$），尿 κ 轻链定量随分期变化不大。λ 亚型 MM 患者血、尿 λ 轻链定量均随分期升高，但无明显统计学意义。不同分型的

MM 患者中，轻链型患者尿 β2-MG 升高较明显（p＜0.05）。重链类型为 IgG 型的血轻链定量结果更高（p＜0.05），尿轻链定量结果在不同亚型之间均无明显变化。
结论 MM 患者血、尿 β2-MG 随分期进展升高。血 β2-MG、轻链定量结果升高更有助于对 MM 患者的病情监控。轻链型患者尿 β2-MG 升高较其他亚型患者更明显，轻链 M 蛋白对肾脏损伤更重。

PU-1418

Correlation analysis of CD4+ T lymphocyte count and viral load in 199 newly diagnosed HIV-infected patients

Tongxin Dai
The Eighth Hospital of Xi'an

Objective To analyze the correlation between the first CD4+ T lymphocyte count and viral load of newly diagnosed HIV-infected patients, and to achieve a preliminary estimation of the patient's viral load through the CD4+T lymphocyte count in areas where viral load testing cannot be carried out.
Methods BD FACS Calibur flow cytometry was used to detect T lymphocyte subsets of 199 HIV-infected patients for the first time. At the same time, Roche COBAS TaqMan real-time fluorescent PCR analyzer was used to detect the viral load of the patients, and SPSS 19.0 was used to compare the data. Analyze the correlation and linear regression relationship between CD4+ T lymphocyte count and viral load.
Results The first CD4+T lymph count of 199 HIV-infected patients was less than 200 cells/μl, accounting for 105 cases (53.8%); CD4+T lymph count was between 200 and 349/μl, accounting for 27 cases (13.6%); CD4+T lymph count was between 350 and 500/μl, accounting for r 34 cases (16.9%); 31 cases (15.1%) with CD4+ T lymphocytes greater than 500/μl. The median distribution of viral load in 199 patients was 7.37x104cps/ml, 10 cases (5.0%)of HIV patients with a viral load of less than 103cps/ml; a total of 102 cases (51.3%) with a viral load of 103-105cps/ml; a total of 87 cases (43.7%) with a viral load of greater than 105cps/ml. CD4+T lymphocyte count was negatively correlated with viral load (r=-0.362, P<0.05), linear regression relationship Y (Lg(RNA))=5.099-0.001X (CD4) (F=17.232, P<0.05). The CD4/CD8 ratio and viral load were also negatively correlated (r=-0.453, P<0.05).
Conclusion About half of newly diagnosed HIV-infected patients have entered the AIDS stage, so early diagnosis of HIV should be strengthened. The viral load of newly diagnosed HIV-infected patients is at a medium-to-high level, and antiretroviral therapy should be carried out in time to reduce the viral content of the patient and enable the patient to obtain a better outcome. CD4+ T lymphocyte count and CD4/CD8 ratio are negatively correlated with viral load. CD4+T lymphatic count can be used to roughly estimate the viral load level in patients without antiviral treatment, and analyze the patient's immune status and disease progression.

PU-1419

肾功能不全对血清人附睾蛋白 4 水平的影响

张晋
中国医科大学附属盛京医院

目的 通过分析肾脏功能损伤对于血清人附睾蛋白 4（human epididymis protein 4, HE4）水平的影响，探讨利用血清 HE4 对卵巢恶性肿瘤进行诊疗时，如何判断伴肾功能不全的患者的血清 HE4 水平与肿瘤之间的关系。

方法 健康对照组（Ⅰ组）50 例，良性疾病组（Ⅱ组）92 例，良性疾病合并肾功能不全组（Ⅲ组）48 例，卵巢癌组（Ⅳ组）78 例，卵巢癌合并肾功能不全组（Ⅴ组）54 例。分别采用电化学发光法、酶法、颗粒增强型免疫透射比浊检测法检测血清 HE4/CA125、血清肌酐/尿素、血清胱抑素 C 水平，比较各组血清 HE4 水平，分析各组 HE4 异常检出率，分析伴有肾功能不全的良性疾病组血清 HE4 水平与肾功能指标肌酐、胱抑素 C 和尿素水平的相关性，分析合并肾功能不全的良性疾病组与合并肾功能不全的卵巢癌组的罗马指数是否存在差异。

结果 良性疾病合并肾功能不全组（Ⅲ组）血清 HE4 水平明显高于良性疾病组（Ⅱ组）和健康对照组（Ⅰ组）（P<0.01），卵巢癌组（Ⅳ组）血清 HE4 水平明也显高于良性疾病组（Ⅱ组）和健康对照组（Ⅰ组）（P<0.01），但良性疾病合并肾功能不全组（Ⅲ组）与卵巢癌组（Ⅳ组）HE4 水平比较差异无统计学意义（P=1.00），良性疾病组（Ⅱ组）与健康对照组（Ⅰ组）血清 HE4 水平比较差异也无统计学意义（P=0.73），卵巢癌合并肾功能不全组（Ⅴ组）血清 HE4 水平显著高于其他组（P<0.01）。血清 HE4 水平与肌酐、胱抑素 C、尿素均呈正相关（P<0.05）。卵巢癌合并肾功能不全组（Ⅴ组）罗马指数高于良性疾病合并肾功能不全组（Ⅲ组）（P<0.05）。

结论 肾功能不全会影响血清 HE4 水平，利用绝经前后罗马指数可有助于鉴别卵巢肿瘤的良恶性。利用血清 HE4 对卵巢恶性肿瘤进行诊疗时，结合肾功能相关指标的检测结果，有助于我们排除肾功能不全导致的血清 HE4 水平升高。

PU-1420

不同类型慢性 HBV 感染者外周血 CD3+、CD8+T 淋巴细胞检测的临床价值

张旭强、李彩东、雷志萍、田鹏飞、陈俏丽
兰州市第二人民医院

目的 分析慢性 HBV 患者外周血 $CD3^+$、$CD8^+$T 淋巴细胞与 HBV DNA 载量、HBV-M 水平和性别等的相关性，探讨 $CD3^+$、$CD8^+$T 淋巴细胞在不同类型慢性 HBV 感染者中的临床价值。

方法 收集甘肃地区 200 例慢性 HBV 感染者，包括乙肝病毒携带者组(ASC)59 例、慢性乙型肝炎组(CHB)51 例、乙肝肝硬化组(LC)31 例、原发性肝癌组(HCC)32 例及健康对照组(Control)27 例。采用 BD FACSCantotM II 流式细胞仪检测 $CD3^+$、$CD8^+$T 细胞水平；采用雅培 i-2000SR 检测 HBV-M 水平；采用荧光定量 PCR 技术检测 HBV DNA 载量。

结果 慢性 HBV 感染者 $CD3^+$水平从 ASC、CHB、LC、HCC 组逐渐降低，与 Control 组相比差异有统计学意义(t_{HCC}=2.106，P=0.044<0.05；t_{LC}=2.003，P=0.049<0.05)，且 HCC 组患者最低；LC 组外周血 CD3+CD8+水平最低，较其他组相比差异有统计学意义($t_{Control}$=2.168，P=0.040<0.05；t_{ASC}=3.019，P=0.005<0.01；t_{CHB}=3.966，P=0.000<0.01；t_{HCC}=2.005，P=0.049<0.05)。与女性患者相比，男性患者有更高的 $CD3^+$水平(t_{CD3}+=2.964，P=0.004<0.01)。HBV DNA 水平与 $CD3^+$、$CD3^+CD8^+$呈负相关(r=-0.232，P=0.012<0.05；r=-0.220，P=0.018<0.05)。各组 HBeAg(+)患者和 HBeAg(-)患者 T 淋巴细胞亚群水平相比，差异无统计学意义(P>0.05)。

结论 随着 HBV 的病程进展，$CD3^+$、$CD8^+$细胞免疫功能均表现为衰竭状态；男性患者感染 HBV 后有更强的 T 细胞免疫应答，推测男性 HBV 感染者更易出现免疫性肝损害，其乙型肝炎进展更快且更易发展为严重肝病；临床可通过持续检测患者的 HBV DNA 载量来推测患者 T 细胞亚群表达情况，进而通过分析患者免疫应答情况来指导抗病毒药物的使用。

PU-1421

IL-35 在慢性乙肝病毒感染中的作用机制研究

徐学静
南京大学医学院附属鼓楼医院

乙型肝炎病毒（Hepatitis B virus, HBV）感染是全球性的公共卫生问题，全球约 20 亿人曾感染过 HBV，其中 3.5～4 亿人为慢性 HBV 携带者。我国 HBV 人群感染率高，2006 年全国乙型肝炎血清流行病学调查显示，人群乙型肝炎表面抗原（HBsAg）阳性率高达 7.18%，推算乙肝表面抗原携带者约 9300 万人。HBV 感染所致的慢性肝炎给患者、家庭和社会造成沉重的经济负担，是我国现阶段最突出的公共卫生问题之一。HBV 感染是一个复杂的免疫调节过程，其中多种细胞因子在 HBV 感染后疾病的发展、转归和治疗反应过程中发挥着重要的作用。白介素 35(IL-35)是近年来新发现的负性免疫调节细胞因子，主要由调节性 T 细胞(Treg)或调节性 B 细胞(Breg)产生。IL-35 可能在 HBV 感染的防治中具有潜在价值。IL-35 可能是在急性 HBV 感染过程具有潜在的抗炎特性对于开发新的乙型肝炎治疗方法可能至关重要。本研究主要探索负性免疫调节细胞因子 IL-35 在 HBV 感染及持续感染时疾病发生、发展过程中的变化规律及其抗 HBV 治疗中的作用和意义；重点分析 HBeAg 阴性和阳性慢性患者中的 IL-35 水平及与 Treg 和 Breg 的关系；以 Treg 和 Breg 为切入点，寻找 IL-35 的来源及可能导致的效应，从细胞因子及相关细胞亚群的变化格局分析可能导致的效应，探索其作用机制。通过以上工作，阐明 IL-35 在 HBV 感染的预防及疾病转归过程中的意义和作用机制，并有望为进一步提高慢性 HBV 感染的防治水平提供新思路，可能具有重要的理论意义和临床价值。

PU-1422

CD64 指数在部分感染性疾病中的诊断价值

朱杰、王娇、吴京学、田瑶
大连医科大学附属第二医院

目的 分析讨论中性粒细胞 CD64 指数在部分感染性疾病中的临床表现和诊断价值。
方法 对我院的 118 例确诊感染患者进行回顾性研究，按照病原学和免疫学诊断进一步分为布氏杆菌病、伤寒、结核、EB 病毒感染、流行性出血热、发热伴血小板减少 6 组，检测患者 CD64 指数、降钙素原和 C 反应蛋白，计算各组数据的阳性率与增长幅度及阳性似然比和阴性似然比，进行比较和讨论。
结果 患者各指标与对照组之间存在统计学差异（$P<0.05$），CD64 指数的阳性率在伤寒（100%）、布氏杆菌（79.49%）、结核（78.95%）及 EB 病毒感染（75.76%）上表达较好，且阳性似然比及阴性似然比均为最优，在流行性出血热（88.89%）与其他指标相比表现一般，在发热伴血小板减少综合征（57.14%，3.12）中无太大参考价值。
结论 CD64 指数在病毒感染和细菌感染上表现有一定差异，在鉴别诊断细菌性感染和病毒性感染上有一定的临床价值，在布氏杆菌、结核及 EB 病毒感染中有一定的诊断价值，在伤寒中表达最高，有较高的诊断价值。

PU-1423

老年男性血液系统损伤红斑狼疮一例

杨美兰、张秀琴、冯磊、白雪晶
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

SLE 是一种由自身免疫介导的累及多脏器多系统的自身免疫性疾病，以多系统受累为主要临床特点。初期多无系统性损伤，仅为单一系统受累，容易误诊漏诊，误诊率达 50-60%，确诊时间 1.7-8 年不等。本病例以血液系统受累为首发症状的系统性红斑狼疮，其原因为老年人造血系统功能逐渐衰退，代偿能力减弱，骨髓长期遭受自身抗体攻击，改变了造血微环境的平衡状态，导致血细胞生成障碍，破坏过多所致。

PU-1424

Overexpression of SCCA in poorly differentiated gastric adenocarcinoma: a case report

Mengyao Yu
Jiangsu Province Hospital

BACKGROUND Squamous cell carcinoma antigen (SCCA) is regarded as a specific indicator of epithelial malignancies and is widely used in the diagnosis of squamous cell carcinoma (SCC). However, the expression of SCCA in gastric adenocarcinoma has not been studied in detail.
CASE SUMMARY A 52-year-old man was admitted to our hospital for a 2.5 cm × 2.5 cm ulcer at the antrum-body junction with dull pain and fullness in the upper abdomen for 2 mo. His pre-surgery serological testing results showed 0.51 ng/mL SCCA (reference interval, < 1.5 ng/mL) and 9.9 ng/mL carcinoembryonic antigen (reference range, < 4.7 ng/mL). He underwent radical distal gastrectomy and Roux-en Y anastomosis and was diagnosed with poorly differentiated mucinous adenocarcinoma (Lauren classification: Diffuse) by pathological examination of the resected lesion. Immunohistochemistry showed that SCCA was highly expressed in the cytoplasm of cancer cells. After surgery, the patient received an S-1 adjuvant chemotherapy regimen for six cycles containing tegafur, gimeracil, and oteracil potassium. He showed no sign of recurrence or metastasis within 24-mo follow-up.
CONCLUSION This is a frontal report of SCCA overexpression in poorly differentiated adenocarcinoma of the stomach.

PU-1425

慢性乙型肝炎患者外周血 IL-37 的表达水平及意义

黄太宏
南京大学医学院附属鼓楼医院

研究慢性乙型肝炎（chronic hepatitis B,CHB）患者外周血血清中白细胞介素-37（IL-37）的表达水平,并探讨 IL-37 在 CHB 中的作用及意义。方法通过 ELISA 检测 35 例 CHB 患者及 35 例健康对照者血清中 IL-37 的含量;全自动生化仪及化学发光仪检测 CHB 患者血清中 ALT,AST,HBsAg,HBeAg 的含量,定量 PCR 及 ELISA 方法检测 CHB 患者血清中 HBV DNA 载量及细胞因子 TNF-α,IL-10 的表达水平,并分析 IL-37 含量分别与 ALT,AST,HBsAg,HBeAg,HBV DNA,TNF-α 及 IL-10 之间的相关性。

PU-1426

特发性炎性肌病自身抗体谱检测在临床应用中的价值

晏颂欣
中国医学科学院北京协和医院

特发性炎性肌病(IIM)是一组以近端对称性肌无力和多器官（如皮肤，关节，肺，胃肠道和心脏）受累为特征的异质性疾病，统称为肌炎。IIM 主要包括多发性肌炎、皮肌炎、包涵体肌炎等临床亚型，其发病机制尚不明确，但肌炎自身抗体被证实在疾病的发展和诊断中发挥着一定的作用。肌炎自身抗体可被分为肌炎特异性自身抗体（MSA）或肌炎相关性自身抗体（MAA）。本文就近年来在肌炎自身抗体领域的进展进行全面的总结和概括，期望能进一步展现肌炎自身抗体的临床价值，促进肌炎自身抗体在临床的应用。

PU-1427

Trust 与 TPPA 联合检测对梅毒初筛的临床意义研究

杨佳新
吉林金域医学检验所有限公司

目的 梅毒，是一种由梅毒螺旋体 TP 所引起的全身各器官的性传播疾病，其传染力强危害性大，能够导致自身性流产或死产甚至是胎传梅毒，大多数是通过性传播途径传。梅毒感染者呈上升趋势，所以梅毒检测已被列为住院的常规检查项目。本文探讨了 TPPA 和 Trust 联合检测对初筛梅毒阳性的诊断及临床诊断意义。
方法 选取 2020 年 1 月至 2020 年 12 月送检我公司的梅毒样本 2000 例，同一时间段分别用 Trust 和 TPPA 两种方法检测，Trust 试剂是上海荣盛生产的试剂，TPPA 是用由富盛生产的试剂，质控为临检中心提供的血清样本，所有的样本均严格按全国临床检验操作规程与试剂说明书上的要求进行，结果为阳性，复查结果仍为阳性，判断为 TP 抗体初筛阳性，再结合临床资料最后确诊为梅毒。
结果 实验表明，2000 例样本中，Trust 和 TPPA 结果如下：Trust 阳性 40 例，TPPA 阳性 106 例，两种方法联合检测阳性 39 例，临床确诊为梅毒 39 例。Trust 与 TPPA 两种方法检测的结果的阳性率分别为 5.30％ 和 2.00％，特异性分别为 96.70％和 98.00％，敏度均为 100％。
结论 人体感染梅毒螺旋体后，体内会产生两种抗体，特异性抗梅毒螺旋体抗体中 IgM 持续时间短 IgG 持续时间长，非特异性抗心磷脂抗体又称反应素。由于 TPPA 抗体治疗后仍可长期存在，因此 TPPA 单独阳性只能说明感染或曾经感染，不能判断是否感染梅毒。Trust 所用的抗原主要是用来检测血清中的反应素，对早期梅毒的辅助诊断能力差。此法操作简便容易判读，但其影响因素也比较多，易受一些生理或病理状态的影响，而出现假阴性或假阳性。在我们的研究中，TPPA 阳性率高于 Trust 的阳性率，这说明一些梅毒患者通过治疗已经痊愈。所以，Trust 和 TPPA 在梅毒临床诊断中的互补作用很强，二者的联合检测，并结合临床进行综合分析，可避免梅毒的误诊与漏诊。

PU-1428

自身免疫疾病或自身抗体作为 PD-1/PDL1 治疗癌症患者的危险因素：一项系统综述和荟萃分析

晏颂欣
中国医学科学院北京协和医院

背景 程序性死亡-1（PD-1）和程序性死亡配体-1（PD-L1）阻断已成为治疗多种癌症的有效方法。越来越需要弄清楚 PD-1/PD-L1 抑制剂在自身免疫性疾病（AID）癌症患者中的安全性和有效性。

虽然 PD-1/PD-L1 抑制剂在 AID 治疗的非小细胞肺癌（NSCLC）患者中通常是安全的，但是需要更大规模的试验来确定这种免疫检查点抑制剂（ICIs）治疗明显自身免疫性患者的风险。
目标 本系统综述的目的是评估抗 PD-1/PD-L1 抗体在癌症患者 AID 治疗中的安全性和有效性。
方法 在 PubMed、科学网和 Cochrane 图书馆的同行评审期刊上系统地搜索相关研究。共获得文献 1049 篇，发表论文 8 篇。
结果 有 AID 的癌症患者和无 AID 的癌症患者的不良事件（耀斑或 IRAE）发生率分别为 57%和 37%。癌症患者接受 AID 治疗的有效率为 33%，而没有 AID 治疗的癌症患者的有效率为 32.7%。
结论 尽管自身免疫性疾病患者发生不良事件的风险较高，但在良好的临床管理条件下，PD-1/PDL1 治疗仍应被视为一种良好的肿瘤治疗选择。

PU-1429

炎症因素在自身免疫性疾病与动脉粥样硬化发病机制中的关联性研究进展

毕千叶、冯磊、马琦欣、邵聪、骆贝贝
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

动脉粥样硬化是许多重要的血管不良事件的基础，严重威胁着人类健康，近年来，炎症及免疫调节因素在动脉粥样硬化发生发展中的作用越来越为人们所重视，人们已经注意到自身免疫性疾病患者心血管病变的风险较常人显著提高，推测自身免疫性疾病与心血管疾病的致病机制之间可能存在交叉。因此本文通过检索国内外相关文献，对自身免疫性疾病与动脉粥样硬化的相关机制做一综述，以期为防治自身免疫性疾病并发心血管疾病提供新思路。

PU-1430

同种异体主动脉移植模型中以 NADPH 氧化酶表达和新生血管形成为特征的早期外膜激活

季健
山东大学齐鲁医院

目的 探讨同种异体主动脉移植模型中 NADPH 氧化酶表达和外膜血管生成反应的动态变化。
方法 将 Fischer 344 大鼠胸主动脉移植至 Lewis 大鼠腹主动脉。分别于第 0.5、3、7、14 天采集移植物标本，进行形态测定、免疫组化、免疫荧光染色和定量 PCR 检测。
结果 移植后第 3 天即发现外膜增厚，第 7 天即发现新生内膜。与正常外膜组织相比，NADPH 氧化酶亚单位 gp91phox 和 p47phox 在移植物外膜中的表达水平从第 3 天开始升高，并在第 14 天进一步升高。免疫组化染色显示，浸润的巨噬细胞可能是 NADPH 氧化酶表达的主要来源。移植物外膜成纤维细胞中 NADPH 氧化酶的表达增加，p47phox 基因沉默显著抑制了移植物成纤维细胞的增殖和迁移。外膜增厚伴随着外膜新生血管的增加，移植后第 14 天外膜微血管密度与新生内膜厚度呈正相关。
结论 移植损伤诱导早期移植物外膜 NADPH 氧化酶的表达和外膜新生血管的形成，提示激活的外膜可能是预防移植血管病变的新靶点。

PU-1431

乙肝病毒 Pre-S 1 抗原测定在乙肝诊治中的应用

邹建文
山东第一医科大学附属省立医院

收集我院门诊就诊及住院的慢性乙型肝炎患者及病毒携带者 355 例(男 247,女 108)，空腹静脉采血进行 Pre-S1、HBV-M、ALT 及 HBV-DNA 检测，结果发现：HBeAg 和 HBV DNA、Pre-S1 高度相关，Pre-S1 同样可以作为 HBV 复制的一个指标。我们还发现,Pre-S1 阳性组 HBV DNA 阳性率 95. 9%，HBeAg 阳性率 77.2%，肝功能异常 46.8%，均明显高于 Pre-S1 阴性组，说明 Pre-S1 阳性组病毒复制较活跃，引起肝功能持续受损。所以在乙肝的诊断、治疗过程中，HBV 五项标志物、HBV DNA 和 Pre-S1 抗原等指标不能互相取代，应联合检测，综合分析，才能对乙肝病情的进展有一个正确认识。

PU-1432

热休克蛋白 90α 在膀胱癌中的表达和意义

季健
山东大学齐鲁医院

目的 研究热休克蛋白 90α（HSP90α）在膀胱癌中的表达和意义。
方法 收集血浆标本侵袭性膀胱癌组 55 例，非侵袭性膀胱癌组 52 例及健康对照组 64 例，应用荧光实时定量 RT-PCR 法检测血浆 HSP90α 的 mRNA 表达量，并应用酶联免疫吸附法（ELISA）检测血浆 HSP90α 表达量；收集侵袭性膀胱癌组织 32 例、非侵袭性膀胱癌组织 25 例及正常膀胱粘膜组织 20 例，应用免疫组织化学技术检测 HSP90α 的表达。
结果 荧光实时定量 RT-PCR 法显示膀胱癌组血浆 HSP90α 的 mRNA 表达量显著高于健康对照组（P<0.01）,并且与膀胱癌浸润程度密切相关（侵袭性膀胱癌组 vs. 非侵袭性膀胱癌组 P<0.01）。ELISA 检测示膀胱癌组血浆 HSP90α 表达量显著高于健康对照组（P<0.01）,但与膀胱癌浸润程度无明显相关（侵袭性膀胱癌组 vs. 非侵袭性膀胱癌组 P>0.05）。免疫组织化学检查显示 HSP90α 在膀胱癌组织及正常膀胱粘膜组织中均表达，但膀胱癌组织阳性细胞百分率显著高于正常膀胱粘膜组织（P<0.01），而侵袭性膀胱癌组织与非侵袭性膀胱癌组织间无显著差异（P>0.05）。
结论 HSP90α 在膀胱癌中高表达，提示其在膀胱癌的发生发展过程中起重要作用，可作为膀胱癌靶向治疗的分子靶标。

PU-1433

外周髓系细胞中的 GSDMD 蛋白促进多发性硬化中神经炎症的发生

吴昱青[1]、李晟[1]、杨冬雪[1]、吴春燕[1]、马春梅[1]、刘雪[1]、Paul N. Moynagh[2]、王冰微[3]、胡刚[3]、杨硕[1]
1. 南京医科大学
2. 爱尔兰梅尔努斯大学
3. 南京中医药大学

目的 NLRP3 炎症小体在 EAE 发病机制中起着关键作用，然而，新近发现的 NLRP3 炎症小体下游的细胞焦亡执行蛋白——GSDMD 在 EAE 中的作用尚未明确。
方法 我们将采用流式细胞检测、免疫荧光、免疫组化等方法探究 GSDMD 在 EAE 发病中的角色和作用机制。

结果 我们观察到在 EAE 小鼠的中枢神经系统中 GSDMD 蛋白的水平显著增强，特别是在血管周围区域。EAE 的发病机制需要 GSDMD，外周血髓系细胞 GSDMD 缺乏可抑制免疫细胞向中枢神经系统的浸润，从而抑制神经炎症和脱髓鞘病变。此外，GSDMD 的丢失降低了 EAE 促发淋巴器官 T 细胞的活化和分化，阻止了 T 细胞向中枢神经系统的浸润。
结论 总的来说，这些发现提供了在 EAE 发病过程中外周髓样细胞驱动神经炎症的 GSDMD 的首次证明。

PU-1434

两种不同流式细胞仪方法学的研究及探讨

沈超飞、刘寒、吴佳莺、张延、王晓鸣、王欣
上海市第一人民医院嘉定分院

目的 流式细胞仪在生命科学领域发挥着至关重要的作用，它可以快速测量、存贮、显示悬浮在液体中的分散细胞的一系列重要的生物物理、生物化学方面的特征参量。起步较早的 BD 生物科技公司通过各项专利技术，在机器、试剂和耗材方面逐步形成了垄断地位，成为行业领域的金标准。然而 BD 流式细胞仪的国产化率非常低，甚至不能在国内进行组装。而国内组装的安捷伦流式细胞仪其性能参数也并不逊色于 BD 公司，于是我们分别在两家公司的仪器上进行常规免疫分析，并且捕获数据分析，从而探讨两种流式细胞仪优劣势及两种仪器的检测结果是否一样可靠。
方法 我们详细对比两家公司高配仪器性能参数的同时，收集了三位志愿者的体检血液，取 50ul 进行流式染色、裂红，并分别在两家公司的流式细胞仪上跑样，通过流式分析软件（flowjo），对数据进行逐级降为解析，以此获得实验结果。
结果 通过对志愿者血液的跑样，显示两者在参数性能上相差无几，基于 Flowjo 软件的数据展示，BD 仪器获得数据更有表现力，但是两者在统计上面没有显著差异。同时我们发现，两种仪器的绝对计数相差无几，从统计学意义上来说两者没有显著性差异。
结论 在绝对计数方面，BD 公司的流式细胞仪需要依赖计数微球，而安捷伦的流式细胞仪不依赖计数微球也可以实现，这是一项重大突破。从后续维修保养来看，安捷伦公司的流式细胞仪国产化程度更高，在国内组装的机器比纯进口的机器更有优势，这也是 BD 流式细胞仪的一大短板。同时实验结果也证明，两种仪器对于细胞成分的测定没有显著性差异，因此，BD LSRFortessa 和 Agilent NovoCyte Advanteon 有着相似的流式细胞术测定能力。

PU-1435

甲状腺功能状态与心血管疾病的相关性

崔洁
宁夏医科大学附属医院

甲状腺功能检查包含甲状腺素：T4、T3、fT 4、fT 3 及促甲状腺素（TSH）检查，TSH 的作用为促进甲状腺滤泡细胞合成及释放甲状腺素，故当甲状腺素升高时，TSH 为降低或检测不到的状态；当甲状腺素降低时，TSH 为升高状态。临床发放化验单过程中，发现部分心血管疾病患者甲状腺素为升高状态，TSH 也为升高状态，与规定不符，故研究特殊模式下甲状腺功能与心血管疾病的相关性，探讨特殊模式甲状腺功能的成因，为临床更清楚的了解疾病做一定的帮助。

PU-1436

不同国产检测系统之间及与 i2000SR 检测系统之间抗 HCV 抗体灰区样本检测结果的一致性分析

陆银华
上海市临床检验中心

目的 探讨 4 种国产检测系统与 ARCHITECT i2000SR 全自动免疫分析仪及配套试剂组成的检测系统（简称 i2000SR 检测系统）检测抗丙型肝炎病毒（HCV）抗体灰区样本的一致性和相关性。
方法 分别使用 4 种国产检测系统（2 种使用酶联免疫吸附试验、1 种使用时间分辨荧光免疫分析法、1 种使用化学发光法）测定不同浓度的抗 HCV 抗体标准品，评价各检测系统的线性关系及不精密度[变异系数（CV）]。分别采用 4 种国产检测系统和 i2000SR 检测系统测定 120 例经重组免疫印迹法（RIBA）确认为阳性的抗 HCV 抗体灰区样本，评价各检测系统的相关性和一致性。
结果 4 种国产检测系统检测不同浓度的标准品，批内 CV 分别为 17.6%～25.1%、0.8%～26.7%、7.8%～36.2%和 0.7%～20.2%，总 CV 分别为 15.9%～25.3%、1.0%～23.5%，7.7%～34.8%和 3.4%～18.9%，线性相关方程分别为 Y=0.634X+0.973、Y=2.495X+0.010、Y=1.348X+0.896、Y=2.510X－0.214。对于 S/CO 值为 1.0～3.0 的样本，4 种国产检测系统与 i2000SR 检测系统符合率为 34.2%～55.2%；对于 S/CO 值为 3.01～6.0 的样本，检测符合率为 57.5%～80.0%；对于 S/CO 值 6.01～9.0 的样本，4 种国产检测系统检测符合率均>90%。4 种国产检测系统均阴性的样本数为 23 份（19.2%），S/CO 值的 ±3s 为 2.80±4.35；4 种国产检测系统均阳性的样本数为 71 份（59.1%），S/CO 值的±3s 为 5.13±7.84。4 种国产检测系统两两之间的 r 值分别为 0.712 5、0.760 0、0.837 0、0.702 2、0.769 4、0.736 4，两两之间的 Kappa 值分别为 0.666 3、0.598 5、0.742 6、0.759 3、0.879 0、0.664 8。
结论 对于灰区（S/CO 值为 1.0～9.41）样本，建议应至少使用 2 种检测系统或使用高特异性的检测系统进行复检。对于低浓度样本或临界值样本，应充分考虑不同检测系统之间可能出现的结果不一致现象，制定合理的灰区范围。

PU-1437

一例 HIV 抗体假阳性的思考

罗宇程
柳州市妇幼保健院

目的 探究 HIV 抗体假阳性的应对方法及分析思路。
方法 实验室所用 HIV 抗体检测酶联免疫法试剂为英科新创（第三代试剂）， 化学发光法试剂为深圳迈瑞（第四代试剂，可同时检测 HIV 抗原抗 体），对弱阳性标本加做化学发光法，可进一步排除一些干扰因素， 最后送疾控中心进行确证实验，最终结果以疾控中心确证报告为准。
结果 我院接诊的某孕产妇进行常规入院筛查，HIV 抗体结果显示弱 阳性（**结果** S/CO 值为 1.34，阳性判断标准为 S/CO 值>1）， 次日进 行酶联免疫法双孔复查，结果仍为弱阳性。标本加做 HIV 抗体化学 发光法，结果为 0.74（>1 判为阳性），外送疾控中心进行检测。疾 控中心确证实验回报为阴性。HIV 抗体结果为阳性，本实验室**结果** 统一发布“HIV 感染待确定”，如果临床回报患者为 HIV 确诊者，报 告单上会备注上“患者已确诊”。针对此类弱阳性结果，实验室**结果** 同样为“HIV 感染待确定”，并及时与临床沟通实验室检验结果，做 好结果解释，虽然有很大可能为假阳性，但最终的结果以疾控中心 的确证报告为准。
结论 孕产妇为特殊人群，出现 HIV 抗体假阳性时， 等待疾控中心的确证报告需要一定的时间，对临床医生的诊断是一 种挑战。新创 HIV 三代酶联试剂产生非特异性反应的原因可能是：1、 样本中含有较多的免疫球蛋白易带来试剂假阳结果；2、样本中含自 身抗体、嗜异性抗体、类风湿因子、

溶菌酶等也易造成假阳结果；3、 一些特殊人群如老人、孕妇、小孩等，由于体内含自身抗体或激素 较多，在免疫测定中也容易产生假阳反应。现代试剂的制备工艺日 趋成熟，这些影响因素在试剂研究过程中也已充分考虑并消除，但 因为人血清成分比较复杂，个体差异较大，总会存在有某些影响特 别强的因素或其他未知的影响因素的样本，造成检验结果的假阳性。 这就需要我们检验人员充分发挥主观能动性，积极联系临床医生与 试剂厂家，及时排查分析原因，为患者提供优质的服务。

PU-1438

慢性乙型肝炎患者病毒复制与肝纤维化五项联合检测的临床应用

熊娟
汉川市人民医院

目的 探讨慢性乙型肝炎患者乙型肝炎病毒（HBV）DNA 复制与肝纤维化五项指标：透明质酸（HA）、Ⅲ型前胶原 N 端肽（PⅢPN）、Ⅳ型胶原（CⅣ）、层粘连蛋白（LN）、甘胆酸（CG）联合检测的临床意义。
方法 选取 109 例慢性乙型肝炎患者为研究对象，选取 40 例健康体检者为对照组，分别检测 HBV DNA 和肝纤维化五项，采用 SPSS19.0 软件对数据进行统计分析。
结果 低载量组和中载量组肝纤五项检测结果与对照组比较，差异无统计学意义（P＞0.05）；高载量组肝纤五项检测结果与对照组比较，差异有统计学意义（P＜0.05）。随着 HBV DNA 载量的增加，肝纤五项各检测指标的数值也在增加。肝纤五项（HA、PⅢPN、CⅣ、LN、CG）的 ROC 曲线下面积（AUC）分别为 0.556、0.763、0.742、0.420、0.695，其中 PⅢPN 的 AUC 最大，表明 PⅢPN 比其他指标对肝脏疾病的诊断准确率最高；LN 的 AUC 最小，小于 0.5，表明其单独诊断的准确率低。
结论 HBV DNA 载量与血清肝纤维化五项指标联合检测是慢性乙型肝炎患者病情监测的一个良好指标，临床应及时关注慢性乙型肝炎患者病毒复制与肝纤维化水平，延缓肝硬化的发生。

PU-1439

前列腺癌与 TAMs

凡慧慧[1]、曾方银[2]
1. 永州市中心医院
2. 南方医科大学第五附属医院

前列腺癌（prostate cancer； PCa） 是指发生在前列腺的上皮性恶性肿瘤，在全球范围内十分常见。近年来，我国前列腺癌的发病率明显上升，且围绕前列腺癌的发生、发展、诊断和治疗进行了大量的研究。前列腺癌治疗手段主要根据患者年龄、肿瘤分期分级等具体情况而定，目前主要是手术切除治疗、放射治疗以及雄激素阻断治疗。但是由于前列腺癌高发的二次转移概率，使得前列腺癌患者总体预后效果不佳。因此，探究更有效的前列腺癌治疗策略，并寻求新的治疗靶点和思路，成为目前前列腺癌的研究热点。近年来，肿瘤免疫治疗备受关注，是肿瘤治疗领域的焦点，同靶向治疗一起有望成为继手术、化疗、 放疗后肿瘤治领域的一场革新。

巨噬细胞是肿瘤微环境中浸润最丰富的炎症细胞，被称为肿瘤相关巨噬细胞（tumor associated macrophages， TAMs）。在原发性肿瘤中，肿瘤细胞分泌细胞因子促进巨噬细胞的募集和增殖； 反过来，巨噬细胞可以刺激新生血管的形成并提高肿瘤细胞的侵袭性、迁移性和血管内渗性；同时巨噬细胞还具有免疫抑制性，保护肿瘤细胞逃避自然杀伤细胞和 T 细胞的攻击。因此，肿瘤的发生发展与肿瘤相关巨噬细胞的作用密切相关。

PU-1440

儿童结核感染 T 细胞 γ 干扰素释放试验的结果分析

吴思宇、张潇钰
中南大学湘雅医院

目的 针对我院儿童可疑结核患者或需排除结核感染患者的结核感染 T 细胞 γ 干扰素释放实验（IGRAs）的结果进行回顾分析，并探讨儿童不确定结果产生与疾病的相关性。
方法 回顾分析 2020 年 4 月-2020 年 12 月中南大学湘雅医院 862 例儿童疑似结核或需排除结核患者的 IGRAs 检测结果，并与此期间 14356 例成人患者 IGRAs 检测结果进行比较分析，同时收集儿童基本资料，运用 SPSS 统计学软件进行数据分析。
结果 862 例儿童检测样本中 IGRAs 检测结果阳性率为 6.3 %，大大低于成人患者阳性率（41.2 %），差异有统计学意义（c2=235.130，P=0.000）；儿童不确定结果发生率为 5.6 %，高于成人不确定结果发生率 3.2 %，差异有统计学意义（c2=24.910，P=0.000）。儿童组中男、女患者 IGRAs 不确定结果发生率为 4.6 %，9.0 %，差异有统计学意义（c2=6.551，P=0.010）；成人组中男女患者不确定结果发生率分别为 2.9 %，3.6 %，差异有统计学意义（c2=6.005，P=0.014）。儿童血液系统恶性肿瘤、感染性疾病、自身免疫性疾病、慢性肝脏疾病、过敏性疾病患者其不确定结果发生率与确定结果（阴性/阳性）发生率的差异具有统计学意义（P＜0.05）。
结论 儿童不确定结果发生与年龄性别因素密切相关，还与患者免疫状态密切相关。

PU-1441

新型冠状病毒疫情前后呼吸道病原体感染情况比较

凡慧慧
永州市中心医院

目的 回顾性分析永州市中心医院 2019 年和 2020 年住院患儿 9 种呼吸道病原体（嗜肺军团菌、肺炎支原体、Q 热立克次体、肺炎衣原体、腺病毒、呼吸道合胞病毒、甲型流感病毒、乙型流感病毒、副流感病毒 1、2 和 3 型）感染的分布差异，了解新冠疫情防控下呼吸道病原体的感染和传播情况，为临床诊疗提供依据。
方法 采用间接免疫荧光法检测患儿血清中 9 种呼吸道病原体 IgM 抗体。
结果 2019 年度检测患儿 3936 例，阳性率 30.6%，2020 年度检测患儿 1176 例，阳性率 17.7%，有统计学意义（P<0.05）；2019 年度和 2020 年度各病原体阳性率分布有显著差异（P<0.05），且有季节差异（P<0.05）。
结论 新冠肺炎疫情常规的防控手段对 9 种呼吸道病原体的感染与传播有明显的阻碍作用，尤其是流感病毒、腺病毒、呼吸道合胞病毒等。

PU-1442

TROCH 筛查的现状

曾静
南方医科大学珠江医院

TORCH 是一个缩写，代表一组病原体，包括弓形虫(TOX)、风疹病毒(RV)、巨细胞病毒(CMV)和单纯疱疹病毒(HSV)，可引起围产期感染，具有类似症状[1]。TORCH 作为优生优育的指标之一，TORCH 特异性抗体筛查可以降低先天性疾病发生率。本文总结 TROCH 筛查的应用现状，指导临床正确合理地使用 TORCH。

PU-1443

CMIA 法与 TPPA 法检测梅毒特异性抗体相关性分析

肖伟利
内蒙古自治区人民医院

目的 对化学发光法检测梅毒特异性抗体（CMIA）与金标准梅毒密螺旋体血凝试验（TPPA）进行比较分析，评价 CMIA 符合率及合理复检范围。
方法 选取 2020 年 6 月至 2021 年 5 月内蒙古自治区人民医院 TPPA 测定梅毒特异性抗体阳性 1355 例为研究对象，同时采用化学发光法（雅培 Ci16200）检测梅毒特异性抗体。以 TPHA 试验为金标准,对 CMIA 诊断梅毒特异性抗体的灵敏度、特异度和准确度进行计算,并采用一致性检验对 CMIA 和 TPPA 的一致性进行分析。根据实验结果探讨 CMIA 检测梅毒特异性抗体复查的合理限度。
结果 1355 例 TPPA 阳性标本用 CMIA 检测，阳性限度为 S/CO≥1 时,阳性 1098 例,阴性 257 例。CMIA 与 TPPA 法的 Kappa 一致性系数为 0.81,灵敏度为 58.35%；准确度为 91.32%；特异度为 95.15%。S/CO 值在>1.0～≤3.5 之间的结果不一致比率为 83.38%，S/CO 值>9.0 时，两者符合率达 100%。
结论 梅毒 CMIA 法用于梅毒特异性抗体检测的灵敏度、准确度高，特异度好，可以用于梅毒筛查检验。同时，鉴于 CMIA 检出限底、灵敏度高，当 S/CO 值<9.0 时必须用确诊方法复检，当两种方法结果明显不一致时，建议定期复查，避免误诊或漏诊。

PU-1444

The Diagnostic Performance of SARS-CoV-2 Antibody Tests for COVID-19: A Systematic Review and Meta-Analysis

Haolong Li
Department of Clinical Laboratory, Peking Union Medical College Hospital, Peking Union Medical College and Chinese Academy of Medical Sciences, Beijing, China

Objective The aim was to systematically evaluate the diagnostic performance of SARS-CoV-2 antibody test for COVID-19 according to officially published data.
Methods Four electronic databases were searched for relevant studies published by 5 May 2020, including PubMed, Web of Science, Embase, and CNKI. The bivariate mixed-effects model was used to calculate the diagnostic indexes from primary data of eligible studies. We evaluated IgM, IgG, either IgM or IgG (at least a positive result detected by IgM and IgG), and total antibody (Ab) tests based on Enzyme-linked immunosorbent assay, Chemiluminescence Enzyme Immunoassays, gold immunochromatographic assay and Fluorescence Immunoassays. The included articles were assessed with the Quality Assessment of Diagnostic Accuracy Studies 2 tool. Subgroup analysis, meta-regression, and publication bias were also performed.
Results Twenty-five articles that met inclusion criteria were performed meta-analysis, there were a total of 2,342 COVID-19 patients and 2979 control participants. Either IgM or IgG and Ab test has the highest sensitivity, as followed by IgG and IgM test. All tests showed high specificity reaching levels above 98%. Meta-regression indicated that the method of antibody detection and the target antigen of antibody detection kits might be the source of heterogeneity for IgM, while no other significant sources of heterogeneity were detected for IgG, either IgM or IgG. In subgroup analysis, we found the heterogeneity could obviously change in some subgroup of IgM, IgG, and either IgM or IgG test. No publication bias was detected in all tests.
Conclusion Antibody test is a reliable supplementary diagnostic tool to identify the suspected COVID-19 patients, simultaneous detection of IgM and IgG is more sensitive than testing one type of antibody.

PU-1445

维生素 D 受体基因多态性在自身免疫性疾病中的研究进展

李昊隆
中国医学科学院北京协和医院

目的 对维生素 D 受体（VDR）基因多态性与多种 AID 易感性之间的相关研究进展进行综述。
方法 检索 PubMed、Web of Science、Scopus、Embase 中已发表的 VDR 基因多态性与多种 AID 易感性之间的相关文献，对已发表的文献进行总结。
结果 VDR 基因在人体多种组织中进行表达，其转录产物 VDR 是介导 1,25(OH)2D3 发挥多种生物学效应的受体，VDR 基因多态性的产生可能影响 1,25(OH)2D3 对机体正常的免疫调节功能。VDR 基因多态性与类风湿关节炎、系统性红斑狼疮、原发性干燥综合征等自身免疫病密切相关。
结论 VDR 基因多态性可能在 AID 的发病过程中扮演某种重要角色，其多态性有望成为诊断 AID 的遗传标志物。目前，国内外研究尚且停留在其多态性表型在疾病分布中的表达情况，还需更多研究去探索多态性分布与疾病临床特点的相关研究。

PU-1446

血液学指标对强直性脊柱炎患者髋关节受累风险的评估价值

Sihui Li、xi li、wei zhou、yanting jiang、min jin、jian wang
The Value of Hematological Indexes in Evaluating the Risk of Hip Involvement in Patients with Ankylosing Spondylitis

Objective To analyze the laboratory data of ankylosing spondylitis (AS) patients with hip involvement, and explore the value of neutrophil to lymphocyte ratio (NLR) and monocyte to lymphocyte ratio (MLR) in evaluating the risk of hip involvement in patients with AS.
Methods Retrospective analysis was performed on a total of 188 patients with AS. According to BASRI score, 84 AS patients with hip radiology score ≥2 were selected as hip involvement group, and 104 AS patients with hip radiology score<2 as non-hip involvement group. During the same period, 173 patients with osteoarthritis (OA) and 181 healthy people by age and sex were selected. The characteristics of hematological indexes of the three groups were compared, and the levels of NLR and MLR in hip involvement group and non-hip involvement group were observed.
Results The values of NLR and MLR in AS group were significantly higher than those in OA group and healthy controls (each P<0.05). The values of NLR and MLR in hip joint involvement group were significantly higher than those in non-hip involvement group (P<0.05). The diagnostic efficiency of combined detection of NLR and MLR in AS-hip involvement group was significantly higher than that in AS-non-hip involvement group and OA group (AUC-AS-hip involvement group=0.863, P<0.001; AUC-AS-non-hip involvement group=0.746, P<0.001; AUC-OA group=0.669, P<0.001).
Conclusion NLR and MLR have certain value in the evaluation of AS patients with hip involvement, and the combined diagnosis of them has higher value.

PU-1447

神经元特异性烯醇化酶对蛛网膜下腔出血早期预后的临床价值

卢英
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨与炎症相关的生物学标志物和神经元特异性烯醇化酶与动脉瘤性蛛网膜下腔出血患者早期预后的相关分析。
方法 将动脉瘤性蛛网膜下腔出血患者临床表现和患者的 CT 检查结果进行比对，根据评分将患者分为预后良好和预后不良组，对比分析两组的临床资料。
结果 预后不良组入院时白细胞计数(WBC)、中性粒细胞计数(N)、C 反应蛋白(CRP)、神经元特异性烯醇化酶(NSE)较预后良好组显著增高，P<0.05，logistics 回归分析表明 WBC、N、 CRP、NSE 与动脉瘤性蛛网膜下腔出血预后不良呈正相关，为其危险因素。当 NSE 升高超过 1000 ng/ml 时，患者预后不良死亡率极高。
结论 入院时 WBC、N、CRP、NSE 的升高是预测动脉瘤性蛛网膜下腔出血预后不良的独立生物学标志。根据患者的病情发展关注 NSE 的变化，判断脑损伤的程度，有利于治疗方案的选择，减少 CT 检查的次数。

PU-1448

系统性红斑狼疮患者血清同型半胱氨酸水平与疾病活动度及血脂异常的相关性

陈希
中国人民解放军北部战区总医院

目的 探究系统性红斑狼疮患者血脂异常发生情况，分析血清同型半胱氨酸与 SLE 活动度以及心血管疾病危险因素的关系。
方法 回顾性分析确诊为系统性红斑狼疮患者 76 例、健康对照组 57 例，用全自动生化分析仪检测 Hcy，总胆固醇（total cholesterol，TC）、甘油三脂（triacylglyceride，TG）、高密度脂蛋白胆固醇（High density liptein cholesterol，HDL-C）、低密度脂蛋白胆固醇（Low-Density Lipoprotein Cholesterol，LDL-C），并检测其抗双链 DNA（anti-double-stranded DNA antibody，anti-dsDNA）抗体与补体 C3、C4 水平，以评估 SLE 患者 SLEDAI 积分。最后采用统计学方法分析 SLE 患者血清 Hcy 水平与疾病活动度及血脂异常的相关性。
结果 SLE 患者血清 Hcy、TC、TG、Hcy 水平均高于健康对照组（P<0.05），血清 HDL-C 水平明显低于对照组（P<0.05）。在 SLE 患者中，伴有血脂异常患者的血清 Hcy 水平明显高于血脂正常的 SLE 患者（P<0.05），高于健康对照组（P<0.05）。SLE 患者血清 Hcy 的水平和 TC 与 TG 水平呈正相关（P<0.05），与 SLEDAI 评分呈显著正相关（P<0.01），伴有血脂异常的 SLE 患者表现出更高的 SLEDAI 评分。Hcy 水平与血脂异常之间存在显著且独立的关联。
结论 血清 Hcy 水平在 SLE 血脂异常患者中明显升高，检测血清 Hcy 水平变化对评估 SLE 患者疾病活动度及预测心血管并发症有重要的临床意义，SLE 患者血清标志物变化的早期识别有助于制定干预策略，从而降低并发心血管疾病的风险。

PU-1449

血清神经元特异性烯醇化酶(NSE)水平和急性心肌梗死患者心功能分级的关系

吴志奇
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨急性心肌梗死(acute myocardial infarction，AMI) 患者的血清神经元特异性烯醇化酶(NSE)水平与心功能分级的关系。
方法 入选 2013 年 12 月 1 日至 2015 年 11 月 31 日入院的冠心病患者，其中 154 名 AMI 患者。由病历收集患者的基本信息、血清 NSE、心电图及血液生化检查资料。依据心功能 Killip 分级分为 Killip 低分级组和 Killip 高分级组。应用 t 检验或 Mann-Whitney U 检验比较不同 Killip 分级组患者血清 NSE 水平的差异。
结果 与 Killip 低分级组相比，Killip 高分级组患者年龄(69 岁 vs 65 岁，P ＜ 0. 05) 和糖尿病患者比例均显著较高(55% vs 25%，P ＜ 0. 05) ，总胆固醇和低密度脂蛋白水平则明显偏低(P ＜ 0. 05) 。Killip 高分级组患者的血清 NSE 水平显著高于 Killip 低分级组患者(19.24 mg /dl vs 17.01 mg /dl，P ＜ 0. 05) 。按疾病史分层分析显示，在非糖尿病(19.45 mg /dl vs 17.02 mg /dl) 或非血脂异常(19.33 mg /dl vs 16.95 mg /dl) 患者中，Killip 高分级组患者的血清 NSE 水平显著性高于低分级组(P ＜ 0. 05) 。
结论 AMI 患者 NSE 水平与 Killip 分级相关，NSE 水平越高，患者 Killip 分级越高。血清 NSE 水平可能是 AMI 患者心功能 Killip 分级的良好预测指标，尤其对于无糖尿病和无血脂异常的患者。

PU-1450

铁蛋白指数作为成人噬血细胞淋巴组织细胞增生症的新型预后标志物

周军、吴志奇、周菁、徐华国
江苏省人民医院（南京医科大学第一附属医院）

目的 先前的研究已经评估了成人噬血细胞性淋巴组织细胞增生症 (HLH) 中铁蛋白水平与存活率之间的关系。然而，从未评估成年 HLH 患者入院至出院时铁蛋白降低百分比（称为铁蛋白指数）水平来预测 6 个月的生存率。
方法 我们收集 102 名新诊断成人 HLH 患者的人口统计学、实验室和临床信息。分析回归分析、接受者操作曲线和 Kaplan-Meier 曲线以探索铁蛋白水平的表现。
结果 存活组和非存活组的铁蛋白指数和铁蛋白水平有显着差异（均 p <0.001）。铁蛋白指数具有最高的预测生存曲线下面积 (AUC) (AUC = 0.802, p < 0.001)，其次是出院铁蛋白 (AUC = 0.746, p < 0.001)。 Kaplan-Meier 分析显示，根据铁蛋白的最佳临界值，存活率存在显着差异指数≥10.19% (p < 0.001) 或出院铁蛋白≤1056.1 μg/L (P < 0.001)。多变量分析证实，铁蛋白指数和出院铁蛋白是 6 个月生存率的独立预测因子（铁蛋白指数：优势比 (HR) 6.237，95% 置信区间 (CI) 2.075-18.774，p = 0.001；出院铁蛋白：HR 6.024, 95 % CI 1.894-19.231，p = 0.002）。此外，铁蛋白指数≥10.19% 和出院铁蛋白≤1056.1 μg/L 的组合具有显着更高的 6 个月生存率（P < 0.001）。
结论 对于成人 HLH 患者，铁蛋白指数比入院和出院时铁蛋白水平更能预测 6 个月生存率。

PU-1451

丁型肝炎：真实流行率和实验室诊断面临的挑战

陈林媛、徐华国
江苏省人民医院（南京医科大学第一附属医院）

丁型肝炎病毒 (HDV) 是一种有缺陷的单负链 RNA 病毒，因为其包膜蛋白的合成依赖于乙型肝炎病毒 (HBV)。研究一致表明，HBV 和 HDV 的共感染是最严重的病毒性肝炎形式，会加速发展为肝硬化甚至肝细胞癌。全世界约有 7400 万 HBV 表面抗原 (HBsAg) 阳性患者也同时感染 HDV。此外，静脉吸毒和高危性行为的患者感染 HDV 的风险更高。 HDV 的治疗方案是有限的，并且在用聚乙二醇化干扰素 α 治疗后已经观察到 HDV 的复发。为减少 HDV 的传播，应对所有 HBV 感染者进行 HDV 筛查。目前，多种血清学和分子检测方法广泛用于 HDV 的诊断。但由于缺乏国际标准的不同实验室的诊断结果往往没有可比性。因此，HDV 的真实患病率仍不清楚。在此，我们分析了影响 HDV 流行率估计的各种因素。我们还讨论了目前可用的 HDV 实验室诊断方法的优缺点，以期为改进 HDV 检测提供一些思路。

PU-1452

Role of cell free microRNA-19a and microRNA-19b in gestational diabetes mellitus patients.

Fang Wang
The Second Hospital of Shandong University

Gestational diabetes mellitus (GDM) is associated with adverse pregnancy outcomes in pregnant women and it’s prevalence is increasing worldwide. A total 100 cases of GDM and 100 healthy controls were included in a study and blood samples were collected in plain vials from all study participant. Difference among several variables which included BMI, glycemia, insulinaemia, HbA1c, total cholesterol, triglycerides, urinary albumin were compared between GDM cases and controls and were found to be statistically significant ($p < 0.0001$). Additionally, GDM cases showed 4.0 fold increase in miRNA-19a and 4.7 mean increase in miRNA-19b expression compared to healthy control individuals. A positive correlation was observed between miRNA-19a and miRNA-19b among GDM cases. However the correlation coefficient was 0.13 between miRNA-19a and miRNA-19b. This suggested that with the increase in miRNA-19a, miRNA-19b also increased. The findings of this study concludes that an increase in microRNA-19a and microRNA-19b is observed in GDM cases and could be linked with increased risk factor for worsening of the disease. MicroRNA-19a and 19b have been linked to alcoholism and smoking and could also be the factors in GDM.

PU-1453

山东地区儿童对 7 种食物不耐受的情况

王芳
山东大学第二医院

目的 调查山东地区儿童对 7 种食物不耐受的情况。
方法 用免疫荧光法(IF)检测 2017 年 1 月至 2020 年 12 月期间山东大学第二医院儿科门诊和住院 1523 例 0—15 岁儿童血清 7 种食物特异性 IgG 抗体浓度。
结果 1523 例儿童中有 1235 例检出食物不耐受,血清食物特异性 IgG 抗体阳性率为 81.09%;7 种食物特异性 IgG 抗体总的阳性比例分别为牛奶 63.2．O%、鸡蛋 65.3%、西红柿 11.4%、大豆 9.6%、

鳕鱼 8.2%、大米 4.36%、牛肉 2.2%、虾 1.2%；男孩 7 种食物的阳性比例均高于女孩。对 1～3 种食物不耐受的男孩和女孩分别占 70.3%和 65.9%。儿童对其中五种食物的不耐受强度存在统计学差异（P〈0．05），其中对牛奶、鸡蛋以重度不耐受为主，对西红柿、大豆、鳕鱼、大米、牛肉以轻度不耐受为主。

结论 所检测儿童群体的食物不耐受以鸡蛋、牛奶等为主，且重度不耐受的比例高；男孩食物不耐受的比例高于女孩；且多数儿童同时对 1～3 种食物不耐受。

PU-1454

降钙素原和 C 反应蛋白，谁更具有指导意义？

孙甜甜
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 分析降钙素原与 C 反应蛋白在感染性疾病临床诊断中的应用效果。降钙素原和 C 反应蛋白在临床上都是反应感染的指标，谁更具有指导意义。

方法 选取所在医院 2019 年 11 月-2019 年 11 月收治的感染性疾病患者 90 例为研究对象,按照随机数字表法分为对照组与观察组两组。对照组采取降钙素原(PCT)诊断方法,观察组采取 C 反应蛋白(CRP)诊断方法,比较分析两组临床诊断效果与患者满意度。

结果 观察组总有效率为 97.78%,对照组为 88.89%,差异有统计学意义(P0.05);观察组患者满意度 100%,对照组为 91.11%,差异有统计学意义(P0.05)。

结论 CRP 作为一种急性时相蛋白，机体炎症反应均可引起 CRP 的升高，故单靠这一指标很难区分是否为感染性疾病，需结合临床表现及其他相关辅助检查进行综合全面考虑机体免疫功能及防御机制。而 PCT 作为一种新的炎症指标，表达水平不受非感染因素影响，因此 PCT 对细菌感染性疾病的诊断价值明显优于白细胞计数及 CRP，是一项灵敏度高、特异性强的指标。而且已被公认为是目前最敏感的脓毒血症诊断指标，其对感染前期的诊断，鉴别感染类型和感染程度，指导抗生素应用等方面有很高的价值，在临床上有很高的指导意义。

PU-1455

抗核抗体和 A3 抗体谱对干燥综合征的临床应用价值

张 凡
滨州医学院烟台附属医院

目的 通过抗核抗体 ANA 和 A3 抗体谱的检测，来诊断研究其与干燥综合征的相互联系。

方法 选取 2019 年 1 月至２０20 年 1 月在本医院就诊疑似干燥综合征的患者，确诊后将其分为干燥综合征（ss）组 150 例和其他疾病组 150 例，分别进行抗核抗体谱 A3 和抗核抗体 ANA 检测，A3 谱分为线粒体 M2 抗体、核糖体Ｐ蛋白（RIB）、组蛋白（HI）、核小体(NUC)、双链ＤＮＡ抗体（ DsＤＮＡ）、ＰＣＮＡ抗体、着丝点Ｂ蛋白（ ＣＢ）、Ｊｏ － １抗体、ＰＭ－Ｓｃｌ抗体、Ｓｃｌ － ７０抗体、ＳＳＢ抗体、Ｒｏ － ５２抗体、ＳＳＡ抗体、Ｓｍ 抗体[1]、抗 U1－nRNP 抗体指标，ANA 分为核型（ANA－X）和抗核抗体（ANA）两项指标。将患者的抗体及核型检测结果与最终确诊疾病类型进行对比研究。

结果 150 例ＳＳ患者中抗核抗体 A3 各项指标表现出特异性变化，相应指标呈现出较高的数值结果，与对照组形成明显对比，差异有统计学意义（ Ｐ ＜０．０５）；其中ＳＳＡ、ＳＳＢ的结果数据分析，表明其与干燥综合征的联系最为密切，Ｐ ＜０．００１，其次抗 U1-ｎＲＮＰ抗体、Ｒｏ － ５２的联系性次之，Ｐ 值＜０．０５，其余相关抗核抗体同样就具有参考价值，Ｐ＜０．０５，特异性表现不如其他抗体。ANA 核型分布以颗粒型、均质型最为广泛。

结论 ANA 核型分布有助于判定其与抗体相互关联性，进而更加精确诊断疾病，判断其阳性率。

PU-1456

黄热病毒 NS1 蛋白在蚊虫监测中的运用

林亚英
南方医科大学珠江医院

目的 检测感染蚊虫中黄热病毒（Yellow Fever virus, YFV）非结构蛋白 1（Nonstructural Protein 1,NS1），评估其在蚊虫黄热病毒感染中预警。
方法 采用含黄热病毒疫苗株人造感染血感染白纹伊蚊（广州株）约 300 只，蚊虫血餐后 7 天，随机 5 只蚊虫一组，研磨后同时采用定量 PCR 方法和前期建立的检测 YFV NS1 的双抗夹心法检测 YFV 17D 疫苗株感染蚊虫研磨上清中病毒 RNA 和 YFV NS1 蛋白。
结果 60 组蚊虫样品中 55 个样品 YFV RNA 阳性，对应 YFV NS1 蛋白也为阳性。5 组 YFV RNA 阴性样品中 YFV NS1 蛋白结果也为阴性。
结论 在感染 YFV 蚊虫中可检测到 YFV NS1 蛋白，提示该 YFV NS1 蛋白可作为 YFV 感染蚊虫监测中检测靶标，用于虫媒传播 YFV 预警监测。

PU-1457

血管内皮生长因子在肿瘤治疗中的应用进展

王青青
滨州医学院烟台附属医院

目的 比较血管内皮生长因子在不同肿瘤和年龄中的表达情况。
方法 采用免疫发光法检测 VEGF 的含量；以 62 岁为年龄的中位数将所有检测为阳性的标本分为低年龄组（<62 岁）和高年龄组（≧ 62 岁）两组对 VEGF 的含量进行比较；所以阳性标本进行癌症分类并比较 VEGF 的表达情况。
结果 510 个检测标本中 VEGF 的阳性率为 17.25%（88/510）, 去掉重复检测后的阳性率为 16.87%（84/498）;在总体检测标本中，VEGF 的表达量与年龄呈正相关（p<0.05,r=0.137）,在阳性标本中 VEGF 表达量与年龄不相关（p=0.0725）；VEGF 的含量在高年龄组和女性中的含量相对较多,（p<0.05）具有统计学意义；VEGF 在各种癌症中的含量比较为肺癌>胃癌>混合型>乳腺癌>肝癌。
结论 VEGF 在恶性肿瘤中含量较多，尤其是在肺癌和胃癌患者体内，且与性别有一定的相关系。

PU-1458

早发性克罗恩病基因多态性及实验室诊断价值分析

詹富国、张泽钦
福建医科大学附属第一医院

目的 探讨 IL-10RA 基因 c.301C>T 和 c.537G>A 位点单核苷酸多态性（SNP）与福建地区早发性克罗恩病（EO-CD）的发病关系；分析几种常见实验室指标在 EO-CD 诊断中的应用价值。
方法 收集 2020 年 10 月至 2021 年 3 月在福建医科大学附属第一医院确诊的 EO-CD 67 例，成人发病 CD 148 例；桑格测序法对 EO-CD 组目的基因进行 SNP 检测；收集并完善入组病例的 EB-DNA 等实验室检测结果、内镜、病理结果进行回顾性研究。
结果 基因检测结果显示 67 例 EO-CD 均无 IL-10RA 基因 c.301C>T 和 c.537G>A 位点突变； EO-CD 组的抗酿酒酵母抗体（ASCA）、抗胰腺腺泡抗体（PAB）、EB-DNA 阳性率明显高于成人发病 CD 组和阴性对照组，差异有统计学意义（P＜0.05）。EO-CD 组的抗小肠杯状细胞抗体（GAB）、粪便钙卫蛋白阳性率明显高于阴性对照组，差异有统计学意义（P＜0.05）；CD 患者

合并 EB-DNA 阳性较 EB-DNA 阴性内镜下更多出现特征性的孤立性深溃疡和浅层弥漫小溃疡，病理出现特征性的上皮淋巴细胞增多和裂隙溃疡，代表病情严重程度的 CDAI 评分明显升高（P＜0.05）。

结论 福建人群 IL-10RA 基因 c.301C>T 和 c.537G>A 位点 SNP 与 EO-CD 发病尚不明确；EB-DNA 阳性可能加重 CD 病情，且在 EO-CD 中表现得更为显著；ASCA 和 PAB 是诊断 CD 的特异性指标；粪便钙卫蛋白可作为 CD 初筛指标和病情监测指标。

PU-1459

血清 IgG4 及 IgG4/IgG 比值对 IgG4 相关疾病的诊断性能评价

魏彬
四川大学华西医院

目的及背景 IgG4 相关疾病(IgG4 related disease, IgG4-RD)是一种可累及多器官的慢性进行性自身免疫性疾病，该病难于诊断，目前缺乏血清 IgG4 及 IgG4/IgG 比值诊断 IgG4-RD 统一标准，本研究旨在评价血清 IgG4 和 IgG4/IgG 比值对 IgG4-RD 的诊断价值，以辅助诊断 IgG4-RD。

方法 纳入 2014 年 4 月-2020 年 12 月我院首次确诊的 IgG4-RD 患者共 226 例，收集其实验室检测及临床信息，同时纳入 1510 例非 IgG4-RD 患者作为对照组，采用受试者工作特征曲线（ROC）评估血清 IgG4 和 IgG4/IgG 比值诊断 IgG4-RD 的最佳 cut-off 值。

结果 IgG4-RD 组患者血清 IgG4 浓度和 IgG4/IgG 比值的中位数分别为 5.89（3.25,13.90）g/L 和 0.29（0.16,0.76），而对照组血清 IgG4 浓度和 IgG4/IgG 比值的中位数分别为 0.53（0.25,1.08）g/L 和 0.038（0.02,0.07）。在鉴别 IgG4-RD 与非 IgG4-RD 时，IgG4 值和 IgG4/IgG 值的最佳 cut-off 值分别为 2.31g/L 和 0.10，相应曲线下面积(AUC)分别为 0.969 和 0.959。受试者工作特性曲线的比较显示这些 AUC 值之间有显著差异(p<0.05)。IgG4 最佳临界值的敏感度、特异度、阳性预测值(PPV)和阴性预测值(NPV)分别为 89.18%、92.24%、62.97%和 98.10%；IgG4/IgG 比值最佳临界值的敏感度、特异度、阳性预测值(PPV)和阴性预测值(NPV)分别为 92.78%、84.42%、43.57%和 98.76%。

结论 血清 IgG4 浓度和 IgG4/IgG 比值升高对 IgG4-RD 的诊断有重要价值。

PU-1460

间接法建立中国西南地区 T 淋巴细胞亚群参考区间

魏彬
四川大学华西医院

目的 采用间接法建立中国西南地区 T 细胞亚群的参考区间，并与厂商提供的参考区间进行比较，验证间接法可靠性。

方法 选取 2018 年 6 月至 2020 年 10 月四川大学华西医院健康体检人群 T 淋巴细胞亚群检测数据共 53822 例，通过偏度-峰度检验分析数据的正态性，非正态数据通过 Box-Cox 转换转变成近似正态，转换后的数据采用 Tukey 法剔除离群值，采用非参数法评估不同年龄段和性别 T 淋巴细胞亚群 P2.5-P97.5 参考区间，选取 2020 年 11 月至 2021 年 2 月的 6116 例健康体检人群对所建立的参考区间进行验证。

结果 男女性之间以及 14-30 岁、31-45 岁、46-60 岁、61-75 岁、76-100 岁年龄段 T 淋巴细胞亚群参考区间均有明显差异（P<0.01）。随着年龄增加，男性和女性人群中各 T 淋巴细胞亚群百分率以及 T 淋巴细胞绝对计数 P2.5-P97.5 参考区间上下限均呈明显下降趋势（具体见表 1）。验证人群各指标在所建立参考区间范围外的比例均小于 5%，符合标准，此次建立的参考区间与厂商提供的参考区间有明显差异。

结论 T 淋巴细胞亚群参考区间与年龄、性别有明显的相关性，间接法建立参考区间结果可靠、应推广应用于不同地区临床实验室各指标参考范围的建立。

PU-1461

两种肺炎支原体抗体检测方法对天津地区不同人群肺炎支原体感染诊断的临床价值

王居鹏、朱黎娜、马明坤、温学红
天津中医药大学第二附属医院

目的 分析两种肺炎支原体抗体检测方法天津地区成人及儿童不同时期肺炎支原体感染检出情况，为临床治疗和预防提供依据。
方法 回顾性研究 2017 年 9 月至 2021 年 5 月，天津中医药大学第二附属医院的呼吸道感染患者经被动凝集法检测肺炎支原体总抗体（IgM、IgG、IgA）和血清间接免疫荧光法（IFA）检测肺炎支原体 IgM 抗体，按成人、儿童不同年龄阶段进行分组比较，分析它们在呼吸道感染性疾病中的检出情况及临床意义。
结果 5666 例呼吸道感染患者肺炎支原体总抗体检测阳性率为 40.13%，成人组阳性率为 19.92%，儿童组阳性率为 77.30%，成人组与儿童组之间有统计学差异（P<0.05）；男性阳性率为 37.89%，女性阳性率为 42.40%，差异有统计学意义（P<0.05）。5746 例呼吸道感染患者肺炎支原体 IgM 抗体检测阳性率为 28.56%，成人组阳性率为 10.37%，儿童组阳性率为 36.82%，成人组与儿童组之间有统计学差异（P<0.05）；男性阳性率为 24.56%，女性阳性率为 33.38%，差异有统计学意义（P<0.05）。秋季为肺炎支原体总抗体和 IgM 抗体阳性率最高的季节。1975 例同时经两种方法检测 MP 抗体的患者中，当肺炎支原体 IgM 抗体阳性时，有 26.71%的患者总抗体为阴性，8.63%的患者滴度在 1：40-1：80 间；而当与肺炎支原体 IgM 抗体阴性时，有 34.94%的患者总抗体滴度≥1：160。
结论 肺炎支原体是引起呼吸道感染的主要病原体，儿童和女性阳性检出率更高，秋季为支原体肺炎告高发季节，应加强筛检。

PU-1462

巨细胞病毒抗原血症检测方法的建立

白敏凤、尹利民
昆明市第一人民医院检验科

巨细胞病毒（ Cytomegalovirus，CMV）属疱疹病毒 β 亚科，成熟的病毒颗粒直径为 150-200 nm，为具有包膜的双链线性 DNA 病毒，基因组全长为 225-240 kb，其翻译后的产物超过 200 种蛋白质。这种病原体的感染在全世界范围内具有很高的流行率。CMV 在有免疫能力的宿主中感染通常是无害的，但在免疫功能低下（如 HIV 感染或接受移植）的病人中感染会有很高的发病率和死亡率[1]。因此，早期检测巨细胞病毒对于指导临床早期治疗至关重要。检测 CMV 的实验室方法包括分子测定、抗原血症检测、组织病理学、病毒培养和血清学检测等。目前临床上常规的巨细胞病毒（cytomegalovirus，CMV）检测目前多数都是通过酶联免疫法（enzymelinked immunosorbent assay,ELISA） 或免疫荧光法（immunofluores cence assay,IFA）检测血清中的 IgG、IgM 抗体以及实时荧光定量 PCR 的方法来检测移植后巨细胞病毒的感染。但对于器官移植人群，对活动性感染或疾病的有效治疗以及采取先发制人的策略都需要准确，早期的诊断才能获得更好的结果，因此需要快速且准确的诊断方法。早在 1988 年，van der 等人就建立了葡聚糖沉淀分离白细胞、固定、间接免疫过氧化物酶染色的直接检测外周血白细胞中 CMV pp65 抗原的方法。研究表明，pp65 抗原血症在指导先发治疗，快速敏感地诊断 CMV 疾病以及指导治疗反应方面可与 CMV 定量核酸检

测相媲美。但目前国内尚无 CMV pp65 抗原血症检测的标准试剂盒，而国外试剂盒价格昂贵。本研究旨在建立免疫荧光法检测 CMV pp65 抗原血症检测的方法，为临床预防指导治疗提供参考。

PU-1463

抗中性粒细胞胞浆抗体检测及相关实验室指标在肺间质纤维化患者中的应用探讨

朱黎娜、王居鹏、马明坤、温学红
天津中医药大学第二附属医院

目的 探讨华北地区肺间质纤维化患者抗中性粒细胞胞浆抗体的发生率以及核型和靶抗原的阳性率，并对常见临床检验指标特征进行分析。
方法 收集 2017 年 8 月至 2020 月 12 月在天津中医药大学第二附属医院呼吸科诊断明确为肺纤维化的住院患者且同时经 ANCA 检测的共 347 例患者资料。其中 77 例 ANCA 阳性且明确诊断为 AAV 并表现为肺纤维化的患者，作为 ANCA 阳性 PF 组，从 ANCA 阴性的 PF 患者中随机选择 78 例作为 ANCA 阴性 PF 组，28 例以非呼吸症状为主的不伴肺纤维化改变的 ANCA 阳性的患者作为 ANCA 阳性非 PF 组、20 例健康体检者作为健康对照组，分析上述患者详细的实验室指标。
结果 ANCA 阳性 PF 组患者更容易表现为 pANCA，对应的靶抗原主要是 MPO。ANCA 阳性 PF 组 CRP、IGM 较 ANCA 阴性 PF 组显著升高，C3 显著降低，差异有统计学意义（P<0.05）；ANCA 阳性 PF 组和 ANCA 阴性 PF 组、ANCA 阳性非 PF 组的 ESR、CRP、d-dimer、PCT、FIB 较健康对照组显著升高，差异有统计学意义（P<0.05）；ANCA 阳性 PF 组的 IgG、IGM 较健康对照组显著升高，C3 显著降低，差异有统计学意义（P<0.05）；ANCA 阳性非 PF 组的 Cr 较 ANCA 阳性 PF 组和健康对照组均显著升高，差异有统计学意义（P<0.05）。16.8%的患者（13 例）在入院后被诊断为中性粒细胞胞浆抗体相关血管炎。
结论 对于肺纤维化患者，诊断时应考虑抗中性粒细胞胞浆抗体相关血管炎的可能，同时应重视患者的 ESR、CRP、d-dimer、PCT、FIB、IgM 和 C3 等检验指标变化。

PU-1464

抗 CCP 抗体及 RF 检测在类风湿性关节炎中的临床价值

屈恩帅
天津医科大学朱宪彝纪念医院
天津市天津医医院

目的 探讨抗环瓜氨酸肽（CCP）抗体和类风湿因子（RF）检测在类风湿性关节炎(RA)中的诊断价值。并探讨两种抗体对判断 RA 活动性和预后价值。
方法 ①研究对象：选择 60 例 RA 患者组成 RA 组。疾病对照组 50 例患者。健康对照组由 50 名体检健康者组成。②检测各组的抗 CCP 抗体及 RF 水平。评价抗 CCP 抗体及 RF 对 RA 的诊断性能。③RA 患者抗 CCP 抗体和 RF 与 X 线分期的相关性，与疾病活动性指标的相关性是通过 Spearman 秩相关来分析的。
结果 ①RA 组抗 CCP 抗体及 RF 的阳性率均明显高于其他两组，差异具有统计学意义（均 P<0.01）。②抗 CCP 抗体的敏感性和特异性分别为 86.67%和 95.00%，RF 的敏感性和特异性分别为 83.33%和 80.00%，两种抗体联合检测的敏感性为 95.00%。③RA 组患者抗 CCP 抗体和 RF 与 X 线分期呈正相关（均 P<0.01）。两种抗体与疾病活动性指标均无相关性（P>0.05）。

结论 ①抗 CCP 抗体在 RA 的诊断中具有较高的诊断价值。②抗 CCP 抗体及 RF 对 RA 均具有预后价值。③抗 CCP 抗体及 RF 两者联合检测可提高 RA 诊断的敏感性。

PU-1465

血清 PCT、CRP 及 IL-6 联合检测诊断细菌性血流感染的临床价值分析

王禺
西安市第一医院

目的 探讨血清降钙素原(PCT)、C 反应蛋白(CRP)及白介素-6(IL-6)联合检测诊断细菌性血流感染(BSI)的临床价值。
方法 选取我院 2015 年 8 月到 2016 年 10 月收治的疑似细菌性 BSI 患者 216 例，入院后均送检血培养，根据培养结果将其分为阳性组(102 例)和阴性组(114 例)。统计细菌性 BSI 阳性率、革兰阳性菌感染率和革兰阴性菌感染率；检测血清 PCT、CRP、IL-6 水平，并比较两组患者的差异，同时绘制 ROC 曲线并计算出各指标及联合检测的灵敏度、特异度、阳性预测值、阴性预测值及约登指数值。
结果 所有疑似 BSI 患者的细菌阳性检出率为 47.22%，革兰阳性菌感染率与革兰阴性菌感染率对比无差异(P＞0.05)；阳性组的血清 PCT、CRP、IL-6 水平均明显高于阴性组(P<0.05)；血清 IL-6 的 AUC 明显大于 PCT 和 CRP(P<0.05)；PCT、CRP 及 IL-6 联合检测的灵敏度、特异度、阳性预测值、阴性预测值及约登指数均明显高于单项检测(P<0.05)。
结论 血清 PCT、CRP 及 IL-6 对于 BSI 均有着一定诊断价值，而各指标联合检测诊断 BSI 的临床价值更高。

PU-1466

血清 IL-6、IL-8、IgM 抗体及 T 细胞亚群水平对新生儿先天性梅毒的诊断价值

李秀娥
西安市第一医院

目的 探讨血清白介素-6(IL-6)、白介素-8(IL-8)、IgM 抗体及 T 细胞亚群对先天性梅毒新生儿的诊断价值。
方法 选择 2015 年 5 月至 2017 年 5 月在我院进行临床治疗的先天性梅毒新生儿 81 例为观察组，另选同期来我院进行健康体检 81 例新生儿为对照组。比较两组患者血清 IL-6、IL-8、T 细胞亚群中 CD3+、CD4+、CD8+、CD4+/CD8+细胞及 IgM 抗体的阳性率。
结果 治疗后，观察组血清 IL-6、IL-8 水平均明显高于对照组(P<0.05)，T 细胞亚群中 CD3+、CD4+、CD4+/CD8+明显低于对照组，而 CD8+ T 细胞比例高于对照组(P<0.05)。19S-IgM-TP ELISA 法检测出 IgM 的阳性率 92.59%，明显高于 TRUST 法(74.07%)及 TP-ELSA 法(70.37%)(P<0.05)。ROC 曲线中，血清 IL-8 特异度为 88.34%明显高于血清 IL-6 特异度 81.48%、IgM 抗体特异度 60.13%、T 细胞亚群特异度 65.34%；IgM 抗体的曲线面积 88.91cm2 明显大于 IL-6 的曲线面积 45.09 cm2、IL-8 的曲线面积 76.19 cm2、T 细胞亚群的曲线面积 77.35 cm2；T 细胞亚群准备性 67.89%明显高于 IL-6 准确性 60.39%、IL-8 准确性 51.09%、IgM 抗体准确性 50.12；IgM 抗体的灵敏度 60.13%高于 IL-6 灵敏度 59.19%、IL-8 灵敏度 42.35%、T 细胞亚群灵敏度 59.37%。具有比较意义(P<0.05)。

结论 血清 IL-6、IL-8 水平、T 细胞亚群中 CD3+、CD4+、CD8+、CD4+/CD8+及 IgM 抗体阳性率是诊断先天性梅毒新生儿的重要指标。

PU-1467

ANA 检测在血细胞减少患者诊疗的应用价值分析

朱敏、姜波
昆明医科大学第一附属医院

目的 探讨抗核抗体（ANA）检测对血细胞减少患者诊疗的应用价值。
方法 采用间接免疫荧光法（IIF）检测血清 ANA，采用流式点阵免疫荧光法检测血清抗可溶性抗原（ENA）抗体，采用日本希森美康 XE-2100 全自动血细胞分析仪检测外周血白细胞（WBC）、红细胞（RBC）、血红蛋白（HGB）、血小板（PLT）等。
结果 血细胞减少患者 ANA 阳性检出率高于血细胞正常组，差异有统计学意义（P<0.05），其中 WBC 减少组共 96 例，ANA 阳性检出 10 例(10.42%)；PLT 减少组共 152 例，ANA 阳性检出 39 例(25.66%)；HGB 减少组共 128 例，ANA 阳性检出 22 例(17.19%)；两系或三系减少统称全血细胞减少组共 124 例，ANA 阳性检出 17 例 (13.71%)。血细胞减少患者 ENA 阳性检出率与血细胞正常组相比，差异无统计学意义（P>0.05）。
结论 自身抗体可导致血液系统损伤，进而引起血细胞减少，ANA 检测对于血细胞减少患者的病因诊断及治疗有一定的应用价值。

PU-1468

血清细胞因子检测在肾移植受者移植物功能延迟恢复中的临床价值初探

黄熙哲[1]、李鸿钏[2]、刘婷婷[3]、罗俐梅[1]、邹远高[1]、徐欢[1]、白杨娟[1]、安云飞[1]、蔡蓓[1]
1. 四川大学华西医院
2. 成都市郫都区中医医院检验科
3. 遂宁市第一人民医院检验科

背景及目的 移植物功能延迟恢复（delayed graft function,DGF）常见于肾移植术后，是移植肾早期急性损伤，可影响移植肾长期存活。免疫炎症反应是导致 DGF 的主要原因。本研究旨在探讨机体炎症因子动态检测对肾移植受者 DGF 的临床评价意义。
方法 本研究回顾性分析我院肾移植受者 97 例，其中发生 DGF 患者 7 例，受者分别进行术前、术后 1-3 天、术后 4-7 天和术后 8-14 天对血清细胞因子的动态分析。应用微粒体化学发光发分析血清细胞因子 IL-1β、可溶性 IL-2R、IL-6、IL-8、IL-10 和 TNF-α 水平，采用 SPSS19.0 统计软件分析数据。
结果 ①发生 DGF 的肾移植受者中女性占比 71.4%显著高于男性占比，女性肾移植患者中发生 DGF 的比例占 17.2%，男性发生 DGF 比例仅为 2.9%（P=0.039）。②动态分析发现，未发生 DGF 受者血清细胞因子可溶性 IL-2R 和 TNF-α 水平在肾移植后逐渐降低（P<0.05），且术前水平>术后 1-3 天水平>术后 4-7 天和术后 8-14 天水平；发生 DGF 受者表现为术后 1-3 天血清可溶性 IL-2R、IL-10、IL-8 和 TNF-α 水平显著增高（P>0.05）；③ 与未发生 DGF 受者相比，发生 DGF 受者表现为术前 IL-6、IL-10 和 IL-8 水平增高（P 均>0.05），可溶性 IL-2R 水平降低（P=0.042）和 TNF-α 水平降低（P>0.05）；术后 1-3 天细胞因子 IL-10、可溶性 IL-2R、IL-6、IL-8 和 TNF-α 水平明显增高，但仅 IL-10 和 IL-8 的增加有统计学差异（P 均<0.05）。

结论 肾移植受者体内细胞因子可能参与 DGF 发生，受者术后一周血清细胞因子的动态检测，尤其是术后 1-3 天血清 IL-10 和 IL-8 检测可作为临床辅助判断 DGF 发生的实验室指标。

PU-1469

血清 IgG4 水平、IgG4/IgG 比值、IgG4/IgG1 比值在鉴别诊断 IgG4 相关性疾病和其它自身免疫性疾病中的价值

任亚萍
中南大学湘雅二医院检验科

目的 探讨血清 IgG4 水平、IgG4/IgG 比值、IgG4/IgG1 比值在 IgG4 相关性疾病和其它自身免疫性疾病鉴别诊断中的应用价值。
方法 收集 2016 年 1 月至 2019 年 12 月 就诊于中南大学湘雅二医院的 36 例 IgG4-RD 患者、146 例自身免疫性疾病患者，40 例体检健康者作为对照组。采用速率散射比浊法检测血清中 IgG 亚型的水平；应用 ROC 曲线，确定最佳临界值及曲线下面积。
结果 与健康对照组相比，IgG4 -RD 组的 IgG4、IgG4/IgG 比值、IgG4/IgG1 比值水平明显增高。与其它自身免疫性疾病组相比，IgG4 -RD 组的 IgG4、IgG4/IgG 比值、IgG4/IgG1 比值水平明显增高。ROC 曲线分析显示血清 IgG4、IgG4/IgG 比值、IgG4/IgG1 比值诊断 IgG4 相关性疾病时，其曲线下面积分别为 0.957，0.976，0.981。与血清 IgG4 的曲线下面积相比，血清 IgG4/IgG 比值和 IgG4/IgG1 比值的曲线下面积更大（P 分别为 0.024 和 0.037)。血清 IgG4/IgG 比值和 IgG4/IgG1 比值的曲线下面积差异无统计学意义（P=0.165）。IgG4 比值诊断 IgG4 相关性疾病的最佳 cut off 值为 2.15g /L,其诊断性能为敏感性为 94.5%，特异性为 94.8%。22 例 IgG4-RD 随访患者中，治疗前患者血清中 IgG4 中位数为 5.72(2.83，9.61) ，治疗 2 个月后血清 IgG4 水平中位数为 3.32(2.15，4.37)，差异有统计学意义（P=0.013）。
结论 IgG4/IgG 比值、IgG4/IgG1 比值鉴别诊断 IgG4 相关性疾病和其它自身免疫性疾病的诊断性能优于 IgG4；IgG4 可以作为对激素治疗后的疗效判断的指标。

PU-1470

粪便钙卫蛋白在炎性肠病的临床应用回顾分析

王梅华[1]、郭智浩[2]、刘锦[1]
1. 福建医科大学附属协和医院
2. 福建医科大学医学技术与工程学院检验系实习生

目的 探讨粪便钙卫蛋白检测在炎症性肠病中的临床应用效果。
方法 收集福建医科大学附属协和医院 2018 年 6 月至 2020 年 12 月，确诊炎性肠病患者的临床检验结果，包括粪便钙卫蛋白、白介素 6、C 反应蛋白以及抗酿酒酵母抗体检验结果。比较粪便钙卫蛋白与血清标志物体之间检测结果的差异性。并跟踪分析粪便钙卫蛋白对炎性肠病患者病程进展的敏感性。
结果 对于 78 例炎性肠病患者的自身免疫性抗体，粪便钙卫蛋白，血清降钙素原，C 反应蛋白结果进行分析，其中 78 例自身免疫性抗体阳性率分别为，ASCA IgA 16.6%、ASCA IgG 20.5%、IGA IGA 1.3%、IGA IgG 34.6%、pANCA 11.5%、pANCA IgA 6.4%、pANCA IgG 0%。其中有 50 例检测粪便钙卫蛋白，36 例阳性，阳性率 69.0%；73 例检测 C 反应蛋白，37 例阳性，阳性率 67.3%；26 例检测血清降钙素原，21 例阳性，阳性率 80.8%，统计学分析粪便钙卫蛋白阳性率显著高于自身免疫性抗体。同时，对 3 例有进行粪便钙卫蛋白，以及 C 反应蛋白复查的炎性肠病患者比较发现粪便钙卫蛋白半定量检测结果与病程变化具有一定相关性。

结论 在本次研究中粪便钙卫蛋白阳性率高于自身免疫性抗体，并且存在粪便钙卫蛋白半定量结果随着病程改变而发生改变现象。

PU-1471

HIV Duo 试剂在艾滋病初筛试验中的价值探讨

任亚萍
中南大学湘雅二医院检验科

目的 评估 HIV Duo 试剂在艾滋病初筛试验中的性能，为更早期检测出 HIV 感染者、减少检测的窗口期提供参考和依据。
方法 通过对 2019 年 10 月-2020 年 9 月就诊于中南大学湘雅二医院进行 HIV 初筛试验的样本进行分析，筛选 HIV 初筛实验阳性的血清标本并使用 HIV Duo 试剂再检测，比较 HIV Duo 与初筛试验的检测结果，同时结合湖南省疾病预防控制中心（CDC）做确证试验结果，综合探讨 HIV Duo 试剂的检测性能。
结果 2019 年 10 月-2020 年 9 月我院共检测 80279 例 HIV 初筛试验样本，218 例呈 HIV 初筛试验阳性，初筛阳性率 0.27%；81 例送检至湖南省 CDC 做确证试验，其中回报阳性 29 例，回报阴性 49 例，回报抗体不确定 3 例，CDC 回报阳性率 35.8%；HIV Duo 试剂检测 81 例有 CDC 回报结果标本，其结果与使用 HIV Combi PT 做初筛试验的 COI 值有高度相关性(r=0.915)，但两者对能否准确反映 CDC 结果有一定差异； HIV Duo 试剂检测灵敏度为 100%，与 CDC 回报结果的符合率为 72.8%。
结论 HIV Duo 试剂有良好的检测性能，利用其检测提供的 HIV p24 抗原、抗 HIV 抗体的综合结果和子结果，能缩短检测窗口期，为优化艾滋病检测流程提供一定依据。

PU-1472

不同类型糖尿病患者 21 羟化酶抗体的分布研究

杨一芬
中南大学湘雅二医院检验科

目的 研究不同类型糖尿病患者胰岛自身抗体和 21 羟化酶抗体（21-OHA）分布情况，为筛查自身免疫性原发性肾上腺皮质功能减退症（Addison 病）提供依据。
方法 收集 2016 年至 2018 年间中南大学湘雅二医院门诊或住院病人，其中 1 型糖尿病（T1DM）患者 179 例，2 型糖尿病（T2DM）患者 198 例，妊娠糖尿病（GDM）患者 154 例以及健康对照 200 例。采用国际标准放射配体法检测 21-OHA 以及谷氨酸脱羧酶抗体（GADA）、蛋白酪氨酸磷酸酶抗体（IA-2A）和锌转运体 8 自身抗体（ZnT8A）等胰岛自身抗体，研究其相互关联以及与临床特征的关系。
结果 ① T1DM 组 GADA、IA-2A、ZnT8A 和 21-OHA 的阳性率分别为 63.7%（114/179）、37.4%（67/179）、33.5%（60/179）和 3.9%（7/179），显著高于健康对照组的 0.6%（1/200）、0、0 和 0（P 值分别为 0.0000、0.0000、0.0000 和 0.005），同时也显著高于 T2DM 组的 6.1%（12/198）、2.0%（4/198）、2.0%（4/198）和 0（P 值分别为 0.0000、0.0000、0.0000 和 0.005），以及高于 GDM 组的 3.2%（5/154）、0.6%（1/154）、0.6%（1/154）和 0（P 值分别为 0.0000、0.0000、0.0000 和 0.013）。② 7 例 21-OHA 阳性的 T1DM 患者中，4 例存在于双胰岛自身抗体阳性组，1 例存在于单胰岛自身抗体阳性组，差异无统计学意义。③ 综合肾上腺皮质功能检查以及其他临床指证，7 例 21-OHA 阳性的 T1DM 患者中，1 例考虑为合并自身免疫性 Addison 病。

结论 T1DM 患者易合并 21-OHA 阳性，对于特别是多抗体阳性的 T1DM 患者，筛查 21-OHA 对于及早识别自身免疫性 Addison 病有着重要的临床意义。

PU-1473

IL-22 在儿童及成人乙肝炎症中的比较研究

董慧、吴万通
天津市东丽医院

目的 探讨乙型病毒性肝病(HB)儿童及成人患者血清 IL-22 水平变化规律，为其诊断及治疗提供依据。
方法 取 55 例乙肝患者静脉血分离血清，其 中包括 13 例大人 CHB，15 例小儿 CHB,13 例大人 LC,14 例小儿 LC.采用 ELISA 方法检测 IL-22 水平，采用 SPSS 软件分析 IL-22 水平。
结果 与健康组(9 例查体健者) 比较，乙肝患者血清 IL-22 水平明显升高，(P＜0．05);大人及儿童随肝损害的程度加重， IL-22 表达水平增高(P＜0．05)。这四组的 IL-22 均与 DNA，ALT,性别无显著相关性。
结论 IL-22 在乙肝的发生、发展中起重要作用，尤其在儿童的乙肝进程中，这可能是儿童本身对乙肝病毒的一种抵抗能力，其水平变化在乙肝临床诊断、病情 分析及预后判断中均具有重要价值。深入研究 IL-22 等细胞因子通路与肝脏损伤机理，可为儿童乙肝免疫干预治疗提供新的靶点，从而减慢乙肝发展进程，减缓炎症及纤维化速度。

PU-1474

Association of Circulating Vascular Endothelial Growth Factor Levels With Autoimmune Diseases: A Systematic Review and Meta-Analysis

Haoting Zhan
Department of Clinical Laboratory, Peking Union Medical College Hospital, Graduate School, Peking Union Medical College, Chinese Academy of Medical Sciences, Beijing 100730, China

Background Autoimmune diseases (ADs) are characterized by immune-mediated tissue damage, in which angiogenesis is a prominent pathogenic mechanism. Vascular endothelial growth factor (VEGF), an angiogenesis modulator, is significantly elevated in several ADs including rheumatoid arthritis (RA), systemic sclerosis (SSc), and systemic lupus erythematosus (SLE). We determined whether circulating VEGF levels were associated with ADs based on pooled evidence.
Methods The analyses included 165 studies from the PubMed, EMBASE, Cochrane Library, and Web of Science databases and fulfilled the study criteria. Comparisons of circulating VEGF levels between patients with ADs and healthy controls were performed by determining pooled standard mean differences (SMDs) with 95% confidence intervals (CIs) in a random-effect model using STATA 16.0. Subgroup, sensitivity, and metaregression analyses were performed to determine heterogeneity and to test robustness.
Results Compared with healthy subjects, circulating VEGF levels were significantly higher in patients with SLE (SMD 0.84, 95% CI 0.25–1.44, P = 0.0056), RA (SMD 1.48, 95% CI 0.82–2.15, P = 0.0000), SSc (SMD 0.56, 95% CI 0.36–0.75, P = 0.0000), Behcet's disease (SMD 1.65, 95% CI 0.88–2.41, P = 0.0000), Kawasaki disease (SMD 2.41, 95% CI 0.10–4.72, P = 0.0406), ankylosing spondylitis (SMD 0.78, 95% CI 0.23–1.33, P = 0.0052), inflammatory bowel disease (SMD 0.57, 95% CI 0.43–0.71, P = 0.0000), psoriasis (SMD 0.98, 95% CI 0.62–1.34, P = 0.0000), and Graves disease (SMD 0.69, 95% CI 0.20–1.19, P = 0.0056). Circulating VEGF levels correlated with disease activity and hematological parameters in ADs.

Conclusion Circulating VEGF levels were associated with ADs and could predict disease manifestations, severity and activity in patients with ADs.

PU-1475

Diagnostic value of D-dimer in COVID-19: a meta-analysis and meta-regression

Haoting Zhan
Department of Clinical Laboratory, Peking Union Medical College Hospital, Graduate School, Peking Union Medical College, Chinese Academy of Medical Sciences, Beijing 100730, China

The prognostic role of hypercoagulability in COVID-19 patients is ambiguous. D-dimer, may be regarded as a global marker of hemostasis activation in COVID-19. Our study was to assess the predictive value of D-dimer for the severity, mortality and incidence of venous thromboembolism (VTE) events in COVID-19 patients. PubMed, EMBASE, Cochrane Library and Web of Science databases were searched. The pooled diagnostic value (95% confidence interval [CI]) of D-dimer was evaluated with a bivariate mixed-effects binary regression modeling framework. Sensitivity analysis and meta regression were used to determine heterogeneity and test robustness. A Spearman rank correlation tested threshold effect caused by different cut offs and units in D-dimer reports. The pooled sensitivity of the prognostic performance of D-dimer for the severity, mortality and VTE in COVID-19 were 77% (95% CI: 73-80%), 75% (95% CI: 65-82%) and 90% (95% CI: 90-90%) respectively, and the specificity were 71% (95% CI: 64-77%), 83% (95% CI: 77-87%) and 60% (95% CI: 60-60%). D-dimer can predict severe and fatal cases of COVID-19 with moderate accuracy. It also shows high sensitivity but relatively low specificity for detecting COVID-19-related VTE events, indicating that it can be used to screen for patients with VTE.

PU-1476

肿瘤相关自身抗体临床应用现状与研究进展

詹皓婷
中国医学科学院北京协和医院

肿瘤相关自身抗体是由肿瘤相关抗原的异常暴露或呈递促进自身免疫反应而产生。该抗体可提前数月或数年于癌症患者体内水平升高，参与肿瘤恶性转化的发生与发展。近年来，肿瘤相关自身抗体的研究和应用为肿瘤的早期预警、危险评估、诊断、预后及治疗效果判断提供了重要的参考依据。本文主要从肿瘤相关自身抗体产生机制、结缔组织病合并肿瘤和恶性肿瘤相关自身抗体的临床应用现状与研究进展展开综述。

PU-1477

特发性肺纤维化生物标志物临床应用进展

詹皓婷
中国医学科学院北京协和医院

特发性肺纤维化（IPF）是临床常见的弥漫性纤维化肺实质疾病，临床表现为组织病理学和/或放射学上的普通型间质性肺炎（UIP）。该病发病机制尚未阐明，且缺乏有效的疾病进展与活动的诊断监测指标，因此在临床管理方面存在一定困难。近年来，蛋白与基因标志物的应用为 IPF 的诊

断、治疗、进展监测及预后评估等提供了重要的参考依据。本文主要对蛋白与基因标志物在 IPF 的临床应用研究展开综述。

PU-1478

系统性红斑狼疮生物标志物临床应用进展

詹皓婷
中国医学科学院北京协和医院

系统性红斑狼疮（SLE）是一种临床常见的累及多系统、多器官的全身结缔组织疾病，临床并发症以狼疮性肾炎、神经精神狼疮、SLE 相关心血管事件为主，确切的发病机制尚未阐明。早期诊断对判断 SLE 严重程度、评估疾病活动度、预测疾病进展、监测治疗效果和改善预后具有重要意义。本文主要对以往在 SLE 患者血清中发现的 SLE 自身抗体及近年发现新型生物标志物的临床应用研究进展展开综述。

PU-1479

69 例特征性神经元抗体阳性患者临床特点及实验室指标分析

彭涣锲、唐浩能
中南大学湘雅二医院

目的 研究特征性神经元抗体阳性人群总体特征，分析神经系统副肿瘤综合征(PNS)发病 的独立相关因素。
方法 回顾性收集 2019 年 1 月至 2021 年 1 月在中南大学湘雅二医院特征性神经元抗体筛查阳性患者 69 例，分析该类人群的总体临床特征；进一步依据 Graus(2004)诊断标准排除 7 例非 PNS 患者后，剩余患者分为 PNS 确证组（31 例），PNS 疑似组（31 例），对比分析两组人群的主要临床特征并分析 PNS 确诊患者发病的独立相关因素。
结果 特征性神经元抗体抗体检测阳性率 8.6%，阳性率最高的特征性抗体是抗-Amphiphysin(44.93%)和抗-CV2(36.32%)；阳性人群大多为中老年人，其中 50.7%表现乏力，26.1%表现精神行为异常；66.7%的患者存在低白蛋白血症，25.0%的患者 D-二聚体升高。PNS 确证组和 PNS 疑似组间除纤维蛋白原和平均红细胞血红蛋白具有显著差异外(P＜0.05)，其余未见显著差异的实验室指标；多变量二元 logistic 回归分析显示纤维蛋白原升高和血钙降低可能与 PNS 发病独立相关(P＜0.05)。
结论 特征性神经元抗体阳性的 PNS 综合征确证患者和疑似患者的实验室指标无特征性的实验室指标特异，血浆纤维蛋白原与血钙水平可能与 PNS 发病相关。

PU-1480

84 例自身免疫性脑炎患者临床特征及实验室指标的回顾性分析

钟健、唐浩能
中南大学湘雅二医院

目的 分析自身免疫性脑炎疑似与确诊患者的临床资料，为临床自身免疫性脑炎早期鉴别诊断寻找联合预测指标。
方法 回顾性收集 2016 年 3 月至 2021 年 3 月在湘雅二医院入院拟诊为自身免疫性脑炎的病例，根据是否满足 Graus 诊断标准划分为确诊组（38 例）和疑似组（46 例），比较两组患者临床特征与

入院首次实验室检查结果，进一步通过多因素二元 Logistic 回归分析自身免疫性脑炎发病的独立影响因素，进一步运用 ROC 曲线评估相关指标对自身免疫性脑炎发病的预测诊断价值。
结果 1、84 名患者就诊时具有相似的临床表现。精神行为异常、言语障碍和口面部或肢体不自主抖动常见于自身免疫性脑炎患者（p 均＜0.05）。2、确诊组患者全血白细胞、中性粒细胞数、中性粒细胞与淋巴细胞比值、总蛋白、肌酸激酶、抗凝血酶 III 活性、D 二聚体和纤维蛋白原降解产物都显著高于疑似组。3、二元 logistic 回归分析显示全血白细胞计数（OR:1.437, 95% CI:1.079-1.914, P=0.013）、发病年龄（OR:0.933, 95% CI: 0.887-0.981, P=0.007）、精神行为异常（OR:5.564, 95% CI: 1.283-24.126, P=0.022）、言语障碍（OR:36.696, 95% CI: 1.889-712.869, P=0.017）时自身免疫性脑炎发病的独立相关因素；4、全血白细胞、发病年龄与精神行为异常多因素联合预测自身免疫性脑炎患病的价值高（AUC=0.860，敏感度为 0.816，特异度为 0.8，约登指数为 0.616）。
结论 自身免疫性脑炎疑似患者和确诊患者入院临床特征缺乏特异性，而实验室指标存在一定差异。综合全血白细胞计数、发病年龄与是否精神行为异常对联合预测自身免疫性脑炎患病具有一定价值。

PU-1481

外周血淋巴细胞亚群、细胞因子与不明原因复发性流产的相关性研究

冯一民
山东大学第二医院

目的 探讨外周血淋巴细胞亚群、细胞因子与不明原因复发性流产(URSA)的相关性.
方法 淋巴细胞亚群和细胞因子检测采用流式细胞术。选取 2020 年 6 月至 2021 年 3 月在山东大学第二医院生殖医学科就诊的 120 例不明原因复发性流产女性患者为 URSA 病例组,选择近半年有健康分娩史的 50 例妇女为正常对照组.分别检测两组人群外周血淋巴细胞亚群的比例和绝对计数、细胞因子(IL-2,IL-4,IL-6 和 IL-10，TNF-α,IFN-γ 和 IL7A)的含量,采用 SPSS 进行统计学分析。
结果（1）URSA 病例组外周血的 CD3+CD4+细胞、CD4+/CD8+、B 细胞以及 NK 细胞比例和绝对值计数结果均高于正常对照组,差异有统计学意义(P＜0.05)；
（2）URSA 病例组外周血中 IL-6、TNF-α、IFN-γ 和 IL-7A 均高于正常对照组,差异有统计学意义(P＜0.05)
结论 URSA 患者外周血的淋巴细胞亚群比例和数量的异常以及细胞因子的失衡可能是导致不明原因流产的重要因素,其发病机制可能与患者体内免疫功能发生了紊乱，导致淋巴细胞和细胞因子的异常增高有关.

PU-1482

IgA 肾炎免疫应答相关生物标志物的研究进展综述

张黎蕾
南京大学医学院附属鼓楼医院

IgA 肾炎（IgA glomerulonephritis）是全球最常见的原发性肾小球肾炎。 它是慢性肾脏疾病的主要原因，在确诊 20 年内，约 30％至 40％患者发展为终末期肾脏疾病。迄今为止，IgA 肾炎诊断金标准是肾穿刺活检病理分型，这种创伤性方法并不适用于长期观察。目前临床常用的长期监测病情指标包括：尿总蛋白、尿微量白蛋白、尿素氮、肌酐、肾小球滤过率，但是他们都代表了肾小球系膜因为发生超敏反应使基底膜损伤后漏出物质，并不能代表肾小球当前所遭受的免疫反应程度。从病原学角度讲，检测免疫相关的生物标志物更加有利于了解疾病的本质，从而得到根本的治疗。但这并没有得到临床普遍的重视。全球肾脏病研究者一直在探索 IgA 肾炎的发病机制，但是本病的

发病机理并未阐明。患者的肾小球系膜区有颗粒状 IgA 和 C3 沉积，提示其发病机理。现在的研究围绕着 IgA 的来源、抗原通过粘膜能力、粘膜屏障是否存在缺陷、免疫调节是否存在缺陷等方面展开。在这篇综述中，我们回顾了这十年基于 IgA 肾炎免疫应答生物标志物的最新进展，以期望结合疾病病原学的研究来更好的了解 IgA 肾炎，这些免疫应答生物标志物将在疾病的预后和治疗方面的有着潜在的巨大作用。

PU-1483

肝素结合蛋白在临床中的应用

杨萌
南方医科大学珠江医院

目的 肝素结合蛋白是由中性粒细胞分泌释放的一种颗粒蛋白，由 Shafer 教授在 1984 年发现并分离成功。由于当时测得的相对分子质量为 37000，因此将其命名为 CAP37。后来学者又从嗜苯胺蓝颗粒中分离出具有杀菌活性的嗜苯胺蓝蛋白，命名为 Azurocidin，即天青杀素。再后来发现其具有极强的肝素结合能力，因此命名为肝素结合蛋白。它能够激活巨噬细胞和单核细胞，有着较强的抗菌活性、趋化及调节炎症反应的作用。本篇文章将系统性阐述肝素结合蛋白的结构、生理特点及其在各系统疾病中的应用。
方法 通过 pubmed、万方、知网等数据库，检索肝素结合蛋白的相关研究，以综合阐述肝素结合蛋白对疾病诊断的价值。
结果 HBP 可通过增加血管通透性、激活单核细胞、调节细胞凋亡的三种途径促进炎症反应，常被用于各个系统疾病中脓毒症相关器官功能障碍的早期预测指标。在呼吸系统疾病中，HBP 比 PCT 和 CRP 以及 WBC 有着更好的诊断效能，特别是在鉴别细菌与非细菌感染时，HBP 的诊断效能最佳。在循环系统疾病中，HBP 可作为预测急性主动脉夹层的敏感指标，并对这些患者的预后评价具有重要意义。神经系统中，细菌性脑膜炎的 HBP 水平高于病毒性，从而可更好的发现术后细菌感染，及时使用抗生素，保证手术效果及患者预后。泌尿系统疾病中，尿肝素结合蛋白可用于预测上尿路感染性结石，指导术前抗生素使用，预防或减少经皮肾镜术后脓毒症的发生。其他系统疾病中，HBP 亦被广泛应用，如，肝硬化腹水继发的自发性腹膜炎、重症胰腺炎继发的细菌感染、脓毒症、脓毒性休克等。
结论 肝素结合蛋白作为蛋白酶样丝氨酸蛋白酶家族之一，可影响炎症反应。在细菌感染的疾病中，肝素结合蛋白明显升高，可作为脓毒症早期诊断的最优指标，并以广泛应用于临床。

PU-1484

农村养老院促甲状腺激素的现状调查

刘建森、向敏、吴国林、马小东、林峰、王丽萍、张莹、叶慧倩
雅安市第四人民医院

目的 了解雅安地区农村养老院老人甲状腺功能现状与异常情况，提高相关养老机构对老年人甲状腺健康的关注。
方法 在养老院人群中随机抽样 329 个为研究对象，按照年龄分为两组：≥70 岁为 A 组（n=126），＜70 岁为 B 组（n=203），分析年龄与 TSH 异常升高的阳性率差异以及年龄与 TSH 水平值的相关性；以性别分组，分为男性组（n=305）和女性组（n=24），比较性别与 TSH 异常升高的阳性率差异；按照甲功状况分 C 组（正常甲功，n=253）和 D 组（亚临床甲功，n=72），分别比较两组异常血糖的阳性率。采用罗氏 Cobas e 411 电化学发光仪和贝克曼 AU680 全自动生化分析仪，检测血清样本甲功和血糖。

结果 本次共检测出亚临床甲减 72 例，占比 21.88%（72/329），甲亢 1 例，占比 0.30%（1/329），亚临床甲亢 3 例，占比 0.91（3/329）；A 组 TSH 异常升高的检出率为 30.16（38/126），明显高于 B 组的 16.74%（34/203），（χ2=8.178，P<0.05）统计学有意义；A 组（n=126，4.59±5.84）TSH 总体水平明显个高于 B 组（n=203，3.00±3.66），p＜0.05，统计学有差异；男性组 TSH 异常升高的阳性检出率为 21.96%（67/305），女性组为 20.83%（5/24），（χ2=0.017，p＞0.05）统计学无明显差异；C 组异常血糖的阳性检出率为 14.23%（36/253），D 组为 18.06%（13/73），（χ2=0.641，p＞0.05）统计学无明显差异。
结论 雅安地区农村养老院老人亚临床甲减发病率远高于甲亢与亚甲亢的发病率，且 TSH 异常升高的阳性率和 TSH 水平与年龄成正相关关系。

PU-1485

CA125、CA199、CEA 检测鉴别结核性浆膜腔积液的诊断价值

王绪山
灌云县人民医院

目的 研究血清肿瘤标记物检测鉴别结核性浆膜腔积液的诊断价值及患者胸腔积液病因分布特点的临床研究。
方法 2018 年 9 月-2020 年 9 月经我院确诊并在我院进行治疗的结核性浆膜腔积液患者纳入 400 例；并检测所有患者血清 CA125、CA199、CEA 的水平和腔液积水。
结果 纳入 400 例浆膜腔积液患者良性组 233 例，其中结核主要占 61.8%（144/233）、肺炎占 16.7%（39/233）、脓胸占 4.7%（11/233）、心功能不全占 8.2（19/233）、其他占 8.5%（20/233）；恶性胸液组占 39%为 156 例，乳腺癌占 3.8%（6/156）、其他恶性肿瘤占 12.1%（19/156）、原发性支气管肺癌占 84%（131/156）、不明原因占 2.7%（11/156）；恶性胸液患者年龄为 41-59 岁占该组 42.3%；浆膜腔积液肿瘤标记物显示 CA125、CA199、CEA 的平均水平显示良性组水平低于恶性组，差异具有统计学意义（P<0.01）。
结论 肿瘤与结核是引起浆膜腔积液的主要原因，可有效鉴别两者是否影响后续患者治疗及临床预后；联合检测 CA125、CA199、CEA 三项指标，可提高特异度、敏感度及准确度从而提高临床诊断价值。

PU-1486

新生儿白细胞介素 6（IL-6）显著升高预后探索

周自城
雅安市人民医院

目的 研究新生儿白细胞介素 6（IL-6）显著升高（>200pg/ml）预后结果。
方法 对我院 2020 年 3 月至 2020 年 11 月收治的 40 例 IL-6 显著升高（>200pg/ml）新生儿患者进行回顾性分析。
结果 治愈出院 26 例；病情不稳定家属主动要求出院 7 例；病情未好转转上级医院 1 例；病情恶化放弃治疗 4 例；死亡 2 例。
结论 新生儿白细胞介素 6（IL-6）显著升高（>200pg/ml）与新生儿预后不良关系密切，加强 IL-6 在新生儿感染事件中的监测。

PU-1487

血清总 IgE 检测在儿童慢性荨麻疹中的诊断价值

逯思显[1]、林婧[2]
1. 呼和浩特金域检验所有限公司
2. 广州金域医学检验中心有限公司

目的 研究血清总 IgE 水平与儿童慢性荨麻疹的关系，为儿童慢性荨麻疹的诊断以及预后提供判断依据。
方法 选取某儿童医院 2018-2019 年荨麻疹患儿 150 名以及健康儿童 90 名，分为 1-5 岁、6-9 岁和 10-18 岁三个年龄段，每个年龄段分为实验组和正常对照组，实验组为慢性荨麻疹确诊患儿 50 名，对照组为健康儿童 30 名，收集各组患儿血清，采用免疫比浊检测各组血清总 IgE 水平。
结果 各年龄段实验组的血清总 IgE 水平均显著高于健康对照组（P<0.05）。
结论 各年龄段慢性荨麻疹患儿血清总 IgE 水平较健康对照组均显著增高，提示血清总 IgE 水平与儿童慢性荨麻疹的发病密切相关，且与年龄无关。提示检测慢性荨麻疹患儿血清总 IgE 水平对于慢性荨麻疹的诊断和预后具有一定的临床意义。

PU-1488

血清 IgG、IgM、IgA 水平与儿童肺炎支原体感染的关系

逯思显、王耀东、杨叶
呼和浩特金域检验所有限公司

肺炎支原体(Mycoplasma pneumoniae，MP) 是引起人类非典型肺炎和其他许多呼吸道感染的主要病原体之一，其易感人群为儿童和青少年，且以秋冬季节多见。近年来，MP 感染发病率呈逐年上升趋势，对儿童以及青少年的生长发育以及生活质量存在较大的影响。MP 具体的致病机制尚未完全明确，但普遍认为其可通过直接损伤及免疫介导等方式致病。因儿童感染 MP 后，机体的免疫功能会受到不同程度的损伤，本文为分析免疫球蛋白指标在肺炎支原体肺炎患儿中的水平变化作一综述，旨在为支原体肺炎感染患儿病情的辅助诊断及治疗提供参考依据。

PU-1489

HIV-1 感染者 HAART 治疗后血清 IL-2、IFN-γ、IL-6 的变化及其临床意义分析

刘洋
内蒙古自治区人民医院

目的 探讨 HIV-1（人类免疫缺陷病毒-1）感染者 HAART（高效抗逆转录病毒）治疗后血清 IL-2（白介素-）、IFN-γ（γ-干扰素）、IL-6（白介素-6）的变化及其临床意义。
方法 现选取 2014 年 3 月-2019 年 3 月经我院确认为 HIV-1 病毒感染的患者 145 例，根据有无接受 HAART 治疗，分为两组，75 例接受治疗为 A 组，70 例未接受治疗为 B 组，选取同时期健康体检者 145 例作为对照组，对比 A 组与对照组、B 组与对照组的血清 IL-2、IFN-γ、IL-6 水平，分析 A 组合 B 组患者 CD4+及 CD8+T 淋巴细胞计数情况。
结果 相比治疗前，治疗后 3 个月-1 年，A 组患者 IL-6 水平逐渐降低，IL-2 和 IFN-γ 水平逐渐上升，A 组患者在治疗前及治疗后 3 个月-1 年的 IL-6 水平都高于对照组，而 IL-2、 IFN-γ 水平都低于对照组（P<0.05）；相比治疗前，治疗后 3 个月-1 年，B 组患者 IL-6 水平逐渐上升，IL-2 和 IFN-γ 水平逐渐下降，B 组患者在治疗前及治疗后 3 个月-1 年的 IL-6 水平都高于对照组，而 IL-2、 IFN-γ 水

平都低于对照组（P<0.05）；随治疗时间增加，A 组患者 CD4+T 细胞数量逐渐上升，CD8+T 细胞数量逐渐降低，CD4+/CD8+水平逐渐上升；随治疗时间增加，B 组患者 CD4+T 细胞数量逐渐减少，CD8+T 细胞数量逐渐增加，CD4+/CD8+水平逐渐降低。
结论 在 HIV-1 感染者接受 HAART 治疗的过程中，血清 IL-2、IFN-γ、IL-6 因子发挥着重要作用，有可能参与免疫重建。

PU-1490

HE4 in comparison with CYFRA 21-1, Pro-gastrin-releasing peptide,neuron-specific enolase, carcinoembryonic antigen and CA125 in the differential diagnosis of lung cancer

guangrong wang、qiang Wang、qin Du、guoyuan Zhang、xiaolan Guo、Xiaolan Lu
Affiliate hospital of north sichuan medical college

Background Conventional biomarkers for lung cancer cannot meet the need of clinical diagnosis. We aimed to assess the the clinical value of human epididymis secretory protein 4 (HE4) for the diagnosis of lung cancer and compare it with other biomarkers.
Methods 242 cases of lung cancer (175 adenocarcinoma, 37 squamous carcinoma, and 30 small cell lung cancer) , 99 cases of benign lung disease and 60 cases of health physical examination were selected. The levels of serum HE4, CYFRA 21-1,proGRP, NSE, CEA and CA125 were detected by chemiluminescence method. The performance of each biomarker in discriminating adenocarcinoma, squamous cell carcinoma and small cell lung cancer (SCLC) from benign lung disease and healthy control were assayed by receiver operating characteristic curve analysis.
Results The serum levels of HE4, CYFRA21-1,proGRP and CEA in lung cancer group were significantly higher than those in benign lung disease group (P<0.05), and the levels of HE4, CYFRA21-1，proGRP, NSE, CEA and CA125 in lung cancer group were significantly higher than those in healthy control group (P<0.05).The serum levels of HE4, proGRP and NSE in patients with SCLC were significantly higher than those in patients with non-small cell lung cancer (NSCLC) (P<0.05),and the serum levels of HE4, CYFRA21-1 and CA125 in patients with squamous carcinoma (SC) were significantly higher than those in patients with adenocarcinoma (AC) (P<0.05). With health physical examination group as normal controls, in comparison to CYFRA 21-1,proGRP, NSE, CEA and CA 125, HE4 was one of the biomarkers with the largest AUC(0.839) for lung cancer diagnosis. In terms of histological results, HE4 was the best biomarker both in AC and SC with AUC of 0.790 and 0.968, and proGRP was the best in SCLC with AUC of 0.974. While with benign lung disease group as normal controls,CEA was one of the biomarkers with the largest AUC(0.679) for lung cancer diagnosis. In terms of histological results, CYFRA21-1was the best biomarker both in AC and SC with AUC of 0.697 and 0.862, and serum proGRP was still the best in SCLC with AUC of 0.949.
Conclusions HE4 is more suitable in distinguishing between lung cancer patients and normal population. HE4 combined with NSE can increase the sensitivity and specificity of screening. In the differential diagnosis of lung cancer and benign lung diseases, CEA, CYFRA21-1 and proGRP are more sensitive and specific than HE4.The combined detection of HE4, CYFRA21-1 and proGRP is helpful to the pathological classification of patients with lung cancer.

PU-1491

乙型肝炎病毒定量新技术的性能验证

魏莘林
雅安市人民医院

目的 对湖南圣湘科技有限公司开发的“一步法”乙型肝炎病毒的检测新技术的性能进行验证
方法 实验性能验证，包含重复性、功能灵敏度、线性、准确性，从志愿参加研究的 2000 名乙肝病毒患者采取血液标本，采用 PCR-荧光探针法检测 HBV DNA 100-5×109 IU/ml 范围内的阳性标本进行相关分析。采取线性回归方程、Spearman 检验、Bland-Altman 分析来统计分析
结果 湖南圣湘对 2000 人份标本检测，有 1724 人份标本含有乙型肝炎病毒，其中有 17 人份病毒含量高于 108IU/mL，有 486 人份病毒含量低于 1000IU/mL ，30 人份病毒含量低于 100IU/mL，罗氏对 2000 人份标本检测，有 1727 人份标本含有乙型肝炎病毒，其中有 16 人份病毒含量高于 108IU/mL，489 人份病毒含量低于 1000IU/mL，33 人份病毒含量低于 100IU/mL。（低于 100IU/mL 已不在试剂盒规定的线性范围，可证实试剂盒所给定的线性范围）
结论 结果在误差范围内，湖南圣湘科技有限公司的“一步法”新技术结果准确，操作简单。

PU-1492

Elevated exhaustion levels and reduced functional diversity of T cells in peripheral blood may predict severe progression in COVID-19 patients

Mi Zhang 、cuixian Yang、xingqi dong
Yunnan Infectious Diseases Hospital

To provide direct evidence on leukocyte homeostasis, we studied the immunological characteristics of peripheral blood leukocytes from 16 patients admitted to the Yunnan Provincial Hospital of Infectious Diseases, Kunming, China. Among them, 10 were mild cases, 6 were severe cases; 7 were ≥50 years old, 11were younger; and 6 had baseline diabetes, hypertension, or coronary atherosclerosis. COVID-19 patients, especially those with severe infection, showed increased levels of regulatory molecules and decreased levels of multiple cytokines in peripheral blood T cells. a Heat maps comparing peripheral blood leukocyte subset concentrations in healthy (n = 6), mild (n = 10), and severe (n = 6) patients. Rainbow-colored squares represent mean values of each group. Red-black-green squares represent log 10 P values, and white asterisk indicates P ≤ 0.05 by post hoc ANOVA test. Comparisons of IL-6, TNF-α, and sCD14 plasma concentrations in healthy, mild, and severe groups. n.s., P > 0.05, *, P ≤ 0.05, by Kruskal–Wallis test. Comparisons of expression levels of activation-, regulation-, and function-related molecules in CD4+ and CD8+ T cells among groups. Rainbow-colored squares represent mean positive cell rate for each group. Comparisons of cell expression modules of exhaustion-related (CTLA-4, PD-1, and TIGIT) and function-related (IFN-γ, TNFα, and IL-2) molecules in CD4+ or CD8+ T cells among groups. “Single” indicates that cell only expresses one of the three molecules, “Multi” indicates that cell expresses at least two of the three molecules, “Non” indicates that cell expresses none of the three molecules. Red-yellow-blue squares indicate average cell expression rates of different modules of three groups, respectively. Correlation network analysis of markers with significant differences among groups. Nodes are colored based on cell type for three groups. Node size indicates relative strength value according to centrality analysis. Thicker lines indicate more correlated genes. Green lines represent significantly positive Spearman’s correlation coefficients ≥0.40; red lines represent significantly negative Spearman’s correlation coefficients ≤-0.40. Hierarchical clustering of participants based on all immunological risk indicators

PU-1493

回顾性分析孕中期唐氏筛查的影响因素

卫仙洪
雅安市人民医院

目的 分析不同因素，包括年龄、体重和标本来源对孕中期唐氏筛查结果的影响，并探讨唐氏筛查在产前诊断中的应用 价值，提高产前筛查的准确率。
方法 对 2018 年 4 月至 2020 年 12 月在我院进行唐氏综合征四联筛查的 7799 例妊娠 15～20+6 周的孕妇采取知情同意原则，进行血清甲胎蛋白（AFP）、总 β－人绒毛膜促性腺激素（Tβ-HCG）游离雌三醇（UE3）和抑制素 A(InhA)水平检测，结合孕妇年龄 、体重 、孕周（孕周计算参照胎儿 BPD）、孕产史、吸烟史、糖尿病史等指标 ，利用配套软件计算胎儿患唐氏综合征、18 三体综合征和开放性神经管缺陷的风险。根据孕妇年龄、体重和标本来源统计分析高危例数和阳性率。
结果 7799 例孕妇中唐氏综合征（DS）高危 182 例（2.33%）；18-三体综合 征（ET）高危 7 例（0.09％）；神经管缺陷（ONTD 高危 70 例（0.90%）。年龄、体重与唐氏综合症筛查阳性率呈正相关，标本来源与唐氏综合症筛查阳性率无关。
结论 年龄和体重对唐氏筛查结果影响较大，应确保相关指标书写规范和准确，提高产前筛查的准确率。

PU-1494

不同离心力对乙肝表面抗原感染标志物定量检测结果的影响

孟静
山东大学第二医院

目的 探讨不同离心力处理后的标本对化学发光微粒子免疫检测检测乙肝表面抗原感染标志物检测结果的影响，以降低乙肝表面抗原假阳性率。
方法 回顾性分析。选取 60 例乙肝表面抗原浓度＞0.05 IU/m 且<1.00 IU/mL 的标本，运用化学发光微粒子免疫分析法在雅培 ARCHITECT i2000 检测平台上定量检测乙肝表面抗原感染标志物。常规离心力为 4000rpm 离心 5 分钟，高速离心力为 10000g 离心 10 分钟。常规离心后乙肝表面抗原阳性的标本进一步进行高速离心，上机检测，比较两种离心力乙肝表面抗原定量结果的变化。
结果 对 60 例乙肝表面抗原浓度＞0.05 IU/m 且<1.00 IU/mL 的标本高速离心后检测， 46 例检测结果<0.05 IU/mL（cutoff 值 0.05 IU/mL），比例为 76.7%；14 例标本前后检测结果保持一致，比例为 23.3%。
结论 化学发光微粒子免疫检测乙肝表面抗原阳性的标本前处理需满足离心条件 10000g 离心 10 分钟，以降低乙肝表面抗原假阳性率。

PU-1495

2020 年医院就诊者 HBsAg 携带率调查分析

李佳
雅安市人民医院

目的 总结和分析医院就诊人群乙型肝炎表面抗原携带情况,为乙型肝炎的预防提供科学的指导。
方法 调取 2020 年在雅安市人民医院就诊人群进行血清乙型肝炎表面抗原（HBsAg）检测，进行不同性别、年龄、类别、科室间率的比较分析。

结果 29542 例携带有 2651 例 HBsAg 携带者，携带率为 8.97%。男性携带率高于女性；高年龄组携带率高于低年龄组；门诊组高于体检组和住院组；在科室分布中，最高为感染科占 60.26%，次为肿瘤科科占 13.95%。
结论 对患者或健康体检者进行感染性标志物检测很有必要的，加强公众乙肝防治知识的普及和宣传，增强公众自我保护识，阻止传染病的传播

PU-1496

高尔基体蛋白、甲胎蛋白、甲胎蛋白异质体 L3 三项肿瘤指标的联合检测对原发性肝癌（PHC）的诊断意义

高晓玉
雅安市人民医院检验科

目的 通过联合检测血清甲胎蛋白（AFP）、甲胎蛋白异质体（AFP-L3）、高尔基体蛋白（GP73）在原发性肝癌患者(PHC)体内的表达水平，探讨其对原发性肝癌的诊断价值。
方法 选取 120 例肝癌、103 例肝炎肝硬化以及健康对照者 100 名，取其空腹血清，用放射免疫定量法检测 AFP，酶联免疫吸附法（ELISA）检测 GP73、AFP-L3。对三组研究对象的 AFP、AFP-L3、GP73 在体内的表达水平进行分组比较。观察 AFP、AFP-L3、GP73 对原发性肝癌的特异性及敏感性。
结果 PHC 患者组三项指标均高于非癌性肝病组（NHC）和正常对照组 （P<0.01）；三项指标联合检测诊断 PHC 的阳性检出率为 95.8%，明显高于单项指标的阳性检出率。
结论 血清 AFP、AFP-L3、GP73 联合检测可以提高原发性肝癌的敏感性，有助于 PHC 的筛查与早期诊断。

PU-1497

脂肪血对 DxI800 化学发光分析仪检测超敏肌钙蛋白 I 结果的影响

麻国芳
青海省人民医院

目的 探讨脂肪血对化学发光免疫分析法检测超敏肌钙蛋白 I（hs-cTnI）结果的影响。
方法 将已知浓度的 cTnI 血清标本与不同浓度的脂肪血标本按 1：9 比例混合，使 cTnI 最终浓度为 40.0pg/mL，甘油三酯（TG）最终浓度分别为 0、1.02、5.27、10.55、13.18、15.82 mmol/L；使用 DxI800 化学发光免疫分析仪检测混合后标本中 cTnI 的浓度，评价脂肪血对 cTnI 检测结果所造成的干扰。
结果 cTnI 基础浓度为 48.46 pg/mL 时，当 TG 浓度为 10.55mmol/L 时，cTnI 结果的偏差为 8.85%，结果可接受；当 TG 浓度为 13.18mmol/L 时，cTnI 结果的偏差为 16.16%，超出可接受范围，同时也小于说明书所给的 33.87mmol/L 的声明。
结论 用 DxI800 化学发光免疫分析仪检测 hs-cTnI 时，TG 浓度≥13.18mmol/L 时，cTnI 结果的偏差＞10%，所以，为了保证检测结果的可靠性，应尽量避免脂肪血所造成的干扰。

PU-1498

CA153、CA125 和 CA199 联合检测对乳腺癌诊断的价值

欧阳健
中国人民解放军联勤保障部队第九二一医院

目的 比较 CA153、CA125、CA199 单项检测和三项联合检测的敏感性、特异性、准确度和阳性预测值差异，以确定三项联合检测是否对检测筛查乳腺癌有更高的价值。
方法 采用回顾性分析法，收集联勤保障部队第 921 医院 2015-2021 年乳腺癌患者标本 100 例，体检健康者 100 例。样本均用罗氏 6000 全自动生化分析仪进行电化学发光法进行检测。
结果 CA153、CA125、CA199 的敏感性分别是 48%、41%、27%；特异性分别是 100%、97%、98%；准确性分别是 0.74、0.69、0.63；阳性预测值分别是 100%、93%、93%。CA153、CA125、CA199 三项联合检测的敏感性、特异性、准确性和阳性预测值分别是 66%、96%、0.81、100%。
结论 1.单项肿瘤标志物检测中 CA153 相比于 CA125、CA199 对于乳腺癌的诊断更有价值 2.CA153、CA125、CA199 三项联合检测对于乳腺癌诊断的敏感性明显高于 CA153、CA125、CA199 各单项检测的敏感性（P<0.05)。三项联合检测的敏感性价值更高，更有利于乳腺癌的筛查。

PU-1499

lincRNA-p21 在病毒性肝炎和肝硬化患者血清中的表达

王顺
山东大学第二医院

目的 lincRNA-p21 参与许多人类疾病的发生和发展。本研究旨在探讨 lincRNA-p21 在在病毒性肝炎和肝硬化患者血清中的表达。
方法 本研究选择 2015 年 1 月至 2017 年 12 月在山东大学第二医院就诊的原发性肝病患者（慢性 HBV 感染患者 80 例、慢性 HCV 感染患者 80 例、乙型肝炎病毒相关肝硬化患者 80 例、乙型肝炎病毒相关 HCC 患者 42 例作为研究对象。采用健康体检者 50 例作为对照，用 RT-qPCR 测定血清中的 lincRNA-p21 水平。并采集患者的临床病理特征。
结果 慢性 HBV 感染患者、慢性 HCV 感染患者、乙型肝炎肝硬化患者、乙型肝炎病毒相关性肝癌患者血清中的 lincRNA-p21 水平均高于对照组（P＜0.001，P＜0.001，P=0.005，P=0.003）。在肝病患者中，lincRNA-p21 水平与 HBV DNA（P=0.03）、ALT（P=0.03）和 AST（P=0.04）呈负相关，但与性别（P=0.35）、年龄（P=0.25）和 AFP（P=0.66）无相关性。
结论 血清 lincRNA-p21 可作为肝炎病毒感染、乙型肝炎肝硬化、HBV 相关 HCC 患者肝细胞损伤的潜在生物标志物。

PU-1500

两种 CA242 检测系统测定结果的一致性分析

李玲[1]、卢小岚[2]、杜鹃[2]、汪光蓉[2]、王强[2]
1. 雅安市人民医院检验科
2. 川北医学院医学检验系

目的 比较 Bioscience 与 Snibe 两种全自动化学发光检测系统测定 CA242 结果的一致性，为临床选择 CA242 检测方法提供依据。

方法 依据 EP5-A2、EP6-A 标准分别对 Bioscience 检测系统测定 CA242 进行重复性和稀释线性分析验证；同时收集 41 例结直肠癌患者、45 例健康体检者血清；分别采用 Bioscience 和 Snibe 检测系统对血清 CA242 含量水平进行检测，并对结果进行一致性分析。
结果 Bioscience 检测系统测定 CA242 的重复性、稀释线性的性能验证合格；Bioscience 检测系统测定健康对照组、结直肠癌组患者血清 CA242 的结果与 Snibe 检测系统测定结果不存在差异(Z=-1.130，-1.664；p=0.327，0.180)(p>0.05)，且两种检测系统测定结果存在显著的线性关系(F=1625.018.000，p<0.0001)，一元线性回归方程为：y=1.018*x + 1.883，R2= 0.9736。
结论 Bioscience 与 Snibe 两种全自动化学发光检测系统测定 CA242 结果具有较高的一致性。

PU-1501

miR-328-3p, a predictor of stroke, aggravates the cerebral ischemia-reperfusion injury

Shun Wang
Department of Clinical Laboratory, the Second Hospital, Cheeloo College of Medicine, Shandong University

Background In the present study, we aimed to identify microRNAs (miRNAs) that affected the prognosis of stroke and assess their biological effects.
Materials and Methods A high-throughput sequencing (HTS) analysis was performed to screen distinctive miRNAs in serum exosomes of stroke patients, and these miRNAs were subsequently validated using individual quantitative real-time polymerase chain reaction (qRT-PCR) in a cohort consisting of 39 stroke patients and 20 normal controls. Briefly, miR-328-3p agomir or agomir NC was injected into rats before ischemia and reperfusion (I/R) injury. Zea-Longa score, neurological severity score (mNSS), triphenyltetrazolium chloride (TTC) staining, terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) assay, transmission electron microscopy, and hematoxylin and eosin (H&E) staining were used to examine the brain injury. Immunohistochemistry was utilized to determine the expressions of TNF-α and IL-6.
Results The expression of serum exosomal miR-328-3p was significantly reduced in patients with an infarct volume >=10 cm3 (P=0.01). Serum exosomal miR-328-3p was associated with the short-term prognosis (P=0.02), and the level of miR-328-3p was an independent relative factor for short-term prognosis (OR 5.276, P=0.02). The sensitivity of miR-328-3p level higher than 1.24 to predict the severity of the patient's 1-week prognosis was 70%, and the specificity was 83% (AUC=0.74, P=0.02). The mNSS was higher in the miR-328-3p agomir group compared with the agomir NC group (P=0.03). Neutrophil infiltration was more serious in the miR-328-3p agomir group.
Conclusions Our study indicated that miR-328-3p played a critical predictive role in the short-term prognosis of stroke, and up-regulation of miR-328-3p aggravated cerebral I/R injury.

PU-1502

ELISA 法联合免疫印迹法检测抗双链 DNA 抗体应用于 SLE 诊断价值分析

朱文波
南京大学医学院附属鼓楼医院

目的 探讨 ELISA 法联合免疫印迹法检测抗双链 DNA 抗体在诊断 SLE 中的价值。
方法 回顾性分析 2018 年 12 月至 2019 年 3 月在本院就诊的患者送检的 7930 例标本，分别采用间接免疫荧光法检测抗核抗体（ANA）、线性免疫印迹法检测抗核抗体谱，以及酶联免疫吸附法检测

抗 ds-DNA 抗体，统计免疫印迹法与 ELISA 法任意一种检测出抗 ds-DNA 抗体阳性的标本信息，分析抗体阳性的病种分布，同时评估抗 ds-DNA 抗体不同检测方法学应用于 SLE 的诊断效能。
结果 检测抗 dsDNA 抗体-IgG 的 7930 份标本中，抗 dsDNA 抗体-IgG 检测结果阳性标本共 179 例。其中，ELISA 法检测阳性标本为 138 例，阳性率为 1.79%；免疫印迹法检测阳性标本 102 例，阳性率为 1.32%。两种方法均为阳性的标本 61 例，占阳性标本的 34.1%；仅 ELISA 法检测结果阳性的标本有 77 例，占阳性标本的 43.0%；仅免疫印迹法检测结果阳性的标本有 41 例，占阳性标本的 29.9%。阳性标本的诊断疾病中分别有系统性红斑狼疮 37.43%（67/179），干燥综合症 17.32%（32/179）、关节疼痛 15.08%（27/179）、混合结缔组织病 4.47%（8/179）、以及其他自身免疫性疾病 25.70%（45/179）。在诊断为 SLE 的 87 例标本中，其中两种方法都是阳性的有 31 例，只有 ELISA 阳性的有 31 例，免疫印迹法阳性的有 5 例，两种方法都阴性的有 20 例。ELISA 法的灵敏度和特异度分别为 71.26%和 99.03%，免疫印迹法的灵敏度和特异度分别为 41.38%和 99.14%。两种方法做卡方检验，P<0.05,具有统计学意义。两种方进行同时检测用于诊断 SLE 的灵敏度为 77.01%，特异度为 98.70%。
结论 ELISA 法检测抗 ds-DNA 抗体的方法优于免疫印迹法，两种方法同时检测时有助于提高系统性红斑狼疮的诊断效能。

PU-1503

联合检测 C1q、IL6、Cys C 在狼疮性肾炎中的诊断意义

李丽
中国人民解放军北部战区总医院

目的 狼疮性肾炎（Lupus nephritis，LN）诊断的金标准肾活检因其创性难以重复进行，现联合检测补体组分 1q（C1q）、白介素-6（IL6）、和胱抑素 C（Cys C），评估其在 LN 不同肾脏损害程度中的诊断意义。
方法 回顾性分析系统性红斑狼疮的患者 410 例，其中病变未累及肾脏者 231 例（SLE 组），狼疮性肾炎活动期患者 100 例（LNA 组），狼疮性肾炎非活动期患者 79 例（LNI 组），再选取 230 例健康体检者（HC 组）。同时测定 C1q、Cys C、和 IL6 以及 Urea、Creat 水平，并计算 eGFRCysC 和 c-aGFR，分析联合检测的 3 种指标与不同程度肾损害的狼疮性肾炎关系。
结果 HC 组、SLE 组、LNA 组和 LNA 组间，指标 C1q、Cys C、和 IL6 的差异均有统计学意义（P<0.05）。且 C1q、Cys C、和 IL6 值与 LN 的活动指数呈正相关（r=0.484，P<0.05; r=0.426，P<0.05; r=0.385，P<0.05）。Logistic 回归分析结果显示 C1q、Cys C、和 IL6 为 LN 发病的危险因素。受试者工作特征（ROC）曲线分析结果显示，各项观察指标单独对 LN 的诊断性能曲线下面积（area under curve，AUC）以 Cys C（0.870）为最大，其后依次为 C1q（0.764）、IL6（0.550），C1q+CysC+IL6 联合检测诊断性能（AUC=0.922），其敏感度为 87.2%，特异度为 91.2%。C1q+Cys C 联合检测也可达到相近于最优的诊断性能。
结论 Cys C 对 LN 有较好的诊断效能。联合检测 C1q、Cys C、和 IL6 可作为评估 LN 疾病活动性和肾功能损伤程度的标志物。

PU-1504

CA125 及 NT-pro-BNP 在中老年心衰患者中的临床诊断价值

李淑璇
中国人民解放军联勤保障部队第九二一医院

目的 分析 CA125 及 NT-pro-BNP 在中老年心衰患者中的临床诊断价值。

方法 收集中国人民解放军联勤保障部队第 921 医院 2016 年 1 月至 2021 年 1 月确诊的慢性心力衰竭患者 104 例，将其中的 71 例按照美国纽约心脏病（NYHA）心功能分级分为 I 级 20 例，II 级 5 例，III 级 25 例，IV 级 21 例、并且选取 97 例慢性心力衰竭患者，查询其急性发作期和好转期数据。收集急性心力衰竭患者 104 例。比较不同组之间血清 NT-pro-BNP 和 CA125 含量。
结果 急性心衰患者急性发作期血清 NT-pro-BNP 含量高于慢性心衰患者，慢性心衰患者急性心衰发作期血清 NT-pro-BNP 含量高于好转期，慢性心衰患者的 NT-pro-BNP 水平与心功能分级有关联，以上结果均具有统计学意义（P<0.05）。
结论 血清 NT-pro-BNP 含量可以体现急性心衰和慢性心衰的差异；也可以利用其在患者急性心衰发作期和好转期两个不同时期进行鉴别；NT-pro-BNP 也可以辅助诊断患者心功能水平。血清 CA125 在急性心衰患者和慢性心衰患者中，以及患者急性心衰发作期和好转期中无明显差异；CA125 和心功能分级无明显相关性。

PU-1505

肝纤四项与生化指标检测在肝硬化诊治中的临床意义

廖家铃
中国人民解放军联勤保障部队第九二一医院

目的 探讨肝纤四项与生化指标联合检测在肝硬化诊断中的运用，为肝硬化诊治提供相关的依据。
方法 选择 2015 年 6 月至 2020 年 12 月在中国人民解放军联勤保障部队第 921 医院的 100 例肝硬化患者作为肝硬化组，分为代偿期肝硬化组和失代偿期肝硬化组两组，每组各 50 例；体检健康者 50 例作为对照组。比较肝硬化组和对照组检测结果及肝硬化组中不同分组间的指标检测结果。
结果 肝硬化组肝纤四项、TBIL、TBA、ALT 和 AST 水平均显著高于对照组，TP、ALB 水平均显著低于对照组；肝硬化失代偿期患者肝纤四项、TBIL、TBA、ALT 和 AST 水平均显著高于肝硬化代偿期患者，TP、ALB 水平均显著低于肝硬化失代偿期患者；联合检测的灵敏度、特异度和曲线下面积均明显高于各单项指标检测。
结论 肝纤四项与生化指标检测对肝硬化的诊断有一定的辅助价值；肝纤四项与生化指标检测可有利于判断肝细胞的损伤程度；肝纤四项和生化指标联合检测可提高肝硬化的诊断效能。

PU-1506

胸苷激酶 1 - 细胞增殖标志物

巫仕霞、黄献中、陈志坚
广州金域医学检验中心有限公司

探讨胸苷激酶 1 作为一种新型细胞增殖标志物，是目前首个血清学细胞增殖标志物，可以监测细胞异常增殖的速度。细胞的异常增殖贯穿于慢性增殖性疾病病情进展、肿瘤发生发展的全过程，这样一种新型癌前病变风险指标在临床上的运用。通过检测血清中的胸苷激酶 1 即可在肿瘤未发生之前就进行全身早早期肿瘤的风险预警，适用于体检和癌前病变评估等；同样也可监测肿瘤患者在进行治疗过程中的细胞增值情况，为临床医生提供患者肿瘤细胞的动态变化和肿瘤细胞的增长速率，来可以预估患者的预后生存率、预测复发风险率、评估癌变进程的风险度等。

PU-1507

SAA 联合 CRP 对小儿感染性疾病的早期鉴别诊断价值

彭剑桥
湖南省人民医院

目的 研究联合 SAA 以及 CRP 的检测在儿童呼吸道感染性疾病的早期诊断中的临床应用价值。
方法 收集湖南省人民医院 2020 年 8 月-2020 年 12 月期间收治的 120 例符合早期呼吸道感染诊断的患病儿童，其中包含病毒感染的患病儿童 80 例，细菌感染的患病儿童 40 例，同时收集同一时期在本院区进行体检的 40 名健康儿童设为对照组，对所有儿童的外周血 SAA 和 CRP 含量进行联合检测分析。根据 ROC 曲线对 SAA、CRP 诊断小儿呼吸道感染为病毒感染或者细菌感染的能力。
结果 SAA 和 CRP 在感染早期都会发生相应的变化，细菌感染早期的外周血 SAA 和 CRP 的含量都会上升，而且其外周血 SAA 和 CRP 的升高的幅度都会大于病毒感染升高的幅度；而病毒感染的前期外周血 SAA 含量会出现上升，但是 CRP 水平不会有太大的变化。通过同时检测 SAA 和 CRP，根据两种感染的这两种指标的特点不同，能够提高细菌感染和病毒感染的鉴别能力。
结论 对于小儿呼吸道感染的早期鉴别诊断，SAA 联合 CRP 的检测具有非常显著的临床意义，可以在早期帮助临床鉴别诊断为病毒感染还是细菌感染。

PU-1508

血清 RF、抗 CCP 抗体及免疫球蛋白联合检测对 RA 的诊断价值分析

谭苑生
中国人民解放军联勤保障部队第九二一医院

目的 探讨分析检测血清类风湿因子（RF）、抗环瓜氨酸肽抗体（抗 CCP 抗体）和免疫球蛋白的含量对类风湿性关节炎（RA）的诊断价值。
方法 选取 2017 年 1 月至 2021 年 1 月在本院确诊的 32 例 RA 患者作为病例组，同期 42 例非 RA 的自身免疫性疾病患者资料为病例对照组，31 例体检健康者资料作为健康对照组，统计分析三种诊断指标及联合检测对 RA 的诊断价值。
结果 RA 组患者血清中 RF、抗 CCP 抗体和 IgM 水平明显高于非 RA 组与健康对照组，组间差异具有统计学意义（P<0.05）；而 IgG 与 IgA 水平的组间差异无统计学。RA 组患者的 RF、抗 CCP 抗体和免疫球蛋白阳性率均显著高于其他两组，差异具有统计学意义（P<0.05）。灵敏度为 RF>抗 CCP 抗体>免疫球蛋白（84.3%>75.0%>40.6%）；特异性为免疫球蛋白>RF=抗 CCP 抗体（90.4%>87.7%=87.7%）；RF+抗 CCP 抗体联合检测的灵敏度为 96.9%，特异度为 79.4%，三项并联检测的灵敏度高达 100.0%，尤登指数最高的是 RF+抗 CCP 抗体联合检测，为 0.76。
结论 RF 与抗 CCP 抗体单独检测也具有较好的灵敏度和特异度，免疫球蛋白则具有高特异度；联合检测有更高的灵敏度和阴性预测值，可辅助临床诊断 RA。

PU-1509

口腔扁平苔藓患者外周血 T 淋巴细胞亚群、免疫球蛋白及补体的水平变化分析

李海波[2]、师志云[1]
1. 宁夏医科大学总医院
2. 宁夏医科大学

目的 研究口腔扁平苔藓（OLP）患者外周血 T 淋巴细胞亚群、免疫球蛋白及补体的变化情况，探讨免疫因素与口腔扁平苔藓的关系及其临床意义。
方法 收集 2019 年 10 月至 2020 年 9 月宁夏某口腔医院就诊的口腔扁平苔藓患者 100 例为实验组，同期体检的健康人群 100 例为对照组。采用流式细胞术检测细胞免疫（淋巴细胞亚群 CD3+、CD3+CD4+T 细胞、CD3+CD8+T 细胞、CD3-CD16+56+NK 细胞、CD3-CD19+B 细胞、CD4+/CD8+）水平，采用免疫散射比浊法检测体液免疫（免疫球蛋白 IgG、IgA、IgM 及补体 C3、C4）水平。应用 SPSS20.0 统计软件对数据进行处理和统计学分析，P<0.05 有统计学意义。
结果 OLP 组与对照组 CD3+T 细胞、CD3+CD4+T 细胞、CD3+CD8+T 细胞、CD3-CD16+56+NK 细胞、CD3-CD19+B 细胞与 CD4+/ CD8+水平虽有差异，但均无统计学差异（p>0.05）；OLP 组免疫球蛋白 IgM 水平相比于对照组有所降低，且差异有统计学意义（p<0.05）。
结论 口腔扁平苔藓患者的免疫功能存在某些方面的失衡。

PU-1510

白癜风的免疫机制

秦玲
西安医学院第一附属医院

白癜风是一种常见的后天性色素脱失性皮肤黏膜疾病。白癜风发病的发病病因是多种多样的，目前来说白癜风的病因及发病机制尚未完全明确, 可能与遗传、氧化应激、自身免疫异常等有关。细胞及体液免疫参与白癜风的发病及病情进展, T 淋巴细胞、单核-巨噬细胞、细胞因子等均在白癜风的发病中有一定作用。本文就以上因素综述了近些年白癜风免疫学机制的研究进展。

PU-1511

鼻咽癌患者血清 Rta-IgG、VCA-IgA、EA-IgA 抗体水平放疗前后变化分析

张扬南、彭玉凤、代国知
郴州市第一人民医院

目的 研究鼻咽癌患者血清 EB 病毒 Rta-IgG、VCA-IgA、EA-IgA 抗体水平放疗前后的变化情况。
材料和方法 本次研究选取在郴州市第一人民医院经病理首次确诊鼻咽癌患者 58 例作为鼻咽癌组，选取同期门诊鼻咽部炎症患者 100 例和健康体检者 100 例分别作为炎症、健康对照组。所有鼻咽癌患者均行根治性放疗，并分别于放疗前、放疗 3 个月、放疗 6 个月检测血清 EB 病毒 Rta-IgG、VCA-IgA、EA-IgA 抗体及全血 EB 病毒核酸载量；对照组检测血清 EB 病毒 Rta-IgG、VCA-IgA、EA-IgA 抗体。
结果 1．鼻咽癌患者放疗前血清 Rta-IgG、VCA-IgA、EA-IgA 抗体阳性率分别为 74.1%(43/58)、62.1%(36/58)、72.4%(42/58)，均高于炎症对照组（阳性率：10.0%、12.0%、18.0%)，健康对照

组（阳性率：2.0%、8.0%、5.0%)（P<0.05）。2．鼻咽癌患者血清 Rta-IgG 抗体的阳性率随放疗时间持续下降，但无显著差异（P>0.05）；血清 VCA-IgA、EA-IgA 抗体的阳性率放疗 3 个月无变化，放疗 6 个月阳性率升高，但均无显著差异（P>0.05）。3．鼻咽癌患者全血 EB 病毒核酸的阳性率放疗前、放疗 3 个月、放疗 6 个月分别为 41.4%、19.0%、12.1%，随放疗时间明显下降，具有显著性差异（P<0.05）。4．EB 病毒载量阳性组 Rta-IgG 的抗体水平放疗前和放疗后均高于阴性组，差异有统计学意义（P<0.05）；5．58 例鼻咽癌患者中放疗后 1 年发生 2 例死亡，1 年存活率为 96.6%（56/58），2 例发生远处转移，1 例发生复发。
结论 1．鼻咽癌患者血清 Rta-IgG、VCA-IgA、EA-IgA 抗体显著升高，可作为鼻咽癌早期筛查、辅助诊断指标。2．鼻咽癌患者放疗后血清 Rta-IgG 抗体明显下降，有望作为鼻咽癌疗效判断的指标。

PU-1512

M1 样巨噬细胞诱导肝癌细胞高表达免疫抑制分子 PD-L1 的机制研究

李娜
山东大学第二医院

目的 本研究证明肿瘤细胞 PD-L1 的过表达是否受 M1 样或 M2 样巨噬细胞的调控。通过体外细胞实验探究巨噬细胞是通过什么机制上调肿瘤细胞 PD-L1 的表达，将小鼠 T 淋巴细胞与肝癌细胞共培养，证明巨噬细胞引起的肿瘤细胞 PD-L1 的过量表达能否抑制 T 淋巴细胞的功能。
方法 1 人肝癌组织中巨噬细胞活化类型免疫组织化学分析以及免疫组织化学染色显示 PD-L1 表达呈异质性，且与 M1 浸润的数量相关。2 小鼠 RAW264.7 来源的 M1 促进了小鼠肝癌细胞 PD-L1 的表达。3 小鼠骨髓来源的 M1 促进了小鼠肝癌细胞 PD-L1 的表达。4 人 THP-1 来源的 M1 样巨噬细胞促进了人肝癌细胞 PD-L1 的表达。5 小鼠 M1 样巨噬细胞通过 MEK/ERK 信号通路促进了小鼠肝癌细胞 PD-L1 表达。6 小鼠 M1 样巨噬细胞通过分泌细胞因子 TNF-α 促进了小鼠 Hepa1-6 PD-L1 的表达。7 人 M1 样巨噬细胞通过 JAK/STAT 信号通路促进了人肝癌细胞 PD-L1 的表达。8M1 样巨噬细胞上清刺激的小鼠肝癌细胞促进了 CD8+T 淋巴细胞的凋亡。
结果 1 PD-L1 在肝癌组织中呈异质性表达，并且肝癌组织 PD-L1 分子的表达与 M1 浸润的数量有关系。2M1 可以上调肝癌细胞免疫抑制分子的表达。3M1 通过不同的信号通路促进了 PD-L1 分子在人和小鼠的肝癌细胞中的表达。4M1 刺激的肝癌细胞促进了 CD8+T 淋巴细胞的凋亡。
结论 本研究揭示了肿瘤微环境中 M1 通过相应的信号通路促进了 PD-L1 的上调表达，拓展了人们对 PD-L1 表达调控的新认识，为靶向 PD-L1 的肿瘤免疫治疗带来了新的思考，提示人们可以针对 PD-L1 分子表达调控关键通路中的分子为靶点，设计小分子药物来阻断 PD-L1 的过量表达，进而提高肿瘤的治疗效果。

PU-1513

A20 抑制肝癌细胞迁移的机制

李娜
山东大学第二医院

目的 肝癌恶性程度高病死率高而且手术后依然具有较高的转移率，癌细胞的转移是一个多步骤多因素的复杂过程，在这过程中，有一些分子发挥着重要作用，比如 A20 分子，A20 是一种重要的免疫负调控分子，因此，我们推测 A20 是否可以抑制肝癌细胞的运动能力以及通过怎样的机制抑制肝癌细胞的运动能力。
方法 首先，选取肝癌病人的组织切片，运用免疫组化技术检测 A20 在癌和癌旁组织的表达是否有区别。再通过转染质粒使肝癌细胞高表达 A20 或底表达 A20，运用 transwell 小室方法进行细胞迁

移和侵袭实验，观察 A20 是否可以抑制肝癌细胞的运动能力。然后再采用 PCR 和 Western-blot 方法检测 A20 对肝癌细胞 EMT 相关分子的影响。再进一步运用 Western-blot 和小干扰的方法检测 A20 通过怎样的机制影响 EMT 相关分子的变化。
结果 免疫组化结果显示癌旁组织中 A20 的表达明显高于癌组织。体外实验结果显示，在 TNF-α 刺激下，当 A20 表达高时，能抑制肝癌细胞的迁移和侵袭能力。当干扰 A20 表达后，肝癌细胞的迁移和侵袭能力增强，未刺激组无论 A20 表达高低与否，对于肝癌细胞的运动能力没有影响。A20 能抑制 TNF-α 诱导的肝癌细胞 EMT 进程，即在蛋白和 RNA 水平均能上调 E-cad,下调 N-cad，随后阻断 NF-KB 信号通路，发现 A20 抑制 EMT 相关分子的现象消失。
结论 A20 与肝癌细胞的转移具有相关性。A20 能抑制 TNF- -α 诱导的肝癌细胞的侵袭和迁移。A20 主要通过 NF-κB 信号通路影响肝癌细胞的侵袭和迁移。

PU-1514

基于免疫荧光层析的产气荚膜梭菌快速检测

段春梅、蒋栋能
陆军军医大学第二附属医院（新桥医院）

目的 产气荚膜梭菌感染在地震等自然灾害时经常发生，对其进行现场快速检测对挽救患者生命十分重要。本研究拟利用表面等离子共振技术和荧光定量免疫层析技术，设计快速检测产气荚膜梭菌的方法，研究其反应特性，以期能用于产气荚膜梭菌的快速检测。
方法 采用柠檬酸三钠还原法制备纳米银溶液，用产气荚膜梭菌抗体标记荧光微球，制备出产气荚膜梭菌荧光免疫检测卡，并对其灵敏度及线性范围、重复性、抗干扰能力作出评价。
结果 该检测方法对产气荚膜梭菌的最低检测限为 1x10^2CFU/ml，灵敏度比较高；线性范围为 10^2~10^7CFU/ml，可以基本满足临床对产气荚膜梭菌检测的要求。本检测卡同板批内重复性较好，CV 值为 1.80%。检测还发现，轻中度溶血、脂血、黄疸对本检测影响不大。
结论 该实验设计出了针对产气荚膜梭菌的快速免疫检测卡，该检测卡灵敏度高，线性范围较宽，能够用于产气荚膜梭菌的快速检测。另还需要进一步改进制作工艺，以减少检测卡间的误差和提高检测卡的抗干扰能力。

PU-1515

过敏原检测及临床类型分析

张芷嘉、蒋栋能
陆军军医大学第二附属医院（新桥医院）

目的 过敏原的检测是临床上常用于诊断过敏性疾病的方法之一, 对找出患者过敏原因, 预防和治疗过敏反应具有十分重要的意义。本实验拟统计分析各类过敏原的分布规律，为临床过敏反应防治提供依据。
方法 收集陆军军医大学第二附属医院皮肤科 2018 年 1 月到 2021 年 1 月间所检测的临床病例, 其中正常对照组 100 例，过敏反应组 300 例, 组间用卡方检验进行差异性分析。
结果 在过敏反应组中，由食物性引发过敏反应的主要因素是虾、蟹有 85 例（28.3%）; 花生过敏 71 例（23.7%）,由呼吸道吸入导致过敏反应的病例包括：屋尘过敏为 91 例（30.73）%;尘螨组合(屋尘螨/粉尘螨)有 77 例（25.7%）, 以上过敏病例经统计学卡方检验,和对照组比较有显著性差异(p <0. 01)。
结论 食入性过敏反应主要是虾、蟹、花生所引起的 I 型过敏反应，与本地区的饮食生活习惯和遗传因素有关。吸入性过敏反应中,常见性过敏原尘螨组合(屋尘螨/ 粉尘螨),这与环境污染、空气质量、

人们的生活卫生习惯有关。通过对变过敏原的类型分析,对患者的诊断、治疗和规避过敏反应有重要的临床指导意义。

PU-1516

一种唾液幽门螺杆菌磁性免疫层析试纸条的研制

韩兴
上海交通大学医学院附属仁济医院(东院)

背景 幽门螺杆菌是世界范围内感染率较高的细菌类型，在中国达 50%以上。研究显示，幽门螺杆菌的感染与胃炎、胃溃疡等疾病有直接关联。目前采用的检测方法都有共同的局限：需要专业仪器、专业技术人员和操作程序复杂。
目的 建立基于纳米磁性免疫层析技术的唾液幽门螺杆菌抗原试纸条检测体系，以达到高效、无创、快速、易操作地筛查幽门螺杆菌感染。
方法 1. 制备幽门螺杆菌抗原（HPS）单克隆抗体，纯化后使用超顺磁性纳米微球颗粒偶联。
2. 针对可能影响试纸条检测表现的因素，对试纸条各组分进行选择和优化。
3. 通过磁信号检测仪记录层析反应过程中信号强度的变化，以确定最佳的反应时间。
4. 用创建的唾液 HPS 试纸条检测体系和唾液 HPS 胶体金试纸条、临床常用的 ^{13}C-UBT 法进行比对，采集 185 例相关症状患者唾液标本，以验证其性能和临床检测的可行性。
结果 1. 构建磁性免疫层析试纸条使用的最佳磁性纳米颗粒粒径大小为 50nm。检测线和质控线磁力强度与抗原浓度呈正相关，最佳反应时间为 15 分钟。
2. 纳米磁性免疫层析法 HPS 试纸条最低的检测限为 1：1000，胶体金试纸条对幽门螺杆菌抗原最低的检测限为 1：100。
3. 创建的试纸条检测体系灵敏度为 93.33%，特异度为 46.25%，阳性预测值为 69.50%，阴性预测值为 84.09%。ROC 分析幽门螺杆菌抗原的 ROC 曲线下面积 AUC=0.634±0.027。
结论 本研究以超顺磁性纳米微球为标记物，代替传统纳米金胶为标记物的免疫层析技术，研制了 HPS 检测试纸条。检测结果明显优于市场在售的 HPS 胶体金试纸条，其灵敏度符合预期，但对于呼气试验的诊断符合率较差，假阳性率较高。其可能原因为唾液中酶类与口腔正常菌群对反应过程的干扰。下一步将对样品垫处理液中添加表面活性剂，对结合垫缓冲液成分进行调整，以期降低假阳性率，提高诊断价值。

PU-1517

不同自动化免疫分析系统对肾移植受者他克莫司和环孢霉素 A 药物浓度检测结果的比对分析

白杨娟、戴鑫华、安云飞、徐欢、万正利、邹远高
四川大学华西医院

目的 评价罗氏®电化学发光免疫分析系统（ECLIA）和西门子®均相酶免疫放大分析系统（EMIT）对肾移植受者 TAC 和 CsA 全血浓度检测结果的一致性。
方法 收集四川大学华西医院就诊的肾移植受者外周血样本（TAC134 份；CsA138 份），同步使用罗氏® Cobase801 和西门子®Viva-E 自动化分析仪及配套试剂盒、严格按照说明书进行外周血 TAC 和 CsA 全血浓度检测。对两个检测系统的检测结果进行相关性和 Bland-Altman 分析。
结果 Cobase801 和 Viva-E 检测系统 TAC 和 CsA 全血浓度结果范围分别为:2.81-10.9&2.9-9.7ng/mL 和 36.9-969&40.1-782.8ng/mL，不同检测系统 TAC 和 CsA 浓度检测结果具有较好相关性(P<0.05)，相关系数分别为 0.92 和 0.93。两个平台上的 TAC 和 CsA 检测结果存在差异:大部分样本（TAC 82.09%；CsA 74.64%）在 Cobas e801 的检测结果高于 Viva-E 的检测结果，TAC 和

CsA 浓度检测结果的平均偏差分别为 14.07%(-39.24%-46.89%)和 13.64%（-40.98-60.76%)，两个检测系统间检测结果差异的大小与样本绝对浓度无相关关系(P>0.05)，两个检测系统 95%一致性界限分别为：TAC 浓度 -16.00%-44.13%；CsA 浓度-21.95%-49.24%。使用不同剂型他克莫司的肾移植受者样本在 Cobas e801 和 Viva-E 的 TAC 浓度检测结果的平均偏差分别为 18.38%（普乐可复®）和 15.73%（新普乐可复®）(P>0.05)。

结论 Cobas e 801 和 Viva-E 自动化分析系统对他克莫司和环孢霉素 A 全血浓度检测结果存在差异，在相关报告解读及实验室拟进行检测平台转换时应做好临床沟通，避免对肾移植受者的临床处置造成不良影响。

PU-1518

Association between complement 4 copy number variation and systemic lupus erythematosus: a meta-analysis

Ziyan Wu
Peking Union Medical College Hospital

Systemic lupus erythematosus (SLE) is a chronic autoimmune disease characterized by multiple genetic mutations. Complement 4 (C4) copy number variation (CNV) is a target-of-interest located on chromosome 6. C4 encodes for either of the two C4 paralogs, C4A or C4B, and low C4 levels have been associated with SLE activity. In this study, we conducted a meta-analysis to comprehensively understand the role of C4 CNV in SLE. Three databases (PubMed, Embase, and Web of Science) were searched for relevant studies. Two investigators independently extracted and evaluated data from eligible studies. Associations between C4 CNV and SLE were estimated by odds ratios (OR) and 95% confidence intervals (95% CI). Further analysis was conducted using the STATA 12.0 software. A total of eight case-control studies were included in the analysis with 4107 SLE patients and 5889 healthy controls. Six studies used TaqMan real-time PCR to genotype C4 CNV, with 1 study used paralog ratio test and other one used multiplex ligation-dependent probe amplification (MLPA). Lower total C4 CNV and C4A CNV were associated with SLE in the overall analysis (pooled OR: 1.55, 95% CI: 1.23-1.95; pooled OR: 1.86, 95% CI: 1.51-2.29). The subgroup analysis found that total C4 CNV and lower C4A CNV were significantly associated with SLE in Caucasians (pooled OR: 1.84, 95% CI: 1.60-2.12; pooled OR: 2.23, 95% CI:1.92-2.59). However, the association was not detected in East Asians. Lastly, SLE was not associated with C4B CNV, long C4 CNV, or short C4 CNV. The meta-analysis confirmed that lower total C4 CNV and lower C4A CNV are associated with SLE in certain populations. Future studies should consider other ethnic groups to further investigate the relationship between the C4 gene and SLE.

PU-1519

早期胃癌筛查生物标志物特征性分析

陈佳琦
丽水市人民医院

目的 研究胃蛋白酶原 I (pepsinogen I，PGI)，胃蛋白酶原 II(pepsinogen II，PGII), PGI/II 比值，胃泌素 17（gastrin-17，G-17）和幽门螺旋杆菌抗体(helicobacter pylori antibody，HP)作为新型胃癌循环生物标志物，对于胃部疾病的评估及在早期胃癌筛查中的价值。

方法 选取 2017 年 6 月至 2019 年 6 月行胃镜检查的门诊及住院患者共 400 例，根据胃镜检查和病理结果分为 5 组，其中非萎缩性胃炎组 80 例，萎缩性胃炎/肠上皮化生组 80 例，上皮内瘤变（异型增生）组 80 例和胃癌组 80 例和同期健康体检组 80 例，及行胃癌根治术组。利用酶联免疫吸附

试验定量检测血清 PGⅠ、PGⅡ和 G-17 水平，并计算 PGI/II 比值,用斑点法检测 HP 现症感染蛋白。**结果** 各组间的 PGⅠ、PGⅡ、G-17、PGI/II 比值及 HP 感染率详见表 1。5 个生物标志物(尤其是 PGⅠ、PGI/II 比值和 G-17)与胃癌前病变及胃癌明显相关，对照组与实验各组间有显著性差异。PGⅡ在实验各组间差异不明显。实行胃癌根治术后 PGⅠ、PGI/II 比值和 G-17 与胃癌对照组有显著性差异。
结论 由五种新型胃癌循环生物标志物组成的血清学活检可以确定高危个体，为进一步胃镜检查，并对其病程诊断进行分层，从而指导靶向筛选和精确预防。

PU-1520

Coagulopathy and Antiphospholipid Antibodies in Patients with Covid-19

Shulan Zhang
Peking Union Medical College Hospital

BackgroundThe authors describe a 69-year-old man with Covid-
19 diagnosed in January 2020 in Wuhan, China, along with two other critically ill patients with Cov id-
19 who were also seen in the same intensive care unit. Coagulopathy and antiphospholipid antib odies were seen in all three patients.
Methods
This department is managed by a multidisciplinary team of Peking Union Medical College Hospita l from the Sino-French Xincheng Branch of Tongji Hospital in Wuhan, China. During the COVID-
19 outbreak, patients with severe disease were treated on the basis of emergency treatment.All p atients were diagnosed with SARS-CoV-
2 infection by either reverse transcription polymerase chain reaction (RT-
PCR) or serological testing.
Results Antiphospholipid antibodies abnormally target phospholipid proteins, and the presence of these antibodies is essential for the diagnosis of antiphospholipid syndrome.However, these anti bodies can also appear briefly in patients with critically ill diseases and a variety of infections.
Conclusions In critically ill patients, the presence of these antibodies may rarely lead to thrombot ic events that are difficult to distinguish from other causes of multifocal thrombosis, such as disse minated intravascular coagulation, heparin-
induced thrombocytopenia, and thrombotic microangiopathy.

PU-1521

IP-10 and MCP-1 as biomarkers associated with disease severity of COVID-19

Yu Chen
Peking Union Medical College Hospital

Background COVID-19 is a viral respiratory disease caused by the severe acute respiratory syndrome-Coronavirus type 2 (SARS-CoV-2). Patients with this disease may be more prone to venous or arterial thrombosis because of the activation of many factors involved in it, including inflammation, platelet activation and endothelial dysfunction. Interferon gamma inducible protein-10 (IP-10), monocyte chemoattractant protein-1 (MCP-1) and macrophage inflammatory protein 1-alpha (MIP1α) are cytokines related to thrombosis. Therefore, this study focused on these three

indicators in COVID-19, with the hope to find biomarkers that are associated with patients' outcome.
Methods This is a retrospective single-center study involving 74 severe and critically ill COVID-19 patients recruited from the ICU department of the Tongji Hospital in Wuhan, China. The patients were divided into two groups: severe patients and critically ill patients. The serum IP-10, MCP-1 and MIP1α level in both groups was detected using the enzyme-linked immunosorbent assay (ELISA) kit. The clinical symptoms, laboratory test results, and the outcome of COVID-19 patients were retrospectively analyzed.
Results The serum IP-10 and MCP-1 level in critically ill patients was significantly higher than that in severe patients ($P < 0.001$). However, no statistical difference in MIP1α between the two groups was found. The analysis of dynamic changes showed that these indicators remarkably increased in patients with poor prognosis. Since the selected patients were severe or critically ill, no significant difference was observed between survival and death.
Conclusions IP-10 and MCP-1 are biomarkers associated with the severity of COVID-19 disease and can be related to the risk of death in COVID-19 patients.

PU-1522

2538 例体检人群 PGⅠ、PGⅡ、G-17 的研究

傅锦芳
中南大学湘雅医院

目的 通过检测长沙市体检人群中血清胃蛋白酶原(PG)、胃泌素-17(G-17)水平及幽门螺杆菌抗体（HP）感染情况，以评估该地区人群中胃功能的整体水平，并为胃部疾病的研究提供流行病学资料。

方法 采用酶联免疫法测定血清中胃蛋白酶原Ⅰ、Ⅱ及胃泌素-17 的含量，按性别、年龄等方式进行分组分析；幽门螺杆菌抗体检测使用胶体金方法测定。

结果（1）2538 例体检者的总异常率为 42.9%，PGⅠ的异常率为 22.18%，PGⅡ异常率为 18.56%，G-17 的异常率为 20.06%，长沙地区的胃功能总异常率处于较高水平。（2）将 2538 例体检人群分为≤30 岁、30-60 岁、≥60 岁三组，30-60 岁组和≥60 岁组的 PGⅠ和 PGⅡ水平高于≤30 岁组；其值有随着年龄增加而升高的趋势。（3）男性组和女性组比较，PGⅠ和 PGⅡ水平无统计学意义，男性组 G-17 低于女性组。（4）将同时做了胃功能检测和 HP 抗体检测的 325 例进行分析，HP 阳性组 PGⅠ、PGⅡ和 PGR 的异常率均高于阴性组。

结论 长沙市 2538 例健康体检者总异常率为 42.9%，处于较高水平；随年龄增加 PGⅠ、PGⅡ、G-17 值升高；HP 抗体阳性的人群 PGⅠ、PGⅡ和 PGR 的异常率也比较高。

PU-1523

快速检测具核梭杆菌的荧光定量 PCR 方法的建立及临床应用

陈颖玮、赵冉、王雪亮、黄维纲
上海市临床检验中心

目的 建立一种快速检测具核梭杆菌的荧光定量 PCR 方法，并探讨其应用于结直肠癌筛查的可行性，为结直肠癌非入侵性的检测提供新的选择。

方法 以具核梭杆菌 nusG 基因作为目的基因，对其保守区域设计特异性的引物及探针，同时根据细菌 16S rDNA 序列保守区域设计简并引物作为内参。通过正交试验优化 PCR 反应体系中的引物探

针比，完善反应条件，建立具核梭杆菌快速定量检测方法，并对方法进行性能验证。收集 100 对结直肠癌患者的癌组织和癌旁组织的临床样本，应用建立的 PCR 方法检测具核梭杆菌在结肠癌组织和癌旁组织中的相对含量。
结果 该方法的最低检测限为 50copies/ml。具核梭杆菌在 5×101-5×108 copies/mL 浓度范围内扩增曲线呈线性，得到的扩增曲线线性方程斜率为−2.8312，R2 值为 0.9952。制备的不同浓度的定量参考样品，检测结果的批内变异系数为 0.57%～2.96%，批间变异系数为 0.82%～1.32%。100 对结直肠癌患者癌组织和癌旁组织样本的检测结果显示具有统计学差异，具核梭杆菌在结肠癌组织内的含量明显高于癌旁组织，配对 t test 的 p 值为 0.02（p<0.05）。
结论 本项研究建立的具核梭杆菌 DNA 定量检测方法具有较高灵敏度及特异性。该方法可以有效的检测临床样本中的具核梭杆菌，具有潜在的结直肠癌筛查的临床应用价值。

PU-1524

三种常用方法检测梅毒螺旋体抗体不确定样本的性能评价

刘蓉、滕文友
郴州市第一人民医院

目的 评价 TRFIA、ELISA 和胶体金法检测梅毒螺旋体抗体不确定样本性能。
方法 以 TP-TRFIA 筛选 1.0≤S/CO 值≤9.9 范围内的梅毒螺旋体抗体不确定标本，同时用 TPPA、TP-ELISA 和胶体金法检测，以 TPPA 为确认方法，比较 TP-TRFIA、TP-ELISA 和胶体金法的灵敏度、特异性、符合率、约登指数、似然比和 ROC 曲线下面积。
结果 与 TPPA 比较，TP-TRFIA、TP-ELISA 和胶体金法的灵敏度分别为 100%、88.57%和 51.43%，特异性分别为 0、96.26%和 85.05%，符合率分别为 24.65%、94.37%和 76.76%，约登指数分别为 0、0.85 和 0.36，阳性似然比分别为 1.00、23.69 和 3.44，阴性似然比分别为 0、0.12 和 0.57，ROC 曲线下面积分别为 0.50、0.92 和 0.68。
结论 TRFIA 灵敏度高，可用于梅毒血清学筛查，ELISA 的灵敏度、特异性和符合率均高，可用于梅毒血清学筛查和诊断，胶体金法的灵敏度低，不宜用于梅毒血清学筛查。检测灰区的梅毒抗体不确定标本需用 TPPA 复查，以减少误诊。

PU-1525

14574 例四川省呼吸道感染病原体 IgM 抗体结果分析

马丽萍、孙思琪
四川金域医学检验中心有限公司

目的 统计四川省 14574 例呼吸道感染的九种常见病原体 IgM 抗体的检出阳性率，分析检出阳性率与年龄、季节之间的关系，为临床的诊断与治疗提供相关的参考性依据。
方法 统计 2020 年共 14574 例患者检测数据，使用 VIRCELL,S.L.的九项呼吸道感染病原体 IgM 抗体检测试剂盒（间接免疫荧光法）检测 Leg-IgM、MP-IgM、CB-IgM、RSV-IgM、ADV-IgM、CP-IgM、IAV-IgM、IBV-IgM、PIVs-IgM。分析不同病原体在不同年龄患者及季节的流行趋势。
结果 九项病原体以 MP-IgM 感染构成比最高，为 3263 例(22.39%)；第二是 PIVs-IgM，为 412 例（2.83%）；第三是 IBV-IgM，为 317 例（2.18%）。从季节来看，春季以 MP-IgM 感染构成比最高，为 494 例(16.27%)；夏季以 MP-IgM 感染构成比最高，为 667 例(25.93%)；秋季以 MP-IgM 感染构成比最高，为 1289 例(27.17%)；冬季以 MP-IgM 感染构成比最高，为 813 例(19.26%)。从年龄来看，≤17 岁组有 2813 例病原体阳性（2813 /68130，4.13%），以 MP-IgM 感染构成比最高，为 2272 例(3.33%)；18~65 岁组有 858 例病原体阳性（858/29619，2.90%），以 MP-IgM 感染构成比最高，为 591 例(2.00%)；66~79 岁组有 395 例病原体阳性（395/20025，1.97%），以 MP-

IgM 感染构成比最高，为 277 例(1.38%)；≥80 岁组有 171 例病原体阳性（171/9639，1.77%），以 MP-IgM 感染构成比最高，为 110 例(1.14%)。

结论 MP-IgM 是四川省各季节呼吸道感染者中检出的主要病原体,其中在秋季 MP-IgM 检出率最高。在四川各年龄段呼吸道感染者中≤17 岁年龄组的 MP-IgM 检出率最高。

PU-1526

HBeAg 阴性慢性乙肝患者转氨酶水平与肝脏功能相关性分析

周觅
山东大学第二医院

目的 分析不同 Child-Pugh 分级 HBeAg 阴性慢性乙肝患者两种转氨酶水平以及 HBV-DNA 的差异,探讨肝脏储备功能与乙肝病毒活动力的相关性。

方法 收集慢性乙肝患者 258 例,按照 Child-Pugh 分级分组,比较各组中谷草转氨酶和谷丙转氨酶水平以及病毒复制能力反应指标 HBV 免疫标志物和 HBV-DNA 的差异,分析病毒复制能力与肝脏储备功能的相关性。

结果 HBeAg 阴性慢性乙肝患者按照 Child-Pugh 分级发现,不同分级的患者 HBV-DNA 表达水平差异有统计学意义(P<0．05),相关性调查发现病毒复制水平与 Child-Pugh 分级呈现明显负相关(r=-0．49,P=0．00)。转氨酶水平与分级水平和 HBV-DNA 并没有统计意义的相关性（R=0.642）,HBeAg 阴性慢性乙肝不同 Child-Pugh 分级的患者免疫血清标志物表现明显不同,差异有统计学意义(P<0．05)；进一步对不同标志物分析发现, HbsAg 和 anti-HBs 表达与 Child-Pugh 分级评分存在相关性。

结论 HBeAg 阴性慢性乙肝患者病毒活动力与患者肝脏储备功能存在相关性,这种相关性的发现有利于乙肝患者病程发展中的药物有效性以及机体耐受力的全面评估,以便乙肝患者的抗病毒治疗正确方案的确定提供可靠的实验室检测数据。

PU-1527

500 例儿童食入物过敏原 IgG 检测结果分析

孙肖涵
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 通过分析特异性过敏 IgG 的检测结果，对儿童食入物过敏性疾病预防和治疗提供理论支持。

方法 采用酶联免疫吸附法对我科 2021 年 1 月～2021 年 6 月 500 例儿童保健门诊、儿科门诊和住院患儿食入物过敏原特异性 IgG，进行统计分析。

结果 在 500 例患儿中检出总阳性率 78.55%.蛋清/蛋黄阳性率最高 12.85%，牛奶次之 9.33%，一份血清标本可出现多种食入物过敏原存在。

结论 食物过敏原中蛋清/蛋黄和牛奶是最主要食入性过敏原，采取有效的预防措施，可以有效降低食入物导致过敏疾病的发生。

PU-1528

1846 例体检者幽门螺杆菌抗体检测结果分析

张法
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 了解济南地区健康体检人群胃幽门螺杆菌（Hp）在不同性别、年龄的感染状况。
方法 选取 2018 年 1 月~2019 年 12 月在我院进行 Hp 检测的 1846 例体检者为研究对象，以性别和年龄进行分组，应用幽门螺杆菌尿素酶抗体检测试剂盒（胶体金法）快速检测体检人群中 Hp 感染情况，并对检测结果进行统计学分析。
结果 1846 例体检者 Hp 总感染率为 48.21%（890/1846），其中男性为 47.49%（718/1512），女性为 51.50%(172/334),女性高于男性但(P>0.05)没有统计学意义;将体检者按年龄分为青年组（18~39）、中年组（40~59）、老年组（60~83），其 Hp 感染率分别为 36.98%（321/868）、42.93%（322/750）、54.82%（125/228）,不同年龄组在 Hp 感染率差异上具有统计学意义（P<0.05）。
结论 健康体检人群中 Hp 阳性率较高，与性别无关，与年龄成正相关。应加强中老年 Hp 诊疗管理，普及 Hp 感染预防知识，从而更有效地预防 Hp 感染疾病的发生。

PU-1529

过敏性鼻炎患者血清 IgE 及 sIgE 结果分析

刘晓丹
中国医科大学附属盛京医院

目的 研究沈阳地区过敏性鼻炎患者血清总免疫球蛋白 E(IgE) 及特异性 IgE (sIgE) 水平检测结果，总结该地区主要过敏原种类，及主要的过敏原随季节的变化情况，为沈阳地区过敏性鼻炎患者的预防、诊断及治疗提供依据。
方法 选取 2019 年 1 月至 2020 年 12 月于中国医科大学附属盛京医院耳鼻咽喉科就诊的过敏性鼻炎患者病例 372 例，采用瑞典 Phadia AB 公司生产的 Phadia 250 全自动体外荧光免疫分析系统，检测过敏性鼻炎患者血清中总 IgE 和过敏原特异性 IgE 水平。
结果 372 例过敏性鼻炎患者中男性 241 例(64.78%) 、女性 131 例(35.22%)，患者年龄高峰为 1-10 岁，波动在 1～ 55 岁之间，其中总 IgE 阳性患者 315 例(85.13%) ，常见吸入性过敏原中，杂草花粉、尘螨、毛屑混合和树木组合为主要的吸入性过敏原。食入性过敏原中，海鲜组合、牛奶蛋白组合及花生芝麻组合为主要食入性过敏原.沈阳地区过敏性鼻炎患者发病高峰期为 7-10 月。在主要的吸入性过敏原中，常年性变应原(尘螨和毛屑混合) 血清特异性 IgE 水平均值随月份变化情况较为相似，季节性变应原(杂草花粉和树木组合) 血清特异性 IgE 水平平均值随月份变化情况与各自的开花季节相同。
结论 沈阳地区过敏性鼻炎患者以幼儿为主。杂草花粉、尘螨、毛屑混合和树木组合为主要的吸入性过敏原，牛奶蛋白组合和花生芝麻组合为主要食入性变应原。在沈阳的每年的 7-10 月，艾蒿及一些常见植物和树木组合的开花季节过敏性鼻炎的发病率最高，过敏性鼻炎患者要注意提前防护自身。

PU-1530

血清核心岩藻糖基化 IgG 与系统性红斑狼疮疾病的关系的研究

李志
大连市中心医院

目的 探讨血清核心岩藻糖基化修饰 IgG 对系统性红斑狼疮疾病（SLE）的诊断价值及其临床意义。
方法 收集 2017 年 3 月到 2019 年 6 月大连市中心医院的 30 例确诊为 SLE 患者的血清样品，采用凝集素印迹方法（Lectin Blot）检测患者血清蛋白核心岩藻糖基化水平；利用高效液相色谱对患者以及野生型小鼠（Fut8+/+）和基因敲除小鼠（Fut8-/-）CD4+T 中核心岩藻糖基转移酶（Fut8）酶活性进行检测；ELISPOT 实验检测 Fut8+/+和 Fut8-/-脾细胞产生抗体的能力。
结果 与正常人相比，SLE 患者血清蛋白核心岩藻糖基化水平显著升高，差异有统计学意义（$p<0.001$）；SLE 患者 CD4+T 细胞中 Fut8 酶的活性显著增强（$p<0.05$）；Fut8-/-小鼠淋巴细胞抗体的含量及产生能力显著下降（$p<0.05$）。
结论 SLE 患者血清蛋白表现出高水平核心岩藻糖基化，提示 Fut8 活性与抗体的活性有关，糖基化在 SLE 的发生发展中起着重要的作用，为 SLE 诊断和治疗提供了新视角。

PU-1531

流式细胞术法检测中性粒细胞 CD64 指数的性能评价及其影响因素探讨

李文敏[1]、周茂华[1]、慕静静[2]、魏晓宁[2]
1. 广东省人民医院
2. 碧迪医疗器械（上海）有限公司

目的 基于 ISO 15189：2012 要求，对中性粒细胞 CD64 指数的性能参数进行评价并探究其影响因素。
方法 应用 BD FACSCanto 流式细胞仪检测来自广东省人民医院住院及体检人群外周血进行外周血中性粒细胞 CD64 指数检测，探究样本血保存时间、样本制备后放置时间、上机检测速度、细胞获取总数等因素对检测结果的影响，并依据《医学实验室质量和能力认可准则》相关文件对该项目的重复性、日间精密度和日内精密度进行评价，建立本实验室正常人群参考范围。
结果 样本血保存时间、样本制备后放置时间、上机检测速度、细胞获取总数等因素对检测结果的影响差异无统计意义（$p>0.05$）。感染组和体检组样本制备重复性分别为 1.84%和 2.95%，样本血重复制备日间精密度实验显示外周血采集 16h 检测结果 CV%＜15%。制备后检测管日内精密度实验显示制备后 6h 内检测结果 CV%＜15%。本实验室检测条件下正常人参考范围为 0-2.02。
结论 中性粒细胞 CD64 指数项目性能能满足临床检测需求，但样本血需在采集后 16h 内进行制备，制备后检测管需在 6h 内进行检测。

PU-1532

Prealbumin as a predictor of prognosis in patients with coronavirus disease 2019

Ying Luo、Feng Wang、Ziyong Sun
Department of Laboratory Medicine, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Background The predictive value of prealbumin for the prognosis of coronavirus disease 2019 (COVID-19) was rarely investigated.
Methods A total of 1,115 patients with laboratory-confirmed COVID-19 were enrolled at Tongji hospital from February to April 2020, and classified into fatal (n=129) and recovered (n=986) group according to the patient's outcome. Prealbumin and other routine laboratory indicators were measured simultaneously.
Results The level of prealbumin on admission was significantly lower in fatal patients than in recovered patients. For predicting the prognosis of COVID-19, the performance of prealbumin was better than most routine laboratory indicators, such as albumin, lymphocyte count, neutrophil count, hypersensitive C-reactive protein, d-dimer, lactate dehydrogenase, creatinine and hypersensitive cardiac troponin I. When the threshold of 126 mg/L was used, the sensitivity and specificity of prealbumin were respectively 78.29% and 90.06% in discriminating between fatal and recovered patients. Furthermore, a model based on the combination of nine indexes showed an improved performance in predicting the death of patients with COVID-19. Using the cut-off value of 0.19, the prediction model was able to distinguish between fatal and recovered individuals with a sensitivity of 86.82% and a specificity of 90.37%.
Conclusions A lower level of prealbumin on admission may indicate a worse outcome of COVID-19. Immune and nutritional status may be vital factors for predicting disease progression in the early stage of COVID-19.

PU-1533

Activation phenotype of Mycobacterium tuberculosis-specific CD4+ T cells promoting the discrimination between active tuberculosis and latent tuberculosis infection

Ying Luo、Feng Wang、Ziyong Sun
Department of Laboratory Medicine, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Background Rapid and effective discrimination between active tuberculosis (ATB) and latent tuberculosis infection (LTBI) remains a challenge. There is an urgent need for developing practical and affordable approaches targeting this issue.
Methods Participants with ATB and LTBI was recruited at Tongji Hospital (Qiaokou cohort) and Sino-French New City Hospital (Caidian cohort) based on positive T-SPOT results from June 2020 to January 2021. The expression of activation markers including HLA-DR, CD38, CD69, and CD25 were examined on Mycobacterium tuberculosis (MTB)-specific CD4+ T cells defined by IFN-γ, TNF-α, and IL-2 expression upon MTB antigen stimulation.
Results A total of 90 (40 ATB and 50 LTBI) and another 64 (29 ATB and 35 LTBI) subjects were recruited from Qiaokou cohort and Caidian cohort, respectively. The expression pattern of Th1 cytokines including IFN-γ, TNF-α, and IL-2 upon MTB antigen stimulation could not differentiate ATB patients from LTBI individuals well. However, both HLA-DR and CD38 on MTB-specific cells showed discriminatory value in distinguishing between ATB patients and LTBI individuals. As for

developing a single candidate indicator, HLA-DR had the advantage over CD38. Moreover, HLA-DR on TNF-α+ or IL-2+ cells had superiority over that on IFN-γ+ cells in differentiating ATB patients from LTBI individuals. Besides, HLA-DR on MTB-specific cells defined by multiple cytokine co-expression had a higher ability to discriminate patients with ATB from LTBI individuals than that on MTB-specific cells defined by one kind of cytokine expression. Specially, HLA-DR on TNF-α+IL-2+ cells produced an AUC of 0.901 (95% CI, 0.833-0.969), with a sensitivity of 93.75% (95% CI, 79.85%-98.27%) and specificity of 72.97% (95% CI, 57.02%-84.60%) as a threshold of 44% was used. Furthermore, the performance of HLA-DR on TNF-α+IL-2+ cells for differential diagnosis was obtained with validation cohort data: 90.91% (95% CI, 72.19%-97.47%) sensitivity and 68.97% (95% CI, 50.77%-82.73%) specificity.
Conclusions We demonstrated that HLA-DR on MTB-specific cells was a potentially useful biomarker for accurate discrimination between ATB and LTBI.

PU-1534

Lymphocyte-related immunological indicators for stratifying Mycobacterium tuberculosis infection

Ying Luo、Feng Wang、Ziyong Sun
Department of Laboratory Medicine, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Background Easily accessible tools that reliably stratify Mycobacterium tuberculosis (MTB) infection are needed to facilitate the improvement of clinical management. The current study attempts to reveal lymphocyte-related immune characteristics of active tuberculosis (ATB) patients and establish immunodiagnostic model for discriminating ATB from latent tuberculosis infection (LTBI) and healthy controls (HC).
Methods A total of 180 subjects consists of 60 ATB, 60 LTBI, and 60 HC were consecutively recruited at Tongji hospital from January 2019 to January 2021. All participants were tested for lymphocyte subsets, phenotype, and function. Other examination including T-SPOT and microbiological detection for MTB were performed simultaneously.
Results Compared with LTBI and HC, ATB patients exhibited significantly lower number and function of lymphocytes including CD4+ T cells, CD8+ T cells and NK cells, and significantly higher T cell activation represented by HLA-DR and proportion of immunosuppressive cells represented by Treg. An immunodiagnostic model based on the combination of NK cell number, HLA-DR+CD3+ T cells, Treg, CD4+ T cell function, and NK cell function was built using logistic regression. Based on receiver operating characteristic curve analysis, the area under the curve (AUC) of the diagnostic model was 0.918 (95% CI, 0.866-0.970) in distinguishing ATB from LTBI, while the cut-off value of 0.674 produced a sensitivity of 80.00% (95% CI, 68.22%-88.17%) and specificity of 91.67% (95% CI, 81.93%-96.39%). Meanwhile, AUC analysis between ATB and HC according to the diagnostic model was 0.918 (95% CI, 0.865-0.971), with a sensitivity of 80.00% (95% CI, 68.22%-88.17%) and a specificity of 90.00% (95% CI, 79.85%-95.34%).
Conclusions Our study demonstrated that the immunodiagnostic model established by the combination of lymphocyte-related indicators could facilitate the status differentiation of MTB infection.

PU-1535

Lymphocyte non-specific function detection facilitating the stratification of Mycobacterium tuberculosis infection

Ying Luo、Feng Wang、Ziyong Sun
Department of Laboratory Medicine, Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Background Inadequate tuberculosis (TB) diagnostics, especially for discrimination between active TB (ATB) and latent TB infection (LTBI), are major hurdle in the reduction of the disease burden. The present study aims to investigate the role of lymphocyte non-specific function detection for TB diagnosis in clinical practice.
Methods A total of 208 participants including 49 ATB patients, 64 LTBI individuals, and 95 healthy controls were recruited at Tongji hospital from January 2019 to October 2020.All subjects were tested with lymphocyte non-specific function detection and T-SPOT assay.
Results Significantly positive correlation existed between lymphocyte non-specific function and phytohemagglutinin (PHA) spot number. CD4+ T cell non-specific function showed the potential for differentiating patients with negative T-SPOT results from those with positive T-SPOT results with an area under the curve (AUC) of 0.732 (95% CI, 0.572-0.893). The non-specific function of CD4+ T cells, CD8+ T cells, and NK cells was found significantly lower in ATB patients than in LTBI individuals. The AUCs presented by CD4+ T cell non-specific function, CD8+ T cell non-specific function, and NK cell non-specific function for discriminating ATB patients from LTBI individuals were 0.845 (95% CI, 0.767-0.925), 0.770 (95% CI, 0.683-0.857), and 0.691 (95% CI, 0.593-0.789), respectively. Application of multivariable logistic regression resulted in the combination of CD4+ T cell non-specific function, NK cell non-specific function, and culture filtrate protein-10 (CFP-10) spot number as the optimally diagnostic model for differentiating ATB from LTBI. The AUC of the model in distinguishing between ATB and LTBI was 0.939 (95% CI, 0.898-0.981). The sensitivity and specificity were 83.67% (95% CI, 70.96%-91.49%) and 90.63% (95% CI, 81.02%-95.63%) with the threshold as 0.57. Our established model showed superior performance to TB-specific antigen (TBAg)/PHA ratio in stratifying TB infection status.
Conclusions Lymphocyte non-specific function detection offers an attractive alternative to facilitate TB diagnosis. The three-index diagnostic model was proved to be a potent tool for the identification of different events involved in TB infection, which is helpful for the treatment and management of patients.

PU-1536

Combination of prealbumin and tuberculosis-specific antigen/phytohemagglutinin ratio for discriminating active tuberculosis from latent tuberculosis infection

Ying Luo、Feng Wang、Ziyong Sun
Department of Laboratory Medicine, Tongji hospital, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Background Given that there is no rapid and effective method for distinguishing active tuberculosis (ATB) from latent tuberculosis infection (LTBI), the discrimination between these two statuses remains challenging. This study sought to investigate the value of nutritional indexes and tuberculosis-specific antigen/phytohemagglutinin ratio (TBAg/PHA ratio) for distinguishing ATB from LTBI.
Methods Participants were consecutively recruited based on positive T-SPOT.TB results between January 2018 and January 2020. ATB was diagnosed by positive mycobacterial culture and/or positive GeneXpert MTB/RIF, with clinical symptoms and radiological characteristics

suggestive of ATB. Individuals with positive T-SPOT.TB but without the evidence of ATB were defined as LTBI. Patients younger than 17 years and undergoing anti-TB treatment were excluded.
Results A total of 709 (312 ATB and 397 LTBI) and another 309 (120 ATB and 189 LTBI) subjects were respectively recruited from Tongji Hospital (Qiaokou cohort) and Sino-French New City Hospital (Caidian cohort). The level of prealbumin was significantly lower in ATB than in LTBI. With a cut-off value of 139 mg/L, the sensitivity and specificity of prealbumin in distinguishing ATB from LTBI were 50.96% (45.41%-56.51%) and 91.69% (88.97%-94.40%). Meanwhile, TBAg/PHA ratio was found statistically higher in ATB compared with LTBI. If using the threshold of 0.29, the sensitivity and specificity of TBAg/PHA ratio were 65.71% (60.44%-70.97%) and 90.93% (88.11%-93.76%), respectively. Moreover, the combination of prealbumin and TBAg/PHA ratio (obtaining by diagnostic model) yielded better specificity (90.18%,[87.25%-93.10%]) and sensitivity (87.18%,[83.47%-90.89%]), while the clinical utility index (CUI) positive and CUI negative were respectively 0.76 and 0.81. After anti-TB treatment, TBAg/PHA ratio was declined while the level of prealbumin was restored (Wilcoxon test,P<0.001). Furthermore, the performance of diagnostic model obtained in Qiaokou cohort was confirmed in Caidian cohort.
Conclusions The diagnostic model based on combination of prealbumin and TBAg/PHA ratio is a rapid and accurate tool for discriminating ATB from LTBI.

PU-1537

铜绿假单胞菌感染肺部疾病的细胞免疫表现

罗燕飞、蓝名伟
广东省人民医院

目的 了解慢性阻塞性肺气肿、慢性支气管炎合并铜绿假单胞菌感染患者的免疫细胞 T、B、NK 水平变化。
方法 通过比较健康人群（对照组），慢阻肺、慢支患者未合并铜绿假单胞菌（No-PA）感染组；慢阻肺、慢支患者合并铜绿假单胞菌（PA）感染组患者外周血免疫细胞。
结果 1.（1）慢阻肺合并 PA 感染患者与正常健康人比较，CD3+增多、CD3+CD4+/CD3+CD8+比值明显降低，B 细胞、NK 细胞减少，分别 P<0.05，差异具有统计学意义（P<0.05）；（2）慢阻肺未合并 PA 感染患者与正常健康人比较，CD3+减少、CD3+CD4+/CD3+CD8+比值明显降低，NK 细胞增多，分别 P<0.05，差异具有统计学意义（P<0.05），B 细胞是没有大太变化（P>0.05）；（3）慢阻肺合并 PA 感染与慢阻肺未合并 PA 感染患者比较，CD3+相对增多、CD3+CD4+/CD3+CD8+比值明显降低 P<0.05，差异具有统计学意义； NK 细胞相对减少，差异具有统计学意义（P<0.05），B 细胞是没有大太变化。2.（1）慢支合并 PA 感染与正常健康人比较，CD3 相对增多，CD3+CD4+/CD3+CD8+比值是明显下降；CD3-CD16+CD56+水平明显降低，差异具有统计学意义（P<0.05）。B 细胞无显著差异（P>0.05）；（2）慢支未合并 PA 感染与正常健康人比较， CD3、B 细胞水平相对减少，CD3+CD4+/CD3+CD8+比值是明显下降；NK 细胞是相对增多，分别 P<0.05，差异具有统计学意义（P<0.05）。（3）慢支合并 PA 感染与未合并 PA 感染患者比较，CD3、B 细胞水相对增多，NK 细胞相对减少，分别 P<0.05，有显著差异（P>0.05）。
结论 慢阻肺、慢支的患者，感染铜绿假单胞菌时进一步打击了体内细胞免疫系统，引起细胞免疫紊乱及免疫功能障碍。

PU-1538

IL-10 与慢乙肝不同血清学标志物模式的相关性研究

延娅娅
西安医学院第一附属医院

目的 探讨 IL-10 与慢性乙肝病毒感染者不同血清学模式的相关性，为慢性乙肝治疗提供指导和实验依据。
方法 随机选取男性乙肝五项检查病例 83 例，其中血清学模式为 135 阳性模式组 20 例，145 阳性模式 21 例，245 阳性模式 22 例，25 阳性模式 20 例。同时，随机选取年健康体检者 24 例作为正常对照组。
结果 慢乙肝不同血清学标志物模式间 IL-10 水平有差异，具有统计学意义（P<0.05）。
结论 血清 IL-10 水平升高，有利于慢性乙肝患者血清学模式由 135、145 阳性模式向 245、25 阳性模式转换。

PU-1539

血清中 PLA2R 抗体、IgG 和 C3 在特发性膜性肾病诊断中的应用价值研究

陈柳勤
广东省人民医院

目的 探讨血清学指标抗磷脂酶 A2 受体抗体（PLA2R 抗体）、IgG 和补体 C3 在特发性膜性肾病中的诊断价值。
方法 回顾性分析广东省人民医院 2019 年 8 月~2021 年 1 月 77 例特发性膜性肾病作为特发性膜性肾病（IMN）组，145 例其他肾病：包含 7 例继发性膜性肾病、59 例糖尿病肾病、60 例 IgA 肾病、10 例狼疮性肾炎、4 例胡桃夹综合征、2 例高血压肾病、2 例尿酸性肾病和 1 例薄基底膜肾病作为其他肾病组，49 例非肾病患者作为对照组，膜性肾病的患者均经临床检查与肾活检病理结果确诊。
结果 IMN 患者血清 PLA2R 抗体阳性率显著高于其他肾病组和对照组（P<0.05）；IMN 组血清 IgG 水平明显低于其他肾病组和对照组（P<0.05）；血清 C3 水平 IMN 组略高于其他肾病组，差异有统计学意义（P<0.05）。IMN 组与其他肾病组中的 IgA 组、糖尿病肾病组比较：PLA2R 抗体、IgG 差异均具有统计学意义（P<0.05），IMN 组与糖尿病肾病组的血清 C3 水平相比差异均具有统计学意义（P<0.05）。IMN 组不同病理分期的实验室指标进行比较：“I+II 期 IMN 组”和“III+IV 期 IMN 组”在血清 PLA2R 抗体、IgG 和 C3 水平上差异均无统计学意义（P>0.05）。
结论 血清 PLA2R 抗体在特发性膜性肾病中的阳性率显著高于其他肾病组和对照组，是一个良好的辅助诊断性指标；血清 IgG、C3 检测有助于临床特发性膜性肾病的判别。

PU-1540

乙肝病毒感染与抗平滑肌抗体相关性分析

马跃飞、贺勤、刘灿、林锦骠、刘晓峰、王炳龙、杨滨、欧启水
福建医科大学附属第一医院

目的 探讨 HBV 感染者病毒活动情况、疾病进程与血清抗平滑肌抗体(ASMA) 产生的相关性。
方法 回顾性分析我院 2014 年 6 月至 2018 年 6 月间慢性乙型病毒性肝炎（CHB）患者的肝病自身抗体检测结果。筛选 51 例合并 ASMA 阳性患者的临床资料和实验室数据进行分析，以自身抗体检

测阴性的 50 例 CHB 患者作为比较。分析两组的临床表现、肝功能、乙肝病毒活动情况和疾病进程的差异。
结果 抗核抗体（ANA）、ASMA、抗线粒体抗体（AMA）和抗肝肾微粒体抗体（LKM-1）在 CHB 受检者中阳性率分别为 13.46%、5.01%、0.60%和 0.07%。ASMA 阳性组和自身抗体阴性组患者的年龄、性别构成、HBsAg 感染年限、HBsAg、HBeAg 和 HBV-DNA 对数值，以及 CHB 的疾病进程的差异无统计学意义。ASMA 阳性组的首发症状多见黄疸，部分合并肝外自身免疫性疾病表现（P<0.05）。ASMA 阳性组 TBIL、ALP、TBA、PT 高于自身抗体阴性组，ALB 低于自身抗体阴性组，差异均有统计学意义（P<0.05）。ASMA 阳性组中肝炎、肝硬化和肝癌患者的 ASMA 滴度差异无统计学意义。
结论 ASMA 与乙肝病毒复制活动性和疾病病程无相关性。

PU-1541

低体重、极低体重早产儿甲甲状腺功能减退的诊断标准探讨 及临床价值分析

叶庭菠、梁河涛
成都市第三人民医院

目的 探讨低体重、极低体重早产儿甲状腺功能低下的筛查切值，及早产儿出生时的胎龄、体重、性别等对甲状腺功能的影响。
方法 收集 2017 年 12 月-2020 年 4 月在我院新生儿科住院的低体重、极低体重早产儿的临床资料，在其出生后 2-4 周采集患儿血清使用雅培 Abbott i2000 化学发光分析仪检测血清中 TT3、TT4、TSH、FT3、FT4 激素水平，分析判断患儿甲状腺激素缺乏状况；同时按出生胎龄＜32 周、或≥32 周、及出生时体重≤1.5KG（极低体重）、或≥1.5KG 而≤2.5KG（低体重）以及性别分组，探讨出生时胎龄、体重、性别因素所致的早产儿甲状腺功能低下的患病率状况。
结果 215 例早产的低体重、极低体重患儿在本院的诊断标准中提高了接受甲状腺素替代治疗比例。在不同胎龄、体重和性别分组中，胎龄<32 周的早产儿甲状腺功能减退患病率明显高于胎龄≥32 周的早产儿（P<0.05），极低体重早产儿的甲状腺功能减退患病率明显高于低体重早产儿（P<0.05），而低体重、极低体重患儿中男婴和女婴甲状腺功能减退患病率无统计学差异。
结论 对早产儿应做甲状腺激素的普查，特别对低胎龄、极低体重早产儿的甲状腺激素更应进行重点筛查，尽早及时的干预治疗不仅可促进早产儿各器官的成熟和发育又可预防或减少呆小症及脑瘫的发病率。

PU-1542

抗磷脂酶 A2 受体抗体在膜性肾病诊断中的价值

黎村艳[1]、王人柯[2]
1. 湖南省人民医院
2. 湖南师范大学医学院

目的 探讨抗磷脂酶 A2 受体抗体（PLA2R 抗体）在膜性肾病诊断中的价值。
方法 选取湖南省人民医院 2020 年 1 月至 2020 年 12 月份膜性肾病患者 50 人（其中特发性膜性肾病 40 人，继发性膜性肾病 10 人）、其他肾病患者 20 人以及健康体检患者 20 人。分为特发性膜性肾病组（A 组）、继发性膜性肾病组（B 组）、其他肾病患者组（C 组）以及健康组（D 组）。比较各组 PLA2R 抗体表达水平以及白蛋白（ALB）、肌酐（Cr）、24h 尿蛋白定量（24h UP）水平。以及选取 A 组中的病例分析其病情不同阶段时 PLA2R 抗体表达水平及肾功能指标（CREA、ALB、24h UP）变化。

结果 A 组 PLA2R 抗体水平高于 B、C、D 组，差异具有统计学意义（P<0.05）。膜性肾病 PLA2R 抗体检测阳性率为 58.3%，特发性膜性肾病 PLA2R 抗体检测阳性率为 82.5%；A、B 组抗 PLA2R 抗体水平高于 C、D 两组，差异具有统计学意义（P<0.05）。A 组抗 PLA2R 抗体水平高于 B 组，差异具有统计学意义（P<0.05）。A 组 Cr、ALB、24h UP 水平与 B、C 组比较，差异无统计学意义（P>0.05）;D 组健康体检者 CREA、ALB 与 A、B、C 3 组比较，ALB 高于其他 3 组，CREA 低于其他 3 组，差异具有统计学意义（P<0.05）。二十四小时尿蛋白、 PLA2R 两项联合检测 ROC 曲线下面积为 0.930 大于 PLA2R 单独检测 ROC 曲线下面积 0.882。从 IMN 患者中收集到 8 例使用免疫抑制剂治疗前后 2-3 个月内病情缓解的患者，治疗前抗 PLA2R 抗体水平为 267.68（190.22，450.87），治疗后抗 PLA2R 抗体水平为 128.61（35.66,351.09），与治疗前相比有明显降低（Z=-2.197,P<0.05）。

结论 抗 PLA2R 抗体在特发性膜性肾病诊断中是一项具有较高诊断效能、可用于联合诊断的指标。

PU-1543

乙肝病毒 P 区耐药突变与患者 T 淋巴细胞表达的相关性研究

杨莉、侯军良
河北省石家庄市第五医院

目的 探讨慢性乙型肝炎患者出现 P 区耐药突变前后不同治疗方案、不同病情及不同突变位点个数 CD3+、CD4+、CD8+ T 淋巴细胞的表达量，为减缓或阻止耐药性出现寻找新的治疗靶点。

方法 选择 2015 年 10 月-2019 年 3 月就诊于石家庄市第五医院的 67 例慢性乙肝患者；在发生耐药突变前后采用流式细胞术检测患者外周血中 CD3+、CD4+、CD8+的表达量，并采用荧光定量 PCR 技术及基因测序法检测所感染的病毒分型、病毒载量及病毒基因 P 区耐药基因位点的变化。

结果 单位点与多位点突变 CD3+/CD4+/CD8+ T 淋巴细胞表达量均明显低于正常水平（P＜0.05），且多位点组有降低趋势，HBV DNA 载量有升高趋势；乙肝患者耐药突变后 CD3+、CD4+ 表达量与突变前相比均明显降低（P＜0.05），CD8+表达量无显著性差异；不同治疗方案的乙肝患者耐药突变后 CD3+、CD4+ 表达量与突变前相比降低(P＜0.05) ，CD8+表达量无显著性差异（P＞0.05）；不同病情 CD3+、CD4+ 表达量随病情加重不断降低（P＜0.05），CD8+表达量无显著性差异（P＞0.05）。

结论 突变位点增多，病毒复制变活跃，患者机体免疫功能受损加重；不同治疗方案下，CHB 患者发生耐药突变后 CD3+、CD4+ T 淋巴细胞功能均受损严重，且随病情加重，CD3+、CD4+ T 淋巴细胞的免疫功能受损加重，临床抗病毒治疗时应重点监测。

PU-1544

石家庄市 2018-2020 年 HIV 抗体筛查及确证结果分析

杨莉、刘腾飞
河北省石家庄市第五医院

目的 比较石家庄地区不同艾滋病病毒（HIV）初筛试剂的筛查阳性结果与确证试验结果的符合率；计算不同 HIV 初筛试剂的特殊阈值；对石家庄地区的 HIV 确证阳性患者进行流行病学调查。

方法 对 1596 例 HIV 初筛阳性样本的初筛检测结果与确证试验结果进行比对分析；制作不同厂家 HIV 初筛试剂的受试者工作特征曲线（ROC），根据曲线得出该试剂的特殊阈值；分析 582 例石家庄地区 HIV 确证阳性病例的基本资料。使用 SPSS 22.0 软件进行 c2 检验和 ROC 曲线的制作与特定阈值的计算。

结果 三种 HIV 初筛方法的确证阳性率有显著性差异，化学发光最低，快速检测最高。ROC 曲线显示罗氏诊断与迈瑞医疗有较好的判断准确度。石家庄地区 2018-2020 年的确证 HIV 阳性病例中，男女比例为 5.9：1；年龄以 20～59 岁（81.62%）为主；人群多分布于石家庄市区。
结论 石家庄地区的 HIV 初筛检测以化学发光法为主，使用化学发光法的罗氏诊断与迈瑞医疗这两种试剂的特定阈值能较好地鉴别出 HIV 感染者。石家庄地区 HIV 防控仍以市区为主，而文化程度较低的、从事农业或服务业的男性中青年人群是宣传 HIV 感染的相关知识及防控的重点人群，同时关于女性的防控今后也应加强重视。

PU-1545

未成熟粒细胞对 ARDS 的临床价值分析

谭超超
湖南省人民医院

目的 探讨未成熟粒细胞百分率（IG%）与急性呼吸窘迫综合症(ARDS)的关系。
资料与方法 统计学分析湖南省人民医院住院治疗 ARDS 患者共 178 例，就诊健康体检人员 51 例。利用血细胞分析仪，血气分析仪,特种蛋白分析仪所得结果收集研究数据 WBC,N%,IG%,CRP,根据柏林定义将 ARDS 患者分轻，中，重三组。使用 ROC 曲线分析评估未成熟粒细胞百分率对 ARDS 的诊断价值。
结果 对于 ARDS 患者，严重组 IG%水平明显高于轻度组(4.72 vs1.80;P＜0.05)和中度组(4.72vs2.55;P ＜0.05)，IG%的升高反映了 ARDS 的发生率和严重程度有明显的上升趋势，IG%的 ROC 曲线下面积 0.885（95%CI：0.815-0.914）明显优于 WBC0.659（95%CI：0.593-0.762）、N%0.795（95%CI：0.727-0.863）曲线下面积，IG%对诊断 ARDS 的诊断价值最大。
结论 IG%可作为急性呼吸窘迫综合征(ARDS)的一种早期生物标志物，也可用于区分 ARDS 患者的严重程度，能够促进对急性呼吸窘迫综合征(ARDS)早期高危人群的及时、有效识别。

PU-1546

乙肝原发性肝癌患者外周血中 CD4+和 CD8+T 淋巴细胞的表达研究

许怡、郭云、黄颖、赵晓霞、张海丛、杨莉
石家庄市第五医院

目的 观察乙肝并原发性肝癌患者外周血中 T 淋巴细胞亚群表达水平的变化，为临床肝癌的诊断及治疗提供理论依据。
方法 收集 167 例乙肝患者、151 例乙肝并原发性肝癌患者以及 30 例健康者抗凝血；根据病程将乙肝病毒感染者进一步分为慢性乙肝组、肝硬化组、肝癌组；根据 BCLC 分期将乙肝肝癌患者分为 A 期组、B 期组、C 期组、D 期组；根据 HBV 载量将乙肝并肝癌患者分为低复制组、中复制组、高复制组，采用流式细胞术对以上各组研究对象外周血中 CD3+、CD4+、CD8+T 淋巴细胞表达量进行检测。
结果 肝癌组患者 CD3+、CD4+、CD8+T 淋巴细胞表达量均明显低于正常水平（P＜0.05）；乙肝病毒感染者中，肝癌组 CD8+表达量明显低于肝炎组、肝硬化组（P＜0.05）；在肝癌的各期患者的 T 淋巴细胞的表达量研究中，D 期患者 CD3+、CD8+表达量较 A、B、C 期明显降低（P＜0.05）；在肝癌不同 HBV 载量患者的 T 淋巴细胞的表达量研究中，中、高复制组 CD4+表达量较低复制组明显降低（P＜0.05）。
结论 乙肝并肝癌患者 CD8+T 淋巴细胞亚群表达水平均明显降低；乙肝病毒感染导致的 CD8+T 淋巴细胞功能受损可能是 HBV 病毒感染患者易诱发肝癌的机制之一；治疗乙肝肝癌的适宜时期为 A、

B 及 C 期；在临床上，当乙肝并肝癌患者体内乙肝病毒开始复制时，应及早采取措施进行抗病毒治疗。

PU-1547

NSG1 在食管鳞状细胞癌的表达及作用机制探讨

林晓青[1]、章良铭[1]、涂铭书[1]、殷晓庆[2]、蔡丽清[1]、张松高[1]、余丽丽[1]、潘小杰[3]、黄毅[1]
1. 福建医科大学省立临床医学院
2. 福建中医药大学中西医结合学院
3. 福建省立医院胸外科

目的 神经元特异性基因家族成员 1（NSG1）是一种神经元细胞特异性表达、分子量 21KDa 的核内体蛋白，目前对 NSG1 的研究主要集中在对神经发育与调控的方面，而对其与肿瘤发生发展的相关性少见关注；我们的前期研究表明食管鳞状细胞癌（ESCC）患者体内存在针对 NSG1 的强烈体液免疫反应，为此，我们拟探讨 NSG1 在 ESCC 的表达及其相关的作用机制。
方法 通过免疫组织化学法检测 20 例 ESCC 患者癌组织和配对癌旁组织 NSG1 蛋白的表达；构建 NSG1 高表达慢病毒转染 NSG1 相对低表达的 KYSE-150 细胞，使 NSG1 过表达；将靶向 NSG1 的 siRNA 转染 NSG1 相对高表达的 TE-1 细胞，敲低 NSG1 表达。分别采用 cck8 法、划痕实验和 transwell 法、transwell 法、流式细胞术检测 NSG1 过表达/敲低 ESCC 细胞活力、细胞迁移、细胞侵袭、细胞周期的变化；western blot 法检测 NSG1 过表达/敲低 ESCC 细胞 MEK/ERK 通路 p-MEK、p-ERK 和 EMT 相关分子标志物表达水平的变化。
结果 NSG1 蛋白在 ESCC 癌组织异常高表达，而在配对癌旁组织中弱表达或不表达。与阴性对照组相比，NSG1 过表达 KYSE-150 细胞活力、侵袭、迁移能力显著增强，G0/G1 期细胞比例明显下降，S 期细胞比例明显升高，MEK/ERK 通路 p-ERK、p-MEK 水平明显升高，EMT 相关转录因子 snail、slug 与间质标志物 Vimentin 表达明显上调，上皮标记物 E-cadherin 表达明显下调；NSG1 敲低 TE-1 细胞的改变则相反。
结论 NSG1 可能在 ESCC 疾病发生发展进程中发挥潜在的致癌作用；NSG1 表达可通过激活 MEK/ERK 通路促进 ESCC 细胞的 EMT。

PU-1548

水通道蛋白 1 与小胶质细胞极化关系的研究进展

李博慧[1]、刘春梅[2]
1. 大庆市第三医院
2. 江苏省苏北人民医院

目的 水通道蛋白 1（AQP1）的主要功能是调节水的运输，它可能参与调节细胞的炎症激活。小胶质细胞是脑中的巨噬细胞，是中枢神经系统的第一道炎症免疫防线，其中，小胶质细胞的极化在神经系统炎症损伤及修复中起到中心调控的作用。本研究的目的是探讨 AQP1 在小胶质细胞中的分布及作用，并对两者关系进行综述。
方法 使用中国知网、PubMed、Embase、Web of Science 网站进行检索，关键词设置为“水通道蛋白 1”和“小胶质细胞极化”、“Aquaporin ”and“Microglia polarization”
结果 共检索出中文文章 4 篇、英文文章 35 篇。
结论 近年来，国外学者对于 AQP 在组织和细胞炎症免疫应答中的作用进行了研究。AQP1 表达降低能够使小胶质细胞从形态和功能上向 M2 型小胶质细胞极化，并且增加小胶质细胞的迁移能力。目前，国内外已有通过调节小胶质细胞的极化治疗缺血性脑卒中、阿尔兹海默病、术后认知障碍及神经胶质瘤的相关研究，而通过 AQP1 调节小胶质细胞极化的作用及机制需要进一步的研究。

PU-1549

低危人群不同梅毒筛查策略的比较

井发红
西安医学院第一附属医院

目的 通过对低危人群梅毒螺旋体不同血清学检测方法试验结果分析，探讨不同筛查策略对梅毒诊断结果的影响，为临床诊断和治疗提供可靠依据。
方法 所有患者，均采用传统筛查方案(TSA) 和逆向筛查方案(RSA)，TSA 即先采用甲苯胺红不加热血清试验（TRUST）检测梅毒螺旋体，若阳性再进行梅毒螺旋体颗粒凝集试验（TPPA）；RSA 则相反，先采用化学发光微粒子免疫分析法（CMIA）进行梅毒血清学初筛试验，阳性标本再进行 TPPA 和 TRUST 试验，CMIA 与 TPPA 结果不相符或 TPPA 弱阳性时采用梅毒螺旋体抗体吸收试验（FTA-ABS）进行验证。
结果 17604 份血清标本中，TSA 检出 148 份（0.84%）TRUST 阳性标本，其中 9 份（6.1%）TPPA 和 CMIA 均为阴性，提示存在生物学假阳性，139 份（93.9%）TPPA 和 CMIA 均为阳性，9 份（6.1%）和 CMIA 阳性而 TPPA 阴性。RSA 经 CMIA 初筛阳性 230 份(1.30%) ，CMIA S/CO 值中位数(25 分位数，75 分位数)为 7.31 (2.12，20.33)，230 份初筛阳性标本中，TPPA 复检仅 200 份(占 86.95%) 阳性，TRUST 148 份(占 64.34%) 阳性。30 份 CMIA 阳性而 TPPA 阴性的标本中，FTA-ABS 验证结果显示，IgM 类抗体均为阴性，其中 3 份标本 IgG 类抗体阳性。当 CMIA S/CO≥1 时进行 TPPA 法复检，TPPA 复检阳性者判断为梅毒感染血清学阳性时，假阴性率为 10% (3 /30) ，假阳性率为 0% 。当 S/CO 界值为 1.07 时 ROC 曲线下面积最大为 0.882。
结论 RSA 比 TSA 能检测出更多阳性血清标本，适合大规模筛查，但 CMIA 法梅毒血清学筛查存在假阳性问题，应依据 TPPA 检测结果综合分析，并确保定期复查。

PU-1550

免疫相关 LncRNA 构建风险模型预测肺腺癌患者生存预后

郭会、顾锦、陈艳
常州市第一人民医院

肺腺癌（LUAD）如今已成为严重威胁人类健康的恶性肿瘤，其 5 年生存率很低，鉴于此我们迫切需要建立新的方法来预测肺腺癌患者生存预后。而在本研究中，我们首先检索了肺腺癌患者原始转录组数据，并通过共表达分析识别免疫相关的非编码 RNA（irlncRNA），其次通过单因素分析和改良的 Lasso 回归鉴定出有效的差异表达的 irlncRNA(DEirlncRNA)对。第三，我们计算并绘制 DEirlncRNA 对的 5 年受试者工作特征曲线（ROC）下的面积（AUC），再通过计算 AIC 值识别最大拐点作为 Cut-off 值以据此建立区分高危或低危 LUAD 患者的最佳模型。最后，利用我们建立的风险模型评估了 LUAD 患者的生存率、肿瘤突变负荷、肿瘤浸润免疫细胞、抗肿瘤药物的耐药情况，以及对高风险和低风险组差异表达基因进行了基因 GO 富集分析和 KEGG 富集分析等。在我们本篇研究中，共鉴定出 28 对 DEirlncRNA，将其纳入 Cox 回归模型分析后，生存分析和和 ROC（AUC）曲线证明该风险模型具有良好的预测效果，低风险组的生存年限要明显高于高风险组。GO 富集分析表明，高风险组和低风险组差异表达基因主要参与的生物学途径为染色质分离和核分裂；主要发挥的生物学功能为细胞粘附与分子结合。KEGG 富集分析表明，高风险组和低风险组之间差异表达的基因主要参与细胞周期、病毒感染病以及钙离子信号通路。肿瘤突变负荷表明，高风险组发生基因突变的几率高于低风险组，且其肿瘤突变负荷（TMB）值也明显高于低风险组。而其他结果表明高风险组浸润的免疫细胞如 NK、CD4+T、CD8+T 降低，且具有较低的半数最大抑制浓度（IC50）。总之，通过我们根据 DEirlncRNA 对而建立的风险模型将有助于 LUAD 患者的预后预测，并为其提供个性化的治疗方案。

PU-1551

血小板计数、NT-proBNP 浓度及降钙素原水平对于血流感染预后的意义

李卫滨[1]、刘星宇[2]
1. 中国人民解放军联勤保障部队第 900 医院(原福州总医院)
2. 联勤保障部队第九〇〇医院

目的 了解血小板计数，NT-proBNP 及降钙素原三项指标对于血流感染性疾病预后的意义。
方法 统计 2016 年 4 月至 2021 年 4 月收治入院的住院患者共计 51 例血流感染患者，以初次入院检测血培养结果阳性并辅助以临床症状、体征、实验室检查等多项检查结果做为判断患者患有血流感染的初始时间。收集患者入院后第 1、3、5、7 天血小板计数、NT-proBNP 浓度及降钙素原水平数据。利用 SPSS20.0 软件进行统计学数据分析。
结果 通过对入院后第 1、3、5、7 天的血小板计数、NT-proBNP、降钙素原分析发现，随着脓毒症症状的加重，血小板下降趋势明显，呈现负相关性；NT-proBNP，降钙素原上升趋势明显，呈现正相关性。随着病程时间的延长，脓毒症死亡患者的血小板水平逐渐减低，而好转患者的血小板水平逐渐回升并有趋于正常值的趋势；同时脓毒症死亡患者的 NT-proBNP 浓度及降钙素原水平始终保持较高水平并有上升趋势，而好转患者的 NT-proBNP 浓度及降钙素原水平不断下降并有趋于正常值的趋势。
结论 血小板计数，NT-proBNP 及降钙素原三项指标可做为临床辅助诊断脓毒症病情严重程度及判断预后疗效的有效指标。

PU-1552

C60@PCN-224 长程有序体系的构建及其光电性能研究

孙倩[1]、杨二利[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学附属中大医院临床检验医学中心
3. 东南大学江苏省重症医学重点实验室

近年来，C_{60} 材料因具有优异的吸电子特性和离域共轭结构而受到研究者们的广泛关注。然而，单一的电子受体特性限制了其在光电领域的应用，构建系统的电子供-受体系对其具有重要意义。金属-有机框架（MOF）具有丰富可调的有机配体、规则的多孔结构和较高的比表面积，不仅可以用于封装小分子材料从而构成主体-客体纳米复合物并且电子性质灵活可控。因此，我们将 C_{60} 与电子互补的卟啉基金属-有机框架（PCN-224）通过 π-π 相互作用进行非共价偶联，形成一个长程有序 C_{60}@PCN-224 供体受体系统，该系统的光电流表现相较于单组分提高了 10 倍左右。C_{60}@PCN-224 供体受体系统具有如此优异的光电性能主要是因为 C_{60} 与 PCN-224 卟啉配体之间的长程有序 D-A 相互作用可以加快光致电子转移和抑制光生载流子的快速复合，实现光生载流子的有效分离，大大提升光捕获效率。本工作为具有较高光电转换效率的 C_{60} 基光电电极的发展提供了一条新的思路。

PU-1553

基于 MOF-Nb 的光电化学免疫传感及其在人附睾蛋白 4 检测中的应用研究

孙倩[1]、沈艳飞[1,2,3]
1. 东南大学医学院
2. 东南大学附属中大医院临床检验医学中心
3. 东南大学江苏省重症医学重点实验室

卵巢癌的早期诊断困难是其致死率居高不下的主要原因之一。人附睾蛋白 4（HE4）被认为是一种新的卵巢癌血清生物标志物。因此，对 HE4 的高效灵敏检测在卵巢癌早期诊断中具有至关重要的意义。金属-有机框架（MOF）作为一种新兴的功能材料，具有高度有序的多孔结构和较大的比表面积，已广泛应用于生物传感领域。然而，这一类材料在光电化学（PEC）生物分析领域的系统研究相对较少，尤其是构建 MOF 基光敏元件用于 PEC 免疫传感器的工作，亟待进一步探究。基于以上背景，我们合成了以羧基官能化卟啉为配体的 MOF 纳米球（nPCN-224）并以此为 PEC 探针，成功构建出用于 HE4 检测的“signal-on”型 PEC 免疫传感器。此外，借助纳米抗体与 nPCN-224 的耦合作用，使用纳米抗体作为识别单元进一步提高了免疫传感器的灵敏度。该传感器可实现 1.00 pg·mL^{-1} 到 10.0 ng·mL^{-1} 的较宽范围的灵敏检测，检测限低至 0.560 pg·mL^{-1}，优于以往报道的大多数方法。更重要的是，该传感器通过检测血清中 HE4 的含量可以对不同患病阶段的卵巢癌患者及健康人群实现有效区分。本工作将为构建具有高灵敏度和准确性的光电化学免疫传感器用于临床诊断和临床疗效评估开辟一条新途径。

PU-1554

甲状腺功能与 2 型糖尿病肾病患者临床分期的关联性研究

李汉秋、冯奕习
东莞市中医院

目的 探讨糖尿病肾病患者的甲状腺功能。
方法 本回顾性病例对照研究选取 2021 年 1 月至 2021 年 2 月的研究对象。25 名健康志愿者、25 名单纯 T2DM 患者和 50 名糖尿病肾病患者纳入本研究。测量研究对象的身高、体重、血压以及实验室的生物标志物如肾功能、甲状腺功能和糖化血红蛋白等指标。
结果 与单纯糖尿病患者相比，糖尿病肾病患者促甲状腺激素 (TSH) 水平更高，游离三碘甲状腺原氨酸 (FT3) 水平更低 (P 值均<0.05)。 Spearman 相关分析显示 TSH 与血清肌酐（r = 0.37，P= 0.004）、尿白蛋白肌酐比（r = 0.36，P= 0.011）；FT3 与估算的肾小球滤过率（eGFR）（r = 0.56，P < 0.001）均呈正相关关系，其差异具有统计学意义。
结论 在糖尿病肾病患者中可观察到高水平的 TSH 和低水平的 FT3。 未来需要前瞻性研究来证实亚临床甲状腺功能减退症与糖尿病肾病之间的关联。

PU-1555

RA-CP 诊断类风湿性关节炎的临床意义

廖军
广州市第一人民医院

目的 探究全新类风湿性关节炎诊断标志物（RA-CP）对于类风湿性关节炎（RA）诊断的临床意义。
方法 现收集广州市第一人民医院 2020 年 9 月至 2021 年 3 月风湿免疫科住院患者和风湿免疫门诊

病人共 158 例，分成两组（RA 组 72 例，非 RA 组 87 例），采用双抗体夹心酶联免疫吸附（ELISA）法检测 RA-CP，并检测类风湿因子（RF）、C 反应蛋白（CRP）和抗环瓜氨酸肽（CCP）抗体。
结果 RA-CP 的灵敏度和阴性预测值（77.78%、81.82%）均高于抗 CCP 抗体（61.11%、73.08%）和 RF（68.06%、 81.11%），特异度和阳性预测值分别为 82.76%、78.87%。RA-CP 的诊断准确度为 80.50%。RA-CP 可检出抗 CCP 抗体（-）或 RF（-）的 RA 患者，阳性率分别为 60.71%、43.49%。11 例抗 CCP 抗体和 RF 双阴性的 RA 患者中有 3 例 RA-CP 阳性。
结论 RA-CP 是一类瓜氨酸化蛋白，用于诊断 RA 的全新抗原类标志物，较其他用于诊断 RA 的抗体如抗 CCP、RF 等具有更高的诊断效能。RA-CP 能够较好地鉴别诊断 RA 。

PU-1556

免疫比浊法检测尿液 λ 轻链的功能灵敏度建立

刘政
吉林大学第一医院

目的 应用 Bio Systems BA400 检测平台，对免疫比浊法尿液 λ 轻链检测的功能灵敏度进行建立和评估。
方法 参考美国临床实验室标准委员会(NCCLS)发布的 EP17-A 文件，对 Bio Systems BA400 检测平台测定尿液 λ 轻链的空白样本和一系列低水平样本，确定该方法的空白限(LOB)、生物检测限（BLD）和功能灵敏度(FS)。
结果 Bio Systems BA400 检测平台检测出的尿液 λ 轻链的 LOB 为 6.725mg/L，BLD 为 15.985 mg/L，FS 为 16.46 mg/L。
结论 实验室应建立本实验室的空白限、生物检测限和功能灵敏度。对于低浓度尿液 λ 轻链检测结果评价具有重要的临床意义。

PU-1557

基于局域表面等离子体共振的金纳米棒在肺癌诊断中的应用研究

陈轶
中南大学湘雅三医院医学检验系

目的 免疫组化是临床上常用的对组织细胞内蛋白质或者多肽进行定位、定性检测技术，但其操作繁琐费时费力。本课题基于金纳米棒其局部等离子共振（LSPR）特性具有的较高的光吸收和散射能力，拟制备不同波长的金纳米棒，选取光信号值最佳的偶连特异性抗体，原位检测组织细胞中抗原，建立一种简单、快速和价廉的方法。
方法 （1）选取氯金酸为原料，通过硫化钠终止法制备具有不同 LSPR 波长的金纳米棒，确定可用于偏光显微镜成像的最佳材料；然后通过巯基十一烷酸修饰金纳米棒，利用 EDC/NHS 活化羧基后加入 RAD21 抗体制备抗体-金纳米棒复合物（2）比较抗体-金纳米棒对 A549 肺癌细胞和其他癌细胞的特异性识别能力，进一步检测抗体-金纳米棒对宫颈癌、乳腺癌、结肠癌、胃癌、肺癌组织切片的检出效果（3）收集临床肺癌病理组织切片 18 例，采用免疫组化和抗体-金纳米棒同时检测比较两者检测效果。
结果 成功制备了 LSPR 在 600-800nm 范围的金纳米棒，在偏光显微镜下发现 LSPR 处于 650nm 处时，金纳米棒的长度 88.2 nm，宽度 37.8 nm 呈现出最强的光学信号。RAD21 抗体-金纳米棒溶液与不同细胞孵育后，在偏光显微镜下观察发现 A549 肺癌细胞呈现高亮红色，而其他细胞没有变化。此外，我们将抗体-金纳米棒用于多种癌组织切片的检测发现，宫颈癌、乳腺癌、结肠癌、胃

癌组织切片在偏光下均没有明显信号，而肺癌组织切片呈现明显的红色。通过对 18 例临床肺癌标本检测发现，抗体-金纳米棒的检出效果和免疫组化一致，差异无统计学意义。
结论 本研究通过硫化钠终止生长反应法实现了金纳米棒 LSPR 的准确调控，得到了偏光成像效果最佳的金纳米棒。将金纳米棒与肺癌抗体 RAD21 偶联后，可用于肺癌细胞和肺癌组织病理切片的有效识别诊断。本文中开发的检测方法是在医学检测诊断中探索的一种新思路，比传统的免疫组化检测操作简单、耗费时间更短，所需成本更低。

PU-1558

免疫荧光法在上呼吸道感染微生物快速检验中的应用分析

王成浩
安徽医科大学第二附属医院

目的 探讨分析免疫荧光法在上呼吸道感染微生物快速检验中的应用效果。
方法 选取我院在 2019 年 5 月-2020 年 5 月确诊并治疗的 220 例上呼吸道感染患儿，采集所有患儿的分泌物样本，并使用免疫荧光法来进行微生物快速检测。观察所有患儿的病毒抗原阳性情况及病毒类型分布；观察阳性患儿在不同年龄段当中的分布情况。
结果 所有 220 例患儿当中，共检测出 190 例（86.4%）病毒抗原阳性。其中，呼吸道合胞病毒：110 例，流感病毒 A 型：22 例，腺病毒：32 例，3 型副流感病毒：10 例，2 型副流感病毒：4 例，B 型流感病毒：4 例，混合型：8 例。不同年龄段患儿占比之间差异显著（P＜0.05），其中阳性占比最高的为 1 个月~6 个月。
结论 在临床微生物快速检验当中免疫荧光法不断完善，且持续跟临当中的其他相关先进技术互相结合，其优点为快捷、高效，可以在给予上呼吸道感染进行微生物检测时广泛性的应用。

PU-1559

两种方法检测乙肝表面抗原结果对比分析

齐莹莹
吉林金域医学检验所有限公司

目的 人感染乙肝病毒后，血液内常有大量的表面抗原剩余下来，形成表面抗原血症。目前最常用的、便捷快速检测乙肝表面抗原方法为胶体金法和酶联免疫法。本文通过酶联免疫法和胶体金法两种方法的检测对乙肝病毒表面抗原的检测结果进行对比，为临床提供参考依据。
方法 选取本实验室 2021 年 1 月～2021 年 5 月收取的血液标本 500 例，分别使用胶体金法与酶联免疫法对标本进行乙肝病毒表面抗原进行检测，并对其结果进行对比分析，比较酶联免疫法和胶体金法检测乙肝表面抗原的阳性率。
结果 其中酶联免疫法检测乙肝表面抗原的阳性率为 17.90%，胶体金法检测乙肝表面抗原的阳性率为 16.40%。两种方法的检测结果相比较没有明显的差异（P>0.05）。
结论 酶联免疫法和胶体金法对乙肝表面抗原均有比较高的阳性检测率,两种方法都是检测乙肝表面抗原的比较可靠的方法。其中胶体金法检测方法具有简便、直观、方便携带、结果更加快捷等特点,并且不需要特殊的仪器设备,适用于紧急状态下患者的检测或者感染者初筛等情况。酶联免疫法具有更高的敏感度,仍然是现今检测乙肝表面抗原的主要方法,适合于对少数胶体金法检测结果呈阳性的患者进行再次筛检,从而很大程度的提高检测结果的准确率。乙肝表面抗原本身不是完整的乙肝病毒，而是乙肝病毒的外壳，它本身没有传染性但有抗原性，它只是乙肝病毒感染的标志之一。它可以表示过去感染过乙肝病毒，或者目前正在受到乙肝病毒的感染。因此，加强对乙肝病毒表面抗原的检测，对于保护自己和身边人的健康有着十分重要的意义。

PU-1560

急性心衰患者心衰标志物检测及预后相关性的研究

刘航
山东第一医科大学第一附属医院

目的 通过对急性心衰患者血清及血浆中心衰标志物的检查筛选对患者预后及心衰等级相关的指标，指导临床对急性心衰患者的诊断及治疗。
方法 建立急性心衰筛选标准，对急性心力衰竭患者测定其外周血 NT-proBNP 、心梗三联、cTnT、心肌酶谱等其他相关心功能参数及患者治疗前后结果的改变对患者的治疗及预后进行评估。
结果 1、NT-proBNP 、心梗三联、cTnT 与患者病情呈正相关；2、NT-proBNP 、心梗三联、cTnT 与心功能有密切相关。3、急性期患者心肌酶谱有改变，但相关性较 NT-proBNP 、心梗三联、cTnT 弱。
结论 1、急性心衰患者的预后与 NT-proBNP 、心梗三联、cTnT 有密切相关性；2、心肌酶谱早期的改变程度与患者预后密切相关。

PU-1561

一例新冠疫苗接种后 TPPA 检测梅毒抗体结果分析

李齐光
清远市人民医院

患者女，24 岁，入职体检，行梅毒螺旋体颗粒凝集试验（TPPA）检测梅毒抗体，结果为“颗粒光滑集聚覆盖孔底，周围有一明显颗粒环”，报告为“阳性”。7 天后前往本院皮肤科就诊，行梅毒特异性抗体化学发光微粒子免疫测定（CMIA）和甲苯胺红不加热血清试验（TRUST）,结果均为阴性。10 天后前往本院体检中心进行 TPPA 复检，结果为“颗粒沉集孔底，中央形成一小点”，判断为“可疑阳性”。鉴于该患者在本院用 2 种不同方法检测梅毒特异性抗体结果的不一致，我们将该患者在本院检查的 3 次血标本送往广东省中医院进行 TPPA 检测，同时在省中医也对该患者再次抽血进行了梅毒相关指标的检测，最终省中医的 TPPA 复测结果与我院的检测结果完全一致，即 TPPA 检测结果凝集中心环随时间推移呈逐渐缩小趋势，而该患者三次不同时间血样新型冠状病毒特异性抗体 IgG 浓度随时间先后其浓度逐渐降低，故我们认为该患者的首次 TPPA 检测梅毒抗体结果为假阳性，且与新冠疫苗接种有关。

PU-1562

精子相关抗原 SPAG9 在肿瘤中的作用机制研究进展

黄强
郴州市第一人民医院

精子相关抗原 SPAG9 是近年新发现的癌睾丸抗原，是 JNK 相互作用蛋白（JIP）家族的新成员。SPAG9 主要表达于人类正常睾丸组织中，研究发现，在肿瘤形成过程中，SPAG9 可异常表达于多种癌组织，并且与肿瘤的发生发展存在密切联系，有望成为潜在的肿瘤标志物和治疗靶点。本文通过对 SPAG9 简要介绍，重点综述 SPAG9 促进肿瘤发生发展的作用机制，为临床诊断和治疗提供新思路。

PU-1563

血清封闭孵育时间对免疫组化染色结果的影响

李志春、刘静、任娟丽、段孟真、吴雨珊
新疆金域医学检验所有限公司

目的 对于免疫组化的每一个步骤以及环节，都会影响到染色的最终后果。本文探讨血清封闭孵育时间长短对免疫组化染色结果的影响，以便分析影响免疫组化染色质量的因素之一,总结提高染色质量的方法。
方法 收集 2021 年 3-5 月送检至新疆金域医学检验所有限公司的手术切除的乳腺癌、肠癌、胃癌、宫颈癌等组织标本共计 210 例，对其中存在明显病变问题的 90 例患者标本进行免疫组化染色。选取常用的正常山羊血清，选用抗体 CK、CK7、CK20、Villin、CK19、CDX2、CEA、HER2、P63、TTF-1 、EMA、P53、LCA、Ki67、p16、MLH1、MSH2、MSH6、PMS2、ER、PR 等试剂盒，对每种组织抗体分别采用 6 分钟、8 分钟、10 分钟、12 分钟以及 15 分钟的孵育时间，按照试剂盒说明书步骤进行染色，DAB 显色，苏木精衬染，中性树胶封固，最后镜检。比较不同的血清封闭孵育时间长短对病变组织免疫组化染色结果的影响。
结果 血清封闭孵育时间的长短对免疫组化染色结果影响较大，其中血清封闭孵育时间≤10 分钟的染色结果较差，血清封闭孵育时间≥10 分钟的染色结果明显较好，孵育 12min 时候染色效果最佳，细胞核 DAB 着色鲜艳，背景清晰，极少出现非特异性背景染色和假阳性反应。
结论 本文通过对临床几种常用抗体在不同的血清封闭孵育时间对免疫组化染色下的表达进行研究表明，血清封闭孵育≥10 分钟的染色结果明显较好。本实验研究血清封闭孵育时间对染色效果的影响进行了较详细、客观的观察分析，对于免疫组化染色效果的好坏，提出了主要的应对措施以及科学合理的建议，供病理同行们在工作中参考。关键字：免疫组化 染色时间 染色效果

PU-1564

新疆喀什地区维吾尔族静脉血栓栓塞症形成的危险因素分析

邝辉、米日姑·依沙木丁、迪力夏提·依明、张媛、努尔比耶·普拉提、麦迪娜·阿迪力、依明江·塞帕尔、尚娟、阿迪莱·买买提明
喀什地区第二人民医院

目的 探讨新疆喀什地区维吾尔族静脉血栓栓塞症（VTE）形成的危险因素及实验室指标变化特点。
方法 回顾性分析维吾尔族 142 例静脉血栓组和 100 例健康对照组的临床资料及实验室指标，对可能导致 VTE 形成的相关因素从年龄、合并症、肿瘤、BMI（kg/m2）指数、凝血四项、D 二聚体（D-D）、同型半胱氨酸(Hcy)、脂蛋白 Lp（a）的数据进行比较，并对其相关因素进行 Logistic 多元回归分析，确定喀什地区维吾尔族 VTE 形成的危险因素。
结果 单因素分析显示，年龄＞50 岁、有肿瘤、有合并症、凝血四项至少 2 项以上异常、D-D＞0.55mg/L、Hcy＞15μmol/L 是维吾尔族 VTE 形成的危险因素(P＜0.05)。多元回归分析显示，年龄＞50 岁(OR= 1.025)、有合并症(OR= 2.354) 、有肿瘤 (OR= 2.436)、D-D＞0.55 mg /L（OR= 0.574）、Hcy＞15μumol/L（OR=1.673）是维吾尔族 VTE 形成的独立危险因素(P＜0.05)。
结论 喀什地区维吾尔族 VTE 形成的危险因素与患者年龄、有肿瘤和合并症、凝血四项异常、D-D＞0.55mg/L 有密切相关性，与 Hcy＞15μmol/L 有相关性，而与 BMI＞28kg/m2 和 Lp（a）＞300mg/L 无相关性。

PU-1565

孕前优生检测对孕前优生保健及婴儿出生缺陷的预防作用

黄肖孝、蒋丽华、戴钰
柳州市妇幼保健院

目的 分析柳州市自愿进行孕前优生检查患者的各项孕前优生检测实验室结果,探讨免费孕前优生检测项目对孕前优生保健及婴儿出生缺陷的预防作用。

方法 回顾性分析 2018-2020 年柳州市自愿接受国家免费孕前优生健康检查的育龄夫妇的实验室检查数据,进行孕前优生检查的妊娠风险评估。男女双方共同享有的免费孕前检测项目包括：血、尿常规,肝肾功能,乙肝两对半(HbsAg、HbsAb、HbeAg、HbeAb、HBcAb)、人类免疫缺陷病毒（HIV），梅毒；女方单独检查项目为孕前优生检测(风疹病毒 IgG、巨细胞病毒 IgG/IgM 及弓形体 IgG/IgM)、促甲状腺激素(TSH)、血糖及分泌物检查(白带常规、淋球菌、沙眼衣原体)。其中梅毒检测采用的是梅毒甲苯胺红不加热实验检测（TRUST）、乙肝两对半、HIV 及孕前优生检测采用酶联免疫吸附试验(ELISA)法；TSH 检测采用电化学发光法,参考范围根据试剂说明书的范围。肝功能检测(谷丙转氨酶)、肾功能检测(肌酐)及空腹血糖测定使用全自动生化分析仪日立 7600,谷丙转氨酶和肌酐检测结果需结合病史,排除干扰因素,若对象复检或其他相关检查均提示异常,则可判为肝肾功能异常；血常规使用全自动血液分析仪检测。检测方法和结果判定均符合《孕前及孕期优生筛查手册》，要求进行一切实验做好质量控制。

结果 得出 HIV,梅毒及乙肝大、小三阳的患病率、好发人群及男女患病比例情况；得出不同年份的各项孕前优生的发病情况；得出育龄妇女患病情况与血色素的相关性。

结论 孕前进行孕前优生健康检查可为不良妊娠结局的预防及干预、提高本市整体出生人口的素质提供理论依据。

PU-1566

不孕患者数睡眠质量对卵巢功能的影响

黄肖孝、戴钰、蒋丽华
柳州市妇幼保健院

目的 了解不孕患者的睡眠质量、婚姻情况及工作环境等因素与其卵巢储备功能指标的相关性，为患者提供有效的个性化治疗方案，达到提高体外受精-胚胎移植的成功率。

方法 采用 2020 年 1 月至 2020 年 12 月在本院行体外受精-胚胎移植(IVF-ET)治疗的不孕患者作为研究对象，根据患者获卵数分成三个组，低反应组（<5 个），正常反应组（5-15 个）和高反应组（>15 个）。实验室检测各组患者血清抗苗勒氏激素(AMH)水平，同时超声测量双侧卵巢内基础窦状卵泡数(AFC)，采用化学免疫发光法检测测患者月经 2-4 天的基础卵泡刺激素(FSH)、黄体生成素(LH)及雌二醇(E2)。经得研究对象的同意后，由专业的调查人员对研究对象进行睡眠质量、婚姻情况及工作环境等的问卷调查。采用 t 检验比较 3 组间各个观察指标的差异；。制定受试者的工作特征（ROC）曲线，以 Youden 指数最大点作为指标的最佳截断值（cut-off 值）。采用 Spearman 相关分析法分析睡眠质量、婚姻情况及工作环境等相关指标与 AMH、AFC、FSH、LH、E2 等卵巢功能指标的相关性。P＜0.05 为差异具有统计学意义。

结果 得出 AMH、AFC、FSH、LH、E2 水平能反映卵巢储备功能并可评估卵巢的反应性；可得出 AMH、AFC、FSH、LH、E2 预测卵巢反应性的程度；得出各项指标得出睡眠质量、婚姻情况及工作环境等相关指标会影响不孕患者的卵巢储备功能指标的分泌水平。

结论 可通过改善患者的睡眠质量、婚姻状况及工作环境提高患者的卵巢储备功能，提高 IVF-ET 的妊娠率，为人类生殖健康事业做贡献。

PU-1567

幽门螺旋杆菌分型在消化系统疾病中的比例分析和临床意义

李一凡、罗迪贤、龚慧、胡庆林、费繁荣
华中科技大学协和深圳医院

目的 了解我院检测幽门螺杆菌(H.pylori)抗体 cagA、vacA 和 iceA 基因亚型分型项目患者的临床诊断类型，并探讨各基因亚型与胃十二指肠疾病类型之间的关系。
方法 对临床患者血清样本幽门螺旋杆菌 CagA, VacA, UreB, UreA IgG 抗体进行检测，并对数据进行统计学分析。
结果 通过统计体检组、慢性胃炎组、胃溃疡组、消化道出血组、十二指肠溃疡组等组别血清标本中幽门螺旋杆菌 IgG 抗体的表达情况，结果显示十二指肠溃疡患者 HP 的 I 型(CagA、VacA)阳性率达 72%，II 型阳性率 21%。慢性胃炎和侵袭性损害（包括十二指肠溃疡、消化道出血、胃溃疡）HP 感染 IgG 抗体偏高，其中以侵袭性损害（十二指肠溃疡、消化道出血、胃溃疡）感染率为最高。胃十二指肠疾病人群男性明显多于女性，临床消化道出血患者占据近一半的比例。I 型(CagA)主要出现在上消化道出血、消化道出血的临床诊断患者中。十二指肠溃疡患者多数为 I 型(CagA、VacA)阳性。通过统计体检组、慢性胃炎组、胃-十二指肠侵袭性损害组(该组合并了胃溃疡组、消化道出血组、十二指肠溃疡组三组患者)等组别血清标本中幽门螺旋杆菌 IgG 抗体的表达情况，结果显示胃-十二指肠侵袭性损害组患者 HP 的 I 型(CagA、VacA)阳性率达 72%，II 型阳性率 21%。
结论 本研究显示，深圳地区各种炎症和出血性消化系统疾病中 HP 感染的比例比对照组高，其免疫分型在在不同年龄和性别中有一定差异。本研究将有助于了解深圳地区幽门螺旋杆菌感染感染率和分型情况，为幽门螺旋杆菌的流行病学研究和防治提供依据。

PU-1568

血蓝蛋白对体外培养 T 细胞的影响

陈聪
南华大学附属第一医院检验科

背景 庆大霉素是一种广谱抗生素广泛用于 T 细胞体外培养，但前期研究表明，庆大霉素显著影响 T 细胞活性。此外，课题组研究证实凡纳滨对虾(L. vannamei)血蓝蛋白具有光谱抗菌性。
目的 探索血蓝蛋白对体外培养 T 细胞活性的影响。
方法 本项目选用 0.05、0.1、0.2μg/ml 三个血蓝蛋白浓度梯度，通过光学显微镜和细胞计数仪分析 T 细胞数量，采用流式细胞技术分析 T 细胞亚型及细胞周期，运用 MTT 实验分析血蓝蛋白对 HepG2 细胞毒性。
结果 相比其他两个血蓝蛋白浓度，细胞计数分析发现，0.2μg/ml 血蓝蛋白显著提高 T 细胞数量；流式细胞分析发现，0.2μg/ml 血蓝蛋白显著上调 CD3 + CD4 +和 CD4+CD25+ T 细胞，且显著下调 G0/G1 期 T 细胞；MTT 分析表明，0.2μg/ml 血蓝蛋白处理显著增加 T 细胞对 HepG2 细胞的细胞毒性。
结论 0.2μg/ml 血蓝蛋白能增加 T 细胞的增殖活性和细胞毒性，此结果说明血蓝蛋白可作为 T 细胞体外培养的潜在抗生素替代品。

PU-1569

YY1 regulated by miR-124-3p promotes Th17 cell pathogenicity through interacting with T-bet in rheumatoid arthritis

Jinpiao Lin、Qishui Ou
the First Affiliated Hospital of Fujian Medical University

Th17 cells are key players in rheumatoid arthritis (RA). Our previous studies have revealed that transcription factor YY1 played an important role in the pathogenesis of RA. However, whether YY1 has any role in Th17 cell pathogenicity and the regulatory mechanism of YY1 in RA remain unclear. Here, we found the proportion of pathogenic Th17 (pTh17) cells was significantly higher in RA than that in osteoarthritis (OA) and health controls. YY1 expression was increased in pTh17, and the pTh17 differentiation was hampered by YY1 knockdown. Mechanistically, YY1 could bind to the promoter region of transcription factor T-bet and interact with T-bet protein to positively regulate the pathogenicity of Th17 cells. Moreover, we found that miR-124-3p negatively correlated with YY1 in RA patients, and it could bind to 3'-UTR regions of YY1 to inhibit the posttranscriptional translation of YY1. Furthermore, knockdown of YY1 decreased the proportion of pTh17 cells and attenuated joint inflammation in CIA mice. These findings indicate that YY1 regulated by miR-124-3p promotes Th17 cell pathogenicity in part through interacting with T-bet, which present promising therapeutic targets in RA.

PU-1570

新疆地区某三级医院妊娠期甲状腺激素水平参考范围的考察及差异性分析

单蕾、李晟彬、刘洁、刘伊宁、吴雄
新疆维吾尔自治区第三人民医院

目的 根据 2019 年由中华医学会内分泌分会和中华医学会围产医学分会联合发布《妊娠和产后甲状腺疾病诊治指南》（第 2 版）的要求，考察本单位检测系统妊娠期（早、中、晚期）特异的血清甲状腺功能指标参考范围，比较不同年龄阶段孕早、中、晚期女性甲状腺激素水平，为妊娠期健康监护提供理论依据。

方法 回顾性分析 2018 年 6 月至 2020 年 6 月本院正常妊娠期女性的甲状腺水平，分析比较不同孕期、不同年龄阶段女性甲状腺水平。

结果 孕早、中、晚期的 FT3 参考范围为 4.45(3.38-5.67)pmol/L、4.08 (3.26-5.308) pmol/L、3.94(3.242-5.012) pmol/L；孕早、中、晚期的 FT415.46 (12.494-20.815) pmol/L、13.66(12.071-18.842)pmol/L、13.27(12.062-16.541)pmol/L；孕早、中、晚期的 TSH 参考范围为 2.14(0.485-3.971) mIU/L、2.11(0.523-3.941)mIU/L 和 2.12(0.611-3.961)mIU/L；TPO 全阶段孕期 TPOAb 参考范围为 2.46(5.562-30.182) IU/Ml。

结论 不同孕期女性的 FT3、FT4、TSH 水平具有显著性差异（P<0.05）,TPO 水平无显著性差异（P>0.05）,不同孕期女性的 FT4 水平分别在四组年龄阶段中（≤25 岁、>25-30 岁、>30-35 岁、>35 岁）均具有显著性差异（P<0.05）。本研究通过对不同年龄阶段的孕早、中、晚期女性甲状腺激素水平的分析发现，孕妇 FT4 在不同年龄阶段存在显著差异，并且在孕早期随着年龄增长，呈逐渐下降的趋势，而在各年龄阶段 FT3、TSH 无明显差异。这可能提示 FT4 在不同年龄阶段孕妇中反馈性抑制更明显，水平波动更大，孕期应加强监测 FT4 水平。

PU-1571

小细胞肺癌患者肺泡灌洗液中 IL-10+CD206+CD14+ m2 样巨噬细胞增多

胡欣彤[1]、谷月[1]、赵崧辰[2]、华树成[1]、姜艳芳[1]
1. 吉林大学第一医院
2. 同济大学

The differences of macrophage distribution and its associated function between SCLC and NSCLC are not fully investigated. Our study showed that the frequency of CD14+, CD206+CD14+ and IL-10+CD206+CD14+M2-like macrophages were significantly increased, with simultaneously elevated IL-10 in BALF of SCLC patients, as compared to those in BALF of NSCLC patients. The increased frequency of IL-10+CD206+CD14+M2-like macrophages and elevated level of IL-10 in BALF of SCLC patients were positively correlated with advanced tumor stage, but negatively correlated with their survival time. Increased IL-10+CD206+CD14+M2-like macrophages were an important feature of SCLC, rather than NSCLC, and it is associated with development of SCLC.

PU-1572

淋巴细胞亚群检验项目自动审核系统的建立及应用

石珏、王盼、张子宁
中国医科大学附属第一医院

目的 建立淋巴细胞亚群检验项目自动审核系统，通过审核流程的标准化与智能化，提高检验结果的准确性和工作效率，为临床诊断和治疗提供更多参考。
方法 收集 2018 年 1 月至 2020 年 8 月 80427 份淋巴细胞亚群检测结果用于建立限值规则，其中有 15000 份来自艾滋病（AIDS）门诊的结果，用于单独设置该门诊检验结果的限值规则。对 2020 年 9 月至 2021 年 3 月中 13975 份结果进行验证，通过对比人工审核与自动审核，验证自动审核系统的有效性。
结果 对 2020 年 9 月至 2021 年 1 月淋巴细胞亚群检测结果进行历史结果验证，自动审核通过率为 70.24%（7000/9966）。通过优化规则后，2021 年 2 月至 3 月在线验证，自动审核通过率提高到 72.69%（2914/4009），其中有 11 个真阳性样本，2703 个真阴性样本，1295 个假阳性样本和 0 个假阴性样本。样本周转时间从 228 分钟减少到 167 分钟。总结了处理触犯自动审核规则结果的指南，基于这些指南，有助于检验人员发现异常淋巴细胞亚群的存在，为临床提供更多诊断信息。
结论 基于流式细胞术检测的淋巴细胞亚群项目，人工操作步骤较多且复杂，应不断完善、优化及验证其自动审核系统，以提高工作效率及报告的准确性，为临床提供更过参考信息。

PU-1573

铁皮石斛多糖对砷中毒大鼠肝损伤的干预作用及氧化应激机制研究

李亚山、李德璇、杜波、张贝基、李虹娟、胡杨丽、赵隽
云南省第三人民医院

目的 观察无急性中毒剂量的砷所造成的 SD 大鼠肝损伤，探讨铁皮石斛多糖对肝氧化损伤的保护作用机制。

方法 在前期建立动物模型的实验数据和文献报道的基础上，进行如下分组:将 50 只健康雄性 SD 大鼠随机分为 5 组，每组 10 只，即正常对照组，每日只饮纯水;砷暴露组，每日饮含亚砷酸钠(NaAsO2)30mg/L 的水溶液; 铁皮石斛多糖干预组（1～3 组），分别以 150mg/kg，300mg/kg.d，450mg/kg.d 的剂量每日灌胃。4 个月实验期结束，末次染毒后次日，大鼠称重，然后乙醚麻醉，抽取心脏血，制备血清样本，检测谷丙转氨酶(ALT)、谷草转氨酶(AST)和白蛋白的活性，作肝功能分析;切除肝脏，计算肝脏系数，肝组织切片染色，观察肝组织细胞形态；制备肝组织匀浆样本，检测谷胱甘肽(GSH)、谷胱甘肽过氧化物酶(GSH-Px)、超氧化物歧化酶(SOD)的活性、检测组织 ROS 的水平以及脂质过氧化水平。采用统计软件 SPSS12.0，对所得数据采用单因素方差分析，各组间的比较采用 SNK-q 检验，检验水准定为 0.05。

结果 与对照组相比，砷暴露组的肝脏系数升高(q=19.53，P＜0.05);ALT 和 AST 水平升高，白蛋白水平降低（q 值分别为 39.56，26.23，13.16，P 均＜0.05），肝功能明显受损;GSH、SOD 和 GSH-Px 的活性降低（q 值分别为 86.74，72.55，36.68，P 均＜0.05），组织中 ROS 与 MDA 水平升高（q 值分别为 38.26，49.54，P 均＜0.05）;而与砷暴露组相比，铁皮石斛多糖联合干预组的各项指标包括肝组织细胞结构均得到明显改善。

结论 (1)慢性砷暴露可以促使肝脏中 ROS 和脂质过氧化产物的增多以及抗氧化酶活性的减弱，致氧化性应激反应增强而引起肝损伤。(2)铁皮石斛多糖可改善慢性砷暴露所引起的大鼠的氧化应激及肝损伤。

PU-1574

自身免疫性疾病患者外周血淋巴细胞亚群表达的临床分析

王莹
吉林大学第二医院

目的 检测自身免疫性疾病（AID）患者外周血的淋巴细胞亚群的表达，探讨 AID 患者外周血淋巴细胞亚群的变化；并分析这种变化与补体 C3、C4 和血沉(ESR)的相关性。

方法 采用流式细胞术分析 72 例 AID 患者及 35 例健康人外周血中淋巴细胞亚群的表达，及 AID 患者外周血 C3、C4 和 ESR 的水平，检测 AID 患者外周血中淋巴细胞亚群的改变，并分析相关参数与补体 C3、C4 和 ESR 的相关性。统计学采用 SPSS16.0 统计软件进行分析，显著性检验标准为 P 值<0.05。

结果 AID 组 CD3+（%）、CD3+CD4+、CD4+/CD8+ 、CD56+和 DNT（%）均明显低于健康对照（Control）组（P<0.05）， CD3+CD8+占淋巴细胞比率（%）高于 Control 组（P<0.05）。系统性红斑狼疮（SLE）组、ANCA 相关性血管炎（AAV）组和干燥综合征（SS）组 CD4+/CD8+比率和 DNT（%）均明显低于 Control 组，有显著性差异（P<0.01）, AAV 组、SLE 组和 SS 组外周血 CD4+ /CD8+比值分别与血清 C3 之间存在明显正相关（r=0.832, P<0.01; r=0.599, P<0.01; r=0.749, P<0.01）；与 C4 和 ESR 均无明显相关性。AAV 组、SLE 组和 SS 组外周血 DNT%与 C3、C4 和 ESR 均无相性关性。

结论 AID 患者体内存在淋巴细胞亚群的多重失衡，且 AAV 组、SLE 组和 SS 组外周血 CD4+/CD8+与补体 C3 存在明显的相关性。分析该类疾病的淋巴细胞亚群的表达尤其 CD4+/CD8+比值对 AID 患者病情严重程度的评估及建立个体免疫治疗方案及判断预后有重要的临床意义。

PU-1575

低 T3 综合征结果分析

周志瑞
昆明市中医医院

目的 探讨低 T3 综合征(low T3 syndrome，LT3S)又称正常甲状腺病态综合征(euthyroid sick syndrome，ESS)的临床情况。
方法 回顾性分析本院住院 2020 年 8 月～2020 年 11 月低 T 3 患者 200 例，同时选择到本院体检中心健康体检者 200 例作为对照组。进行统计分析临床情况 、病因。
结果 住院组在全身性疾病、严重的心肺疾病 、禁食、精神创伤、恶性肿瘤、重症感染及术后多种应激状态下各原发疾病类型患者的 T 3 水平明显低于体检对照组，差异具有统计学意义（ P ＜ 0.05）；
结论 低 T 3 综合征临床住院患者发病率高 ,与多种疾病存在一定相关性，尤以危重症出现的一种综合征。

PU-1576

ENA 多肽抗体谱和抗核抗体在临床上对自身免疫性疾病的应用

周万彩
昆明市中医医院

自身免疫性疾病(autoimmune diseases,AID)是指由于机体的自身细胞和体液对自身产生反应，主要表现为血清中多种自身抗体的形成及全身多脏器损伤的疾病。而多种抗体联合检测项目在临床上对自身免疫性疾病筛查与诊断工作中起到了很好的辅助作用，有效提高了 AID 的确诊效率。

PU-1577

血清抗线粒体抗体 M2 亚型检测的回顾性分析

张兴保
昆明市中医医院

目的 研究抗线粒体 M2 亚型抗体的实验室检测指标的回顾性分析及在临床诊疗中的意义。
方法 选取 2019-2020 年医院就诊的 30 例抗线粒体抗体 M2 亚型阳性患者作为 AMA-M2（+）组，另随机选取 30 例年龄阶段一致、身体健康、AMA-M2（-）患者作为 AMA-M2（-）组，就两组患者的性别、年龄、生化指标碱性磷酸酶、γ-谷氨酰转肽酶指标进行研究，并对结果进行统计学分析。
结果 抗线粒体 M2 亚型抗体阳性患者性别男女比例为 1:1.5，其中以中老年人患者阳性居多，平均 62（30,86）岁，阳性率高于 AMA-M2（-）组。抗线粒体抗体 M2 亚型阳性患者的生化指标碱性磷酸酶、γ-谷氨酰转肽酶均明显升高，差异有统计学意义（P<0.05）。
结论 抗线粒体 M2 亚型阳性患者以中老年女性为主，出现血清碱性磷酸酶、γ-谷氨酰转肽酶升高，联合检测对疾病的诊断及鉴别诊断有重要意义。

PU-1578

降钙素原(PCT),C 反应蛋白((CRP)、白介素 6 联合测定在老年急性感染疾病中的诊断价值

苏斌斌
昆明市中医医院

目的 评价 PCT、IL-6、CRP 联合检测在老年急性感染疾病中的诊断价值，帮助临床医生对其所患疾病进行鉴别诊断。
方法 对我院 2019 年 10 月—2020 年 10 月诊断 60 例急性感染老年患者的临床资料进行回顾性分析，根据其致病原因分为细菌组（30 例）、病毒组（30 例），再选取同期健康体检的 30 例老年人为对照组，检测 3 组血清 PCT、IL-6、CRP 水平，对比其水平差异。
结果 细菌组 PCT、IL-6、CRP 水平均高于病毒组，病毒组 PCT、IL-6、CRP 水平均高于对照组，三组之间对比差异有统计学意义（$p<0.05$）），细菌组 PCT、IL-6、CRP 的阳性率比病毒组高，病毒组 PCT、IL-6、CRP 的阳性率比对照组对高，三组之间对比差异有统计学意义（$p<0.05$））。
结论 血清 PCT、IL-6、CRP 联合测定对老年急性感染疾病有较高鉴别诊断价值，对指导临床用药有重要意义。

PU-1579

肺炎支原体抗体检测的两种方法学比较

李田妹
云南省中医药大学第三附属医院-昆明市中医医院

目的 比较间接免疫荧光法(IFA)和免疫胶体金法(GIA)在肺炎支原体感染早期检测中的应用价值。
方法 选取我院 2020 年 3 月～2020 年 11 月可疑肺炎支原体感染的患者 467 例，分别采用间接免疫荧光法和免疫胶体法检测患者血清中的肺炎支原体抗体，比较这两种检测方法阳性检出率的差异，以协助临床早期诊断肺炎支原体感染。
结果 间接免疫荧光法 MP-IgM 阳性检出率为 35.12%，免疫胶体金法 MP-IgM 阳性检出率为 36.40%，2 种检测方法阳性检出率无显著差异（$P>0.05$）。
结论 两种方法检验肺炎支原体，均有一定临床使用价值，探索联合检验，可提高肺炎支原体感染早期检出率。

PU-1580

丙肝抗体阳性与 HCV RNA 的检测分析

李少萍
昆明市中医医院

目的 探讨丙肝抗体阳性者血清中 HCV—RNA 的阳性率及丙型肝炎病毒抗体与 RNA 对于丙型肝炎的诊断及治疗具有重要的实用价值和临床意义。
方法 用 ELISA 法检测我院住 2019 年 5 月 一 2019 年 11 月住院及门诊患者血清中的丙型肝炎抗体，同时丙肝抗体阳性患者血清进行了 HCV—RNA 检测。
结果 22 例 HCV 抗体阳性的患者 HCV-RNA 阳性 12 列，阳性率为 54.54%。
结论 抗-HCV 和 HCV-RNA 的联合检测 ，对丙型肝炎的临床诊断和治疗有一定的意义和价值.

PU-1581

两种不同免疫检验方法对乙肝病毒感染血清标志物的临床效果观察

王菁、金亚莉、张涛、张志平、刘家云
空军军医大学西京医院

目的 评估乙肝病毒感染患者实施两种不同免疫检验方法的临床效果。
方法 对 72 例本医院实施治疗的乙肝病毒感染予以项目研究，选于 2019 年 12 月至 2020 年 12 月，全部患者均应用酶联免疫吸附法检验、电化学发光法检验，分析两组方案的检验结果、血清标志物情况。
结果 （1）疑似乙肝病毒感染患者确诊结果阳比 77.78%；阴性比 22.22%。酶联免疫吸附法检验阳性比 73.61%；阴性比 26.39%。电化学发光法检验阳性比 76.39%；阴性比 23.61%。（2）疑似乙肝病毒感染患者乙肝病毒表面抗体、乙肝病毒核心抗体结果具有一致性，P>0.05 说明其差异相对较低。实验组的疑似乙肝病毒感染患者经由检验后，与参照组的患者检验后进行对比，其乙肝病毒表面抗原、乙肝病毒 E 抗原、乙肝病毒 E 抗体比例较高，P<0.05 说明其差异相对较高。
结论 乙肝病毒感染患者行电化学发光法进行血清标志物检验的准确性较高。

PU-1582

Preconditioning with a TLR2 ligand-Pam3CSK4 enhances methicillin-resistant Staphylococcus aureus presentation of dendritic Cells to Tcell

Yiguo Chen
Medical Laboratory, Jiangxi Provincial People's Hospital Affiliated to Nanchang University

Our previous studies showed pretreatment with TLR2 agonist Pam3CSK4 attenuated the sepsis-induced cytokine burst and protected mice from MRSA pneumonia, suggesting that ligands of TLR2 enhance immune responses against bacteria. Pretreatment of Pam3CSK4 also reduced bacteremia and mortality in mouse models of polymicrobial peritonitis, colitis , inflammatory responses . However, few studies have examined the effects of Pam3CSK4 pretreatment on Dendritic cells and T cell immunity against MRSA, Toll-like receptor 2 (TLR2), a pattern recognition receptor, is an essential component in host innate defense system against S. aureus infection. However, little is known about the adaptive immune response, specifically TLR2 activation, against MRSA infection. In the present study we have examined the effects of Pam3CSK4 pretreatment on Dendritic cells and T cell immunity against MRSA. We found that Phenotypies of these BM-DCs is affected by TLR2 agonists Pam3CSK4 or LTA, and BM-DCs pretreated with Pam3Csk4 express a lower level of CD40 and CD86 not CD80, and those BM-DCs pretreated with Pam3CSK4 for 24h, 48h significantly enhanced their phagocytic ability towards HK-MRSA; Mixed leukocyte reaction (MLR) showed that Pam3CSK4 treated BM-DCs increased CD69 express on surfer of naïve T-cell in time-dependent manner, and induced significently proliferation of CD4 T cell and CD8 T cell in a time-dependent manner but LTA. Conclusion, Pam3CSK4 activate T immunity to Staphylococcus aureus by sensitizing BM-DCs pretreatment with Pam3CSK4 .

PU-1583

CEA、CA125 和 CA19-9 及其联合检测在胰腺肿瘤诊断中的价值及其临床应用

韦莉
江苏省人民医院（南京医科大学第一附属医院）

目的 研究血清学肿瘤标志物 CEA、CA125、CA19-9 及其联合检测在胰腺肿瘤诊断中的价值及其临床应用。
方法 收集 2017 年 5 月至 2018 年 1 月南京医科大学第一附属医院胰腺中心收治并经病理确诊的 172 例胰腺肿瘤患者和 73 例健康体检者，其中胰腺肿瘤患者按照 WHO 消化道肿瘤分为良性肿瘤组、癌前病变组和胰腺癌组。采用电化学发光法检测血清 CEA、CA125 和 CA19-9 并进行各组间的分析；采用受试者工作曲线（ROC）分析其在胰腺癌中的诊断价值。
结果 胰腺癌组血清 CEA、CA125 及 CA19-9 水平均明显高于健康对照组、良性肿瘤组和恶性前病变组，差异均有统计学意义（P<0.05）；并且血清 CA19-9 水平在恶性前病变组明显高于健康对照组，差异有统计学意义（P<0.05）。ROC 曲线显示，血清 CA199 的 AUC 高于其他单项指标，灵敏度和特异性分别 76.0%和 89.7%，三项联合检测效能均优于单项检测，其灵敏度和特异性分别为 81.4%和 92.2%。
结论 血清学肿瘤标志物联合检测可提高胰腺肿瘤早期诊断的检测效率。

PU-1584

25-羟基维生素 D 在斑秃患者外周血的表达及临床意义探讨

张晓洁、夏晓红
江苏省人民医院（南京医科大学第一附属医院）

目的 通过检测斑秃患者外周血中 25-羟基维生素 D[25-Hydroxy VitaminD, 25(OH)D] 的表达量，初步探讨其与斑秃的相关性，探索斑秃的发病机制，为斑秃治疗提供新的靶点。
方法 选取 2019 年 1 月-2020 年 1 月在南京医科大学第一附属医院皮肤科门诊初诊的斑秃患者 83 例为观察组，并选取同期体检中心健康对照者 80 例为对照组，回顾性分析其临床资料, 分析斑秃与血清 25-羟基维生素 D 水平之间的关系。
结果 共纳入斑秃患者 83 例，健康对照 80 例。结果显示，观察组患者的血清 25(OH)D 水平为（49.81±18.74）nmol/L，对照组为（56.96±19.81）nmol/L，两组比较差异有统计学意义（P＜0.05）。83 例斑秃患者中 25(OH)D 严重缺乏 4 例(4.82%)，缺乏 40 例（48.20 %），不足 29 例（34.94 %），充足 10 例（12.05%）；80 例正常对照组中 25(OH)D 严重缺乏 2 例(2.50%)，缺乏 20 例（25.00 %），不足 42 例（52.50 %），充足 16 例（20.00%），两组血清 25(OH)D 分布比较差异有统计学意义（P<0.05）。组内分析显示，斑秃组和正常对照组男性和女性血清 25(OH)D 的水平及分布比较差异均具有统计学意义（P<0.05）。
结论 斑秃患者的血清 25(OH)D 水平和分布与正常人相比差异均有统计学意义。斑秃组和正常对照组男性和女性的血清 25(OH)D 水平和分布同样存在显著性差异。

PU-1585

血清 FSH、LH、TSTO 检测在多囊卵巢综合征患者诊断中的临床价值探讨

张晓洁、张立涛、黎青
江苏省人民医院（南京医科大学第一附属医院）

目的 为了提高临床对多囊卵巢综合征(PCOS)的诊断和治疗，分析和研究性激素水平变化和多囊卵巢综合征发生的相关性。
方法 从就诊的多囊卵巢综合征患者中按照随机原则选取 70 例作为试验组研究对象，应用同样方法从 2019 年 1 月-2021 年 1 月在我院进行健康查体者中选取 70 例作为对照组研究对象，采用化学发光法分别检测两组患者血清的黄体生成素(LH)、卵泡刺激素(FSH)及睾酮(TSTO)含量并进行对比分析。
结果 经过研究发现，试验组中共发现 37 例患者出现 FSH、LH、TSTO 含量异常，发生率为 52.90％。对照组受检者 LH 阳性 2 例 TESTO 阳性者 0 例，发生率为 2.86%。试验组患者的 FSH 水平和对照组相比差异不具有统计学意义(P＞0.05)，试验组患者的 LH、TSTO 含量和对照组相比明显升高，两组比较差异具有统计学意义(P＜0.05)。
结论 多囊卵巢综合征患者多伴有性激素含量异常，FSH 水平偏低或正常，以黄体生成素(LH)、睾酮(TSTO)水平异常最为显著，具有较高的临床诊断价值。故而临床发现育龄女性体内 LH 和 TESTO 的含量升高情况应当及时予以全面诊断，为患者提供针对性治疗，以预防罹患 PCOS 风险。

PU-1586

乙型肝炎表面抗原阴性/核心抗体阳性患者 HBV DNA 阳性率及临床意义

蔡婧瑶、吴伟民、吴佳丽、陈芷阳、吴紫薇、唐亚梅、胡敏
中南大学湘雅二医院

目的 本研究将估算出 HBsAg 阴性/HBcAb 阳性患者的 HBV DNA 阳性检出率，探讨 HBV DNA 阳性样本的病毒载量与乙肝病毒血清学标志物、肝功能和凝血功能指标的相关性。同时，分析免疫抑制治疗是否影响 DNA 复制。
方法 选取 2019 年 1 月至 12 月在中南大学湘雅二医院就诊的 HBsAg 阴性/HBcAb 阳性患者 2013 例。观察其血清学标志物、HBV DNA 病毒载量、肝功能和凝血功能指标以及免疫功能状态。
结果 HBsAg 阴性/HBcAb 阳性患者的 DNA 阳性率为 5.4％，并且随着 HBV 血清学特征不同 DNA 阳性率和病毒载量也有明显差异。在 DNA 阳性患者中，DNA 载量与谷丙转氨酶和谷草转氨酶的活性呈正相关，而与抗凝血酶Ⅲ活性呈负相关。并且在接受免疫抑制治疗的患者中，血清 ALT 与 AST 水平均高于未接受免疫抑制治疗的患者；HBeAb 阳性组患者血清 ALT 与 AST 水平明显高于 HBeAb 阴性组。
结论 对 HBsAg 阴性/HBcAb 阳性患者，临床医生应关注患者免疫功能状态，如果不能及时检测 HBV-DNA，也可观察 ALT、AST 以及 ATⅢ的水平变化，推测病毒复制情况，从而减少该类患者 HBV 的发病风险和传播风险。

PU-1587

Vertical transmission rate of hepatitis C in China：A systematic review and meta-analysis

Hongyan Li 、Li He、Yongjun Wang
Second Xiangya Hospital of Central South University

Vertical transmission is one of the main transmission routes of hepatitis C virus infection.The main purpose of this paper is to explore the vertical transmission rate of Chinese mainland hepatitis C virus (HCV) infection in recent decades by meta analysis, which has a certain reference value for controlling HCV mother-to-child transmission and improving the public health system.

Methods PubMed, CNKI, WanFangData, SinoMed, EMBASE and VIP were searched and 17 articles were included.the literatures about Chinese mainland HCV mother-to-infant transmission published from between 1 January 1994 and 30 December 2019 were collected . Subgroup analysis and Meta regression analysis were used to identify potential sources of heterogeneity among the included studies, and sensitivity analysis was used to explore the effect of a single study on the combined effect.

Results Among the 17 studies included, the vertical transmission rate of HCV was between 1.1% and 86.7%, and there was significant heterogeneity among the studies (I^2=86.2%,P<0.001). The combined vertical transmission rate of Chinese mainland HCV based on random effect model was 17.38% [95%CI(9.60,26.88)]. Subgroup analysis showed that the vertical transmission rate of HCV was the highest in intrauterine infection (31.49%). The vertical transmission rate of HCV in pregnant women with other infections was significantly higher than that in the south. In Chinese mainland area, the mother-to-infant transmission rate of HCV in the north was higher than that in the south.

Conclusion The rate of vertical transmission of HCV in Chinese mainland area is relatively high, suggesting that more attention should be paid to mother-to-child transmission of hepatitis C, and case identification and prevention strategies should be expanded and strengthened to detect and monitor HCV infected women and children, so as to reduce the risk of mother-to-child transmission of hepatitis C.

PU-1588

丙肝病毒感染相关检测技术及筛查诊断策略新进展

李红燕、贺理、王勇军
中南大学湘雅二医院

高效抗病毒药物（DAAs）可以治愈 95%以上的丙肝病毒感染者，世卫组织（WHO）新的战略目标是将丙肝病毒感染率、死亡率分别减少 90%和 65%。目前，丙肝病毒（HCV）感染的筛查和诊断主要是基于抗 HCV 抗体和/或 HCV RNA 检测，但其检测时间长、价格昂贵且有部分隐匿性 HCV 感染者血清 HCV 抗体、HCV RNA 检测均阴性。因此，采用简单快速、高灵敏度、高特异性的检测方法来简化 HCV 的筛查、诊断，对实现 2030 年消灭丙肝病毒性肝炎的目标至关重要。本文对丙肝病毒的抗体、核心抗原、RNA 的相关检测技术及国内外丙肝筛查诊断策略进展进行了综述并对简化 HCV 筛查和诊断作出思考和展望。

PU-1589

基于 BAS 化学发光技术中一种全自动化抗生物素干扰方法及性能评价

刘栋[1,2]、王晓琴[2]、周莉莉[1]、胡健[2]、张宁[2]、陈斌[1]、仝慧[1]
1. 铜川市人民医院
2. 西安交通大学第一附属医院

目的 在采用生物素-链霉亲和素的化学发光技术中，建立和评价一种可实现全自动化的抗生物素干扰方法。
方法 筛选适宜的链霉亲和素磁微粒（M）浓度，在全自动仪器中对加入一定浓度的生物素样品进行检测，评价该方法的精密度、正确度和检出限。
结果 （1）M 浓度越高，抗生物素干扰能力越强；但 M 浓度越高，对光信号的屏蔽作用也越强。（2）在夹心法项目人绒毛膜促性腺激素 β 亚基（β-HCG）和竞争法项目孕酮（Prog）中，当 M 浓度为 2.16 mg/ml（M6）时，至少可抵抗 500 ng/ml 的外源性生物素干扰，且对光信号的屏蔽作用相对较小；（3）应用 M6 进行抗生物素干扰时，尽管该方法的空白限（LOB）、检出限（LOD）和定量检出限（LOQ）均较原倍 M（0.72mg/ml）有一定增大，但总不精密度<1/3 允许总误差、正确度<1/2 允许总误差，能满足实际需要。
结论 在全自动仪器中使用 M6 是一种经济、便捷、有效、准确的抗生物素干扰方法。

PU-1590

宝鸡地区 2 型糖尿病患者亚临床甲状腺功能减退及骨密度异常发生率分析

葛君琍
宝鸡高新人民医院

目的 分析 2 型糖尿病患者亚临床甲状腺功能减退及骨密度减低的相关性。
方法 选择我院诊断为 2 型糖尿病者 2986 例，其中男性 1763 例女性 1223 例。体检中心健康体检人群 1200 例，其中男性 600 例，女性 600 例。采用美国雅培全自动化学发光免疫分析仪，罗氏全自动生化分析仪检测分别检测血清 T3、T4、FT3、FT4、TSH，空腹血糖、糖化血红蛋白含量。双能 X 线吸收法测定骨密度。
结果 糖尿病组甲状腺功能异常、骨量减少、骨质疏松检出率均高于对照组 P＜0.001；2 型糖尿病组显示，各年龄段亚临床甲状腺功能减退、骨量减少及骨质疏松发生率，均高于对照组，并且随着年龄增长而发生率升高，青年老年组＞中年组＞青年组。
结论 2 型糖尿病患者亚临床甲状腺功能减退与骨密度减低发生率高于普通人群。建议对糖尿病患者定期进行甲状腺功能及骨密度检测筛查。做到早期预防及早期诊断，便于临床针对性的采用治疗措施，提高糖尿病患者的生活质量。

PU-1591

矮小儿童生长激素治疗后 IGF-1 和甲状腺功能的变化研究

张志平
空军军医大学西京医院

目的 探讨矮小儿童经基因重组人生长激素治疗前后甲状腺功能和胰岛素样生长因子-1（IGF-1）的变化。
方法 选取 2017 年 5 月至 2019 年 5 月期间在西京医院就诊的 60 例矮小症的患儿（全部为甲状腺功能正常患儿），采用基因重组人生长激素(rhGH)治疗 2 年。比较患儿治疗前后的生长发育情况、甲状腺功能指标，分别于治疗前 、治疗 3 个月、治疗 6 个月，取患儿清晨空腹血 ，测定游离三碘甲状腺原氨酸（fT3）、游离甲状腺素（fT4）及促甲状腺素（TSH）水平分以及胰岛素样生长因子 1（IGF-1），分析比较几个点测量指标的均数以及两组治疗前后生长参数。
结果 在 rhGH 治疗后身高的标准差计数 、生长速度均有所改善 。提示经人生长激素治疗后甲状腺功能差异无统计学意义，IGF-1 差异有统计学意义。
结论 治疗前甲状腺功能正常的矮身材患儿治疗后对甲状腺功能影响不大，IGF-1 增长与儿童生长指数成正比，可作为监测疗效的安全指标。

PU-1592

炎症性肠病与肠易激综合征的鉴别诊断

葛秋霞
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨粪便中钙卫蛋白(calprotectin，CPT)在炎症性肠病(Inflammatory bowel disease，IBD)及肠易激综合征鉴别诊断中的临床应用。
方法 选择 2018 年 5 月至 11 月在我院初诊为 IBD 的住院患者 221 例，其中溃疡性结肠炎(Ulcerative colitis, UC)57 例，克罗恩病(Crohn's disease, CD)164 例，肠易激综合征（irritable bowel disease，IBS-D）30 例，收集患者内镜检查前的粪便及对应外周血，检测各组粪便 CPT 水平和血常规相关指标。
结果 CD 组、UC 组粪便 CPT 阳性率均显著高于 IBS 组（P<0.05），CPT 水平也显著高于 IBS 组（P<0.01），且 UC 组显著高于 CD 组（P<0.05）。当按肠道炎症严重程度分组时，UC 轻度者明显高于 CD 轻度者（P<0.05），UC 中、重度者与 CD 中、重度者之间无明显差异（P>0.05）。CD 组、UC 组 WBC、N、PLT 均较 IBS 组显著升高（P<0.05），其中 UC 组 WBC 和 N 较 CD 组更高（P<0.05），UC 组 RBC 显著低于 CD 组和 IBS 组（P<0.05）。CPT+WBC+N+PLT+RBC 联合的敏感性在 CD、UC 为 92.4%、94.5%，特异性分别达 97.7%,、98.4%。
结论 粪便中 CPT 水平可作为 IBD 活动性强弱的评估并且与血常规指标联合可提高诊断即鉴别诊断的敏感性和特异性。

PU-1593

血清脂肪因子 Vaspin 与 Adropin 蛋白水平联合检测在冠心病临床诊断中的应用

陈峻
武汉市第一医院

目的 探讨血清脂肪因子 Vaspin 与 Adropin 蛋白水平联合检测对冠心病临床诊断的意义。
方法 选取 2020 年 8 月至 2021 年 2 月在我院诊治的老年冠心病患者 100 例为观察组，及同期我院健康老年体检者 100 例为对照组。采用酶联免疫吸附(ELISA)法检测各组血清脂肪因子 Vaspin 和 Adropin 蛋白表达水平，绘制 ROC 曲线，分别计算 Vaspin、Adropin 用于诊断冠心病的曲线下面积（AUC）。评价各项指标联合检测时对冠心病患者临床诊断的意义。
结果 与对照组相比，观察组患者 Vaspin 和 Adropin 水平均显著降低（$p<0.05$）。Vaspin 诊断冠心病的 AUC 为 0.898，Adropin 诊断冠心病的 AUC 为 0.883，Vaspin 和 Adropin 联合诊断冠心病的 AUC 为 0.955；Vaspin 和 Adropin 联合检测用于冠心病诊断的敏感度、特异度及准确度均显著增加（$p<0.05$）。
结论 血清脂肪因子 Vaspin 与 Adropin 蛋白水平联合检测可改善冠心病的预后，明确诊断。

PU-1594

甲状腺功能五项在甲状腺功能亢进中的诊断价值

汪旭
吉林金域医学检验所有限公司

目的 甲状腺激素对人体有着十分重要的作用，几乎作用于所有组织。本文分析了甲状腺功能五项检测结果，探讨其在甲状腺功能亢进诊断中的应用价值，为临床提供参考依据。
方法 选取 2020 年 8 月份到 2021 年 3 月份送检样本 100 例，其中 60 例为已知晓为甲状腺功能亢进患者作为 A 组，其余 40 例为甲状腺功能正常的患者作为 B 组，对这两组患者都进行甲状腺功能五项检测,对这两组患者检测结果进行比较分析,对游离三碘甲状腺原氨酸(FT-3)、游离甲状腺素(FT-4)、促甲状腺激素(TSH)、甲状腺过氧化物酶抗体(TPO)、抗甲状腺球蛋白抗体(TGAb)抗体含量进行对比与评定，对比这两组甲状腺功能的阳性检出率与阴性检出率。
结果 A 组患者 TSH 水平明显低于 B 组且部分小于下限($P<0.05$),A 组的 FT-3、FT-4、TPO、TGAb 水平明显高于 B 组且部分高于上限($P<0.05$),A 组阳性检出率明显高于 B 组,A 组阴性检出率明显低于 B 组($P<0.05$)。
结论 人体的生长发育、能量代谢甚至于生殖系统都不同程度上受甲状腺激素的影响。其中促进生长发育是甲状腺激素对人体最为显著的作用。因此甲状腺功能的检测对诊断成年人的甲亢所致的多汗、消瘦、易怒和儿童甲低所致的生长发育迟缓型呆小症都有重要的临床意义。实验表明，甲状腺功能五项指标对甲状腺功能亢进有明显的检出作用,有助于帮助患者明确病症,为临床治疗提供参考,甲状腺功能五项指标检测法可作为临床医学检验甲状腺功能亢进的主要手段。

PU-1595

串联液滴微流控芯片化学发光免疫分析系统

刘大渔
广州市第一人民医院

目的 发展一种基于串联液滴微流控芯片的化学发光免疫分析方法，可用于现场条件下的生物标志物快速检测。
方法 研究设计并加工了一种包含串联液滴微流控芯片与相关分析仪器的化学发光免疫分析系统。仪器的结构紧凑，其内包含了温度控制、磁力控制、机械运动以及光学检测模块，可配合微芯片实现“样本进，结果出”的自动化分析。芯片的主要结构是通过狭缝串联的一系列反应微池，其内预储存了含有不同试剂的油包水型液滴。通过外部磁力控制，可使磁珠在微液滴之间程序性转移，并依次完成抗原抗体反应、磁珠洗涤以及酶促化学发光反应，而最终产生的化学发光信号将通过仪器内集成的光电倍增管来读出。
结果 为了验证串联液滴微流控芯片免疫化学发光系统的检测性能，研究建立了基于该系统的降钙素原（PCT）检测方法。在优化了各项实验条件的基础上，该系统能够以自动化的形式在 15 分钟以内对 PCT 进行高度灵敏、特异以及定量准确的检测，其检出限为 0.044 ng·ml-1。研究分析了 105 份感染性疾病患者的临床样本，所测得的 PCT 浓度与临床所用 Cobas E602 电化学发光免疫分析仪的检测结果呈现出了良好的线性相关性（R2=0.98）
结论 研究发展的串联液滴微流控芯片化学发光免疫分析方法具有检测快速灵敏，定量准确以及自动化分析的特点和优势，有望用于解决现场环境下的生物标志物快速检测问题。

PU-1596

补体 C5b-9 在系膜增生型 IgA 肾病中的作用机制及其临床应用初探

谢梦晓
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨补体终末复合物 C5b-9 在系膜增生型 IgA 肾病病变中的作用及其调控机制，并初步评估其在 IgA 肾病中的应用价值。
方法 1）复制大鼠 Thy-1 肾炎（Thy-1N）模型，或利用 C5b-9 刺激大鼠肾小球系膜细胞（GMC）。2）RNA、抗体芯片以及 IB 等进行分析并验证。3）CCK-8 及报告基因等分析相应基因或蛋白对 GMC 增殖的影响与调控机制。4）免疫共沉淀及质谱等分析相应蛋白激酶磷酸化修饰转录因子对 GMC 增殖及其转录调控的作用。5）采用慢病毒肾动脉灌注的方式沉默上述基因以观察 Thy-1N 大鼠病变的改善。6）免疫组化以及 ELISA 检查在 IgA 肾病患者及对照的肾组织或血清中 C5b-9 以及相应蛋白的表达水平。
结果 1）成功复制 Thy-1N 的动物与细胞模型。2）转录因子 SOX9 以及细胞周期蛋白 Cyclin D1 表达上调，而 ERK1/2 激酶磷酸化水平显著升高。3）ERK1/2、SOX9 和 Cyclin D1 均能增强 GMC 的增殖，ERK1/2 和 SOX9 均能上调 Cyclin D1 的表达，SOX9 能够直接结合于 Cyclin D1 启动子区域，而该过程受 ERK1/2 影响。4）ERK1/2 磷酸化 SOX9 丝氨酸 64 和 181 位点是促进其调控 GMC 增殖以及 Cyclin D1 表达的关键位点。5）沉默上述基因能显著改善 Thy-1N 大鼠病变。6）C5b-9、p-ERK1/2、p-SOX9、SOX9 或 Cyclin D1 在系膜增生型 IgA 患者肾组织或血清中的表达水平显著升高。
结论 C5b-9 能通过调控 ERK1/2 磷酸化修饰 SOX9 促进 Cyclin D1 表达，进而导致 GMC 增殖并引起系膜增生型 IgA 肾病患者病变。C5b-9、p-ERK1/2、p-SOX9、SOX9 和 Cyclin D1 的表达在系膜增生型 IgA 患者的肾组织或血清中显著升高，提示其在该疾病的诊断中具有潜在的应用价值。

PU-1597

CXCL7 在肺癌外泌体中的表达及其临床意义

陈良远、赵秋荣、杨国溜、陈发林
福建省立医院

目的 探讨趋化因子 7（CXCL7）在外泌体中的表达对肺腺癌的早期诊断的重要意义。
方法 选取 2020 年 10 月至 2021 年 2 月于福建省立医院确诊的肺腺癌患者例和健康体检正常人标本，采集其外周血样 1ml,取血清标本进行外泌体的提取，用裂解液破坏外泌体得到蛋白，再用 ELISA 方法检测 CXCL7 的含量。数据用 SPSS 20.0 软件进行分析，最后采用受试者工作曲线（ROC）曲线，分析 CXCL7 早期诊断肺腺癌的灵敏度和特异度，以及与健康人比较是否具有统计学意义。
结果 趋化因子 7（CXCL7）的表达水平在肺腺癌患者的外泌体中较健康人表达显著增加(P 值＜0.001)，差异有统计学意义，ROC 曲线所得的结果为：Cut-of 值：433.6pg/ml SN:72.0% SP:86.67% AUC:86.53%。
结论 CXCL7 在外泌体中的表达对肺腺癌的早期诊断有一定的意义。

PU-1598

血清白细胞介素（IL-6）和 C 反应蛋白（CRP）在胰腺癌中的应用

吴文冰、沈菁、徐如梅、陈发林
福建省立医院

目的 检测胰腺癌患者手术前后血清中的 IL-6 和 CRP 水平，同时与健康体检者和胰腺炎患者进行比较，探讨 IL-6 和 CRP 在胰腺癌诊断中的价值。
方法 收集标本，将其分为三组• 健康对照；,胰腺炎组；*f* 胰腺癌组；记录相关的临床资料。将标本分别保存到-20℃。用免疫比浊法和化学发光法分别检测三组标本中 IL-6 和 CRP 水平。
结果 胰腺癌患者血清白介素-6 和 C-反应蛋白水平高于健康受试者，低于急性胰腺炎患者。
结论 血清白介素-6 和 C-反应蛋白在胰腺癌和急性胰腺炎的诊断鉴别有重要意义。

PU-1599

抗 CCP 抗体和 RF 联合检测在类风湿性关节炎诊断中的应用进展

逯思显、胡文霞、杨叶
呼和浩特金域检验所有限公司

类风湿性关节炎(rheumatoid arthritis,RA)是医学当中比较常见的疾病,也是一种临床表现比较隐匿且复杂的多发病。如今，RA 成为了越来越多现代都市人的健康威胁，而此类疾病的诊断手段并没有十分显著的特性，以及临床治疗的不规范，可能造成病情容易发展为关节强直及畸形，严重的话，将会导致残疾。目前临床上对于 RA 早期诊断,有两个重要指标。一是类风湿因子(rheumatoid factor,RF),常被用作诊断 RA 的指标。二是环瓜氨酸肽(cyclic citrullinated peptide,CCP),RA 患者血清中常见的抗体，它与 RF 相比,在 RA 诊断中，敏感度相似但特异度更高。本文综述了近年来抗 CCP 抗体和 RF 在 RA 诊断中的应用进展。

PU-1600

多重微珠流式免疫荧光法检测系统性红斑狼疮患者自身抗体的临床应用

肖倩
广东省中医院

目的 分析多重微珠流式免疫荧光法检测系统性红斑狼疮患者自身抗体的结果和临床应用。
方法 选取确诊系统性红斑狼疮患者 46 例，健康体检者 30 例，利用多重微珠流式免疫荧光法和免疫印迹法检测各组自身抗体，进行两种方法的结果分析。
结果 试验组采用多重微珠流式免疫荧光法和免疫印迹法检测 ANAs 阳性率分别为 73.9%和 80.4%，差异无统计学意义（p>0.05）。多重微珠流式免疫荧光法检测抗 Sm 抗体、抗 SSA、抗 dsDNA 灵敏度分别为 28.2%、34.7%、23.9%，检验效能分别为 56.5%、60.5%、53.9%。利用多重微珠流式免疫荧光法检测两组 ANAs，除抗 Jo-1 抗体、抗着丝点抗体外 7 种常用自身抗体水平差异具有统计学意义（p＜0.05）。
结论 多重微珠流式免疫荧光法是一种检测新方法，定量，快速，可以一次性同时进行多种自身抗体的联合检测，可为临床提供良好指标。

PU-1601

血清 CEACAM1 对结直肠癌诊断的临床价值分析

黄晨蕾、王莹莹、刘小岑、李小宁、陶绍能
皖南医学院弋矶山医院

目的 检测血清癌胚抗原相关细胞粘附分子 1 (CEACAM1)在结直肠癌患者血清中 的水平，以探讨其在结直肠癌中的诊断价值并分析其与临床病理资料之间的关系。
方法 采 用 ELISA 法测定了 50 例结直肠癌患者、30 例结直肠良性疾病患者和 30 例健康对照血清 CEACAM1 水平，并进一步分析其与临床病理特征的相关性及诊断效能。
结果 结直肠癌 组 CEACAM1 血清浓度[469.1（258.1～637.5）pg/mL]明显较结直肠良性疾病组[246.8（206.9～ 311.3）pg/mL]和健康对照组[245.2（207.1～287.9）pg/mL]升高（P＜0.05）；Ⅲ/Ⅳ期结直肠 癌患者血清 CEACAM1 浓度明显高于Ⅰ/Ⅱ期患者（P＜0.01）。有淋巴结转移与远处转移的 结直肠癌患者血清 CEACAM1 浓度均明显升高，差异有统计学意义（P＜0.05）。ROC 曲线 分析表明，血清 CEACAM1 是筛选结直肠癌患者的一种潜在生物标志物(AUC 为 0.749，54.0%)。CEACAM1 对结直肠癌的诊断特异度（96.7%）略高于 CEA（86.7%）；CEACAM1 与 CEA 联合检测效能（AUC=0.822）和灵敏度（76.0%）略提高。
结论 血清 CEACAM1 可能是结直肠癌的一种潜在生物标志物。与 CEA 联合检测可略提高结直肠癌的诊断效能并 与结直肠癌的分期、转移相关。

PU-1602

时间与溶血因素对孕中期产前筛查项目 AFP 和 Free-β-HCG 的影响探讨

王玉萍、武其文、付夏、余冬黎
皖南医学院弋矶山医院

目的 探讨时间与溶血因素对孕中期产前筛查项目血清甲胎蛋白(AFP)和游离绒毛膜促性腺激素(Free-β-HCG)的影响。

方法 收集 50 例孕 14-21 周之间孕妇血清，一份 1 小时内分离血清，一份室温 22－26℃放置 3 小时分离血清，一份为溶血标本，1 小时内分离血清，放置-20℃冰箱中保存，若一周无法测定，则放置-75℃冰箱保存，同样条件进行测定。

结果 原始数据 AFP46.225±17.403, Free-β-HCG20.914±18.279，3 小时为 AFP47.899±19.424，Free-β-HCG24.759±18.145，溶血标本为 AFP54.522±41.174，Free-β-HCG24.049±17.774，室温放置 3 小时与溶血标本 AFP 和 Free-β-HCG 与原始标本 AFP 和 Free-β-HCG 相比较 P>0.5，差异无显著性。

结论 孕中期产前筛查标本室温放置 3 小时及溶血标本对检测结果无影响。

PU-1603

炎症性肠病与肠易激综合征鉴别诊断中相关炎症指标的临床应用

娄鉴芳、葛秋霞
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨粪便中钙卫蛋白(calprotectin，CPT)在炎症性肠病(Inflammatory bowel disease，IBD)及肠易激综合征鉴别诊断中的临床应用。

方法 选择 2018 年 5 月至 2019 年 7 月在我院初诊为 IBD 的住院患者 175 例，其中溃疡性结肠炎(Ulcerative colitis, UC)88 例，克罗恩病(Crohn's disease, CD)87 例，肠易激综合征（irritable bowel disease，IBS-D）30 例，收集患者内镜检查前的粪便及对应外周血，检测各组粪便 CPT 水平和血常规相关指标。

结果 CD 组、UC 组粪便 CPT 阳性率均显著高于 IBS 组（P<0.05），CPT 水平也显著高于 IBS 组（P<0.01），且 UC 组显著高于 CD 组（P<0.05）。当按肠道炎症严重程度分组时，UC 轻度者明显高于 CD 轻度者（P<0.05），UC 中、重度者与 CD 中、重度者之间无明显差异（P>0.05）。CD 组、UC 组 WBC、N、PLT 均较 IBS 组显著升高（P<0.05），其中 UC 组 WBC 和 N 较 CD 组更高（P<0.05），UC 组 RBC、Hb、Hct 在 UC 显著低于 CD 组和 IBS 组（P<0.05）。CPT+WBC+N+PLT+RBC 联合检测的敏感性在 CD、UC 分别为 92.4%、94.5%，特异性分别达 97.7%、98.4%。

结论 粪便中 CPT 水平可作为 IBD 活动性强弱的评估并且与血常规指标联合可提高诊断及鉴别诊断的敏感性和特异性。

PU-1604

川东北地区耐头孢哌酮/舒巴坦鲍曼不动杆菌耐药基因检测

刘亮华、刘海波、林芳、胡娟、赵明才
遂宁中心医院

目的 通过聚合酶链式反应（PCR）检测 β-内酰胺酶相关耐药基因，探讨耐头孢哌酮/舒巴坦鲍曼不动杆菌 β-内酰胺酶基因分布特点。
方法 收集 2018 年 1 月至 2019 年 6 月我院微生物室采用 VITEK 2 Compact 全自动微生物系统鉴定的醋酸钙-鲍曼不动杆菌复合群共 157 株，聚合酶链式反应检测 β-内酰胺酶相关耐药基因，包括 A 类（ESBLs 类）GES、TEM，B 类（金属酶类）IMP、VIM、DNM，D 类（苯唑西林酶类）OXA-51、OXA-23、OXA-24、OXA-58；利用基质辅助激光解吸电离飞行时间质谱（MALDI-TOF MS）对耐药基因 OXA-51、TEM 和 OXA-23 共表达型进行聚类分析。
结果 药敏分析发现对头孢哌酮/舒巴坦耐药的鲍曼不动杆菌对临床多种药物耐药，亚胺培南、头孢他啶耐药率 99.4%，阿米卡星、庆大霉素、妥布霉素耐药率超过 70%，米诺环素耐药率 45.2%。替加环素较为敏感，耐药率仅为 5.7%。β-内酰胺酶基因检出率：OXA-51 100%、TEM 98.7%、OXA-23 93.6%、GES 53.5%、VIM 47.8%、IMP 17.8%、OXA-58 16.6%，未检出 NDM、OXA-24 基因。共有 11 种耐药基因组合型，其中以耐药基因组合 A 为主，OXA-51、TEM 和 OXA-23 共表达（n=62，39.74%）。随机选取 14 株 OXA-51、TEM 和 OXA-23 共表达菌株，聚类分析成同一簇分布。
结论 β-内酰胺酶基因 OXA-51、TEM 和 OXA-23 共表达模式是我院耐头孢哌酮/舒巴坦鲍曼不动杆菌的主要耐药机制之一；MALDI-TOF MS 技术有望成为分子流行病学研究新型手段。

PU-1605

肿瘤住院患者输血前传染性指标检测结果分析

贺元
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 探讨肿瘤住院患者的常见输血传染性疾病的感染状况及其与年龄大小和肿瘤类别的相关性。
方法 对本院 2016 年 1 月～2019 年 12 月期间，输血前传染性标志物(乙型肝炎表面抗原（HBsAg）、丙型肝炎病毒抗体（抗-HCV）、人类免疫缺陷病毒抗体（抗-HIV1/2）、梅毒螺旋体抗体（抗-TP）)阳性肿瘤住院患者的检验结果进行回顾性统计分析。
结果 在 59370 例患者中共发现 HBsAg 阳性 7820 例、抗-HCV 阳性 269 例、抗-TP 阳性 1041 例、抗 HIV 阳性 82 例，总阳性率分别为 13.17%、0.45%、1.75%、0.14%。输血前各传染性标志物感染者在各个年龄段均有分布，主要集中在 41~70 岁，占总阳性率的 60%以上。输血前传染性标志物感染者几乎于医院各个病种均有发现，检出率较高（20%左右），疾病谱较宽。
结论 通过统计分析发现 HBsAg、抗-HCV、抗-HIV 的阳性率无明显变化处于平衡发病状态，抗-TP 在 2016 年至 2019 年有增加趋势但 2019 年又无明显变化也趋于平衡。感染者在各个年龄段均有分布，主要集中在 41~70 岁。HBsAg 阳性的以肝癌为主；抗-HCV 阳性的以肝癌的检出率最高，其次以宫颈癌和乳腺癌；抗-TP 阳性的患者检出率较高的为宫颈癌，其次为卵巢癌患者；HIV 阳性患者则以头颈部肿瘤所占构成比较高，其次为占位性病变。

PU-1606

ProGRP 在小细胞肺癌诊断中的价值

朱波
宜宾市第一人民医院

目的 探讨胃泌素释放肽前体（ProGRP）检测在小细胞肺癌 (small-cell lung cancer，SCLC)中的价值；
方法 选取我院 2018 年 12 月一 2019 年 9 月呼吸科、肿瘤科 SCLC 患者 96 例，非小细胞肺癌(non-small-cell lung cancer，NSCLC)患者 48 例，肺部良性疾病患者 42 例，健康体检者 60 例，分别进行 ProGRP 和神经元特异性烯醇化酶(NSE)的检测并对结果进行统计分析；ProGRP 采用微粒子化学发光法，用美国雅培 ARCHITECT i2000SR 全自动化学发光仪进行定量检测，NSE 采用安图全自动免疫仪作定量测定；
结果 SCLC 组血清 ProGRP、NSE 水平均显著高于 NSCLC 组、肺良性疾病组和正常对照组，差异有统计学意义(P<0.05)；ProGRP、NSE 对诊断 SCLC 的灵敏度分别为：81.25%、67.71%、特异性为 94.67%、81.33%；
结论 对 SCLC 的诊断，血清 ProGRP 比 NSE 拥有更高的灵敏度和特异性，具有重要的临床应用价值，值得大力推广。

PU-1607

子宫内膜癌中 PDCD5 的下调表达及临床意义

高梦
山东大学第二医院

目的 子宫内膜癌是女性生殖系统最常见的恶性肿瘤之一。程序性细胞死亡 5 (PDCD5)是新近发现的与细胞凋亡相关的基因，在一些人类肿瘤的发生发展中发挥着重要作用。然而，PDCD5 在子宫内膜癌中的表达及临床意义尚未被研究。
方法 我们通过 qRT-PCR、western blot 和免疫组化技术研究了 PDCD5 在子宫内膜样癌及正常对照子宫内膜中的表达，并分析了 PDCD5 表达与患者临床病理参数的关系。此外，我们通过免疫细胞化学方法检测了正常子宫内膜腺上皮细胞和子宫内膜样子宫内膜癌来源细胞株 KLE 中 PDCD5 的表达。
结果 PDCD5 蛋白主要表达于腺上皮细胞和子宫内膜癌细胞的细胞质中，且子宫内膜癌标本中 PDCD5 蛋白水平明显低于对照子宫内膜。PDCD5 表达降低与肿瘤分化程度相关。中、低分化子宫内膜癌中 PDCD5 蛋白表达低于正常子宫内膜癌和高分化子宫内膜癌。而正常子宫内膜增殖期与分泌期、高分化子宫内膜癌与正常对照间 PDCD5 表达无显著差异。免疫细胞化学在对照腺上皮细胞和 KLE 细胞中验证了这一结果。
结论 PDCD5 可能在子宫内膜癌的发病机制中发挥关键作用，可能成为诊断和治疗子宫内膜癌的新靶点。

PU-1608

一种适用于移液器的清洗消毒装置

程孟浩
西安金域医学检验所有限公司

目的 本实用新型属于医学仪器清洁技术领域，具体涉及一种适用于移液器的清洗与消毒。

方法 上述发明柜体内底部被第一隔离板分成左清洗箱和右消毒箱，左清洗箱和右消毒箱的上部设置有移动机构,移动机构上安装有升降机构,升降机构底端安装有用于夹紧移液器的夹紧机构，左清洗箱顶部安装有用于限定枪管伸入的弹性限位垫，左清洗箱内设置有搅拌装置和清洗刷能够快速干净清洁移液器枪管，右消毒箱内安装有超声波雾化喷头和电磁微波装置。本装置能够自动彻底清洗移液器的枪管,并且通过电磁微波装置，产生的电磁微波能够加热超声波雾化喷头喷 出的水分子，也能够加热病毒细菌内的水分子，使消毒液在较高温下快递杀灭细菌，从而保证移液器干净安全。
结果 本装置结构设计合理，解决了针对移液器枪管清洗的难题,不仅可以彻底清洗枪 管内外部,还可以对移液器本体进行彻底消毒，有助于提高实验的精度。
结论 研究所设计装置申请了使用新型专利并取得授权，专利号：CN 210995650 U

PU-1609

抗缪勒氏管激素与 FSH、LH 检测的相关性研究及临床应用

严湘红[1]、黄新媛[2]、吴菲[1]
1. 长沙市中心医院
2. 湖南医药学院

目的 探讨抗缪勒氏管激素（AMH）与卵泡刺激素（FSH）及黄体生成素（LH）的相关性，进一步分析三种激素水平检测的临床应用。
方法 选择 2019 年 8 月-2020 年 5 月，在长沙市中心医院检验科进行了 AMH 和性激素六项检测的健康女性标本 218 例，按年龄分为育龄组、超育龄组及围经组，进一步选取其中健康女性 44 例作为正常组，并选取同期妇科门诊及住院部年龄 34~42 岁之间患有子宫肌瘤的患者共 15 例和患有卵巢囊肿的患者共 12 例作为患病组。
结果 在不同年龄组中，血清 AMH 水平随着年龄的增长呈现逐渐下降趋势，育龄组、超育龄组及围经组 3 组间比较差异有统计学意义（P<0.05）；Pearson 相关分析显示，AMH 与 FSH 间呈线性相关，与 LH 间非线性相关，在卵巢囊肿辅助诊断中，FSH 水平检测与正常组相比具有差异（P<0.05）。
结论 育龄组、超育龄组及围经组女性随年龄增长，AMH 水平逐渐下降，AMH 与 FSH 检测水平呈负相关，FSH 在卵巢囊肿辅助诊断中要优于 AMH、LH，有利于辅助临床判断卵巢囊肿对女性患者卵巢功能的影响程度。

PU-1610

肺炎支原体抗体不同测定方法在儿童肺炎支原体肺炎诊断中的应用评价

穆原[1]、高岭[2]
1. 江苏省人民医院（南京医科大学第一附属医院）
2. 南京市儿童医院

目的 比较肺炎支原体（Mycoplasma pneumoniae，MP）抗体两种检测方法对儿童肺炎支原体肺炎（Mycoplasma pneumoniae pneumonia，MPP）诊断的应用价值。
方法 回顾性收集南京市儿童医院呼吸科于 2019 年 6 月至 2019 年 7 月收治入院的疑似 MP 感染患儿共 80 例。采集病例临床与实验室检查资料，依诊断标准分别归入非 MPP 组、普通 MPP 组、RMPP 组。MP 抗体检测同时采用明胶被动凝集法（PA）与直接化学发光免疫测定法（CLIA）。采用 Shapiro-Wilk 正态性检验考察计量资料的分布情况，偏态资料以中位数（四分位间距）[M(P25，P75)]表示，多组间比较采用 Kruskal-Wallis 秩和检验，率的比较采用卡方检验，等级相关采用 Spearman 秩相关分析，指标诊断性能评价采用非参数 ROC 分析。

结果 非 MPP、普通 MPP 与 RMPP 三组患儿在男女比、热程、热峰温度、GGT、ALB 与 PLT 间的差异无统计学意义（*P* 均> 0.05），而在年龄、住院天数、咳嗽天数、CHE、A/G、IgA、IgM 与 IgG 间存在显著差异（*P* 均< 0.05）。ROC 分析显示 PA 法与 CLIA 法 MP-IgM 联合检测，用于 MPP 诊断的 AUC 为 0.862，其效能高于单一方法检测。
结论 MPP 患儿年龄显著大于非 MPP 组，PA 法与 CLIA 法 MP-IgM 联合检测可提高对 MPP 的诊断效能。

PU-1611

巨噬细胞自噬在动脉粥样硬化中的作用

彭琪、关秀茹
哈尔滨医科大学附属第一医院

动脉粥样硬化（atherosclerosis，AS）的基本病理机制为炎症反应，巨噬细胞在炎症反应中起关键作用。自噬是一种进化保守的亚细胞过程，参与溶酶体内蛋白质的降解和细胞器的损伤是维持细胞内稳态的关键，自噬在抑制炎性反应和细胞凋亡以及促进胆固醇流出方面起着重要作用。而巨噬细胞的自噬可促进脂质代谢,减少泡沫细胞的形成,减弱炎性反应信号,进而抑制动脉粥样硬化。而自噬失调已被认为与包括动脉粥样硬化在内的多种疾病有关，诱导巨噬细胞自噬可能在治疗动脉粥样硬化上具有深远的意义。本文就巨噬细胞自噬在 AS 中的作用作一综述。

PU-1612

应用酶联免疫系统与胶体金检测艾滋抗体的检测效果

邵贝贝
山东省千佛山医院

目的 讨论分析应用酶联免疫法与胶体金法检测艾滋抗体的检测效果
方法 选取我院 2019 年 6 月至 10 月的就诊患者为对象，将患者随机分为的对照组和研究组 105 例对照组患者采用酶联免疫法进行检测，105 例研究组采用胶体金法进行检测，对两组患者的检测效果进行分析。
结果 研究组采用的酶联免疫法检测率为 4.3%，与对照组采用的胶体金法检测率相比无明显差异（P>0.05）。
结论 应用酶联免疫法与胶体金法两种方法对艾滋抗进行检测均具有良好的效果能直观的对艾滋病毒进行检测，值得在临床上进一步用推广。

PU-1613

孕妇葡萄糖耐量及血清胰岛素、C-肽释放水平检测的特点

任丽芬
空军军医大学西京医院

妊娠糖尿病（Gestational diabetes mellitus ,GDM）是妊娠期最常见的并发症之一，其发病率呈明显升高趋势。GDM 对母婴的健康及生命安全都会有一定的威胁，因此为保证母婴健康，应及时发现并接受治疗。为保证临床诊断的准确性，在妊娠糖尿病的筛查诊治中，糖耐量、胰岛素、C 肽释放是常用检测项目。对血中 C 肽、胰岛素浓度进行检测， 能够了解胰岛 β 细胞贮备功能。 同时由于 C 肽的抗干扰性和稳定性， 还能弥补测定胰岛素的不足。本次研究回顾性分析我院门诊

420 例孕妇的临床资料，分析葡萄糖耐量（ oral glucose tolerance test，OGTT）、胰岛素、C-肽释放曲线特点，探讨其对妊娠糖尿病的诊断价值。

PU-1614

呼吸道感染致免疫性血小板减少性紫癜 1 例

吕路路
空军军医大学西京医院

女 16 岁，因皮肤瘀点瘀斑伴牙龈出血 4 天入院。平素身体健康，无过敏史及血液病家族史。2 周前有呼吸道感染史。入院检查：体温正常，全身浅表淋巴结未见明显肿大，全身皮肤可见密集针尖大小淤点和散在融合的瘀斑，呈暗紫色，压之不褪色，微痛。可见牙龈粘膜渗血，咽部充血，扁桃体轻度肿大。心肺听诊正常，肝脾肋下未触及，双肾未见叩击痛。神经系统检查未见异常。实验室检查:血常规白细胞 5.3×1012/L，血红蛋白 125g/L，血小板 11×109L。

PU-1615

雅培 i2000SR 化学发光法测血浆 HBsAg 出现假阳性结果的分析及处理

吕路路
空军军医大学西京医院

目的 探讨雅培 i2000SR 全自动化学发光仪检测血浆 HBsAg 出现假阳性结果的原因及相应处理。
方法 对 2020 年 9 月至 11 月我院门诊患者，i2000SR 检测血浆中 HBsAg 结果在 0.05-0.3IU/ml 的标本分别进行原标本原机复查、金标法复查、ELISA 法复查等，同时重新抽取对应患者标本用其血清复查。
结果 共复测 HBsAg 结果≥0.05IU/ml 标本 167 例（排除仪器、质控、试剂等原因后，确定为假阳性），其中 18 例原机复查结果仍≥0.05IU/ml，金标复查均阴性，16 例 ELISA 法复查阴性，2 例弱阳性。18 例患者原管高速离心后 5 例弱阳性。18 例患者重新抽黄色促凝管离心（10000 g RCF,10 min），分离血清后复查 HBsAg 结果均<0.05IU/ml。
结论 检验前标本质量对结果准确性至关重要，选用患者血浆或者血清，以及两者分离是否完全，离心质量等均有可能影响实验结果的准确性，导致出现假阳性结果，因此，对 HBsAg 弱阳性标本，应进行多方法复查，以保证实验结果的准确性。

PU-1616

肾移植患者不同诊断切点下的高同型半胱氨酸血症的肾损伤研究

刘杨、张志平、彭道荣、邢瑞青
空军军医大学西京医院

探讨肾移植患者不同诊断切点下的高同型半胱氨酸（homocysteine，Hcy）血症对早期肾功能损伤的影响。
方法 收集 2016 年至 2019 年空军军医大学第一附属医院行肾移植术的患者 64 例为肾移植组，同期健康体检查 44 例为健康对照组，所有研究对象测定血 Hcy，肌酐（Cr），半胱氨酸蛋白酶抑制剂 C（Cys C），尿素（BU）及尿酸（UA），采用中国人改良 MDRD 计算肾小球滤过率（eGFR）,当 eGFR<60ml/min.1.73m2 认为肾移植患者有早期肾功能损伤。肾移植组以血 Hcy 水

平的四分位点分为四个亚组，各组间的肾功能指标比较采用方差分析；影响因素采用多元线性回归分析；以 10umol/L、12umol/L 及 15umol/L 三个不同高 Hcy 血症诊断点，校正性别、年龄、移植年限、FK506 的影响，用多元 Logistic 回归模型评估不同诊断点高 Hcy 血症对早期肾功能损伤的影响。

结果 与健康对照组比较，肾移植组四个亚组的血 Cr，CysC，UA、BU 及 eGFR 差异均有统计学意义（P<0.001）

PU-1617

DA-DRD5 信号调节结肠巨噬细胞极化影响结肠炎发生的研究

吴昱青[2]、刘璐[2]、王冰微[3]、姜玉莹[2]、林琳[1]、李晓曦[2]、杨硕[2]
1. 南京医科大学第一附属医院（江苏省人民医院）
2. 南京医科大学
3. 南京中医药大学

目的 多巴胺（Dopamine，DA）是一种重要的儿茶酚胺类神经递质，其水平的降低与炎症性肠病（Inflammatory bowel disease，IBD）的发展密切相关，然而 DA 对 IBD 发生的作用和潜在的机制目前仍不清楚，本研究旨在探索 DA 调节结肠炎的免疫相关作用机制，为临床炎症性肠病的诊治提供新的线索。

方法 1、 采用 DSS 诱导的小鼠结肠炎模型，对分笼或合笼饲养的野生型及 DRD5 敲除小鼠进行造模研究，分析 DRD5 对结肠炎发生的影响；

2、 体外运用 qPCR、western blot、流式细胞术以及 RNA 测序分析检测 DA-DRD5 信号影响结肠炎的具体分子机制；

3、体内实验验证 DA-DRD5 信号影响结肠炎的具体机制以及激活 DRD5 后对 DSS 诱导的结肠炎有何作用。

结果 1、 DSS 结肠炎模型研究显示 DRD5 在结肠炎发生过程中有保护作用，野生型和 DRD5 敲除鼠合笼实验及菌群测序结果表明 DRD5 在 DSS 诱导的结肠炎中的保护作用与菌群关联性不大；

2、 运用 RNA-seq 结果分析表明 DA-DRD5 信号能够通过抑制 NF-κB 通路进而抑制 M1 型巨噬细胞的极化以及通过提高 CREB 信号通路来促进 M2 型巨噬细胞的极化；

3、 体内实验表明 DA-DRD5 信号能够调节巨噬细胞的极化进而影响结肠炎的发生发展。

结论 本项研究发现 DA-DRD5 信号能够通过负调节 NF-κB 信号传导抑制 M1 巨噬细胞的极化，并通过激活 CREB 途径促进 M2 巨噬细胞极化，最终在小鼠结肠炎的发生发展中起到保护作用。

PU-1618

Exosomal KRAS mutation promotes the formation of tumor-associated neutrophil extracellular traps and causes deterioration of colorectal cancer by inducing IL-8 expression

Anquan Shang 、Dong Li
Tongji Hospital of Tongji University

Background Colorectal cancer (CRC) remains one of the leading causes of cancer-related death. The current study aimed to elucidate the mechanism by which exosomes carrying KRAS mutant contribute to neutrophil recruitment as well as the formation of the neutrophil extracellular trap (NET) in CRC.

Methods APC-WT and APC-KRASG12D mouse models were initially developed. Peripheral blood, spleen, bone marrow (BM) and mesenteric lymph nodes (mLN) were isolated to detect neutrophil content. Then, APC-WT and APC-KRASG12D mice were injected with exosomes isolated from APC-WT and APC-KRASG12D mice. The ratio of neutrophils, NETs formation and IL-8 protein content were subsequently quantified in colon tissues. DKs-8 (wild type) and DKO-1 (KRAS mutant) cells were employed for in vitro experimentation. Then, DKs-8 cells were cultured with exosome-treated PMA stimulated neutrophil-forming NETs culture medium, with cell viability, invasion, migration, and adhesion evaluated.
Results Compared with APC-WT mice, the numbers of polyps and neutrophils in the peripheral blood, spleen and mLNs were increased in APC-KRASG12D mice, accompanied with increased NET formation, IL-8 expression and exosomes. Meanwhile, IL-8 upregulation, neutrophil recruitment and NET formation were observed in the mice injected with exosomes derived from APC-KRASG12D. The in vitro investigation results revealed that more NETs were formed in the presence of DKO-1-Exos, which were inhibited by DNAse. In addition, DKs-8- and DKO-1 cells-derived exosomes could adhere to NETs under static conditions in vitro. Exosomal KRAS mutants were noted to exert stimulatory effects on the IL-8 production and NET formation to promote the growth of CRC cells.
Conclusion The results provide evidence suggesting that exosomes may transfer mutant KRAS to recipient cells and trigger increases in IL-8 production, neutrophil recruitment and formation of NETs, eventually leading to the deterioration of CRC.

PU-1619

外周血 Th9,Th22,Treg 细胞及细胞因子在变应性鼻炎中的研究

李志、杨婷婷
大连市中心医院

目的 检测过敏性鼻炎患者外周血辅助 T 细胞 9（Th9）、辅助 T 细胞 22（Th22）、调节性 T 细胞（Treg）的比例及血清中白细胞介素-9（IL-9）、白细胞介素-22（IL-22）、转化生长因子 β（TGF-β）和总 IgE 的表达水平，讨论其与过敏性鼻炎的关系以及临床意义。
方法 选择 48 例过敏性鼻炎患者为患者组，40 例健康成人作为对照组，采用流式细胞术检测外周血单个核细胞（PBMCs）中 Th9、Th22 和 Treg 细胞的比例；用酶联免疫吸附法（ELISA）检测血清中细胞因子 IL-9、IL-22 和 TGF-β 的含量；用速率散射比浊法检测血清中总 IgE 的水平。测得数据用 SPSS 24.0 统计软件进行分析，用 Pearson 相关分析进行相关性检验。
结果 同对照组相比，AR 患者组 Th9 细胞的百分比显著升高（P<0.0001），Treg 细胞的百分比显著降低（P<0.0001），Th22 细胞的百分比与健康对照组相比无显著差异（P=0.63）。与对照组相比，AR 患者组血清 IL-9、IL-22 和总 IgE 表达水平显著升高（P<0.0001），而 TGF-β 则呈现明显下降（P＜0.0001）。AR 患者血清 IL-9 与总 IgE 水平呈正相关（r=0.487, P<0.05），TGF-β 与总 IgE 水平呈负相关（r=-0.679, P<0.05）。
结论 外周血 Th9、Treg 细胞及细胞因子的分泌异常、比例失调在过敏性鼻炎的发病过程中起着重要作用，可作为病情诊断的重要参考指标，也可为临床病因的分析研究提供理论依据，而 Th22 细胞目前不明确，可能没有参与 AR 的发病机制。

PU-1620

依达拉奉通过抑制神经胶质细胞免疫炎性反应改善1-溴丙烷诱导神经毒性

索金宁[1]、赵秀兰[2]
1. 山东大学第二医院
2. 山东大学公共卫生学院

目的 观察 1-溴丙烷（1-BP）对运动神经元的损伤及自由基清除剂依达拉奉（EDV）的干预效果，探究小胶质细胞激活及 M1/M2 极化失衡在 1-BP 神经毒性中的作用。
方法 SPF 级雄性 Wistar 大鼠随机分为对照组、200、400、800 mg/kg·bw 1-BP 组、800 mg/kg·bw 1-BP+6 mg/kg·bw EDV 组、6 mg/ kg·bw EDV 组。分别按以上剂量给予相应组别动物 1-BP 和 EDV，持续 6 周，期间每周测定大鼠后肢抓力。实验结束后采用硫堇染色观察神经元形态，免疫组化观察小胶质细胞及星形胶质细胞激活、运动神经元丢失和凋亡情况。western blot 检测大脑皮层还原型硫氧还蛋白（Trx）、ASK1/MAPK 通路蛋白表达及蛋白硝基化水平。
结果 1-BP 暴露 6 周导致实验动物后肢抓力呈剂量依赖性下降，病理形态学观察到大脑运动皮质小胶质细胞及星形胶质细胞激活、伴随运动神经元丢失；同时，观察到 1-BP 染毒大鼠大脑皮层 nNOS 活性和 NO 水平明显升高，蛋白硝基化增强；Trx-ASK1-p38/MAPK 凋亡通路激活，表现为还原性 Trx 表达减少、ASK1 和 P38 磷酸化增强。动物染毒同时给予 EDV 干预可显著抑制小胶质细胞和星形胶质细胞活化、减轻运动神经元丢失，下调 Trx-ASK1-p38/MAPK 凋亡信号传导通路激活，有效改善 1-BP 染毒导致的后肢抓力下降。来自 1-BP 染毒大鼠大脑的外泌体可导致体外原代培养神经元轴突缩短、消失，给予 EDV 保护神经元损伤明显减轻。
结论 1-BP 暴露可导致实验动物大脑运动神经元损伤及运动功能障碍，与 Trx-ASK1-p38/MAPK 凋亡信号传导通路激活密切相关，清除自由基可有效减轻 1-BP 的神经毒性。

PU-1621

调节组蛋白乙酰化对肝癌细胞 IFI16 的诱导调控作用

赵霞
山东省千佛山医院

染色质核小体组蛋白 N 端的乙酰化、甲基化、磷酸化、泛素化修饰可影响组蛋白与 DNA 的亲和性而改变染色质的状态，对基因表达调控具有类似 DNA 遗传密码的作用。组蛋白乙酰化是一由组蛋白乙酰化酶(histone acetyl transferase,HAT)和脱乙酰化酶(histone deacetylase,HDAC)调控可逆的动态过程，。许多研究证实了组蛋白低乙酰化或 HDACs 的高表达与肿瘤的发生、发展密切相关。干扰素诱导蛋白 16（IFI16）属于 IFI200 蛋白家族，主要通过 JAK1-STAT 信号通路激活表达，在抑制肿瘤、促进细胞分化方面起重要的作用。研究表明 IFI16 蛋白表达减少或缺失与多种肿瘤的发生、发展密切关联，增加 IFI16 表达，会明显抑制细胞增殖周期、诱导细胞凋亡。选择 HepG2、BEL7402、SMMC7721 等肝癌细胞系应用 HDAC 抑制剂 VPA、TSA 进行干预，观察干预后细胞 IFI16 蛋白、mRNA 表达水平变化、细胞增殖、凋亡变化以确定 HDAC 抑制剂 VPA、TSA 对肝癌细胞 IFI16 的调控作用及其与细胞增殖变化的关系，以及调控作用是否与细胞表型相关。

PU-1622

代谢物柚皮素通过 TGF-β1 通路恢复 NK 细胞对 Tfh 样细胞抑制功能缓解类风湿性关节炎

王洪星
山东大学齐鲁医院

背景 类风湿关节炎(RA)是一种自身免疫性疾病。最近，研究者在 RA 的 ELSs 中发现一群特异的 Tfh 样细胞，被称为 Tph 细胞（Tph）。Tph 样细胞通过促进 B 细胞的活化促进 RA 的进展。然而，Tph 细胞参与 RA 进展的上游调控机制尚不清楚。
方法 本研究拟在体内、体外和临床三个方面，通过制备柚皮素纳米制剂，探究柚皮素对 RA 的作用及机制。
结果 代谢组学分析 RA 和 OA 患者滑液中代谢物的变化，OPLS-DA 显示 RA 和 OA 分群清晰。火山图和热图显示了 22 个差异代谢物，其中柚皮素在 RA 中降低。用 WGCNA 的方法分析了代谢物临床指标的关系，将 250 个代谢物分成了 7 个模块。其中 Brown 模块与 RA 患者 anti-CCP 抗体显著负相关（R=-0.59，p=0.006）与 CIA 组相比，NAR 组大鼠足趾炎症缓解，NAR 联合 TGF-β1 足趾炎症变化无统计学差异。NAR 组 NK 细胞比例升高，联合 TGF-β1 组 CD94 (bright) CD161 (bright) NK 细胞比例变化无差异。Tph 细胞与 NK 相反。收集 RA 患者的滑液，用 100ng/ml 的 NAR 纳米粒或联合 TGF-β1 处理 24h 后，流式检测 NK 细胞、Tph 细胞比例。与对照组相比，NAR 纳米粒组 NK 细胞比例升高，Tph 细胞比例降低。NAR 纳米粒组穿孔素升高。用靶向代谢组的方法测定了 OA 和 RA 患者滑液中 NAR 的表达，结果表明， NAR 在 RA 中的含量显著降低。NAR 与 RF 和 anti-CCP 抗体显著负相关，与 CD94 (bright) CD56 (bright) NK 细胞显著正相关。
结论 NAR 可能通过 TGF-β1/Smad3 通路恢复 CD94 (bright) CD56 (bright) NK 细胞对 Tph 细胞的抑制作用，缓解 RA 进展。

PU-1623

Oncostatin M inhibits HBV replication by promoting antiviral proteins and immune-regulatory factor expression

Yuchen Ye、Zhen Xun、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Interferon-α (IFN-α) is an approved anti-HBV drug with higher rate of HBsAg seroconversion than nucleos(t)ide analogues. However, the efficacy of IFN treatment varies among individuals. It's urgent to find new therapy that can inhibit HBV replication and augment antiviral immunity, replacing IFN-α or in combination with IFN-α to improve the efficacy of curing. Recently, a research reveals that oncostatin M (OSM) enhances the anti-HAV and anti-HCV effect of type I Interferon by inducing a chain of antiviral genes. This study was designed to determine whether OSM could inhibit HBV replication and promote the expression of antiviral proteins and immunoregulatory factors, farther to rate the value of OSM in predicting the efficacy of IFN-α for CHB patients. In vitro, HepG2.2.15 cells were in the presence or absence of recombinant OSM. We found that different concentration OSM can significantly suppress the secretion of HBsAg and HBV DNA. In vivo, HBV-infected mice were subcutaneously injected with OSM. These studies confirmed that OSM can significantly inhibit HBV replication. Interestingly, OSM activated JAK-STAT signaling pathway and upregulated interferon-stimulated genes (such as IFITMs, TRIMs, GBPs and so on) expression in liver cells. Moreover, OSM promoted interleukin-7 and interlerkin-15 receptor alpha production, which were critical for the activation and expansion of CD8+ T cells in HBV-infected mice. Thus, our results elucidates that OSM shows strong

immune regulation function and inhibits HBV replication in vitro and in vivo that is promising to be a new therapy for CHB.

PU-1624

Downregulation of SUMO2 inhibits hepatocellular carcinoma cell proliferation, migration, and invasion

Jintu Chen、Zhishan Zhang
Department of Clinical Laboratory, Quanzhou First Hospital Affiliated to Fujian Medical University, Quanzhou, Fujian, China

This study aimed to evaluate the prognostic value and biological function of small ubiquitin-like modifier 2 (SUMO2) in hepatocellular carcinoma (HCC). SUMO2 expression in HCC tissues was markedly higher than that in normal liver tissues, and patients with high SUMO2 expression had significantly shorter median overall survival than those with low SUMO2 expression. Furthermore, SUMO2 expression was closely correlated with lymph node metastasis and vascular invasion and was a predictor of poor prognosis. The knockdown of SUMO2 in two HCC cell lines (SMMC-7721 and Bel-7404) dramatically suppressed their proliferation, migration, and invasion. Western blot analysis showed that the downregulation of SUMO2 significantly reduced the expression of Ki-67, matrix metalloproteinase-9 (MMP-9), and vascular endothelial growth factor (VEGF) in SMMC-7721 and Bel-7404 cells. Similarly, quantitative reverse transcription-polymerase chain reaction revealed consistently decreased expression of MMP-9 and VEGF. Our data suggest that SUMO2 promotes proliferation, migration, and invasion of HCC cells via mechanisms involving MMP-9 and VEGF. Therefore, SUMO2 may be a prognostic factor and a promising therapeutic target for patients with HCC.

PU-1625

RIG-I enhances interferon-α response by promoting antiviral protein expression in patients with chronic hepatitis B

Shu Wu、Qishui Ou
The First Affiliated Hospital of Fujian Medical University, Fuzhou, China

Background Interferon (IFN)-α is widely used for the treatment of chronic hepatitis B (CHB) infection due to the high rate of hepatitis B surface antigen (HBsAg) seroconversion. However, IFN-α treatment has a number of side effects. Thus, identification of molecular biomarkers to predict IFN-α therapeutic effect would be useful in the clinic. In this study, we aimed to investigate the role of retinoic acid-inducible gene-I (RIG-I) in prediction of IFN-α curative effect of CHB patients.
Methods A total of 65 CHB patients treated with pegylated IFN-α weekly for 48 weeks were enrolled. Real-time PCR was performed for detection of RIG-I and IFN-stimulated gene (ISG) expression. In vitro, the HepG2 cells were transfected with siRNA and levels of RIG-I and anti-HBV proteins were detected by western blot. The P-values were calculated in SPSS 18.0. The statistical significance level was accepted as $P<0.05$.
Results In this study, we found RIG-I expression in peripheral blood mononuclear cells was higher in responder than non-responder CHB patients treated with IFN-α therapy. In HBV-transfected HepG2 and Huh7 cells, RIG-I enhanced IFN-α response by promoting anti-HBV protein expression such as double-stranded RNA-dependent protein kinase (PKR), oligoadenylate synthetase (OAS), adenosine deaminase (ADAR1) and Mx protein. Knocking

down of RIG-I could downregulate the expression of these proteins. Inhibited RIG-I expression by RIG-I siRNA deceased STAT1 phosphorylation.
Conclusions Our results revealed RIG-I enhanced IFN-α response by promoting antiviral protein expression via the STAT1 pathway. RIG-I may be a new predictive factor for prediction of IFN-α efficacy in CHB patients.

PU-1626

抗磷脂抗体升高和住院患者院内血栓事件的相关性研究

史晓敏
北京大学第一医院

目的 针对抗磷脂抗体升高的住院患者，评估抗磷脂抗体对于血栓事件发生的判断价值。
方法 回顾性研究。以 2015 年 1 月至 2019 年 12 月于北京大学第一医院住院，并且抗磷脂抗体谱中任意一项检测结果为阳性的 385 例患者为研究对象。依据住院期间是否检测到血栓将所有受试者分为血栓组和非血栓组。记录患者的临床资料及实验室数据，包括 aCL-IgM/IgG、抗 β2GPI-IgM/IgG、LA。比较两组之间的年龄、性别、吸烟、肥胖、高血压、高血脂、糖尿病的发生率以及抗磷脂抗体中位数水平。通过 logistic 多因素回归分析判断血栓事件发生的危险因素。用 ROC 曲线评估 LA 判断血栓的最佳 cutoff 值。用 c2 趋势检验确立 aCL 的中高滴度数值。
结果 血栓组的年龄以及男性、吸烟、高血压、糖尿病的比率明显高于非血栓组。血栓组的抗 β2GPI- IgG、dRVVT 的阳性率明显高于非血栓组，dRVVT 的中位数水平也高于非血栓组，差异有统计学意义。aCL-IgM 的中位数水平，非血栓组高于血栓组。aCL-IgG 的阳性率，血栓组略高于非血栓组。logistic 多因素回归分析显示，男性、高血压、糖尿病、高龄、dRVVT 升高、抗 β2GPI-IgG 升高是血栓的高危因素。ROC 曲线显示，dRVVT 判断血栓的曲线下面积为 0.608（0.558~0.605），最佳诊断界值为 1.20。以 36 GPL 作为 aCL-IgG 的中高滴度数值，与 12 GPL 的临界值相比，血栓事件的 OR 值从 1.93 提高到 2.61。
结论 抗磷脂抗体谱中，DRVVT 方法检测的 LA 是对住院患者血栓事件最有价值的指标，其次是抗 β2GPI-IgG。aCL-IgG 的中高滴度数值设立在 36 GPL 合适。aCL-IgM 在非血栓性疾病显著升高。

PU-1627

抗心磷脂抗体和抗 β2GPI 抗体阈值的确立以及在相关疾病中的应用

史晓敏
北京大学第一医院

目的 确立抗心磷脂抗体和抗 β2 糖蛋白 I 抗体用于预测血栓的阈值。
方法 选取 2021 年 3 月～2021 年 4 月北京大学第一医院 197 份体检样本作为正常人群，采用 ELISA 法对其抗心磷脂抗体和抗 β2 糖蛋白 I 抗体进行检测，统计分析，计算第 99 百分位数。选取 2015 年 1 月～2021 年 5 月[1] 至少有一项 APL 阳性的 545 例患者，根据出院诊断是否为血栓分为血栓组和非血栓组，查阅临床资料得到抗心磷脂抗体和抗 β2 糖蛋白 I 抗体水平。分别计算以正常人群第 99 百分位数原倍、2 倍、3 倍数值作为阈值的情况下发生血栓的 OR 值，比较得出最适阈值。
结果 抗心磷脂抗体（ACL）-IgG/IgM、抗 β2 糖蛋白 I 抗体-IgG/IgM 正常人群的第 99 百分位数分别为 8.68GPL、14.25MPL、22.33RU/ml、19.09RU/ml，ACL-IgG 用于预测血栓的最适阈值为 17.36GPL，抗 β2 糖蛋白 I 抗体-IgG 用于预测血栓的阈值为 22.33RU/ml。ACL-IgM 和抗 β2 糖蛋白 I 抗体-IgM 无法确定阈值（OR<1）。

结论 确立了 ACL-IgG/IgM、抗 β2 糖蛋白 I 抗体-IgG/IgM 正常人群的第 99 百分位数；ACL-IgG 和抗 β2 糖蛋白 I 抗体-IgG 以最适阈值可以用于血栓的预测。

关键词：抗心磷脂抗体，抗 β2 糖蛋白 I 抗体，血栓

PU-1628

胃泌素释放肽前体、糖类抗原 19-9、神经元特异性烯醇化酶（NSE）联合检测对小细胞肺癌的诊断价值

王参军
东南大学附属中大医院

目的 探讨胃泌素释放肽前体（ProGRP）、糖类抗原 19-9（CA19-9）、神经元特异性烯醇化酶（NSE）联合检测对小细胞肺癌的诊断价值。

方法 选择 120 例小细胞肺癌患者、70 例肺部良性病变患者及 70 例健康体检者,分别作为小细胞肺癌组、肺部良性病变组及健康对照组,检测并比较 3 组研究对象的血清胃泌素释放肽前体（ProGRP）、糖类抗原 19-9（CA19-9）、神经元特异性烯醇化酶（NSE）水平,比较不同病理类型小细胞肺癌患者的血清胃泌素释放肽前体（ProGRP）、糖类抗原 19-9（CA19-9）、神经元特异性烯醇化酶（NSE）水平。绘制受试者工作特征（ROC）曲线,分析血清胃泌素释放肽前体（ProGRP）、糖类抗原 19-9（CA19-9）、神经元特异性烯醇化酶（NSE）单独及联合检测对小细胞肺癌的诊断效能。

结果 小细胞肺癌组患者的血清胃泌素释放肽前体（ProGRP）、糖类抗原 19-9（CA19-9）、神经元特异性烯醇化酶（NSE）水平均高于肺部良性病变组和健康对照组,差异均有统计学意义（$P < 0.05$）;肺部良性病变组和健康对照组的血清胃泌素释放肽前体（ProGRP）、糖类抗原 19-9（CA19-9）、神经元特异性烯醇化酶（NSE）水平比较,差异均无统计学意义（$P > 0.05$）;小细胞癌患者的血清 ProGRP 水平高于腺癌和鳞状细胞癌患者（$P < 0.05$）。ROC 曲线分析结果显示,血清胃泌素释放肽前体（ProGRP）、糖类抗原 19-9（CA19-9）、神经元特异性烯醇化酶（NSE）单独检测诊断小细胞肺癌的曲线下面积（AUC）分别为 0.913、0.942 及 0.976,均低于三者联合诊断的 0.997。

结论 血清胃泌素释放肽前体（ProGRP）、糖类抗原 19-9（CA19-9）、神经元特异性烯醇化酶（NSE）联合检测可提高小细胞肺癌的诊断效能,利于小细胞肺癌的早期筛查及诊疗。

PU-1629

Blocking of YY1 reduce neutrophil infiltration by inhibiting IL-8 production via the PI3K-Akt-mTOR signaling pathway in rheumatoid arthritis

Jinpiao Lin、Qishui Ou
the First Affiliated Hospital of Fujian Medical University

Our previous study revealed that Yin Yang 1(YY1) played an important part in promoting interleukin (IL)-6 production in rheumatoid arthritis (RA). However, whether YY1 has any role in regulation of IL-8 in RA remains unclear. YY1 and IL-8 expression in RA patients were analyzed by real-time polymerase chain reaction (PCR). Ingenuity pathway analysis (IPA) was used to analyze the signaling pathway involved in YY1-induced IL-8 production. The expression of YY1 and proteins involved in the pathway were detected by Western blot and enzyme-linked immunosorbent assay (ELISA). Migration of neutrophils was performed by chemotaxis assay. In this study, we found that high expression of IL-8 was positively associated with YY1 expression in

RA. Blocking YY1 expression by YY1-short hairpin (sh)RNA lentivirus reduced IL-8 production. Mechanistically, we showed YY1 activated IL-8 production via the phosphatidylinositol-3-kinase/Akt/mammalian target of rapamycin (PI3K/Akt/mTOR) signaling pathway. Further, using a co-culture system consisting of peripheral blood mononuclear cells (PBMC) and neutrophils, we found that migration of neutrophils would be inhibited by YY1 RNA interference. Finally, using the collagen-induced arthritis animal model, we showed that treatment with the YY1-shRNA lentivirus led to reduction of IL-8 levels and attenuation of inflammation and neutrophil infiltration in vivo. Our results reveal a role of YY1 involved in neutrophil infiltration in RA via the PI3K/Akt/mTOR/IL-8 signaling pathway. YY1 may be a new therapeutic target for treatment of RA.

PU-1630

血清标志物对桥本甲状腺炎的诊断价值

马庆海
山东省千佛山医院

目的 探讨桥本甲状腺炎患者自身抗体的变化对疾病的诊断价值及临床意义。
方法 选取 2020 年 6~10 月本院诊断为桥本氏甲状腺炎的患者 100 例作为研究组，同期选择本院体检健康人员 100 例作为对照组。两组人员标本分别行游离三碘甲状腺原氨酸（FT3）、游离甲状腺素（FT4）水平、促甲状腺激素（TSH）、甲状腺过氧化物酶抗体（anti-TPO）及甲状腺球蛋白抗体（anti-TG）检测并记录结果。
结果 研究组 FT3、FT4、anti-TPO 及 anti-TG 均高于对照组，差异有统计学意义（P<0.05）。
结论 临床诊断桥本甲状腺炎时，不应只检测甲功三项，应联合 anti-TPO 及 anti-TG 检测，可作为诊断的关键依据，对疾病诊断有重要意义。

PU-1631

Association of serum lipids with autoantibodies and inflammatory markers in rheumatoid arthritis patients

Longjie Gan、Qishui Ou
Department of Laboratory Medicine, the First Affiliated Hospital of Fujian Medical University

Background We studied the relationship between serum lipids and autoantibodies and inflammatory markers in rheumatoid arthritis (RA) patients to explore the effect of serum lipids on the diagnosis and judgment of disease activity in RA patients.
Methods Serum lipids including TCHO, TG, HDLC and LDLC and anti-CCP, RF, CRP, ESR of RA patients from May 2013 to August 2017 were retrospectively analyzed in the First Affiliated Hospital of Fujian Medical University.
Results With the dilution factor increased, the concentrations of serum lipids and anti-CCP, CRP and RF showed the same downward trend, indicating that the detection Methods of the above indicators were reasonable and would not be affected by hyperlipidemia. CRP and ESR levels were negatively correlated with HDLC concentration in male and female RA patients. However, the concentration of anti-CCP and RF were closely related to TG. In all the RA patients and female RA patients, the RF level was negatively correlated with the TG concentration. Moreover, with the TG concentration increased, the proportion of patients with high concentrations of anti-CCP levels decreased. In addition, in male RA patients, anti-CCP and ESR concentration increased with the increase of LDLC.
Conclusion The concentrations of HDLC, TG and LDLC were associated with the concentration of anti-CCP, RF, CRP and ESR in RA patients. Therefore, clinical diagnosis of RA and

determination of disease activity should consider the impact of the concentration of serum lipids in order to make a reasonable judgment on the diagnosis of the disease.

PU-1632

Alteration of the gut microbiota in tumor necrosis factor-α antagonist-treated collagen-induced arthritis mice.

Binglong Wang、Jinpiao Lin
the First Affiliated Hospital of Fujian Medical University

Aim Gut microbiota play an important role in rheumatoid arthritis (RA). Biological therapies targeting tumor necrosis factor-α (TNF-α) have been used for treatment in RA patients. However, whether TNF-α antagonist has some influence on gut microbiota is still unknown. This study aims to investigate the distribution of gut microbiota in collagen-induced arthritis (CIA) mice treated with the TNF-α antagonist etanercept.
Methods Collagen-induced arthritis mice were induced by type II collagen. Cytokine expression was detected by real-time polymerase chain reaction. 16S ribosomal RNA sequencing was performed to characterize the gut microbiota in CIA mice treated with vehicle or etanercept. Sequencing reads were processed by Microbial Ecology software program.
Results Compared with vehicle-treated mice, we showed that CIA mice treated with etanercept led to attenuation of inflammation and reduced expression of TNF-α, interferon (IFN)-γ, interleukin (IL)-6 and IL-21. Meanwhile, results showed operational taxonomic units, richness estimators and the diversity indices of gut microbiota in etanercept-treated mice were lower than that in vehicle-treated mice. Moreover, bacterial abundance analyses showed that genus Escherichia/Shigella was more abundant in etanercept-treated mice, and Lactobacillus, Clostridium XlVa, Tannerella were less abundant. The altered bacterial genus was correlated with TNF-α, IFN-γ, IL-6, IL-21 and IL-10.
Conclusion Our results revealed that TNF-α antagonist treatment can reduce the abundance and diversity of gut microbiota in CIA mice. Targeted gut microbiota may be a new therapeutic strategy for the treatment of RA.

PU-1633

A critical role of transcription factor YY1 in rheumatoid arthritis by regulation of interleukin-6

Jinpiao Lin、Qishui Ou
the First Affiliated Hospital of Fujian Medical University

Previous studies have revealed a critical role of YY1, a "Yin Yang" transcription factor, in cancer development and progression. However, whether YY1 has any role in rheumatoid arthritis (RA) remains unknown. This study aims to explore the potential role of YY1 in RA pathogenesis. In this study, we found that YY1 was over-expressed in RA patients and CIA mice. Blocking of YY1 action with YY1 shRNA lentivirus ameliorated disease progression in CIA mice. We further analyzed the signaling pathway involved by ingenuity pathway analysis (IPA), results showed IL-6 signaling and JAK/Stat signaling pathway was significantly inhibited by LV-YY1-shRNA treatment. Moreover, we observed that blocking of YY1 reduced IL-6 production and downregulated Th17 population. Finally, we showed YY1 positively regulated IL-6 transcription by binding to the promoter region of the IL-6 gene. In conclusion, YY1 plays a critical role in promoting IL-6 transcription in RA which contribute to the inflammation of RA via stimulation of Th17 differentiation. Thus, YY1 is likely a key molecule involved in the inflammation process of RA. Targeting of YY1 may be a novel therapeutic strategy for RA.

PU-1634

抗 CCP 抗体检测在类风湿性关节炎中的临床意义

陈永新
山东省千佛山医院

目的 通过收集抗 CCP 抗体的检测结果，分析抗 CCP 抗体检测在类风湿性关节炎患者中的临床意义。
方法 选取 2020 年 6 月~11 月在本院风湿免疫科确诊的类风湿性关节炎患者 100 例作为实验组，同期非类风湿性关节炎的自身免疫病患者 100 例作为对照 A 组，同期健康体检者 100 例作为对照 B 组，分别对 3 组标本进行抗 CCP 抗体检测，记录数据并分析比较。
结果 实验组分别与对照 A 组、对照 B 组比较，抗 CCP 抗体均有明显的升高，差异有统计学意义(P<0.05)。
结论 抗 CCP 抗体对 RA 诊断有着较高的特异性和敏感性，是 RA 早期诊断的一个高度特异指标，所以对 RA 的早期实验室检查诊断时，可以对患者进行抗 CCP 抗体单独检测。

PU-1635

骨髓基质细胞诱导分化中基因表达谱变化的研究

许苗
山东省千佛山医院

目的 利用基因表达谱芯片研究大鼠骨髓基质细胞向成骨细胞分化中基因表达谱的变化。
方法 分离、培养大鼠骨髓基质细胞，以地塞米松、β-甘油磷酸钠和维生素 C 诱导分化，抽提细胞 mRNA 并逆转录成 cDNA，用基因表达谱芯片检测相关基因的差异表达。
结果 经诱导后的细胞可见有钙化结节，与正常传代的细胞相比有 27.7%基因的差异表达超过了 3 倍，而参与转录、翻译、糖基化修饰和调节细胞外基质、信号分子形成及参与代谢的相关基因表达均有不同程度的上调。
结论 基因表达谱芯片技术可显示细胞在诱导分化中多基因的差异表达，这些差异表达基因是大鼠骨髓基质细胞在增殖和成骨分化诱导中所必需参与的基因。

PU-1636

CA-125 联合 BDNF 对老年急性心梗患者急性心衰的预测价值

汪雅婷
安徽医科大学第二附属医院

目的 探讨糖类抗原 125 联合脑源性神经营养因子（brain-derived neurotrophic factor，BDNF）在早期预测老年急性心肌梗死（AMI）患者发生急性心衰(AHF)的诊断价值；分析两者水平与急性心衰严重程度的相关性；
方法 医院心内科收治的急性心肌梗死（AMI）患者 144 例，收集所有患者入院时的临床资料，入院后抽取患者空腹静脉血，采用全自动免疫分析仪测定血清 CA-125 和 BDNF 水平，根据冠脉再灌注治疗后 1 周内是否发生急性心衰分为心衰组和对照组，对比两组患者临床资料，采用多因素 logistic 回归方程分析影响 AMI 患者发生 AHF 的独立危险因素；采用 Spearman 线性方程分析 CA-125、BDNF 水平和急性心衰患者心功能分级的相关性；绘制受试者工作特征曲线，分析 CA125 联合 BDNF 对老年急性心梗患者急性心衰的预测价值；

结果 144 例 AMI 患者共发生 42 例急性心衰，据此分组后对比两组患者临床资料显示，心衰组患者在肌钙蛋白（cTnI）、心房脑钠肽（BNP）、CA-125、BNDF 及病变支数方面与对照组比较存在统计学差异（P<0.05）；多因素 logistic 回归分析显示，BNP（OR=1.015）、CA-125(OR=23.228)、BNDF（OR=1.455）水平升高是导致 AMI 患者发生 AHF 的独立危险因素（P<0.05）；Spearman 线性方程显示，CA-125、BDNF 水平与心功能分级呈正相关（ρ=0.981,0.808,P<0.05）；ROC 曲线显示，CA-125 联合 BNDF 在早期预测 AMI 患者发生 AHF 的曲线下面积高于 CA-125 和 BDNF 单独预测，其诊断敏感度为 78.57%，特异度为 89.22%；
结论 通过监测血清 CA-125 和 BNDF 水平能够有效预测老年 AMI 患者发生 AHF 风险，并且水平高低与临床心功能严重程度相关。

PU-1637

Tim-3 对三阴性乳腺癌增殖、迁移、侵袭中的作用及机制研究

韩福燕
山东大学第二医院

目的 T 细胞免疫球蛋白及黏蛋白结构域分子-3（T cell immunoglobulin and mucin-domain containing molecule-3,Tim-3）是一种负性免疫调节分子，不但表达于免疫细胞上，也表达于肿瘤细胞上，在肿瘤免疫中发挥重要的功能。研究发现 Tim-3 在宫颈癌、黑色素瘤、肺癌细胞上的表达明显高于癌旁组织。本文我们研究 Tim-3 在三阴性乳腺癌细胞中的表达情况及对其增殖、迁移、侵袭和凋亡的影响。
方法 通过 Western 检测乳腺癌细胞株 Tim-3 的表达；利用 CCK-8、划痕、Transwell 及 Annexin V/FITC，检测 Tim-3 对乳腺癌细胞增殖、迁移、侵袭、凋亡的影响。
结果 运用 Western blotting 检测发现 Tim-3 在 MCF-7 中表达相对较高，在 MDA-MB-231 中表达相对较低。利用 CCK-8 检测发现 Tim3-siRNA 组细胞的增殖能力明显低于 NC 组；转染 ADV-Tim3 组细胞的增殖能力明显强于 Control 组（P<0.05）。划痕实验发现 Tim3-siRNA 组 24h 的迁移距离显著小于 NC 组，ADV-Tim3 组细胞的迁移距离显著大于 Control 组（P<0.05）。利用 Transwell 来验证 Tim-3 对侵袭能力的作用，我们发现 Tim3-siRNA 组穿过膜的细胞数量明显比 NC 组低，ADV-Tim3 组穿过膜的细胞个数显著高于 Control 组（P<0.05）。
结论 Tim-3 可表达乳腺癌细胞上。Tim-3 可促进三阴性乳腺癌细胞的增殖、迁移、侵袭能力及抑制其早期凋亡，为三阴性乳腺癌的防治提供新靶点。

PU-1638

miR-16-5p 对 HIV 感染者抗病毒治疗后 T 细胞功能影响的研究

吕俊楠、李佳琦、宋成博、蔡红娇、李思瑶、张子宁
中国医科大学附属第一医院

目的 我们的前期结果发现了 HIV 感染者 ART 治疗后免疫重建不良患者的血浆中 miR-16-5p 表达量较高，并且可作为疾病进展的预测标志物之一。因此我们拟探索 miR-16-5p 是否对 HIV 感染者 T 细胞增殖和凋亡情况产生影响，并进一步探索 miR-16-5p 影响 T 细胞功能的基因和功能调节机制，明确 miR-16-5p 对 HIV 感染者 ART 治疗后免疫恢复的影响作用。
方法 本研究选取了 31 例 ART 治疗 1 年以上的 HIV 感染者。通过在 T 细胞中转染 miR-16-5p mimics，采用流式细胞术观察过表达 miR-16-5p 的 CD4+、CD8+ T 细胞增殖和凋亡的变化情况。对 miR-16-5p 过表达的 HIV 感染者 T 细胞的基因表达情况进行转录组测序分析，并根据转录组分析结果，采用流式细胞术分析 miR-16-5p 对 CD4+、CD8+ T 细胞活化时钙离子内流的影响情况。
结果 过表达 miR-16-5p 的 CD4+和 CD8+ T 细胞在活化后 72 小时的增殖水平明显下降，而在活化

48 小时的凋亡情况无明显变化。过表达 miR-16-5p 的 T 细胞的差异表达基因显著富集于阳离子转运通路，并且 CACNB2 基因的表达明显降低。过表达 miR-16-5p 的 CD4+ T 细胞活化时细胞内钙离子内流与对照相比显著降低，而 CD8+ T 细胞活化时钙内流仅有下降趋势。
结论 通过观察 miR-16-5p 对 CD4+、CD8+ T 细胞增殖和凋亡变化的影响及深入探索，发现 miR-16-5p 通过影响细胞活化时钙内流过程进而影响 T 细胞增殖，对 HIV 感染者 ART 治疗后的免疫恢复产生抑制作用。

PU-1639

Study on the diagnostic value of three microRNAs in serum for gastric cancer

Xing Ke 、Xinyu Cai、Lisong Shen
Xinhua Hospital, Shanghai Jiao Tong University School of Medicine

Objective To explore the diagnostic values of combined detection of serum miRNA-181c, miRNA-99a and miRNA-27a for gastric cancer.
Methods The expressions of serum miRNA-181c, miRNA-99a and miRNA-27a were determined by fluorescence quantitative PCR in 44 gastric cancer patients and 36 healthy controls. The expressions of three miRNAs were compared to detect whether there are significant differences. The correlations between the three miRNAs levels in serum and clinicopathological characteristics of gastric cancer patients were analyzed. The receiver operating characteristic curve (ROC) is constructed to evaluate the diagnostic performance of each miRNA and combined detection of common tumor markers, including CEA, CA 19-9, CA 724, and CA 242 for gastric cancer, and to explore the best combined detection plan. A gastric cancer risk model was conducted via binary Logistic Regression, and the diagnostic efficacy of the model was detected by the ROC curve.
Results The expressions of serum miRNA-181c and miRNA-99a were low in gastric cancer patients, while the expression of serum miRNA-27a was high ($P<0.05$). The expression of serum miRNA-181c and miRNA-27a in gastric cancer was correlated with the degree of gastric cancer invasion, lymph node metastasis, and clinical stage ($P<0.05$). The area under the ROC curve (AUC) of serum miRNA-181c, miRNA-99a, and miRNA-27a were 0.803, 0.755 and 0.627, respectively. The diagnostic efficiency of three miRNAs was higher than that of commonly used tumor markers, including CEA, CA 19-9, CA 724 and CA 242 ($P=0.007$). The combined detection of three miRNAs and four antigens had high diagnostic efficiency (AUC=0.881). Using three miRNAs to diagnose gastric cancer with all negative tumor markers, the AUC values were 0.820, 0.813 and 0.558. The gastric cancer risk model is described by the following equations: probability of malignancy=ex/(1+ex), X=36.966 - (21.477×miRNA-181c) - (4.614×miRNA-99a) + (8.568×miRNA-27a) - (0.025×LYM%) - (2.016×LYM#) - (0.084×Hb) + (0.005×HCT) - (0.006×PLA) - (0.375×Alb) - (0.008×UA). A calculated cancer probability of ≥0.94 prompts a high risk of gastric cancer, and a probability of ≤0.52 denotes a low risk of gastric cancer.
Conclusion The combined detection of serum miRNA-181c, miRNA-99a and miRNA-27a has a high diagnostic value for gastric cancer and a certain effect on predicting the risk of gastric cancer, which can be promoted and applied in clinical practice.

PU-1640

HIV 不同亚型免疫活化与疾病进展的关系研究

熊旋
中国医科大学附属第一医院

目的 HIV 流行和传播过程中不断进化出新的亚型及重组亚型。不同 HIV 亚型感染后疾病进展速度不同，其中 CRF01AE 亚型感染者疾病进展速度较快。免疫活化因素在 HIV 感染疾病进展中发挥重要作用，其是否与 CRF01AE 亚型进展较快尚未阐明报道。本研究对 CRF01AE 亚型患者和 B/B′亚型患者之间免疫活化与疾病进展的关系进行研究，明确 CRF01AE 亚型是否通过影响免疫活化度而导致疾病进展速度不同，B′亚型及 B 亚型免疫状态是否存在差异，为解析不同亚型之间疾病进展不同的免疫机制等提供依据。
方法 选取 281 例来自中国辽宁、吉林和河南的未治疗汉族 HIV/AIDS 患者。根据近全长 HIV 基因组测序和病毒序列亚型鉴定结果将患者分为 CRF01AE 亚型组和 B/B′亚型组。使用流式细胞仪检测淋巴细胞计数、CD38 和 HLA-DR、浆细胞样与髓系 DC，使用 ELISA 检测趋化因子 RANTES，MIP-1α，MIP-1β 和 SDF-1 水平。
结果 1、B 亚型的活化指标 CD4+CD38+T 细胞、CD8+CD38+T 细胞高于 B′亚型，CD11c+DC 细胞低于 B′亚型；2、CRF01AE 亚型的活化指标 CD8+HLA-DR+T 细胞高于 B/B′亚型；CD8+T 细胞计数高于 B/B′亚型；而 MIP1α、MIP1β、CD123+DC 细胞、CD11c+DC 细胞均显著低于 B/B′亚型。3、活化指标 CD4+CD38+T 细胞与病毒载量显著相关（r=0.245，P<0.001）；CD4+HLA-DR+T 细胞、CD8+HLA-DR+T 细胞、CD8+CD38+T 细胞均与 CD4+T 细胞呈负相关，与病毒载量呈正相关；CD123+DC 细胞、CD11c+DC 细胞与 CD4+T 细胞均呈正相关，与病毒载量呈负相关。
结论 不同亚型的进展不同的内在机制可能与 T 细胞免疫活化、DC 细胞的保护作用的差异有关，为 HIV 不同亚型进展不同的内在免疫机制提供了新的依据。

PU-1641

High proportion of Circulating CD8+CD28− senescent T Cells is an Independent Predictor of Distant Metastasis in Nasopharyngeal Cancer after Radiotherapy

Xiaotian Xu、Lin Xiao、Wei Cui
National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College

Background Immunosenescent CD8+CD28− T cells are a unique subset of T cells that are increased in human peripheral blood with increasing age and declining immune function. CD8+CD28− T cells also have an antigen-non-specific immunoregulatory function. Therefore, CD8+CD28− T cells may profoundly influence tumor progression. To gain novel insights into the role of CD8+CD28− T cells in nasopharyngeal carcinoma (NPC), we investigated the proportion and clinical relevance of CD8+CD28− T cells in the peripheral blood of patients with NPC.
Methods Flow cytometry was performed to explore the frequency of peripheral CD8+CD28− T cells in 351 pretreatment patients with NPC, including a training (n = 123) and validation (n = 228) cohort. Statistical analyses were conducted to determine an association between the CD8+CD28− T cells proportion and clinical characteristics of the patients. After a 5-year follow-up period, progression-free survival (PFS) and distant metastasis-free survival (DMFS) analyses were performed with the Kaplan-Meier method.
Results The proportion of CD8+CD28− T cells in peripheral blood was significantly increased in patients with NPC and was unrelated to age, sex, plasma Epstein Barr virus (EBV)-DNA level, or clinical staging. High pretreatment levels of peripheral CD8+CD28− T cells were closely

associated with recurrence and distant metastasis after radiotherapy in both the training ($p < 0.0001$; hazard ratio [HR], 4.96; 95% confidence interval [CI], 2.20–9.96) and validation ($p = 0.0008$; HR, 2.20; 95% CI, 1.38–3.49) cohorts. After multivariable adjustment, the proportion of CD8+CD28− cells remained a strong independent prognostic factor for PFS and DMFS in both the training and validation cohorts.
Conclusions A high proportion of pretreatment CD8+CD28− T cells is an independent risk factor for recurrence and distant metastasis in patients with NPC after radiotherapy. The incorporation of circulating CD8+CD28− T cells can improve the prognostic value of plasma EBV-DNA and clinical staging.

PU-1642

潜在细胞因子 CCDC134 对免疫抑制性肿瘤微环境的调节作用及机制研究

肖琳、崔巍
中国医学科学院肿瘤医院

目的 肿瘤微环境（TME）对肿瘤的发生发展至关重要，它具有免疫抑制特性，使其中的细胞毒性 T 细胞（Tc）发生功能障碍，亟需寻求解除 TME 免疫抑制的分子机制，以建立 Tc 细胞长久有力的抗肿瘤免疫。已知 MAPK 通路在 TME 中异常激活，参与抑制性 TME 的形成。CCDC134 是 MAPK 通路抑制分子，我们首次报道它是 γ_c 家族新细胞因子，通过 Tc 细胞抑制肿瘤生长。然而，CCDC134 能否有效抵御 TME 对 Tc 细胞的免疫抑制，以及重塑 TME 免疫状态的机制尚不清楚。
方法 以原创发现的新细胞因子 CCDC134 为研究对象，以 TCGA 肿瘤数据分析为依据，通过肿瘤种植模型和 TCR 刺激模型，利用 CCDC134 重组蛋白和基因工程鼠，集中研究其重塑 TME 免疫特征的作用及机制。
结果 在深入研究中，申请人对 TCGA 数据库 33 种癌症近 2 万例患者的数据进行了分析，获得了重要的临床证据和线索提示。首先，在绝大多数癌种中，CCDC134 转录水平在 TME 中高于正常组织；更重要的是，在宫颈癌、乳腺浸润癌、胃癌、直肠癌、胸腺癌中，肿瘤组织 CCDC134 的转录水平与患者预后呈正相关，进一步证实了 CCDC134 有效的抑瘤效应。接下来，申请人重点分析了 CCDC134 在这五种癌症中的表达共性：1）与文献报道一致，CCDC134 mRNA 水平均与 ERK/MAPK 通路的活性成反比，提示 CCDC134 是 MAPK 通路的抑制分子。2）申请人重点分析了 AP-1 家族、免疫抑制性分子、调节免疫抑制性分子表达和降解的因子、调节 T 细胞耗竭过程的关键因子等近四十个基因与 CCDC134 转录水平的相关性，发现在所有受益癌种中，CCDC134 的表达水平均与 c-Jun、c-Fos 和 NR4A TFs 成反比，这些基因均参与免疫抑制性 TME 的形成，并均受 MAPK 通路调控。
结论 CCDC134 通过抑制 MAPK 通路解除 TME 对 Tc 细胞的免疫抑制，进而促进其介导的肿瘤免疫。

PU-1643

肝素结合蛋白在髓系白血病中的应用价值研究

杨涛[2]、方莉[1]
1. 川北医学院附属医院
2. 三台县人民医院

目的 探讨 HBP 在髓系白血病患者中的应用价值，对 HBP 的应用领域进行有效的补充和完善。
方法 检测 122 髓系白血病患者（其中白血病合并感染患者 16 例，非感染患者 106 例）、32 例非恶性血液病的白细胞缺乏患者、33 例门诊急性上呼吸道细菌感染患者和 29 例健康体检肝素结合蛋

白（HBP）、白细胞（WBC）、中性粒细胞百分比（N%）、降钙素原（PCT）和 C 反应蛋白（CRP）水平，根据结果进行统计学分析。
结果 1.经差异性检验显示 HBP 在感染组与其他组之间均具有统计学差异（均 P<0.001）。2.Spearman 相关分析显示在感染对照组中 HBP 仅与 PCT 呈正相关（P=0.035）；Logistic 回归显示 HBP 与急性上呼吸道感染密切相关(P=0.011）；所有受试者 ROC 分析显示 HBP 对患者感染状态具有筛查性能（AUC=0.625，P=0.004），由此说明 HBP 可作为感染性标志物。3.Spearman 相关分析显示在白血病组中 HBP 仅与 WBC 呈正相关（P<0.001）；多元线性回归偏相关分析显示白细胞缺乏和白血病患者 HBP 与 WBC 密切相关（均 P<0.05），由此证实 HBP 水平与 WBC 水平密切相关。4.采用 ROC 分析检测指标对白血病患感染状态的筛查性能发现，HBP、WBC 和 N%（均 P>0.05）对白血病患者感染状态无筛查性能，而 PCT（AUC=0.963）和 CRP（AUC=0.883）对白血病患者感染状态仍具有筛查性能。
结论 在髓系白血病患者以及非恶性白细胞缺乏症患者中，HBP 水平仅与 WBC 水平呈密切正相关，对于筛查髓系白血病患者是否发生感染方面，除了传统的标志物 PCT 和 CRP 可供使用外，HBP、WBC 和 N%均对不具备感染筛查能力，因此不建议使用 HBP 来诊断髓系白血病中的感染发生。

PU-1644

多囊卵巢综合征患者性激素结合球蛋白水平与糖脂代谢相关性

陈莉
南山区蛇口人民医院

目的 探讨多囊卵巢综合征(PCOS)患者性激素结合球蛋白(SHBG)水平与糖脂代谢相关性。
方法 选取本院接诊的 96 例 PCOS 患者(实验组)及同期体检的 80 例育龄女性(对照组)，实验组根据 SHBG 水平分为两个亚组，进行血清激素、胰岛素及血脂检测，分析 SHBG 与糖脂代谢的关系。
结果 低 SHBG 组的 FAI、FINS、TG、TC、ApoB 水平均高于 SHBG 正常组，HDL-C、ApoA 水平均低于 SHBG 正常组(P<0.05)，SHBG 正常组与对照组上述各指标比较无差异(P>0.05)。PCOS 患者的 SHBG 水平与 HDL-C、ApoA 有正相关关系，与 FAI、FINS、TG、TC、ApoB 均有负相关关系(P 均<0.05)。
结论 PCOS 患者 SHBG 与 FAI、FINS、及血脂指标关系密切，SHBG 水平的变化也可以作为 FINS 和血脂变化的提示指标。低 SHBG PCOS 患者更易发生血糖、血脂异常，SHBG 水平降低可能是患者发生血脂紊乱的危险因素。从而为临床提早诊断及及时治疗 PCOS 提供重要的参考依据。

PU-1645

弥漫大 B 细胞淋巴瘤患者免疫治疗期间外周血淋巴细胞亚群数量和活性的动态变化

侯红艳、汪峰、吴士及
华中科技大学同济医学院附属同济医院

目的 分析初诊弥漫大 B 细胞淋巴瘤（DLBCL）患者免疫治疗期间外周血淋巴细胞亚群数量和活性的动态变化。
方法 本研究共纳入 33 例 DLBCL 患者，使用流式细胞术检测其外周血淋巴细胞亚群数量、表型和功能，并对其中 18 例患者进行淋巴细胞的活性变化进行动态分析。
结果 初诊 DLBCL 患者的 CD3+ T、CD4+ T、CD8+ T 细胞和 NK 细胞数量低于健康对照组，特别是在国际预后指数（IPI）评分较高组。高风险组（IPI 评分 3-5）和低风险组（IPI 评分 0-2）患者的淋巴细胞数量无显著差异，但 CD4+ T 细胞表面 CD28 和 CD8+ T 细胞表面 HLA-DR 在高风险组的表达增高。高风险组患者调节性 T 细胞比例增高，且 CD4+ T 和 CD8+ T 细胞分泌 IFN-γ 的能力

降低，提示该组患者细胞免疫功能受损。该研究进一步分析了 R-CHOP 治疗期间淋巴细胞数量和功能的动态变化，由于化疗的细胞细胞毒性，CD3+ T, CD4+ T, CD8+ T 细胞和 NK 细胞数量进一步降低，6 周期 R-CHOP 治疗后逐渐恢复。CD4+ T 和 CD8+ T 细胞功能在 2 周期 R-CHOP 治疗后恢复，而 NK 细胞功能在整个病程中影响较小。结果表明 DLBCL 患者淋巴细胞数量和功能降低，特别是 CD4+ T 和 CD8+ T 细胞。

结论 DLBCL 患者 CD4+T 和 CD8+T 细胞数量和功能降低，有效治疗后逐渐恢复。因此，T 细胞数量和功能的联合检测在实施 DLBCL 的个体化治疗及探寻新的预后指标中具有重要临床价值。

PU-1646

Dynamic changes in peripheral blood lymphocyte subset counts and functions in patients with diffuse large B cell lymphoma during chemotherapy

Hongyan Hou 、Feng Wang、Shiji Wu
Tongji Hospital, Tongji Medical College, Huazhong University of Science and Technology

Background This study aimed to analyze the lymphocyte subsets, their activities and their dynamic changes during immunochemotherapy in patients newly diagnosed with diffuse large B cell lymphoma (DLBCL).

Methods Patients with DLBCL (n=33) were included in the present study. Their peripheral lymphocyte subsets, phenotypes and functions were detected using flow cytometry. The dynamic results of lymphocyte activities were available for 18 patients.

Results Compared with healthy controls (HCs), the counts of CD3+, CD4+, and CD8+ T cells as well as those NK cells decreased in patients newly diagnosed with DLBCL, mainly attributed to patients with high risk of prognosis assessed by International Prognostic Index (IPI) score. Lymphocyte counts didn't present significant difference between high risk (IPI scores 3-5) and low risk patients (IPI scores 0-2), but CD4+ T cells and CD8+ T cells expressed higher levels of CD28 and HLA-DR, respectively, in patients with IPI score ranging from 3 to 5. Patients at high risk harbored higher percentage of regulatory T cells (Tregs), and their CD4+ and CD8+ T cells produced lower levels of IFN-γ, reflecting an impaired cellular immune response. The dynamic changes of lymphocyte numbers and functions during treatment were further investigated. Total counts of CD3+, CD4+, CD8+ T and NK cells progressively decreased because of the cytotoxicity of chemotherapy and then gradually recovered after six cycles treatment (rituximab combined with cyclophosphamide, doxorubicin, vincristine and prednisone, R-CHOP). The functions of CD4+ and CD8+ T cells recovered by the end of two cycles R-CHOP treatment, although NK cell function was not significantly affected throughout treatment. These results suggest that the counts and functions of lymphocytes are significantly decreased in patients with DLBCL, particularly those of CD4+ and CD8+ T cells.

Conclusions The absolute counts and functions of CD4+, CD8+ T cells, which were significantly lower in patients with DLBCL, gradually recovered after effective treatment. Therefore, combined detection of T cell counts and functions are critically important for administering effective personalized immunotherapy as well as for identifying new prognostic markers or DLBCL.

PU-1647

胰岛素瘤手术中胰岛素、C-肽、血糖的动态观察及分析

李世蕊、王芃
中日友好医院

目的 评价胰岛素瘤患者手术治疗在术中进行胰岛素、C-肽、血糖动态监测的作用和意义

方法 在本院收治的一例胰岛素瘤患者，男性，69 岁，依据 Whipple 三联征症状及血糖、B 超等检测结果确诊后，入院实施腹腔镜手术治疗。在该患者手术前、后不同时间点采集血样，检测血清胰岛素、血清 C-肽、指尖血糖，确定肿瘤切除是否完全，与患者手术转归进行分析。
结果 该患者在手术麻醉前检测外周血胰岛素、血 C-肽、血糖分别为 18.55uIU/mL、1.98ng/mL、4.1mmol/L 腹腔镜切除肿瘤组织，在肿物切除后 1min、5min、10min、15min、30min、60min、90min 分别测定外周血胰岛素、C-肽及相应指尖血糖变化，结果显示外周血中胰岛素明显而迅速地降低，分别为 59.68uIU/mL、37.62uIU/mL、24.12uIU/mL、17.61uIU/mL、8.83uIU/mL、2.74uIU/mL、2.17uIU/mL，血 C-肽也明显降低，分别为 6.58ng/mL、5.87ng/mL、5.12ng/mL、4.71ng/mL、3.74ng/mL、3.65ng/mL、2.16ng/mL，血糖则相应有所恢复，分别为 3.7mmol/L、3.7mmol/L、4.2mmol/L、4.2mmol/L、3.6mmol/L、4.1mmol/L、4.9mmol/L。在术后 2 日的空腹的血胰岛素和 C-肽分别为 7.88 uIU/mL 和 1.70 ng/mL，均较术前显著降低，在正常范围之内。
结论 在胰岛素瘤切除术中,血胰岛素、血 C-肽和血糖的动态监测观察良好地反映了手术对肿瘤负荷是否清除及清除程度，并且血胰岛素的检测也为常规的血糖检测提供了交叉验证的方法和灵敏的确认性指标，因此是术中必要的检测手段和疗效预测指标。

PU-1648

血清 IFN-γ、IL-17 水平与耐多药肺结核患者化疗预后的相关性

张裕祥
新疆医科大学第六附属医院

目的 观察血清干扰素-γ（IFN-γ）、白细胞介素-17（IL-17）在耐多药肺结核（MDR-TB）患者中表达，并分析二者与 MDR-TB 化疗预后的关系。
方法 回顾分析，收集 2017 年 1 月-2018 年 10 月医院完成标准化疗 87 例 MDR-TB 患者病历资料，全部患者于化疗前、化疗 3 个月、化疗 6 个月时接受实验室指标检测，且检测结果资料完整；重点记录患者各时点血清 IFN-γ、IL-17 表达；根据 24 个月标准化化疗预后分为治愈组（57 例）、失败组（30 例），分析血清 IFN-γ、IL-17 与 MDR-TB 患者化疗预后关系。
结果 随着治疗时间延长，两组 IFN-γ 水平逐渐升高，IL-17、IL-10、超敏 C 反应蛋白（hs-CRP）水平逐渐降低，但失败组各时点 IFN-γ 水平低于治愈组，IL-17、IL-10、hs-CRP 水平均高于治愈组（P＜0.05）；相关性检验发现，MDR-TB 患者化疗预后情况与不同时点血清 IFN-γ 水平呈正相关（r＞0，P＜0.05），与 IL-17 水平呈负相关（r＜0，P＜0.05），且在化疗前相关系数 r 最大；化疗前血清 IFN-γ、IL-17 水平之间呈负相关（r=-0.922，P＜0.001）；绘制 ROC 曲线，化疗前血清 IFN-γ、IL-17 预测化疗失败的 AUC 均＞0.80，有一定预测价值，且当二者 cut-off 值分别取 14.583pg/ml、53.881ng/L 时，可获得最佳预测价值。
结论 MDR-TB 患者化疗前 IFN-γ 低表达、IL-17 过表达与化疗失败有一定联系，早期监测患者血清 IL-17、IFN-γ 水平，对预测 MDR-TB 患者化疗预后有一定价值。

PU-1649

血清 CTX-II 蛋白在股骨头坏死早期诊断及监测中的临床意义

黄俊远、周迎春
广州中医药大学第一附属医院

目的 探讨检测血清 CTX-II 蛋白在股骨头坏死早期诊断及病情监测中的应用价值。
方法 纳入符合标准的病例 132 例作为实验组，根据不同病因、不同分期将实验组再分组，纳入体检正常的健康人群 68 例作为对照组。采用 ELISA 法检测两组受试者血清 CTX-II 浓度（ng/mL）。

结果 实验组血清 CTX-II 浓度显著高于对照组（P<0.001）；不同病因患者血清 CTX-II 浓度无显著差异（P>0.05）；在不同 ARCO 分期，Ⅱ期患者血清 CTX-II 浓度与Ⅲ期、Ⅳ期分别比较，差异没有统计学意义（P>0.05），Ⅲ期与Ⅳ期比较，差异有统计学意义（P<0.05）；用 ROC 曲线分析实验组和对照组的血清 CTX-II 浓度，曲线下面积为 0.7554，P<0.0001；实验组血清 CTX-II 浓度与 ARCO 分期之间的相关系数为 0.293，该相关具有统计学意义（P<0.05）。
结论 血清 CTX-II 在诊断 ONFH 时有一定的灵敏度和特异性，ONFH 患者血清 CTX-II 浓度会随着股骨头坏死程度的加重而升高。在 ONFH 的诊断和病情监测中,血清 CTX-II 表现出一定的临床应用价值，可作为临床诊断和病情监测的参考指标之一。

PU-1650

Construction and application of tolerant dendritic cells modified with NF-κ B oligodeoxynucleotides decoy in rat of collagen-induced arthritis

Lichang Ning
The First Affiliated Hospital of Nanhua University

Objective In rheumatoid arthritis (RA)，dendritic cells (DCs) play a crucial role in the initiation of autoimmunity ; therefore, we explored the construction of stable, tolerant DCs from the spleen of collagen-induced arthritis (CIA) rats by the NF-κB oligodeoxynucleotide (ODN) decoy strategy.The CIA rat-derived DC-loaded bovine collagen type II (BIIC) was injected into the self-CIA rats for in vivo intervention test, and the intervention effect was observed,which seeks new targets and strategies for the treatment of RA.
Methods In vitro cell experiments, mononuclear cells derived from the spleen of CIA rats were induced to DCs by the cytokines GM-CSF and IL-4. DCs were treated with NF-κB ODN decoy for morphological observation, viability evaluation, phenotypic identification and tolerance assessment.In an in vivo rat experiment, DCs derived from the spleen of CIA rats were induced by ODN decoy and loaded with BIIC, and then infused into self-CIA rats via the tail vein for intervention in the course of disease. That is, on the 20th day of the primary immunization of the bovine type II collagen, the CIA has already occurred in the rat.The degree of joint swelling in each group of rats was observed every day, and then the arthritis index was calculated. On the 42nd day, rats in each group were treated to detect the pathological changes of synovial tissue and the contents of cytokines IFN-γ and IL-10 in serum..
Results In vitro cell experiments, the spleen-derived DCs of CIA rats were treated with ODN Decoy, and the expression of surface co-stimulatory molecules CD80 and CD86 and mean fluorescence intensity were decreased. In the mixed lymphocyte co-culture, the ability of DCs treated with ODN Decoy to stimulate lymphocyte proliferation was decreased; lymphocytes were in a state of low secretion of IFN-γ and high secretion of IL-10.This indicates that CIA rat-derived DCs have the characteristics of immature DCs induced by NF-κB ODN Decoy, and the immature characteristics after stimulation with LPS are unchanged.In the in vivo rat experiment, the arthritis index of CIA rats was significantly increased; the pathological changes of joint synovial tissue were obvious, and the secretion of inflammatory factors IFN-γ and IL-10 in serum was imbalanced. After returning BIIC-Decoy DC to CIA rats on the 20th day, the arthritis index and the synovial tissue pathological score were significantly reduced, and the serum inflammatory factors IFN-γ and IL-10 were balanced.
Conclusion The spleen-derived DCs of CIA rats successfully constructed morphological, phenotypic and functionally stable tolerant DCs by NF-κB ODN Decoy strategy, which effectively reduced the arthritic symptoms and histopathological damage of CIA rats during the course of disease.This research indicates that, according to the actual clinical situation, it is possible to prepare a specific tolerant DC from the patient who has already developed RA, and then inject

the tolerant DC into the patient for therapeutic intervention. This is a very feasible method for treating patients who have developed rheumatoid arthritis.

PU-1651

CIA 大鼠经耐受性 DC 干预后血清中 IL-4、TGF-β、IFN-γ 及 IL-17 水平变化

宁丽常
南华大学附属第一医院

目的 探讨 NF-κ B 寡脱氧核苷酸诱骗剂(NF-κB ODN decoy)构建的耐受性树突状细胞(DC)对胶原诱导性关节炎(CIA)大鼠血清 IL-4、TGF-β、IFN-γ 和 IL-17 表达水平的影响。

方法 以 SD 雌性大鼠为实验动物，分为空白对照组、CIA 模型组、BⅡC-Decoy DC 实验组和 BⅡC-Decoy DC 对照组，共四个组。CIA 模型组在大鼠左足注射牛Ⅱ型胶原(BⅡC)，空白对照组注射生理盐水，BⅡC-Decoy DC 实验组在 CIA 模型组的基础上在初次免疫第 20 天尾静脉注射耐受性 DC。从建模开始，每周观察各组大鼠各关节肿胀程度，计算关节炎指数(AI)，用酶联免疫吸附法(ELISA)检测各组大鼠血清 IL-4、TGF-β、IFN-γ 和 IL-17 水平。

结果 与 CIA 模型组相比，BⅡC-Decoy DC 实验组大鼠较少出现关节肿胀和关节畸形等情况，关节炎指数评分明显降低（p＜0.05）；BⅡC-Decoy DC 实验组大鼠血清 IL-4、TGF-β 水平显著升高，IFN-γ、IL-17 水平显著降低（p<0.05）。

结论 耐受性 DC 通过纠正 CIA 大鼠血清中 IL-4、TGF-β、IFN-γ 和 IL-17 水平失衡来减轻大鼠关节炎症状。

PU-1652

新型冠状病毒肺炎流行前后成都地区健康体检者体液免疫指标分析

邓君
四川省医学科学院·四川省人民医院

目的 了解新型冠状病毒肺炎流行前后成都地区健康体检者体液免疫状况，探讨新型冠状病毒肺炎流行期是否对普通人群的身体免疫力存在影响。

方法 2019 年 3-4 月和 2020 年 3-4 月，对来自四川省人民医院体检中心健康体检者的体液免疫－免疫球蛋白 A（IgA）、免疫球蛋白 G（IgG）、免疫球蛋白 E（IgE）和免疫球蛋白 M（IgM）数据进行分析统计，其中 2019 年 482 例（男性 252 例，女性 230 例），2020 年 427 例（男性 215 例，女性 212 例）。

结果（1）与 2019 年相比，女性 2020 年的 IgE 和 IgM 降低（P<0.05），IgG 和 IgA 无显著性差异（P>0.05）；

（2）与 2019 年相比，男性 2020 年的 IgE 降低（P<0.05），IgG、IgM 和 IgA 无显著性差异（P>0.05）；

（3）2020 年，女性 IgE 高于男性（P<0.05），男性 IgM 高于女性（P<0.05），IgG 和 IgA 则无显著性差异（P>0.05）。

（4）2020 年 40 岁以上女性的 IgM 低于 40 岁以下女性（P<0.05），IgG、IgE 和 IgA 无显著性差异（P>0.05）；

（5）2019 年 40 岁以上女性的 IgM、IgG、IgM 和 IgA 与 40 岁以下女性无显著性差异（P>0.05）；

（6）2019 年和 2020 年 40 岁以上男性的 IgM、IgG、IgM 和 IgA 与 40 岁以下男性无显著性差异（P>0.05）。

结论（1）疫情期间，男女体液免疫水平产生差异，特别是 40 岁以上的女性，免疫能力可能有所下降，这和疫情期间宅在家中，缺乏锻炼和饮食等可能有关系；

（2）COVID-19 已经构成世界大流行，严重威胁全人类的生命健康，造成重大的经济损失，虽然目前在我国已得到有效控制，我们更应该大力加强健康管理、积极主动锻炼身体提高免疫力、完善营养膳食、倡导良好生活方式以及融入心理健康辅导,加强自我保健,预防疾病发生,提高全民健康水平。

PU-1653

Characteristics and diagnostic significance of the repertoire features of peripheral blood T cell receptor in patients with lung indeterminate nodules

Huaichao Luo
Sichuan Cancer Hospital & Institute, Sichuan Cancer Center, School of Medicine, University of Electronic Science and Technology of China

Background The T-cell receptor (TCR), located on the surface of T cells, is responsible for the recognition of the antigen-major histocompatibility complex, leading to the initiation of an inflammatory response. Analysing the TCR repertoire may help to gain a better understanding of the immune system features and of the aetiology and progression of diseases, in particular those with unknown antigenic triggers. Current clinical management of patients with pulmonary nodules involves either repeated LDCT/CT scans or invasive procedures yet causes significant patient misclassification. An accurate non-invasive test is needed to identify malignant nodules and reduce unnecessary invasive tests . The aim of this study was to determine the basic characteristics and diagnostic significance of the peripheral blood T-cell receptor (TCR) repertoire in patients with indeterminate nodules;

Method Multiplex PCR amplification of CDR3 of the TCR β chain (TRB) was conducted including PCR1 and PCR2, inclusively and semi-quantitatively.To amplify all possible V(D)J combinations, a set of 32 V forward and 13 J reverse primers was used to perform multiplex PCR1 assays as follows: 1 cycle at 95 _x0001_C for 15 min, 10 cycles of denaturation at 94 _x0001_C for 30 s, and 10 cycles of annealing at 60 _x0001_C for 90 s and extension at 72 _x0001_C for 30 s. In the second round, PCR2 was performed using universal primers. Sequencing libraries were loaded onto the Illumina XTen System, and reads of 151-bp fragments were obtained. The CDR3 sequence was defined as the amino acids between the second cysteine of the V region and the conserved phenylalanine of the J region, according to the ImMunoGeneTics (IMGT) V, D, and J gene references. Then, high throughput sequencing was used to identify hypervariable rearrangements of complementarity determining region 3 (CDR3) of the TCR β chain in peripheral blood samples.Shannon’s entropy was calculated on the clonal abundance of all productive TCR sequences. The normalized Shannon’s entropy (Shannon index) was determined by dividing Shannon’s entropy by the natural logarithm of the number of unique productive TCR sequences prospectively 48 indeterminate nodules are determined as suspected malignant by thoracic doctors, which were divided into the training cohort and testing cohort randomly.Differences between groups were compared using the Mann–Whitney or Kruskal–Wallis tests. Correlations between variables were analyzed using Spearman’s rank test. Relationships between clinical benefit and the TCR repertoire were determined using Fisher’s exact test. All statistical analyses were calculated using R(V3.4.4).

Results We found that the TCR repertoire differed substantially between stage I and benign group in terms of CDR3 clonotype, diversity, V/J segment usage, and sequence. Specifically, baseline diversity correlated with several clinical characteristics. Interestingly, we construct one model base one Shannon Index and two CT features, which is robust for discriminating the

indeterminate nodules, even whose size is less than 20mm. In training group, receiver operating characteristic (ROC) value is 0.92, and in the test group the receiver operating characteristic (ROC) value is 0.82.
Conclusions In conclusion, TCR repertoire analysis served as a useful indicator of indeterminate nodules diagnosis, moreover, model based on TCR repertoire analysis in indeterminate nodules may be utilized to direct indeterminate nodules screening. This study suggests that the TCR repertoire analysis model may provide a better test for classifying pulmonary nodules, which could help facilitate the accurate diagnosis of early-stage lung cancer from pulmonary nodule patients and guide clinical decisions.

PU-1654

一种优化带齿离心管的设备

杜江涛
西安金域医学检验所有限公司

该设备主要用来优化带齿离心管的离心以及拿取，以免在拿取过程中震荡或出现其他生物安全事故。

该设备采用塑料与磁吸作为连接，将带齿离心管放置于样本架上，利用该设备可以将离心管轻松提取并放置于离心机内，离心完毕后可利用该设备将离心管取出。

该设备可折叠变形以适用于各种样本架和离心机。

PU-1655

丙肝抗体阳性患者血清中丙肝 RNA 数量和肝功能损伤程度指标和糖蛋白的关系

张小颖
西安医学院第一附属医院

目的 探讨丙肝患者血清中丙肝抗原和丙肝核糖核酸（HCV-RNA）载量与其肝功能指标 AST、ALT 以及糖蛋白甲胎蛋白的关系。
方法 分别用化学发光法、实时荧光定量 PCR 法、全自动生化仪对本院 2017 年 1 月至 2019 年 12 月的 146 例丙肝抗体阳性患者血清进行 HCVRNA 载量及肝功能相关指标进行检测。
结果 146 例丙肝抗体阳性患者中有 120 例丙肝 RNA 阳性，占总比例的 82%，丙肝 RNA 与丙肝抗体阳性有相关性。对丙肝 RNA 含量与 ALT、AST、AFP 相关性进行分析发现丙肝在载量的高低与 ALT、AST、AFP 呈相关性（$P<0.05$）
结论 综合检测 HCV 抗体和 HCVRNA 载量可以明确诊断慢性丙肝感染及判断病毒复制情况。病毒复制可造成肝脏炎症，在一定程度上肝功能指标和糖蛋白 AFP 可反映丙肝病毒复制载量，因此在有条件的情况下可联合 ALT、AST、AFP 为指导临床诊断和鉴别诊断肝炎相关疾病。

PU-1656

Identification of potential biomarkers associated with immune infiltration in the esophageal carcinoma tumor microenvironment

Zhicheng Wang、Wenling Zhang
Xiangya third hospital of central south university

Tumor immune cell infiltration was significantly correlated with the progression and the effect of immunotherapy in cancers including esophageal carcinoma (ESCA). However, nobiomarkers were identified which were associated with immune infiltration in ESCA. In thepresent study, a total of 128 common differentially expressed genes (DEGs) were identifiedbetween esophageal squamous cell carcinomas (ESCC) and esophageal adenocarcinomas(EAC). The results of gene ontology (GO) enrichment and Reactome pathway analysis displayed that the up-regulated DEGs were mainly involved in the regulation of extracellularmatrix (ECM), while the down-regulated DEGs were mainly involved in the regulation ofcornification and keratinocyte differentiation. The most significant module of up-regulatedDEGs was selected by Molecular Complex Detection (MCODE). Top ten similar genes ofCOL1A2 were explored, then validation and the prognostic analysis of these genes displayed that COL1A2, COL1A1, COL3A1, ZNF469 and Periostin (POSTN) had the prognostic value which were up-regulated in ESCA. The expressions of COL1A2 and its four similargenes were mainly correlated with infiltrating levels of macrophages and dendritic cells (DCs)and showed strong correlations with diverse immune marker sets in ESCA. To summarize,COL1A2 and its four similar genes were identified as the potential biomarkers associatedwith immune infiltration in ESCA. These genes might be applied to immunotherapy for ESCA.

PU-1657

Vitamin D deficiency and risk factors in patients with Crohn's disease

Ruixia Yang
Jiangsu Province Hospital （The First Affiliated Hospital of Nanjing Medical University）

Background To explore vitamin D(VD) levels in patients with Crohn’s disease, and the correlation between VD levels and seasons, disease activity, lesion region, hormone therapy. To find the risk factors of VD deficiency and the role of VD in the pathogenesis and treatment of Crohn’s disease.
Methods Between March 2018 and December 2019, 86 patients diagnosed with CD at the First Affiliated Hospital of Nanjing Medical University were identified, and 86 healthy people were selected as the control group at the same time. VD, counts of white blood cells (WBC), hemoglobin (Hb), counts of platelet(PLT), C-reactive protein (CRP), erythrocyte sedimentation rate (ESR), albumin (ALB) levels were recorded at the same time of colonoscopy. Logistic regression analysis of the relationship between disease activity, lesion region, hormone therapy and vitamin D deficiency in patients with Crohn’s disease, and analyze possible risk factors.
Results The levels of VD in patients with CD was significantly lower than that in the healthy controls (35.10 nmol/L vs 67.60 nmol/L), the difference was statistically significant (Z= -10.527, P<0.001).The summer autumn group was significantly higher than the winter spring group (z = -2.215, P = 0. 027). Patients with ileum lesions have a higher proportion of vitamin D deficiency than patients with non-ileum lesions. vitamin D deficiency rate of patients in activity stage is higher than that of patients in remission stage. With the increase of the degree of inflammation, the level of vitamin D decreased. Logistic regression analysis shows that platelet count > 250 ×

10^9 /L, CRP ≥ 8 mg / L, ALB < 30 g/L and hormone therapywere risk factors for vitamin D deficiency(P<0.05).
Conclusions Patients with CD have low levels of VD, which is related to seasons. platelet count > 250 × 109 /L, CRP ≥ 8 mg / L, ALB < 30 g/L, and hormone therapy were risk factors for V D deficiency in patient with CD.

PU-1658

ELISA 检测梅毒螺旋体抗体的最佳临界值和可疑区间

沈玲英
福州市第一医院

目的 探讨酶联免疫法（ELISA）检测梅毒螺旋体抗体（TP-Ab）诊断阳性的最佳临界值（Cut-off 值）和可疑区间，降低本实验室检测 TP-Ab 的假阳（阴）性率。
方法 选取在在联勤保障部队第九〇〇医院就诊的患者经 ELISA 初筛 TP-Ab 结果为阳性和 Cut-off 值附近（阴性）的血清标本（OD＝0.1～0.6）共 26 例，并采用梅毒螺旋体特异性抗体明胶凝集试验（TPPA）作为确认试验。通过软件 SPSS22.0 绘制受试者工作特征(receiver operating characteristic，ROC)曲线，取约登(Youden)指数最大时的吸光度值作为最佳 Cut-off 值，并进一步确定可疑区间。
结果 ELISA 检测 TP-Ab 诊断阳性的最佳 Cut-off 值为 0.3055，可疑区间为[0.168,0.351]。
结论 确定适合本实验室 ELISA 检测 TP-Ab 最佳 Cut-off 值和可疑区间能够有效降低其假阳（阴）性率，减少临床的漏诊率和误诊率，为临床诊断工作提供有力依据。

PU-1659

南京地区女性人群维生素 D 营养状况及其与血脂的相关性

杨瑞霞
江苏省人民医院

目的 了解南京地区女性人群维生素 D 的营养状况，并探讨其与血脂的关系。
方法 收集 2019 年 1 月至 2020 年 9 月在江苏省人民医院体检中心进行健康体检者 358 例，检测其 25-(OH)D 及血脂水平，分析其与血脂代谢指标的关系。
结果 358 例研究对象血清 25-(OH)D 水平为 44.05(19.10 - 98.80)nmol/L，其中 25-(OH)D 缺乏者 252 例，占 70.39%；25-(OH)D 不足者 99 例，占 27.65%；25-(OH)D 充足者 7 例，占 1.96%。随着年龄增长，25-(OH)D 水平呈下降趋势，差异有统计学意义(χ^2= 59.588，P= 0.000)。夏秋组 25-(OH)D 水平显著高于冬春组(z= -5.682，P= 0.000)。25-(OH)D 与 TG 呈负相关（r= -0.63，P=0.000），与 LDL 呈负相关（r= -0.411，P= 0.000）、与 TC 呈弱相关（r= -0.137，P= 0.010）、与 HDL 不相关（r= -0.007，P= 0.894），以 25-(OH)D 为应变量，其他各项指标为自变量，进行多元线性回归分析，TG、TC、LDL 与 25-(OH)D 独立相关。不同 25-(OH)D 营养状况下，TG、TC、LDL 水平有显著差异，25-(OH)D 缺乏组的 TG、TC、LDL 水平均显著高于 25-(OH)D 不足组（P 均<0.05），25-(OH)D 缺乏组的 TG、TC、LDL 水平均显著高于 25-(OH)D 充足组（P 均<0.05）
结论 南京地区女性人群普遍存在维生素 D 营养缺乏，25-(OH)D 水平与血脂指标存在相关性。

PU-1660

梅毒螺旋体特异性抗体快速稀释方法

王雍璇
西安金域

通过使用八通道加样枪，提高梅毒螺旋体特异抗体前处理加样速度。

取出梅毒螺旋体特异性抗体试剂，恢复室温 30min，取出配套的加样板，使用八通道加样枪分别给加样板第一列加入样本稀释液 100ul，第二列、第三列、第四列加入样本稀释液 25ul，第一列加入待测样本 25ul，然后使用八通道加样枪更换新的吸嘴调整加样量为 25ul，放入第一列加有待测样本的稀释液中开始轻柔捶打混匀左右两边各吹打 20 次左右，尽量避免气泡产生，吸液 25ul 至第二列轻柔吹打混匀以此类推倍比稀释至第四列，第四列吹打混匀后吸出 25ul 稀释后的样本弃去，依次给第三列、第四列板孔中加入稀释均匀后的未致敏粒子和致敏粒子，整板振荡混匀，放置暗盒反应 2 小时后判读结果。梅毒螺旋体特异性抗体半定量实验也可使用上述方法操作，倍比稀释至第 12 孔。

PU-1661

不同方法检测高血压五项相关性分析

王欣
吉林大学第一医院

目的 采用不同方法检测高血压五项：醛固酮(ALD)、肾素（REN）、血管紧张素Ⅱ(AⅡ)、皮质醇(COR)和促肾上腺皮质激素(ACTH)水平，并探讨用化学发光法检测高血压五项水平对原发性和继发性高血压分型诊断及治疗评估。

方法 选取本院 186 例 (收缩压≥140mmHg，舒张压>90mmHg)的高血压患者，清晨采静脉血。分别用索灵生物化学发光试剂盒和放射免疫试剂盒测定醛固酮、肾素浓度并计算其比值；分别用 ENZO 酶联免疫试剂盒和安图生物化学发光试剂盒测定 AⅡ浓度；分别用 ROCHE 全自动电化学发光测定仪及配套试剂和 BECKMAN 全自动化学发光测定仪及配套试剂检测 COR 及 ACTH 浓度。

结果 不同厂家试剂盒检测高血压五项存在一定的偏差，但相关性良好(相关系数 R>0．95)，化学发光的方法较放射免疫及酶联免疫法的灵敏性及特异性更强。

结论 化学发光法做为一种灵敏度高、特异性强、准确性高、检测便利的定量检测方法，定量检测高血压 5 项对原发性和继发性高血压分型诊断及治疗效果评估更具有优势。

PU-1662

滤泡性辅助 T 细胞通过 CD40/CD40L 轴介导微小病变型肾病（MCD）发病机制的探讨

李涛
山东大学齐鲁医院

目的 研究在微小病变型肾病发病过程中滤泡性辅助 T 细胞起到的功能作用及调节方式。

方法 选取微小病变型肾病（MCD）初发确诊患者 18 名，排除继发性肾病，肿瘤等干扰因素，另取 10 名健康体检患者作为对照组(HC)。收集所有参与者外周血抗凝标本进行流式细胞学分析，同时收集所有参与者临床肾功能损伤指标（24H 尿蛋白水平）留待进行统计学相关性分析。

结果 与正常健康对照组相比，所有微小病变型肾病 MCD 患者外周血单个核细胞(PBMC)分析 T 细胞亚群中：PD1+CXCR5+CD4+Tfh 细胞，CD40L+PD1+CXCR5+CD4+Tfh 细胞水平高表达(P 值>0.05)，其他 PD1+Tfh 细胞亚群未见显著性差异。B 细胞亚群中：CD38+CD19+浆细胞，活化的 CD40+CD38+CD19+浆细胞水平高表达(P 值>0.05)，其他浆 B 细胞亚群未见显著性差异。同时微小病变型肾病患者的尿蛋白水平显著高于正常对照组(P 值>0.05)。统计学相关性分析发现：PD1+CXCR5+CD4+Tfh 细胞与 CD38+CD19+B 细胞，CD40L+PD1+CXCR5+CD4+Tfh 细胞与 CD40+CD38+CD19+B 细胞具有显著性正相关(P 值>0.05)，且两者与肾功能损伤指标尿蛋白水平具有显著性正相关(P 值>0.05)。
结论 通过结果我们发现在微小病变型肾病（MCD）发病过程中存在 T/B 细胞免疫平衡失调，其中高表达的滤泡性辅助 T 细胞可能通过 CD40/CD40L 轴介导了浆 B 细胞的发展活化，诱导了大量异常免疫蛋白的产生，导致了微小病变型肾病（MCD）患者肾脏功能受损，蛋白尿表达。

PU-1663

肿瘤异常蛋白在肺癌中的诊断价值

朱梅、朱志军、童红芳
安徽医科大学附属巢湖医院

Objective To explore the application value of TAP on the diagnosis of lung cancer.
Methods All specimens were tested for TAP and tumor markers.
Results The serum levels of TAP, ProGRP, CEA, CYFRA21-1 and CA72-4 in the patients with lung cancer were significantly higher than those with benign lung diseases ($P < 0.05$), while the serum levels of NSE and SCC showed no difference between the two groups ($P > 0.05$). The sensitivity of TAP and CYFRA21-1 in the lung cancer group was significantly higher than that of the other detection indexes ($P < 0.01$). Of all the indexes, the accuracy of CYFRA21-1 was the highest, followed by TAP.
Conclusions TAP is suitable for lung cancer screening in normal population and high-risk population.

PU-1664

Treponema pallidum flagellar filament outer layer protein Tp0664 induce THP-1 cells to express IL-6 via TLR2 pathway

Yafeng Xie
The Second Affiliated Hospital of University of South China

Objective This study is to investigate the mechanisms by which Treponema pallidum flagellar filament outer layer protein Tp0664 induces proinflammatory cytokine IL-6 in human THP-1 cells.
Methods The tp0664 gene was amplified by polymerase chain reactions (PCR) and then subcloned into the prokaryotic expression vector pET28a. The recombinant protein Tp0664 was expressed in E. coli by the induction of IPTG and purified by Ni2+-NTA affinity chromotography. Protein concentration was determined by using a bicinchoninic acid protein assay kit. Polymixin B was used to remove the endotoxin in the recombinant protein. Human THP-1 cells were cultured for transient transfection with plasmids or siRNA of TLR2, TLR4, TLR5, TLR6 and MyD88, or pretreated with the ERK1/2 inhibitor PD98059、p38 inhibitor SB203580、NF-κB inhibitor BAY11-7082 and then stimulation with recombinant protein Tp0664 for indicative time intervals. After incubation with recombinant protein Tp0664, cells were collected and disrupted, before being

tested for the transcription of IL-6 mRNA, expression of IL-6, and the phosphorylation of several signaling molecule using RT-PCR, ELISA, and Western bloting, respectively.
Results Recombinant plasmid pET28a-Tp0664, confirmed by colony PCR and sequence, was successfully constructed. The recombinant protein was expressed as supernatant with a molecular weight of 34 kDa. After Ni-NTA affinity purification, the purity of the recombinant protein reached up to 95%. Western bloting showed the molecular weight was consistent with the predicated. After processed with polymixin B, the endotoxin in the recombinant protein was found to be less than 0.04 EU/mL. When THP-1 cells were stimulated by recombinant protein Tp0664 ranging from 0.1μg/mL to 10μg/mL, the transcription of IL-6 mRNA and the expression of IL-6 significantly increased. When THP-1 cells were pretreated with the inhibitors of ERK1/2, p38, and NF-κB, the transcription of IL-6 mRNA and the production of IL-6 decreased significantly. However, inhibition of JNK was insufficient to attenuate IL-6 mRNA transcription and IL-6 expression. Moreover, Tp0664-induced IL-6 mRNA transcription and IL-6 expression were also abrogated by transfection with dominant negative (DN) plasmid of TLR2 and TLR6. There are significant statistical differences between group transfected with dominant negative (DN) plasmid of TLR2 and control groups ($P<0.05$), but no statistical significance between group transfected with DN plasmid of TLR6 and control groups ($P>0.05$).
Conclusions Treponema pallidum flagellar filament outer layer protein Tp0664 could induce THP-1 cells to express interleukin-6 in which TLR2, ERK1/2, p38, NF-κB are involved.

PU-1665

多发性骨髓瘤病人血浆白介素-6 水平动态监测的研究

付笋笋
山东省千佛山医院

目的 探讨多发性骨髓瘤病人白细胞介素-6 在发病及治疗中的动态变化及预后，为临床治疗提供帮助。
方法 采用双抗体夹心酶联免疫吸附法检测 30 例多发性骨髓瘤患者血浆中 IL-6 的含量，观察其在治疗 4 个疗程后的水平变化并进行统计学分析。
结果 1、多发性骨髓瘤病人血浆 IL-6 水平均明显升高，与对照组相比差异有统计学意义；2、血清 IL-6 水平随着临床分期的增加及病情的严重程度呈现出相关性；3、治疗有效的患者其血浆 IL-6 的水平明显降低，治疗无效的患者其水平无明显变化。
结论 多发性骨髓瘤病人血浆 IL-6 水平明显升高，其血浆水平变化与疾病严重程度和化疗效果有关，检测病人血浆 IL-6 水平对评估病情变化和治疗效果有重要意义。

PU-1666

多发性骨髓瘤患者血浆白介素-6 水平动态监测的研究

付笋笋
山东省千佛山医院

目的 探讨多发性骨髓瘤病人白细胞介素-6 在发病及治疗中的动态变化及预后，为临床治疗提供帮助。
方法 采用双抗体夹心酶联免疫吸附法检测 30 例多发性骨髓瘤患者血浆中 IL-6 的含量，观察其在治疗 4 个疗程后的水平变化并进行统计学分析。
结果 1、多发性骨髓瘤病人血浆 IL-6 水平均明显升高，与对照组相比差异有统计学意义；2、血清 IL-6 水平随着临床分期的增加及病情的严重程度呈现出相关性；3、治疗有效的患者其血浆 IL-6 的水平明显降低，治疗无效的患者其水平无明显变化。

结论 多发性骨髓瘤病人血浆 IL-6 水平明显升高，其血浆水平变化与疾病严重程度和化疗效果有关，检测病人血浆 IL-6 水平对评估病情变化和治疗效果有重要意义。

PU-1667

Tim-3 blockade elicits potent anti-multiple myeloma immunity of natural killer cells

Wen Jiang、Yun Luan、Jue Wang、Qian Xin
Second Hospital of Shandong University

Tim-3 is an immune checkpoint blocking molecule. Multiple myeloma (MM) is a plasma cell tumor that has not been cured to date. Natural killer (NK) cells are characterized by an efficient anti-tumor activity, and its activity has been exploited as the basis of cancer immunotherapy strategies. In the present study, in order to augment the efficiency of NK cell cytotoxicity to MM cells, we used anti-Tim-3 antibodies to block the Tim-3 pathway of the NK cells, to augment the efficiency of NK cell cytotoxicity to MM cells. We investigated the natural cytotoxicity of Tim-3 blocking NK cells against MM cells in vitro and in vivo. NK cells with Tim-3 blockade displayed a significantly stronger cytolytic activity against both human MM cell lines and primary MM cells compared to parental NK cells. The increased cytolytic activity of Tim-3 blocking NK cells was associated with upregulation of cytotoxicity-related moleculars, such as perforin, granzyme B, TNF-α and lFN-γ. Antibody blocking experiments confirmed that ligands combination blocking played more important roles in the system of NK cells cytotoxicit to MM cells. Encouragingly, NK cells with Tim-3 blockade could significantly inhibit MM tumor growth in a xenograft model and prolonged the survival of MM-bearing NOD/SCID mice. These results suggest that Tim-3 blocked NK cells could be suitable for the future development of cell-based immunotherapeutic strategies for MM.

PU-1668

呼吸道感染患儿九项病原体 IgM 抗体检测分析

梁友宝
蚌埠市第一人民医院

目的 对我院呼吸道感染患儿进行九项病原体 IgM 抗体检测，回顾性分析患儿感染情况。
方法 采用呼吸道九项病原体 IgM 抗体荧光检测方法，对 490 例呼吸道感染患儿血清标本进行检测。
结果 与其它病原体 IgM 抗体相比，肺炎支原体 IgM 抗体与副流感病毒 IgM 抗体阳性百分率明显增加，分别占 47.55%和 44.49%，差异有统计学意义（P<0.05）；单项病原体 IgM 抗体阳性率为 35.71%，混合病原体 IgM 抗体阳性率为 34.49%；在患儿感染单一病原体组，单一肺炎支原体 IgM 抗体阳性组和单一副流感病毒 IgM 抗体阳性组明显高于其它单一病原体阳性组，阳性率分别占 15.10%和 14.29%；在混合感染病原体中，肺炎支原体和副流感病毒 IgM 抗体同时阳性组明显高于其它混合感染组，阳性率占 16.94%；在不同年龄组中：0-1 岁，>1-3 岁，>3-6 岁，>6 岁，四个年龄组患儿肺炎支原体 IgM 抗体与副流感病毒 IgM 抗体阳性百分率明显高于其它病原体阳性率。
结论 呼吸道感染患儿九项病原体 IgM 抗体检测分析有利于疾病早期诊断，肺炎支原体和副流感病毒是常见感染病原体，应引起临床重视。

PU-1669

高危型 HPV 持续感染在宫颈癌发生中的研究进展

杨奕、汪琴诗、张平、冯同保
常州市第二人民医院

目的 宫颈癌是全世界仅次于乳腺癌导致妇女死亡的第二大恶性肿瘤，近年来其发病率逐年升高并有年轻化趋势。人乳头瘤病毒(human liapillomavirus, HPV)与宫颈癌的发生发展密切相关。本文主要研究 HPV 感染与宫颈炎症以及宫颈癌发生的关系以及临床意义。
方法 收集我院 HPV 检测阳性的感染患者纳入实验研究，其中体检患者 452 例，宫颈炎症患者 449 例，宫颈癌患者 132 例，对所有受检者均进行 TCT 检查、病理活检等，对不同类型的病例 HPV 检测阳性率进行分析比较。
结果 体检患者中单一基因高危险感染阳性率为(98/452, 21.68%); 多基因高危感染率为(75/452, 16.59%); 宫颈炎症患者中单一基因高危险感染阳性率为(185/449, 41.20%); 多基因高危感染率为(135/449, 30.06%); 宫颈癌患者中单一基因高危险感染阳性率为(70/132, 53.03%); 多基因高危感染率为(55/132, 41.67%)
结论 随着宫颈疾病的发生与进展，高危 HPV 单基因以及多重感染率显著增加，可通过 HPV 检测及早确定患者病情，也为 HPV 疫苗的临床应用提供实验基础。

PU-1670

尿源性干细胞对急性肾损伤的保护作用及机制研究进展

杨博鑫、杨硕、崔丽艳
北京大学第三医院

急性肾损伤（Acute Kidney Injury，AKI）是一种发病急，死亡率高并且预后差的疾病，目前除了透析和替代疗法外没有更加及时有效的治疗手段。尿源性干细胞（urine-derived stem cells，USCs）是从尿液中分离获得的一种多能干细胞，具有自我更新和多向分化的潜能，作为易于获得、无创且易体外培养的干细胞资源，与泌尿系统高度同源，通常不产生免疫排除反应，在膀胱组织再生、尿道重建中均具有较好的潜能，可以减少炎症和纤维化。同时 USCs 具有抗氧化、抗炎和抗凋亡的细胞保护作用，可以抑制组织损伤，在 AKI 的治疗中具有较好的应用前景。本文重点阐述 USCs 在 AKI 中的保护作用和相关机制研究进展，为 AKI 的临床防治、预后改善提供新的思路。

PU-1671

肿瘤的靶向自噬

蒋兵[1]、王涛[2,3]、苏海翔[2,3]
1. 甘肃中医药大学
2. 甘肃省肿瘤医院
3. 甘肃省医学科学研究院

目的 自噬是一个保守的自我降解系统，在应激状态下对维持细胞内稳态至关重要，本文对近年来肿瘤靶向自噬方面的研究进展做一综述。
方法 通过文献学习，综述自噬生物学的主要进展、靶向自噬研究方法以及自噬在肿瘤免疫中的潜在作用，了解具有临床潜力的下一代自噬抑制剂的最新进展。
结果 失调的自噬对健康和疾病都有影响，在肿瘤中，自噬通过抑制肿瘤发生、支持肿瘤进展起着双向作用。部分试验研究成果表明，抑制自噬可能是治疗晚期癌症的一种有希望的方法。

结论 自噬是肿瘤药物开发的一个较有前景的靶点。

PU-1672

金属基质蛋白酶 3 在类风湿关节炎早期诊断与治疗中的临床价值

杨平、沈瀚
南京大学医学院附属鼓楼医院

目的 探讨血清基质金属蛋白酶 3（matrix metalloproteinase 3，MMP-3）在类风湿关节炎（rheumatoid arthritis，RA）早期诊断与疗效观察中的应用评价。
方法 病例对照研究。选取 2020 年 5 月至 2021 年 4 月期间就诊于南京大学医学院附属鼓楼医院风湿免疫科，经确诊为 RA 的患者 130 例（男 24 例，女 106 例），年龄（52.98±13.24）岁，中位数 51 岁。同期南京大学医学院附属鼓楼医院体检中心的健康对照者 50 名（男 28 名，女 72 名），年龄（45.04±11.55）岁，中位数 44 岁，排除肿瘤、糖尿病、肝肾疾病、近期感染以及其他自身免疫性疾病。根据 ROC 曲线判断 MMP3 对 RA 的诊断效能。同时根据判断 RA 活动度的 ESR 和 CRP 水平进行分组，采用 Sperson 相关评判 MMP-3 与 RA 疾病活动的相关性。同时我们收集经甲氨蝶呤（MTX，Methotrexate）稳定剂量治疗的活动性类风湿关节炎患者各个时期的血样进行 MMP3 的检测，判断 MMP3 在 RA 疗效观察方面的价值。
结果 MMP-3 诊断 RA 患者的曲线下面积（AUC）为 0.76，敏感度为 73.1%，特异度为 93%。另外，血清 MMP-3 与 CRP、ESR、MCV、RF、CCP、ASO 相关（r 分别为 0.3762，0.5507，02324，0.4287，0.2737，0.1784），其中与 CRP 相关性最强（r=0.5507）。
结论 MMP-3 可以用于临床诊断 RA 的一个有价值的标志物，并且其水平的高低可以用于评估类风湿关节炎的病情活动程度。

PU-1673

CTC 簇与乳腺癌转移

王涛[1,2]、江秀娟[1,2]、苏海翔[1,2]
1. 甘肃省医学科学研究院
2. 甘肃省肿瘤医院

目的 循环肿瘤细胞（CTCs）是肿瘤远处转移的前体，本文综述 CTCs 技术在乳腺癌患者肿瘤细胞播散和转移机制研究中的应用。**方法** 通过文献学习，综述 CTC 簇在乳腺癌转移中的作用及 CTC 簇的起源，转移优势和临床意义。
结果 在肿瘤患者血液中，CTCs 可以是单个细胞，也可以是肿瘤细胞聚集体，称为 CTC 簇。CTC 簇具有不同的生物学特性，如提高生存率和转移潜能，在转移性肿瘤的预后评估、诊断和治疗方面有很大的应用前景。
结论 CTC 簇的分析为肿瘤转移机制的研究提供了新思路，可指导肿瘤转移的诊断和治疗策略的制定。由于发展了检测 CTC 和 CTC 集群的改进技术，目前这种分析已成为可能。但仍需要发展更有效的方法来解决有关 CTC 转移潜能和未来临床应用的重要问题。

PU-1674

血清正五聚蛋白 3 在类风湿关节炎诊断中的价值

葛贤、史兵伟、丁志祥
南京中医药大学附属常州市中医医院

目的 探讨血清正五聚蛋白 3 在类风湿关节炎诊断中的价值。
方法 应用 ELISA 法检测 30 例类风湿关节炎（rheumatoid arthritis，RA）、30 例骨关节炎（osteoarthritis，OA）和 30 例正常人血清正五聚蛋白 3（pentraxin-3，PTX3）的水平；应用单因素方差检验分析 PTX3 在三组间的差异，绘制 ROC 曲线分析 PTX3 对 RA 的诊断价值，应用 Pearson 相关分析评估 PTX3 与疾病活动指数（DAS28）之间的相关性。
结果 RA 患者血清 PTX3 水平显著高于 OA 患者和正常人（P < 0.001）；血清 PTX3 在关节炎患者中诊断 RA 的 ROC 曲线下面积为 0.857（95%CI：0.761-0.953），PTX3 的最佳临界值为 1.465 ng/mL，此时诊断敏感性 80.0%，特异性为 80.0%；RA 患者血清 PTX3 水平和疾病活动指数（DAS28）呈正相关（r = 0.484，P = 0.007）。
结论 PTX3 在 RA 患者血清中显著增高，可作为 RA 一个较好的诊断标志物。

PU-1675

血清白细胞介素-26 水平与肝功能指标相关指标对慢性丙型肝炎预后相关性

朱建光、周汉义、周俊豪
咸宁市中心医院

目的 通过检测慢性丙型肝炎患者血清中白细胞介素-26（IL-26）、C-反应蛋白（CRP）、总胆红素（TBIL）、谷丙转氨酶（ALT)、天冬氨酸氨基转移酶（AST）等水平，探讨血清 IL-26 与肝功能相关指标对慢性丙型肝炎预后的相关性和存在的潜在意义。
方法 选取 2018 年 1 月-2019 年 12 月于本院就诊的慢性丙型肝炎患者 140 例，其中高病毒载量慢性丙型肝炎患者 68 例（高病毒组），低病毒载量慢性丙型肝炎患者 72 例（低病毒组）；慢性丙型肝炎患者进展为肝硬化、失代偿肝硬化、肝衰竭或肝癌的患者 55 例为不良预后组，未发生进展的患者 85 例非不良预后组。另随机选取同期于本院进行体检的健康人群 140 例为对照组。采用全自动生化分析仪检测血清天冬氨酸氨基转移酶（AST）、丙氨酸转氨酶（ALT）及总胆红素（TBIL）水平；采用免疫比浊法测定 CRP 水平；采用酶联免疫吸附（ELISA）法检测血清 IL-26 水平；采用 Logistic 回归分析影响慢性丙型肝炎患者发生不良预后的危险因素。
结果 高病毒组与低病毒组慢性丙型肝炎患者血清 IL-26 水平均显著高于对照组，且高病毒组显著高于低病毒组（P＜0.05）；不良预后组血清 CRP、TBIL、ALT、AST 及 IL-26 水平均显著高于非不良预后组（P＜0.05）；Logistic 回归分析结果显示，血清 CRP、ALT、AST 及 IL-26 水平均是影响慢性丙型肝炎患者发生不良预后的独立危险因素（P＜0.05）。
结论 慢性丙型肝炎患者血清 IL-26 水平升高，且随患者病毒载量升高而升高，血清 CRP、ALT、AST 及 IL-26 均与患者预后存在一定相关性，可能是评估慢性丙型肝炎患者预后的潜在参考指标。

PU-1676

七项呼吸道病毒抗原检测试剂多中心评价

徐韫健
广州医科大学附属第一医院

目的 考核和信七项呼吸道病毒抗原检测试剂盒（免疫荧光法）与“金标准”病毒分离培养鉴定方法对检测甲型流感病毒、乙型流感病毒、呼吸道合胞病毒、腺病毒和副流感病毒 1/2/3 型的等效性。
方法 在广州医科大学附属第一医院、武汉市第三医院及湖北省疾病预防控制中心共计进行了 1710 例人鼻咽拭子样本的临床试验，评价试剂与对比方法同时对同一临床样本进行检测，记录结果，并对结果进行对比分析，计算评价试剂的灵敏度、特异性、总符合率及其 95%的置信区间和 Kappa 值，评价两者检测性能的等效性。
结果 评价试剂与“金标准”病毒分离培养检测结果不一致的样本共 28 例，七个项目的两种检测结果均高度一致；七种呼吸道病原体感染患者主要来自于 0～21 岁人群，其中以甲、乙型流感病毒的感染率最高（9.50%），尤以 5～≤21 岁为主，各年龄段合并感染率较低；呼吸道合胞病毒、甲型流感病毒、乙型流感病毒和副流感病毒 3 型在各年龄段的阳性率，差异均有统计学意义；把广州地区和湖北地区来源的标本呼吸道病毒的检出率进行比较，0～≤5 岁段，两个地区呼吸道合胞病毒、腺病毒检出率差异均有统计学意义；5～≤21 岁，两个地区甲型流感病毒、乙型流感病毒、腺病毒出率差异均有统计学意义。
结论 和信七项呼吸道病毒抗原检测试剂盒（免疫荧光法）与“金标准”-病毒分离培养鉴定方法在临床应用中对人鼻咽拭子样本中 7 种病毒的检测性能基本等效，且特异性好。

PU-1677

胃镜下病理改变与血清幽门螺杆菌抗体分型的关系分析

刘庆华、李真、张红
山东第一医科大学第二附属医院

目的 探讨血清幽门螺杆菌感染在该地区的流行状况及幽门螺杆菌抗体分型与胃镜下病理改变的关系。
方法 选取 2018 年 8 月到 2020 年 1 月在山东第一医科大学第二附属医院行胃镜检查并同期进行 H.pylori 抗体检测的患者 705 例，其中男性 389 例，女性 316 例，年龄 13 至 88 岁。采用免疫印迹法检测 H.pylori 的四种抗体，根据性别分组比较两组间幽门螺杆菌各基因型感染率； 根据研究对象的资料将其按年龄分为七组，并分别计算各组各抗体检测的阳性率及 H.pylori 感染Ⅰ型和Ⅱ型的感染率； 根据胃镜诊断结果将 705 例患者大体分为 6 组，浅表性胃炎组（195 例）、浅表性胃炎伴糜烂组（75 例）、胃溃疡组（245 例）、食管炎组（40 例）、胃癌组（25 例）、慢性萎缩性胃炎（125 例），比较各组间抗体检测的阳性率。
结果 血清幽门螺杆菌四种抗体分型感染率最高的是 CagA 抗体，且Ⅰ型 H.pylori 感染率高于Ⅱ型；不同性别分组间两组比较差异无统计学意义（P>0.05）；不同年龄组间血清幽门螺杆菌感染呈现极端分化，<20 岁年龄组和>70 岁年龄组感染人数最少，中间年龄段感染人数最多；胃镜下病理改变分组中，胃癌组 CagA 阳性率最高，食管炎组的 UrcA+UreB 抗体阳性的检出率高达 45%，VacA、UreA 和 UreB 抗体单独阳性率在各组都较低。
结论 血清幽门螺杆菌感染与胃部病理改变密切相关，是导致大部分胃部疾病的关键原因。

PU-1678

甘氨酸脱羧酶在 p53 突变 B 细胞淋巴瘤中的表达研究

李向东
山东省千佛山医院

目的 本研究旨在探讨甘氨酸脱羧酶（GLDC）与 p53 突变 B 细胞淋巴瘤的关系。
方法 采用 PCR-SSCP 方法检测人淋巴瘤细胞点突变。用定量实时 PCR（qRT-PCR）和免疫印迹法分别检测 SU-DHL-9 和 SU-DHL-1 细胞中 GLDC 含量。应用 siRNA 技术对 SU-DHL-1 细胞进行 GLDC 转染，westernblot 证实转染成功。建立的 SU-DHL-1 和 SU-DHL-9b 细胞淋巴瘤小鼠模型，检测 GLDC 基因（qRT-PCR）和蛋白（免疫印迹）表达水平。
结果 SU-DHL-9 无点突变，SU-DHL-1 和 SU-DHL-8 细胞各有一点突变。SU-DHL-1 细胞的 GLDC mRNA 和蛋白表达水平增加，与空白对照组和阴性对照组相比 SU-DHL -9 在 siRNA 组中 GLDDC 蛋白表达显著。动物实验显示，SU-DHL-1 诱导小鼠淋巴瘤 GLDC 基因和蛋白表达水平都较高。人 B 细胞淋巴瘤实验显示 P53 阳性组人 B 细胞淋巴瘤细胞 GLDC 蛋白含量高于 P53 阴性对照组。
结论 我们的研究表明 GLDC 表达与 p53 基因突变的 B 细胞淋巴瘤之间有直接关系，GLDC 的研究可能为治疗 B 细胞淋巴瘤提供新的靶点。

PU-1679

妊娠期甲状腺功能减退对妊娠结局的影响

江家红、张立涛
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨妊娠期甲状腺功能减退(甲减)对妊娠结局的影响。
方法 选取 2019 年 12 月至 2020 年 12 月江苏省妇幼保健院产科门诊行产前检查及分娩的孕妇 682 例为研究对象，于孕期接受甲状腺功能筛查,发现妊娠期甲状腺功能减退者 63 例(甲减组)，其中及时发现并接受规范甲减治疗的孕妇 44 例(甲减治疗组),发现时已接近足月妊娠而未接受规范甲减治疗的孕妇 19 例(甲减未治疗组)，其余未发现甲减的 700 例孕妇归为对照组。比较甲减组与对照组各种不良妊娠结局的发生率，比较甲减治疗组与甲减未治疗组不良妊娠结局的发生率。
结果 (1)甲减组孕妇妊娠期高血压疾病、妊娠期糖尿病和自然流产发生率均高于对照组(17.20%:2.85% 、14.45%:3.26% 、13.14%:3.07%)，差异均有统计学意义($\chi 2$ =40.947、26.560、23.602,均 P<0.01)。(2)甲减治疗组孕妇妊娠期高血压疾病、妊娠期糖尿病和自然流产的发生率均低于甲减未治疗组(9.48%:35.33% 、8.18%:26.94% 、8.66%:23.93%),差异均有统计学意义($\chi 2$ =7.692、6.766、5.316,均 P<0.01)。
结论 妊娠期甲减对于妊娠结局具有不良影响，以妊娠期高血压疾病、妊娠期糖尿病和自然流产多见,通过补充外源性甲状腺素，可在一定程度上改善妊娠结局。

PU-1680

25-羟基维生素 D 在新生儿败血症中的水平以及影响因素分析

张立涛、江家红
江苏省人民医院（南京医科大学第一附属医院）

目的 新生儿败血症是因感染引起的全身炎症反应综合征（SIRS），是新生儿期死亡的重要原因，也是新生儿重症监护室（NICU）常见危重症之一，其发病率及病死率均较高。本研究通过测定新生儿败血症患儿的 25-羟基维生素 D 水平，并与同期无败血症新生儿做比较，了解本地区新生儿败

血症患儿中 25-羟基维生素 D 水平；研究分析 25-羟基维生素 D 在新生儿败血症中的水平以及影响水平的影响因素。
方法 采集 100 例新生儿静脉血，58 例新生儿败血症患儿为病例组，42 例无败血症新生儿为对照组，采用 ELISA 法检测两组新生儿 25-羟基维生素 D，分析两者的相关性，并分析新生儿 25-羟基维生素 D 影响因素。
结果 1.新生儿败血症患儿血清 25-羟基维生素 D 水平（7.70±4.17）ng/ml 明显低于对照组（13.02±6.27）ng/ml（P<0.05）。2.剔除感染因素后，单因素分析结果显示，民族、胎龄、出生体重、母亲年龄、母亲学历、孕期补充维生素 D 情况、出生季节与新生儿 25-羟基维生素 D 水平有关。3.通过多因素回归分析，25-羟基维生素 D 水平与出生季节、孕期补充维生素 D 情况、出生胎龄相关，差异有统计学意义（P<0.05）。
结论 1. 25-羟基维生素 D 水平与新生儿败血症相关，2.影响 25-羟基维生素 D 水平的因素有出生季节、孕期补充维生素 D 情况、出生胎龄。

PU-1681

呼吸道病原体抗体检测的干扰现象及其干扰因素回顾性研究

张铁
中日友好医院

目的 分析我院呼吸道病原体抗体阳性样本来源和阳性率分布情况，同时评估阳性样本与临床表现等相关性，分析是否存在干扰因素影响检测结果。
方法 回顾性统计分析 2017 年 1 月-2019 年 9 月在我院进行呼吸道病原体检测的不同科室就诊患者 EB 病毒衣壳抗原（EB VCA）Ig M、Ig A、Ig G 抗体与巨细胞病毒（CMV）IgM、IgG 抗体阳性率，进一步分析风湿免疫科发病率前四名疾病呼吸道病原体阳性率、及其与自身抗体结果等指标相关性。
结果 全院各科室 CMV IgM、CMV IgG 阳性率不同，差异有统计学意义（P<0.001）。风湿科与全院其他各科室的 CMV IgG 阳性率比较，差异有统计学意义（P<0.05）。不同科室 EB VCA IgM、EB VCA IgG、EB VCA IgA 阳性率不同，差异有统计学意义(P<0.001)。风湿科与儿科、消化科以及感染科的 EB VCA IgG 阳性率比较，差异有统计学意义(P<0.05)。风湿科内常见的类风湿关节炎、系统性红斑狼疮、肌炎、干燥综合征以及其他疾病的病原体 CMV IgM、CMV IgG、EB VCA IgA 的阳性率不同，差异有统计学意义（P<0.05）。抗核抗体阳性患者 CMV IgM、EB VCA IgA 的阳性率明显高于抗核抗体阴性者（P<0.001）类风湿因子阳性者 EB VCA IgM、EB VCA IgA 的阳性率高于阴性者（P<0.05），而类风湿因子阳性者病原体 EB VCA IgG 的阳性率低于阴性者（P<0.05）。抗核抗体类风湿因子双阳组 CMV IgM、EB VCA IgA 的阳性率高于单阳组（P<0.05）。
结论 全院各科室 CMV IgM、CMV IgG 阳性率有显著差异，而风湿免疫科的相关病原体阳性率均较高，风湿免疫科发病率前四名疾病病原体阳性率与 CMV IgM、CMV IgG、EB VCA IgA 阳性率相关。

PU-1682

2 型糖尿病患者血糖指标与骨转换标志物水平的相关性分析

冀承杰
简阳市人民医院

目的 探讨 2 型糖尿病患者体内骨转换标志物 β-胶原特殊序列(β-CTX)、25-羟基维生素 D(25(OH)D)、骨钙素(OC)、Ⅰ型胶原氨基末端延长肽（PⅠNP）的表达水平以及与空腹血糖、糖化血红蛋白 HbA1c 的相关性。

方法 选取 2 型糖尿病患者男性 39 例，女性 46 例设为实验组；非糖尿病患者男性 52 例，女性 44 例作为对照组。做病例对照研究，测定患者空腹血糖、糖化血红蛋白，同时测定两组四项骨转换标志物,比较两组的临床资料和体内标志物的差异并进行统计学分析。
结果（1）2 型糖尿病女性患者体内 β-CTX、骨钙素、25(OH)D、PⅠNP 水平低于非糖尿病患者；（2）2 型糖尿病男性患者体内 PⅠNP 高于非糖尿病患者，体内 25(OH)D 水平较低；（3）男性患者体内 25(OH)D 水平与空腹血糖以及糖化血红蛋白水平呈负相关；但女性患者 PⅠNP 与糖化血红蛋白 HbA1c 呈正相关，骨钙素与空腹血糖、糖化血红蛋白 HbA1c 呈正相关，而数据表明 25(OH)D 与糖化血红蛋白 HbA1c 呈负相关。
结论 2 型糖尿病与骨转换标志物水平之间存在着相关性，同时骨转换标志物水平与糖化血红蛋白、空腹血糖水平存在相关性。

PU-1683

MxA 蛋白对儿童呼吸道病毒感染的研究进展

邹悦[1]、叶辉铭[2]
1. 厦门大学
2. 厦门市妇幼保健院

目的 运用系统评价方法分析评价 MxA 蛋白在儿童呼吸道病毒感染诊断方面的临床应用进展。
方法 中英文数据库检索 MxA 蛋白抗呼吸病毒及在呼吸道感染中临床应用的文献，进行阅读归纳。
结果 呼吸道感染是儿童的常见病和多发病，目前临床应用的感染检测指标并不能很好地鉴别出病毒感染和细菌感染，均存在特异性和敏感性不高的问题。MxA 蛋白是 I 型干扰素诱导产生的一种广谱抗病毒蛋白，其表达严格依赖于干扰素 α/β 信号，而其他的细胞因子对 MxA 蛋白的表达水平无明显调节作用。研究表明，MxA 蛋白在病毒感染后迅速诱导，感染后 1-2 小时开始积累，16 小时达到峰值，且在外周血液中含量较高，可作为急性病毒感染良好的生物标志物，此外 MxA 蛋白广谱抗病毒作用可为临床治疗提供指导。该文介绍了 MxA 蛋白作为病毒感染检测标志物的机制及其目前主要的检测方式，着重介绍了 MxA 蛋白能识别的病毒种类以及在儿童呼吸道感染疾病中早期诊断病毒感染以及病毒感染和细菌感染的鉴别作用的研究进展。同时，也简要讨论了 MxA 蛋白与其他检测指标联用对呼吸道病毒感染和细菌感染的鉴别作用。
结论 MxA 蛋白在儿童早期呼吸道病毒感染的早期诊断有一定的临床价值，可结合其他生物标志物进行早期病原体识别，更好的应用于临床。

PU-1684

MxA 蛋白对呼吸道病毒感染诊断价值的 meta 分析

邹悦[1]、陈祺[2]、赵丽[2]、叶辉铭[3]
1. 厦门大学
2. 厦门大学医学院
3. 厦门市妇幼保健院，医学检验科

目的 运用诊断性试验 Meta 分析评价 MxA 蛋白对儿童呼吸道病毒感染的诊断价值。
方法 在 EMbase、PubMed 和 The Cochrane Library 英文数据库及中国知网、万方和维普中文数据库中检索至 2021 年 1 月的相关文献。两位研究者按照制定的文献纳入和排除标准进行文献初筛、二筛、三筛，最终筛选出文献用 QUADAS-2 量表进行文献质量评价，用 Revman 5.3 软件绘制偏倚风险图，用 Meta-Disc、STATA 15.0 软件进行灵敏度、特异度等数据分析。
结果 中英文数据库检索 1157 篇文献，排除重复文献 256 篇，通过阅读题目和摘要排除 880 篇，通过阅读全文排除 15 篇，最终共纳入 6 篇文献，其中包括 1 篇中文，5 篇英文文献。QUADAS-2

评价工具对选入的 6 篇文献质量进行评价，对每篇文献的病例选择、待评价试验、诊断金标准、病例流程及进展情况逐一评价，纳入的文献总体偏倚风险较低，适用性较好。分析结果为：MxA 异质性检验的灵敏度Q＝14.68，P=0.01，I2＝65.95%，特异度Q＝10.82，P=0.06，I2＝53.79%。合并灵敏度(Sen)=0.91[95%CI(0.85,0.94)]、合并特异度(Spe)=0.89[95%CI(0.81,0. 93)]、合并阳性似然比(PLR)=8.00[95%CI(4.90,13.10)]、合并阴性似然比(NLR)=0.11[95%CI(0.07,0.16)]、合并诊断比值比(DOR)=76.00[95%CI(43.00,135.00)]，SROC 曲线下面积 AUC=0.95[95% CI(0.93,0.97)]。Deeks 漏斗图显示，各研究的发表偏倚并无显著性差异（P＝0.91）。
结论 MxA 蛋白对儿童早期呼吸道病毒感染有一定的诊断价值。

PU-1685

乙型肝炎病毒表面抗原与乙型肝炎病毒外膜蛋白前 S1 抗原之间的相关性

孙文肖
广饶县人民医院

目的 探讨乙型肝炎病毒表面抗原与乙型肝炎病毒外膜蛋白前 S1 抗原在乙型肝炎携带者中相关性及乙型肝炎病毒外膜蛋白前 S1 抗原在临床中的应用。
方法 乙型肝炎病毒表面抗原与乙型肝炎病毒外膜蛋白前 S1 抗原都采取化学发光法。选择 2021 年 4 月到 5 月一个月的乙肝表面抗原同时做过前 S1 抗原的患者 562 例，两者数据对比。
结果 不同患者前 S1 抗原会随着表面抗原的升高而升高，其中表面抗原为阴性的患者中，乙型肝炎病毒外膜蛋白前 S1 抗原也为阴性。
结论 在乙型肝炎携带者中前 S1 抗原与表面抗原存在正相关性。在非乙肝携带者中两者都为阴性。在临床上前 S1 可以协助表面抗原的检测，可以进一步判断病人的病情。

PU-1686

蛋白芯片法在幽门螺杆菌感染中的应用研究

吴 峥
沈阳金域医学检验所有限公司

目的 研究幽门螺杆菌(（Helicobacter pylori，H.pylori)抗体在慢性胃炎、消化性溃疡、血小板减少性紫癜及其他消化道外疾病组血清中的阳性情况；探讨不同类型 H.pylori 感染与胃肠疾病发病的关系及蛋白芯片技术在幽门螺杆菌感染诊断中的应用价值。
方法 应用蛋白芯片法检测 1341 例血清标本中(包括消化性溃疡组、血小板减少性紫癜组、慢性胃炎组及对照组）细胞毒素相关基因蛋白(CagA)、空泡毒素(VacA)、尿素酶(Ure)抗体的表达情况，计算阳性率，用统计学方法比较各组的差异。
结果 在一定年龄范围内（5～15 岁）H.pylori 感染率随年龄的增长有升高趋势(P<0.01)溃疡组组、胃炎组三种抗体（CagA VacA Ure）阳性率明显高于正常对照组(P<0.01)。而消化道出血组抗体阳性率与对照组无明显变化。
结论 CagA 阳性的 H.pylori 感染是胃肠疾病发生和发展的关键因素。蛋白芯片法用于 H.pylori 感染的分型诊断以及治疗后的复查有其独特的优点，是一项简单易行、结果准确可靠的实验室方法，值得临床推广。

PU-1687

结核分枝杆菌检验及结果分析

王舒灏
沈阳金域医学检验所有限公司

目的 肺结核是由结核分枝杆菌引起的慢性传染性疾病，现对结核患者的结核分枝杆菌进行检验和分型，并对检验结果进行分析，以此为临床诊断及用药提供参考。
方法 筛选疾病控制中心的非重复肺结核痰标本 80 例，80 例痰液标本均来自各个医院收治的肺结核患者，且均经影像学检查诊断为肺结核。同时选取相同时间段非肺结核肺部疾病患者 80 例痰液标本作为健康对照组。而后进行检验，检验方法主要分为涂片法和培养法。涂片法：将 160 例标本直接涂片，进行抗酸染色，镜检。培养法：采用罗氏培养法进行培养，痰液进行碱处理后，在 30 分钟内完成接种。
结果 80 例肺结核患者培养法检验阳性率高于直接涂片法，80 例非肺结核肺部疾病患者两种检验均未出现阳性。直接涂片检验及罗氏培养检验均为阳性，相符率为 100%。
结论 肺结核患者主要有盗汗、乏力、低热、咳嗽、咯血、胸痛等临床表现，严重影响患者生活质量，潜伏者一般无明显症状，发病者多为慢性过程。一般临床对患者的痰液进行检验，用来与其他肺部疾病进行诊断，早期一般采用直接涂片染色、集菌等方法。临床发现，采用直接涂片法敏感性相对较低，阳性率较低，但罗氏培养检出率高，还可以再进一步做菌种鉴定、药敏试验等。本次研究结果显示罗氏培养法对于肺结核的诊断较为准确且高效。

PU-1688

CD4+T 细胞是影响 QFT-GIT 在矽肺合并肺结核患者中灵敏度下降的主要因素

黄丽娜
苏州市第五人民医院

目的 分析矽肺病与 QFT-GIT 试验的相关性，找出矽肺患者 QFT-GIT 灵敏度降低的主要因素，并探索提高灵敏度的方法。
材料与方法 收集结核杆菌培养阳性的矽肺病患者，QFT-GIT 试验、流式细胞计数、CD4+T 细胞富集实验。
结果 1.TB 和 TB＆SILs 组中外周血淋巴细胞亚群的比值和绝对值存在差异。与 TB 组相比，TB＆SILs 组患者外周血 B 细胞比例显著增加（P<0.05），但绝对值无统计学差异。2.TB＆SILs-N 组患者外周血 CD4+T 细胞比例（P<0.05）和绝对值（P<0.01）明显比 TB＆SILs-P 组低，且差异显著。3.矽肺病合并结核病的患者 QFT-GIT 试验灵敏度（60.0%）与单纯的肺结核患者（90.1%）相比明显降低，且其灵敏度与 CD4+T 细胞数量呈正相关（P<0.01），利用 CD4 细胞富集实验可以提高 QFT-GIT 灵敏度。
结论 IFN-γ 体外释放试验（TB-IGRA）是一种可早期诊断临床肺结核病的新检测方法，这种测试 IFN-γ 的体外释放量的检测方法可帮助诊断结核病或者查明机体是否存在结核分枝杆菌感染。现有研究已确认，TB-IGRA 是检测矽肺病合并肺结核患者的最灵敏的测试。本研究发现 TB＆SILs 组患者的 QFT-GIT 的诊断效率显著降低。进一步研究还发现，TB＆SILs-P 组患者外周血中 CD4+T 细胞的比率和数量明显高于 TB&SILs-N 组。增加 CD4+T 细胞可以提高 QFT-GIT 的灵敏度。以上结果表明，矽肺患者的免疫缺陷状态影响了 QFT-GIT 试验的检测效率，而 QFT-GIT 试验的检测效率可以通过增加 CD4+T 细胞的数量来进行恢复。这项研究为矽肺并发症的诊断及免疫疗法提供了理论上的依据，且对于临床诊断及治疗来说具有重要价值。

PU-1689

丁螺环酮与经颅电刺激对精神分裂症脑损伤治疗的变化

尹石华、崔吉俊
东营市胜利医院

目的 观察丁螺环酮联合经颅电刺激对精神分裂症患者的临床治疗效果，以及对患者 GFAP、S100、神经元烯醇化酶（NSE）含量变化、阴性症状和阳性症状的影响。
方法 选择精神分裂症患者 196 例为研究对象，首发 62 例，复发 134 例，随机分为观察组和对照组，每组 98 例。2 组患者均给予常规杭精神分裂症药物治疗，观察组(1.2)加用丁螺环酮联合经颅电刺激治疗。观察两组患者临床治疗效果，对患者的认知功能，生活质量进行评定比较，以及对四组患者 GFAP、S100、神经元烯醇化酶（NSE）含量进行分析对比。
结果 (1)观察组临床总有效率为 91.8 % (90 /98)，对照组为 75.5% (74/98)，差异有统计学意义(p<0.05);(2)治疗后观察组 MoCA 认知功能评分为(29. 1 士 1.36)分，对照组为(27. 89 士 1. 13)分，差异有统计学意义(p<0.05) ；(3)观察组患者阴性症状评分(87. 93 士 5. 87)分显著高于对照组评分(82. 37 士 4. 32)分，差异有统计学意义(p<0.05); 观察组患者阳性症状评分(78. 93 士 5. 87)分，显著低于对照组(89. 37 士 4. 32)分，差异有统计学意义(p<0.05); (4)治疗后观察组患者(GFAP 浓度(24.61 士 3. 89) ng/ml，显著低于对照组(31. 08 士 4. 87) ng/ml ，差异有统计学意义(p<0.05); S100/NSE. …。
结论 丁螺环酮联合经颅电刺激治疗精神分裂症患者的临床疗效较好，能改善患者的认知功能，提高患者的生活质量，抑制 GFAP 过度表达，S100/NSE.脑损伤指标降低，有较好的临床应用价值。

PU-1690

光激化学发光法与其他梅毒血清学检测方法的联合应用

尹石华、邓宽国
东营市胜利医院

目的 为了探讨光激化学发光（LICA）免疫分析技术在梅毒感染血清检测中的应用。
方法 用 LICA 免疫分析、梅毒螺旋体明胶颗粒凝集试验（TPPA）和快速血浆反应素环状卡片试验（RPR）对 LICA 梅毒螺旋体抗体初筛阳性标本进行进一步检测，并以 TPPA 为金标准，对 LICA 检测阳性的标本进行确认。
结果 19156 例血清标本经 LICA 检测梅毒螺旋体抗体阳性的 318 例，318 例梅毒螺旋体抗体阳性标本经 TPPA 复检阳性 231 例，阳性检出率为 72.6%；而 RPR 检测 78 例，阳性检出率为 24.5%。以 TPPA 为金标准，用 LICA 对 TPPA 检测阳性及阴性标本各 50 例进行复检，LICA 敏感性为 100%（50/50），特异性为 98%（49/50）。
结论 LICA 敏感性优于 TPPA 和 RPR，重复性好，操作简便，可自动化，宜用于梅毒的临床初筛，但梅毒螺旋体抗体 LICA 检测值在 1-5 区间为灰区，必须用 TPPA 试验进行确证。

PU-1691

肺结核与非结核分枝杆菌肺病淋巴细胞及因子分析

邓宽国、刘玉霞
东营市中医院

目的 通过淋巴细胞亚群和细胞因子的检测，结合影像学等其他检查尽快的诊断肺结核和非结核分枝杆菌肺病（NTM-PD）患者，指导临床及时选择合适的治疗方案。

方法 选择我院结核病防治所确诊肺结核患者 60 例，非结核分枝杆菌肺病患者 30 例，健康查体 30 例，三组试验者分别采血用流式细胞术检测血液中 CD3+、CD4+、CD8+、CD19+、CD16+CD56+淋巴细胞亚群的绝对数和百分数以及血浆中 IL-2、IL-4、IL-6、IL-10、TNF-α、IFN-γ 细胞因子水平，用 SPSS 统计软件分别两两比较三组试验者各指标的 P 值。
结果（1）肺结核组、NTM-PD 组及对照组 CD3+、CD4+、CD8+、CD19+淋巴细胞亚群的绝对数比较，差异有统计学意义（p<0.05），各组间两两比较，除 CD8+的 NTM-PD 组与对照组、CD19+的肺结核组与 NTM-PD 组差异无统计学意义（p>0.05）外，其余组间两两比较差异均有统计学意义（p<0.05）；三组试验者淋巴细胞亚群的百分数比较，除 CD19+在三组间有统计学意义（p<0.05）外，其余组间差异无统计学意义（p>0.05）； (2)肺结核组、NTM-PD 组及对照组 TNF-α、IFN-γ、IL-4 的细胞因子水平差异有统计学意义（p<0.05），各组间两两比较，除 IL-4 的肺结核组与 NTM-PD 组差异无统计学意义（p>0.05）外，其余各组间两两比较差异均有统计学意义（p<0.05）。
结论 对肺结核患者进行 CD3+、CD4+、CD8+、CD19+、CD16+CD56+淋巴细胞亚群以及 IL-2、IL-4、IL-6、IL-10、TNF-α、IFN-γ 细胞因子的检测，对及时判断肺结核和 NTM-PD 患者有重要意义。

PU-1692

乙肝表面抗体 ELISA 法的性能验证

杨厚禄
沈阳金域医学检验所有限公司

目的 对乙肝表面抗体（HBsAb）ELISA 法进行性能验证。
方法 精密度测定①重复性精密度：使用购买弱阳性康彻斯坦质控品（浓度为 30IU/ml），重复检测 20 次，计算结果 CV<15%为重复性精密度验证通过。②批间精密度： 使用购买弱阳性康彻斯坦质控品（浓度为 30IU/ml）每天重复检测 4 次，连续检测 5 天，共计 20 个数据，计算结果 CV<25%为批间精密度验证通过。检出限测定：使用购买弱阳性康彻斯坦质控品（浓度为 30IU/ml）进行倍比稀释，并检测稀释后样本结果。确定结果为阳性的最低浓度值。直接配置足够检测 20 次的该浓度的质控品，一次完成复测 20 次，且满足最多有一个结果不为阳性，即可确定此值即为乙肝表面抗体（HBsAb）的检出限。符合率:选择 20 例化学发光定量法乙肝表面抗体（HBsAb）阳性结果的样本，结果应分布在弱阳性、阳性结果范围内。使用乙肝表面抗体（HBsAb）ELISA 法检测留存的 20 例样本，检测结果≥80%为满意即符合率验证通过。
结果 重复性精密度验证结果为，4.45%，CV<15%；批间精密度验证结果为 14.52%，CV<25%,。检出限为 7.5mIU/ml，符合率结果为 95%，＞80%。
结论 乙肝表面抗体（HBsAb）ELISA 法的性能验证通过，符合项目开展要求。

PU-1693

肿瘤标志物联合检测对原发性肝癌的诊断价值

王乾曜
沈阳金域医学检验所有限公司

目的 本文拟通过探讨外周血中性粒细胞与淋巴细胞比值（NLR）以及联合血清甲胎蛋白（AFP）、高尔基体蛋白 73（GP73）、α-L-岩藻糖苷酶（AFU）、分泌蛋白 Dickkopf 同源物 1（DKK1）检测、异常凝血酶原（DCP）、碱性磷酸酶（ALP），为原发性肝癌的诊断提供依据，提高原发性肝癌的检出率。

方法 1.1AFP、DCP、高尔基体跨膜糖蛋白 73 的联合检测 1.2 AFP、DCP、DKK1 的联合检测 1.3 AFP、α-L-岩藻糖苷酶、碱性磷酸酶的联合检测
结果 1.1 AFP、DCP、高尔基体跨膜糖蛋白 73 的联合检测
联合检测阳性检出率最高，绝代诊断原发性肝癌特异度敏感度等方面更优势，表明较单独检测，联合检测的实践更能确保原发性肝癌诊断的准确性。
1.2 AFP、DCP、DKK1 的联合检测
86 例肝癌患者作为自己的研对象，分别检测其 AFP、DCP、DKK1 水平，分析相关数据得 出单独检测 AFP、DCP、DKK1 时其敏感度为 58.13%、74.42%、73.26%，特异度为 29.00%、30.00%、44.00%，联合检测时敏感度与特异度分别为 93.02%、78.00%。
1.3AFP、α-L-岩藻糖苷酶、碱性磷酸酶的联合检测
单独检测患者 AFP、AFU 和 ALP 水平，敏感度分别为 67.16%、73.13% 和 71.64%，3 项指标联合检测敏感度可达 88.06%。AFP、AFU 和 ALP 的联合检测可以明显提高单项检测的敏感度，这对于肝癌的诊断至关重要。
结论 肿瘤标志物的联合检测已经成为临床工作中的趋势，但在没有更好治疗方式被发掘时，通过联合检测这些标志物能在早期，甚至在更早期进行诊断肝癌，从而进行更早的干预，这对于提高患者的生存率、改善患者的预后有重要意义。

PU-1694

多种自身抗体在原发性胆汁性胆管炎中的临床意义

李齐光
广州医科大学附属第六医院/清远市人民医院

目的 探讨多种自身抗体在原发性胆汁性胆管炎(PBC)诊疗中的临床意义。
方法 收集 58 例原发性胆汁性胆管炎患者(PBC 组)、60 例病毒性肝炎组和 60 名正常对照组。应用间接免疫荧光法分别检测抗核抗体(ANA)、抗线粒体抗体(AMA),用线性免疫印迹法分别检测自免肝谱,分析各种自身抗体单独检测及并联检测在 PBC 诊断中的意义.
结果 PBC 组、病毒性肝炎组和正常对照组患者的 ANA 阳性率比较差异有统计学意义(P < 0.05),其中 PBC 组的 ANA 阳性率最高、正常对照组的 ANA 阳性率最低,组间两两比较差异均有统计学意义(P 均< 0.017).3 组的 ANA 阳性者中,PBC 组以中高滴度为主,中高滴度者比例均高于病毒性肝炎组及正常对照组(P 均< 0.017),低滴度(1 : 100)者比例低于病毒性肝炎组(P 均< 0.017).PBC 组 54 例 ANA 阳性患者中,ANA 荧光核型以胞浆颗粒型(43%)与着丝点型(20%)为主.PBC 组患者的 ANA、AMA、AMA-M2、抗 gp210、抗 sp100 及并联检测[ANA、AMA 等]的阳性率均高于病毒性肝炎组和正常对照组(P 均< 0.017),PBC 组中并联检测的阳性率高于单独检测抗 gp210 和抗 sp100(P 均< 0.05).ANA(1 : 320 及以上)、AMA、AMA-M2、抗 gp210 和抗 sp100 以及并联检测在 PBC 患者中的灵敏度分别为 88%、85%、78%、29%、16%和 90%;特异度分别为 92%、97%、98%、98%、100%和 92%;阳性预测值分别为 91%、96%、98%、94%、9/9 和 91%;阴性预测值分别为 89%、87%、82%、59%、55%和 90%。
结论 临床筛查 PBC 时,仅行 ANA 检测的患者出现中高滴度胞浆颗粒型结果时,应追加自身免疫肝抗体谱检测;并联检测自身抗体能够提高 PBC 的灵敏度,为临床提供更多诊断依据。

PU-1695

对磁条码免疫荧光发光法与流式免疫荧光法检测抗核抗体谱结果及检测时间之间的比较

李齐光
广州医科大学附属第六医院/清远市人民医院

目的 对磁条码免疫荧光发光技术(CILIA）和多重微球流式荧光免疫技术(MBFFI）检测抗核抗体谱结果以及所用检测时间进行比较。
方法 同时用磁条码免疫荧光技术和多重微球流式荧光免疫技术检测 93 例自身免疫病患者（其中 52 例系统性红斑狼疮（SLE）、16 例干燥综合征（SS）和 21 例其他自身免疫性疾病）和 50 例健康者血清的抗核抗体谱,进行结果的一致性比较,同时对两种方法在 SLE 诊断中的灵敏度、特异度、阳性预测值和阴性预测值进行比较。
结果 在自身免疫疾病组中，磁条码免疫荧光发光技术与 MBFFI 标本中抗核抗体谱各指标一致率在 86.02%-98.92%之间；在正常对照组[刘 1] 中，磁条码免疫荧光发光技术与 MBFFI 标本中抗核抗体谱一致率在 96.0%-100%之间；所有标本[刘 2] 一致率为在 90.90%-97.91%之间。两种不同检验方法检测各指标在诊断系统性红斑狼疮中的灵敏度、特异度、阳性预测值和阴性预测值，详见表二[刘 3]，两种方法检测抗核抗体谱项目总的灵敏度、特异度、阳性预测值和阴性预测值分别是 94.23%、90.38%，96.00%、98.00%，96.07%、97.91%，94.11%、90.74%，无统计学差异（P>0.05）；前者所用平均检测时间为 60±5min，后者为 180±30min，前者所用时间明显少于后者，具有统计学意义（P<0.01）。
结论 磁条码免疫荧光技术检测抗核抗体谱与多重微球流式荧光免疫技术相比，一致性较高，各指标之间灵敏度、特异度、阳性预测值和阴性预测值均无显著差异，可互相替代用于自身免疫性疾病诊疗，而且前者所用检测时间显著低于后者，其检测效率明显高于后者。

PU-1696

荧光免疫层析法检测 2019-nCoV 特异性抗体用于新冠病毒感染筛查价值探讨

李齐光
广州医科大学附属第六医院/清远市人民医院

目的 探讨荧光免疫层析法检测 2019-nCoV 特异性抗体 IgM 和 IgG 用于一般人群新冠病毒感染筛查价值。
方法 选取 2019 年 2 月至 2020 年 10 月某医院共 2 322 例诊疗患者,采用免疫荧光层析法对血清中 2019-nCoV 特异性抗体 IgM 和特异性抗体 IgG 分别进行检测。记录光免疫层析法 2019-nCoV 抗体检测结果,包括阳性率、疑似阳性率。观察 2019-nCov 特异性抗体 IgG 检测结果为阳性和疑似阳性的样本中年龄分布情况。
结果 在 2 322 例 2019-nCoV 特异性抗体检测中,荧光免疫层析法检测总阳性病例 28 例,即阳性检测率为 1.21%;特异性抗体 IgG 检测阳性率为 0.78%;特异性抗体 IgM 中,阳性率为 1.18%。2019-nCov 特异性抗体 IgG 检测结果为阳性和疑似阳性的样本中年龄>45 岁的比例为 61.54%（1 429/2 322）;2019-nCov 特异性抗体 IgM 检测结果为阳性和疑似阳性的样本中年龄>45 岁的比例为 72.00%（1 672/2 322）。
结论 荧光免疫层析法检测 2019-nCoV 血清抗体用于一般人群筛查假阳性率低,可作为核酸检测的补充手段,用于疑似人群初筛,节省医疗资源。

PU-1697

血清抗苗勒管激素与抑制素 A 在青春期多囊卵巢综合征诊断中的价值

李正秋
湖南省儿童医院

目的 探讨青春期多囊卵巢综合征患者血清抗苗勒管激素与抑制素的变化及其对诊断的价值。
方法 选取本院 2018 年 3 月-2019 年 5 月门诊确诊为 PCOS 青春期女性 39 例（PCOS 组）与同期接受体检的健康同龄女性 26 例（健康组）作为研究对象，检测血清性激素水平、胰岛素抵抗（HOMA-IR）、AMH、INH-A 与 INH-B 的浓度，比较两组血清指标的差异，并结合超声检查结果分析差异指标与卵巢体积之间的关系，采用 ROC 曲线分析差异指标对 PCOS 诊断的价值。
结果 PCOS 组促黄体生成素(LH)、睾丸酮 T、HOMA-IR、AMH 与 INH-A 均高于健康组（P＜0.05），两组卵泡刺激素(FSH)、雌二醇(E2)、催乳素(PRL)与 INH-B 水平没有显著差异（P＞0.05）；pearson 相关性分析显示：AMH 与 LH、INH-A 与 HOMA-IR 呈显著正相关（P＜0.05），INH-A 与 AMH、LH 与 HOMA-IR 呈显著正相关（P＜0.05），INH-B 水平与 BMI、FSH 与 HOMA-IR 呈显著正相关（P＜0.05）；AMH 与左卵巢体积呈现显著正相关关系（P＜0.05），INH-A 与右卵巢体积呈现显著正相关关系（P＜0.05）；ROC 曲线分析显示：AMH 预测 PCOS 的 AUC 为 0.885，以 6.38μg/L 为临界值时，其灵敏度、特异度与准确度分别为 0.821（32/39）、0.808（21/26）与 0.815（53/65），INH-A 预测 PCOS 的 AUC 为 0.865，以 17.52ng/L 为临界值时，其灵敏度、特异度与准确度分别为 0.897（35/39）、0.692（18/26）与 0.815（53/65）。
结论 AMH、INH-A 在青春期 PCOS 女性患者血清中显著升高，其对青春期 PCOS 有着较高的诊断价值。

PU-1698

肿瘤相关巨噬细胞:乳腺癌发展过程中的重要参与者

黄心群、曹劲松、申莹莹、祖旭宇
南华大学附属第一医院

乳腺癌是一种常见的女性恶性肿瘤,在肿瘤患者中死亡率位列第二。乳腺肿瘤微环境中,肿瘤相关巨噬细胞为含量最多的免疫细胞,通过多种方式参与和调节乳腺癌发展。在乳腺癌发展过程中，肿瘤相关巨噬细胞通过促进血管生成、癌细胞转移、诱导癌细胞干性、参与免疫抑制和能量代谢调节,为乳腺肿瘤生长提供支持。可塑性是肿瘤巨噬细胞的特性,将肿瘤相关巨噬细胞复极化为 M1 型巨噬细胞可发挥肿瘤杀伤作用。本文对肿瘤相关巨噬细胞在乳腺癌发展过程中的作用与机制进行综述,为肿瘤相关巨噬细胞作为乳腺癌有效的治疗靶点提供依据。

PU-1699

Th17 细胞/Treg 细胞及其相关炎性因子在川崎病冠脉损伤中的作用

周玉杰、袁华敏、彭艳华
湖南省职业病防治院

目的 分析辅助性 T 细胞 17(Th17)和调节性 T 细胞(Treg)及其相关炎症因子，探讨它们与川崎病的发生及其冠脉损伤的临床意义。

方法 选取 2018 年 1 月至 2018 年 12 月本院川崎病住院患者 40 例作为 KD 组，根据是否出现冠状动脉病变又划分为冠状动脉病变组（CALs），以及非冠状动脉病变组（NCALs），另选取健康体检者 40 例为健康对照组。在患儿发病的急性期以及健康对照组抽取外周静脉血，用流式细胞仪检测外周血中辅助性 T 细胞 17(Th17)和调节性 T 细胞(Treg)的百分含量，同时用酶联免疫吸附试验（ELISA）测出各细胞因子的含量，收集他们的基本临床信息，分析它们与川崎病的发生及其冠脉损伤的临床意义。
结论 1. Th17 细胞百分率、Treg 细胞百分率、Th17/Treg 与川崎病的发生发展相关。2.Th17 细胞、Treg 细胞、Th17/Treg 及其相关炎症因子对于冠状动脉损伤的预测及判断有一定的临床价值。

PU-1700

成人急、慢性荨麻疹血清过敏原特异性 IgE 的比较分析

杨术生
上海市东方医院南院检验科

目的 探讨成人急、慢性荨麻疹的发生与过敏原的关系。
方法 采用免疫印迹法对该院皮肤科门诊 2017 年 1 月—2020 年 11 月的急、慢性荨麻疹患者血清过敏原特异性 IgE（sIgE）抗体进行检测及分析。
结果 563 例荨麻疹患者以女性为主，女性荨麻疹例数占比（61.10%）显著高于男性（38.90%），差异有统计学意义（χ2=55.506，P=0.000）。共检出 sIgE 阳性病例 228 例（40.50%）；吸入性过敏原 sIgE 阳性率（30.91%）高于食入性过敏原 sIgE 阳性率（22.20%），差异有统计学意义（χ2=10.933，P=0.001）。急、慢性荨麻疹患者年龄构成、性别分布等差异均无统计学意义（P＞0.05）。急性荨麻疹患者较慢性荨麻疹患者猫毛、艾蒿 sIgE 阳性率更高，差异有统计学意义（χ2 分别为 6.156 和 7.843，P 分别为 0.013 和 0.005），慢性荨麻疹患者较急性荨麻疹患者鸡蛋白 sIgE 阳性率更高，差异有统计学意义（χ2=8.203，P=0.004）。
结论 急、慢性荨麻疹过敏原种类存在差异，可能与其发病机制、临床表现等有关，临床应重视过敏原种类的筛查以便更好地进行荨麻疹患者诊治和管理。

PU-1701

AFP-L3%、DCP 和 GALAD 模型在 AFP 低浓度 HCC 诊断中的作用

杨术生
上海市东方医院南院检验科

目的 探讨血清甲胎蛋白异质体比率（AFP-L3%）、异常凝血酶原（DCP）和 GALAD 模型对甲胎蛋白（AFP）低浓度肝细胞肝癌（HCC）中的应用价值。
方法 采用回顾性研究方法，纳入 2020 年 1 月至 2021 年 2 月上海市东方医院就诊的 120 例低浓度 AFP 的研究对象，根据诊断分为 HCC 组 47 例、非 HCC 组 73 例，测定血清中 AFP-L3%、DCP 浓度并进行统计分析。
结果 HCC 组血清 AFP、AFP-L3%和 DCP 水平以及 GALAD 模型评分均明显高于非 HCC 组，差异有统计学意义（P＜0.05）；联合检测 AFP、AFP-L3%和 DCP 的曲线下面积为 0.954，对应的诊断灵敏度为 89.4%、特异性为 97.3%，明显高于 AFP、AFP-L3%和 GALAD 模型（分别为 Z=3.418，P=0.001；Z=2.965，P=0.003 和 Z=3.184，P=0.002），但与 DCP 差异无统计学意义（Z=1.684，P=0.092）。

结论 AFP、AFP-L3%及 DCP 联合检测或有助于提高低浓度 AFP 肝癌的诊断效能，为 AFP 低浓度肝癌早期诊断提供可靠依据。

PU-1702

郑州部分地区健康成年人群血清促甲状腺激素受体抗体参考区间的调查研究

徐海娈
郑州安图生物工程股份有限公司

目的 调查郑州地区健康人群血清促甲状腺激素受体抗体（thyrotrophin receptor antibody，TRAb）水平分布，建立本地区 TRAb 的参考区间，以期为临床诊断、用药和预后提供可靠依据。
方法 收集从 2020 年 4 月至 2020 年 12 月于郑州唯爱康健康体检中心进行常规体检的人群，按照美国国家临床生化协会建议的正常成人入选标准进行严格筛选，将入组的 936 人按性别及年龄段分为两组：男性（18-40 岁 394 人和大于 40 岁 104 人），女性（18-40 岁 339 人和大于 40 岁 99 人），采用郑州市安图生物工程有限责任公司开发的磁微粒化学发光免疫试剂检测血清 TRAb 水平，对检测结果进行分析。
结果 936 名健康人血清 TRAb 呈偏态分布，男性与女性各年龄组血清 TRAb 之间水平差异均无统计学意义（P＞ 0.05），可建立统一参考区间（0.3-1.17 IU /L）。
结论 建立适合本地区健康人群的 TRAb 参考区间，为郑州地区医院临床实验室的应用提供了参考依据。

PU-1703

类风湿关节炎患者中性粒细胞/淋巴细胞比值和血小板/淋巴细胞比值对病情活动度的评估价值研究

张丽中
山西白求恩医院

目的 研究类风湿性关节炎患者中性粒细胞/淋巴细胞比值和血小板/淋巴细胞比值在评估病情活动度中的价值。
方法 收集 2019 年 12 月—2021 年 2 月山西白求恩医院类风湿性关节炎患者 150 名，同时随机抽取年龄、性别相匹配的健康体检者 81 名作为健康对照组。RA 患者按类风湿性关节炎疾病活动度 DAS28 进行评分，分为 RA 缓解期组（41 例）和 RA 活动期组（109 例），记录患者的临床资料（关节肿胀数，关节压痛数，患者自我感觉评分）和实验室指标（PLT，LYM，NEUT，WBC，CRP 等），计算 NLR，PLR 比值;比较健康对照组，RA 缓解期和活动期患者 NLR，PLR 的差异性，并进行相关性分析。符合正态分布的组间使用独立样本 t 检验，相关性分析采用 Spearman 检验，对 RA 病情进展的评估价值则用 ROC 曲线。
结果 健康对照组 PLT, WBC，NEUT，NLR，PLR 水平显著低于 RA 患者 PLT，WBC，NEUT，NLR，PLR；健康对照组 LYM 明显高于 RA 患者 LYM，差异有统计学意义（p<0.05）；缓解期 RA 患者 NLR，PLR 和 CRP 明显低于活动期 RA 患者 NLR，PLR 和 CRP 水平，差异有统计学意义(P<0.05)。RA 活动期患者 NLR，PLR 与 DAS28-CRP 呈显著正相关（r=0.297,r=0.381，P<0.05）。ROC 曲线表示，NLR，PLR 评估类风湿性关节炎疾病活动的曲线下面积（AUC）分别为 0.728 和 0.675，当 cut-off 值为 2.45 和 161.0（即检测量值为 2.45 和 161.0 时），NLR，PLR 诊断 RA 的敏感性为 0.572 和 0.527 特异度为 0.877 和 0.827。

结论 RA 的病情活动与 NLR，PLR 存在正相关关系，NLR，PLR 对评估类风湿性关节炎进入活动期具有较高的价值。

PU-1704

GrpE Immunization Protects Against Ureaplasma urealyticum Infection in BALB/C Mice.

Guozhi Dai[2]、Yanhong Tang[1]、Fangyi Guo[2]
1. 广州医科大学呼吸疾病国家重点实验室
2. 郴州市第一人民医院

Nucleotide exchange factor (GrpE), a highly conserved antigen, is rapidly expressed and upregulated when *Ureaplasma urealyticum* infects a host, which could act as a candidative vaccine if it can induce an anti-*U. urealyticum* immune reaction. Here, we evaluated the vaccine potential of recombinant GrpE protein adjuvanted by Freund's adjuvant (FA), to protect against *U. urealyticum* genital tract infection in a mouse model. After booster immunization in mice with FA, the GrpE can induced both humoral and cellular immune response after intramuscular injection into BALB/c mice. A strong humoral immune response was detected in the GrpE-immunized mice characterized by production of high titers of antigen-specific serum IgG (IgG1, IgG2a, and IgG3) antibodies. At the same time, the GrpE also induced a Th1-biased cytokine spectrum with high levels of IFN-γ and TNF-α after re-stimulation with immunogen GrpE in vitro, suggesting that GrpE could trigger the Th1 response when used for vaccination in the presence of FA. Although GrpE vaccination in the presence of a Th1-type adjuvant-induced had readily detectable Th1 responses, there wasn't increase inflammation in response to the infection. More importantly, the robust immune responses in mice after immunization with GrpE showed a significantly reduced *U. urealyticum* burden in cervical tissues. Histopathological analysis confirmed that tissues of GrpE-immunized BALB/c mice were protected against the pathological effects of *U. urealyticum* infection. In conclusion, this study preliminarily reveals GrpE protein as a promising new candidate vaccine for preventing *U. urealyticum* reproductive tract infection.

PU-1705

血清 NSE、S-100 和 CRP 水平在脑损伤中的变化及意义

凌芸、束梅燕、钱香、臧晓陵
江苏省人民医院（南京医科大学第一附属医院）

目的 评估血清中神经元特异性烯醇化酶（NSE）、中枢神经特异蛋白（S-100）、和 C 反应蛋白（CRP）水平与脑损伤的关系，探讨其与患者病情严重程度及结局的关系。
方法 选取 203 例脑损伤患者作为观察组，另选取同期 200 例健康体检者作为对照组，比较两组血清中 NSE、S-100、和 CRP 水平，并分别比较观察组不同结局患者血清中的水平。
结果 观察组血清中 NSE、S-100 和 CRP 水平均明显高于对照组，差异具有统计学意义($P<0.05$)。不良结局组患者血清中 NSE、S-100、和 CRP 水平均明显高于良好结局组，差异均有统计学意义($P<0.05$)。
结论 血清中 NSE、S-100、和 CRP 水平与脑损伤病情严重程度及结局存在关联，检测三者水平有助于病情评估和结局判断，对临床治疗有积极意义。

PU-1706

浓缩清洗缓冲液浓度对乙肝表面抗原定量结果的影响

郑欢欢
吉林金域检验所有限公司

目的 探讨浓缩清洗缓冲液浓度对乙肝表面抗原定量结果的影响
方法 选取 2020 年 1 月至 2020 年 3 月之间送检我公司的健康体检项目为乙肝表面抗原检测的标本 100 例，将标本平均分为 2 份，分别为 A、B 两组。A 组 100 例体检患者为实验组，将浓缩 Bffer 液用纯水以 1:9 的稀释倍数进行稀释；B 组 100 例体检患者为对照组，用纯水对浓缩 Bffer 液以 1:9.5 的稀释倍数进行稀释，将所有样本进行高速离心后，A、B 组均采用雅培 i2000ISR 进行乙型肝炎病毒表面抗原检测，检测试剂为乙型肝炎病毒表面抗原检测试剂盒，检测方法为化学发光微粒子免疫检测法，均使用配套试剂进行检测。对实验组（1:9 倍雅培 Buffer 液进与纯水稀释）与对照组（1:9.5 倍的雅培 Buffer 液与纯水稀释）的乙型肝炎病毒表面抗原检测结果进行分析。
结果 根据乙型肝炎病毒表面抗原检测标准，浓度＜0.05IU/ml 的样本视为非反应性（阴性）；浓度≥0.05IU/ml 的样本则视为反应性（阳性）。一般情况下健康人的乙型肝炎病毒表面抗原浓度很低(多为 0.00-0.01）。实验组乙肝表面抗原定量（HBSAg）1:9 倍雅培浓缩清洗液结果为 0.00-0.01(IU/ml)；对照组乙肝表面抗原定量（HBSAg）1:9.5 倍雅培浓缩清洗液结果为 0.03-0.04(IU/ml)，表面抗原结果高于正常值。
结论 结果表明浓缩清洗缓冲液浓度为 1:9 时，结果更准确。雅培浓缩清洗液浓度过低会导致吖啶脂标记的乙肝表面抗原抗体结合反应混合物冲洗不干净，从而导致表面抗原结果有差异。乙型肝炎病毒表面抗原通常用于辅助诊断疑似乙型肝病（HBV）感染的患者并对抗病毒治疗效果和感染者的状态进行检测，如果表面抗原结果不准确，可能会耽误病情的检测或者疾病的诊断，我们要严格按照厂家提供的稀释倍数进行配比，消除可能因清洗液浓度过低对乙肝表面抗原的影响。

PU-1707

血清 GPC-3 在肝细胞癌诊断中的应用

崔俊华、杨静、周佳烨、王蓓丽、郭玮
复旦大学附属中山医院

目的 研究血清 GPC-3 在肝细胞癌诊疗中的应用。
方法 围绕 GPC-3 生物学特征、血清 GPC-3 检测手段及其在肝细胞癌诊断中的应用作一综述。
结果 据世界卫生组织数据统计，HCC 是全球第五大常见肿瘤，第二大癌症致死病因。HCC 的早期发现和治疗与良性肝病灶或正常肝相比，大多数 HCC 中 GPC-3 信使 RNA（mRNA）显着增加，同时免疫组织化学研究表明，GPC-3 在 HCC 中会有表达，而在正常肝脏和良性肝脏疾病的肝细胞中则无法检测到。与此相符的是，在健康人群和肝炎患者的血清中未检测到 GPC-3。
结论 通过检测血清 GPC-3，并结合甲胎蛋白、异常凝血酶原等其它血清标志物可辅助肝细胞癌的诊断。

PU-1708

新疆地区某三甲医院呼吸道病原体感染情况分析

王玲玲、庞秀慧、黄睿
新疆维吾尔自治区人民医院

目的 分析研究新疆地区某三甲医院呼吸道病原体的感染率及季节分布情况。

方法 回顾性分析该院 2020 年 4 月至 2021 年 3 月进行呼吸道病原体 IgM 抗体检测的 7231 例住院患者的结果，采用间接免疫荧光法检测 8 种呼吸道感染病原体 IgM 抗体（包括腺病毒、肺炎衣原体、甲型流感病毒、乙型流感病毒、副流感病毒、嗜肺军团菌、肺炎支原体、呼吸道合胞病毒），对感染阳性率及感染的季节分布进行分析。
结果 7231 例患者中，呼吸道感染病原体 IgM 抗体阳性检出率 28.34%（2049/7231），主要以肺炎支原体感染为主，阳性率为 6.47%（468/7231）；混合感染以甲型流感病毒+乙型流感病毒为主，阳性率为 1.31%（392/7231）。呼吸道感染以秋季（9-11 月）最高，7.79%（563/7231）；春季（3-5 月）次之，7.23%（523/7231）。
结论 新疆地区呼吸道病原体感染主要以肺炎支原体为主，混合感染以甲型流感病毒+乙型流感病毒为主，秋季发病率最高。

PU-1709

Interleukin-18 is a prognostic marker and plays a tumor suppressive role in colon cancer

Xiaodong Feng、Xiaodong Feng
The Affiliated Hospital of Qingdao University

Interleukin-18 (IL-18) belongs to the IL-1 family, and is an essential proinflammatory and immune regulatory cytokine. The present study was designed to investigate the expression and function of the IL-18 in colon cancer. In clinical analyses, mRNA and protein expression of IL-18 were decreased in tissues of colon cancer patients. This decreased expression of IL-18 was significantly correlated with the tumor size (P=0.001) and American Joint Committee on Cancer (AJCC) stage (P=0.013). Patients with IL-18 positive tumors had a better survival than patients with IL-18 negative tumors. Moreover, up-regulation of IL-18 inhibited colon cancer cells proliferation. Our data suggest that the decreased expression of IL-18 in colon cancer was associated with prognosis and tumor proliferation. IL-18 may be considered as a novel tumor suppressor and a potential therapeutic target for colon cancer patients.

PU-1710

南京地区妊娠女性甲状腺功能指标参考区间的建立

王参军
东南大学附属中大医院

目的 检测南京地区健康妊娠女性不同孕期的甲状腺功能指标水平,建立该地区孕早、中、晚期女性的甲状腺功能指标参考区间。
方法 选取 2019 年 1 月至 2020 年 12 月在该院建档、产检的孕妇 160 例,并选择 160 例育龄期健康非妊娠女性作为健康对照,采用罗氏全自动化学发光分析仪检测 120 例妊娠女性在孕早、中、晚期的血清游离甲状腺素（FT4）、促甲状腺激素（TSH）水平,并对检测结果进行分析,建立该地区妊娠女性 FT4、TSH 的参考区间。
结果（1）孕早、中、晚期 FT4 水平分别为（13.97±1.51）、（11.36±0.87）、（11.47±1.09）pmol/L,TSH 水平分别为 1.253（0.081,2.639）、1.573（0.517,3.42）、1.563（0.515,3.168）mIU/L。（2）孕早期女性与孕中期、孕晚期女性的 FT4、TSH 水平比较,差异均有统计学意义（P<0.05）,但孕中期、孕晚期女性的 FT4、TSH 水平比较,差异无统计学意义（P>0.05）。（3）TSH 在孕早期较低,之后逐渐上升,孕早期女性 TSH 水平与健康非妊娠女性比较,差异有统计学意义（P<0.05）。FT4 在孕早期较高,之后逐渐下降,孕早、中、晚期女性与健康非妊娠女性 FT4 水平比较,差异均有统计学意义（P<0.05）。

结论 妊娠期女性较健康非妊娠女性甲状腺功能指标水平有明显变化,孕早期、孕中期、孕晚期也有差别,应建立该地区孕早、中、晚期女性的甲状腺功能指标参考区间。

PU-1711

梅毒螺旋体 Hsp40 蛋白的表达、纯化及免疫学活性分析

伍仙
湖南中医药高等专科学校附属第一医院（湖南省直中医医院）

目的 表达梅毒螺旋体（Tp）Hsp40 蛋白并分析其免疫学活性。
方法 利用软件预测 TpHsp40 蛋白的 B 细胞表位，构建重组质粒 pET28a-TpHsp40，转化大肠埃希菌 BL21 star（DE3），培养后利用 IPTG 诱导重组 TpHsp40 蛋白的表达。收集菌体，破碎、离心后用 Ni2+层析柱进行纯化。收集 80、120 和 200 mmol/L 咪唑洗脱蛋白，经脱盐、去内毒素后取纯度良好的一组 TpHsp40 蛋白免疫小鼠，制备抗血清，采用 ELISA 检测抗体效价并分型。取小鼠脾脏，制成脾细胞悬液，采用 CCK-8 法检测淋巴细胞增殖情况，ELISA 法测定淋巴细胞分泌的细胞因子水平。
结果 生物信息学分析 TpHsp40 含有多个 B 细胞表位。构建的重组质粒转染 DE3 后经 IPTG 诱导表达分子质量单位约为 42.4 ku 的重组 TpHsp40 蛋白，经亲和层析纯化后免疫小鼠，能够刺激产生高滴度（105log10）的血清抗体。且能够诱导小鼠淋巴细胞增殖(SI 值为 2.41)和 IFN-γ、TNF-α 高表达，但不能够诱导 Th2 型细胞因子表达。
结论 重组表达的梅毒螺旋体 TpHsp40 蛋白能够诱导小鼠产生 Th1 型应答，有望成为 Tp 疫苗的新靶点。

PU-1712

自动光激化学发光检测仪 LiCA500 的性能验证

李恒[1]、陈煌炜[2]、杨宏伟[1]
1. 天津市天津医院
2. 天津医科大学 医学检验学院

目的 验证医院新引进的 LICA500 自动光激化学发光检测仪系统性能。
方法 根据 CNAS-GL038: 2019《临床免疫学定性检验程序性能验证指南》的要求，对 LICA 500 自动光激化学发光检测仪检测乙肝表面抗原（HBsAg）、乙肝表面抗体（Anti-HBs）、乙肝 e 抗原（HBeAg）、乙肝 e 抗体（Anti-HBe）、乙肝核心抗体（Anti-HBc）、丙肝抗体(Anti-HCV)和梅毒螺旋体抗体(Anti-TP)7 个项目的符合率、精密度、检出限、临界值、线性范围进行性能验证及评价。
结果 检测 7 个项目的方法符合率均为 100%，批内变异系数 CV%为 0.16%~8.61%，批间变异系数 CV%为 0.17%~13.93%，线性范围斜率为 1.0038~1.0074，r2 在 0.9999~1.0000，满足相关文件要求；检出限阳性结果次数、最低检测限以及临界值均满足厂家要求，在其规定的范围之内。
结论 自动光激化学发光检测仪 LiCA500 检测系统检测 7 个项目的符合率、精密度、检出限、临界值、线性范围验证通过，可满足临床需要并投入使用。

PU-1713

发热和呼吸困难患者九联检 IgM 抗体检测结果分析

杨耀永、唐满玲、蒋最明、何聪玲、吴莹
株洲市中心医院

目的 了解本地区发热和呼吸困难患儿的病原谱, 为临床抗感染及病原体检测提供依据。
方法 收集 1033 例临床症状表现为发热和呼吸困难患儿的血清标本, 采用间接免疫荧光法检测其中 9 种常见病原体的 IgM 抗体。
结果 1033 例患儿中肺炎支原体抗体阳性 495 例,春季、夏季和秋季都是肺炎支原体高发期。
结论 湖南株洲地区引起儿童发热和呼吸困难的主要病原体是肺炎支原体，并且春季、夏季和秋季感染率都很高。

PU-1714

建立基于 HCC 相关特异性血清标志物的诊断模型

刘晓文、周佳烨、朱晶、邵文琦、王蓓丽、郭玮
复旦大学附属中山医院

目的 本研究旨在探讨肝癌诊疗中应用的血清标志物之间的联系和关系，期望能建立相应的诊断模型探讨肝癌（Hepatic Cell Carcinoma，HCC）患者的预后情况。
方法 选取影像学诊断或是病理诊断为 HCC 的患者 227 例数，依据其治疗前后（术前、术后；化疗前、化疗后）的样本检测 HCC 相关特异性血清标志物（AFP、AFU、PIVKA、AFP-L3）等，在随访患者一定时间后，依据其终点事件（复发、死亡、肿块大小、肝功能分级情况）与血清标志物的关系，模拟出含有血清标志物的诊断模型（可以用 logistics 回归，逐步进入计算风险相关系数）。
结果 根据特异性的血清标志物，对入组患者进行回顾性的研究，提出相应血清标志物的诊断模型。
结论 通过 HCC 相关特异性血清标志物的检测结果，分析 HCC 患者治疗前后的预后情况，得出能用以推断 HCC 患者预后情况的模型或是指导治疗的潜在诊断模型。

PU-1715

金属离子稳定剂对神经元特异性烯醇化酶样本稳定性提升影响

郑迪文
郑州安图生物工程股份有限公司

目的 肺癌是最常见的恶性肿瘤之一，且由于在发病早期症状和体征不明显，约 60%-80%的患者在确诊时已发展为中晚期，5 年生存率不到 10%。肿瘤标志物 NSE、ProGRP、SCC、Cyfra21-1、CEA 对于肺癌的早发现、早确诊具有明确指导意义，其中 NSE 是小细胞肺癌的首选肿瘤标志物，但是由于 NSE 抗原本身的不稳定性对临床检验工作的复检及留样考核带来较大困难。本文主要对金属离子稳定剂是否能延长 NSE 样本保存时间进行研究。
方法 选择经规范采血及处理得到的血清样本 38 例，取上清并分成 2 部分。实验组：按照 5%（质量体积比）的比例在其中 1 份样本中添加金属离子稳定性；对照组：按照 5%的比例在另外 1 份样本中添加 PB 缓冲；分别混匀后再次将实验组及对照组样本各分成 2 份，一份放置室温，一份放置 2-8℃。检测时间点：处理后 0 小时/4 小时/1 天/3 天/7 天/14 天。本次检测使用磁微粒化学发光法在安图 AutoLumo A2000 Plus 全自动化学发光测定仪上进行，比较实验组与对照组样本保存时间是否具有差异。

结果 添加金属离子稳定性的实验组在室温条件下可保存 3 天，样本与 0 小时比较检测偏差在 8.33%以内，明显优于对照组（室温条件下可保存 1 天）；实验组在 2-8℃条件下样本可稳定保存 7 天（与 0 小时比较检测偏差在 8.33%以内），明显优于对照组（2-8℃条件下可保存 3 天）。
结论 金属离子稳定剂的添加有利于神经元特异性烯醇化酶样本稳定性的提升，在进行一些需要样本短期保存的实验时，可使用并提升样本保存时间。另外可用于体外诊断试剂研发用样本添加以延长样本使用时效。

PU-1716

甲状腺刺激性免疫球蛋白临床效能应用评估

徐世骥、吴群、邵文琦、朱晶、王蓓丽、郭玮
复旦大学附属中山医院

目的 研究 TSI 在监测甲亢治疗疗效中的作用；通过间接法获得 TSI 参考范围。
方法 选取 2020 年 7 月至 12 月门诊及住院患者 TSI 检测数据，使用偏度-峰度值检验分析数据正态性，非正态分布数据通过 BOX-COX 变换转变为近似正态分布，采用四分位间距法剔除离群值，最后使用 Hoffman 法得出参考区间，并与直接法得到的行业标准参考区间比较，以参考变化值（reference change value，RCV）作为标准。通过比较甲亢组、肝病组、肾病组之间 TSI 水平差异，研究 TSI 与甲亢相关性。通过比较甲亢患者药物治疗或放射性治疗前后 TSI 水平变化，研究 TSI 在监测甲亢治疗疗效中的作用。
结果 TSI 间接法参考范围为 0-0.55；甲亢组中 TSI 水平显著高于肝病组和肾病组，$p<0.005$；肝病组和肾病组之间 TSI 水平无显著差异。甲亢患者经药物治疗后病情得到控制的患者中 TSI 水平下降。甲亢患者经放射性治疗后病情得到控制的患者中 TSI 水平下降。
结论 TSI 是甲亢的显著相关指标，并对监测甲亢疗效具有良好相关性。

PU-1717

罗氏 e602 全自动免疫分析仪性能验证及评价

邱美菊、杨丽红、胡道波、施立超
杭州迪安医院检验中心

目的 在仪器投入使用前，为了能够保证临床检验结果的准确性，提高临床检验的检测质量，有效的提高服务质量，现对罗氏 e602 全自动免疫分析仪进行验证及评价。
方法 根据 ISO15189 的要求，现对在该全自动免疫分析仪上检测的甲胎蛋白（AFP）、癌胚抗原（CEA）、糖类抗原 125（CA12-5）、糖类抗原 153(CA15-3)、糖类抗原 199(CA19-9)、糖类抗原 724(CA72-4)、铁蛋白(Ferr)、非小细胞肺癌相关抗原 21-1(CYFRA21-1)、总前列腺特异性抗原（PSA）、游离前列腺特异性抗原（fPSA）、神经元特异性烯醇化酶（NSE）共 11 个项目的精密度、正确度、分析测量范围、参考区间、临床可报告范围进行性能的验证与评价。
结果 批内精密度均小于 1/4CLIA’88（6.25%），批间精密度均小于 1/3CLIA’88（8.33%）；正确度允许误差均小于 1/2CLIA’88（12.5%）；分析测量范围的实际偏倚均小于允许偏倚（12.5%）；健康人群的 20 例样本进行验证，应不超过 2 例（10%）在验证区间外，若超过 2 例在参考区间外，则需要重复检测另外一组 20 例标本，参考区间的 20 例样本均不超过 2 例（10%）在验证区间外，验证通过；可报告范围的高限，至少选用 3 个高浓度样本，稀释倍数应为方法性能标明的最大稀释倍数并适当增加或减小稀释比例，每个高值样本重复测定 3 次，其相对偏倚均在允许范围（8.33%）之内。
结论 通过对罗氏 e602 全自动免疫分析仪进行验证及评价后，其分析性能符合质量目标和要求，能够保证临床检验结果的真实性、准确性和可靠性，能够更好的满足和服务于临床。

PU-1718

两种检测肺炎支原体 IgM 抗体的方法学比较

杨琴
胜利油田中心医院

目的 支原体肺炎是肺炎支原体引起的急性呼吸道感染伴肺炎，过去称为“原发性非典型肺炎”的病原体中，肺炎支原体最为常见。可引起流行，约占各种肺炎的 10%，严重的支原体肺炎也可导致死亡。肺炎支原体抗体分为 IgG 抗体和 IgM 抗体两种，因为肺炎支原体感染的潜伏期为 2 周-3 周，当患者出现症状而就诊时，IgM 抗体已达到相当高的水平，因此，IgM 抗体阳性可作为急性期感染的诊断指标。如 IgM 抗体阴性，也不能否定肺炎支原体感染，还需检测 IgG 抗体。IgG 较 IgM 出现晚，需动态观察。本文将对两种检测肺炎支原体 IgM 抗体的方法学进行比较。
方法 采用欧蒙间接免疫荧光法定性检测、亚辉龙化学发光法定量检测
检测人群： 202101-2021-04 我院住院及门诊就医患者，临床上有呼吸系统症状，以检测肺炎支原体 IgM 抗体来排除是否有其感染。年龄为 1M-94 岁之间，不区分性别，平行用这两种方法进行检测。
结果 定性按照弱阳性、阳性、阴性来判定，弱阳性和阳性均在阳性率统计范围内。定量按照无反应性 0-0.9；灰区：0.9-1.1；有反应性>0.9，结果在 0.9 以上均在阳性率统计范围内。
在 725 例患者中，肺炎支原体 IgM 抗体用间接免疫荧光法定性检测：阳性+弱阳性，230 例，阳性率为 31.72%；化学发光法定量检测：大于 0.9，138 例，阳性率为 19%。
结论 肺炎支原体 IgM 抗体结果在临床上的应用较为重要，因检测方法学不同，敏感性也不同，通过以上比较，采用欧蒙间接免疫荧光法检测比亚辉龙化学发光法检测更为敏感。

PU-1719

临床免疫检验报告自动审核系统的规范化建立和验证

朱晶、周佳烨、邵文琦、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 探讨临床免疫乙肝两对半、甲状腺功能和肿瘤标志物结果（共 30 个检测项目）自动审核系统的规范化建立和验证。
方法 复旦大学附属中山医院检验科的免疫报告自动审核系统自 2018 年建立并应用至今，将所有自动审核规则建立于实验室信息系统（Laboratory information system，LIS)，采用仪器报警信息、复检规则、各检测项目的审核范围、Delta check，以及检测项目之间的逻辑关系共 5 部分审核规则。通过人工审核与自动审核相互比对，验证自动审核系统的有效性。
结果 临床免疫报告自动审核的灵敏度和特异性分别为 89.6%和 65.0%，阳性预期值和阴性预期值分别为 78.9%和 88.2%。自动审核系统与两位实验室高年报告审核人员判断的一致性达到 99.78%。自动审核系统的报告总通过率为 85.06%。统计 kappa 分析结果为 0.99（P<0.001）。
结论 实施临床免疫报告自动审核系统可降低 TAT，大大减少需要人工审核的工作量，使工作人员有更多的时间关注在疑难报告上。有效提高分析后环节的工作效率，进一步确保检验报告的准确性。

PU-1720

COVID-19 住院患者抗体 IgM、IgG 产生时效性和量化标准

段丽、林国跃*、李远达、秦莹、蔺志强、王泉、刘艳、史长音、杨振萍、何雪、贾婷、木尼热·库尔班
新疆医科大学第八附属医院（新疆新冠肺炎医疗救治定点医院）

目的 探讨新冠肺炎患者不同时间阶段自然产生的抗体 IgM、IgG 含量变化及 CT 值与浓度量化对应关系，为病情判断评估提供依据。
方法 收集 200 例 COVID-19 患者临床特征信息资料，应用磁微粒化学发光法多次检测新冠住院患者抗体 IgG 和 IgM 含量，统计并方差分析。
结果 COVID-19 患者随着病情变化住院时间延长体内 IgG 和 IgM 含量逐步增加，第 1-5d 产生浓度较低，第 6-10d 和第 11-20d 大幅度快速上升，在第 21-30d 内达到最高峰，第 31-40d 仍在高峰期并处于稳定状态，第 41-50d 后开始下降，几乎呈正态分布。恢复期较发病早期明显的高（P＜0.05）。不同年龄、性别、民族和临床分型的患者产生的 IgG 抗体含量随着病情进展天数延长是逐步增加的，到第 31-40 天仍保持较高浓度，但以 51-60 岁患者抗体 IgG 增加幅度最大，但早期第 1-5 天抗体 51-60 岁以上患者较年轻人产生明显的低、速度慢，而 IgM 抗体在早中期是逐步增加，到第 31-40 天后却是逐步减少的。女性 IgG 抗体增加明显高于男性（P＜0.05），IgM 抗体无明显差异（P＞0.05）。汉族第 10-20 天和第 21-30 天患者 IgG 和 IgM 抗体含量均明显高于维族（P＜0.05），而早期与后期其基本一致。IgG 和 IgM 抗体含量重型较轻型患者显著增高（P＜0.05），且重型患者抗体浓度变化较大不稳定，仅 IgM 抗体在第 31-40 天后明显下降。抗体 ct 值与浓度量化关系：1.61-7 之间为 1:2 浓度，8-15 为 1:4 浓度，16-25 为 1:8 浓度，17-35 为 1：16,36-80 为 1:32,81-115 为 1:64,116-350 为 1:128，351 以上为 1:256。
结论 COVID-19 患者在自然免疫状态下体内产生抗体 IgM、IgG 含量与年龄、性别、病程轻重有密切关系，其含量大小有提示患者清除病毒能力和预示病情转归的重要作用。

PU-1721

基于 CD169 表达量对小鼠脾红髓巨噬细胞进行的分型研究

杨施琪
上海交通大学医学院附属第九人民医院

目的 基于小鼠脾中红髓巨噬细胞唾液酸黏附蛋白（sialoadhesin, Sn，CD169）分子的表达水平，研究 CD169+和 CD169-红髓巨噬细胞亚群的基因表达谱差异。
方法 采用流式细胞术和免疫荧光法，检测 C57BL/6J 野生型（WT）小鼠脾中红髓巨噬细胞中 CD169 的表达，以 CD169 敲除（CD169 KO）小鼠为阴性对照。富集 F4/80+的脾红髓巨噬细胞并分选出 CD169+和 CD169- 2 个亚群，对它们进行 RNA 测序。利用 DESeq2 软件在 P <0.05 &|log2FC|≥ 1 时筛选出差异基因，通过京都基因与基因组数据库（Kyoto Encyclopedia of Genes and Genomes, KEGG）富集功能分析，将差异基因按照参与的通路或功能进行分类。通过实时荧光定量 PCR（quantitative real-time PCR, qPCR）验证部分差异基因。
结果 流式细胞术和免疫荧光法证实部分红髓巨噬细胞表达 CD169。CD169+和 CD169- 亚群拥有 485 个差异表达基因，其中有众多与介导炎症相关的基因在 CD169-群中高表达，提示这 2 个亚群有不同的功能。
结论 CD169+ 和 CD169- 红髓巨噬细胞有不同的转录谱，CD169- 红髓巨噬细胞亚群具有更多 M1 型巨噬细胞的特征。

PU-1722

血清肿瘤标志物联合检测在宫颈癌中的应用价值

杨军[1]、冯悦爽[2]
1. 天津市天津医院
2. 天津医科大学 临床医学院

目的 探讨新的肿瘤标志物热休克蛋白 90α（Hsp90α）与传统肿瘤标志物糖类抗原 125(CA125)，癌胚抗原(CEA)在宫颈癌中的应用价值。
方法 回顾性检测分析 2018 年 5 月—2020 年 3 月于天津市天津医院、和田地区人民医院妇科初诊的宫颈癌患者 70 例（宫颈癌组），平均年龄为 (46±15) 岁，选择同期体检中心 50 例女性健康体检者（对照组），平均年龄为 (51±24) 岁。均无心肝肾等系统疾病，检测期间未使用过任何药物。所有研究对象均于入院后未治疗前取静脉血，采用 ELISA 双对数拟合曲线法行 Hsp90α 检测，传统肿瘤标志物 CA125，CEA 的检测采用化学发光法，所有检测结果均采用 SPSS 19.0 统计学软件进行统计学分析，计量数据用均数±标准差表示；采用 t 检验分别比较不同组间各检测指标水平的差异，以 P<0.05 为差异有统计学意义；宫颈癌组 Hsp90α 与传统肿瘤标志物的相关性采用 person 相关性分析，以 P<0.05 为具有相关性。
结果 宫颈癌组患者外周血 Hsp90α、CA125、CEA 检测水平均高于健康对照组，两组经比较差异均具有统计学意义 （P 均<0.05)。经 person 相关性分析，在宫颈癌患者中 Hsp90α 与 CA125、CEA 之间没有相关性，P 均>0.05。
结论 本研究结果显示 Hsp90α 与传统肿瘤标志物在早期初诊未经治疗的宫颈癌患者外周血中均高表达，具有临床早期检测价值。Hsp90α 对宫颈癌具有独立的早期检测意义。

PU-1723

茯苓多糖联合 CD47 免疫检查点抑制剂增强巨噬细胞抗肺癌作用

龙婷婷、张春莹、江虹
四川大学华西医院

目的 明确茯苓多糖免疫调节抗肺癌作用及与 CD47 抗体联用增强巨噬细胞吞噬肺癌细胞、达到协同抗癌的疗效。
方法 经茯苓多糖处理 Lewis 肺癌细胞及 Lewis 肺癌荷瘤小鼠，分别检测茯苓多糖对 Lewis 细胞的抑制率及对荷瘤小鼠的抑瘤率、脏器指数、血清细胞因子水平的影响。利用流式和免疫荧光技术检测肺癌细胞系和肺癌组织中 CD47 的表达，以及肿瘤相关巨噬细胞表面 SIRPα 的表达情况。构建巨噬细胞与肺癌细胞的混合培养体系，检测 CD47 抗体阻断 CD47-SIRPα 信号通路后巨噬细胞对肺癌细胞吞噬活性的影响。最后利用茯苓多糖与 CD47 抗体联合作用于巨噬细胞和肺癌细胞的共培养体系及肺癌荷瘤小鼠模型，比较二者联用较单一用药的体内外疗效差异。
结果 茯苓多糖可抑制 Lewis 肺癌细胞体外培养活性，提高荷瘤小鼠的抑瘤率及胸腺、脾脏指数，促进免疫细胞因子的分泌，达到体内外免疫调节抗肺癌作用。CD47 抗体可有效阻断肺癌细胞上高表达的 CD47 与巨噬细胞上的 SIRPα 结合，打开吞噬信号通路，促进巨噬细胞吞噬肿瘤细胞过程。茯苓多糖与 CD47 抗体联用，体外可增强巨噬细胞对肺癌细胞的吞噬功能，体内可增强抑瘤作用、减缓癌细胞扩散速度、增强免疫器官脏器指数、提高生存率等。
结论 茯苓多糖可激活巨噬细胞的吞噬活性，CD47 抗体阻断抑制吞噬的信号通路实现巨噬细胞吞噬肿瘤细胞过程，二者联用可促进巨噬细胞的免疫调节功能，发挥协同抗肺癌作用。

PU-1724

COVID-19 infection induces readily detectable morphologic and inflammation-related phenotypic changes in peripheral blood monocytes

Rui Guo
Xi,an Eight Hospital

Objective To explore the value of morphological and phenotypic changes of peripheral blood mononuclear cells in the early recognition of COVID-19 infection and inflammation
Method Peripheral blood samples of 34 COVID-19 patients were detected by flow cytometry
Results The monocytes of COVID-19 patients in the intensive care unit (ICU) are larger than normal, and they are easier to identify on the forward scatter (FSC). Then we perform side scatter analysis by conventional flow cytometry and find that the FSC is high. Compared with the normal control group, these CD14+CD16+, FSC-high monocytes showed the characteristics of mixed M1/M2 macrophage polarization. Compared with other monocytes with low FSC, CD80+ and CD206+ The expression is higher and it secretes higher levels of IL6, IL-10 and TNF-α.
Conclusion Detection and continuous monitoring of this subpopulation of inflammatory monocytes may guide the prognosis and treatment of COVID-19 patients, and deserves further evaluation.

PU-1725

中国西南地区高血压患者 24h 尿儿茶酚胺及其代谢物参考区间的建立

戴鑫华、安云飞、邹远高、万正利、白杨娟
四川大学华西医院

目的 在探究中国西南地区非嗜铬细胞瘤的高血压患者 24h 尿液中儿茶酚胺及其代谢物的水平分布，建立中国西南地区的生物水平参考区间。
方法 收集 2020 年 10 月至 2021 年 3 月四川大学华西医院的 526 例高血压患者 24 h 尿液儿茶酚胺及其代谢物的检测数据，其中男性 277 例，女性 249 例，排除诊断为嗜铬细胞瘤的病例。尿液采集送检前均加入 10 mL 浓盐酸抗氧化，通过超高效液相色谱-串联质谱（UPLC-MS/MS）对尿液儿茶酚胺及其代谢物进行检测。所有数据采用偏度-峰度值检验数据的正态性，非正态分布数据采用 U 检验和 Z 检验对参考区间是否需要以性别分组进行验证，并通过非参数方法建立 2.5%-97.5%的参考区间及其 90%置信区间。
结果 E、NE、DA、MN、NMN、3-MT、HVA、VMA 水平均表现为男性高于女性，其差异具有统计学意义（$p<0.05$），且 Z 检验提示需要根据性别进行参考区间分组；HVA 在性别组间的差异无统计学意义（$p=0.178$）且不需要根据性别进行参考区间分组。HVA 参考区间为：1.21~11.37mg/24h；男性 E、NE、DA、MN、NMN、3-MT、VMA 参考区间分别为：0.26~18.67、3.03~102.63、36.29~483.62、2.10~46.29、1.60~51.53、4.51~70.87μg/24h、1.09~8.46mg/24h；女性 E、NE、DA、MN、NMN、3-MT、VMA 参考区间分别为：0.26~15.51、4.82~89.24、36.22~369.58、2.49~33.86、2.88~43.28、6.35~57.22μg/24h、1.06~7.44mg/24h。
结论 本研究建立了非嗜铬细胞瘤高血压患者 24h 尿液儿茶酚胺及其代谢物的生物水平参考区间，为中国西南地区实验室提供参考，有助于高血压患者的病因筛查、诊断及预后评估。

PU-1726

超高效液相色谱-串联质谱法检测血浆中马钱子碱和士的宁的方法学研究

戴鑫华、安云飞、邹远高、万正利、白杨娟
四川大学华西医院

目的 利用超高效液相色谱-串联质谱（UPLC-MS/MS）建立马钱子碱和士的宁的检测方法，同时检测血浆中马钱子碱和士的宁的浓度。
方法 取 200 μL 血浆，依次加入内标（200 ng/mL 乌头碱）50 μL 和 10%氢氧化钠溶液 50 μL，使用 1 mL 混合溶剂正己烷-二氯甲烷（2:1）萃取，涡旋振荡后离心取上清液，于 40℃氮气流下挥干，残渣用 200 μL 流动相复溶。液相色谱采用 PC HILIC（2.0 mm I.D × 150 mm，3μm）色谱柱，流动相 A 相为 10mmol/L 甲酸铵+0.1%甲酸，流动相 B 相为乙腈，设置梯度洗脱程序，流速 0.3 mL/min，进样量 5 μL。质谱采用电喷雾离子源（ESI），在正离子多反应监测模式下检测血浆中马钱子碱和士的宁。定量分析离子对分别为马钱子碱 m/z 395.20→244.20、士的宁 m/z 335.20→184.00、乌头碱 m/z 646.50→586.40（内标）。对方法的专属性、线性、检出限、精密度、提取回收率和基质效应进行验证。
结果 UPLC-MS/MS 检测血浆中马钱子碱和士的宁的专属性良好。马钱子碱在 1-500 ng/mL 范围内线性良好，最低检测限为 0.5 ng/mL，日内精密度（RSD）为 3.2-9.6%，日间精密度（RSD）为 3.9-11.5%，提取回收率为 79.4%-108.2%，基质效应为 90.6%-97.4%。士的宁在 0.5-200 ng/mL 范围内线性良好，最低检测限均为 0.2 ng/mL，日内精密度（RSD）为 2.8-7.6%，日间精密度（RSD）为 4.2-12.1%，提取回收率为 92.3%-105.1%，基质效应为 92.2%-98.1%。
结论 本研究成功建立了同时检测马钱子碱和士的宁的 UPLC-MS/MS 检测方法，方法操作简便、快捷，在准确性、精密度和提取效果中能够满足临床对马钱子中毒检测的需求。

PU-1727

1630 例患者伏立康唑血药浓度监测结果分析

戴鑫华[1]、陈思宇[2]、白杨娟[1]、安云飞[1]、万正利[1]、邹远高[1]
1. 四川大学华西医院
2. 成都市双流区第一人民医院-四川大学华西空港医院

目的 探究多种因素对伏立康唑（VRC）血药浓度的影响，为临床合理使用伏立康唑提供参考。
方法 对 2017 年 1 月-2020 年 10 月在四川大学华西医院行伏立康唑治疗性药物监测（TDM）的 1630 例住院患者的监测结果及相关病例资料进行回顾性分析，比较性别、年龄和使用科室等不同因素对伏立康唑血药谷浓度的影响。
结果 本研究纳入了 1630 例住院患者共计 3758 例次伏立康唑血药浓度监测结果，其中男性 1098 名，女性 532 名，平均年龄为 50.14±16.42 岁。从整体检测结果分析，伏立康唑血药谷浓度具有较大的个体间差异，平均血药谷浓度为 3.47±4.01mg/L，其中 2605 例次（69.32%）在推荐浓度（0.5-5.0mg/L）范围内。不同年龄组的伏立康唑血药谷浓度具有统计学差异，与患者的年龄呈显著的正相关性，随患者年龄的增加药物浓度逐渐增加；男性与女性的伏立康唑血药谷浓度具有统计学差异，表现为男性高于女性。
结论 伏立康唑血药浓度受性别、年龄、肝肾功能等多种因素影响，个体差异较大，在进行个体化治疗时需进行血药浓度监测，以保障患者用药安全和有效。

PU-1728

UCH-L1 在脑出血性疾病中的诊断价值研究

王虹霏、史清海
新疆军区总医院

目的 脑出血是一种起病急，发展迅速，能够导致高死亡率、高致残率的严重疾病。泛素羧基末端水解酶 L1(UCH-L1)在神经细胞中高度特异性表达。本研究旨在通过分析脑出血患者血清中 UCH-L1 的浓度变化，研究其诊断及评估脑出血疾病病情和预后的临床意义。
方法 收集 60 例经头颅 CT 确诊的高血压性脑出血患者发病后 12 小时内和入院后 1 至 10 天内及出院时的静脉血作为待测样本，采用酶联免疫吸附法进行分析血清中 UCH-L1 的浓度。用格拉斯哥昏迷评分对患者临床状况进行评估，同时分析患者的年纪，入院时的瞳孔变化，血压，体重，不同发病部位的颅内压对病情预后的影响。
结果 脑出血患者与健康体检者相比，血清中 UCH-L1 水平明显升高，诊断疾病的最佳截止值为 0.3ng/ml，[ROC 分析曲线下面积 0.925 (95% CI，(0.766 - 1)，p＜0.001],入院时精神表现正常患者（格拉斯哥昏迷评分 15 分）与健康体检者相比，UCH-L1 诊断精神表现正常患者的价值并不确定,(ROC 分析曲线下面积 0.598,p=0.467）,发病 12 小时内患者血清中 UCH-L1 的浓度与格拉斯哥昏迷评分相比，有显著相关性（相关系数 0.694，p=0.002),患者的年纪，瞳孔变化和 UCH-L1 都是影响患者死亡相关。
结论 UCH-L1 可以作为诊断脑出血疾病特异性的生物标志物，也可以作为评估脑出血患者预后的有价值的指标。

PU-1729

维持性血液透析患者血浆心肌酶学、NT-proBNP 和血肌酐水平变化与心功能衰竭的相关性分析

漆星
四川大学华西医院资阳医院·资阳市第一人民医院

目的 分析维持性血液透析（MHD）患者血浆心肌酶学、氨基末端脑钠肽前体（NT-proBNP）和血肌酐（SCr）水平变化与心功能衰竭的相关性。
方法 选取 2019 年 7 月～2020 年 7 月资阳市第一人民医院收治的行 MHD 治疗患者 100 例，根据是否并发心力衰竭（HF）将其分为 MHD 并发 HF 组 33 例、MHD 未并发 HF 组 67 例。检测患者血浆肌酸激酶同工酶（creatine kinase-MB，CK-MB）、NT-proBNP 和 SCr 水平；检测患者心脏每搏量（SV）、左室射血分数（LVEF）等心功能指标，计算左心室心肌质量指数（LVMI）。采用 Pearson 相关性分析 CK-MB、NT-proBNP 及 SCr 水平与心功能之间的相关性，采用受试者工作特征（receiver operating characteristic，ROC）曲线评估各项指标在 HF 预测中的应用价值。
结果 MHD 并发 HF 组患者的 CK-MB、NT-proBNP、Scr 指标均明显高于 MHD 未并发 HF 组（P＜0.05）。MHD 并发 HF 组患者的 SV、LVEF 指标均明显低于 MHD 未并发 HF 组（P＜0.05），LVMI 则明显高于 MHD 未并发 HF 组（P＜0.05）。Pearson 相关性分析结果显示，CK-MB、NT-proBNP 及 SCr 水平均与 SV、LVEF 指标呈负相关关系，而与 LVMI 指标呈正相关关系，相关系数有统计学意义（P＜0.05）。ROC 结果显示，CK-MB、NT-proBNP 及 SCr 用于预测 MHD 患者伴发 HF 的 AUC 分别为 0.802、0.878、0.740，NT-proBNP 的 AUC 值显著高于 SCr（P＜0.05）。
结论 MHD 并发 HF 患者的血浆 CK-MB、NT-proBNP 及 SCr 水平均明显升高，且与患者的心功能指标关系密切，检测上述指标对于预测 MHD 患者并发 HF 具有积极意义。

PU-1730

广东省成人血清 25-羟基维生素 D 水平调查分析

李云珍、张玲、李玲、姚少濠、洪卓凡
广州金域医学检验中心

目的 了解广东省成人血清 25-羟基维生素[25（OH）D]的水平状态，为成人合理补充维生素 D（VD）提供科学依据。

方法 选取 2019 年 1 月~2020 年 12 月送检本检验中心常规体检的成人 31309 例，其中男性 10984 例，女性 20325 例，通过采集静脉血进行血清 25（OH）D 检测。

结果 （1）31309 例成人血清 25（OH）D 水平均值为（23.01±9.01）ng/mL，男性明显高于女性（P<0.01），分别为（25.03±9.65）和（21.92±8.45）ng/mL 。25（OH）D 缺乏及不足率高达 81.04%，充足率为 18.93%，过量为 0.03%。（2）青年组、中青年组、中年组、中老年组和老年组血清 25（OH）D 水平均值分别为（21.64±8.62）ng/mL、（22.26±8.14）ng/mL、（22.51±8.50）ng/mL、（24.29±9.14）ng/mL 和（25.14±10.53）ng/mL，青年组＜中青年组＜中年组＜中老年组＜老年组，各组比较差异均有统计学意义（均为 P<0.01），25（OH）D 平均水平随着年龄增大而升高。（3）25（OH）D 水平比较，夏季高于其他三季有统计学意义（P＞0.05），其他三季组间比较无差异（P<0.05）。不同季节间 25（OH）D 不足及缺乏率比较，冬季（82.84%）＞秋季（81.63%）＞春季（81.54%）＞夏季（79.00%），冬季不足及缺乏率最高。

结论 广东省成人 VD 平均水平总体呈现不足，VD 水平随着年龄增长而升高，青年组水平最低，男性 VD 平均水平明显女性高。VD 总体不足及缺乏率较高。夏季不足及缺乏率低于其他三季。

PU-1731

桂林临桂区 15867 例急性呼吸道感染病原体流行性分析

冷俊[1]、王迪[2]、向晓华[1]、李宁[1]、韦传东[2]
1. 桂林医学院
2. 桂林医学院第二附属医院

目的 通过分析桂林临桂区各年龄段急性呼吸道感染患者所感染的病原体流行特点，为临床科室诊疗计划提供依据。

方法 收集 2017 年 3 月－2020 年 2 月于桂林医学院第二附属医院 15867 例拟诊为急性呼吸道感染患者血清，用间接免疫荧光法检测 9 种常见呼吸道感染病原体的血清 IgM 抗体，并且进行统计学分析。

结果 15867 例患者中，IgM 抗体呈阳性的占 5469 例，阳性率 34.5%，以肺炎支原体（MP）检出率最高，占 23.9%。女性患者检出率明显高于男性，差异存在统计学意义。儿童组、青壮年组、中老年组病原体阳性率依次为 46.3%、31.4%、24.5%，不同年龄段阳性率差异有统计学意义。MP、FluB、PIV、RSV、ADV 在不同年龄段检出率差异有统计学意义。636 例患者存在混合感染（2 种及 2 种以上），检出率为 4.0%。其中 MP+FluB 的混合感染最多，共 169 例，检出率为 1.07%，其次是 MP+FluB+PIV，共 117 例，检出率为 0.74%。儿童组中 MP 检出率全年均高，以春、夏、冬季明显，FluB、RSV、FluA 在春、冬季多发，PIV 在冬季多发，ADV 在春季多发，LP、CP 及 COX 均偶有散发。

结论 桂林临桂区呼吸道感染病原体以 MP 和 Flu B 为主，不同性别、不同年龄、不同季节的感染阳性率均存在差异，混合感染主要为 MP+FluB 模式。

PU-1732

中国上消化道或结直肠癌患者中 p53 抗体升高的患病率

王敏、谢素红、卢仁泉、郭林
复旦大学附属肿瘤医院

背景 包括 p53 抗体在内的肿瘤标志物已用于癌症治疗。
目的 我们旨在描述中国人群中新诊断或复发的上消化道癌（GI）或结直肠癌（CRC）患者中 p53 抗体和其他肿瘤标志物升高的患病率，并评估对已确立的肿瘤标志物阴性的患者，增加 p53 抗体检测是否会提高癌症检出率。
方法 招募 187 名健康人，169 名 GI 患者和 217 名 CRC 患者。所有受试者均需提供最多 10 毫升的血液。对每个纳入的受试者测量以下生物标志物：p53 抗体，CEA，CA19-9，CA125，CA15-3，CA72-4，CYFRA 21-1，HE4，ProGRP 和 SCC。
结果 在 0.02μg/ml 的临界值下，中国人群中上消化道癌和 CRC 的 p53 抗体敏感性较低（分别为 9.47％和 25.93％）。在该临界值时，健康人群中 p53 抗体的特异性非常高，为 98.4％。通过在其他肿瘤标记物中添加 p53 抗体，检测 CRC 的敏感性提高 18-26％，检测上 GI 的敏感性提高 8-10％，特异性降低 1-2％。
讨论 目前的研究表明，p53 抗体在上消化道和结直肠的患病率较低，但在健康对照中的特异性很高（98.4％，95％CI，95.38-99.67）。在健康对照的基础上，在肿瘤标志物中添加 p53 抗体可以提高检测癌症的敏感性，同时特异性的损失却最小。在大肠癌患者中，敏感性的改善最大，而在上消化道癌的肿瘤标志物中添加 p53 抗体的获益较小。 总之，使用 p53 抗体的多标记分析可以提高对大肠癌患者的诊断价值。但是，有必要进行进一步的研究以验证 p53 抗体自身抗体在中国的临床应用。这些研究应在具有适当良性疾病对照的多中心环境中评估 p53 抗体和结直肠癌标志物。

PU-1733

肝癌肿瘤标志物在肝癌高危人群预防治疗中的应用研究

冉盼盼、渠文涛、史小芹
郑州安图生物工程股份有限公司

目的 肝癌肿瘤标志物在肝癌高危人群预防治疗中的应用研究。
方法 将影像学尚不能明确为肝癌的乙型肝炎患者 30 例，将 30 例患者按照年龄和性别均匀的分配两组。分别是中药治疗组 15 例，对照组 15 例，其中对照组采用一般消炎、抗病毒、抗纤维化等中西医结合对症治疗法；中药治疗组采用“肝复安”(主要成分:茯苓、党参、白术、苡仁、冤丝子、桑寄生、川断、灵芝等),每日 2 剂；随症加减：脘腹饱胀：加枳壳、鸡内金；鼻蛆齿血：加生蒲黄、牛膝；肝区胀痛：加旋复花、茜草根；另全蝎、蜈蚣、参三七、贝母共研细末，每日 8g；人参鳖甲煎丸每日 6g 吞服。治疗期间，每日记录临床症状、体征，每月检测以下项目：（1）肝癌标志物 AFP(磁微粒化学发光法)、AFP-L3(磁微粒化学发光法)、PIVKA-Ⅱ(磁微粒化学发光法)；(2)肝脏生化指标(按医院常规方法进行)，定期进行 B 超、CT 检查。
结果 中药治疗组患者 AFP-L3 和 PIVKA-Ⅱ转阴率分别为 83%(5/6)和 86%(6/7)，对照组无一例转阴；肝癌发病例数中药组 1 例，对照组 10 例，呈显著差异（表格见附件）。
结论 ①中药（肝复安）能有效降低肝癌高危患者肿瘤标志物水平，并能延缓或阻止肝癌的发生；②肝癌肿瘤标志物在肝癌高危人群治疗中能够预测肝癌的发生。

PU-1734

HE4 在女性卵巢癌的应用研究

俞晓晨[1]、孙妍[2]
1. 哈尔滨医科大学附属第一医院
2. 黑龙江省哈尔滨市医科大学附属第一医院

目的 探讨 HE4（人附睾蛋白 4）在女性卵巢癌中的研究新进展
方法 分析 HE4 在早期卵巢癌，在鉴别卵巢良恶性疾病中的应用。
结果 1 正常卵巢组织不表达 HE4，而在卵巢癌中高表达 HE4，特异性高。
2 HE4 在卵巢癌早期和晚期表达均可升高。
3 HE4 可以监测卵巢癌患者的预后。
4 HE4 与 CA125 联合应用可以辅助鉴别卵巢的良恶性疾病。
5 HE4 不受女性月经周期及激素的影响，比较稳定
结论 HE4 是卵巢癌检测的良好标志物，与 CA125 联合应用可以提高卵巢癌检测的敏感性和特异性。

PU-1735

两种方法检测抗中性粒细胞胞浆抗体的结果分析

姜茜
中国医科大学附属盛京医院

目的 通过对抗中性粒细胞胞浆抗体（anti-neutrophil cytoplasmic antibody，ANCA）检测结果的分析，了解 ANCA 在就诊患者中的检出率及其分布特征。
方法 采用化学发光免疫分析法（Chemiluminescent assays，CLIA）和间接免疫荧光法（indirect immunofluorescence，IIF）联合检测 25822 例血清样本，比较两种检测方法的一致性，分析 ANCA 阳性率、荧光核型、靶抗原的分布。
结果 两种检测方法总符合率为 98.03%，一致性较好；25822 例样本中，ANCA 阳性率为 4.09%，其中男性为 3.67%，女性为 4.38%，两组差异有统计学意义（P＜0.05）。60 岁以上年龄组阳性检出率高于其他年龄组（P＜0.01）；1056 例阳性样本中，荧光核型以 pANCA 阳性率最高（51.14%），靶抗原以 MPO 为主（37.03%），不同靶抗原的分布有统计学差异（P＜0.01），男性与女性的年龄构成差异有统计学意义（P＜0.05）；靶抗原 MPO 的含量在不同年龄组中有统计学差异（P＜0.05）。
结论 CLIA 法和 IIF 法联合检测 ANCA 的效果更佳，更有助于了解 ANCA 的阳性率及分布特征。

PU-1736

血液中 ANGPTL7 蛋白水平与 2 型糖尿病肾病病程进展的关系研究

刘影[1]、张宏毅[2]、张诗田[1]、王雅茹[1]、刘霖霖[1]、牛文彦[1]
1. 天津医科大学朱宪彝纪念医院
2. 天津医科大学

目的 研究 ANGPTL7 在单纯 2 型糖尿病和 2 型糖尿病肾病患者中的表达差异，以及 ANGPTL7 的表达量与 2 型糖尿病肾病病程进展的相关性。
方法 将 130 例 2 型糖尿病患者按 2 型糖尿病发生进程分为单纯 2 型糖尿病（T2DM）组（35 例）、糖尿病肾病微量蛋白尿(尿蛋白：30-300mg/24h)组（45 例）、糖尿病肾病大量蛋白尿(尿蛋

白：>300mg/24h)组（50 例）。三组分别采用酶联免疫法检测各组血清中 ANGPTL7 的含量，比较三组标本血清中 ANGPTL7 表达量的差异。检测三组标本中 FPG、HbA1c、Cre、BUN、GFR、mALB、UTP、TG、TC、LDL 、HDL 的含量，分析以上各指标在各组中的差异，以及 ANGPTL7 表达与以上指标含量的相关性。

结果 三组中 ANGPTL7 的水平随着 2 型糖尿病肾病的发生进程有升高的趋势，但无显著性差异。糖尿病肾病大量蛋白尿组的 mALB、UTP、Cre、GFR、BUN、TG、TC、LDL 水平均显著高于糖尿病肾病微量蛋白尿组和单纯 T2DM 组，糖尿病肾病大量蛋白尿组和糖尿病肾病微量蛋白尿组的 HbA1c 水平均高于单纯 T2DM 组。ANGPTL7 水平与 FPG、HbA1c、Cre、BUN、TG 均呈正相关，与 GFR 呈负相关。与 mALB、UTP、TC、HDL、LDL 不相关。

结论 ANGPTL7 的表达水平随着 2 型糖尿病肾病的发生发展有逐渐上升的趋势，ANGPTL7 的表达与肾功能指标存在相关性，但是能否作为监测、预测 2 型糖尿病肾病发展的指标还需要进一步研究。

PU-1737

血红蛋白与转铁蛋白联合检测对消化道出血的临床诊断价值

兰丽媛
吉林金域医学检验所有限公司

目的 评价便潜血两项，同时检测血红蛋白（Hb）和转铁蛋白（Tf）粪便隐血实验在消化系统肿瘤筛查检测中的临床诊断价值。

方法 收集住院患者的粪便标本 253 例以及健康对照者的粪便标本 100 例，受试者标本均采用单纯血红蛋白定量诊断试剂和血红蛋白和转铁蛋白双指标定量检测试剂盒两种检测方法进行粪便隐血检测实验。

结果 血红蛋白和转铁蛋白双指标定量检测试剂盒联合试剂检测上消化道出血的阳性率为 46.4%,检测下消化道的阳性率为 58.7%.检测健康组阳性率为 8.7%。单纯血红蛋白定量诊断试剂检测上消化道出血的阳性率为 41.4%.检测下消化道出血的阳性率为 54.7%.检测健康组阳性率为 2.1%。

结论 粪便隐血检测中的血红蛋白和转铁蛋白双指标定量检测试剂盒联合检测可大大提高消化道出血及结直肠癌肿瘤的阳性检出率， 单纯血红蛋白定量诊断试剂检测在消化道出血中有较高的检出率，一般情况下具有很高的检测灵敏度，但是游离血红蛋白容易被消化道的胃酸、酶及共生菌等分解，易出现假阴性结果。转铁蛋白其稳定性好，活性持 续时间长，具有很强的耐胃酸和耐肠道细菌分解能力，血红蛋白和转铁蛋白联合检测可以在检测中起到相互补充的作用，对提高恶性肿瘤患者伴发消化道出血的检出率具有重要的临床指导价值。

PU-1738

联合检测血清 GADA、ICA、IAA 在糖尿病分型的临床意义

兰丽媛
吉林金域医学检验所有限公司

目的 通过联合检测血清中谷氨酸脱羧酶抗体（GAD)、胰岛素自身抗体（IAA)、胰岛细胞抗体（ICA)在糖尿病鉴别 1 型、2 型诊断中的价值。**方法** 将 2019 年 1 月至 2020 年 12 月在我检验所检测并确诊为糖尿病的患者 100 例作为观察组,同一时期在我检验所进行员工健康体检的无糖尿病的体检者 100 例作为对照组。均同时进行糖尿病自身免疫抗体三项化学发光法联合检测，对患者的血清中谷氨酸脱羧酶抗体（GAD)、胰岛素自身抗体（IAA)、胰岛细胞抗体（ICA)进行单项及联合检测,分析阳性率,并分析这些指标对不同在糖尿病分型中的阳性占比。

结果 糖尿病患者的谷氨酸脱羧酶抗体（GAD)、胰岛素自身抗体（IAA)、胰岛细胞抗体（ICA)阳性率明显高于正常对照组（P<0. 05)，其中 1 型糖尿病患者的谷氨酸脱羧酶抗体（GAD)、胰岛素自

身抗体（IAA)、胰岛细胞抗体（ICA)阳性率分别为 54. 94%、30. 11%和 27. 57%,明显高于 2 型糖尿病组（P<0. 05).谷氨酸脱羧酶抗体（GAD)、胰岛素自身抗体（IAA)、胰岛细胞抗体（ICA)三项抗体联合检测结果，阳性率显著提高。

结论 联合检测有助于提高青少年 T1DM 早期的检出率和诊断率，1 型糖尿病患者可能存在胰岛功能损伤，可以提高诊断患者敏感性，并且对鉴别 1 型糖尿病与 2 型糖尿病有着重要价值。

PU-1739

粪便钙卫蛋白联合血液指标在诊断及评估溃疡性结肠炎活动度中的临床价值

丁红梅
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨粪便钙卫蛋白（FC）联合血液指标在诊断及评估溃疡性结肠炎（UC）活动度中的临床价值。

方法 将 2017 年 12 月至 2020 年 10 月在江苏省人民医院诊断为 UC 的 100 例患者进行回顾性分析，并选择同期在我院诊断为功能性胃肠病的 100 例患者作为对照组，分别检测 FC 含量，比较两组 FC。再根据 UCEIS 将 100 例 UC 患者分为缓解组、镜下活动轻度组、镜下活动中度组、镜下活动重度组，分别检测各组血液指标（CRP、ESR、WBC、NLR、Hb、Alb）。比较不同 UC 组患者 FC 及相关血液指标，并绘制 ROC 曲线分析 FC 联合血液指标对判断 UC 内镜下是否活动的诊断效能。

结果 UC 患者 FC 浓度明显高于对照组，活动期各组 UC 患者 FC 水平亦高于对照组(P<0.05)。FC 分别联合血液指标作 ROC 曲线，发现单 FC 在评估 UC 是否活动中已具有较高的诊断价值，同时 FC 联合血液指标评估价值更优于 FC 单一指标。

结论 FC 是一种判断 UC 患者病情活动程度的较好评估指标,其可作为临床上 UC 患者进行病情活动评估辅助指标。

PU-1740

Usefulness of Mean Platelet Volume for Differential Diagnosis of Rheumatoid Arthritis and Osteoarthritis

Fengfeng Zhao
Department of Clinical Laboratory of Zhongda Hospital, Southeast University

Objective The clinical manifestations and pathological changes of in osteoarthritis (OA) are similar to in rheumatoid arthritis(RA) , such as joint swelling, pain, morning stiffness, and so on, which may lead to joint dysfunction with the development of the disease. OA is easy to be confused with RA in clinic. The expression of mean platelet volume (MPV), hypersensitive C-reactive protein (hsCRP) and rheumatoid factor (RF) in RA, OA and normal human serum were compared. The difference of sensitivity and specificity and the application value of the three indexes in differential diagnosis of RA and OA were evaluated by using the receiver operating characteristic curve. It provides reference for the diagnosis and differential diagnosis of RA and OA.

Method From June 2017 to August 2018, we collected 159 patients with RA who were hospitalized in the Department of Rheumatology, affiliated Hospital of Chinese University of Southeast University, as RA group and 91 patients with OA as OA group. At the same time, 100 cases who passed the physical examination in our hospital were set as the normal control group.SPSS 18.0 statistical software was used for analysis.

Results 1. There were significant differences in MVP, RF and hsCRP among RA group, OA group and normal control group (all P < 0 05). The levels of serum RF and hsCRP in RA group were higher than those in OA group and normal control group (P < 0. 05), MVP), which were lower than those in OA group and normal control group (all P < 0. 05). The serum levels of MVP, RF and hsCRP in OA group were higher than those in normal control group (all P < 0 05). 2. According to the ROC curve, the area under the ROC curve of RA diagnosed by MVP was 0.825 (95%CI = 0.733~0.812, P < 0.000), taking non-RA patients as reference. The AUC of RA diagnosed by hsCRP was 0.726 (95%CI = 0.804 ~ 0.894), and the AU of RA diagnosed by); RF was 0.781 (95%CI = 0.893 to 0.964, P = 0.000). The AUC of RA diagnosed by MVP+hsCRP was 0.906 (95%CI = 0.840 ~ 0.918, P < 0.000), and the AUC of RA diagnosed by MVP+RF was 0.939 (95%CI = 0.910 ~ 0.968, P = 0.000). The AUC of RA diagnosed by hsCRP+RF was 0.830 (95%CI = 0.865-0.925, P = 0.000).
Conclusion MVP, hsCRP and RF can be used as effective reference indexes for differential diagnosis of RA and OA, and the combined detection of these indexes can improve the accuracy of RA diagnosis. Therefore, the clinical diagnosis of large joint as OA patients, should pay active attention to MVP and RF indicators, in order to distinguish the possibility of RA, reduce missed diagnosis, misdiagnosis.

PU-1741

Combined with serum pro-gastrin releasing peptide(Pro-GRP) and CA72-4 in diagnosis of colorectal cancer

Fengfeng Zhao
Department of Clinical Laboratory of Zhongda Hospital, Southeast University

Objective Colorectal cancer (Colorectal cancer, CRC) is one of the common malignant tumors of digestive tract. In recent years, the incidence and death of colorectal cancer in China are on the rise, the incidence and mortality are higher than the world average level, which seriously endangers the health of Chinese residents and places a heavy burden on the social economy. Therefore, it is of great significance to find serum tumor markers which can assist in the diagnosis of colorectal cancer. With the deepening of the study of colorectal cancer, we found that Pro-GRP and CA72-4 increased in some patients with colorectal cancer, but the related content has not been reported in the literature. In this study, Pro-GRP and CA72-4 in patients with colorectal cancer were evaluated to evaluate the clinical value of combined detection of these two tumor markers in the auxiliary diagnosis of colorectal cancer.
Method From October 2017 to April 2019, 82 patients with diagnosed colorectal cancer were selected as colorectal cancer group, and 100 healthy patients were selected as control group.Serum Pro-GRP and CA72-4 were detected by electrochemical luminous method in 82 patients with colorectal cancer and 100 healthy people. SPSS 19 was used for data processing.
Results The levels of serum Pro-GRP and CA72-4 in patients with colorectal cancer were significantly higher than those in healthy subjects (P < 0.05). The sensitivity and specificity of single detection of Pro-GRP in the diagnosis of colorectal cancer were 47.0% and 51.6%, CA72-4 was 43.8% and 58.8%, and the combined detection of Pro-GRP and CA72-4 was 61.4% and 73.6%, respectively.
Conclusion The levels of serum tumor markers Pro-GRP and CA72-4 in patients with colorectal cancer are abnormally increased. Combined detection of Pro-GRP and CA72-4 can effectively improve the sensitivity and specificity of diagnosis, and has certain clinical value in the diagnosis and early screening of colorectal cancer.Pro-GRP not only has obvious clinical value in the diagnosis of small cell lung cancer, but also has certain clinical significance in the diagnosis of colorectal cancer.

PU-1742

NLR、RDW 联合血清肿瘤标志物在乳腺癌鉴别诊断中的价值及与病理特征的关联

邹红
福建医科大学附属协和医院

目的 探究中性粒细胞与淋巴细胞比值（NLR）、红细胞分布宽度（RDW）和血清肿瘤标志物在乳腺癌（BC）与乳腺纤维腺瘤（FA）鉴别诊断中的价值以及与 BC 患者组织病理学指标和分子分型之间的关联。
方法 收集整理 653 例 BC 患者与 100 例 FA 患者的病理资料和常规临床检验指标。比较 BC 与 FA 组间上述常规临床检验指标的水平差异，统计学分析检验指标做 ROC 曲线，探讨二分类 Logistic 回归和 ROC 曲线综合分析有差异指标联合模式在鉴别诊断 BC 与 FA 中的价值。运用有序多分类 Logistic 回归分析 BC 患者的常规临床检验指标与 BC 病理特征，包括 TNM 分期、组织学分级与分子分型等指标间的相关性。
结果 CEA、NLR 和 CA19-9 等三项指标水平在 BC 组与 FA 组间有显著性差异（P<0.05），它们将 FA 患者与 BC 患者相鉴别的 ROC 曲线下的面积（AUC）分别为 0.799、0.747 和 0.711，其最佳 cutoff 值分别为 1.35ng/mL、1.58 与 8.55U/mL。二分类 Logistic 回归和 ROC 曲线综合分析结果显示，CEA、NLR 和 CA19-9 这三项临床检验指标对鉴别诊断 BC 与 FA 有一定效能，其中诊断效能最高的单项指标为 CEA，两项指标联合优于单项指标，三项指标联合效能最佳；三项指标联合时的 AUC 为 0.886。敏感度和特异度分别为 76.5%和 88.9%。有序多分类 Logistic 回归分析结果显示，NLR、CEA 和 CA15-3 均与 BC 的 TNM 分期呈正相关，RDW 与 BC 组织学分级呈负相关，RDW、CA15-3 和 CA125 均与 BC 分子分型关联明显（P<0.05）。
结论 CEA、NLR 和 CA19-9 这三项指标联合对鉴别诊断 BC 与 FA 有一定效能。NLR、CEA 和 CA15-3 等三项指标与 BC 的 TNM 分期、RDW 与 BC 组织学分级以及 RDW、CA15-3 和 CA125 等三项指标与 BC 分子分型等具有关联。

PU-1743

被嫌弃的“牛奶血”患者

王梅华、石安然、陈莺
福建医科大学附属协和医院

综合性大医院门诊大楼每天门庭若市，患者和医护人员都很不容易，大家都知道医患沟通很重要，真正要做到提高病人满意度很是艰难，我们门诊服务中心是个不错的沟通缓冲区，这位患者在门诊服务中心得到联系检验人员的渠道，检验者也能通过服务中心联系到临床相应科室的医生护士。招人嫌弃的“牛奶血”标本不能一退了之，如果能明确患者是真正的空腹 12 小时，并排除患者输注脂乳等的用药干扰，应采取相应对策加以解决，尽快帮病人检验标本。

PU-1744

糖化白蛋白酶法测定的初步评价及其与糖化血红蛋白相关性研究

黄鋆
福建医科大学附属协和医院

目的 应用 EP10-A3 文件对酶法检测糖化白蛋白（GA）的临床应用性能进行初步评价，并对糖尿病患者糖化血红蛋白(HbA1c)和糖化白蛋白（GA）的一致性、相关性及阳性率进行分析，评价其临床应用价值。
方法 使用酶法测定 GA 浓度，采用美国临床实验室标准化委员会(CLSI)颁布的《定量临床检验方法的初步评价；批准指南 EP10－A3》文件中规定的方法对其总不精密度、非线性、偏差、互染率、斜率、漂移等指标进行评价。并通过测定 90 例糖尿病患者的 HbA1c 和 GA 浓度，对两者相关性、一致性以及阳性率进行分析。
结果 低，中，高 GA 样本浓度偏差分别为-0.61,-0.28,0.34μmol/L。总不精密度分别为 1.48%，1.37%，0.84%。斜率、互染率、非线性、漂移（t 值分别为 1.38,0.097，-1,37,0.013）差异均无统计学意义（P>0.01）。GA 与 HbA1c 回归分析方程为 Y = 2.8048X-0.2681（r2= 0.7141）。GA 与 HbA1c 一致性采用 Kappa 检验，Kappa 值为 0.655，说明两者一致性较好。HbA1c 检测结果阳性率与 GA 检测结果阳性率，两者差异无统计学意义（P>0.05）。
结论 糖化白蛋白试剂盒准确度、精密度良好，均在允许范围内，线性良好，携带污染率低，稳定性较好，性能指标符合临床应用要求。GA 可作为糖尿病诊断的补充指标，并用于临床糖尿病疗效监测

PU-1745

肺炎支原体检测的三种方法学比较

范玲芳
福建医科大学附属协和医院

目的 比较被动凝集法（PPA）、酶联免疫吸附法（ELISA）、间接免疫荧光法（IIF）在检测肺炎支原体（mycoplasma pneumoniae,MP）感染时的差异性与一致性，探讨如何更好的进行方法间的组合与利用。
方法 收集疑似 MP 感染的患者血清，采用 PPA、ELISA、IIF 等三种血清学方法检测 MP 抗体,采用统计学的方法对检验结果的差异性与一致性进行分析。
结果 三种方法间的比较均存在统计学差异（P<0.05）,三种方法的一致性均不好,其中 PPA 与 ELISA 法的一致性相对其他两组较好。
结论 PPA 与 ELISA 法联合检测可提高肺炎支原体病原体诊断的速度及敏感性，为临床及时准确的诊断提供依据。

PU-1746

异常凝血酶原与甲胎蛋白在肝癌疗效监测中的比较

陈思妍
福建医科大学附属协和医院

目的 探讨血清异常凝血酶原（PIVKA-Ⅱ）和甲胎蛋白（AFP）在肝癌中的诊断以及疗效监测中的价值。

方法 选取 2018 年 1 月至 2019 年 4 月 24 日期间就诊于福建医科大学附属协和医院的 2109 例患者血清的 PIVKA-Ⅱ和 AFP 的检测结果，分析 PIVKA-Ⅱ和 AFP 对诊断肝癌的敏感度和特异度。回顾性分析 175 例肝癌患者治疗前后血清 PIVKA-Ⅱ和 AFP 的实验室检查结果，比较 PIVKA-Ⅱ和 AFP 在手术治疗前后的血清学水平变化。

结果 血清 PIVKA-Ⅱ在肝癌患者手术治疗前后水平降低（或阴转）率 88（154/175）%高于血清 AFP42.8（75/175）%，差异具有统计学意义（P<0.05）。在 1125 例肝癌患者中，血清 PIVKA-Ⅱ阳性率为 68.4（769/1125）%；血清 AFP 阳性率为 50.7（570/1125）%，差异具有统计学意义（P<0.05）。肝癌组血清 PIVKA-Ⅱ和 AFP 阳性率均高于其他各组，差异具有统计学意义（P<0.05）。血清 PIVKA-Ⅱ和 AFP 检测对肝癌的诊断的敏感度分别为 68.4%和 50.7%，特异度分别为 81.9%和 87.7%，PIVKA-Ⅱ、 AFP、
PIVKA-Ⅱ联合 AFP 诊断肝癌的 ROC 曲线下面积分别为 0.786、0.736、0.835，PIVKA-Ⅱ联合 AFP 诊断肝癌的 ROC 曲线下面积大于 PIVKA-Ⅱ及 AFP。

结论 血清 PIVKA-Ⅱ的检测有助于提高肝癌的诊断价值，与 AFP 联合检测可提高肝癌的检出率。肝癌患者术后血清 PIVKA-Ⅱ水平监测有助于判断肝癌手术疗效，并对预后判断有一定的参考价值。

PU-1747

TB-IGRA 在诊断结核感染中的应用分析

林光华
福建医科大学附属协和医院检验科

目的 研究 γ-干扰素释放试验（TB-IGRA）与传统检测方法在临床诊断结核分枝杆菌感染的应用价值。

方法 对我院 1127 例受检者的 TB-IGRA 试验与痰涂片找抗酸杆菌，血清检测结核抗体，结核菌 DNA 检测结果进行回顾性比较分析。并分析 1127 例受检者的人群年龄分布情况。

结果 1127 例受检者分为结核组和非结核组，TB-IGRA 灵敏度 74.7%，特异度 79.9%，ROC 曲线下面积 0.821。497 例 TB-IGRA 与痰涂片找抗酸杆菌比较，灵敏度分别为 77.4%与 9.3%，特异度分别为 92.3%和 99%。721 例 TB-IGRA 与血清检测结核抗体比较，灵敏度分别为 75.4%和 32%，特异度分别为 95.1%和 78.3%。191 例 TB-IGRA 和痰结核菌 DNA 比较，灵敏度分别为 77.1%和 27.1%，特异度分别为 92.1%和 97.4%。老年人人群结核分枝杆菌感染率高于年轻人群。

结论 TB-IGRA 作为临床诊断结核分枝杆菌感染的辅助诊断方法之一，相比痰涂片找抗酸杆菌，血清检测结核抗体，结核菌 DNA 检测等方法，有更高的灵敏度和特异性。老年人结核分枝杆菌感染率较高，TB-IGRA 作为筛查手段可助于结核病的诊断及预防。TB-IGRA 对于鉴别现症病人还是既往感染人群的能力较差。

PU-1748

联合检测 HIF-1α 和 HIF-2α 在肾癌诊断中的意义

李蓉、袁改玲
新疆生产建设兵团第五师医院

目的 探讨联合检测 HIF-1α 和 HIF-2α 在肾癌诊断中的临床意义。

方法 选取 2019 年 4 月至 2021 年 4 月在新疆生产建设兵团第五师医院及下属医院就诊并确诊为肾癌的患者，分为肾癌组 1（肾癌 II 期及以上，25 名），肾癌组 2（肾癌 I 期及癌前病变，31 名）及

健康对照组（60 名），采用实时荧光定量 PCR（q RT-PCR）定量检测患者外周血清 HIF-1α 和 HIF-2α 水平。

结果 对于 HIF-1α，肾癌组 1 患者水平[(984.41±121.04)pg/mL]明显高于健康对照组[(315.87±64.52)pg/mL]及肾癌组 2[(572.33±51.42)pg/mL]，差异均有统计学意义(P<0.05)，对于 HIF-2α，肾癌组 2 患者水平[(433.98±65.81)pg/mL]高于健康对照组[(123.63±12.14)pg/m L]及肾癌组 1[(224.51±42.24)pg/mL]，差异存在统计学意义(P<0.05)；对现存的病理切片进行 HIF-1α 及 HIF-2α 免疫组织化学染色，其结果与血清结果具有一致性。

结论 HIF-1α 与恶性程度更高的肾癌有关，相反，HIF-2α 与侵袭性较低或低度肾癌相关度更高，联合检测 HIF-1α 和 HIF-2α 可以用于辅助评估肾癌患者肿瘤的恶性程度。

PU-1749

探究血清游离轻链对初诊多发性骨髓瘤患者预后生存的影响及临床意义

陶安福、谭宛昀、任丽
天津医科大学肿瘤医院

目的 分析多发性骨髓瘤患者血清游离轻链（serum free light chain，sFLC）比值对初诊多发性骨髓瘤患者预后生存的影响及临床意义。

方法 选取并回顾性分析 2017 年 1 月至 2018 年 12 月我院收治的 49 例初诊 MM 且有行 sFLC 检查的患者临床资料，将血清游离轻链等可能影响预后的因素进行分析，通过 Kaplan-Meier 生存分析探讨 sFLC 在初诊 MM 患者预后中的作用及临床意义。

结果 在长达 1017 天的随访中我们发现 49 例患者中有 19 例出现终末死亡结局事件，患者中位随访时间 359（120-1017）天。生存组的 κ 值和 κ/λ 比值明显高于死亡组（P=0.040，P=0.024），而死亡组的 λ 值水平高于生存组（P=0.032）。我们进一步进行 Kaplan-Meier 生存分析，发现 κ/λ 比值高的患者预后生存明显好于 κ/λ 比值低的患者（P=0.023），这是预测游离轻链影响初诊 MM 患者预后好坏的有力证据。

结论 初诊 MM 患者预后生存与 sFLC 检测结果密切相关，κ 值水平和 sFLC 的 κ/λ 比值越高，患者的预后生存结局越好。

PU-1750

幽门螺杆菌抗体分型在东营地区老年体检人群中的结果分析

杨琴
胜利油田中心医院

目的 幽门螺杆菌病在世界卫生组织国际癌症研究机构公布的致癌物清单初步整理参考，幽门螺杆菌感染在一类致癌物清单中。当体内出现了免疫原性的一种反应，因为菌体的刺激而导致抗体的产生。这一类抗体对身体是没有保护性的，仅代表患者曾经感染过幽门螺杆菌或如今正处于幽门螺杆菌的感染期。幽门螺杆菌抗体分型可分为高毒型和无毒型两种。统计东营地区 2021 年 3-4 月份老年体检人群幽门螺杆菌抗体分型在老年体检人群中的结果情况。

方法 采用蛋白芯片法将幽门螺杆菌抗体分为细胞毒素抗体 CagAb、空泡毒素抗体 VacAb、尿素酶抗体 UreAb。

检测人群：2021 年 3-4 月份老年体检人群，年龄大于 60 岁，不分性别。

结果 1400 例老年体检人群中，CagA 抗体阳性 690 例，VacA 抗体阳性 752 例，单一 Ure 抗体阳性 414 例。

按照：CagAb、VacAb 任一项阳性则患者感染为Ⅰ型有毒株。UreAb 单一阳性为Ⅱ型无毒株。各项指标全部阴性：无 Hp 感染或者根除治疗成功后较长一段时间。

综合分析：Ⅰ型为 752 例，Ⅱ型为 414 例，全阴性为 234 例。东营地区 60 岁以上老年体检人群的幽门螺杆菌抗体分型的情况如下：Ⅰ型幽门螺杆菌占人群：53.71%，Ⅱ型幽门螺杆菌占人群：29.57%，无幽门螺杆菌感染者占人群：16.71%。

结论 Ⅰ型为高毒力菌株：毒性较强,和消化性溃疡、胃癌等密切相关，应该引起医生及病人高度重视。Ⅱ型为无毒力菌株毒性较小，致病力弱，一般表现为轻微消化不良或者无临床症状。体检人群若感染为无毒株，可不必盲目选择根除治疗。

幽门螺杆菌抗体分型检测有助于了解Ｈｐ感染患者体液免疫反应状态；通过体检筛查按照结果分型，可到临床就医根据分型检测结果，结合临床症状选择性进行抗生素治疗，避免抗生素过度使用，减少细菌耐药性的产生，实现精准诊断。

PU-1751

丙型肝炎患者中 HCVRNA 和肝功能联合检测意义

牛登冉
山东省立医院

目的 探讨丙肝患者超敏丙肝病毒核糖核酸 HCVRNA 与 AST、ALT 和 AFU 的相关性及其临床应用价值。

方法 实时荧光定量 PCR 法检测 904 例丙肝患者的超敏丙肝病毒核糖核酸（HS-HCVRNA）、全自动生化分析仪检测 AST、ALT 和 α-L-岩藻糖苷酶（α-L-fucosidase，AFU）。

结果 HS-HCVRNA 阳性率女性明显高于男性（χ2=28.165，P＜0.05）；HS-HCVRNA 病毒载量不同分组间 AST、ALT 和 AFU 的水平有显著性差异（P＜0.05）；异常率最高的是 AST（41.58%）；肝功能单项检测 AUC 最高是 AST（0.747），联合检测的 AUC 为 0.894；ALT 的特异度最高（80.15%）；AST 检测的灵敏度最高（76.65%）；联合检测的灵敏度和特异度高于单项检测。

结论 肝功能单项检测与联合检测均有诊断价值，可以全面了解患者病情进程，为患者和临床治疗提供可靠的依据。

PU-1752

血清胃蛋白酶原、胃泌素-17 与幽门螺杆菌抗体分型检测临床分析

张培莉
山东省立医院

目的 检测体检人群幽门螺杆菌（Helicobacter Pylori，HP）感染情况，以及血清中胃蛋白酶原Ⅰ(PGI)、胃蛋白酶原Ⅱ（PGII）和胃泌素-17(G-17)的含量，探讨其与 HP 感染发生的相关性。

方法 选择 2017 年 2 月至 4 月到本院体检中心体检的 781 例人群，分别用幽门螺杆菌抗体分型试剂盒和酶联免疫吸附试验检测此人群的血清 HP 抗体分型、PGI、PGII、G-17 水平。运用用 SPSS22.0 分析系统，对该人群 HP 感染率，HP 感染者与非感染者间及不同分型感染者间 PGI、PGII、PGI/PGII（PGR）、G-17 水平差异进行分析，并对不同年龄不同性别体检者感染率及各水平差异进行分析。

结果 HP 阳性感染者占 49.81%，不同年龄组间有显著性差异（P<0.05）。HP 阳性与阴性者比较，血清中 PGI、PGII、PGR、G-17 水平有显著性差异（P<0.05）。将感染者按 HPI 型和 HPII 型分组比较，PGII、PGR 水平有显著性差异（P<0.05）。不同性别不同年龄组血清中 PGI、PGII 水平

均有显著性差异（P<0.05），PGI、PGII 水平男性较女性偏高；随年龄升高，PGI、PGII、G-17 有升高趋势，而 PGR 呈下降趋势。
结论 该地区体检人群中，血清 PG 水平与性别、年龄、HP 是否感染有关，且与 HP 感染分型密切相关。将 HP 抗体分型及血清 PG、G-17 水平联合作为胃功能常规检测，对早期胃部疾病的评估和筛查有重要的意义。

PU-1753

甲状腺功能五项指标联合检测评价甲状腺功能的临床意义

高俊杰、李严
郑州安图生物工程股份有限公司

目的 探讨促甲状腺激素（TSH）、总三碘甲状腺原氨酸（T3）、总甲状腺素（T4）、游离三碘甲状腺原氨酸（FT3）、游离甲状腺素（FT4）联合检测评价甲状腺功能临床意义。
方法 选择 2019 年 5 月~7 月来本院的体检人群 1346 例，其中，男 801 例，女 545 例，按照不同年龄分为 5 组，使用安图 AutoLumo A2000 plus 化学发光检测仪进行甲状腺功能五项指标的检测，并对检测结果进行统计分析。
结果 1346 例体检人群中，甲状腺功能异常在体检人群中的总检出率为 6.98%，其中其中亚临床甲减检出率最高（4.01%），甲减检出率最低（0.30%），亚临床甲状腺疾病的检出率明显高于临床甲状腺疾病的检出率，差异有统计学意义（c2＝34.569，P＜0.05）；甲状腺功能异常的发病率女性明显高于男性(男性 4.49%，女性 10.64%)，在性别差异上具有显著统计学意义（c2=18.871，P＜0.05）；不同年龄段发病率也均存在差异，甲减、亚临床甲减、亚临床甲亢均以 60 岁以上年龄段女性发病率最高，甲亢以 41~50 年龄段发病率最高；随着年龄的增加，无论男性群体还是女性群体，亚临床甲状腺疾病均呈现出增加的趋势。
结论 TSH、FT3、FT4、T3 和 T4 联合检测，对甲状腺功能异常的鉴别、诊断和判断预后具有重要作用，值得在临床进行推广应用。

PU-1754

广东地区老年呼吸道疾病患者呼吸道病原体 IgM 抗体检测结果分析

李云珍、姚少濠、李玲、苏坤华
广州金域医学检验中心

目的 探讨广东地区老年人呼吸道疾病患者的病原学流行特征，为临床诊疗提供病原学依据。
方法 采用间接免疫荧光法检测患者血清是否存在嗜肺军团菌血清 1 型(LP1) 、肺炎支原体(MP) 、Q 热立克次体（CB）、肺炎衣原体(CP) 、腺病毒(ADV) 、呼吸道合胞病毒(RSV) 、甲型流感病毒(INFA) 、乙型流感病毒(INFB) 和副流感病毒（1、2 和 3 型 PIVs）9 种呼吸道病原体的 IgM 抗体，根据不同性别、不同年龄和不同季节的病原体阳性率以及合并感染情况进行统计分析。
结果 （1）3192 例患者中有 368 例阳性，阳性率为 11.53%，女性阳性率 13.29%高于男性阳性率 10.48%，差异有统计学意义（p<0.05）；（2）不同年龄组感染阳性率无差异（P＞0.05）；（3）阳性患者中，93.75%为单一一种病原体感染，6.25%为两种病原体同时感染，以 MP 最常见，其次是 INFB 和 CB，最常见的混合感染模式为 MP+INFB；（4）病原体流行的时间段为春夏两季，MP、CB、ADV 和 PIVs 好发于春季和夏季，其他 5 种病原体感染未见明显季节性变化。
结论 该地区老年人呼吸道疾病发病率高，女性较男性易感，感染病原体以 MP 最高，其次为 INFB 和 CB。呼吸道病原体不同季节流行情况不同，采用 9 项病原体 IgM 抗体联检可快速检测出病原体，为当地老年人呼吸道疾病的早期诊疗提供科学依据。

PU-1755

血清学指标在甲状腺髓样癌诊断中的应用

韩筱点、卢仁泉、胡昊昀
复旦大学附属肿瘤医院

目的 探索肿瘤标志物降钙素（CT）、癌胚抗原（CEA）、神经元特异性烯醇化酶（NSE）、胃泌素释放肽前体（Pro-GRP）和嗜铬粒蛋白 A (CgA) 在鉴别甲状腺髓样癌（Medullary thyroid carcinoma, MTC）中的价值。
方法 本回顾性研究选取 2017 年 2 月至 2019 年 8 月复旦大学附属肿瘤医院检验科检测的 105 例甲状腺髓样癌，65 例非髓样癌的甲状腺恶性肿瘤，50 例甲状腺良性疾病，30 例非甲状腺恶性肿瘤以及 50 例健康对照血清 CT 含量。选取其中 79 例 MTC，30 例非 MTC 的甲状腺恶性肿瘤及 30 例健康对照者，检测血清 CEA、NSE、Pro-GRP 和 CgA 含量。利用受试者工作曲线明确各指标区分不同组之间的曲线下面积（AUC）、敏感性和特异性。
结果 MTC 患者 CT 含量显著高于甲状腺其他病变、非甲状腺恶性肿瘤和健康对照。CT 区别 MTC vs 非 MTC 患者的敏感性为 96.2%，特异性为 99.3%，AUC 为 0.99。MTC 结节最大直径（>1cm, P=0.001, OR=15.74）与 MTC 结节个数（>1 个, P = 0.04, OR=3.4）是 CT 升高的两个独立危险因素。CEA（AUC=0.94）、NSE（AUC=0.65）、Pro-GRP（AUC=0.94）以及 CgA (AUC=0.83) 均能够区分 MTC vs 非 MTC 的甲状腺恶性肿瘤。联合 CT、CEA、NSE、Pro-GRP 和 CgA 区分 MTC vs 非 MTC 的甲状腺恶性肿瘤的的 AUC 为 1，敏感性 100%，特异性 100%。
结论 CT、CEA、NSE、Pro-GRP 和 CgA 对于 MTC 的辅助诊断具有重要的意义。联合这些指标诊断 MTC 具有很高的敏感性和特异性。

PU-1756

A randomized controlled trial about Evaluation of plasma Epstein-Barr virus biomarker for early diagnosis in patients with nasopharyngeal carcinoma

Minjie Mao
Department of Clinical Laboratory, Sun Yat-sen University Cancer Center, State Key Laboratory of Oncology in South China, Collaborative Innovation Center for Cancer Medicine

Introduction Early diagnosis of nasopharyngeal carcinoma (NPC) still remains a major problem in Southern China. Epstein-Barr virus (EBV) biomarkers have been widely used in NPC screening. This study aims to evaluate the early diagnostic performances of individual EBV biomarker in NPC.
Methods The levels of EBV biomarkers: IgA antibodies against EBV nuclear antigen 1 (EBNA1-IgA), EBV capsid antigen (VCA-IgA), EBV early antigen (EA-IgA), EBV BZLF1 transcription activator protein (Zta-IgA) and IgG antibodies against EBV BRLF1 transcription activator protein (Rta-IgG) from 106 NPC patients (stage I and II) and 150 normal subjects were measured. VCA-IgA and EA-IgA were detected by immunofluorescence assay (IFA), EBNA1-IgA, Rta-IgG and Zta-IgA were measure by enzyme-linked immunosorbent assay (ELISA), and EBV DNA was detected by qPCR. Statistical analyses of single index were conducted to evaluate the significance in NPC early diagnosis and TNM classification.
Results The level of EBNA1-IgA, EBV DNA, VCA-IgA, EA-IgA, Rta-IgG, Zta-IgA in early-stage NPC was significantly higher than healthy controls (all $P < 0.001$). EBNA1-IgA yielded the biggest area under the curve (AUC) of 0.962 in distinguishing early-stage NPC patients from the normal, with a sensitivity of 91.5% and a specificity of 98.7%. However, EBV biomarkers levels were not associated with tumor size (all $P > 0.050$). Whereas, four biomarkers levels (EBNA1-IgA, EBV DNA, VCA-IgA, EA-IgA) were related to the lymph node metastasis (N0 and N1-2),

among which EBNA1-IgA and EBV DNA showed pretty good performance. Finally, high correlation was found between VCA-IgA and EA-IgA ($r > 0.800$).
Conclusion A single EBNA1-IgA exhibits excellent discrimination performance in early diagnosis of NPC and could become a promising marker for NPC screening.

PU-1757

我国多地区孕妇与孕前育龄妇女间 ToRCH 感染率的案例配对比较

夏玲芝
南京金域医学检验所有限公司

目的 了解孕妇与孕前育龄妇女间 ToRCH 感染率的差异。
方法 收集 10 年来（2009.01 -2019.12）在国内杂志上发表的各地有关 ToRCH 抗体筛查结果的论文，从中筛选出同一实验室在同一时期内用相同方法和试剂盒分别对本地区孕妇和孕前育龄妇女进行 ToRCH 筛查的文献，归类总结其数据，并对多实验室的案例配对数据采用 GraphPad Prism 5 软件进行配对 t 检验，分析两组间的每种 ToRCH-IgM 阳性率的差异，$p<0.05$ 为有显著差异；同时对这些数据进行非配对 t 检验和 Metal 分析，观察其合并效应量。
结果 双向配对 t 检验显示 TOX-IgM 和 RV-IgM 在孕妇群体中的阳性率高于孕前育龄妇女群体，统计有显著性差异（$P = 0.0299$; $P = 0.0499$）；Metal 分析显示无论是单种 ToRCH-IgM 阳性率，还是 4 种 ToRCH 病原体的总阳性率，在两个群体中都呈现有效差异，OR 值均小于 1。从 I2 值和发表偏差看，只有 TOX-IgM 和 RV-IgM 阳性率的合并效应分析较为可信，I2 值均为 0%，漏斗图正常。尽管其他三项的 OR 值也小于 1，但 I2 值均较大（81% - 90%），漏斗图显明显偏倚。但是，非配对 t 检验显示 4 种病原体的 IgM 抗体阳性率在两个群体间均无显著性差异。
结论 经配对 t 检验和 Metal 分析，我国孕妇群体的刚地弓形虫和风疹病毒感染率显著高于孕前育龄妇女群体，而巨细胞病毒和单纯疱疹病毒在两个群体间的感染率差异无统计学意义。

PU-1758

2017.8-2020.7 年江苏地区 γ-干扰素检测结果分析

任雪芳、白文丽、袁杭
南京金域医学检验所有限公司

目的 分析 2017 年-2020 年间江苏地区 γ-干扰素检测结果，为结核病诊断及防治提供理论依据。
方法 统计南京金域近三年来送检的疑似结核病人标本，采用 QFT-GIT 和 CLIA 法检测 γ-干扰素结果，统计分析时间趋势，地区分布，性别比例，年龄层分布及检测方法学对 γ-干扰素检测阳性率的比较，用 $\chi 2$ 检验进行统计分析。
结果 2017.8-2020.7 江苏地区结核病就诊人群及阳性结果逐年上升，而就诊人群分布为苏南苏中无差异，均大于苏北，阳性结果苏中大于苏北大于苏南；阳性结果的男女性别比例约为 2:1，男性明显多于女性；阳性结果主要集中在 50 岁以上人群，占比 71.12%；化学发光法的检出率明细高于酶免法。
结论 江苏地区近年来对结核的识别和诊断意识逐年增加，检测手段更加便捷，同时反映出结核病疫情逐年上升，结核病防控形势不容乐观，应加强中老年结核病患者的防控工作。

PU-1759

上海宝山区九项呼吸道病原体 IgM 抗体检出率分析

刘灵燕、钟政荣、王萍、许蓓妮、喻成飞、郭竹英
上海交通大学医学院附属第九人民医院

目的 分析上海宝山区 9 项呼吸道病原体 IgM 抗体的检出情况。
方法 收集我院 2017 年 1 713 例呼吸道感染患者的血清标本，采用间接免疫荧光法检测 Lp1 、MP 、COX 、 CP、 ADV 、 RSV 、IFA 、IFB 和 PIV (1、2 和 3 型) 这 9 项病原体的 IgM 抗体，从年龄、季节和性别等方面分析其检出情况。
结果 1 713 例患者中总阳性率为 19． 61% (336 /1 713) ; 其中 COX 和 IFA 未检出; 单一病原体阳性率 15． 29% (262 /1713) ; 混合病原体阳性率 4． 32% (74 /1 713) ，主要是两种病原体的混合感染，以 MP 合并其他病原体感染为主。9 项病原体的阳性率以 MP 最高，其次是 PIV(1、2 和 3 型) ，再次是 IFB，其阳性率分别为 16． 64% 、3． 44% 和 2． 16% 。从季节来看，春、夏、秋、冬季 9 项病原体检出率分别为 17． 15% 、21． 05% 、22． 31% 和 18． 85% ，各季节之间检出率无差异。从年龄来看，0 ～ 12 岁组的检出率高于 13 ～ 59 岁组，而 13 ～59 岁组的检出率高于 60 ～岁组，三组的检出率依次为 38． 49% 、15． 07% 和 8． 86% 。从性别来看，男性检出率为 16． 25% ，女性为 24． 30% ，女性高于男性(P ＜ 0． 001) 。
结论 MP 是上海宝山区不同季节和人群呼吸道感染者中检出率最高的病原体，呼吸道病原体的感染与年龄和性别相关，提示针对性的防范具有临床意义。9 项呼吸道病原体联合检测快速、简便、检测范围广，有利于非典型病原体的早期诊断和治疗。

PU-1760

抗 Yo 抗体阳性的帕金森综合征 1 例分析及文献复习

时丽丽、王金玲、刘霞、吴艳艳、王培昌
首都医科大学宣武医院

神经系统副肿瘤神经综合征（paraneopstic neurological syndrome，PNS）是一类与肿瘤相关的影响中枢神经系统和外周神经肌肉系统的综合征。包括抗 Hu 抗体、抗 Yo 抗体、抗 Ri 抗体、抗脑衰蛋白反应介导蛋白（collapsin response mediator protein，CRMP5）抗体、抗 Aamphiphysin 抗体在内的特异性抗体检测可辅助诊断副肿瘤综合征[1]。副肿瘤性小脑变性（paraneopstic cerebellar degeneration，PCD）是一种罕见的神经系统副肿瘤神经综合征，与抗 Yo 抗体阳性相关，其患者大多数为患宫颈内膜癌和乳腺癌的女性患者[2-3]。PCD 的临床表现为眼球震颤、构音障碍以及躯干和肢体共济失调。抗 Yo 抗体阳性在男性中极为罕见，本研究报道 1 例抗 Yo 抗体阳性男性患者。

PU-1761

南京地区腹泻患儿艰难梭菌感染情况分析

岳玉林
南京市儿童医院（南京医科大学附属儿童医院）

目的 了解南京地区不同原因腹泻患儿艰难梭菌(Clostridium difficile,CD)感染情况及其感染特征，为腹泻患儿 CD 感染的预防和治疗提供帮助。

方法 选取 2018 年 1 月～2020 年 12 月在南京医科大学附属儿童医院就诊的腹泻患儿 2 957 例作为研究对象，通过酶联免疫层析方法检测患儿和健康体检儿童粪便标本中艰难梭菌抗原和毒素 A、毒素 B，并结合临床资料进行回顾性分析。
结果 南京地区腹泻患儿和健康体检儿童 CD 的总感染率分别为 23.31%(689/2 957)和 6.67%(4/60)；2018 年、2019 年、2020 年感染率分别为 23.44%(117/499)、27.04%(318/1 176)、19.81%(254/1 282)；各年龄组 CD 感染有所不同，学龄前为 25.25%(558/2 210)，学龄后 17.53%(131/747)；男童为 23.96%(460/1 920)，女童为 22.08%(229/1037)；城区和农村儿童 CD 感染率为别为 23.00%(490/2 130)、24.06%(199/827)；抗生素相关性腹泻组 CD 感染率为 32.77%(176/537)明显高于健康体检儿童，质子泵抑制剂组、肝损害组 CD 感染率分别为 28.91%(198/685)、28.12%(115/409)，与健康体检组比较差异差异具有统计学意义(P 均<0.05)；急性肠炎组和肠易激综合征组感染率分别为 15.04%(119/791)和 15.14%(81/535)，与健康体检组比较差异无统计学意义(P 均>0.05)。
结论 腹泻患儿感染艰难梭菌风险较大，抗生素相关腹泻的艰难梭菌感染率最高，在治疗腹泻患儿过程中艰难梭菌感染情况应引起重视。

PU-1762

T 细胞斑点实验与培养液腺苷脱氨酶联合检测在结核快速诊断中的价值

李秀玉、刘文娜、刘畅、郭在广、王红彦、王培昌
首都医科大学宣武医院

目的 使用 T 细胞斑点实验（T-SPOT）配合淋巴细胞培养液中腺苷脱氨酶（ADA）的检测，研究二者联合应用对结核菌感染快速检测的价值。
方法 随机选取原发性肺结核、结核性胸膜炎、儿童肺结核和中枢神经系统结核患者，进行 T-SPOT、淋巴细胞培养液 ADA、血清 ADA、胸水 ADA 及脑脊液 ADA 等检测。
结果 原发性肺结核等结核组患者组的血清 ADA、胸水 ADA 和 20 h 培养液 ADA 均显著高于对照组（P<0.05），但疾病组间差异无统计学意义（P>0.05）。在相应时间点检测淋巴细胞培养液 ADA 可有效诊断原发性肺结核、结核性胸膜炎、儿童肺结核及神经系统结核。培养液 ADA 检测能将结核性胸膜炎和儿童肺结核的诊断时间由单纯 T-SPOT 的 20 h 缩短至 8 h。
结论 在进行 T-SPOT 试验的同时进行淋巴细胞培养液的 ADA 检测能帮助提高检测的时效性，二者联合应用能有效提高对结核病的诊断效能。

PU-1763

乳腺癌患者腋窝淋巴结 CD8+T 细胞功能及其表面 PD-1 表达的研究

毛敏静、史册、王剑飚
上海交通大学医学院附属瑞金医院

目的 分析乳腺癌患者腋窝淋巴结洗脱液标本中 CD8+T 细胞表面 PD-1 及胞内因子表达，为评估机体免疫应答状态提供依据，并探索评估乳腺癌患者疾病严重程度的新指标。
方法 采用流式细胞术分析患者转移淋巴结组和阴性淋巴结组穿刺液洗脱液中 CD8+T 细胞的比例、亚群分布、细胞表面 PD-1 及胞内 IFN-γ、TNF-α 和 Granzyme B 的表达，以反映不同类型淋巴结中 CD8+T 细胞的亚群格局和功能；通过分析转移淋巴结中 CD8+T 细胞表面 PD-1 表达与乳腺癌患

者病理参数之间的关系，探讨在转移淋巴结穿刺洗脱液中 PD-1 作为参考指标评估乳腺癌严重程度的可能性。
结果 与阴性淋巴结组相比，乳腺癌患者腋窝转移淋巴结组 CD8+T 细胞中初始 T 细胞（TNaive）比例降低，效应记忆 T 细胞（TEM）比例升高，中央记忆 T 细胞（TCM）和 CD45RA+效应记忆 T 细胞（TEMRA）比例无明显变化。与阴性淋巴结组相比，转移淋巴结组 CD8+T 细胞表面 PD-1 表达增高，胞内 IFN-γ 和 TNF-α 表达增强；但 PD-1+CD8+T 细胞内 IFN-γ、TNF-α、Granzyme B 的表达降低，而 PD-1－CD8+T 细胞内上述因子表达增高。转移淋巴结中 CD8+T 细胞表面 PD-1 表达与乳腺癌 TNM 分期及淋巴结转移数量呈正相关。
结论 我们发现 US-FNAC 洗脱液是一种新颖的标本来源，利用流式细胞仪对乳腺癌腋窝淋巴结洗脱液中淋巴细胞进行分析，在揭示转移淋巴结中 CD8+T 细胞抗肿瘤能力的变化的同时，发现 CD8+T 细胞表面 PD-1 表达的比例可以作为参考指标评估乳腺癌患者疾病严重程度。

PU-1764

Knockout 血清替代品联合生长因子对小鼠胚胎干细胞向神经细胞分化的影响

王贝
东南大学附属中大医院

目的 探讨 Knockout 血清替代品（KSR）对小鼠胚胎干细胞（mESCs）向神经细胞分化过程中的影响。
方法 2%、10%、15%KSR 分别与碱性成纤维细胞生长因子（bFGF）、血小板衍化生长因子（PDGF-AA）为主要成分的复合诱导液诱导 mESCs 向神经细胞方向分化，第 28 天行 NFH、O4 以及 GFAP 免疫细胞化学染色鉴定诱导后的神经细胞，观察不同浓度 KSR 对 mESCs 分化的影响。
结果 2%KSR 组仅强阳性表达 O4；10%KSR 组和 15%KSR 组仅强阳性表达 NFH，组间无差异；三组均无 GFAP 表达。
结论 KSR 影响 mESCs 分化为神经元和神经胶质细胞的方向，并与 KSR 的浓度有一定的关系。

PU-1765

辛伐他汀对慢性阻塞性肺疾病稳定期患者肺功能及血清 IL-13、IL-4 等指标的影响

田文君、王光海
山东第一医科大学第一附属医院

目的 研究辛伐他汀对于稳定期慢性阻塞性肺疾病(COPD)患者肺功能和血清白细胞介素-13(IL-13)、白细胞介素-4(IL-4)等指标的影响。
方法 将 2020 年 5–12 月共 158 例在山东第一医科大学第一附属医院呼吸与危重医学科住院治疗的 COPD 患者以随机抽样法分成常规组(79 例)及辛伐他汀药物组(79 例)。常规组实施常规疗法，辛伐他汀药物组则另加服辛伐他汀;同时选取 79 例健康体检者作为对照组。测定患者及健康体检者血清 IL-13、IL-4 等检验指标与肺功能指标,进行对比分析。
结果 辛伐他汀药物组临床疗效显著优于常规组,差异有统计学意义(P<0.05)。相比于治疗前，辛伐他汀药物组患者治疗后的 IL-4、第一秒用力呼气量(FEV1)及用力肺活量(FVC)的比值、FEV1 占预计值的百分比(FEV1/预计值,FEV1%)等水平明显上升(P<0.05);而 IL-13 等指标水平均明显下降(P<0.05)。相比于常规组治疗后，辛伐他汀药物组患者治疗后的血沉(ESR)、红细胞压积(HCT)、血

浆纤维蛋白原(FIB)、IL-13 均下降,但 IL-4、FEV1%、FEV1/FVC 等水平明显上升,差异均有统计学意义(P<0.05)。
结论 辛伐他汀药物组治疗稳定期 COPD 患者具有较好的临床疗效,值得临床推荐。

PU-1766

中孕期血清学产前筛查两联法和四联法对唐氏综合征假阳性分析

张力
雁江区妇幼保健计划生育服务中心

目的 血清学产前筛查根据使用的筛查指标数量不同分别两联法、四联法等[1]，了解两种方法在唐氏综合征假阳性方面的差异，以便选用更好的筛查策略。
方法 是从我院开展血清学产前筛查起所获得的两联法和四联法数据进行分析。
结果 从分析结果来看采用四联法进行血清学产前筛查唐氏综合征假阳性率明显低于两联法[2]。
结论 我院开展的四联法能显著降低中孕期血清学产前筛查唐氏综合征的假阳性率，减少假阳性所致的介入性产前诊断额外支出和胎儿丢失风险。

PU-1767

Clinical Significance of an IgM and IgG Test for Diagnosis of Highly Suspected COVID-19

Xingwang Jia[3]、Pengjun Zhang[4]、Yaping Tian[5]、Junli Wang[2]、Huadong Zeng[2]、Jun Wang[2]、Jiao Liu[1]、Zeyan Chen[1]、Lijun Zhang[1]、Haihong He[1]、Kunlun He[6]、Yajie Liu[7]
1. Department of Clinical Laboratory Medicine Center, Shenzhen Hospital, Southern Medical University, Shenzhen, China.
2. Department of Respiratory and Critical Care Medicine, Shenzhen Hospital, Southern Medical University, Shenzhen, China.
3. Department of Clinical Laboratory Medicine Center, Shenzhen Hospital, Southern Medical University, Shenzhen, China.
4. Key Laboratory of Carcinogenesis and Translational Research (Ministry of Education/Beijing), Interventional Therapy Department, Peking University Cancer Hospital & Institute, Beijing, China.
5. Department of Translational Medicine, Chinese PLA General Hospital, Beijing, China.
6. Key Laboratory of Ministry of Industry and Information Technology of Biomedical Engineering and Translational Medicine, Chinese PLA General Hospital, Beijing, China.
7. Department of Neurology, Shenzhen Hospital, Southern Medical University, Shenzhen, China.

Background Nucleic acid detection and CT scanning have been reported in COVID-19 diagnosis. Here, we aimed to investigate the clinical significance of IgM and IgG testing for diagnosis of highly suspected COVID-19.
Methods A total of 63 patients with suspected COVID-19 were observed, 57 of whom were enrolled (24 males and 33 females). The selection was based on the diagnosis and treatment protocol for COVID-19 (trial Sixth Edition) released by the National Health Commission of the People's Republic of China. Patients were divided into positive and negative groups according the first nucleic acid results from pharyngeal swab tests. Routine blood tests were detected on the second day after each patient was hospitalized. The remaining serum samples were used for detection of novel coronavirus-specific IgM/IgG antibodies.
Results The rate of COVID-19 nucleic acid positivity was 42.10%. The positive detection rates with a combination of IgM and IgG testing for patients with COVID-19 negative and positive nucleic acid test results were 72.73% and 87.50%, respectively.
Conclusions We report a rapid, simple, accurate detection method for patients with suspected COVID-19 and for on-site screening for close contacts within the population. IgM and IgG antibody detection can identify COVID-19 after a negative nucleic acid test. Diagnostic accuracy

of COVID-19 might be improved by nucleic acid testing in patients with a history of epidemic disease or with clinical symptoms, as well as CT scans when necessary, and serum-specific IgM and IgG antibody testing after the window period.

PU-1768

湘南地区健康体检人群与生殖中心患者维生素 D 水平分析

贺安
郴州市第一人民医院

目的 对湘南地区 25-羟基维生素 D [25(OH)D] 检测结果进行分析，了解各类人群体内 25(OH)D 水平及状况，以及健康体检人群与生殖中心患者体内 25(OH)D 水平及状况有无不同。
方法 使用化学发光法测定 2020 年 7 月至 2021 年 1 月 2709 例健康体检人群与 2122 例生殖中心患者体内 25(OH)D 水平，使用统计学软件对两组进行性别及年龄分析。
结果 2709 例体检者血清 25(OH)D 的平均水平为 27.31ng/mL，正常率为 88.70%，不足率为 11.07%，缺乏率为 0.22%；2122 例生殖中心患者的平均水平为 29.56ng/mL，正常率为 92.93%，不足率为 6.83%，缺乏率为 0.24%。健康体检人群男性 25(OH)D 平均水平为 27.72ng/mL，正常率为 91.07%，不足率为 8.75%，缺乏率为 0.19%；健康体检人群女性 25(OH)D 平均水平为 26.71ng/mL，正常率为 85.23%，不足率为 14.50%，缺乏率为 0.27%；生殖中心患者中男性 25(OH)D 平均水平为 30.71ng/mL，总体正常率为 94.07%，不足率为 5.55%，缺乏率为 0.38%；生殖中心患者中女性 25(OH)D 平均水平为 28.84ng/mL，正常率为 92.25%，不足率为 7.60%，缺乏率为 0.15%。
结论 湘南地区人群 25(OH)D 正常率较高，健康体检人群正常率低于生殖中心患者，且女性正常率率明显低于男性。

PU-1769

TRAb 检测对甲状腺疾病诊断意义

李秀
新疆维吾尔自治区人民医院

目的 探讨促甲状腺激素受体抗体（TRAb）对甲状腺疾病诊断价值。
方法 用电化学发光法检测甲状腺疾病组和健康体检组 TRAb；
结果 观察组 TRAb 阳性率达 32.7%，TRAb 检测值 14.61±3.08，两者均高于健康组，且 P<0.05 有统计学意义。
结论 TRAb 可作为诊断甲状腺疾病重要指标。

PU-1770

人类白细胞抗原 HLA-G5 过表达慢病毒载体的构建以及 JAR-HLA-G5 稳转细胞株的建立

曹维维
德阳市人民医院

目的 构建过表达 HLA-G5 慢病毒载体，筛选建立稳定表达 HLA-G5 的 JAR 细胞株。

方法 根据 HLA-G5 基因序列设计合成引物并使用 PCR 扩增目的基因片段。将目的基因定向接入经 BamHI/AgeI 酶切的载体质粒 GV492 中构建重组慢病毒质粒 GV492-HLA-G5。经 PCR 筛选阳性克隆和测序鉴定后，使用三质粒系统包装将含有目的基因的重组质粒 GV492-HLA-G5 和辅助包装质粒共转染至 293T 细胞进行病毒包装并测定慢病毒滴度。设置对照 (NC)组和实验(OE)组，在感染复数（MOI）为 20 的条件下感染 JAR 细胞。用荧光显微镜观察各组 GFP 表达情况。采用 2μg/mL 嘌呤霉素筛选出稳定表达 HLA-G5 的 JAR 细胞株。Real-time PCR 检测 JAR 细胞内 HLA-G5mRNA 的表达水平。Westernblotting 法检测 JAR 细胞内和上清液中 HLA-G5 蛋白表达水平。
结果 经 PCR 及测序鉴定证明，序列与设计合成序列一致，成功构建重组慢病毒载体。GV492-HLA-G5 慢病毒滴度为：2x108TU/ml，阴性对照组滴度为 4X108。RT-PCR 显示实验组 JAR 细胞中的 HLA-G5mRNA（108.690±4.249）表达水平较对照组（1.002±0.760）明显增高（P<0.01）。Westernblotting 表明实验组 JAR 细胞中的 HLA-G5 蛋白表达(65.844±14.11)水平较对照组(1.350±0.366)明显升高（P<0.01）。在上清液中 OE 组（）的的 HLA-G5 蛋白表达水平较 NC 组显著增高。
结论 成功构建 HLA-G5 慢病毒载体并建立 HLA-G5-JAR 稳转细胞株，且 HLA-G5-JAR 稳转株中 HLA-G5 的 mRNA 和蛋白水平明显上升。且 HLA-G5 可分泌至细胞外。为进一步探讨 HLA-G5 对类风湿性关节炎潜在的调控机制提供细胞模型。

PU-1771

NK 细胞在癌症中的作用机制及免疫治疗应用的进展研究

袁成良、曹维维
德阳市人民医院

NK 细胞是机体固有免疫系统的重要组成部分,以非特异性的方式对靶细胞发挥细胞毒性作用，还可诱导效应性 T、B 淋巴细胞的反应性从而增强适应性免疫功能。NK 细胞的功能受一系列种系编码的激活型受体和抑制性受体的信号平衡调节，可对异常细胞中相应配体的表达变化进行快速行识别和应答，在机体抵抗病毒感染、癌症等免疫过程中发挥重要的防御作用。本文将从 NK 细胞的分化、成熟、抗肿瘤作用机制及其在免疫治疗应用方面的进展进行综述。

PU-1772

Bioinformatics analysis of DNA methylation profile in rheumatoid arthritis

weiwei cao
People's hospital of deyang city

Objective To analyze the expression profile of DNA methylation chip by bioinformatics method, and to explore the relationship between DNA methylation and the mechanism of occurrence and development of rheumatoid arthritis (Rheumatoid arthritis RA) from an epigenetic perspective.
Method Download the raw data of DNA methylation chip GSE42861 from GEO database, which contains DNA methylation data of peripheral blood lymphocytes in 354 RA patients and 337 control groups. After the original data was processed by quality control, the differential methylation sites and differential methylation regions were screened and the differential methylation regions were annotated. Kyoto Encyclopedia of Genes and Genomes KEGG pathway enrichment analysis and Gene Ontology GO functional enrichment analysis were performed on abnormally expressed methylated genes.
Results There were 159076 methylation sites with significant difference between RA patients and normal control group (Q <0.05, | Δβ |> 1), of which 159076 were high methylation sites and 146449 were low methylation sites. 192953 differentially methylated regions were obtained (Q

<0.05). 141 differentially methylated genes were annotated to the differentially methylated region. KEGG and GO analysis showed (P <0.05): 20 signaling pathways involvedherpesvirus type Ⅰ infection, Th17 cell differentiation, Th1 / Th2 cell differentiation, systemic lupus erythematosus, etc. Mainly involves the processing and presentation of antigens and immune response regulating cell surface receptor signaling pathways, negative regulation of immune system processes, γ-interferon-mediated signaling pathways and other biochemical processes as well as antigen peptide binding, transmembrane transport activity, ubiquitin Various molecular functions such as protein ligase binding.

Conclusion Abnormal DNA methylation may be an important epigenetic mechanism leading to the occurrence and development of RA, and provide new diagnostic ideas for the follow-up analysis of RA-related biomarkers and targeted therapy of diseases.

Keywords: rheumatoid arthritis; methylation; bioinformatics analysis

Rheumatoid arthritis (RA) is a kind of autoimmune disease characterized by joint damage and destruction as well as inflammation and proliferation of synovium tissue. It often involves articular cartilage, resulting in joint deformity and rigidity, thus causing joint dysfunction. The global prevalence is about 0.5% ~ 1% [1]. At present, the main clinical treatment is to delay the disease and improve the joint function, but because of its long course and high disability rate, the prevention and treatment of RA has important public health significance. The research shows that the pathogenesis of RA is complex, mainly involving genetic susceptibility, virus infection, environment and lifestyle and other factors.

The epigenetic mechanism synthesizes the environmental and genetic factors of RA, and has been paid more and more attention in recent years [2]. Epigenetics mainly involves the regulatory mechanisms of histone methylation, DNA methylation and noncoding RNA [3-5]. DNA methylation, as the most widely studied epigenetic modification, refers to the reaction of modifying cytosine to 5-methylcytosine with S-adenosylmethionine as the methyl donor under the catalysis of DNA methyltransferase [6]. It is characterized by direct mutation and complementation of DNA sequence to regulate gene expression and cell function without changing DNA sequence, through covalent modification of DNA base and other potential changes in chromatin structure, thus affecting the development of disease.

In recent years, the research of DNA abnormal methylation is mostly focused on cancer and other fields, and there are few reports on autoimmune diseases such as RA. In this study, geo database is used to mine chip data, and bioinformatics analysis method is used to analyze methylation sites, regions and related pathways of abnormal differential expression, so as to further clarify the epigenetic mechanism of DNA methylation in RA and provide new ideas for subsequent analysis of biomarkers and targeted treatment of diseases.

PU-1773

Bioinformatic prediction of immunodominant regions in spike protein for early diagnosis of the severe acute respiratory syndrome coronavirus 2（SARS-CoV-2）

Siqi Zhuang
the second xaingya hospital of CSU

Background To contain the pandemics caused by SARS-CoV-2, early detection approaches with high accuracy and accessibility are critical. Generating an antigen-capture based detection system would be an ideal strategy complementing the current Methods based on nucleic acids and antibody detection. The spike protein is found on the outside of virus particle and appropriate for antigen detection.

Methods In this study, we utilized bioinformatics approaches to explore the immunodominant fragments on spike protein of SARS-CoV-2.

Results The S1 subunit of spike protein was identified with higher sequence specificity. Additionally, glycosylation sites and high-frequency mutation sites on spike protein were circumvented in the antigen design. Three immunodominant fragments, Spike56-94, Spike199-264, and Spike577-612, located at the S1 subunit were finally selected via bioinformatics analysis. All these fragments present qualified antigenicity, hydrophilicity, and surface accessibility. A recombinant antigen with a length of 194 amino acids (aa) consisting of the selected immunodominant fragments as well as a universal Th epitope was finally constructed.
Conclusion The recombinant peptide encoded by the construct contains multiple immunodominant epitopes, which could stimulate strong immune response in mice and generate qualified antibodies for SARS-CoV-2 detection.

PU-1774

肝纤四项与肝功的联合诊断对慢性乙肝肝硬化的影响研究

郑欢欢
吉林金域检验所有限公司

目的 探讨肝纤四项与肝功能指标联合检测对慢性乙肝肝纤维化诊断中的诊断价值。
方法 回顾性分析 2020 年 6 月 1 日至 2020 年 12 月 30 日送检的 100 例慢性乙肝患者及 40 例健康患者的肝纤四项[透明质酸（HA）、层粘连蛋白（LN）、Ⅲ型前胶原（PC-Ⅲ）、Ⅳ型胶原（Ⅳ-C）]及肝功能[天门冬氨酸氨基转移酶（AST）、丙氨酸氨基转移酶（ALT）和 AST/ALT 比值]检查结果，分为两组，100 例慢性乙肝患者为乙肝组，40 例健康患者为对照组。肝纤四项使用安图全自动免疫分析仪，检测方法为磁微粒法。肝功能指标检测采用罗氏 c702 全自动生化分析仪进行检测，检测方法为速率法。均使用配套试剂进行检测。并对乙肝组和对照组的肝纤四项及肝功能检测结果进行对比分析。
结果 乙肝组透明质酸（HA）、层粘连蛋白（LN）、Ⅲ型前胶原（PC-Ⅲ）、Ⅳ型胶原（Ⅳ-C）、天门冬氨酸氨基转移酶（AST）、丙氨酸氨基转移酶（ALT）和 AST/ALT 比值水平均高于对照组血清测定结果，差异具有统计学意义（P＜0.05），肝纤四项与肝功联合检测阳性率高于肝纤四项及肝功阳性检出率，差异具有统计学意义（P＜0.05）。
结论 肝纤四项与肝功联合检测在慢性乙肝肝纤维化诊断中临床效果显著，优于单纯检测肝纤四项或肝功的检测。肝纤维化较为常见，如不及时治疗，则多数患者将进展至肝硬化，进而发生肝功能衰竭、门静脉高压等。积极有效的干预则有望延缓或阻止肝纤维化病情进展，延长患者生存期，提高患者的生活质量。

PU-1775

Artemisinin Ameliorates Intestinal Inflammation by Skewing Macrophages to the M2 Phenotype and inhibiting epithelial–mesenchymal transition

Junxiang Zeng
Xinhua hospital, School of Medicine, Shanghai Jiaotong University Shanghai, China

Background Inflammatory bowel disease (IBD) is a self-destructive intestinal diseasewhose etiology is unclear but complex and the effective treatment is deficient. Increasing evidences have indicated that immune dysfunction and epithelial–mesenchymal transition (EMT)-related intestinal mucosal barrier impaired hold critical position in the pathogenesis of IBD. Artemisinin (ART) is a sesquiterpenoid compound extracted from Chinese herbal medicine which has good immunomodulatory effects. Studies have shown that artemisinin and its analogues have

therapeutic effects on a variety of tumors and immune-related disorders. The purpose of current study was to research the effect and mechanism about artemisinin induced macrophage polarization to M2 phenotype and inhibiting the process of EMT.
Methods In vitro, the anti-inflammatory effect of artemisinin is mainly verified by RAW264.7 cells and tissue (colon tissue and PBMC) from CD patients with active intestinal inflammation. RAW264.7 cells stimulated with LPS to induce inflammatory state and ART were used as therapeutic treatment in different concentration. Then the expression levels of pro-inflammatory factors, macrophage polarization and ERK pathway were analyzed. Colon tissue and PBMC from CD patients were treated with ART in different concentrations and macrophage polarization, pro-inflammatory factors expression, EMT-related protein were analyzed. In vivo, DSS-induced colitis mice were treated by ART for seven days. The DAI score was calculated and the colons andspleens were harvested after the animals were sacrificed. The expression of macrophage markers and EMT-related markers in the intestines of mice in each group were monitored by qPCR and western blot.
Result ART treatment could decrease thelevels of pro-inflammatory coefficient expressed in theRAW264.7 cells and human PBMC. Moreover, ART could ameliorate the intestinal inflammation in vivo through down-regulating the expression of pro-inflammatory factors, promoting macrophagepolarization to M2 phenotype and inhibiting the process of EMT.
Conclusion Taken together, our findings demonstrated that artemisinin might ameliorate inflammation by inducing macrophage polarization to M2 phenotype and inhibiting the process of EMT, suggesting that ART may be applied to the rehabilitation of IBD in the future.

PU-1776

Development and validation of a novel noninvasive index based on Chitinase-3-like protein 1 for predicting significant fibrosis in patients with chronic hepatitis B

chuanshang zhuo、Xu-Jiang Lu、Hui-Juan Feng、Hui-Lin Mo、Zhi Ye、Li-Ping Zheng、Jun-Ping Ke、Li-Juan Liu
Mengchao Hepatobiliary Hospital of Fujian Medical University

Backgrounds Identification of significant liver fibrosis plays an important role in the management of patients with chronic hepatitis B. However, most existent indices remains unsatisfied in the diagnosis of significant fibrosis in CHB patients. This study try to develop a noninvasive index based on Chitinase-3-like protein 1 (CHI3L1) and other laboratory parameters for predicting significant fibrosis in patients with chronic hepatitis B (CHB) with a better performance.
Methods A cohort of 279 consecutive subjects undergoing percutaneous biopsy was enrolled and randomly divided into training and validation groups. The Scheuer's score was introduced as the reference for fibrosis staging and significant fibrosis was defined as the Scheuer's stages ≥S2. A novel index of multivariate binary (stepwise) logistic regression analysis was developed and compared to APRI, FIB-4, and GPR.
Results Multivariate analysis showed that CHI3L1, Laminin, international normalized ratio (INR), and platelet were the independent predictors of significant fibrosis, and then a new index called CLIP was suggested. The area under the receiver-operating characteristic curve (AUC) of the latest CLIP index for predicting significant fibrosis was 0.842 (95% CI 0.773-0.897), higher than those of APRI (0.679, 95% CI 0.601-0.751), FIB-4 (0.764, 95% CI 0.690-0.827) and GPR (0.738, 95% CI 0.663-0.804) in the training group. The CLIP's AUCs in the validation group, the overall CHB population, CHB patients with normal ALT, and CHB patients with elevated ALT were 0.841, 0.838, 0.807, and 0.875, respectively, higher than those of APRI, FIB-4, and GPR. The optimum cutoff value for CLIP for diagnosing significant fibrosis in CHB was >0.04 with a sensitivity of 76.54% and specificity of 79.10% in the training group.

Conclusions The new index CLIP has a better diagnostic performance than APRI, FIB-4, and GPR in diagnosing significant fibrosis in CHB patients, and its application may reduce the need for liver biopsy among CHB patients.

PU-1777

Dense fine speckled immunofluorescence pattern in a Chinese population: Prevalence and clinical association

Keyi Zhang、Zhuochun Huang、Bin Yang
West China Hospital of Sichuan University

Objective To provide information on prevalence and possible clinical association in a Chinese population for medical practice of the dense fine speckled pattern (DFS pattern).
Methods A retrospective study was conducted with patients who had the DFS pattern from June 2018 to December 2019 in West China Hospital.
Results A total of 469 patients (1.27% of patients with positive ANA IIF test results) revealed the DFS pattern, of which 92.96% had isolated DFS pattern and 23.67% had titers above/equal to 1:320. The average age of patients with the DFS pattern was 43.45 years, and females accounted for 76.97% of them. Ten different kinds of diseases made up the vast majority of the disease spectrum, in which inflammatory or infectious diseases (46.11%), mental diseases (21.45%) and systemic auto-immune rheumatic diseases (SARDs) (18.23%) ranked in the top three. The most common SARDs were rheumatoid arthritis (RA), undifferentiated connective tissue disease (UCTD) and systemic lupus erythematosus (SLE). Forty-six patients (10.55%) had positive or suspicious ENA antibodies test Results Patients with positive ENA antibodies test results had a higher risk of suffering from SARDs, however, we discovered that not all SARDs patients had positive/suspicious ENA antibodies test Results If negative ENA antibodies test result was considered as exclusion criterion of SARDs, 47 patients would be missed.
Conclusions The DFS pattern is basically isolated and with low titer. Middle-aged individuals and females are the majority of patients with DFS pattern and deserve attention. Auto-immune diseases related antibodies such as ENA antibodies, clinical information of patients and long term follow-up are of great importance to avoid missed or delayed diagnosis of SARDs, not just because of the existence of the DFS pattern.

PU-1778

Breast cancer cells regulate macrophages toward the M2 activation status by recruiting peripheral blood monocytes

Yu Liu
West China Hospital，Sichuan University

Macrophages play a major role in monitoring the tumor microenvironment (TME), especially M2 macrophages, considered correlated with poor prognosis and therapy resistance. In breast cancer patients, tumor microenvironment can attract peripheral blood monocytes by secreting IL-4,IL-10 and IL-12 rather than TNF-αand subsequently regulate the transformation of macrophages to M2.Flow cytometric analysis found that CD206+ macrophage strongly increased, while MHC-II+ macrophage reduced comparatively. The secretion of cytokines could activate the IL-10- associated pathway via stat1 inhibition and stat3 activation. the breast cancer patients with high expression of M2 macrophage showed recurrence and related complications more common, suggesting a poorer prognosis. It provides a new therapeutic strategy and potential target for the treatment of breast cancer patients.

PU-1779

免疫检查点 CD47 分子表达与自身免疫性甲状腺炎相关性研究

何雪
中国医科大学附属第一医院

目的 免疫检查点 CD47 能够抑制巨噬细胞吞噬，参与自身免疫性胰岛炎、狼疮肾炎等自身免疫性疾病发病。前期研究发现自身免疫性甲状腺炎小鼠体内存在巨噬细胞吞噬能力异常，目前巨噬细胞功能和 CD47 在自身免疫性甲状腺炎患者中障碍机制和表达水平尚不明晰。本研究旨在探究自身免疫性甲状腺炎患者 CD47 表达及其与疾病相关性。
方法 收集因甲状腺结节而手术的甲炎患者（AIT 组）和年龄、性别匹配的非甲炎患者（CON 组），采集病理证实的桥本甲状腺炎组织、正常甲状腺组织以及患者血清。ELISA 检测 CON 组（n＝26）和 AIT 组（n＝29）血清中 CD47 分泌情况；免疫组化实验比较甲状腺组织 CD47 蛋白表达情况。
结果 AIT 组患者血清中 CD47 表达显著增高，差异有统计学意义（p<0.05）。且血清 CD47 水平与 TPOAb 存在相关性。免疫组化实验比较甲状腺组织 CD47 蛋白表达情况，与 CON 组比较，AIT 患者甲状腺组织内 CD47 表达明显增加；炎症浸润中心区域，CD47 表达未明显改变，炎症浸润区域周围的甲状腺滤泡上皮细胞细胞膜 CD47 表达增加明显，暂未受炎症累及区域 CD47 表达增加不明显。
结论 免疫检查点 CD47 分子在自身免疫性甲状腺炎患者中高表达，可能为自身免疫性甲状腺炎的预防和治疗策略提供新的靶点。

PU-1780

应用自身抗体对抗凝脂综合征继发肾损伤进行诊断的初步研究

王子霞[1]、范立民[2]、孟玥[1]、陈晓忠[1]、陆慧琼[1]、廖建枫[1]、侯铁英[1]
1. 广东省人民医院
2. 广州医科大学

目的 探讨抗 β2 糖蛋白-1IgG 抗体（β2GP1-IgG）、抗 β-2 糖蛋白-1IgM 抗体（β2GP1-IgM）、抗心磷脂抗体（ACL）等多种抗体检测在抗磷脂综合征继发肾损伤（APSN）诊断中的应用价值。
方法 采用 ELISA 检测方法，检测抗磷脂综合征（APS）患者的抗 β-2 糖蛋白-1IgG 抗体（β2GP1-IgG）、抗 β-2 糖蛋白-1IgM 抗体（β2GP1-IgM）、抗心磷脂抗体（ACL）的抗体水平，以蛋白尿、血尿为尿沉渣阳性，统计尿沉渣阳性组与尿沉渣阴性组之间的抗体水平是否有统计学差异。
结果 APS 患者中 53 例尿沉渣阳性组的 β2GP1-IgM 的抗体水平明显高于 31 例尿沉渣阴性组的抗体水平（P<0.05）；53 例尿沉渣阳性组的 β2GP1-IgG 的抗体水平高于 31 例尿沉渣阴性组的抗体水平（P>0.05）。53 例尿沉渣阳性组中 ACL-IgM 阴性率为 54.72%，ACL-IgM 阳性率为 45.28%；31 例尿沉渣阳性组中 ACL-IgM 阴性率为 70.97%，ACL-IgM 阳性率为 29.03%（P>0.05）。而 53 例尿沉渣阳性组中 ACL-IgG 阴性率为 88.68%，ACL-IgM 阳性率为 11.32%；31 例尿沉渣阴性组中 ACL-IgM 阴性率为 90.32%，ACL-IgM 阴性率为 9.68%(P>0.05)。
结论 尿沉渣阳性组的 β2GP1IgM 的抗体水平明显高于尿沉渣阴性组的抗体水平，APS 患者出现肾损伤时 β2GP1IgM 的抗体水平会升高。

PU-1781

利妥昔单抗对不同疾病患者外周血 B 淋巴细胞计数的影响

严琳、冯伟华
四川大学华西医院

目的 探讨视神经脊髓炎、天疱疮、膜性肾病三种自身免疫性疾病患者以及肾移植受者，使用利妥昔单抗治疗后，外周血 B 淋巴细胞计数的变化。
方法 本研究纳入视神经脊髓炎患者 10 例、天疱疮患者 29 例、膜性肾病患者 37 例、肾移植受者 24 例，根据疾病类型分为四个组：视神经脊髓炎组、天疱疮组、膜性肾病组、肾移植组。比较四组疾病的 B 淋巴细胞计数的基线水平，并分析在使用利妥昔单抗治疗后四类患者外周血 B 淋巴细胞计数的变化情况。
结果 视神经脊髓炎、天疱疮、膜性肾病、肾移植受者在年龄 (44.0 vs 46.3 vs 47.7 vs 30.4，P<0.0001) 和男女比例 (男性占比：0% vs 31.0% vs 64.9% vs 66.7%，P<0.0001) 上均有统计学差异。在使用利妥昔单抗治疗前，四组患者 B 淋巴细胞计数的基线水平有显著差异 (269 个/ul vs 404 个/ul vs 245 个/ul vs 190 个/ul，P=0.002)。使用利妥昔单抗治疗后，四组患者的 B 淋巴细胞计数均显著减少 (P<0.05)，且在治疗后 6 个月内维持与治疗初期相同的低水平，从治疗后第 9 个月开始逐渐回升。
结论 虽然视神经脊髓炎患者、天疱疮患者、膜性肾病患者以及肾移植受者基线 B 细胞计数水平不同，但是利妥昔单抗对四类患者的 B 淋巴细胞计数的影响趋势一致。B 淋巴细胞计数可作为使用利妥昔单抗治疗后的有效的免疫监测指标，监测周期建议每月一次。

PU-1782

Characterization of anti-Neutrophil cytoplasmic antibodies and their clinical associations

Yang Wen
Department of Laboratory Medicine, West China Hospital, Sichuan University,

Background anti-Neutrophil cytoplasmic Antibodies (ANCA) are frequently tested by indirect immunofluorescence method. They can present different fluorescent patterns, whose diagnostic value for diseases is still obscure. Through researching the clinical and laboratory characteristics of them, we aimed at providing reference for the diagnosis of diseases associated with ANCA.
Method We collected the diagnosis, clinical features and laboratory tests data of ANCA-positive patients in West China Hospital in the last two years. Stratified analysis of diseases distribution and laboratory tests results were performed according to different fluorescent models.
Results In 652 ANCA-positive patients, pANCA accounted for 76.4%, cANCA were 12.4%, and aANCA were 11.2%. pANCA mainly related to ANCA-associated vasculitis(68.22%), lupus nephritis(12.46%),and connective tissue diseases(9.35%). As for cANCA, they were ANCA-associated vasculitis(90.90%), osteoarthritis(9.09%), and ANCA-associated nephritis(9.09%). In pANCA and cANCA-positive patients, the lungs and kidneys were most involved. (The total proportion of these two was more than 50%). Procalcitonin(PCT) and C-reactive protein which reflect the inflammatory status were significantly increased(p=0.00), while the anemia indicators: HGB and RBC decreased(p=0.00). CYS-C, eGFR and CREA, representing the renal function, were obviously abnormal(p=0.00).
Conclusion ANCA-positive patients mainly suffered from vasculitis, and their lungs and kidneys were often affected. We should pay attention to their anemia status and susceptible organs, trying to prevent the progression of the diseases and improve the quality of life of these patients.

PU-1783

术前 DNLR 评估经肝切除术后的Ⅰ期肝细胞癌患者预后价值-基于 nomogram 模型

杜琴
川北医学院附属医院

目的 探讨术前中性粒细胞/（白细胞计数-中性粒细胞计数）评估Ⅰ期肝细胞癌（HCC）患者在 肿瘤切除术后死亡的价值。

方法 2009 年 1 月至 2015 年 12 月诊治的Ⅰ期 HCC 患者 129 例，均接受肝癌切除术。绘制受试者工作特征(ROC)曲线，由最高约登指数确定 DNLR 的截断点，比较不同 DNLR 组患者临床和病理学特征。应用 COX 回归分析影响 HCC 术后死亡的危险因素。基于危险因素建立 nomogram 模型，运用 C 指数、内部验证的校准曲线、临床决策曲线对模型准确性进行评估。

结果 术前 DNLR 选取 1.77 为最佳截点，低 DNLR(<1.77)组与高 DNLR (≥1.77)组年龄、性别、吸烟、饮酒、肝切缘、肿瘤数量、门脉高压、BCLC 分期、胸腔积液等均无统计学意义（P＞0.05）。DNLR(≥1.77)、术后胸腔积液是 HCCⅠ期患者 OS 较短的独立危险因素。基于 DNLR 及术后胸腔积液构建了 nomogram 模型，C 指数是 0.629(95%CI: 0.54 -0.718)。校准曲线、临床决策曲线也表明模型的准确性。

结论 高 DNLR 及术后胸腔积液 对预测 Ⅰ期 HCC 患者术后死亡具有潜在的应用价值。

PU-1784

全血 miR-499 作为 RA 疾病生物标志物的评价分析

黄卓春、谭慧玲、王雪安、张丽静、杨滨
四川大学华西医院

目的 类风湿关节炎（RA）是一种多基因自身免疫性疾病，其特征是全身性炎症伴关节进行性损伤。MicroRNA（miRNA）是小的非编码 RNA 分子。 最近的研究表明，不同 miRNA 表达水平的改变可能与自身免疫性疾病的发生发展相关。在本研究中，我们拟评估 RA 患者与健康对照之间 5 种 miRNA 的表达差异，并评估它们作为 RA 生物标志物的潜力。

方法 纳入 19 例新诊断的 RA 患者和 21 例性别年龄匹配的健康对照者，结合我们课题组的前期研究结果和文献报道，选择 miR-499，miR-146a，miR-15a，miR-149a-3p 和 miR-155-5p 作为候选 miRNA，采用实时定量 PCR（qRT-PCR）检测 miRNA 的表达，并评估这 5 种 miRNA 作为 RA 潜在生物标志物的性能。

结果 MiR-146a（p = 0.107），miR-15a（p = 0.935），miR-149a-3p（p = 0.560）和 miR-155-5p（p = 0.136）的表达在 RA 患者组和健康对照组间未见显著性差异。与健康对照相比，RA 患者外周血 miR-499 的表达显著高于健康对照组（p <0.05）。受试者研究曲线（ROC）分析提示 miR-499 对 RA 具有较好的诊断价值（AUC = 0.688，95％CI = 0.52-0.83，灵敏度= 0.79，特异性 = 0.57）。结合 ESR，CRP 和 RF，可以进一步提高 miRNA-499 对 RA 的诊断价值（结合 ESR 的 AUC = 0.971，结合 CRP 的 0.865，结合 RF 的 0.931）。

结论 本研究结果提示，miR-499 可能是中国人群 RA 疾病诊断相关的新的潜在的非侵入性诊断生物标志物。

PU-1785

肺癌血清肿瘤标志物联合检测诊断模型的建立与性能验证

龙天娣
南方医科大学珠江医院

目的 比较分析癌胚抗原（CEA）、细胞角蛋白 19 片段（CYFRA21-1）、神经元特异性烯醇化酶（NSE）、糖类抗原 125(CA125）、糖类抗原 153（CA153）等五种血清肿瘤标志物检测在肺癌诊断中的价值，建立肺癌的诊断模型，并验证其性能。
方法 采用电化学发光法（CLIA）检测血清肿瘤标志物 CEA、CYFRA21-1、NSE、CA125、CA153 的水平。采用 SPSS19.0 软件对所得数据进行统计分析，计量资料用中位数(四分位数间距)表示，采用 kruskall-wallis 检验，阳性率的比较采用卡方检验；以肺癌确诊情况为因变量(Y=0,1)，五个血清肿瘤标志物为自变量，采用逐步回归法建立二项分类 Logistic 回归模型；以回归方程产生的 Logistic(P)为新变量，作 ROC 曲线分析；比较新变量与单个参数的 ROC 曲线，并求出最佳诊断界值；用新的临床病例分析模型预测的符合率，验证回归模型应用性能。以 P<0.05 为差异有统计学意义。
结果 肺癌组 CEA、CYFRA21-1、NSE、和 CA153 的表达水平明显高于健康对照组和肺良性疾病组，差异有统计学意义(P<0.01)，肺癌组和肺良性疾病组 CA125 水平均高于健康对照组(P<0.01)，肺癌组和肺良性疾病组 CA125 水平差异无统计学意义(P>0.05）；将血清肿瘤标志物的临床检测数据代入 Logistic 回归模型中，求出 P 值，以 P 值>0.579 判断为肺癌，应用 Logistic 回归模型预测的符合率为 83%。
结论 血清肿瘤标志物联合检测诊断肺癌的灵敏度和准确度均优于单项检测，对鉴别肺癌具有一定临床价值。Logistic 回归模型代表了预测肺癌发生的综合概率，预测肺癌的价值高于单一参数，是肺癌筛查的新的可靠方法。

PU-1786

探讨检测孕中期血清 β-HCG、ACA 和孕后期尿酸浓度对先兆子痫的预测价值

张懿
南方医科大学珠江医院

目的 通过比较先兆子痫患者和正常孕妇孕中期 β-HCG、抗心磷抗体 ACA 和孕后期尿酸的浓度变化，探讨这三项指标对该疾病的预测价值。
方法 回顾性分析 2012.1-2016.8 在南方医科大学珠江医院接受孕中期筛查并成功随访直至分娩的 65 例单胎妊娠孕妇，其中 30 例经诊断为子痫前期患者，对照组有 35 例血压正常的孕妇。比较两组孕妇的 BMI 指数，孕中期（15-20 周）血清的 β-HCG 浓度，β-HCG MoM 值和抗心磷脂抗体 ACA 水平，以及孕妇孕后期（20 周以后）尿酸浓度，分析这些指标与孕妇发生子痫前期的相关性。
结果 （1）子痫前期组孕妇 BMI 指数、β-HCG MoM 值、尿酸均显著高于正常对照组(P<0．05)。(2)多因素 Logistic 回归分析显示 BMI 指数、血清尿酸浓度都是子痫前期的预测指标，其中尿酸水平的预测能力最强 ,BMI 次之。
结论 抗心磷脂抗体 ACA 对孕妇患子痫前期的预测意义不明显，先兆子痫患者组的 BMI 值、尿酸水平均显著高于正常对照组，与疾病具有一定的相关性。子痫前期患者孕中期的 β-HCG 水平显著升高，可作为预测子痫前期的一个指标，经修正的 β-HCG MoM 值诊断效能更强。

PU-1787

肝细胞癌患者诊断时血清异常凝血酶原水平对肿瘤生物学特性与预后的预测价值分析

罗俐梅、苏真珍、袁宇珊、张可依、蔡蓓、李立新
四川大学华西医院

目的 探讨肝细胞癌（HCC）患者在诊断时血清异常凝血酶原（PIVKA-Ⅱ）水平对肿瘤生物学特性的预测价值。
方法 回顾性纳入 2017 年 6 月-2018 年 12 月在四川大学华西医院经病理确诊的 HCC 患者 478 例，获取患者在确诊时 PIVKA-II 的血清学浓度，并以 40 mAU/mL 作为截断值将 HCC 患者分为 PIVKA-II 阴性组（≤40 mAU/mL）与 PIVKA-II 阳性组（>40 mAU/mL），分析 PIVKA-II 水平与肿瘤生物学特性（肿瘤大小、肿瘤数目、肿瘤细胞分化程度、有无微血管浸润、有无远处转移、有无门静脉癌栓等）以及复发之间的相关性。
结果 与 PIVKA-II 阴性组相比，PIVKA-II 阳性组 HCC 患者更容易发生微血管浸润（39.4% vs 13.9%，$\chi2$=15.839，P<0.001），更容易形成门静脉癌栓（17.0% vs 5.6%，$\chi2$=10.164，P=0.001），肿瘤直径≥5cm 更常见（83.4% vs 16.6%，$\chi2$=21.599，P<0.001），具有更高的 TNM 分期（34.1% vs 17.5%，$\chi2$=12.289，P<0.001），更高的 BCLC 分期（38.6% vs 21.7%，$\chi2$=10.956，P=0.001），且更容易术后复发（47.8% vs 32.3%，$\chi2$=4.643，P=0.031）。
结论 HCC 患者在诊断时高 PIVKA-II 水平与肿瘤的不良生物学特性相关，且更容易复发。检测 HCC 患者 PIVKA-II 水平可对临床预后判断提供一定依据。

PU-1788

Immunosuppression has long-lasting effects on circulating follicular regulatory T cells in kidney transplant recipients

Qian Niu[1]、Aleixandra Mendoza Rojas[2]、Marjolein Dieterich[2]、Dave L. Roelen[3]、Marian C. Clahsen van Groningen[2]、Lanlan Wang[1]、Teun van Gelder[2]、Dennis A. Hesselink[2]、Nicole M. van Besouw[2]、Carla C. Baan[2]
1. Department of Laboratory Medicine, Wset China Hospital, Sichuan University
2. Erasmus MC, University Medical Center Rotterdam
3. Leiden University Medical Center

Background FoxP3+ follicular regulatory T cells (Tfr) have been identified as the cell population controlling T follicular helper (Tfh) cells and B cells which, are both involved in effector immune responses against transplanted tissue.
Methods To understand the biology of Tfr cells in kidney transplant patients treated with tacrolimus and mycophenolate mofetil (MMF) combination immunosuppression, we measured circulating (c)Tfh and cTfr cells in peripheral blood by flow cytometry in n = 211 kidney transplant recipients. At the time of measurement patients were 5–7 years after transplantation. Of this cohort of patients, 23.2% (49/211) had been previously treated for rejection. Median time after anti-rejection therapy was 4.9 years (range 0.4–7 years). Age and gender matched healthy individuals served as controls.
Results While the absolute numbers of cTfh cells were comparable between kidney transplant recipients and healthy controls, the numbers of cTfr cells were 46% lower in immunosuppressed recipients (P<0.001). More importantly, in transplanted patients, the ratio of cTfr to cTfh was decreased (median; 0.10 vs. 0.06), indicating a disruption of the balance between cTfr and cTfh cells. This shifted balance was observed for both non-rejectors and rejectors. Previous pulse methylprednisolone or combined pulse methylprednisolone + intravenous immunoglobulin anti-rejection therapy led to a non-significant 30.6% (median) and 51.2% (median) drop in cTfr cells, respectively when compared to cTfr cell numbers in transplant patients who did not receive anti-

rejection therapy. A history of alemtuzumab therapy did lead to a significant decrease in cTfr cells of 85.8% (median) compared with patients not treated with anti-rejection therapy (P<0.0001). No association with tacrolimus or MMF pre-dose concentrations was found.
Conclusions This cross-sectional study reveals that anti-rejection therapy with alemtuzumab significantly lowers the number of cTfr cells in kidney transplant recipients. The observed profound effects by these agents might dysregulate cTfr functions.

PU-1789

类风湿关节炎患者血清骨转换标志物的水平分析

牛倩[1]、谢中华[2]、苗强[1]、徐欢[1]、万正利[1]、蔡蓓[1]、张君龙[1]
1. 四川大学华西医院
2. 内江市东兴区人民医院

目的 探讨类风湿关节炎（RA）患者血清骨转换标志物水平的变化及其与炎性因子水平的关系。
方法 纳入 2020 年 10 月~12 月符合 2010 年美国风湿病学会/欧洲抗风湿病联盟（ACR/EULAR）修订的 RA 诊断标准的患者 58 例作为疾病组，性别、年龄匹配的健康体检者 49 例作为对照组，采用电化学发光法检测血清 β-I 型胶原羧基端交联肽（β-CTx）、总 I 型胶原氨基端延长肽（tPINP）、骨钙素 N 端中分子片段（N-MID）、抗环瓜氨酸肽抗体（ACPA）和白介素 6（IL-6）水平，化学发光法检测血清骨型碱性磷酸酶（BALP）和可溶性白介素 2 受体（sIL-2R）水平，速率散射比浊法检测血清 C 反应蛋白（CRP）水平。分析骨转换标志物 β-CTx、tPINP、N-MID 和 BALP 在疾病组与对照组间的表达差异，及其与炎性指标 CRP、IL-6 和 sIL-2R 的相关性。
结果 与健康对照组相比，RA 患者组血清 β-CTx、CRP、IL-6 和 sIL-2R 的水平明显升高（P<0.05），tPINP、N-MID 和 BALP 的水平轻微升高但差异无统计学意义（P>0.05）。ACPA>500 U/mL 的 RA 患者其血清 β-CTx 水平明显高于健康对照者（P<0.05），但与 ACPA<500 U/mL 的患者相比差异无统计学意义（P>0.05）。Spearman 相关性分析显示，RA 患者血清 β-CTx 水平与其病程、CRP 和 sIL-2R 水平呈正相关关系（P<0.05）。
结论 RA 患者表现出以骨吸收活性明显增强为特征的高骨转换过程，其骨吸收活性与病程的长短和炎症反应的强度有关；骨标志物 β-CTx 在评价 RA 患者骨质破坏中具有潜在价值。

PU-1790

Elevated soluble Tim-3 correlates with disease activity of systemic lupus erythematosus

赵地
山东大学齐鲁医院

Tim-3 has been found to play important roles in systemic lupus erythematosus (SLE), but whether sTim-3 is involved in development of SLE remains unknown. In this study, we firstly observed an increased expression of plasma sTim-3 in SLE patients, especially active SLE patients. The plasma sTim-3 levels were positively correlated with anti-dsDNA, SLEDAI score, ESR, and urine albumin. The plasma sTim-3 levels were negatively correlated with C3 and C4. The AUC values indicated that the plasma sTim-3 level was significantly discriminative of early active SLE from stable SLE and HC with high sensitivity and specificity. The present results suggest that sTim-3 might serve as a potential biomarker for promising the disease activity of SLE.

PU-1791

抗 Chrom 抗体和抗 dsDNA 抗体阳性 SLE 患者实验室及临床特点研究

张帆[1,2,3,4]、刘微芬[1]、崔晓花[2,3,4]、钟敏[2,3,4]
1. 曲靖市第一人民医院
2. 昆明医科大学第一附属医院
3. 云南省实验诊断研究所
4. 云南省检验医学重点实验室

目的 研究系统性红斑狼疮（SLE）患者抗核染色质（Chrom）抗体和抗双链 DNA（dsDNA）抗体阳性实验室指标和临床特点的差异。
方法 选择 2020 年昆明医科大学第一附属医院收治并检测抗 Chrom 抗体和抗 dsDNA 抗体的 156 例 SLE 患者相关信息，分为抗 Chrom 抗体阳性组（C 组 50 例）、抗 dsDNA 抗体阳性组（D 组 46 例）和双抗体阳性组（CD 组 60 例），分析 3 组患者实验室指标和临床特点的差异。
结果 C 组年龄高于 D 组（P<0.05）。C 组累及血液系统阳性率高于 D 组（P<0.05）；D 组累及肾脏阳性率高于 C 组（P<0.05）；CD 组累及浆膜腔阳性率高于其他两组（P<0.05）。C 组以核颗粒型为主，D 组以核颗粒型及核均质型为主；CD 组以核均质型为主（P<0.05）。C 组和 C+D 组中抗 Sm 抗体和抗 SmRNP 抗体阳性率高于 D 组（P<0.05）；C 组和 CD 组中抗 RNP 抗体、抗 RNP-A 抗体阳性率高于 D 组（P<0.05）。C 组 PLT 水平低于 CD 组（P<0.05）；C 组和 D 组 C3 水平均高于 CD 组（P<0.05）。
结论 抗 Chrom 抗体阳性 SLE 患者发生血液系统疾病风险较高，抗 dsDNA 抗体阳性组患者发生肾脏疾病风险较高，当两种抗体同时存在时，应密切关注浆膜腔积液症状出现，应重视 SLE 患者诊疗中相关指标变化，做到早预防、早干预。

PU-1792

重度抑郁症患者血浆前列腺素 E 含量水平的检

蒋娅玲
江门市第三人民医院

检测前列腺素 E 在重度抑郁症患者血浆中的改变情况。方法选取江门市第三人民医院精神科门诊 2018 年 1 月—2019 年 12 月治疗的 80 例重度抑郁症患，根据治疗方式的分成研究组和对照组，采用高效液相色谱在 40 例重症抑郁症患者作为研究组和 40 例健康患者作为对照组，在队列中检测血浆中 PGE1 和 PGE2 的含量。

PU-1793

血清 HE4、CA125 和 ROMA 指数对卵巢肿瘤良恶性评价及疗效判断的初步分析

暴旭广
南方医科大学珠江医院

目的 探讨血清人附睾上皮分泌蛋白 4（HE4）、CA125 和卵巢癌风险预测值（ROMA 指数）卵巢肿瘤良恶性评价及对卵巢癌患者预后疗效判断的临床意义。

方法 收集珠江医院 2015 年 1 月~2016 年 3 月经手术病理学确诊为卵巢肿瘤的患者 91 例，其中卵巢癌患者 31 例，良性肿瘤患者 60 例,另外收集 30 例健康体检者，测定其血清 HE4、CA125 及 ROMA 指数值。
结果 卵巢癌组血清 HE4、CA125 及 ROMA 指数值明显高于良性肿瘤组（P<0.01）；卵巢癌患者组治疗后血清 HE4、CA125 及 ROMA 指数值化疗后均低于术前（P<0.05）；复发或转移后，患者血清 HE4、CA125 及 ROMA 指数值均不同程度升高，结果有统计学差异（P<0.05）。
结论 联合检测血清 HE4、CA125 及 ROMA 指数来评价卵巢肿瘤的良恶性以及卵巢癌治疗后的评估方面具有重要的临床意义，血清 HE4、CA125 及 ROMA 指数在卵巢癌患者复发或转移中有监测意义。

PU-1794

6 岁以下儿童布鲁菌病患者的流行病学及临床特点分析

何晶晶
黑龙江省农垦总局总医院

目的 了解学龄前布鲁菌病（简称布病）患儿的流行病学和临床特点，以提高对儿童布鲁菌病的认识及诊断水平。
方法 收集 2016 年 12 月至 2018 年 11 月黑龙江省农垦总局总医院收治确诊的学龄前布病患儿，回顾分析患儿的流行病学特征、临床症状、实验室检查、治疗和转归情况。
结果 共纳入 45 例学龄前布病患儿，其中男性 29 例，女性 16 例，年龄（3.7±1.6）岁，范围 6 月 ～ 6 岁，主要集中在 > 3 ～ 6 岁（64.44%，29/45）；居住地以农村为主（97.78%，44/45）；发病时间主要集中在 3 – 6 月（46.67%，21/45）。临床症状以发热、关节痛居多，分别占 97.78%（44/45）、57.78%（26/45）；淋巴结及肝脾肿大较多见，分别占 42.22%（19/45）和 35.56%（16/45）。患儿治疗前、后 ALT、AST、CK-MB、HBDH 及 LDH 比较，差异有统计学意义（t = 4.774、2.970、2.229、5.664、5.805，P 均 < 0.01 或 < 0.05）。血标本培养布鲁菌阳性 36 例（80.0%），治疗后均转为阴性。
结论 学龄前儿童布病流行病学和临床特点不典型。在布病流行区域及多发季节，对于不明原因发热的患儿，临床医生应详细询问其流行病史并结合临床特征，考虑布病的可能，争取早诊早治。

PU-1795

TROCH 筛查的应用现状

曾静
南方医科大学珠江医院

TORCH 是一个缩写，代表一组病原体，包括弓形虫(TOX)、风疹病毒(RV)、巨细胞病毒(CMV)和单纯疱疹病毒(HSV)，可引起围产期感染，具有类似症状[1]。TORCH 作为优生优育的指标之一，TORCH 特异性抗体筛查可以降低先天性疾病发生率。本文总结 TROCH 筛查的应用现状，指导临床正确合理地使用 TORCH。

PU-1796

桥本甲状腺炎患者血液中炎症因子水平的研究

何春燕
苏州大学附属第二医院

目的 探讨桥本甲状腺炎（Hashimoto's thyroiditis，HT）患者的肾功能指标与疾病的关系，为防止临床误诊提供依据，同时我们研究了 HT 患者血清中的炎症因子，为探索 HT 的发病机制提供了依据。
方法 回顾性分析 1270 例桥本甲状腺炎门诊及住院患者的甲状腺功能指标和肾功能指标，将患者按 TSH 水平分为正常和升高组，分析两组病人 IgA、IgG、IgM、C3、C4、Cr、尿素、尿酸、尿隐血指标之间是否有差异，并进行相关性分析。采用竞争 ELISA 方法检测 53 例 HT 患者血清中的细胞因子如白介素，干扰素、共刺激分子如 B7-H3 和肿瘤抗原如 CEA 等指标，探讨它们与 HT 发病的关系。
结果 HT 患者体内的 IL-2、IL-6、IFN-γ 的水平明显高于正常对照组 IL-2(3.814.07vs.1.92±0.68)，IL-6(3.34±2.06vs.2.12±1.59)，IFN-γ(2.85±3.98 Vs. 1.53±0.82)而 IL-10 的水平明显低于正常对照组(1.61±0.53 Vs.2.25±1.18)。HT 患者体内的 CEA 水平高于正常对照，可溶性 B7-H3 水平明显低于健康对照者。TSH 水平升高组肌酐、尿酸、IgG、IgM 较 TSH 水平正常组明显增高（P<0.05），TSH 水平升高组 C3、C4 与较正常组明显降低（p<0.05），TGAb、TPOAb、TSH 与肾功能、补体以及免疫球蛋白指标之间存在相关性。其中血清肌酐（Cr）水平与 TSH 呈正相关。IgG、IgM 与 TPOAb、TGAb、TSH 呈正相关，C3 与 TPOAb、TSH 呈负相关。C4 与 TPOAb 呈负相关。
结论 HT 患者体内存在 Th1/Th2 失衡，分泌的细胞因子以 Th1 型为主；HT 患者与甲状腺癌的发生有一定的相关性；HT 患者的肾功能和甲状腺功能存在相关性，甲状腺功能的异常可以导致肾功能的异常。

PU-1797

Analysis of PD-1 expression in different monocyte subsets and serum soluble PD-1 from patients with sepsis

Yang Fu、Shuang Wang、Qi Zhang、Binwu Ying
West China Hospital, Sichuan University

Objective Negative costimulatory molecule programmed death-1 (PD-1) play an important role in dysregulation of immune responses of sepsis. We aimed to investigate the PD-1 expression in monocyte subsets and serum soluble PD-1 level in sepsis patients with different degrees of severity.
Materials and Methods The observational clinical study on the different expression of PD-1 in peripheral blood monocytes from patients with sepsis was conducted in West China Hospital of Sichuan University. This study included 42 sepsis patients and 16 healthy controls (HCs) with matched age and sex. PD-1 expression was determined on the monocyte subsets (classical, intermediate, non-classical) by flow cytometry. Monocytes in different groups were stained by anti-human CD45 per-cp, anti-human CD16 FITC, anti-human CD14 APC, anti-human CD279 (PD-1) PE. In addition，serum soluble PD-1 was examined by Luminex MagPix.
Results Monocytes in peripheral blood can be divided into three subsets according to the CD14 and CD16 expression: $CD14^{+}CD16^{-}$(classical monocyte, CL Mo), $CD14^{+}CD16^{+}$ (intermediate monocyte, IM Mo) and $CD14^{low}CD16^{+}$ (non-classical monocyte, NC Mo). The results showed that the percentage of CL Mo in septic shock group were significantly decreased and the percentage of IM Mo in sepsis and septic shock group were significantly increased when compared to HC group. Moreover, the expressions of PD-1 on IM Mo were significantly higher in both sepsis and

septic shock patients than HCs. Further analysis of serum PD-1 in sepsis patients showed that serum PD-1 level was decreased in sepsis patients compared with HCs.
Conclusions Our results suggested that the difference of PD-1 expression in peripheral blood monocyte subsets were associated with the severity of sepsis.

PU-1798

自身免疫性肝病中多种自身抗体的检测及应用进展

郑燕妮
南方医科大学珠江医院

自身免疫性肝病(AILD)是由于机体异常的免疫反应攻击自身的肝脏而引起的以肝脏组织损害和肝脏功能异常为主要表现一组自身免疫性疾病。主要包括自身免疫性肝炎(AIH)、原发性胆汁性胆管炎(PBC)、原发性硬化性胆管炎(PSC)。该病在我国其确切发病率和患病率尚不清楚，但国内文献报道的病例数呈明显上升趋势。大多数病人表现为慢性肝炎，也有部分患者无任何症状，仅因发现肝功异常而就诊。自身免疫性肝病患者血清中存在特异性自身抗体，自身抗体的检测已成为 AILD 诊断和鉴别的重要工具。本文主要对 AILD 相关血清自身抗体的研究进展作一概述, 以有助于临床对自身抗体意义的解读。

PU-1799

肝素结合蛋白联合降钙素原与中性粒细胞计数在全身及消化系统局部炎症疾病中的临床价值

何仁栋[1,2,3]、李婕妤[1,2,3]、何莉萍[1,2,3]、谢宁[1,2,3]、王强[1,2,3]、郭晓兰[1,2,3]、郭斌[1,2,3]
1. 川北医学院附属医院检验科
2. 川北医学院医学检验系
3. 川北医学院转化医学研究中心

目的 评估肝素结合蛋白（HBP）、降钙素原（PCT）、中性粒细胞计数在消化系统局部炎症疾病和全身炎症疾病中的鉴别及联合诊断价值
方法 选取 58 例急性胆囊炎患者作为消化系统局部炎症疾病组，62 例细菌感染引起的脓毒症患者作为全身炎症疾病组，以同期 30 例健康体检者为对照组。采用免疫荧光干式定量法测定 HBP 水平，全自动化学发光免疫分析仪和全自动血细胞分析仪分别测定 PCT 和中性粒细胞水平。正态分布的定量资料采用单因素方差分析，非正态分布定量资料采用 Mann-Whitney U 检验，定性资料采用 χ2 检验，两变量间相关性采用 Spearman 相关分析，建立受试者工作特征(ROC) 曲线评估各指标诊断效能。
结果 全身炎症疾病患者 HBP、PCT 和中性粒细胞水平较消化系统局部炎症疾病患者以及健康体检者明显增高（p 均=0.000），而消化系统局部炎症疾病患者仅 HBP 较健康体检者明显增高（p=0.000），PCT 和中性粒细胞均无明显差异（p 均＞0.05）。全身炎症疾病患者 HBP 与 PCT 呈正相关（p=0.006，r=0.344），消化系统局部炎症疾病患者 HBP 升高率高于 PCT 升高率（χ2=16.06，p=0.000）。消化系统局部炎症疾病患者，当中性粒细胞绝对值小于 7.5×109/L 时，HBP 和中性粒细胞水平呈正相关（p=0.012，r=0.305），而全身炎症疾病中两者无相关性。HBP 用于消化系统局部炎症疾病诊断时曲线下面积（AUC）为 0.750；HBP 用于鉴别诊断全身炎症疾病和消化系统局部炎症疾病时 AUC 为 0.783；HBP、PCT 和中性粒细胞联合诊断全身炎症疾病时 AUC 为 0.994
结论 HBP 可用于鉴别全身炎症疾病和消化系统局部炎症疾病。更为重要的是 HBP、PCT 和中性粒细胞计数三指标联合诊断炎症疾病时具有更优的临床价值。

PU-1800

化学发光法检测抗双链 DNA 抗体

晋晶
南方医科大学珠江医院

目的 评价两种全自动、定量和随机上样化学发光法(CLIA) 检测抗双链 DNA 抗体的临床应用价值，为临床检测方法的选择提供参考。
方法 对 40 例 SLE 患者及 31 例非自身免疫病患者的血清样本分别应用重庆科斯迈 SMART6500 磁微粒全自动化学发光仪、苏州浩欧博自身抗体检测试剂和美国 INOVA 公司 BIO-FLASH 全自动化学发光检测系统采用 CLIA 平行检测抗双链 DNA 抗体，与传统的间接免疫荧光法(IFA) 检测抗双链 DNA 抗体结果进行比较与数据分析。
结果 两种 CLIA 检测系统与 IFA 针对抗双链 DNA 抗体的检测表现出良好的符合率，其中，浩欧博检测系统与 IFA 总符合率为 88.7%，阳性符合率 85.7%，阴性符合率 90%。BIO-FLASH 全自动化学发光检测系统与 IFA 总符合率为 87.3%，阳性符合率 100%，阴性符合率 82%。
结论 与 IFA 比较，两种 CLIA 检测试剂在检测抗双链 DNA 抗体均具有良好的符合率。CLIA 检测方法不仅提供了客观的检测数据，同时具有较高的检测通量，实现了自动化。建议实验室开展检测方法选择时，应同时结合样本临床信息以及方法学自身特点、实验室自身条件等因素进行判断和评价。

PU-1801

探讨标本保存条件对高血压五项结果的影响

汪旭
吉林金域医学检验所有限公司

目的 探讨不同温度保存条件对高血压五项检测结果的影响
方法 收集 2020 年 8 月到 2021 年 1 月期间送检的 60 例高血压五项患者样本。把检测结果记录，作为对照组；检测后的样本分成两份，分别保存在室温和－20℃冷冻冰箱内。24h 后，将室温样本和冷冻样本（需充分复融）上机检测，得到两组数据，室温样本检测结果为 A 组，冷冻样本检测结果为 B 组。比较对照组、A 组、B 组的高血压五项检测结果。
结果 A 组的 Renin 浓度与对照组相比在 24h 内呈下降趋势且部分小于线性下限，而 B 组 Renin 浓度与对照组相比在 24h 内呈上升且稳定。A 组的 ACTH 浓度与对照组相比在 24h 内大幅度下降且部分小于线性下限，而 B 组的 ACTH 浓度与对照组相比在 24h 内基本稳定。A 组和 B 组的 ALD 和 Cortisol 浓度与对照组相比变化影响较小。A 组 AII 浓度与对照组相比在 24h 内大幅度下降且大部分小于线性下限，B 组 AII 浓度与对照组相比在 24h 内基本稳定且部分下降。
结论 检测高血压五项时，应在收到样本后尽快检测，如果不能尽快检测，需要把离心好的样本冷冻保存，并尽快检测完毕，本次研究为高血压五项提供了样本保存条件的依据。

PU-1802

IgA 类抗磷脂抗体对抗磷脂综合征的诊断价值研究

杨滨[1]、谭慧玲[1]、胡朝军[2]
1. 四川大学华西医院
2. 中国医学科学院北京协和医院

目的 分析多种抗磷脂抗体（aPL）亚型在健康人群与抗磷脂综合征（APS）患者中的分布情况，并探讨 IgA-aPL 检测在 APS 诊断中的临床应用价值。

方法 依据 2006 年悉尼国际 APS 分类标准，连续纳入 2019 年 7 月至 12 月就诊于北京协和医院或四川大学华西医院的 APS 患者共计 218 人，其中原发性 APS 患者 148 人，继发性 APS 患者 70 人，并同期 1：1 收集年龄、性别匹配的健康对照。以化学发光免疫分析法检测研究对象血清样本中 IgA/IgG/IgM 型抗心磷脂抗体（aCL）及抗 β2 糖蛋白Ⅰ抗体（aβ2GPI）。以独立样本 t 检验、χ2 检验、受试者工作曲线（ROC）和 logistic 回归进行统计学分析。
结果 APS 患者中，IgA-aCL、IgA-aβ2GPI 的阳性率分别为 20.6%、15.6%，而二者各自的独立阳性率仅为 2.3%、0.9%。IgA-aCL、IgA-aβ2GPI 独立阳性不能用于有效识别 APS 患者（P 值分别为 0.216，1）。联合 IgG/IgM-aCL 的诊断效能明显优于 IgG-aCL（P<0.001），而加入 IgA-aCL 并不能进一步提升对 APS 的诊断价值（P=0.287）。对 aβ2GPI 而言，联合 IgG/IgM 或 IgA/IgG/IgM 型抗体的诊断效能与 IgG-aβ2GPI 单独使用时相较，均无显著差异（P 均>0.05）。此外，IgA-aPL 阳性 APS 患者更易发生心脏瓣膜损伤（P=0.044）及血小板减少症（P=0.014）。
结论 在已有的狼疮抗凝物、IgG/IgM 型 aCL 和 aβ2GPI 等血清学标志物基础上，增加 IgA-aCL 与 IgA-aβ2GPI 并不能进一步提升实验室检查对 APS 的预测价值，但 IgA-aPL 与心脏瓣膜损伤及血小板减少症等临床症状相关。

PU-1803

评价肿瘤标志物 CA199、CEA、CA125 在胰腺癌临床诊断及分期中的作用

王晓瑞
河南省漯河医学高等专科学校第三附属医院

目的 分析肿瘤标志物 CA199、CEA、CA125 在胰腺癌临床诊断及分期中的作用。
方法 选定本院 2018 年 6 月至 2019 年 6 月收治的 228 例胰腺癌患者作为实验组，以及同期门诊体检的 228 例健康人员作为参照组，检测并对比两组血清 CA199、CEA、CA125 水平，对比不同 TNM 分期组血清 CA199、CEA、CA125 水平，对比复发和未复发组血清 CA199、CEA、CA125 水平。
结果 实验组血清 CA199、CEA、CA125 水平均比参照组高，III-IV 期组血清 CA199、CEA、CA125 水平均比 I-II 期组，复发组血清 CA199、CEA、CA125 水平均比未复发组高，P<0.05（差异均具有统计学意义）。
结论 血清 CA199、CEA、CA125 水平与胰腺癌患者 TNM 分期及复发情况呈正相关性，值得借鉴。

PU-1804

不同检测系统检测 SCC 结果对比分析及探究

肖含、李姗姗、崔思洋
吉林金域检验医学检验所有限公司

目的 比较雅培化学发光检测 SCC 和博奥赛斯化学发光法检测 SCC 结果的是否具有可比性,两种不同的检测方法进行对比分析，探讨不同的系统间检测 SCC 结果的相关性。
方法 依据美国临床实验室标准化委员会 EP9-A 文件要求, 使用雅培化学发光仪 i2000SR 和博奥赛斯全自动化学发光仪 Axceed 260，每天测定 8 例临床样本，每样本各测定 1 次，连续测定 5 天，共 40 例样本，样本浓度覆盖试剂检测范围。进行数据统计，计算线性回归方程，计算 R^2。
结果 使用雅培化学发光仪 i2000SR 和博奥赛斯全自动化学发光仪 Axceed 260 两台仪器检测 SCC 的回归方程为 Y=0.836X+0.1892。R^2=0.9934。具有良好的相关性。

结论 两种检测系统测定 SCC 的结果是具有可比性的，两种不同方法学的差异对检测结果没有明显影响。可以根据临床需要选择不同的检测系统，从而更好的满足临床的需要，为临床服务。

PU-1805

输卵管卵巢脓肿患者血清 ACTA、INHB 和 FSH 检测及临床意义

林花、冯颖
吉林大学第一医院

目的 探讨血清激活素 A(ActivinA，ACTA)、抑制素 B（InbibinB，INHB）和卵泡刺激素（Follicle-stimulatng hormone，FSH）在输卵管卵巢脓肿（Tubo-Ovarian abscess,TOA）发病机制中的作用。
方法 采用酶联免疫（ELISA）法和放射免疫（RIA）法检测 55 例 TOA 患者及 20 例正常对照组的血清 ACTA、INHB 和 FSH 水平。
结果 TOA 患者血清 ACTA 和 INHB 水平明显高于对照组（P<0.01），FSH 水平明显低于对照组（P<0.01）。
结论 ACTA、INHB 和 FSH 可能均参与了疾病的发生，联合检测三项指标，对指导治疗及病情评估具有实际意义。

PU-1806

肺泡灌洗液肝素结合蛋白在肺内感染诊断与鉴别诊断中的临床价值

毕惠娟[1]、沈继录[1]、方文浩[2]、吴珊[1]、尹丽娜[2]、徐倩[2]、薛莹[2]、柯晨阳[1]
1. 安徽医科大学第四附属医院
2. 安徽医科大学第四附属医院检验科

目的 探讨肺泡灌洗液肝素结合蛋白（Heparin binding protein, HBP）在肺内感染诊断与鉴别诊断中的临床价值。
方法 选取 2019 年 1 月—2020 年 6 月安徽医科大学第四附属医院呼吸科收治的 80 例肺内感染患者，其中细菌性肺内感染 44 例，非细菌性肺内感染 36 例，另选取同期 40 例非肺部感染性疾病患者为对照组，检测各组患者肺泡灌洗液中 HBP、PCT、IL-6 水平，并分析上述各指标鉴别细菌性和非细菌性肺内感染的临床效能。
结果 细菌性肺内感染患者肺泡灌洗液 HBP、PCT、IL-6 水平均较非细菌性肺内感染及对照组明显升高，差异有统计学意义（P<0.05）。ROC 曲线结果显示 HBP、PCT 及 IL-6 可有效辅助诊断细菌性肺内感染，AUC 分别为 0.923、0.774、0.884，HBP cut-off 值为 16.88ng/ml 时，灵敏度为 77.3%，特异度为 92.5%。HBP、IL-6 可有效辅助细菌性与非细菌性肺内感染的鉴别诊断，AUC 分别为 0.778、0.696，灵敏度分别为 63.6%、54.5%，特异度分别为 88.9%、77.8%。
结论 肺泡灌洗液 HBP 在细菌性肺内感染的诊断及鉴别诊断中，具有较 PCT、IL-6 更优的临床价值。

PU-1807

CD3+T, CD4+T, CD8+T, CD4+T/CD8+T ratio, expression of γδT cells in peripheral blood of HIV-infected/AIDS patients and its clinical significance

Nange Zhao[1]、Keqiang Wang[2]
1. Xianyang Central Hospital of Shaanxi Province
2. 山东第一医科大学第二附属医院

To investigate the expression of CD4+T, CD4+T, CD8+T and γδT cells in peripheral blood of HIV-infected /AIDS patients, and to explore the possible role of CD4/CD8 ratio and γδT cells in the progression of HIV /AIDS, so as to provide evidence for the diagnosis and treatment of AIDS. According to different T cell antigen receptors (TCR), T cells are divided into αβT cells and γδT cells. The latter is composed of γ chains and δ chains, and the number is relatively small, accounting for 0.5%-5% of healthy adult lymphocytes. γδT cells originate from the thymus, but mature in peripheral tissues and organs. Most of γδ T cells are CD4- and CD8- cells, and a few are CD4+ and CD8+ cells. In this study, by detecting the peripheral blood CD3+T, CD4+T, CD8+T, γδT cells of HIV-infected/AIDS patients, the number of γδT cells, CD4+T, CD8+T cells and HIV infection in HIV-infected/AIDS patients The relationship with disease progression provides a basis for adoptive immunotherapy and other treatment Methods for AIDS.

PU-1808

BioSystems BA400 全自动特定蛋白分析仪尿轻链生物参考区间建立

连丽丽
吉林大学第一医院

目的 分析 BioSystems BA400 全自动特定蛋白分析仪与 SIEMENS BNⅡ全自动蛋白分析仪的尿 k 轻链、λ 轻链检测结果线性回归分布规律，由已通过确认的 SIEMENS BNⅡ检测系统尿轻链生物参考区间建立本实验室 BioSystems BA400 检测系统尿 k 轻链、λ 轻链生物参考区间。
方法 分析 2020 年 11 月在吉林大学第一医院就诊的 210 例住院及门诊检测尿 k 轻链、λ 轻链的患者样本检测结果。其浓度分布整个线性范围，不使用超出线性范围的标本。分别用 BioSystems BA400 全自动特定蛋白分析仪与 SIEMENS BNⅡ全自动蛋白分析仪检测 220 份样本各 1 次，收集检测数据，设 SIEMENS BNⅡ全自动蛋白分析仪测定结果为 x 值（比较方法），BioSystems BA400 全自动特定蛋白分析仪测定结果为 y 值（实验方法）。对检测数据进行离群值检验，若有显著离群值应予剔除。经剔除离群值，筛选出 192 例成对的尿 k 轻链、199 例成对的尿 λ 轻链的检测数据。对两个检测系统的成对测定数据进行一元线性回归分析，制作实验方法对比较方法散点图，得到回归方程 y=bx+a，其中 a、b 分别为回归直线的截距和斜率。对该直线进行相关性检验，若 r≥0.975 或 r2≥0.95，则认为该线性拟合满意。如果 r2＜0.95,则必须分析更多的样品以扩大数据浓度分布范围，然后再重新分析全部数据。对回归方程的进行方差分析，判断回归方程是否成立。根据线性回归分析计算 x 为本室 SIEMENS BNⅡ检测系统尿 k 轻链、λ 轻链参考值时的 y 值，即为通过线性回归分析建立的 BioSystems BA400 检测系统尿 k 轻链、λ 轻链参考值结果尿 k 轻链项目回归方程 y=1.084x-3.760，r2＝0.989。线性拟合满意。对回归方程的方差分析结果，F=3225.179，P=0.000，差异有统计学意义，该回归方程成立。x 为本室 SIEMENS BNⅡ检测系统尿 k 轻链参考值＜7.19 mg/L 与＜14.20 mg/24h 时，y 值为＜6.62 mg/L 与＜14.48 mg/24h。尿 λ 轻链项目回归

方程 y=1.083x+1.099，r2＝0.992。线性拟合满意。对回归方程的方差分析结果，F=8345.163，P=0.000，差异有统计学意义，该回归方程成立。x 为本室 SIEMENS BNⅡ检测系统尿 λ 轻链参考值＜3.90 mg/L 与＜7.80 mg/24h 时，y 值为＜5.32 mg/L 与＜9.55 mg/24h。由此建立本室 BioSystems BA400 检测系统生物参考区间为尿 k 轻链＜6.62 mg/L 或＜14.48 mg/24h，尿 λ 轻链＜5.32 mg/L 或＜9.55 mg/24h。经验证该参考区间适用于本实验室。

结论 BioSystems BA400 全自动特定蛋白分析仪与 SIEMENS BNⅡ全自动蛋白分析仪的尿 k 轻链、λ 轻链检测结果一元线性回归方程成立，线性拟合满意。由此建立 BioSystems BA400 检测系统尿 k 轻链、λ 轻链参考区间可向临床提供参考。

PU-1809

抗磷脂抗体升高和住院患者院内血栓的相关性研究

史晓敏
北京大学第一医院

针对抗磷脂抗体升高的住院患者，评估抗磷脂抗体和院内血栓事件之间的相关性，比较不同种类的抗磷脂抗体对于血栓的意义大小。

方法 回顾性研究。以 2015 年 1 月至 2019 年 12 月于北京大学第一医院住院，并且抗磷脂抗体谱中任意一项检测结果为阳性的 385 例患者为研究对象。依据住院期间是否检测到血栓将所有受试者分为血栓组和非血栓组。记录患者的临床资料及实验室数据，包括 aCL-IgM/IgG、抗 β2GPI-IgM/IgG、LA。比较两组之间的年龄、性别、吸烟、肥胖、高血压、高血脂、糖尿病的发生率以及抗磷脂抗体中位数水平。通过 logistic 多因素回归分析判断血栓事件发生的危险因素。用 c2 趋势检验确立 aCL 的中高滴度数值，并用 logistic 回归验证。

结果 血栓组的年龄以及男性、吸烟、高血压、糖尿病的比率明显高于非血栓组。血栓组的抗 β2GPI- IgG、dRVVT 的阳性率明显高于非血栓组，dRVVT 的中位数水平也高于非血栓组，差异有统计学意义。aCL-IgM 的中位数水平，非血栓组高于血栓组。aCL-IgG 的阳性率，血栓组略高于非血栓组。logistic 多因素回归分析显示，男性、高血压、糖尿病、高龄、dRVVT 升高、抗 β2GPI-IgG 升高是血栓的高危因素。以 36 GPL 作为 aCL-IgG 的中高滴度数值，血栓风险增加 2.45 倍。

结论 抗磷脂抗体谱中，DRVVT 方法检测的 LA 和抗 β2GPI-IgG、aCL-IgG 是对住院患者院内血栓事件最有价值的实验室指标。aCL-IgG 的中高滴度数值设立在 36 GPL 可以很好地区分血栓风险。aCL-IgM 在非血栓性疾病显著升高。

PU-1810

ALDH2 在类风湿关节炎滑膜的表达及临床意义

王洪星
山东大学齐鲁医院

目的 观察类风湿关节炎(rheumatoid arthritis, RA)患者膝关节滑膜组织中乙醛脱氢酶 2（aldehyde dehydrogenase, ALDH2）蛋白表达情况，并分析其临床意义。

方法 选取在我院进行膝关节置换术的 RA 患者为实验组（n=24），选取同期进行关节镜手术的半月板损伤患者为对照组（n=12），收集滑膜组织 WB 检测 ALDH2 蛋白表达水平，实验组患者检测抗环瓜氨酸多肽抗体（抗 CCP 抗体），类风湿因子水平（RF），采用 DAS28 评分评估 RA 疾病活动度，采用 Pearson 相关性分析 RA 患者滑膜组织 ALDH2 表达水平与其临床检验指标间的相关性。

结果 RA 实验组 ALDH2 表达水平高于对照组；RA 实验组 ALDH2 表达水平与抗 CCP 抗体呈正相关(r=0.71, P=0.04)，与 DAS28 评分和 RF 无相关性(P>0.05)。

结论 RA 患者膝关节滑膜组织中 ALDH2 表达增高，并可能与 RA 疾病进展正相关。

PU-1811

分析糖化血红蛋白、血脂检测应用于诊断 2 型糖尿病的临床价值

张兴红
安岳县人民医院

目的 对 2 型糖尿病患者予以糖化血红蛋白、血脂检测，对其检测效果予以探究。
方法 68 例糖尿病患者及 68 例健康检查者选自 2018 年 4 月-2019 年 4 月期间，将糖尿病患者设为 A 组，健康检查者设为 B 组。 2 组采取糖化血红蛋白、血脂检测，对比 2 组指标（FBG、HbA1c、TC、TG、HDL-C、LDL-C）。
结果 A 组指标：FBG（7.35±0.43）mmol/L、HbA1c（8.68±4.21）%、 TC（6.78±0.23）mmol/L、TG （2.56±0.31）mmol/L、HDL-C（0.93±0.43）mmol/L、LDL-C（3.57±0.46）mmol/L。B 组指标： FBG （ 4.92±0.35 ） mmol/L 、 HbA1c （ 5.31±0.36 ） % 、 TC （ 4.47±0.38 ） mmol/L 、 TG （2.17±0.24）mmol/L、HDL-C（1.25±0.26）mmol/L、LDL-C（2.34±0.36）mmol/L。A 组 FBG、HbA1c 指标高于 B 组，对比差异具备统计学含义 P<0.05，A 组 TC、TG、LDL-C 高于 B 组，其 HDL-C 指标低于 B 组，对比具备统计学含义 P<0.05。
结论 本次研究对 2 型糖尿病予以进行糖化血红蛋白、血脂检测，可作为 2 型糖尿病有效诊断指标，该方法可推广应用。

PU-1812

探究 CA125、HE4 水平在临床卵巢癌诊断中的意义

武诗曼
沈阳金域医学检验所有限公司

目的 探究 CA125、HE4 水平在临床卵巢癌诊断中的意义。
方法 使用电化学发光分析法对恶性组、良性组、健康对照组的三组实验对象的血清进行 CA125 和 HE4 检测，分析其单项、联合检测水平、阳性率、敏感度及特异性。并采用受试者工作特征（ROC）曲线，评价 CA125、HE4 水平及联合检测水平对卵巢癌的诊断价值。
结果 恶性组中 CA125、HE4 的单项、联合检测水平及其阳性率均显著高于其他两组，组间差异具有统计学意义（P<0.05），其中 CA125 的灵敏度为 81.7%，但是其特异性为 73.6%明显低于 HE4 95.9%。ROC 曲线分析结果显示：CA125、HE4 对卵巢癌均具有良好的诊断价值（P<0.05），并且其联合检测水平准确性高于单项指标检测，差异有统计学意义（P<0.05）。
结论 血清 CA125、HE4 在卵巢癌患者中高表达,随病程进展而提高,联合检测 CA125、HE4 能够提高卵巢癌诊断的正确率，具有较高的诊断价值。

PU-1813

抗 PDL1 纳米抗体展示文库的构建与筛选

王清
青岛大学附属医院

目的 利用噬菌体展示技术进行纳米抗体库的构建和筛选，获得抗程序性死亡配体 1(PDL1)的高亲和力、强特异性纳米抗体，为建立血清外泌体 PD-L1 化学发光免疫检测方法的应用奠定基础。

方法 使用重组 PDL1 抗原免疫羊驼，分离免疫后羊驼的外周血淋巴细胞，提取总 RNA 后通过 RT-PCR 技术扩增羊驼重链抗体可变区（VHH）片段，构建纳米抗体文库。采用噬菌体展示技术和固相淘选方法，筛选得到强阳性克隆，经大肠杆菌表达和镍离子亲和层析获得纳米抗体，最终利用 Biacore 分析其亲和力和特异性。
结果 通过 3 轮的淘选，获得一株纳米抗体亲和力达到 1.4 x 10-10 mol·L-1，对其他免疫检查点蛋白 PD1、VEGFC、CTLA4、HER2 及 VEGFR3 均无交叉反应性。
结论 利用噬菌体展示技术成功获得了程序性死亡配体 1(PDL1)的高亲和力、强特异性纳米抗体，可用于后续癌症治疗疗效监控和评价。

PU-1814

四种 POC 仪器检测 PCT 与罗氏仪器电化学发光法分析性能比较

黎春宝、黄亚萍
上海金域医学检验所有限公司

目的 通过对四种平台 POC 法检测 PCT 与罗氏电化学发光法的性能比较，了解各平台 POC 方法性能参数比对情况。
方法 以 Cobas e602 仪器为参考仪器，其余四台仪器检测结果与参考仪器进行比对，分别对正确度、精密度、线性和一致性进行数据统计。
结果 血浆中的精密度高于全血中的精密度。AQT90 平台无论是血浆样本还是全血样本均表现出很好的重复性；Getein 1100 平台仅在血浆高浓度表现出较好的重复性，而 mLabs 平台仅在血浆低浓度的重复性验证达标；Finecare 平台仅血浆高浓度重复性验证不通过。在正确度验证中，AQT90 和 Getein 1100 与参考方法表现出较好的相关性，四个 POC 平台与罗氏平台检测结果比对相对偏倚均小于 1/2 最大允许误差。比对所有 4 种 POC 分析都有很好的线性。我们还发现这些方法之间存在着较好的一致性。
结论 在用于检测 PCT 的四种 POC 方法中，与 Cobas e602 相比，AQT90 有较高的精密度和正确度。

PU-1815

PD-1 抗体的临床疗效分析

高骞
中南大学湘雅医院

目的 探讨 PD-1 抗体在肺癌、结肠癌的单药治疗以及联合化疗的临床疗效，为免疫治疗用于癌症的临床应用提供参考。
方法 选取 2018 年 7 月至 2019 年 11 月就诊于中南大学湘雅医院确诊的肺癌、结肠癌的患者，并从中选取使用过 PD-1 抗体治疗的 90 例患者。同时跟踪这 90 例患者，了解其临床信息，动态监测其各种检验、影像学指标。
结果 PD-1 对肺癌、结肠癌的治疗有一定的效果，联合治疗效果要优于单药治疗。

PU-1816

血清 sST2 与 NT-proBNP 在 DKD 合并心衰患者中的应用价值

浦春[1,2]、胡蝶[2]、国慧敏[1]、张艳珍[2]、朱 萍[2]、张博超[2]、路 勇[1]
1. 皖南医学院检验学院
2. 皖南医学院第一附属医院

目的 探讨可溶性生长刺激表达基因 2 蛋白（sST2）、血清 N 末端 B 型脑钠肽前体（NT-proBNP））的水平在 DKD 合并心衰患者中的临床价值。
方法 收集单纯糖尿病（DM）患者 41 例、DKD 患者 119 例（DKD 早期 28 例，DKD 中期 47 例，DKD 晚期 44 例）；同期选择 32 例健康体检者作为对照组。检测全部研究对象的血清中 sST2、NT-proBNP 和 IL-33 的水平。
结果 对照组、DM 组和 DKD 组患者的性别、CHOL、HDL、AST、TG 和 LDL 的组间差异均无统计学意义（P＞0.05）；年龄、BUN 和 Cr 的差异有统计学意义（P＜0.05）。与对照组、DM 组相比，DKD 患者的血清中 sST2、NT-proBNP 水平显著升高（P＜0.05），对照组与 DM 组之间 sST2 水平差异无统计学意义（P＞0.05）。DKD 病变程度不同的患者血清 NT-proBNP 水平随 DKD 病变的严重程度的加重而升高（P＜0.05），而血清中 sST2 水平的差异无统计学意义（P＞0.05）；sST2、NT-proBNP 水平在心衰患者和无心衰患者的血清中的差异有统计学意义（P＜0.05）。统计分析提示，血清 sST2 水平是预测 DKD 合并心衰的独立危险因素（OR=1.034，P=0.005）。单独检测 DKD 合并心衰患者的血清 sST2、NT-proBNP 的曲线下面积（AUC）分别为（0.827、0.887）；ROC 曲线显示 sST2 与 NT-proBNP 联合检测的 AUC 为 0.903。
结论 在 DKD 患者中，sST2 和 NT-proBNP 水平均与心功能衰竭有关，但血清 sST2 水平不受肾功能的影响，有望作为预测 DKD 合并心衰的独立危险因素之一，与 NT-proBNP 联合检测可在一定程度上提高两指标单独检测的特异度，提高诊断效能。

PU-1817

生化检测在高血压的诊断和管理中的意义

卞林翠
合肥金域医学检验实验室有限公司

高血压是心血管疾病的一个重要的可治疗的危险因素，在普通人群中发病率很高。原发性高血压病因复杂，多为遗传及环境等因素相互作用导致；而目前继发性发高血压的研究及诊断仍存在不足。高血压被称为“无形杀手”，通常无明显症状。患者血压越高，患心血管、脑血管、周围血管和肾病的风险越大。常规和专门的生化检测对于评估高血压患者状况及其后续处理都是至关重要的。常规生化检测可基于高血压常见并发症，如血糖异常、血脂异常、肾脏损伤或靶器官损伤等确定高风险的高血压患者，并对患者进行风险分层，有助于后续开展针对性管理和治疗。专门的生化检测包括肾素-血管紧张素-醛固酮系统(RAAS)和肾上腺素能标记物的检测，有助于识别具有特定和可治疗的高血压病因。生化检测在高血压患者评估中是复杂的，但其结果的分析能够为临床医生提供患者血压分型、临床表现及混杂因素（如药物或方法干扰）等临床证据。因此临床检验实验室与临床专家及临床生化研究科学家之间的相互合作是至关重要的；以期达到对患者进行生化检查的标准化方法，以确保患者血压的最佳管理。

PU-1818

高血压患者血小板活化标志物及血小板参数与颈动脉内膜中层厚度的相关性

胡传玺
上海交通大学医学院附属第九人民医院

目的 探讨高血压患者血小板活化标志物尿 11-脱氢-血栓素 B2（11-DH-TXB2）及其参数与颈动脉内膜中层厚度（CIMT）的相关性。
方法 依据颈动脉内膜中层厚度，选取上海市虹口区四川北路街道社区卫生服务中心的高血压患者并分为：无病变组（CIMT<0.9 mm）74 例，斑块组（CIMT≥1.3 mm）155 例，共计 229 名。测量两组高血压患者尿液 11-DH-TXB2 含量及血小板数量（PLT）、平均血小板体积（MPV）、血小板分布宽度（PDW）、血小板容积（PCT）、大血小板比率（P-LCR）、同型半胱氨酸（Hcy）等指标，并进行统计学分析。
结果（1）斑块组患者 HCY、11-DH-TXB2、P-LCR、MPV、PDW 水平比无病变组高（P＜0．05）；（2）Spearman 相关分析表明 CIMT 与尿 11-DH-TXB2、P-LCR、MPV、PDW 及 HCY 呈正相关。
结论 高血压患者血小板活化标志物（尿 11-DH-TXB2）及其参数（P-LCR、MPV、PDW）与颈动脉内膜中层厚度具有相关性。

PU-1819

SAA、D-dimer、Cys-c 与慢性心力衰竭患者病情程度相关性分析

宋娟、马明坤、韩敬华、赵立杰、温学红
天津中医药大学第二附属医院

目的 研究 SAA、D-dimer、Cys-c 与慢性心力衰竭患者病情程度之间的关系。
方法 以我院心内科病区 2020 年 4 月至 2021 年 4 月收治的 117 例慢性心力衰竭患者作为研究对象，按照 NYHA 心功能分级分成心功能Ⅱ级组 30 例、Ⅲ级组 54 例、Ⅳ级 33 例。另选取本院非冠心病心衰患者 30 例作为对照组，分析不同组间 SAA、D-dimer、Cys-c 表达差异，以及与病情程度的相关性。
结果 Cys-c 随心功能级别升高而升高，组间两两比较差异有统计学意义（<0．05)，SAA 在对照组和心功能 II 级组、II 级组和 III 级组之间无明显差异，对照组、心功能 III 级组、Ⅳ级组之间比较差异有统计学意义，随着心功能的级别升高其值相应升高。D-dimmer 随着心功能恶化有逐渐升高的趋势，但在 II 级组和 III 级组、II 级组和Ⅳ级组之间差异无统计学意义。SAA、D-dimer、Cys-c 水平与心功能分级和 NT-proBNP 水平呈正相关。
结论 SAA、D-dimer、Cys-c 与慢性心衰患者病变程度间呈正相关，SAA 和 Cys-c 是诊断和评估心衰患者病情的较好指标，值得临床探索应用。

PU-1820

25-(OH)D 检测在妇科生殖疾病中的应用

张莹、胡玉皎、胡娟娟、冯玉洁、王昊、刘家云
空军军医大学西京医院

目的 探索 25-(OH)D 在妇科生殖疾病患者体内的含量及临床应用的重要性。
方法 使用液相色谱串联质谱技术，分析 2020 年妇科生殖中心 1976 例病例、健康对照组 551 例，评估 25-(OH)D 在妇科生殖中心患者和对照组间的差异，男性和女性组间差异，以及不同 25-(OH)D 水平在不同组别中的分布情况。
结果 妇科生殖中心患者 25-(OH)D 含量 19.52±8.85，健康对照组 25-(OH)D 含量 19.70±10.11，两组间差异无统计学意义（P=0.290>0.05）。妇科生殖中心男女患者间 25-(OH)D 结果分别为 21.40±8.75、15.83±8.02，差异有统计学意义（P=0.000<0.05）；健康对照组男女组间 25-(OH)D 结果分别为 21.69±10.21、18.69±9.93，差异有统计学意义（P=0.001<0.05）；妇科生殖中心患者与健康对照组男性组间 25-(OH)D 结果差异没有统计学意义（P=0.724>0.05），女性组间 25-(OH)D 结果差异有统计学意义（P=0.000<0.05）。

PU-1821

新生儿脐血与母血血脂水平的相关性研究

堵一乔[1]、徐刚[2]、钮静[1]、杨叶怡[2]、杨卫华[1]、董玲娣[1]、陈允钦[3]、王文惠[1]、杨振华[1]
1. 上海市宝山区中西医结合医院
2. 上海交通大学附属仁济医院宝山分院
3. 复旦大学附属中山医院心内科

目的 分析新生儿脐血与母血血脂水平的相关性。
方法 选取 2020 年 10 至 2021 年 4 月在上海市宝山区中西医结合医院住院的孕 37～41 周的临产孕母 100 例(孕母组)，自然分娩胎儿娩出时采集新生儿脐血 100 例（脐血组），同期在本院体检的健康育龄期未妊娠妇女 100 例(对照组)。采集孕母组产前清晨空腹静脉血，新生儿娩出后近脐端脐静脉血，对照组清晨空腹静脉血，采血后 2 小时内分离血清。采用 BECKMAN AU5800 自动生化分析仪检测 3 组对象血清总胆固醇(TC)、甘油三酯(TG)、高密度脂蛋白胆固醇(HDL-C)、低密度脂蛋白胆固醇(LDL-C)、载脂蛋白 A1 (ApoA1)、载脂蛋白 B(ApoB)和脂蛋白 a（LPa）水平。
结果 3 组对象血清 TC、TG、HDL-C、LDL-C、ApoA1、ApoB、LP（a）水平比较，差异有统计学意义(P＜0.05)；孕母组高于对照组和脐血组，对照组高于脐血组，差异有统计学意义(P＜0.05)。脐血组 TC（1.8553±0.5503）mmol/L，TG（0.32±0.1）mmol/L、HDL-C（0.932±0.264）mmol/L、LDL-C（0.908±0.306）mmol/L、 ApoA1（0.8628±0.1711）g/L、ApoB（0.218±0.057）g/L、LP(a)（16.8±14.2）mg/L，各项血脂指标均低于孕母组和对照组，差异有统计学意义(P＜0.05)；单变量相关性分析显示，新生儿性别、母亲分娩年龄，对新生儿脐血 TC、TG、HDL-C、LDL-C、ApoA1、ApoB、LP(a)水平的影响差异无统计学意义(P＞0.05)。双变量相关性分析显示，母血血脂水平、新生儿出生时体质量与脐血血脂水平无相关性(P＞0.05)。
结论 妊娠期间，母体血脂水平生理性升高，脐血血脂与母血血脂水平不相关。

PU-1822

上海地区健康成人 VITROS 干化学法血清胆红素参考区间的建立及其与湿化学检测结果的比对

宋晓冬、陆美娟
复旦大学附属华山医院

目的 目前国内干化学法测定胆红素尚无标准参考区间（RI），本研究通过使用奥森多医疗（Ortho Clinical Diagnostics）VIRTOS5600 全自动生化免疫分析仪及配套胆红素测试试剂，旨在建立上海地区健康人群的干化学法胆红素各成份参考区间。同时本研究使用罗氏湿化学分析仪同步测试，对两种方法测得的参考区间进行比较，以分析二者的一致性。

方法 经问卷调查，体格检查和实验室筛查，共计筛选出健康人群 256255 例（男 121 例，女 135134 例）建立 RI。在 VITROS5600 全自动生化免疫分析仪进行总胆红素（TBIL）、非结合胆红素（BU）及结合胆红素（BC）检测，在对照湿化学 Roche Cobas 检测平台上，进行 TBIL、直接胆红素（DBIL）和间接胆红素（IBIL）（计算值）分析。经过统计学分析后，得到 RI 及胆红素各组分干湿化学法间相关性评估结果。

结果 我们为健康人群建立了性别特异的干化学参考区间，包括 TBIL 5~17.7 μmol/L（男）、4.5~14.3 μmol/L（女）；BU 3.1~15.6 μmol/L（男）、2.9~13.3 μmol/L（女）；δB 0.4~3.2μmol/L（男）、0~3.1μmol/L（女）；所有 BC 测定值均为 0。除此之外，由于干湿化学两种方法均采用重氮法测定 TBIL，所以两种方法间具有良好一致性，其相关系数为 0.970。与之相对，由于干化学 BU 和湿化学 IBIL 检测原理不同，如同预期，二者检测结果之间平均差异超过 50%，不具一致性。

结论 本课题组成功建立了男女特异的干化学法血清胆红素各成份 BU、BC 及 δB 的参考区间，可为临床医师和检验人员提供参考。另一方面，我们认为干湿化学法测定的 TBIL 具有一致性，BU 和 IBIL 不具一致性。因此本课题组建议应该正确理解干、湿生化胆红素各组分（BC≠DBIL，BU≠IBIL），以避免临床混淆。

PU-1823

Center of Clinical Laboratory, Zhongshan Hospital, School of Medicine, Xiamen University, Xiamen, China

huilin zhang
Center of Clinical Laboratory, Zhongshan Hospital, School of Medicine, Xiamen University, Xiamen, China

The aim of the study was to assess the analytical performance of the HISCL NT-proBNP assay, a newly developed chemiluminescence immunoassay, for the detection of NT-proBNP.

The within-run and total imprecision of the NT-proBNP assay were determined with HISCL cardiac marker controls. Two hundred serum samples were evaluated to compare the HISCL NT-proBNP and Elecsys NT-proBNP assays. Five additional high NT-proBNP concentrations serum samples were evaluated to assess if there was high-dose hook effect in the HISCL NT-proBNP assay.

The total and within-run imprecision values of the HISCL NT-proBNP assay were 5.85%, 0.81%, 2.56% and 0.54% and 6.07%, 0.73%, 2.61% and 0.59% at 6.1, 129.83, 3732.84and39737.33 pg/ml, respectively. The
assay was verified to be linear for NT-proBNP levels ranging between 6.1 and 39737.33 pg/ml.

The HISCL NT-proBNP chemiluminescence immunoassay showed good analytical and diagnostic performance for the detection of NT-proBNP and could be used in routine clinical practice.

PU-1824

上海市月浦社区老年 2 型糖尿病患者视网膜病变与糖化血红蛋白等检测指标的相关性研究

李超男、吴成志、董成林、徐灵、程材
上海中冶医院

目的 探讨 2 型糖尿病患者（type 2 diabetes mellitus，T2DM）视网膜病变（diabetic retinopathy，DR）与糖化血红蛋白（HbA1c ）和空腹血糖（FPG）、尿微量白蛋白（MA）水平的关系。
方法 选择共 245 例月浦社区老年体检患者为研究对象，通过眼底检查结果，根据是否发生糖尿病视网膜病变将收集资料患者分为糖尿病视网膜病变（DR）组 116 例，和正常眼底无视网膜病变（NDR）对照组 129 例。收集患者一般临床资料和化验指标，包括 HbA1c 、FPG、MA 等资料进行回顾性分析。
结果 DR 组与 NDR 组之间性别、年龄比较差异无统计学意义(P＞0.05)；DR 组患者的 HbA1c、FPG、MA/ UCRE 明显高于 NDR 组，差异具有显著统计学意义(P＜0.01)，同时 DR 组 MA 水平增高，差异具有统计学意义（P＜0.05）；进一步 Binary logistic 回归分析结果显示，高水平的 HbA1c 是糖尿病视网膜病变发生的独立危险因素(P＜0.05）。
结论 1，DR 患者视网膜病变与 HbA1c 存在关联。 2，临床应积极关注糖尿病患者的 HbA1c 和 FPG、MA、MA / UCRE 比值水平，注意视网膜病变的早期筛查并积极干预，可降低 DR 的发生。

PU-1825

Comparison of electrolyte and glucose levels measured by a blood gas analyzer and an automated biochemistry analyzer among hospitalized patients

Yong Lin
Zhongshan Hospital, Xiamen University

Blood gas analyzers are capable of delivering results on electrolytes and metabolites within a few minutes and facilitate clinical decision-making.
In total, arterial and matched venous blood samples were collected from 200 hospitalized patients. Arterial blood samples were evaluated using a RAPIDPOINT 500 to test electrolyte and glucose levels, then the samples were cen_x0002_trifuged and the same parameters were measured with an AU5800.

Paired t tests showed that all parameters tested were significantly differ_x0002_ent between the two analyzers except chloride. The biases calculated indicated that blood gas analyzers tend to underestimate the parameters, and the linear regression showed a strong correlation between the two analyzers.

The significant reduction in parameter estimation and diagnostic perfor_x0002_mance we observed suggested that clinicians should interpret results from blood gas analyzers more cautiously. The reference interval of blood gas analyzers should be adjusted accordingly, given that values are underestimated.

PU-1826

血清钙磷比值在原发性甲状旁腺功能亢进的诊断效能研究

银梦婷[1]、李贵星[2]
1. 四川大学
2. 四川大学华西医院

目的 研究血清钙磷比值在原发性甲状旁腺功能亢进症中的诊断效能。
方法 收集 2015 年 1 月至 2020 年 12 月四川大学华西医院收治的诊断为原发性甲状旁腺功能亢进症并行甲状旁腺切除术患者 155 例和对照组 153 例，将实验组按照血钙水平，分为高血钙 A 组和血钙正常 B 组，比较各组患者的血钙、血磷、甲状旁腺激素、25 羟维生素 D 水平。通过 ROC 曲线，确定血清钙磷比值在诊断原发性甲状旁腺功能亢进中的诊断效能。通过斯皮尔曼相关，性分析探讨钙磷比值与 PTH 的关系。
结果 实验组血清钙磷比值高于对照组（P＜0.001）。钙磷比值用于诊断原发性甲状旁腺功能亢进症的最佳临界值为 2.94（AUC:0.993， 95%CI：0.976-0.998），敏感度和特异度分别为 95.5%（90.9-98.2）和 98.7%（95.4-99.8）。
结论 当钙磷比值＞2.94 时，我们可以很好的诊断原发性甲状旁腺功能亢进症。这一指标对于一些缺乏甲状旁腺激素检测的基层医院非常有帮助。

PU-1827

血浆纤维蛋白原水平与锁骨骨折术后骨不连的相关性研究

李明[1]、赵洁[2]、王蓉蓉[1]、范卫华[1]、董振芳[1]、张庆晨[1]、王大伟[1]、唐琪[1]、白晓卉[1]、卢志明[1]
1. 山东省立医院
2. 济南市中心医院

目的 锁骨骨折是一种常见的骨损伤类型，约占成人骨折的 5%，容易出现骨不连等并发症。血浆纤维蛋白原检查是一种评估手术安全性的常规术前检查。在本研究中，我们旨在评估锁骨骨折病人在接受切开复位内固定术后血浆纤维蛋白原水平与骨不连之间的关系。
方法 对 2010 年 1 月至 2019 年 5 月在山东第一医科大学附属省立医院创伤骨科收治并接受切开复位内固定术后的锁骨骨折患者的基线数据，包括性别、年龄、从受伤到手术的时间(Time from Injury to Surgery，TIS)、吸烟史、酗酒史、骨折原因、活动能力、是否畸形和美国麻醉师协会(American Society of Anesthesiologists，ASA 美国麻醉师协会)分级，以及实验室标记物（血浆纤维蛋白原水平、d -二聚体、凝血酶原时间、活化部分凝血酶时间）进行了回顾性分析。根据严格的诊断标准，患者根据随访结果分为两组：正常愈合组和骨不连组。对所有变量都进行了单变量分析。排除对血浆纤维蛋白原水平可能产生影响的混杂因素后开展多变量 Logistic 回归分析。构建平滑拟合曲线，以确定血浆纤维蛋白原水平和锁骨术后骨不连之间的相关性。
结果 研究共纳入锁骨骨折患者 251 例（男性 180 例，女性 71 例），其中正常愈合组 237 例，骨不连组 14 例。单变量分析表明，TIS（OR=1.21）和纤维蛋白原水平（OR=1.82）与骨不连的发生率显著相关（P<0.05）。多变量 Logistic 回归分析和平滑拟合曲线表明，无论有无混杂因素（患者年龄和 TIS），纤维蛋白原水平与骨不连（患者年龄和 TIS）发生显著正相关（OR>1）。
结论 血浆纤维蛋白原水平与锁骨骨折术后骨不连显著相关。

PU-1828

胱抑素 C 联合尿蛋白标志物检测在儿童过敏性紫癜早期肾损害辅助诊断中的价值探讨

毕婧
丹东市第一医院

目的 探讨血清胱抑素 C(Cys-C)联合尿蛋白标志物检测在过敏性紫癜（HSP）患儿早期肾损害诊断中的应用价值。
方法 对本院儿科门诊及住院 2018 年 9 月至 20120 年 9 月收治首次发作的 142 例 HSP 患儿[（按有无肾脏损害分为紫癜性肾炎组(HSPN 组，69 例）和 HSP 组,73 例）]和 70 例同期在本院健康体检的儿童（对照组）的血液样本和随机晨尿样本进行血清 Cys-C、尿视黄醇结合蛋白（URBP）、尿转铁蛋白（TRF)和尿 α1-微球蛋白（Uα1-MG）检测，采用 Minitab 17 统计学软件分析检测结果的差异。
结果 HSP 组 Cys-C、URBP、TRF 和 Uα1-MG 检测结果均高于对照组，组间比较差异有统计学意义（p＜0.05）；HSPN 组 Cys-C、URBP、TRF 和 Uα1-MG 检测结果显著高于 HSP 组，组间比较差异有高度统计学意义（p＜0.01）。Cys-C 检测水平与 URBP、TRF 和 Uα1-MG 检测水平呈正相关（r 值分别为 0.728，0.512,0.603，p 均＜0.05）。HSP 组和 HSPN 组联合检测的阳性检出率均高于各组单项检测的阳性检出率，比较差异有统计学意义（p＜0.05）；HSPN 组四项指标单项检测和联合检测阳性检出率均高于 HSP 组，比较差异有统计学意义（p＜0.05）.
结论 Cys-C、URBP、TRF 和 Uα1-MG 可作为判断儿童 HSP 早期肾损害重要的检测指标，通过血尿指标联检能明显提高 HSP 患儿肾损害的早期诊断阳性率和临床诊断准确性，为 HSP 的早期诊治、病情判断、预后等方面提供参考依据。

PU-1829

血清脂蛋白(a)检测在肾脏疾病诊断中的应用价值

孙昱
德州市陵城区人民医院检验科

目的 分析血清脂蛋白(a)检测在肾脏疾病诊断中的应用价值。
方法 选取自 2018 年 1 月至 2020 年 11 月在我院住院的患者。其中肾早期损害组 40 例，肾病综合征组 30 例，尿毒症组 32 例作为研究对象，另选 50 例健康体检者作为对照组。采用免疫透射比浊法检测血清脂蛋白(a)水平，分析其水平变化与肾病病变程度之间的关系及在临床中的应用价值。结果与健康对照组相比,肾早期损害组,肾病综合征组和尿毒症组 LP(a)水平升高,差异有统计学意义(P< 0.05);肾病综合征组与尿毒症组 LP(a)明显高于肾早期损害组，差异有统计学意义(P< 0.05)。
结论 血清 LP(a)在监测肾脏疾病患者病程进展上有重要意义,可作为肾脏疾病病变程度判断的一项有效指标。

PU-1830

两种不同样本急诊生化项目检测结果一致性及临床应用分析

张兴宗、林云、张清文、邹映东
云南省中医医院（云南中医药大学第一附属医院）

目的 探讨采用肝素抗凝血浆替代血清，在罗氏 Cobas c702 全自动生化分析仪上用于急诊生化项目检测，为临床更快速的提供检验报告，利于挽救患者生命。

方法 对门诊及住院急诊患者 125 例,采用常规方法采集静脉血 3ml 于未加抗凝剂的血清管中，作为对照组进行血清分离(血清样本组) ，采集静脉血 3ml 于含有肝素抗凝剂的血浆管中分离血浆作为试验组(血浆样本组)，应用罗氏 Cobas c702 全自动生化分析仪对两组样本的 18 项急诊生化项目进行检测及结果比较分析。

结果 两组样本检测结果显示：18 项急诊生化检测项目中，除了钾（K+）试验组低于对照组，差异有统计学意义(P＜0.05)外，其余 17 项生化急诊项目检测**结果** 天门冬氨酸氨基转移酶(AST)、肌酸激酶（CK）、肌酸激酶同工酶 MB(CK-MB)、乳酸脱氢酶(LDH)、肌钙蛋白 I（cTnI）、尿素氮(BUN)、肌酐（Cr）、尿酸（UA）、血糖（GLU）、 钠（Na+）、氯（Cl-）、钙（Ca）、磷（P）、镁（Mg）、二氧化碳（CO2）、超敏 C 反应蛋白（Hs-CRP）及淀粉酶（AMY)，结果比较差异均无统计学意义(P＞0.05) ,两组急诊生化项目检测结果间的相关系数和回归方程显示二者间存在较好的相关性。虽然试验组 K+低于对照组，差异有统计学意义(P＜0.05)，但 K+相关系数 r=0.942，具有较好的相关性，通过对检测结果一致性分析，18 项检测结果均在临床可接受范围内，表明检测结果具有一致性，可为临床提供准确的检验结果。

结论 肝素抗凝血浆在急诊生化检验中，其结果与血清检测结果具有一致性，抗凝血浆采样后可及时离心分离血浆，及时上机检测，快速为急诊患者提供准确可靠的检验报告，为临床医师在抢救、诊断、治疗过程中提供了宝贵时间，利于挽救患者生命。

PU-1831

血清 β-羟基丁酸检测在糖尿病酮症酸中毒临床诊断中的应用

陈涌泉
厦门弘爱医院

目的 探讨血清 β-羟基丁酸和血糖水平检测在糖尿病酮症酸中毒（diabetic ketoacidosis，DKA）临床诊断中的应用价值。

方法 纳入 2018 年 9 月至 2021 年 3 月就诊于我院的 I 型糖尿病患者 42 例、II 型糖尿病患者 50 例和健康对照人群 50 例作为研究对象；采集血液样本进行血清 β-羟基丁酸和血糖水平检测，同时记录糖尿病患者 DKA 发病情况；分析 I 型糖尿病患者和 II 型糖尿病患者、DKA 患者和非 DKA 患者血清 β-羟基丁酸和血糖水平差异，同时对糖尿病患者血清 β-羟基丁酸与血糖水平的相关性进行分析。

结果 经 Kruskal-Wallis 秩和检验，I 型糖尿病组血清 β-羟基丁酸和血糖水平均高于健康对照组和 II 型糖尿病组（P<0.05），II 型糖尿病组血清 β-羟基丁酸和血糖水平均高于健康对照组（P<0.05）；经卡方检验，I 型糖尿病患者 DKA 发病率高于 II 型糖尿病患者（P<0.001）；经 Kruskal-Wallis 秩和检验，I 型糖尿病和 II 型糖尿病中 DKA 患者血清 β-羟基丁酸和血糖水平均高于非 DKA 患者（P<0.05）；相关性结果显示 I 型糖尿病和 II 型糖尿病患者血清 β-羟基丁酸水平与血糖水平均存在明显的相关性（tI 型=0.740，PI 型<0.001，R2I 型=0.547；tII 型=0.575，PII 型<0.001，R2II 型=0.331）。

结论 I 型糖尿病患者血清 β-羟基丁酸和血糖水平升高幅度、DKA 发病率均高于 II 型糖尿病患者；I 型糖尿病和 II 型糖尿病 DKA 患者血清 β-羟基丁酸和血糖水平均高于非 DKA 患者；I 型糖尿病和 II 型糖尿病患者血清 β-羟基丁酸水平随血糖水平升高而升高。

PU-1832

运用功效函数图法设计部分生化项目的室内质控方案

张真铭
昆明医科大学第一附属医院

目的 结合昆明医科大学第一附属医院临床化学检验室的情况，利用功效函数图，选择合适的质控规则和质控测定个数，要求质控方案经济高效。
方法 确定本实验室生化检测项目的临床允许总误差（TEa），项目测定方法的不精密度（CV）和不准确度（Bias），计算临界系统误差（ΔSEc）并利用功效函数图，选择合适的质控规则和质控测定个数。
结果 不同生化检测项目的质控规则和质控测定个数不相同。
结论 根据实验室生化检测项目的临界系统误差，利用功效函数图选择最佳质控方案，即满足临床质量要求，达到期望的误差检出率且控制假失控概率，提高质控效率。

PU-1833

双相情感障碍抑郁相患者血清 CD38 和 TRPM2 浓度变化

唐亚梅[1]、周乐[2]
1. 中南大学湘雅二医院
2. 中南大学湘雅医学院检验专业

目的 研究双相情感障碍抑郁相患者血清 CD38 和 TRPM2 蛋白水平及铁代谢相关指标血清 TRF、NGAL、Fe 和 TIBC 的浓度变化，探讨上述指标与双相情感障碍抑郁相发生的关系及其临床意义。
方法 收集 2020 年 10 月至 2021 年 4 月于湘雅二医院精神科门诊就诊的 27 例双相情感障碍抑郁相患者的血清和汉密尔顿量表资料；同时收集 20 例于湘雅二医院体检中心体检的正常人血清，采用 ELISA 法测定血清样本中的 CD38 和 TRPM2 水平，应用 IMMAGE800 和 HITACHI7600-DDP 仪器检测血清转铁蛋白（TRF）、NGAL、铁（Fe）和 TIBC 的水平。
结果 双相情感障碍抑郁相患者血清 CD38（1006.57±118.06ng/ml）和 TRPM2（116.38±29.15 ng/ml）浓度较健康对照组（812.99±188.57ng/ml）和（49.78±18.62 ng/ml）均显著升高（P＜0.01），差异有统计学意义；NGAL（121.51±52.38 ng/mL）和 TIBC（54.89±7.90）较对照组（154.31±62.98 ng/mL）和（60.14±6.20）显著降低（P＜0.05），差异有统计学意义；Pearson 相关分析显示 TRF 与 HAMD 量表总分相关（P<0.05）。
结论 双相情感障碍抑郁相患者血清 CD38 、TRPM2 和 NGAL 水平及 TIBC 比值存在异常，上述指标与双相情感障碍抑郁相的发生有关。

PU-1834

免疫比浊法检测血液透析患者的血清白蛋白水平及白蛋白检测的干扰因素研究

黄文婷、赖婉婷、倪艳丽、蔡桂君、彭永正
南方医科大学珠江医院

目的 低白蛋白水平是影响进行血液透析的慢性肾脏病（CKD）患者预后的的重要因素之一。我们研究了免疫比浊法和溴甲酚绿法（BCG 法）检测此类患者血清白蛋白水平的差异情况，并对比了在血液透析前或透析后采集的血清标本的白蛋白结果，以确定合适的采集时间。

方法 收集 104 位 CKD 患者血液透析前和透析后的剩余血清标本，分别用免疫比浊法和 BCG 法进行白蛋白测定，并分析各种球蛋白对这两种血清白蛋白检测方法的影响，将结果绘制散点图、柱状图，进行配对 t 检验分析。
结果 免疫比浊法与 BCG 法检测的血清白蛋白结果呈线性相关。我们发现两种方法的差异随白蛋白浓度的变化而变化，血清白蛋白水平接近 37-38g/L 时，差异较小；白蛋白水平偏高或偏低时，两者差异逐渐？增大。两种方法检测的血液透析患者透析前或透析后白蛋白结果之间都有明显统计学差异（P＜0.0001）。免疫比浊法测定的透析前后血清白蛋白平均差值为 5.7g/L；BCG 法测定的平均差值为 4.7 g/L。本实验中两种方法测定透析后-透析前最大差值分别为 18.2 g/L（免疫比浊法）、14.9 g/L（BCG 法）。不同球蛋白组分对白蛋白检测结果的影响不同，不添加球蛋白时，两种方法的检测结果都与靶值一致；存在球蛋白时，两种检测方法的偏差都随着白蛋白浓度的升高而减小；球蛋白对免疫比浊法检测的干扰小于 BCG 法。
结论 对于低血清白蛋白的血液透析 CKD 患者，BCG 法检测的结果较免疫比浊法有明显偏差，而血清中的球蛋白是干扰因素之一，使用免疫比浊法检测的结果更准确。血液透析前与透析后白蛋白检测结果有显著差异，透析后血清白蛋白水平更适合用于血液透析 CKD 患者的营养评估。

PU-1835

山东地区 744 例儿童全血微量元素检测结果分析

徐艳秋
山东第一医科大学附属省立医院临床医学检验部

目的 了解山东地区儿童全血元素镁（Mg）、钙(Ca)、铁(Fe)、铜(Cu)、锌(Zn)的含量，为山东地区儿童生长发育情况进行评估及科学合理补充微量元素提供依据。
方法 对本院儿科 744 例儿童全血采用电感耦合等离子体质谱法（ＩＣＰ －ＭＳ）对进行 Mg、Ca、Fe、Cu、Zn 元素的检测，将受检儿童根据年龄不同分组分为三组：幼儿组（<3 岁，300 例)，其中男童 174 例，女童 126 例；学龄前组（<6 岁,252 例)，其中男童 163 例，女童 89 例；学龄组（<13 岁,192 例)，其中男童 142 例，女童 50 例。应用 SPSS19.0 统计学软件对检测结果按年龄和性别分别进行统计分析 。
结果 山东地区儿童各年龄组全血元素 Mg、Ca、Fe、Cu、Zn 的含量均值水平均在参考值范围内 ，但各组间均值水平的差异具有统计学意义(P＜ 0 .05) 。 微量元素 Mg、Ca、Fe、Cu、Zn 缺乏普遍存在，锌缺乏率最高，铁缺乏率第二，钙缺乏率次之，铜和镁水平异常率很低,年龄段越小 ,锌和铁缺乏率越高 ,各年龄组间锌和铁缺乏率的差异具有统计学意义(P＜ 0 .05)， 男女儿童之间缺乏率的差异无统计学意义(P＞ 0 .05)。
结论 山东地区儿童锌 、铁元素缺乏率较高 ,应加大对儿童微量元素的监测力度，大力加强儿童保健，均衡儿童营养，平衡膳食 ，做到及时合理的补充微量元素，保证儿童健康成长。

PU-1836

河南省孕期妇女同型半胱氨酸的水平以及同型半胱氨酸检测重要性

陈明
郑州金域临床检验中心有限公司

Hcy 是一种含巯基的氨基酸，主要来源于饮食摄取的蛋氨酸，是蛋氨酸和半胱氨酸代谢过程中一个重要的中间产物，其本身并不参加蛋白质的合成。Hcy 水平与心血管疾病密切相关。是心血管疾病发病的一个重要危险因子。血液中增高的 Hcy 因为刺激血管壁引起动脉血管的损伤，导致炎症和管壁的斑块形成，最终引起心脏血流受阻。高同型半胱氨酸尿症患者，由于严重遗传缺陷影响

Hcy 代谢，造成高 Hcy 血症。轻微的遗传曲线或 B 族维生素营养缺乏会伴随中度或轻度的 Hcy 升高，也会增加心脏病的危险。Hcy 升高还可引起神经管畸形及先天畸形等出生缺陷类疾病。

PU-1837

妊娠期糖尿病患者妊娠中期维生素 D 组分水平与妊娠中期及分娩前肾功能指标的相关性

冯跃
绵阳市中心医院

目的 有研究指出，25(OH)D 或 25(OH)D3 水平可能与肾功能相关，妊娠早期此二者水平也可能与妊娠期糖尿病(gestational diabetes mellitus, GDM)相关。然而，妊娠中期 25(OH)D 或 25(OH)D3 水平与 GDM 相关性以及其肾功能变化的相关性少有报道。本研究的目的旨在探究妊娠中期维生素 D 组分 25(OH)D2、25(OH)D3、25(OH)D、25(OH)D2 与 25(OH)D3 的比值 D2/D3 与 GDM 的相关性，以及与 GDM 患者妊娠中期与分娩前的肾功能指标的相关性。
材料与方法 招募 GDM 患者与同期健康妊娠者(healthy pregnant, HP)(两组均为单胎妊娠)，于妊娠中期用液相色谱-串联质谱(liquid chromatography-tandem mass spectrometry, LC-MS/MS)的方法检测其血清维生素 D 组分水平，并检测第一次血清肾功能指标尿酸 Urea、 尿肌酐 Creat、 血糖 GLU、 尿酸 UA、胱抑素 C(cys C)、肾小球滤过率 GFR，于产前入院时检测其第二次血清肾功指标。维生素 D 状态根据 25(OH)D 水平分为三组(A 组,充足: 25(OH)D≥30ng/ml; B 组,不足: 20≤25(OH)D<30ng/ml; C 组, 缺乏:25(OH)D<20ng/ml)。
结果 本研究共纳入 GMD 组 77 例，HP 组 121 例。两组的年龄、妊娠中期采样时孕周、总孕周均无显著性差异(Table 1)。孕中期 GDM 组 25(OH)D2、GLU 水平显著高于 HP 组(p=0.008)，但 25(OH)D3、25(OH)D、D2/D3、Urea、 Creat、 UA、cysC、GFR 水平在两组间无显著性差异(Table 1)。此外，HP 组维生素 D 不足的比例显著高于 GDM 组（p=0.037）(Table 1)。除 Urea 外，分娩前 GDM 组与 HP 组的肾功能各指标水平无显著性差异(Table 2)。分娩前与妊娠中期相比，GDM 组与 HC 组均有 Urea、 Creat、 UA、cysC 显著升高，GFR 显著性降低（all p<0.05）(Table 2)。
结论 妊娠中期 GDM 患者 25(OH)D2 水平显著高于健康妊娠者，但 25(OH)D3、25(OH)D、D2/D3 水平两组无显著差异。两组妊娠晚期肾功能指标较妊娠中期均显著降低，但在两组间无显著性差异(Urea 除外)。结果表明，妊娠中期 25(OH)D2 可能与 GDM 相关。妊娠中期 25(OH)D2 与 GDM 可能均不是影响妊娠中期及晚期肾功能的显著因素。

PU-1838

HCPT 对肿瘤细胞增殖、细胞凋亡、细胞周期影响及作用机制的研究

胡洪华
四川省医学科学院·四川省人民医院

目的 观察羟基喜树碱对肿瘤细胞周期、细胞增殖及细胞凋亡的影响；选择多种既有不同特征的肿瘤细胞为研究对象；探讨 HCPT 对 Bcl-2 家族基因表达水平的影响，研究 HCPT 对肿瘤细胞凋亡的分子机制。
方法 羟基喜树碱处理 A549 细胞后用 CCK-8 法检测 HCPT 对细胞增殖，吖啶橙/溴化乙锭（AO/EB）染色观察细胞形态学变化，琼脂糖凝胶检测 DNA 片段化，用流式细胞仪测定其对细胞周期影响。利用 Annexin V-FITC/PI 检测细胞凋亡，RT-PCR 检测凋亡相关基因 Bcl-2 的表达变化。

结果 CCK-8 结果表明不同浓度的 HCPT 对肿瘤细胞的生长抑制作用不同;HCPT 对不同肿瘤细胞的抑制细胞增殖效应不相同。HCPT 处理的 pc12 细胞和 A549 细胞的琼脂糖凝胶电泳可见调亡细胞 DNA 的梯状条带,荧光显微镜下观察到经 AO/EB 染色的典型凋亡细胞，FCM 提示这种抑制作用可能与细胞周期与细胞凋亡有关;HCPT 对 H22 细胞的抑制效果不明显。
结论 HCPT 对肿瘤细胞有生长抑制作用有选择性,对不同的肿瘤细胞的抑制机制也不相同；HCPT 可抑制 pc12 和 A549 细胞增殖，诱导细胞凋亡,其细胞凋亡与细胞周期分布有关;HCPT 对 H22 细胞无生长抑制作用,无凋亡作用,未见其干扰细胞分裂周期作用;HCPT 对肿瘤细胞的抑制作用存在细胞特异性。

PU-1839

联合检测尿微量白蛋白与尿肌酐比值和血胱抑素 C 的必要性

邱洪
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 探讨评价肾功能损伤时,联合检测 UmAlb/UCr 与 Scys-C 值的必要性。
方法 分别收集符合条件的病人尿液和对应的血清标本,散射比浊法测定出病人尿液标本 UmAlb 值,肌氨酸氧化酶法测出 UCr 值,参考美国糖尿病联合会（ADA）的糖尿病临床指南,将病人血清标本按照尿 mAlb/UCr 比值进行粗略分组，乳胶散射增强免疫比浊法测出各血清胱抑素 C（Scys-C）值。应用 SPSS19.0 统计学软件作 t 检验等统计学方法分析各组间血胱抑素 C（Scys-C）值间差异有无统计学意义,并对各组中所得的尿 mAlb/UCr 比值和血胱抑素 C（Scys-C）作 Spearman 相关性检验分析其相关性,探究在评价肾功能损伤时,联合检测 UmAlb/UCr 与 Scys-C 值的必要性。
结果 各组间血胱抑素 C（Scys-C）值间差异有统计学意义,各组中所得的尿 mAlb/UCr 比值和血胱抑素 C（Scys-C）没有相关性。
结论 在评价肾功能损伤时,联合检测 UmAlb/UCr 与 Scys-C 值有很大的必要性。

PU-1840

血清高敏肌钙蛋白 I、心肌酶及白介素-6 联合检测在慢性心衰患者心功能评价中的应用价值

吉永、杜如佳
昆明市延安医院

目的 探讨血清高敏肌钙蛋白 I（cTnI）、心肌酶及白介素-6（IL-6）联合检测在慢性心衰患者心功能评价中的应用价值。
方法 选择 2021 年 2 月至 2021 年 5 月在昆明市延安医院心内二科 33 例慢性心衰患者作为研究组，根据心功能分级分为心功能 I 级、II 级、III 级、IV 级共四组，另选择同期在该院排除慢性心衰等疾病的门诊病人 10 例作为对照组，分别对五组进行 cTnI、心肌酶及 IL-6 等指标进行联合检测，分析上述指标与 NYHA 心功能分级的相关性，同时分析联合检测的特异性和敏感性，为慢性心衰的诊断提供依据。
结果 研究组 BNP 水平均明显高于对照组，差异有统计学意义（P<0.05）；研究组 cTnI、心肌酶和 IL-6 水平均明显高于对照组，差异有统计学意义（P<0.05）。研究组 cTnI 与心功能分级呈正相关关系（r>0）；心肌酶、IL-6 与心功能分级差异有统计学意义（P<0.05），呈正相关关系（r>0），其中 CK、IL-6 与心功能分级呈低度相关(0.3<r<0.5)，CK-MB、AST、LDH 与心功能分级呈中度相关（0.5<r<0.8）。cTnI、IL-6 对慢性心衰诊断价值较低（0.5<AUC<0.7），心肌酶对慢性心衰无诊断价值（AUC<0.5），差异均无统计学意义（P>0.05）。

结论 慢性心衰患者 cTnI、心肌酶及 IL-6 水平明显高于正常健康人群，联合检测上述指标，其水平随慢性心衰患者心功能分级严重程度而升高，联合检测可提示心功能受损程度，但对 CHF 无诊断价值。

PU-1841

血清可溶性 PD-1 在预测急性胰腺炎感染并发症中的临床价值

杨海燕
江苏连云港市第一人民医院新海院区

目的 临床急性胰腺炎(AP)患者中约有 15%-20%发展为严重急性胰腺炎(SAP)或中度急性胰腺炎(MSAP)伴局部或全身并发症，在中、重度患者中，感染并发症(ICS)高达 40%-70%，导致死亡率明显升高。因此，早期鉴别 ICS 具有重要的临床价值。许多研究表明，血清可溶性程序性细胞死亡蛋白(sPD - 1)或程序性细胞死亡 1 配体 sPD-L1 含量变化在严重脓毒症患者中可以预测死亡的能力。然而，血清 sPD-1/sPD-L1 在 AP 中是否有同样的的作用尚不清楚，本研究旨探讨血清 sPD-1/sPD-L1 是否可以预测 AP 患者发生 ICS 死亡率。
研究方法 研究对象为本院临床确诊的 65 例 MSAP 和 SAP 患者，其中男 35 例，女 30 例，年龄 52.21±14.51 岁；同时选择 31 例健康体检自愿者作为对照组。应用 ELISA 法检测血清 sPD-1 和 sPD-L1。对危险因素进行单因素和多因素回归分析，并于 APACHE II 评分进行比较。
结果 AP 患者在术后第 1、3 和 10 天的血清 SPD-1 水平与对照组比较显著升高（P<0.01）。AP 合并 ICS 患者血清 SPD-1 水平高显著高于无 ICS 的 AP（266.03 ± 130.37 185.17 ± 78.79，P<0.01）。而 AP 血清中的 SPD-L1 水平与健康对照组比较，P>0.05。ROC 曲线下面积为 0.826。单因素和多因素回归分析均显示升高的血清 SPD-1 水平是 AP 中 ICS 的独立危险因素。
结论 在 AP 患者中，血清 SPD-1 水平可能是一个独立危险因素，在预测 AP 患者 ICS 发生具有一定的临床价值。

PU-1842

化学发光微粒免疫分析法检测 PIVKA-II 的性能评价

杨佳
四川省医学科学院·四川省人民医院

目的 用化学发光微粒免疫分析法（CMIA）测定血清维生素 K 缺乏或拮抗剂Ⅱ诱导的蛋白质（PIVKA-II）从而了解其检测性能。
方法 用雅培公司的 ARCHITECT 系统 i2000SR 化学发光分析仪,使用配套的试剂、校准品和质控品，参照美国临床和实验室标准化研究院（CLSI）推荐的相关文件要求对该项目检测方法的精密度、准确度、线性范围、携带污染率、灵敏度等进行评价，并验证其参考值区间[1]；
结果 (1)CMIA 法测定 PIVKA-II 的批内和批间精密度，三水平的批内及批间精密度的 CV 值均小于 5.0%；(2) PIVKA-II 的准确度测定值与靶值的偏倚在 0.88%～5.60%之间；(3) PIVKA-II 的线性范围在 0～5000pg/ml 间呈良好的线性关系，$R^2 = 0.998$ ；(4)携带污染率实验中，PIVKA-II 表现出良好的抗污染能力；(5) PIVKA-II 检测的分析灵敏度（最低检测限）在厂家提供的范围之内；（6）PIVKA-II 的参考值区间的验证，均符合厂家提供的参考范围。
结论 CMIA 法测定 PIVKA-II 的结果评价其精密度和准确度、线性、抗干扰能力、携带污染率、灵敏度，均表现出良好的性能结果，满足临床要求。

PU-1843

围绝经期女性 25（OH）D3 水平与血脂、血糖的相关性研究

潘俊希
昆明医科大学第一附属医院检验科
云南省检验医学重点实验室
云南省实验诊断研究所

目的 探究围绝经期女性 25（OH）D3 水平与血脂、血糖的关系，为女性围绝经期管理提供科学理论依据。
方法 收集到本院体检的围绝经期女性 295 例,记录其年龄、身高、体重、收缩压（SBP）、舒张压（DBP）,饮食及运动情况,月经情况及改良 Kupperman 评分表等。测定 25（OH）D3、血糖（FPG）、甘油三酯（TG）、总胆固醇（TC）、高密度脂蛋白胆固醇（HDL-C）、低密度脂蛋白胆固醇（LDL-C）、维生素 A（VA）、红细胞（RBC）、尿酸指标（UA）。
结果 维生素 D3 水平缺乏 74 例（25.1%）,不足 115 例（39.0%）,正常 106 例（35.9%）;TG、LDL-C、FPG 水平呈负相关。25（OH）D3 不足组血脂异常患病危险是适宜组的 1.6 倍（95% CI:1.05-2.6）,25（OH）D3 缺乏组血脂异常的患病危险是适宜组的 2.3 倍（95%CI:1.52-3.3）。
结论 围绝经期女性 25（OH）D3 不足组与缺乏组 TG 异常和 HDL-C 异常率均高于适宜组，25（OH）D3 水平与 TG、LDL-C 水平相关,且 25（OH）D3 缺乏组血脂异常患病的独立危险因素。

PU-1844

二型糖尿病引发的骨相关疾病的诊断

高乐
湘西土家族苗族自治州人民医院

随着大众的生活水平逐渐提高，对于饮食追求呈现新的特点：糖与脂肪的摄入日益升高，现在已普遍出现摄入过量现象，而由此引发以二型糖尿病、高脂血症等相关疾病。根据之前的大量研究表明，二型糖尿病与心脑血管疾病和骨相关疾病都息息相关，其中对于骨骼危害极大。糖类摄入过多会通过以下方式影响骨代谢：首先，糖类物质可通过氧化应激干扰骨代谢，先前的研究表明，二型糖尿病患者中的糖基化终产物 (AGEs)和同型半胱氨酸水平都异常升高由此造成骨细胞和成骨细胞不同程度的的功能障碍，并且其中可能与 AMP 依赖的蛋白激酶（Adenosine 5‘-monophosphate (AMP)-activated protein kinase，AMPK）有关， AMPK 作为生物体内一种重要的能量代谢感受器，受血糖波动影响较大，并会通过一些氧化应激反应影响骨代谢，从而导致骨关节炎、骨质疏松症等骨相关疾病，因此 AMPK 作为糖与骨代谢的至关枢纽，在机体内的糖代谢中发挥着重要作用。其次，胰岛素也会影响骨代谢。二型糖尿病的影响因素之一就是胰岛素抵抗，胰岛素作为一种降低血糖的重要激素，也会通过一系列的信号通路调节骨形成和骨吸收，而最近的研究表明，生物体内的骨骼和胰岛素抵抗之间似乎存在一种双边关系，当机体内血糖浓度过高时，胰岛 β 细胞会分泌大量的胰岛素来降低血糖，同时激活相关细胞通路对骨骼产生一定影响。而在一些骨质疏松症和骨关节炎患者的体内，又能发现胰岛素样生长因子 (IGF)的相对增高，而 IGF1 的生理作用是促进生长和发育以及刺激细胞增殖，骨骼和胰岛素之间的这种双边关系对于骨平衡也维持着一定作用。最后，糖代谢与脂代谢。机体摄入过度的糖类物质后，胰岛素会通过将其转换为其他物质来降低血糖，其中一类主要物质就是脂肪。骨细胞是由骨髓间充质干细胞分化而来，而骨髓间充质干细胞作为一种具有多项分化潜能的干细胞，也能分化为脂肪细胞、神经细胞、破骨细胞等，而有研究表明，当小鼠持续高糖饮食后，就可能会引起体内成骨分化减弱、成脂分化增强，导致骨细胞数量减少，骨合成过程减弱，另一方面，破骨细胞的大量分化也会破坏骨平衡，使破骨过程大于成骨过程，从而出现骨密度降低、骨脆性增加等一些列骨质疏松等症状，同时还会引发二型糖尿病。综上所述，这些

研究都表明了糖类物质可通过各种途径对骨代谢和骨平衡造成不同程度的影响和破坏，而现有诊断二型糖尿病的检测手段与方法都已经不适合现代的待诊人群，应该将氧化应激水平、胰岛素抵抗相关指标以及成骨成脂分化相关因子结合起来，并与骨相关疾病的生化指标与影像学结果联结，为二型糖尿病引发的骨相关疾病提供新的联合诊断思路和模式。

PU-1845

潍坊地区孕期妇女碘营养状况监测分析

于北凯
潍坊市中医院

目的 了解 2019 年潍坊地区孕期妇女碘营养情况，为指导优生优育提供依据。
方法 以 2019 年 1 月至 2019 年 12 月来我院进行产前检查的孕期妇女为研究对象，检测其尿碘浓度，并对结果进行分析。
结果 共收集到符合条件的尿液标本 2510 份，尿碘浓度均值为 179.7 ug/L，中位数为 181.0ug/L，其中尿碘浓度<150 ug/L 的占 33.35%，150~249 ug/L 的占 54.22%，≥250 ug/L 的占 12.43%；群体年龄分布 19~44 岁，各年龄组间尿碘值无统计学差异；孕早期群体尿碘中位数为 199.0 ug/L，孕中期为 185.0 ug/L，孕晚期为 162.0 ug/L，随着孕期进展，尿碘水平呈降低趋势。
结论 潍坊地区孕期妇女总体碘营养状况尚可，但仍存在较大比例的碘缺乏群体，需要加大宣传力度，采取有效措施，保证孕妇特别是孕晚期妇女的碘营养充足。

PU-1846

探讨 CKMB(活性法)/CK 在感染轮状病毒患儿中诊断心肌损伤的应用价值

赵丽娜
潍坊市中医院

目的 探讨 CKMB/CK 在感染轮状病毒患儿中诊断心肌损伤的应用价值，从而减少轮状病毒患儿心肌损伤的过度诊断。
方法 选取本院 2021 年 1 月到 2021 年 5 月腹泻患儿 40 例，采集新鲜大便，用胶体金法检测轮状病毒，其中轮状病毒阳性者 20 例为观察组，轮状病毒阴性者 20 例为对照组。分别于早晨空腹抽血，避免标本溶血，检测 CKMB、CK，计算 CKMB 与 CK 比值，并进行统计分析。
结果 CKMB/CK 在轮状病毒阳性组和阴性组差异有统计学意义。
结论 CKMB/CK 在感染轮状病毒患儿中诊断心肌损伤有临床价值，通过 CKMB/CK 的检测可以减少轮状病毒患儿心肌损伤的过度诊断。

PU-1847

血气分析仪 ABL800 检测电解质、乳酸与 生化分析仪 Cobas702 检测结果的相关性和差异性分析

杨武发、杨文秀、崔华、蔡冬竹
贵州医科大学附属医院

目的 由于血气分析仪 ABL800 检测项目和生化分析仪 CobasC702 在电解质和乳酸项目上是相同的，但一直存在差异，本次回顾性分析旨在比对两者检测结果的相关性和差异性。为临床报告解读提供可靠实验室数据。
方法 回顾性分析本院住院患者 33 例，每个患者皆进行血气分析（ABL800）和生化电解质和乳酸(Cobas702)的检测。包括钠离子（Na+）、钾离子（K+）、氯离子（CL-）、乳酸（Lac）、碳酸氢根离子（HCO3-）检测，依据其检测结果随机分为低值、中值、高值三个组，每个组 11 例。参照临床实验室标准化协会 EP9-A2 文件，进行 pearson 相关性分析和配对样本 T 检验。
结果 两种检测仪器的差异性分析 雷度 ABL800 与罗氏 Cobas702 检测结果如下：A 组 K+、CL-、Lac、HCO3-结果比较，差异均有统计学意义（ P＜0.05）。B 组 Lac 结果比较,差异具有统计学意义（P＜0.05）。C 组 Na+、CL-结果比较差异均有统计学意义（P＜0.05）。相关性分析 雷度 ABL800 与罗氏 Cobas702 检测结果的回归相关分析显示，A 组 K+、CL-、Lac、HCO3-结果比较差异均有统计学意义（P＜0.05）。 B 组 Na+、HCO3-结果比较差异均有统计学意义（P＜0.05）。C 组 Na+、K+、CL-、Lac、HCO3-结果比较差异均有统计学意义（P＜0.05）。
结论 血气分析仪和生化分析仪在电解质和乳酸检测上，两者的相关性和差异性并不那么显著。在电解质检测中，当两者结果出现很大差异时，检测结果应以生化分析仪结果为准，血气分析仪结果作为参考。乳酸检测中，当检测结果低值和高值时，血气分析仪检测更加准确及时。

PU-1848

羟基喜树碱对肺癌 A549 细胞抑制作用的初步研究

胡洪华
四川省医学科学院·四川省人民医院

目的 研究羟基喜树碱对肺癌 A549 细胞生长抑制、细胞周期和细胞凋亡的影响。
方法 用 CCK-8 试剂盒(cell counting kit - 8)法测定羟基喜树碱对肿瘤细胞的生长抑制作用，吖啶橙/溴化乙锭(AO/EB)染色观察细胞形态变化情况，琼脂糖凝腔电泳验证细胞调亡的特征性 DNA 条带，用流式细胞仪测定一定浓度下不同作用时间抗癌药物羟基喜树碱对细胞凋亡和细胞周期的影响。
结果 不同浓度的羟基喜树碱对肿瘤细胞的生长抑制作用不同，羟基喜树碱可明显抑制 A549 细胞的生长，琼脂糖凝胶电泳可见调亡细胞 DNA 的梯状条带，经 AO/EB 染色，荧光显微镜下观察到早期凋亡细胞细胞核被染成绿色，呈碎片状，晚期凋亡细胞核染色质为橘红色并呈固缩状或圆珠状，细胞周期 S 期由 20%升高到 60%。经 1μmol/L 羟基喜树碱处理 24 h 后，流式细胞术显示 A549 细胞的凋亡率为 18.11%，明显高于对照组细胞凋亡率（0.09%， P<0.05）。
结论 羟基喜树碱对 A549 细胞有生长抑制作用，可诱导 A549 细胞细胞凋亡，其细胞凋亡与细胞周期分布有关。

PU-1849

高血脂对临床生化检验结果的影响与解决方法

郭群
南京鼓楼医院

目的 分析和探究高血脂对临床生化检验结果的干扰及消除方法。
方法 选择我院 2020 年 9 月～2020 年 10 月临床生化检验的 70 例高脂血症患者 (设为实验组) 以及同期 80 例血脂正常人员 (设为对照组) 作为研究对象, 比较两组受试人员血清标本经乙醚提纯前后送检的检验结果。
结果 实验组血清标本经乙醚提纯前后送检的检验结果显示， 生化检验项目中的 ALT、AST、Cr、TP、TB 水平对比具有明显差异 (P<0.05) ，且提纯前明显偏高，GGT、CK 水平对比无显着差异 (P>0.05) ；对照组血清标本经乙醚提纯前后送检的检验结果显示，生化检验项目中的 ALT、AST、Cr、TP、TB、GGT、CK 水平对比均无显着差异 (P>0.05) 。
结论 对照组血清标本经乙醚提纯前后, 各生化检验结果无显着变化，说明血清标本经乙醚提纯后不影响以上生化检验结果。实验组血清标本经乙醚提纯前多项生化检验结果受高血脂干扰而偏高，而经乙醚提纯后, 各生化结果均有明显下降, 说明了乙醚提纯能够有效消除脂血对临床生化检验项目造成的干扰。

PU-1850

血清胰岛素样生长因子-1（IGF-1）的动态监测对心梗患者经皮冠状动脉介入治疗（PCI）后的临床意义

沈东海
潍坊市中医院

目的 分析心肌梗塞（AMI）患者经皮冠状动脉介入治疗(PCI)后，血清中胰岛素样生长因子（IGF-1）的变化水平，为临床检测心梗患者术后恢复状况提供新的生物学标志物。
方法 前瞻性研究，连续入选 2021 年 7 月至 2022 年 1 月潍坊市中医院心血管病科心梗患者 80 例作为实验组，同期入选无心梗患者 30 例为对照组。在患者入院时采集血样标本，送至医学检验科采用全自动化学发光法检测肌红蛋白、肌酸激酶、肌酸激酶同工酶、肌钙蛋白 I 和肌钙蛋白 T 等血清学指标；同时对患者的进行心脏血管造影或心脏彩超等影像学诊断作为患者心肌梗塞的临床指征。我们采用全自动化学发光法检测心梗患者和对照组患者血清中胰岛素样生长因子（IGF-1）的水平。80 例心梗患者中我们收集采取经皮冠状动脉介入治疗(PCI)后的心梗患者的血清，检测肌红蛋白、肌酸激酶、肌酸激酶同工酶、肌钙蛋白 I 和肌钙蛋白 T 等血清学指标以及监测患者心脏彩超等影像学指标作为心梗患者经皮冠状动脉介入治疗(PCI)后恢复的临床指征，同时继续检测患者血清中胰岛素样生长因子（IGF-1）的水平。
预期**结果** 在入院时，心梗患者与无心梗患者的血清中 IGF-1 的水平存在明显差异。心梗患者经皮冠状动脉介入治疗(PCI)后，血清中 IGF-1 的水平较未采取 PCI 治疗的心梗患者存在显著差异。
结论 血清胰岛素样生长因子（IGF-1）可作为评估心梗患者经皮冠状动脉介入治疗(PCI)后恢复的生物学标志。

PU-1851

利用尿碘评价孕期妇女碘营养状况的研究进展

于北凯
潍坊市中医院

甲状腺激素参与机体多种代谢过程的调节，是人体内的重要激素，其合成需要碘元素的参与，碘缺乏或碘过量均会引起甲状腺激素水平异常进而影响身体健康。妊娠期作为一个特殊时期，机体的激素水平和碘营养需求在此期会发生变化。加强关于孕妇碘营养的研究对优生优育至关重要，目前，评价孕妇碘营养状况的指标主要有孕妇尿碘检测、孕妇血清甲状腺功能指标检测、孕妇甲状腺体积测量以及新生儿足跟血促甲状腺激素测定等，其中以孕妇尿碘检测应用最为广泛。

本文将针对利用尿碘评价孕妇碘营养状况的研究，从判断标准、尿液留取和检测方式、检测方法学等方面进行综述。

PU-1852

女性高尿酸血症与血脂血糖的相关性研究

潘俊希
昆明医科大学第一附属医院检验科
云南省检验医学重点实验室
云南省实验诊断研究所

目的 通过了解体检人群生化指标、糖代谢相关指标，调查女性高尿酸血症患病率，探讨女性高尿酸血症的危险因素，以及血尿酸升高与糖、脂代谢异常的相互关系。
方法 收集 2019 年间我院体检人群的资料，包括基本资料、既往病史、饮食情况和用药史等，采集静脉血后全自动生化分析仪检测血尿酸、血脂、血糖等指标。采用统计分析软件 SPSS 22.0 进行统计分析。
结果 共检出女性高尿酸血症 243 例，检出率为 2.3%，女性高尿酸的患病率随着年龄的增加呈上升趋势（18～29、30～39、40～49、50～59、60～69 和≥70 岁组的 HUA 患病率分别为 0.6%、0.7%、1.1%、2.9%、3.5%和 5.8%）。高尿酸血症组中高胆固醇血症、高甘油三酯血症、空腹血糖升高的检出率均高于血尿酸正常组，差异有统计学意义（P＜0.05）。多重线性回归分析，TG、TC、空腹血糖均与血尿酸水平呈正线性相关。
结论 女性血脂异常和血糖代谢紊乱与高尿酸血症密切相关，高脂血症、血糖代谢紊乱是高尿酸血症的危险因素。女性尿酸血症检出率随年龄增加而升高，应针对性的开展宣传教育，倡导合理饮食，积极锻炼，养成良好的生活习惯，以期能有效控制高尿酸血症的患病率。

PU-1853

标本放置时间对血糖检测的影响

赵苓旭
川北医学院附属医院

目的 探讨标本放置时间对血糖检测结果的影响；
方法 将肝素抗凝全血与同一健康体检者的肝素抗凝血浆设为对照（共 21 组检测标本），分别测定标本在放置 30min、1h、2h、3h 后的血糖值；
结果 （1）血浆组：30min 后的测量结果与 2h 的测量结果无明显差异，与 3h 的测量结果有差异(p〈0.05)；（2）全血组：30min 后的测量结果与 1h 的测量结果有差异（p〈0.05），与 2h 的测量结果有差异（p〈0.001）；

结论 血糖检测结果随标本放置时间增加而降低，2h 后血糖含量开始下降，放置 3h 后血糖检测结果显著降低，提示血糖检测标本至少应在 3h 内完成测定，以保证检测结果的可靠性。

PU-1854

Estimation of 24 hour urine protein excretion using urine creatinine/albumin ratio

Xin Liu [1]、Yonghong Zhao[2]、Daqing Hong[1]、Yunlin Feng[1]
1. Department of Laboratory Medicine, Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China
2. 四川大学

Purpose To study the correlation between 24 hour urine protein excretion (24h UPE) and urine creatinine/albumin ratio (ACR) and develop a prediction model for 24h UPE.
Methods All individuals with paired urine ACR and 24h UPE tested on the same day in Sichuan Provincial People's Hospital during September 1st, 2018 to December 31st, 2019 were enrolled. Correlation and agreement between urine ACR and 24h UPE were evaluated. A prediction model of 24h UPE was further developed and validated.
Results 671 subjects were identified. Urine ACR had a good correlation with 24h UPE in general population (Spearman's coefficient = 0.939; p<0.001) but the agreement between these two measurements was not consistently good (overall ICC = 0.870; 95% CI: 0.849-0.888; p<0.001). Our multivariable transform model of 24h UPE had good performance (R2=0.829) and validated high accuracy (RMSE=0.0227, rRSME=3.1%).
Conclusions Urine ACR has a good correlation with 24h UPE in general population but is not a reliable surrogate for 24h UPE. Our prediction model is a useful tool for estimating 24h UPE, however, 24h UPE is still mandatory in situations when accurate quantification of proteinuria is required.

PU-1855

孕妇糖化血红蛋白水平对新生儿低血糖发病风险的影响

杨富强
襄樊市第一人民医院

目的 探讨孕妇糖化血红蛋白（HbA1c）水平对新生儿低血糖及阈值低血糖发病风险的影响。
方法 选取 2016 年 12 月至 2018 年 10 月该院收治的 375 例孕妇作为研究对象，根据血清 HbA1c 水平分为 3 组，A 组 HbA1c 为＜5.5％，317 例；B 组 HbA1c 为 5.5％～6.5％，49 例；C 组 HbA1c 为＞6.5％，9 例。观察并记录新生儿出生 1、4、8h 血糖值，分析新生儿低血糖及阈值低血糖发生率。
结果 C 组与 B 组新生儿出生后 1h 低血糖发生率明显高于 A 组，差异有统计学意义（P＜0.05）；C 组新生儿出生后 4、8h 低血糖发生率明显高于 A 组与 B 组，差异具有统计学意义（P＜0.05）。A 组与 B 组新生儿出生后 1、4、8h 低血糖发生率随时间延长逐渐下降，差异有统计学意义（P＜0.05）。C 组与 B 组新生儿出生后 1、4、8h 阈值低血糖发生率明显高于 A 组，差异具有统计学意义（P＜0.05）。A 组新生儿出生后 1h 阈值低血糖发生率明显高于 4、8h，差异有统计学意义（P＜0.05）；B 组新生儿出生后 1、4h 阈值低血糖发生率明显高于 8h，差异有统计学意义（P＜0.05）。
结论 妊娠期孕妇 HbA1c 水平升高会增加新生儿低血糖及阈值低血糖发病风险。

PU-1856

TEG 和 CCTs 在急性胰腺炎患者病情评估中的价值

杨林飞[1]、陆珊[2]
1. 湖南省人民医院
2. 湖南师范大学医学院

目的 分析血栓弹力图联合凝血四项常规指标在急性胰腺炎患者病情评估中的价值。
方法 选取湖南省人民医院 2020 年 8 月～2021 年 4 月诊治入院的急性胰腺炎患者 84 例为研究对象。根据临床诊断的病情严重程度分为轻症急性胰腺炎组 44 例与重症急性胰腺炎组 40 例，另外选取同期体检的健康志愿者 18 例作为对照组。检测所有研究对象的血清 C 反应蛋白，生化指标脂肪酶，血栓弹力图指标血块成型时间(K)、血凝时间(R)、血块强度(MA)、血凝块形成起始点至描记图最大曲线弧度做切线与水平线所成夹角（α 角）及凝血常规四项指标活化部分凝血活酶时间(APTT) 、凝血酶时间(TT) 、纤维蛋白原(Fib) 及凝血酶原时间(PT)。
结果 轻症急性胰腺炎组、重症急性胰腺炎组生化指标脂肪酶、血清 C 反应蛋白、血凝时间(R)、血块成型时间(K)较健康对照组高，血块强度（MA）、α 角较健康对照组低，且重症急性胰腺炎组生化指标脂肪酶、血清 C 反应蛋白、血凝时间(R)、血块成型时间(K)较轻症急性胰腺炎组高，血块强度（MA）、α 角较轻症急性胰腺炎组低（P＜0.05）；轻症急性胰腺炎组、重症急性胰腺炎组纤维蛋白原（FIB）、凝血酶原时间(PT)、凝血酶时间(TT)、活化部分凝血酶原时间（APTT）均较健康对照组高，且重症急性胰腺炎组纤维蛋白原、凝血酶原时间、凝血酶时间、活化部分凝血酶原时间较轻症急性胰腺炎组高（P＜0.05）。
结论 临床可根据生化指标脂肪酶、血清 C 反应蛋白、血栓弹力图、凝血四项指标检测结果评估急性胰腺炎患者病情程度，初步对 AP 患者炎症浸润程度和微循环障碍情况进行了解，以期对 AP 的病情严重程度进行判断以及把握病情的演变，对早期预防和治疗 SAP 提供依据。

PU-1857

奇怪的胎儿血红蛋白峰：胎母输血综合征 2 例报告

卢妮娜、叶雅丽、杨再兴、阮荣华
台州市第一人民医院

目的 探讨应用 Tosoh HLC-723 G8 糖化仪检测产妇血中胎儿血红蛋白(fetal hemoglobin,HBF)的浓度联合甲胎蛋白以快速辅助诊断胎母输血综合征(fetomaternal hemorrhage syndrome, FMH)的可行性。
方法 收集临床怀疑 FMH 的新生儿 2 例，采用 Tosoh HLC-723 G8 糖化仪高效液相色谱法（HPLC）来检测患者母血术前、产后第 5 天、第 10 天的 HBF 以及血清甲胎蛋白，同时收集手术当天五位剖宫产出后血红蛋白≥170g/L 的新生儿作为正常对照，检测其母血的 HBF 值以及甲胎蛋白。
结果 HPLC 图谱示病例 1 母血术前有较高 HBF 峰，HBF 为 5.1%，甲胎蛋白(AFP)为 1600.36ng/ml，产后第 5 天，第 10 天测得 HBF 分别下降至 4.8%和 4.5%；病例 2 母血术前 HBF 为 2.8%，甲胎蛋白(AFP)为 2747.69ng/ml，产后第 5 天，第 10 天测得 HBF 分别下降至 1.7%和 0.7%。患者母血的 HbF 值比正常妊娠者明显升高，排除 HBF 遗传性增高，结合临床症状以及 AFP 结果，可以诊断为 FMH。
结论 Tosoh HLC-723 G8 糖化仪检测的 HBF 联合甲胎蛋白是可供选择的快速辅助诊断 FMH 的方法。

PU-1858

A noninvasive diagnostic model for significant liver fibrosis in patients with chronic hepatitis B based on CHI3L1 and routine clinical indicators

Qingyong Huang、Jianhua Wu、Chunse Huang、Xiuli Wang、Zhenxing Xu
Xiamen Hospital of Traditional Chinese Medicine

Background In consideration of the limitations of liver biopsy, the past years have seen a great advance in the application of noninvasive indices in assessing liver fibrosis. However, the accuracies of the existing indices to determine liver fibrosis in patients with chronic hepatitis B (CHB) are still unsatisfactory. Here, we established a noninvasive diagnostic model for assessing significant liver fibrosis (SLF) in CHB patients based on serum chitinase 3-like 1 (CHI3L1) and routine clinical indicators.

Methods A total of 537 CHB patients who had received a liver biopsy at Xiamen Hospital of Traditional Chinese Medicine from December 1, 2019, to September 30, 2020 enrolled in this study. Overall, 173 patients were excluded base on exclusion criteria, 27 patients were excluded due to insufficient data; 337 patients were included as the eventual participants in this cross-sectional study. All the included cases were randomly divided into a training cohort (n=270) and a validation cohort (n=67). The training cohort was further divided into a non-significant liver fibrosis (NSLF) group (stages S0–S1; n=189; used as the control group) and an SLF group (stage S2–S4; n=81) based on the Scheuer scoring system. Univariate and multivariate logistic regression analyses were performed to screen for independent predictors of SLF in CHB patients and to establish a diagnostic model.

Results The results of univariate and multivariate logistic regression analysis showed that CHI3L1, AFP and PLT were independent predictors of SLF in CHB patients, and the diagnostic model was established as follows: CHI3L1/AFP/PLT (CAP) = 0.600 × CHI3L1/upper limit of normal (ULN) + 0.252 × AFP/ULN– 1.424 × PLT/lower limit of normal (LLN) – 1.223. The area under the receiver operating characteristic (AUROC) of this model for the diagnosis of SLF in the training cohort and the validation cohort was 0.805 and 0.819, respectively, showing no statistically significant difference (P>0.05), and the AUROC for the diagnosis of SLF in the whole cohort was significantly higher than those of other noninvasive markers including aspartate transaminase to platelet ratio index (APRI), fibrosis 4 score (FIB-4) and CHI3L1 (all P<0.05). CAP was further applied to the staging of liver fibrosis. The Jonckheere-Terpstra trend test revealed that the CAP value tended to increase gradually with the severity of liver fibrosis (Ptrend<0.001) and had a good correlation (Spearman correlation coefficient: 0.486). Dunn's test for paired comparisons showed CAP had good performance in distinguishing S2–S4 from S0–S1; however, the difference in CAP among S2, S3, and S4 was not statistically significant. The efficacy of CAP in diagnosing SLF (S2–S4) was also analyzed in subgroups with different ALT levels and HBeAg statuses. It was found that the AUROCs of CAP in diagnosing SLF were not significantly different among the 3 ALT subgroups [≤ULN, (1–2) × ULN, and >2×ULN] and between the HBeAg-positive and HBeAg-negative subgroups.

Conclusions The newly established model has a good diagnostic efficacy for SLF in CHB patients and is superior to other noninvasive markers including APRI, FIB-4, and CHI3L1. Thus, it can be used as a noninvasive diagnostic index for liver fibrosis in CHB patients.

PU-1859

四川某大型三甲医院体检人群异常空腹血糖分析

廖凤慧
电子科技大学附属医院 四川省人民医院临床医学检验中心

目的 分析体检人群中异常空腹血糖的检出情况，为人群血糖异常的防治提供一定的思路。
方法 收集 2020 年 1 月 1 日到 2020 年 12 月 31 日于四川省人民医院体检中心行空腹血糖检测的体检者的血糖结果。
结果 共收到 14366 名体检者的空腹血糖测定结果，其中女 6568 名，男 7798 名。14366 名体检者中，低血糖阳性率为 1.10%，其中男女分别为 1.20%和 1.03%；空腹血糖受损患者阳性率为 4.88%，其中男女分别为 5.80%和 3.19%；糖尿病的阳性率为 4.50%，其中男女分别为 6.19%和 2.41%；其中，春季（3 月,4 月和 5 月）空腹血糖受损阳性率（5.12%）和糖尿病阳性率（5.65%）明显高于其他三季（3.93%、4.86%和 4.55%，4.34%、4.76%和 4.93%）。随着年龄的增加，低血糖的阳性率逐渐降低，且男女的差距逐渐增大；而空腹血糖受损和糖尿病的随着年龄的增大，阳性率逐渐增加，男性明显多于女性。
结论 对于各个年龄阶段的人群，筛查空腹血糖都具有重要意义。对于青年人群，低血糖的发生不容忽视，而对于中年和老年人群，尤其是对男性，空腹血糖受损和糖尿病是关注的重点。春季空腹血糖受损阳性率和糖尿病阳性率相对较高可能与春节饮食有关。

PU-1860

Trimethylamine N-oxide and its nutrient precursors are differently associated with cardiovascular risk factors and kidney function

Yan Song、Jie Zhang、Li Zhao
Renji Hospital affiliated to Shanghai jiaotong university school of medicine

Objective We analyzed the association of plasma trimethylamine N-oxide (TMAO) and its nutrient precursors with cardiovascular risk factors and kidney function in humans.
Method A total of 318 individuals were included in our study. Plasma concentrations of free TMAO, choline, L-carnitine, and betaine were measured with the use of liquid chromatography–tandem mass spectrometry (LC-MS/MS). Plasma crea, urea and uric levels were assessed with the use of Hitachi 7600. Multiple linear regression and spearman correlation test were used to analyze the associations of plasma concentrations of TMAO and TMAO-related compounds with kidney function.
Results Participants were 59% male with an average age of 44±10. Older age was significantly associated with high concentrations of carnitine, choline, TMAO and betaine (ρ=0.222, P<0.001; ρ=0.246, P<0.001; ρ=0.139, P=0.013; ρ=0.179, P=0.001; respectively). Being male was significantly associated with high levels of carnitine, choline, and betaine (ρ=0.359, P<0.001; ρ=0.283, P<0.001; ρ=0.241, P<0.001; respectively). The difference in plasma TMAO levels between men and women was NS (ρ=0.359, P=0.438). The Higher concentrations of Carnitine and choline were correlated with characteristics of both an unfavorable cardiovascular risk-factor profile (lower HDL cholesterol, and higher triglycerides and NHDL) and kidney markers (higher urea, crea and uric). Moreover, TMAO was significantly positively associated with triglycerides, urea, crea and uric.
Conclusion TMAO and its dietary precursors choline and carnitine have differential associations with cardiovascular risk factors and kidney markers.

PU-1861

绝经相关的宫颈癌差异甲基化位点的筛选及关联基因的初步分析

王蓉、杨金豪、张文帆
天津医科大学医学检验学院

目的 筛选与绝经相关的宫颈癌差异甲基化位点，并分析其关联基因的功能。
方法 从 TCGA 数据库提取 307 例宫颈癌患者的 450k 甲基化芯片数据和临床信息；采用 R 软件处理分析数据，对甲基化位点 β 值采用 Wilcoxon 秩和检验，筛选未绝经组和绝经组异常的甲基化位点，对其差异位点基因采用 GO、KEGG、STRING 数据库分析其功能和信号通路。
结果 共检出未绝经组、绝经组的差异明显甲基化位点 7 个(P.adjust<0.05)，分别位于 5 个基因(KAZN、AC069368.1、SEMA6A-AS2、SUSD1、miR-99a)。GO 和 KEGG 分析，上述基因有蛋白质结合，钙离子结合分子功能，参与 miRNA 沉默基因通路，负向调控白介素-6 介导的信号通路和负向调控 STAT 级联通路等。STRING 分析发现差异基因编码的蛋白之间没有相互作用，KAZN 的作用蛋白是 PPL、EVPL、PKP1，AC069368.1 的作用蛋白是 MED10，SUSD1 的作用蛋白是 MFSD2B、TMEM245、KIAA0368、ZNF462、ZNF483。
结论 未绝经和绝经的宫颈癌患者存在差异甲基化位点和基因，它们的主要功能与蛋白结合，信号通路有关。结合 TCGA 数据库和 R 语言可用于绝经相关的差异甲基化位点的初步筛选。

PU-1862

超氧化物歧化酶在甲状腺癌和结节性甲状腺肿外周血中的意义

徐艳秋
山东第一医科大学附属省立医院临床医学检验部

目的 研究超氧化物歧化酶(superoxide dismutase,SOD)在甲状腺癌和结节性甲状腺肿外周血中的活性水平。
方法 收集甲状腺癌患者 84 例、结节性甲状腺肿患者 21 例和正常人对照组 63 例，酶法检测外周血清中 SOD 活性，电化学发光法检测游离甲状腺原氨酸（FT3）、游离甲状腺素（FT4）、促甲状腺激素（TSH）水平，分析各组 SOD 活性差异及 SOD 活性与甲状腺激素相关性。
结果 甲状腺癌组 SOD 活性（164.536±18.095 U/ml）、结节性甲状腺肿组 SOD 活性（157.667±15.189 U/ml）和正常人对照组 SOD 活性（179.529±11.625 U/ml），甲状腺癌组和结节性甲状腺肿组 SOD 活性分别低于正常人对照组，差别有统计学意义（$p<0.05$）。甲状腺癌组 FT3、FT4 水平与 SOD 活性成呈正相关（$r=0.346$ $p<0.05$，$r=0.3278$ $p<0.05$），正常人对照组 FT3 水平与 SOD 活性成呈负相关（$r=-0.5522$ $p<0.05$）。
结论 甲状腺发生结节和肿瘤后 SOD 活性降低，观察 SOD 活性变化可了解甲状腺组织损伤的情况并作为甲状腺肿瘤发生辅助指标。

PU-1863

在甲状腺功能亢进和甲状腺功能低下外周血中超氧化物歧化酶的意义

徐艳秋
山东第一医科大学附属省立医院临床医学检验部

目的 研究超氧化物歧化酶(superoxide dismutase,SOD)在甲状腺功能亢进和甲状腺功能低下外周血中的意义。

方法 收集甲状腺功能亢进患者 75 例、甲状腺功能低下患者 56 例和正常人对照组 63 例，酶法检测外周血清中 SOD 活性，电化学发光法检测游离甲状腺原氨酸（FT3）、游离甲状腺素（FT4）、促甲状腺激素（TSH）水平，分析各组 SOD 活性差异及 SOD 活性与甲状腺激素相关性。
结果 甲状腺功能亢进症组 SOD 活性（173.376±15.942 U/ml）、甲状腺功能低下症组 SOD 活性（174.827±19.895 U/ml）和正常人对照组 SOD 活性（179.529±11.625 U/ml），甲状腺功能亢进组与甲状腺功能低下组、甲状腺功能亢进组与正常人对照组、甲状腺功能低下组与正常人对照组之间 SOD 活性差别均无统计学意义（$p>0.05$）。正常人对照组 FT3 水平与 SOD 活性成呈负相关（$r=-0.5522$ $p<0.05$）。
结论 通过本研究我们发现当甲状腺功能亢进和甲状腺功能低下时 SOD 活性变化不大。

PU-1864

BECKMAN AU5800 型全自动生化分析仪检测免疫球蛋白的性能评价

徐艳秋
山东第一医科大学附属省立医院临床医学检验部

目的 评价 BECKMAN AU5800 型全自动生化分析仪检测血清免疫球蛋白的性能评价。
方法 评估 AU5800 生化仪检测血清免疫球蛋白的性能评价的正确度、精密度、线性范围、可报告范围、参考区间。
结果 AU5800 型全自动生化分析仪检测血清免疫球蛋白的性能评价的正确度取室间质评的样本进行比对，结果 SDI≤2 符合要求；依据卫生部室间质量评价标准批内精密度小于允许总误差 CV 的 1/4、批间精密度小于允许总误差 CV 的 1/3，结果均符合要求；线性范围采用线性回归分析线性方程 $Y=Ax+b$，a 值在 0.97-1.03 范围内，相关系数 $r2>0.95$,则线性范围符合要求；可报告范围以 80%≤R≤120%为可接受限，对应的稀释倍数为最高稀释倍数；参考区间依据中华人民共和国卫生行业标准“临床实验室项目参考区间的制定”（WS/T402-2012）文件要求，R≥90%符合要求。
结论 德赛诊断试剂在 AU5800 型全自动生化分析仪上的检测性能均可接受，符合要求。具有检测快、准确性高、可靠性好，可满足本实验室要求，适用于临床需求。

PU-1865

过敏性紫癜患儿尿蛋白/肌酐比值与 24 小时尿蛋白定量关系及其临床应用的研究

司文
山东省立医院

目的 研究过敏性紫癜患儿随机尿蛋白/肌酐比值与 24 小时尿蛋白之间的定量关系，探讨过敏性紫癜患儿随机尿蛋白/肌酐比值的临床应用价值
方法 测定测定 104 例过敏性紫癜患儿的 24 小时尿蛋白总量,随机尿样本中尿蛋白肌酐含量,计算尿蛋白肌酐比。收集患儿相关数据,分析 24h 尿蛋白总量与尿蛋白肌酐比之间的相关性。
结果 随机尿蛋白/肌酐比值与 24 小时尿蛋白定量之间有良好
的相关性，24h 尿蛋白总量与尿蛋白肌酐比的相关系数 $r=0.65$($P<0.01$),随机尿蛋白/肌酐比值作为反映过敏性紫癜患儿蛋白质的排泄情况，效果良好。
结论 随机尿蛋白/肌酐比值能够反映过敏性紫癜患儿蛋白质的排泄情况，可以替代 24 小时尿蛋白测定应用于临床。

PU-1866

乙肝病毒 DNA 与两对半及血清 ALT 之间关系的探讨

兰星宇、李霞
新疆兵团第一师医院

目的 研究乙肝病毒 DNA 与两对半及血清 ALT 之间关系，并且通过对其数据结果进行分析，从而可以找到最佳的治疗方案。
方法 选取 2018 年 7 月至 2019 年 7 月来我院就诊的乙肝病毒患者为研究对象，通过问卷调查并筛选后选取 130 例乙肝病毒患者为研究对象，对病毒的 DNA 定量与两对半及血清中的 ALT 进行检测，并根据相应的指标对结果进行分析。
结果 通过检测结果得出，其中经过两对半检测结果为大三阳、小三阳的患者，HBV DNA 定量检测的阳性率为 55.38%，97.25%，数据差异明显，具有统计学意义（P<0.05）。
结论 通过上述对比分析研究，其中乙肝病毒 DNA 定量与两对半及血清 ALT 之间有密切的关系，在今后的临床治疗中可以联合的治疗使用。

PU-1867

维生素 C 对临床化学检测项目的干扰分析

张华、李燕、赵红光、孙艳、兰星宇
新疆兵团第一师医院

目的 研究分析维生素 C 对 ADA、ALP、AST、CR、FMN、GGT、Mg 7 个临床化学检测项目的干扰。
方法 将 40 例新鲜的血清标本，混合成 ADA、ALP、AST、CR、FMN、GGT 和 Mg 的高、低两个浓度标本。参考 EP7-A2 文件制备干扰物维生素 C 贮存液，通过“配对差异”试验对维生素 C 影响 ADA、ALP、AST、CR、FMN、GGT 和 Mg 项目检测结果进行筛查确认。对 ADA、CR、FMN 干扰确定时, 则进一步采用“剂量关系 ”试验分析维生素 C 干扰物浓度与对 ADA、CR、FMN 干扰情况二者间关系。
结果 50mg / d L 维生素 C 对 ADA、CR 高、低浓度干扰效应点估计值大于 cut off 值（dobs>dc），50mg / d L 维生素 C 对 FMN 高、低两个浓度干扰效应点估计大于值 cut off 值（dobs>dc）。维生素 C 对 ADA 测定呈线性负干扰，对肌酐（Cr）测定呈线性负干扰，对 FMN 测定呈线性正干扰。
结论 维生素 C 对 ADA、CR 测定存在负干扰，对 FMN 测定存在正干扰，而且与维生素 C 干扰物质浓度呈线性关系，所以在临床诊断和治疗过程中需关注病人服用维生素 C 情况

PU-1868

利用基于拉曼光谱的无标记血清检测诊断和分级胶质瘤

张晨曦
首都医科大学附属北京天坛医院

胶质瘤是中枢神经系统最常见的恶性肿瘤可导致严重的死亡和发病,相对准确无创地诊断胶质瘤诊断具有重要意义

在这项研究中，我们使用拉曼光谱学鉴别神经胶质瘤患者与健康人群。

血清样本采自 86 名健康个体，脑胶质瘤[高级别胶质瘤(HGG) n = 75，低级别胶质瘤(LGG) n = 60]。用 785nm 波长的激光采集了所有的光谱/n 射程 400-1800 立方厘米-1/n。每个样本共录得三个光谱每个频谱被积分 12 秒，平均超过 5 秒积累主成分分析和线性判别分析结合模型对不同基

团的拉曼光谱进行了分类。正常组、hGG 组和 LGG 组的正确分类率分别为 95.35% 、93.33% 、93.34% ,总准确率为 94.12%。鉴别 HGG 组和正常组的敏感性，特异性和准确性分别为 96.00% 、96.51% 和 96.27%，曲线下面及未 0.997。鉴别 LGG 组与正常对照组的敏感性、特异性、准确性分别为 96.67% 、98.84% 、98.84%，97.95% ，曲线下面积为 0.999。我们的研究提出基于拉曼光谱的主成分分析和线性判别分析，可以快速无创对早期胶质瘤进行诊断

PU-1869

新型冠状肺炎患者实验室生化指标检测结果的评价

邢小平
安徽省铜陵市人民医院

目的 探讨感染新型冠状肺炎患者肝功能和肾功能的变化。
方法 整理 2020 年元月-2020 年 2 月收治住院的确诊新型冠状肺炎和一般肺炎患者肝功能和肾功能资料，比较两类肺炎患者导致肝功能和肾功能的变化与区别。
结果 在肝功能指标上，新型冠状肺炎患者的总胆红素（TBIL）、直接胆红素（DBIL）、总蛋白（TP）、白蛋白（ALB）、谷丙转氨酶（ALT）、谷草转氨酶（AST）、碱性磷酸酶（ALP）与一般肺炎患者存在显著差异（P＜0.05），但是两类肺炎患者的 r-谷氨酰转肽酶（r-GT）差异并不显著（P＞0.05）。在炎症指标上，新型冠状肺炎患者的 C-反应蛋白（CRP）与一般肺炎患者存在显著差异（P＜0.05），但是两类肺炎患者的肾功能指标差异并不显著。
结论 新型冠状肺炎会对患者的肝脏造成一定的影响并引起相关炎症。

PU-1870

24h 尿蛋白定量与随机尿 ALB/CR 一致性分析

张鹏[1]、李志豪[2]
1. 南方医科大学南方医院
2. 南方医科大学检验与生物技术学院

目的 探究 24h 尿蛋白定量（24hUTP）与随机尿白蛋白肌酐比（Alb/Cr）一致性。
方法 选取南方医院 2020 年 11 月至 2021 年 4 月的患者 164 例，收集所有患者的 24 小时尿及近一两天内的某一次随机尿测定 24hUTP 和随机尿 ALB/CR，使用 GraphPad Prism 5 软件进行统计分析，对患者的 24hUTP 和随机尿 ALB/CR 的进行 spearman 相关性分析并进行回归分析得出随机尿 Alb/Cr 预测 24hUTP 的预测方程，采用 ROC 曲线分析法得出在不同尿蛋白水平下随机尿 Alb/Cr 预测 24UTP 的最佳临界点。
结果 24hUTP 和随机尿 Alb/Cr 的 spearman 相关系数 r=0.8216（P＜0.0001），存在显著相关关系，且按照申请科室分组其相关性也显著。根据散点图构建随机尿 Alb/Cr 预测 24hUTP 的预测方程 lg（24hUTP）=1.2143lg(Alb/Cr)+1.3273。根据正常临界值及 KDIGO 指南定义 24 小时尿蛋白定量的三个临界点，即 24hUTP＞0.14g/24h、＞0.5g/24h、＞1g/24h、＞3.5g/24h，做 ROC 曲线分析得随机尿 Alb/Cr 得最佳诊断临界值为＞ 2.735mg/mmol 、＞ 11.16 mg/mmol 、＞ 19.96 mg/mmol、＞38.20 mg/mmol。
结论 24hUTP 和随机尿 Alb/Cr 的相关性良好，可用随机尿 Alb/Cr 预测 24hUTP。重点分析的内分泌科糖尿病患者中，可用随机尿 Alb/Cr 替代 24hUTP 作为门诊病患的随访及定期筛查。而对于产科子痫前期的患者，其相关性受多种关系影响而低于整体，但也可应用随机尿 Alb/Cr 代替 24hUTP 作为紧急情况下如用于早发型重型子痫前期病人以提供及时快速的诊断帮助临床。

PU-1871

血清 CD5L 水平在肝纤维化进展中的临床价值研究

杨澜
中国人民解放军空军军医大学第二附属医院

目的 探讨巨噬细胞凋亡抑制因子-CD5L 作为新型血清生物标志物在肝纤维化中的变化，及其鉴别诊断价值。
方法 本研究纳入 41 例慢性肝炎、21 例肝硬化、171 例肝硬化失代偿、69 例肝癌（HCC）、23 例自身免疫性肝炎（AILD）患者和 136 例健康对照（HC）。采用 ELISA 方法测定血清 CD5L 水平。利用全自动生化分析仪测定血清肝功指标总蛋白（TP）、白蛋白（ALB）、球蛋白（GLO）、白球比（A/G）、总胆红素（T-BIL）、直接胆红素（D-BIL）、间接胆红素（I-BIL）、谷丙转氨酶（ALT）、谷草转氨酶(AST)、碱性磷酸酶(ALP)、总胆汁酸（TBA）水平。并测定了血小板（PLT）、国际标准化比值（INR）的水平。同时采用 Spearman 相关性分析对 CD5L 和以上指标进行分析。
结果 肝硬化患者血清 CD5L 水平（52.79(IQR 32.22-140.7)ng/ml）明显低于健康对照组（208.85(IQR 141.22-326.72)ng/ml）（p<0.0001）、肝炎患者（89.65(IQR 52.65-304.6)ng/ml）(p=0.0268)和肝癌患者（112.22(IQR 46.02-306.87)ng/ml）(p=0.0331)。相关性分析结果显示：在肝炎患者中，CD5L 与 PLT（r=0.45,p=0.01）,T-BIL(r=0.37,p=0.02),D-BIL（r=0.39,p=0.01）and I-BIL(r=0.35,p=0.02) 显著相关，但与其他指标无明显相关。肝硬化患者中，CD5L 与 TP（r=0.51,p=0.02）显著相关，与其他指标无明显相关。肝癌患者中，CD5L 与 ALP（r=0.66,p<0.0001）强相关。
结论 与健康对照和肝炎患者相比，CD5L 在肝硬化患者中显著降低，可作为一种新型血清生物标志物鉴别诊断肝纤维化。

PU-1872

心肌标志物在 COVID-19 患者风险分级和管理中的意义

张静、夏欣一
中国人民解放军东部战区总医院

目的 发现敏感且可靠的 COVID-19 患者的早期预警生物标志物，以优化管理和改善预后。
方法 选取 2954 例 2 月 4 日至 4 月 10 日在武汉火神山医院就诊的 COVID-19 患者。入院后测定血清心肌标志物。记录冠状动脉疾病诊断及生存情况。对不同分类的非 COVID-19 患者进行单细胞 RNA 测序，分析 SARS-CoV-2 受体表达情况。
结果 2954 例 COVID-19 患者的年龄中位数为 60 岁（50-68 岁），其中重症/危重症 1515 例（51.3%）。与轻症/中症患者（1439 例，48.7%）相比，重症/危重症患者入院 1 周内血清心肌标志物水平明显升高。在这些病人中，血清 BNP（42[24.6%] vs 7 [1.1%]）,hs-TNI（38[48.1%] vs 6[1. 0%]）,α- HBDH（55[10.4%] vs 2[0.2%]）,CK-MB（45[36.3%] vs 12[0.9%]）,和 LDH（56 [12.5%] vs 1[0.1%]）水平异常的患者死亡率明显高于这些指标正常的患者。ICU 入院率也有相同的趋势。患有冠状动脉疾病（CAD）的重症/危重症患者（165/1155 [10.9%]）相比那些没有 CAD 的患者更有可能有异常指标：BNP（52 [46.5%] vs 119 [16.5%]）, hs-TNI（24[26.7%] vs55（9.6%）,α- HBDH（86[55.5%] vs 443 [34.4%]）,水平（27 [17.4%] vs 97[7.5%]）,和 LDH（65[41.9%] vs 382 [29.7%]）。CAD 患者 SARS-CoV-2 受体表达较健康对照组增强。回归分析显示，有 5 项心肌指标升高的患者有更高的死亡风险（危险比 3.4 [95% CI 2.4-4.8]）。
结论 既往有 CAD 的 COVID-19 患者心脏标志物的异常百分比较高，死亡率和 ICU 入院率较高。值得注意的是，未患冠心病且心脏标志物水平异常的 COVID-19 患者的死亡率也很高。BNP 与 hs-TNI、α-HBDH、CK-MB 和 LDH 联合可作为第 1 周高死亡风险早期预警的预后生物标志物，因为

入院后第 1 周及住院期间心脏标志物水平异常的患者可能预示病情恶化或进展。(本文部分内容已发表于 Crit Care， IF=6.407)

PU-1873

叶酸水平与脑卒中的相关性研究

张云芳
昆明市延安医院医学检验科

目的 探讨血清叶酸（folate）水平与脑卒中发生的相关性，为脑卒中的预防、筛查、病情变化、预后提供更多的监测指标。
方法 选择脑卒中患者 40 例作为卒中组，46 例健康体检人群作为对照组。所有检测项目均质控在控。叶酸（folate）使用化学发光法进行测定，血脂中总胆固醇(totalcholesterol，TC)、甘油三酯（total triglyceride,TG）采用氧化酶法测定，高密度脂蛋白胆固醇(highdensity lipoproptein,HDL-C)采用抗体阻碍均相法测定，低密度脂蛋白胆固醇(lowdensity lipoproptein,LDL-C)采用表面活性剂清除法测定。检测结果用统计学软件 spss23.0 进行 t 检验、线性回归分析及 ROC 曲线分析。
结果 卒中组血清叶酸（8.11±3.92）μg/L 较对照组血清叶酸（11.79±5.68)μg/L 明显降低，差异具有统计学意义(P<0.05)。卒中组血清 TG(1.56±1.03) mmol.L-1 浓度较对照组 TG(1.11±0.26) mmol.L-1 浓度高，卒中组 HDL-C(1.13±0.36)mmol.L-1 较对照组 HDL-C(1.51±0.34) mmol.L-1 降低，差异具有统计学意义(P<0.05)。卒中组 TC（4.24±1.07）mmol.L-1、LDL-C（2.56±0.96）mmol.L-1 浓度较对照组 TC（4.52±0.37）mmol.L-1、LDL-C（2.61±0.37）mmol.L-1 变化不明显，差异无统计学意义(P>0.05)。卒中组的血清叶酸水平与年龄、性别、血脂（TG、TC、HDL-C、LDL-C）指标均无显著相关(P>0.05)。
结论 脑卒中患者血清叶酸（folate）水平低于健康人，叶酸的低水平与脑卒中的发生相关。

PU-1874

肝损伤对 COVID-19 患者疾病进展和临床结局的影响

吴秋月、夏欣一
中国人民解放军东部战区总医院

目的 SARS-CoV-2 感染与肝功能障碍和肝脏损伤密切有关。本研究旨在评估肝损伤对 COVID-19 患者疾病进展及临床结局的影响。
方法 共纳入武汉市火神山医院 COVID-19 重症或危重症患者 1520 例，包括 127 例慢性肝病患者，其中 64 例乙肝患者，20 例丙肝患者，37 例脂肪肝患者和 6 例肝硬化患者。收集这些患者的年龄、性别、基础疾病、肝功检验结果、临床治疗及预后等数据进行统计分析。利用 scRNA-seq 数据和大量基因表达谱数据识别不同类型患者肝脏组织中与 SARS-CoV-2 病毒结合的受体靶标 ACE2 和 TMPRSS2 的表达差异。收集实验室指标建立了风险评分系统，预测住院期间肝损伤的风险和严重程度。
结果 10.98% 的重症或危重症 COVID-19 患者在入院后出现肝损伤，并有较高的死亡率（21.74%，p<0.001）和 ICU 入住率（26.71%，p< 0.001）。既往携带有慢性肝病的 COVID-19 患者并未有更高风险的病死率和疾病严重程度。相反，脂肪肝和肝硬化 COVID-19 患者疾病进展更严重，这一结果被 scRNA-seq 数据和大量基因表达谱数据所证实，这些患者肝脏组织中携带有更多与 SARS-CoV-2 结合的受体靶标 TMPRSS2+ 细胞，更易于被 SARS-CoV-2 感染。根据入院后 3 天内进行的 22 项常规实验室检查建立了风险评分系统，成功预测住院期间肝损伤的风险[AUC：95%CI；0.85（0.83-0.88）]和严重程度[AUC：95%CI；0.92（0.89-0.95）]。

结论 治疗过程中发生肝损伤及既往有脂肪肝和肝硬化基础病的 COVID-19 患者，具有更高的疾病严重程度和病死率。基于 ALT、AST、LDH 和 CRP 等指标建立的一个风险评分模型，可以预测 COVID-19 患者在住院期间是否发生肝损伤或进入高风险阶段。（本文部分内容已发表于 Hepatol Int，IF=5.102）

PU-1875

不同保养方案对贝克曼 AU5821 全自动生化分析仪电解质

胡帅、何仁栋
川北医学院附属医院

目的 探讨两种不同保养方案对贝克曼 AU5821 全自动生化分析仪电解质分析紧密度以及电极稳定性和使用寿命的影响。
方法 采用两个不同方案对贝克曼 AU5821 全自动生化分析仪电解质模块进行日常维护保养，收集不同浓度血浆样本重复测定，评估批内及批间紧密度，同时观察电极的稳定性和使用寿命。
结果 本研究发现采用维护保养方案一的情况下，钾、钠和氯三个项目的批内及批间紧密度分别为 0.789，0.677，0.664 和 0.800，0.684，0.674，均优于方案二（0.791，0.681，0.671 和 0.84，0.718，0.724）。同时采用维护保养方案一的情况下，钾、钠和氯三个项目校准结果的均数和变异系数分别为 56.49，54.34，52.36 和 0.50，0.50，0.67，均优于方案二（51.46，50.63，48.64 和 1.36，1.07，1.70）。并且电极使用寿命（方案一：10 个月左右，方案二：6 个月左右）。
结论 在实际使用贝克曼 AU5821 全自动生化分析仪的过程中，应当根据实验室具体情况建立最佳的日常维护保养方案从而保障检验过程的高效，保证检验结果的精确。

PU-1876

家兔急性肠系膜缺血模型血清髓过氧化物酶活性变化

雷燕、唐伟、胡帅、王黎、郭斌
川北医学院附属医院

目的 观察家兔急性肠系膜缺血(Acute mesenteric ischemia，AMI)模型血清中髓过氧化物酶(myeloperoxidase，MPO) 活性变化与 AMI 组织病理学和影像学评分之间的相关性，探讨 MPO 活性在 AMI 疾病病程中作为实验室诊断指标的可能性。
方法 选用 3 个月左右月龄新西兰兔 21 只，随机分为对照组、假手术组、缺血 0.5h 组、1h 组、2h、4h 和 6h。采用手术结扎肠系膜上动脉根部制备 AMI 模型，小肠和盲肠放回腹腔，按标准程序缝合手术切口。在各规定时间点进行 CT 扫描、采血及切取肠组织，分别进 AMI 的影像学评分、HE 染色病理组织学 Park/Chiu 评分，检测血清 MPO 活性。
结果 与对照组和假手术组比较，兔 AMI 模型组各时相血清中 MPO 活性逐渐升高(P<0.05); 缺血组血浆 MPO 值与肠组织缺血损伤的病理学评分呈正相关（相关系数 R 为 0.76，P<0.05）；缺血组血浆 MPO 值与与肠道缺血损伤的 CT 影像学评分呈正相关（相关系数 R 为 0.79, P<0.05）。
结论 随着 AMI 兔模型缺血时间延长和缺血损伤的肠组织 Park/Chiu 评分和影像学评分增加，血清中 MPO 活性也逐渐增加，血清 MPO 活性的检测可以作为一个早期的 AMI 疾病的实验室诊断标志物之一。

PU-1877

尿 NGAL 与血 CysC 在系统性红斑狼疮肾损伤中的诊断价值

李海英
湖南中医药大学第一附属医院

目的 探讨尿中性粒细胞明胶酶相关脂质运载蛋白（uNGAL）和血清胱抑素 C（CysC）对系统性红斑狼疮肾脏病变的早期诊断价值及临床意义。
方法 收集 103 例 SLE 患者，据尿白蛋白/肌酐比（ACR）分成 3 组，正常白蛋白尿组（NA）33 例，ACR<30mg/mg；微量白蛋白尿组（MA）36 例，ARC 30~300mg/mg；大量白蛋白尿组（CA）34 例，ACR≥300mg/mg。同时选取 30 例健康体检者作为健康对照组（NC）。留取血及尿液标本，用乳胶增强免疫比浊法测 uNGAL，用免疫比浊法测血清 CysC。
结果 SLE 患者的 uNGAL 和血清 CysC 水平，除 NA 组与 NC 组之间无差异（P>0.05），其他各组间两指标的差异均有统计学意义（P<0.01），且 CA 组的 uNGAL 和血清 CysC 均明显高于 MA 组（0.85±0.38 vs 0.47±0.29，P<0.01；2.54±1.59 vs 1.44±0.51， P<0.01）；诊断微量白蛋白尿 SLE 时，uNGAL 和血清 CysC 的 AUCROC 分别为 0.54、0.65，特异度和敏感度分别为 19.9%和 73.5%，39.1%和 100.0%；判断大量白蛋白尿 SLE 时，uNGAL 和血清 CysC 的 AUCROC 分别为 0.89、0.85，特异度和敏感度分别为 74.3%和 100.0%，60.4%和 90.9%。
结论 uNGAL 和血清 CysC 在 SLE 患者肾脏病变的早期诊断与病情监测中均具有重要意义。其中，CysC 对早期诊断更灵敏，而 NGAL 更利于病情监测。

PU-1878

甘胆酸检测试剂盒的性能验证

部小霞[1]、龚俊[2]
1. 中日友好医院
2. 北京九强生物技术有限公司

目的 验证北京九强生物技术股份有限公司甘胆酸检测试剂盒的性能。
方法 根据厂家的说明书和技术参数在 HITACHI 7180 上进行了重复性、室内总不精密度、线性、正确度（回收实验）、特异性等实验，并检测了 200 例体检样本以验证厂家的参考范围。
结果 该试剂重复性、室内总不精密度的测值在 5%左右。线性范围为 1.0-40 μg/ml。试剂对甘胆酸纯品的回收率为 90%-100%。特异性方面 ，甘氨脱氧胆酸和胆酸钠对九强试剂的干扰率分别为 18.60%和 61.17%。检测 200 例体检样本，九强试剂检测均值为 0.57 μg/ml，有 3 例样本测值大于参考范围 1.5 μg/ml。
结论 北京九强生物甘胆酸试剂盒性能与说明书一致，基本能满足临床检测需求

PU-1879

脑脊液外泌体中 miR-21 诊断神经胶质瘤的价值初探

朱迎星
徐州医科大学附属医院

目的 探讨脑脊液外泌体 miR-21 检测对神经胶质瘤的诊断价值。
方法 选择 2017 年 1 月至 2020 年 1 月本院收治的神经胶质瘤患者 60 例为观察组,选择同期于本院健康体检者 60 例为对照组. 使用 Exoquick 试剂盒提取新鲜脑脊液中的外泌体。通过透射电子显微镜（transmission electron microscope，TEM）、蛋白质印迹法对提取的外泌体进行形态学及蛋白

标志物鉴定。用 TRIZOL 法从外泌体中提取总 RNA，实时荧光定量 PCR 检测 miR-21 的表达水平并对结果进行统计分析。
结果 蛋白质印迹法检测到外泌体标志蛋白 CD63，CD81，TSG101，透射电子显微镜下见到多个直径为 40-120nm、内含低电子密度物的囊泡，表明 Exoquick 试剂盒成功提取到脑脊液外泌体。实时荧光定量 PCR 结果表明神经胶质瘤患者脑脊液外泌体中 miR-21 的相对表达量明显高于健康体检者(P＜0.05)，其诊断神经胶质瘤患者灵敏度为 83％,特异度为 87％。
结论 脑脊液外泌体 miR-21 在神经胶质瘤患者中的表达显著上调，有望为神经胶质瘤诊断的潜在的新的标志物。

PU-1880

STAT 对人胃癌细胞凋亡的影响

童书青
山东第一医科大学附属省立医院

目的 信号传导子与转录激活子 (Signal.transducers-and-activators-of transcription ,STAT)是一种存在于细胞浆中与酪氨酸磷酸化信号通道相偶联的双功能蛋白，并与肿瘤的增殖、凋亡、侵袭、转移、血管生成和免疫逃逸等密切相关，被看作是肿瘤治疗的潜在靶点。
本文章研究 siRNA 干扰 STAT 基因表达后对人胃癌细胞株凋亡的影响。
方法 1. 设计并合成两个 STAT-siRNA 片段，经脂质体介导分别转染胃癌细胞株。
2. Western blot 及流式细胞术检测 STAT-siRNA 对细胞凋亡的影响。
结果 1. Western blot 结果显示，RNA 干扰下调细胞中 STAT 表达后，影响凋亡相关因子的表达，与 si-NC 转染对照组相比差异有统计学意义。
2. 流式细胞术结果显示，RNA 干扰下调细胞中 STAT 表达后，凋亡率增加，与 si-NC 转染对照组相比差异有统计学意义。
结论 1. siRNA 干扰沉默 STAT 在胃癌细胞中的表达后可促进胃癌细胞的凋亡。
2. 提示 STAT 可能是胃癌治疗的潜在靶点之一。

PU-1881

线性和非线性定量在同位素稀释质谱法中应用的比较

马妍慧
上海交通大学医学院附属新华医院

目的 同位素稀释质谱法被越来越多的临床实验室用于高通量复杂成分的定量分析。多数时候采用具有线性响应函数用于制作校准和/或标准曲线，但同位素稀释方法有时候表现为非线性响应曲线。
方法 实验室建立的同位素稀释质谱法检测伊立替康及其三种主要代谢产物，血清样品制备包括蛋白质沉淀、氮吹后有机溶剂复溶。在 ABSciex API 3200 上进行分析，使用 C18 反相柱梯度洗脱，总运行时间为 9 分钟，正离子模式下的电喷雾电离和多反应监测用于质谱分析。稳定同位素标记内标为：CPT-11 D10、SN-38 D3、SN-38G D3 和 APC D3。目前大多数同位素稀释的校准，或通过使用具有显著不同分子量的内标来消除非线性，或经验性采用多项式拟合以提高准确度。在这里我们利用伊立替康及其代谢的同位素稀释定量结果作为数据，应用线性函数、二次函数、三次函数和新的线性最小二乘法 Padé [1,1]近似拟合分析，比较四种拟合方法对三种浓度 QC 样本结果的偏差。
结果 CPT-11，SN-38G 和 APC 在 4.6~4.7 分钟出现洗脱峰；SN-38 在~5.2 分钟时出现洗脱峰。此外，我们发现 CPT-11 D10 中存在低含量的 SN-38 杂质（在 SN-38 D3 中含量较低），这导致了低

浓度时分析物定量的问题。初步实验中没有发现关于残留效应、精度、准确性和基质效应的重大问题。
结论 结果适合线性标准曲线时，优先推荐应用线性；非线性校准曲线时，使用三参数有理函数，y = （a0 + a1x）/（1- a2x）此功能一定程度上可以消除同位素稀释分析中不必要的误差源。

PU-1882

西门子 BNII 特定蛋白分析仪测定 ASO 的分析性能验证与评价

代蓉蓉
昆明医科大学第一附属医院

目的 验证和评价西门子 BNII 特定蛋白分析仪测定抗链球菌溶血素 O(ASO)的分析性能。
方法 依据美国临床实验室标准化组织(CLSI) 文件和科室制定的相关文件的实验方案，分析西门子 BNII 特定蛋白分析仪测定 ASO 的精密度、正确度、携带污染率、线性及可报告范围,对结果与质量标准比较。
结果 批内精密度 CV 分别为 2.9% 、2.8% ，符合判断标准≤6.3% 。批间精密度 CV 分别为 3.94% 、2.70% ，符合判断标准≤8.3% 。正确度:平均偏倚为 4.03%,符合判断标准≤12.5% 。携带污染率为 0.24% 。线性: Y = 0.9834X －1.704 4，a = 0.9834，r2 = 0.99，实测线性范 52.8～1500 IU /ml。
结论 仪器分析性能验证是为保证检验结果的准确性。西门子 BNII 特定蛋白分析仪测定 ASO 的精密度、正确度、携带污染率、线性及可报告范围，结果与质量目标比较，均符合要求，可用于临床标本检测。

PU-1883

分析肿瘤标志物检测对高龄肝硬化患者的临床诊断价值

李玲
湖北省中西医结合医院

目的 分析肿瘤标志物检测对高龄旰硬化串者的临床诊断价值。
方法 选取 2019 年 6 月至 2020 年 6 月期间我院收治的 76 例高龄肝硬化患者作为研究组，另 76 例健康体检患者作为对照组。纳入标准:患者及患者家属均签署研究知情同意书;年龄均>60 岁。排除标准:年龄<60 岁;伴有合并心肝肾等重大疾病及其他恶性肿瘤。所有研究对象均在清晨进行空腹静脉采血 5ml，采用全门子 XP 全自动化学发光免疫分析仪，由日立 7600 全自动生化分析仪进行测量全部操作均严格按照操作规程流程执行。记录并对比两组串者血清中的 AEP、 CEA、CA125、CA199 水平和阳性检出率，按照肝功能分级，将研究组患者分为 A、B、C 三级，对比不同程度肝硬化患者血清中的 AEP、CEA、CA125、CA199 水平。
结果 研究组患者血清中的 AEP、CEA、CA125、CA199 水平及阳性检出率明显高于对照组，对比差异有统计学意义(P<0.05);按肝功能分级:B、C 级的肿瘤标志物水平均明显高于 A 级;C 级的 AEP、CA125、CA199 水平高于 B 级，以上比差异无统计学意义(P>0.05)。
结论 血清 AFP、CEA、CA125、CA199 联合检测高龄肝硬化有较高的敏感性和特异性，肿瘤标志物可作为肝硬化病情程度的诊断对高龄肝硬化串者具有较高的诊断价值，值得临床推广和应用。
关键词肿瘤标志物检测;肝硬化;高龄患者;临床诊断价值

PU-1884

不同因素及疾病与 Lp(a)的相关性分析

张文娟
中南大学湘雅二医院

目的 调查中南大学湘雅二医院住院患者血清脂蛋白（a）水平(Lp(a))，分析 Lp(a)与性别、年龄、吸烟、饮酒、不同疾病、其他血脂指标的相关性。
方法 从湘雅二医院住院患者中选取 2013-2020 年来院就诊的 7395 例患者，统计血脂 8 项数据及其它病历资料，使用 SSPS 24.0 软件统计分析患者 Lp（a）水平变化与临床指标的相关性。
结果 Lp（a）在各个年龄段的差异具有统计学意义（P＜0.05），青年组＜中年组＜老年组。吸烟组 Lp（a）高于不吸烟组，差异具有统计学意义（P＜0.05）。各疾病组数据比较显示，AS 组以及 AS 合并其它疾病的患者与对照组的比较，Lp（a）的差异均有统计学意义，发生心梗和脑卒中的患者与对照组的比较，差异均有统计学意义，糖尿病组、高血压组与对照组的差异无统计学意义。Lp(a)在血脂指标中与 ApoB、CHO、HDL-C、LDL-C 的相关性，相关系数（95%CI）分别为 0.179（0.130~0.227）、0.132（0.082~0.181）、0.143（0.094~0.192）、0.143（0.094~0.192）。线性回归分析显示校正年龄和性别后，Lp(a)水平与年龄（β=0.101，P＜0.001）、是否吸烟（β=0.042，P=0.001）、AS（β=0.086，P＜0.001）、心梗（β=0.119，P＜0.001）有相关性。与性别、饮酒、糖尿病、高血压、脑卒中无相关性。二元逻辑回归分析显示，AS 的影响因素包括 Lp(a)、性别、年龄、糖尿病、高血压和是否吸烟，χ2＝384.1，P＜0.001；心梗的影响因素为 Lp(a)、LDL-C、Apo-A1 、年龄、性别、高血压和糖尿病，χ2＝404.8，P＜0.001。
结论 Lp(a)与 APO-B、CHO、HDL-C、LDL-C 具有相关性。Lp(a)水平与 AS、心梗和 CKD 有相关。Lp(a)水平与年龄、吸烟具有相关性，需要进一步研究证实。

PU-1885

谷胱甘肽还原酶在早期肝损伤诊断中的应用价值

赵瑾超、杨进波
襄阳市第一人民医院

目的 研究检测血清谷胱甘肽还原酶（GR）水平在早期肝损伤诊断中的应用价值。
方法 选取 210 例各类急性病毒性肝炎的患者作为实验组,另选取体检中心健康者 280 例作为对照组,检测两组研究对象的血清丙氨酸氨基转移酶（ALT）、门冬氨酸氨基转移酶（AST）、碱性磷酸酶（ALP）、GR 以及总胆红素（TBIL）水平。采用组间比较和分层比较评估 GR 水平与早期肝损伤的相关性和诊断效能。
结果 实验组 ALT、AST、TBIL、ALP、GR 水平均显著高于对照组,差异具有统计学意义（P<0.05）。对 ALT、AST、TBIL、ALP 和 GR 进行受试者工作特征（ROC）曲线分析可知，血清 GR 活性水平对早期肝损伤的诊断界值为 61.5 U/L,曲线下面积（AUC）为 0.882[95%CI=（0.845, 0.919）, P<0.05],灵敏度为 78.6%,特异度为 89.3%。将实验组研究对象按 GR 活性水平四分位数间距（Q）进行分层:ALT、AST、TBIL、ALP 活性水平均随 GR 活性水平的升高而升高（P<0.05），且升高时间晚于 GR。
结论 血清 GR 活性水平升高与早期肝损伤显著相关,检测血清 GR 活性水平可作为辅助诊断、治疗各类肝病、评估肝损伤程度的方法。

PU-1886

肝硬化患者 IMA 与 CHE 浓度的改变及相关性研究

宋能
湖北省中西医结合医院（湖北省职业病医院）

目的 研究肝硬化患者 IMA 与 CHE 浓度的改变及相关性。
方法 以我院消化内科病历资料完整的乙肝肝硬化患者 46 例为研究对象，其中男性 25 例，女性 21 例，年龄 46.1±10.3 岁。选择同期健康体检者 35 例（无任何肿瘤既往史，无自身免疫性疾病、肝脏疾病、心脑血管疾病，无感染等）。两组静脉采血对比测试研究两组之间 IMA 与 CHE 血清浓度差异，再进一步验证 IMA 与 CHE 在肝硬化进程中的变化规律，通过相关性检验分析其相关关系。
结果 病例组与健康组两组人群在 CHE 与 IMA 的血清含量上有统计学差异，患者组的血清 CHE 值平均为（3.67±1.41）KU/L，明显低于健康对照组（5.64±1.13）KU/L，患者组的血清 IMA 值平均为（109.1 ±21.5）KU/L，明显低于健康对照组（54.9±11.4）KU/L（$p<0.05$）。患者血清中 CHE 含量（3.67±1.41）KU/L 与健康组（5.64±1.13）KU/L 比较患者组 CHE 值明显升高（$p<0.05$）。通过散点图可知，随着 CHE 水平降低，血清 IMA 水平逐渐升高，可见两者在肝硬化进程中 CHE 与 IMA 含量的改变呈负相关关系，经过相关分析可知 R2＝0.98。
结论 肝硬化患者血清 IMA 与 CHE 含量会随着疾病的发生发展而分别升高和降低，同时两者的升高和降低程线性负相关。

PU-1887

长沙地区健康人群血浆血氨水平变化及参考区间的建立

张文娟
中南大学湘雅二医院

目的 对湖南省长沙地区健康人群血氨水平进行调查，并初步建立参考区间。
方法 选取 2021 年 4-5 月在我院健康管理中心进行体检的健康者 228 例（男 111 例，女 117 例）。采用德国 Roche Diagnostics GmbH 公司生产的血氨检测试剂盒（比色法）在罗氏 cobas c702 全自动生化分析仪上进行检测。所得检测结果剔除离群值后，按照性别与年龄进行分组，采用 SPSS 26.0 软件对血氨检测结果进行统计学分析。
结果 各个检测时间的血氨水平差异有统计学意义（$P<0.05$），男性与女性的 1 小时、2 小时、3 小时血氨水平差异均有统计学意义（$P<0.05$），但各年龄段的血氨水平差异均无统计学意义（$P>0.05$）。各个检测时间、不同性别的血氨水平均呈正态分布，故需按照检测时间、性别，取双侧 95%（X±1.96S）的结果为参考区间，分别建立参考区间。长沙地区健康男性 1h 血氨参考区间为 15.8~47.5μmol/L，健康女性 1h 血氨参考区间为 12.4~39.6μmol/L，健康男性 2h 血氨参考区间为 22.3~56.5μmol/L，健康女性 2h 血氨参考区间为 19.1~48.0μmol/L，健康男性 3h 血氨参考区间为 27.9~65.7μmol/L，健康女性 3h 血氨参考区间为 24.6~56.7μmol/L。
结论 长沙地区不同检测时间男性与女性的血氨水平存在差异，应按照检测时间和性别初步建立适合该地区健康人群血氨的参考区间，为临床诊断提供更好的相关依据。

PU-1888

Adenosine deaminase activity associate with arthritis, new-rash and hypocomplementaemia symptoms in systemic lupus erythematosus

Zhao-wei Gao、Ke Dong
Tangdu hospital, Air Force Medical University

Aim Serum adenosine deaminase (ADA) activity was increased in SLE patients and positively correlated with SLE disease activity, which suggested that ADA might be involved in SLE development. In order to further clarify the clinical significance of ADA activity in SLE patients, we investigated the relationship between serum ADA activity and clinical characteristics of SLE patients.
Methods A total of 120 SLE patients were included. The relationship between serum ADA activity, laboratory indexes and 14 clinical symptoms were analyzed.
Results The results showed that serum ADA activity was significantly increased in SLE patients with arthritis, new-rash or hypocomplementaemia compared with patients without these symptoms ($p = 0.003$; $p = 0.016$; $p = 0.002$). In contrast, there were no significant differences between SLE patients with or without the other symptoms ($p > 0.05$). Based on Spearman's rank correlation analysis, serum ADA activity was significantly negative correlated with complement C3 and C4 ($p < 0.01$), while was not correlated with the other laboratory indexes in SLE patients.
Conclusion These findings suggested that ADA correlated with arthritis, new-rash and hypocomplementaemia in SLE patients, which suggested that ADA activity detection may act as laboratory markers for the clinical subtypes of SLE patients.

PU-1889

多功能介孔中空 ZrO2 包覆 NIR-PLNPs 用于磁-光双模态成像及近红外长余辉发光激活的化疗-光动力学协同肿瘤治疗

吴伯岳
天津医科大学

目的 发展一种基于空心二氧化锆基质的具有多模态成像能力的长余辉药物载体的构建针对肿瘤组织的活体多模态成像、可控药物释放以及化疗-光动力学联合治疗的肿瘤诊疗平台。
方法 通过层层自组装方式合成 NIR-PLNPs@ZrO2，并通过特异性共价结合、静电结合等方式最终合成 NIR-PLNPs@ZrO2-Ce6-Gd。随后评价材料的药物负载与释放能力、光动力学治疗能力、磁-光双模态成像能力、细胞负载能力、体内化疗/光动力学联合治疗效果以及材料生物毒性。
结果 在近红外区发光的上转换-长余辉纳米颗粒（NIR-PLNPs）基础上，制备以 NIR-PLNPs 为核心的中空二氧化锆纳米颗粒（NIR-PLNPs@ZrO2），并通过光致热效应，构建高载药量可控释放的纳米载药系统；在此基础上，在其表面修饰光敏剂 Ce6，实现化疗与光动力学治疗的联合。在 NIR-PLNPs@ZrO2-Ce6 基础上，进一步提高活体示踪的灵敏度和空间分辨率。通过结合优势互补的磁共振成像探针，构建长余辉发光/磁共振多模态成像纳米诊疗系统（NIR-PLNPs@ZrO2-Ce6-Gd），用于高灵敏度和空间分辨率的光学和磁共振成像示踪以及针对肿瘤的化疗/光动力学联合治疗。该体系的构建，旨在解决传统长余辉纳米颗粒不适于作为药物传输载体的缺陷，同时实现活体针对肿瘤组织的高灵敏度和空间分辨率的多模态成像示踪及靶向、可控药物传递。
结论 建立了以近红外长余辉纳米颗粒为核心并基于空心二氧化锆基质的具有多模态成像能力的药物载体的构建针对肿瘤组织的活体多模态成像、可控药物释放以及化疗-光动力学联合治疗的肿瘤诊疗平台。

PU-1890

人血清 CEA 发光免疫分析方法的建立及性能评价

杨进波
襄阳市第一人民医院

本研究建立了一种人血清 CEA 发光免疫分析方法并进行了性能评价。根据生物学上抗原与抗体会发生特异性反应的原理，将 CEA 捕获抗体包被在羧基磁珠表面，与血清中的 CEA 抗原以及吖啶酯标记的 CEA 抗体反应形成双抗夹心“三明治”免疫复合物，清洗复合物后，加入预激发液和激发液，用化学发光免疫分析仪检测反应过程中的光强，四参数方程拟合后计算出样本中 CEA 浓度，并对线性范围、准确度、精密度及与雅培试剂盒相关性进行了性能评估。本方法空白限为 0.2 ng/mL，线性范围为 0.4~1000 ng/mL，批内精密度为 5.12%~5.17%，批间精密度为 5.52%~5.60%，与雅培 CEA 检测试剂盒测定结果拟合方程为 Y=1.0046X+0.0734，相关系数 r=0.9949。本方法各项性能指标均能满足医院检验需求，与进口试剂相比有很好的相关性，可用于医院临床检验。

PU-1891

血清铁、铁蛋白和转铁蛋白与妊娠期糖尿病的相关性研究

黎青
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨妊娠期糖尿病（GDM）患者与血清铁（serum iron，SI）、血清铁蛋白（serum ferritin，SF）和转铁蛋白（transferrin，TRF）水平变化的关系及临床意义。
方法 选择 2019 年 1 月～2019 年 8 月该院孕周为 24～28 周妊娠期糖尿病孕妇 145 例作为妊娠期糖尿病组（GDM 组），血糖正常孕妇 170 例作为对照组。分别测定两组孕妇 SI、SF、TRF、Hb、MCV、MCH 和 MCHC 水平并进行比较。
结果 与对照组孕妇相比，GDM 组孕妇 SI、SF、TRF 水平均显著升高（P<0.05），差异有统计学意义；而两组孕妇 Hb、MCV、MCH 和 MCHC 比较差异均无统计学意义（P>0.05）；SI、SF 及 TRF 与空腹血糖、1h 血糖、2h 血糖均呈正相关（P<0.05）；进行单因素 Logistic 回归分析，当显著性水平 α=0.05 时，SI、SF 和 TRF 水平与 GDM 的发生均有统计学意义（P<0.01）。
结论 孕妇体内铁储存水平的升高与妊娠期糖尿病的发生密切相关。

PU-1892

The prognostic value of serum high-density lipoprotein in adult hemophagocytic lymphohistiocytosis

军 周
First affiliated Hospital of Nanjing Medical University / Jiangsu Provincial people's Hospital

Objective To investigate the prognostic value of absolute lymphocyte count (ALC) in adult patients with hemophagocytic lymphohistiocytosis (HLH).
Methods The clinical and laboratory data of 171 newly diagnosed adult HLH patients from January 2012 to July 2018 were retrospectively analyzed. First, ROC curve was used to determine the optimal threshold of ALC. Second, the difference between the low ALC group (≤0.51×10^9/L) and the high ALC group (＞0.51×10^9/L) was analyzed; Third, univariate and multivariate analysis were conducted to verify ALC was an independent prognostic

factors. Finally, K-M survival curve was used to verify whether ALC was related to the survival time.

Results ①The optimal threshold of ALC was 0.51×10^9/L, the curve area was 0.740(0.668-0.804). Compared with the low ALC group; There is a significant difference between low ALC patients and high ALC patients in the levels of leukocyte, neutrophil, hemoglobin, platelet, urea nitrogen and creatinine (all P values <0.05). ②Multivariate analysis showed that ALC, platelets and urea nitrogen can be used as independent indicators to predict the prognosis of patients. ③ K-M curve showed that to patients with HLH and its subgroups, there is a significant difference in survival time between low ALC patients and high ALC patients.

Conclusion ALC is an independent prognostic factor for adult HLH patients.

PU-1893

降钙素原对细菌感染的临床意义研究

张翠英
吉林金域医学检验所有限公司

目的 感染是造成人类死亡的最重要因素。约占人类每年总死亡率的 25.5%，尽管临床监测感染手段众多，但仍缺乏敏感而特异的检测指标。而降钙素原克服了上述监测手段的缺点，近年在临床感染诊断、预后判断上应用越来越广泛，本文就降钙素原对细菌感染的临床意义进行研究，旨在为临床提供参考依据。

方法 通过查阅大量文献，及了解各大医疗机构及第三方医检机构对降钙素原的应用程度、频次及效果，分析降钙素原的临床意义。

结果 1.细菌感染的判断在细菌引起的全身性炎性反应时，血清 PCT 浓度会明显增高，但在病毒感染、自身免疫性疾病和器官移植排斥反应等炎性反应时，血清 PCT 浓度仅维持低水平，提示血清 PCT 浓度可以鉴别诊断细菌性或非细菌性炎症。

2.感染程度的判断 感染组织的范围和严重程度与血浆 PCT 浓度呈正相关。

3. 指导抗生素选择及调整

4.治疗效果的评定血 PCT 浓度是评定疗效的灵敏指标，严重细菌感染病人在抗菌治疗后，血 PCT 浓度迅速降低或恢复正常，临床症状明显好转。

结论 PCT 是临床应用价值很高的诊断感染状态的微生物学指标。虽然血细胞分析可反应患者细菌感染的情况，但在创伤、应激时也会升高；血菌培养只在大量细菌入血时才能获阳性结果；急性期反应蛋白在严重细菌感染时表现为血浆浓度明显升高，但手术、病毒感染、局部细菌感染及非感染因素下也升高，升高水平与感染严重程度不一致，受激素影响。因此，降钙素原可成为细菌感染的新的预防及诊断途径。

PU-1894

Differential Performance of Neutrophil Gelatinase-associated Lipocalin and Cystatin C to Predict Ischemic Stroke

Ling Peng
Departmant of Clinical Laboratory, Mianyang Central Hospital, School of Medicine, University of Electronic Science and Technology of China

Objectiv Both cystatin C (CysC) and neutrophil gelatinase-associated lipocalin (NGAL) are markers of kidney injury and may also be marker candidates for neuroinflammation. The aim of this article is to explore the relationship between kidney injury and ischemic stroke (IS).
Methods 498 IS patients were enrolled from March 2017 to October 2020, and 173 IS-related disease control (DC) patients and 293 healthy control (HC) subjects were randomly selected. We collected serum kidney function markers (including NGAL, Cre, Ure, CysC and eGFR)，analyzed the relationship between the levels of serum kidney function markers and the occurrence of IS.Then all IS patients were divided into IS patients with normal kidney function (NKF-IS, n=408) and IS patients with CKD (CKD-IS, n=90),observed the difference performanceof renal function markers between the NKF-IS and CKD-IS.
Results Except Ure ($\chi2=3.862$, $P=0.145$), there were statistical differences in the levels of Cre ($\chi2=36.695$, $P<0.001$), CysC ($\chi2=46.0304$, $P<0.001$), eGFR $\chi2=34.072$, $P<0.001$) and NGAL ($\chi2=153.953$, $P<0.001$) among those three groups.By multiple comparisons,the NGAL level of patients with first-onset IS when they were admitted to the hospital,was higher than that of both HC group ($z=5.964$, $P<0.001$) and DC ($z=12.191$, $P<0.001$); The level of CysC of them was higher than that of HC group ($z=5.762$, $P<0.001$), and was the similar with that of DC group ($z=1.663$, $P=0.289$). The partial correlation coefficient between NGAL and the occurrence of IS was the highest ($rp=0.341$, $P<0.001$) in IS patients with normal kidney function(NKF-IS), and significantly higher than the partial correlation coefficient of other indicators except coronary heart disease ($z=4.812$-7.622, all $P<0.001$). However, the partial correlation coefficient between CysC and IS was the highest ($rp=0.460$) , $P<0.001$) in IS patients with chronic kidney disease (CKD-IS), and significantly higher than the partial correlation coefficient of other indicators except eGFR ($z=3.504$-6.920, all $P<0.001$). When HC, DC, and no-IS were used as references, NGAL had the best predictive performance for IS, with AUC of 0.761 ($z=15.347$, $P<0.001$). 0.711 ($z=10.010$, $P<0.001$) and 0.749 ($z=14.821$, $P<0.001$), respectively, by ROC analysis. For patients with normal kidney function, only NGAL was a risk factor for IS [OR(95%CI)=6.54(3.75,11.41)], and had the certain predictive performance AUC=0.734($z=12.928$, $P<0.001$). However, for CKD patients, CysC has better predictive performance for IS occurrence AUC=0.835 ($z=11.343$, $P<0.001$) and risk assessment ability [OR(95%CI)=5.97(2.45, 14.56)] than NGAL.
Conclusion This study found that the level of NGAL in IS patients was higher than that of HC and DC, while the levels of the other four renal function markers were only higher than HC. It indicates that serum NGAL level may be increased in both kidney function impairment and IS occurrence. This may also indicate that the risk of IS in patients with kidney injury is extremely high, and the patients with IS may have renal function impairment for a long time.IS is related to kidney injury and neuroinflammation. NGAL and CysC are suitable for IS prediction in patients with normal kidney function and CKD,respectively.Researchers should pay attention to the changes of NGAL and CysC for the prevention and treatment of stroke in these two types of patients, respectively.

PU-1895

原发性肝癌患者血清中 AFP、DCP、AFP-L3%水平分析

袁丹[1]、田小军[2]
1. 四川省科学城医院
2. 绵阳市中心医院

目的 探讨原发性肝癌患者血清甲胎蛋白（AFP），异常凝血酶原（DCP）和甲胎蛋白异质体比率（AFP-L3%）的变化情况。
方法 测定 62 例健康体检者、28 例非肝癌肝脏疾病患者、36 例肝癌患者血清中 AFP、DCP 和 AFP-L3%的水平。
结果 肝癌患者血清 AFP(578.65±605.29,p=0.000),DCP(373.85～783.45, p=0.000) 和 AFP-L3%(7.68±2.62, p=0.000)水平均显著高于健康体检组和非肝癌患者组。ROC 曲线分析显示，AFP、DCP 和 AFP-L3%的最佳临界点分别为 30.90ng/ml、49.97ng/ml 和 5.05%，其 AUC 分别为 0.777、0.882 和 0.782。三项联合检测 AUC 为 0.956，灵敏度 97.2%，特异性 79.1%。
结论 单项检测 DCP 较 AFP 与 AFP-L3%更具有诊断敏感性，联合检测更有利于评估肝癌的诊断效能。

PU-1896

Cys-C 与尿 RBP 联合检测对糖尿病早期肾损伤的诊断价值研究

高科、李如飞
重庆市重钢总医院

目的 分析胱抑素 C（Cys-C）与尿视黄醇结合蛋白（RBP）联合检测在基层医院糖尿病患者早期肾损伤中的诊断价值。
方法 选择 120 例 2019 年 6 月-2020 年 12 月我院收治的糖尿病患者作为病例组，根据尿微量白蛋白排泄率（UAER）分为单纯糖尿病组（UAER<30mg/24h）65 例和糖尿病肾损伤组（30mg/24h≤UAER<300mg/24h）55 例；同时，选择同期健康体检者 60 例作为对照组。检测空腹血标本 Cys-C 和晨尿 RBP，比较各组 Cys-C、尿 RBP 表达水平，分析 Cys-C、尿 RBP 单一和联合检测的阳性率、灵敏度、特异性。Cys-C 阳性临界值为 1.5mg/L、RBP 阳性临界值为 3mg/L。采用 SPSS 17.0 软件对数据进行统计学处理。
结果 糖尿病肾损伤组 Cys-C 2.65±0.52mg/L，尿 RBP 1.65±0.35mg/L；单纯糖尿病组 Cys-C 0.98±0.15mg/L，尿 RBP 0.51±0.16mg/L；对照组 Cys-C 0.62±0.12mg/L，尿 RBP 0.22±0.11mg/L。糖尿病肾损伤组 Cys-C、尿 RBP 水平明显高于单纯糖尿病组，单纯糖尿病组明显高于对照组，差异均具有统计学意义（P<0.05）。糖尿病肾损伤组 Cys-C 阳性率 60%，灵敏度 58.25%，特异性 69.3%；尿 RBP 阳性率 63.64%，灵敏度 55.36%，特异性 68.5%；Cys-C 与尿 RBP 联合检测阳性率 94.55%，灵敏度 82.63%，特异性 90.16% 。Cys-C 与尿 RBP 联合指标的阳性率、灵敏度、特异性均高于单一指标，差异具有统计学意义（P<0.05），说明联合指标具有较高诊断价值。
结论 糖尿病肾病是糖尿病最主要的并发症之一，在糖尿病患者中发病率约占 40%。Cys-C 是一种反映肾小球滤过率变化的理想内源性标志物，能更早反应肾小球滤过功能，RBP 是反映肾小管重吸收功能最直接的指标，具有较理想的时效性。血 Cys-C 和尿 RBP 指标检测在中小型医院更易开展，可作为临床评估糖尿病早期肾损伤的理想指标。该研究结果显示，Cys-C 与 RBP 二者联合检测对中小型医院开展糖尿病患者早期肾损伤的预测具有重要的价值和临床意义。

PU-1897

补充维生素 D 对维生素 D 缺乏或不足的糖尿病及糖尿病前期患者糖稳态和胰岛功能的影响：系统综述和 Meta 分析

邹雨桐
中国医学科学院北京协和医院

目的 探讨补充维生素 D 对维生素 D 不足或缺乏的糖尿病和糖尿病前期患者糖稳态、胰岛功能及糖尿病进展的影响。
方法 采用 Medline、Embase、web of science、Cochrane 图书馆、OpenGrey、www.controlled-trials.com 等检索工具检索从最早的时间到 2020 年 5 月底的文献，辅以历史搜索的方式。纳入最初设计针对 25（OH）D<30 ng/mL 的糖尿病和糖尿病前期的随机对照试验。所有数据均根据 Cochrane 指南进行提取和分析，并根据 PRISMA 指南进行呈现。
结果 共有 27 篇文章（n=1932）纳入本研究，其质量参差不齐。在基线 25（OH）D<30 ng/mL 时，补充维生素 D 可显著改善糖尿病和糖尿病前期患者的 FBG、PPBG 和 QUICKI。影响大小分别为-3.36（-5.83，-0.89）、-14.72（-28.15，-1.29）和 0.02（0.01，0.03）。维生素 D 补充组从糖尿病前期到正常血糖状态的比例较高[1.60（1.19，2.17），p=0.002，n=564]，从糖尿病前期到糖尿病的比例较低[0.68（0.36，1.27），p=0.23，n=569]，且研究间异质性较低。补充维生素 D 对 BMI、腰围、HDL-C、LDL-C 和 CRP 也有积极影响。
结论 补充维生素 D 对 25（OH）D<30ng/mL 的糖尿病和糖尿病前期患者的短期糖稳态、胰岛素敏感性和疾病发展有一定改善，但仍需进一步研究以支持临床应用

PU-1898

西藏人群尿碘和血清碘状况评价：不再是缺碘地区

邹雨桐
中国医学科学院北京协和医院

背景 碘是合成甲状腺相关激素的一种重要微量元素，低碘或高碘状态均可导致甲状腺功能障碍。本研究旨在了解西藏人群碘营养状况。
方法 2016 年 9 月至 2018 年 8 月，选择西藏 3 个不同海拔地区 1499 名健康成人作为研究对象。采用电感耦合等离子体质谱法测定尿碘浓度（UICs）、校正 UICs 和血清碘浓度（SICs）。
结果 平均 UIC、校正 UIC 和 SIC 为 137.90μg/L，118.40μg/gCr 和 58.30μg/L。30.40%的受试者 UICs<100μg/L，63.00%的患者 UIC 在 100-300 之间 μg/L 和 9.60%的人 UICs>300μg/L。UIC、校正 UIC 与 SIC 的相关性良好（r>0.65，p<0.01）。SICs 较 UICs 稳定，与年龄、性别无关。临床甲状腺功能亢进、临床甲状腺功能减退、亚临床甲状腺功能亢进、亚临床甲状腺功能减退、TPO-Ab 阳性、Tg-Ab 阳性、二者均阳性的患病率分别为 0.50%、1.30%、1.70%和 17.90%、9.30%、6.50%、12.50%和 2.50%。几乎所有甲状腺疾病的患病率女性高于男性。
结论 根据世界卫生组织的标准，这项多中心横断面研究发现西藏成年人的碘状况是适量的。

PU-1899

维生素 D 和强直性脊柱炎相关性的研究

张萍
昆明市中医医院

目的 检测强直性脊柱炎（ankylosing spondylitis，AS）患者及健康对照组血清中 25(OH)D 水平，并与 AS 患者其他相关实验室指标进行相关性分析，探讨维生素 D 与强直性脊柱炎的相关性。
方法 收集浙江大学医学院附属邵逸夫医院 2013 年至 2017 年门诊或住院共 69 例血清 25(OH)D 数据，包括初诊 AS 患者 41 例，健康体检者 28 例，其他临床资料包括：年龄、性别、血沉（ESR）、C 反应蛋白（CRP）、类风湿因子（RF）、碱性磷酸酶（ALP）、Ca、P、HLA-B27 基因等指标。按年龄分组用 SPSS19.0 统计软件进行分析。
结果 AS 组和体检组的 25(OH)D 水平与性别和年龄均无显著差异（$p>0.05$）。AS 组和体检组的 25(OH)D 的分布情况具有显著差异（$Z=-4.167$，$p<0.001$），且 AS 组明显低于体检组。与体检组相比，AS 组的 25(OH)D 与 ESR，CRP，Ca，P，HLA-B27 基因均有显著差异（$p<0.05$），与 RF，ALP 无显著差异（$p>0.05$）。AS 组 HLA-B27 基因阳性率高达 63.4%，而健康体检者的 HLA-B27 基因阳性率为 3.5%。
结论 与体检组相比，AS 组 25(OH)D 水平显著降低，提示强直性脊柱炎可能与维生素 D 缺乏相关，但具体机制仍需进一步研究。我们研究也表明，除了 HLA-B27 基因外，强直性脊柱炎与 ESR，CRP 也有密切联系。

PU-1900

Logistic 回归模型在冠心病鉴别诊断中的临床价值

黄本林、王宁、朱星成
曲靖市第二人民医院

目的 探讨基于一般临床资料和常规实验室检查建立的 Logistic 回归模型在冠状动脉粥样硬化性心脏病鉴别诊断中的临床价值。
方法 选取 2019 年 3 月~2020 年 11 月以胸闷胸痛为主诉就诊的 253 例患者为研究对象，根据冠状动脉造影结果分为冠心病组和非冠心病组，回顾性分析这些患者的常规指标，建立诊断冠心病的 Logistic 回归模型，进一步探讨其在临床中的实际意义。
结果 多因素 Logistic 回归分析发现，体重指数、吸烟史、糖尿病史及高血压史是冠心病的独立危险因素。单核细胞/高密度脂蛋白胆固醇比值是预测冠心病的强烈独立危险因子。基于上述指标，建立预测冠心病的 Logistic 回归模型。受试者工作特征曲线和校准曲线显示模型具有较好的区分度（曲线下面积为 0.838[95%CI，0.790~0.857)]）和校准度(平均绝对误差为 0.017)。
结论 Logistic 回归模型在冠心病诊断中具有较好的鉴别和预测价值。

PU-1901

肌钙蛋白与非阻塞性冠状动脉疾病

赵若莲
昆明市中医医院

本文系统性总结了最新的非阻塞性冠状动脉疾病中肌钙蛋白增高的证据。通常肌钙蛋白的增高被认为表明出现了心肌损伤，在这一认识基础上而产生的一些未被证实的假说（例如肌钙蛋白仅来自于心肌）使我们要准确地解释肌钙蛋白增高变得困难。要全面理解心脏标志物的临床意义首先必

须了解心脏标志物释放入血的病理生理机制。我们尤其需要在病因学上区分影响心脏标志物合成与清除的各种心脏和非心脏混杂因素。心脏标志物的应用帮助我们更好地对患者进行危险分层及预后管理。临床中经常出现难以诊断的肌钙蛋白增高，我们的目标是进一步阐明其临床意义以有利于明确诊断和制定个体化治疗策略。

PU-1902

肺癌患者血清中肌酸激酶及 同工酶含量的分析

吴苑、吴琳露
中南大学湘雅三医院

目的 分析肺癌患者血清中肌酸激酶（CK)和肌酸激酶同工酶（CK-MB)的含量，为肺癌的辅助诊断和分型提供参考和帮助。
方法 收集 2021 年 1 月-4 月在中南大学湘雅三医院确诊为肺癌且未经抗肿瘤治疗的 124 例肺癌患者作为观察组，另选本院同期 20 例健康体检者作为对照组。采用活性法检测两组肌酸激酶（CK），采用活性法和质量法检测两组肌酸激酶同工酶（CK-MB)在血清中的含量。采用 Wilcoxn 秩和检验进行组间比较及不同病理类型间比较，采用 spearman 相关分析和回归分析评估活性法和质量法两种检测方法的相关性，计算不同检测项目灵敏度和特异度。
结果 1.活性法检测 CK 水平，观察组血清 CK 水平低于对照组，差异具有明显统计学意义（P<0.001）；活性法和质量法检测 CK-MB 水平，观察组和对照组差异无明显统计学意义。2.小细胞肺癌组、鳞癌组 CK 水平低于对照组，差异具有明显统计学意义（P<0.001），腺癌组和对照组差异无明显统计学意义。3.采用活性法和质量法检测 CK-MB 的相关系数为 0.9218，且在小细胞肺癌组中二者相关系数为 0.981，有很好的相关性，在鳞癌组、腺癌组中相关系数分别为 0.2288、0.0541，相关性低。
结论 肺癌患者血清 CK 明显降低，且与病理类型密切相关，肺癌患者 CK-MB 含量与健康者无明显差异，采用活性法检测时，鳞癌、腺癌患者血清中 CK-MB 的含量可能受到 CK-BB 的影响。

PU-1903

估算法和测量法在血清残余胆固醇评估中的比较分析

黄本林、王宁、朱星成
曲靖市第二人民医院

目的 探讨估算法与测量法检测血清残余胆固醇（RLP-C）的差异。
方法 表面活性剂清除法定量检测血清 RLP-C，再运用 Bland-Altman 法和 ICC 法评估 RLP-C 定量测定值与 Friedewald 方程估算值的一致性。
结果 Bland-Altman 法的结果显示：7.0%个体（70/996）位于 95%一致性界限外。相对于定量测定法，Friedewald 方程估算法的平均阳性偏倚为 0.2mmol/L [95%CI (0.18~0.23)]。ICC 法的结果显示，ICC=0.551 [95%CI，0.192~0.732)，P<0.001]。Friedewald 方程估算的 RLP-C 与 RLP-C 测量值存在正相关关系（r=0.4，P<0.001）。此外，随着 TG 及 RLP-Ce 浓度逐渐升高，估算值与测量值的差异越来越大，其平均阳性偏倚为 0.2mmol/L（P<0.001）。
结论 测量法与方程估算法一致性欠佳，在临床实践中能否替代使用有待进一步验证。

PU-1904

49 例 IgG4 相关性疾病的临床分析

郭利利
南京大学医学院附属鼓楼医院

目的 提高对 IgG4 相关性疾病(IgG4-related disease,IgG4-RD)的认识及诊治水平。
方法 分析就诊于南京鼓楼医院 49 例 IgG4-RLD 患者,收集并分析其基本临床特征、实验室检查、影像学检查、组织病理学检查、治疗与随访结果等资料。并使用 IgG4-RD 应答者指数评估疾病活动和损害。
结果 50 例患者中,男 36 例,女 23 例,平均年龄(59.1±9.12)岁,起病到诊断的中位时间为 10(1～120)个月。最常见的首发症状是颌下腺肿大 10 例(20.4%)、腹痛 9 例(18.4%)、眼睑肿物或水肿 9 例(18.4%)、黄疸 8 例(16.3%)。最常见的受累器官为颌下腺 30 例(61.2%),其次为淋巴结 23 例(46.9%)、泪腺 22 例(44.9%)、腮腺 20 例(44.9%)和胰腺 15 例(30.6%)。影像学主要表现为 2 个及 2 个以上受累器官增大和(或)占位,主要以唾液腺为主，其次是淋巴结、泪腺、胆道等。IgG4-RD 应答者指数为 7.13±3.25,与受累器官呈正相关(r=0.15,P<0.0001)。93.55%的患者血清 IgG4 升高,且与血清 IgG 呈正相关(r=0.54,P<0.01)。组织病理学检查 46 例(93.9%)可见淋巴细胞、浆细胞增多,26 例(53.1%)患者伴纤维组织增生。单药糖皮质激素治疗者 23 例(46.9%),糖皮质激素联合免疫抑制剂者 20 例(40.8%),手术治疗者 3 例(6.1%),病情较轻观察者 2 例(4.1%)。47 例(95.9%)患者对初始治疗反应良好。23 例糖皮质激素单药治疗组有 10 例(43.5%)复发,20 例糖皮质激素联合免疫抑制剂治疗组有 6 例(30.0%)复发,复发患者再次给予足量糖皮质激素联合免疫抑制剂治疗仍有效。
结论 IgG4-RD 是一种多器官受累的慢性炎症伴纤维硬化性改变的疾病, 唾液腺、淋巴结、泪腺及内脏器官肿大是常见的临床表现,血清 IgG4 水平升高,病理组织大量 IgG4 阳性浆细胞浸润, 是确诊的金标准。糖皮质激素和免疫抑制剂治疗有效,总体预后良好，但存在复发现象。

PU-1905

7473 例健康体检者血脂和血糖检测结果分析

王宁、李晓东、孙继芹
云南省曲靖市第二人民医院

目的 对健康体检者血脂中总胆固醇、甘油三酯、高密度脂蛋白、低密度脂蛋白、空腹血糖水平分布情况进行分析。
方法 将我院体检中心 2019 年 7473 例健康体检者按照年龄分为 7 组，并对总胆固醇、甘油三酯、高密度脂蛋白、低密度脂蛋白、空腹血糖检测结果进行统计分析。
结果 不同年龄组血脂、血糖比较有统计学差异，31-50 岁年龄组血脂不正常率较高，31-59 岁年龄组血糖不正常率较高。
结论 高脂血症、糖尿病的发生和人们的年龄增长、饮食习惯、生活水平有着密切关系；高血脂、高血糖的发病呈现年轻化趋势，重视健康体检者血脂、血糖筛查结果，倡导良好饮食习惯、生活方式，预防高血脂、高血糖疾病。

PU-1906

液相色谱串联质谱法分析血清中 17-α-羟孕酮、双氢睾酮、脱氢表雄酮、脱氢表雄酮硫酸酯的性能评价

郑东[2]、邱骏[1]
1. 苏州大学附属第一医院临床检测中心
2. 苏州大学附属第一医院临床检测中心

目的 建立液相色谱串联质谱法定量检测血清中 17-α-羟孕酮、双氢睾酮、脱氢表雄酮、脱氢表雄酮硫酸酯的方法，并对其进行性能分析评价。
方法 采用液相色谱串联质谱法定量检测血清中 17-α-羟孕酮、双氢睾酮、脱氢表雄酮、脱氢表雄酮硫酸酯的含量。根据《中国药典》（2015 年版）通则中 9012“生物样品定量分析方法验证指导原则”对所建方法的线性范围、检出限、精密度、样本稳定性、回收率和携带污染率等基本性能进行确认。
结果 液相色谱串联质谱法定量检测血清中 17-α-羟孕酮、双氢睾酮、脱氢表雄酮、脱氢表雄酮硫酸酯的线性范围分别为 0.16～40 ng/ml、32～8000 pg/ml、0.16～40 ng/ml、2～500 ug/dl，检出限分别为 0.008 mg/L、0.0032 mg/L、0.008 mg/L、1 mg/L，定量下限分别为 0.032 mg/L、0.0064 mg/L、0.016 mg/L、4 mg/L，批内变异系数（CV）和批间 CV 均小于 5 %，回收率分别为 89.79 %～101.23 %、91.79 %～101.10 %、90.01 %～94.30 %、86.35 %～108.35 %。
结论 建立的液相色谱串联质谱法基本性能符合评价标准，能够高灵敏且准确地检测血清中 17-α-羟孕酮、双氢睾酮、脱氢表雄酮和脱氢表雄酮硫酸酯含量。

PU-1907

惠中 MQ-8000 糖化血红蛋白分析仪性能评价

邵明希、曹文俊
复旦大学附属眼耳鼻喉科医院

目的 本研究将采用惠中 MQ-8000 全自动糖化血红蛋白分析仪（MQ-8000）对样本 HBA1c 水平进行检测，从而对 MQ-8000 的性能进行全面的评价。
方法 采用 MQ-8000 对 100 例样本的 HBA1c 水平进行检测，综合分析评价该仪器的重复性、精密度、携带污染、正确度、线性范围以及与 ArkrayADAMSTMA1c HA-8180 糖化血红蛋白分析仪(HA-8180)进行样本比对。
结果 MQ-8000 检测糖化血红蛋白（HbA1c）的重复性、室内不精密度（CV）均小于 1%，高值样本对低值样本的结果无明显携带污染（携带污染率为-1.69%）；线性范围为 2.9%-20.5%，覆盖范围广；采用美国国家糖化血红蛋白标准化计划溯源样本进行正确度验证，测得的偏离度（-1.02%、0.97%）＜3%，正确度验证通过。与 HA-8180 糖化血红蛋白检测仪样本比对结果呈正相关（r=0.9953），相对偏差为 1.36%，在医学决定水平 6.5%处的偏移＜1%，验证结果均符合国家及国际行业协会相关标准。
结论 MQ-8000 具有良好的重复性、精确度、线性和较低的携带污染率，表明该仪器性能良好，可满足临床检测诊断的应用需求。

PU-1908

高同型半胱氨酸高血压相关因素分析

周勇军
益阳市中心医院

目的 探讨血清同型半胱氨酸(Hcy) 与高血压病的和生活习惯的关系。
方法 采用整群随机抽样方法，随机选取 832 名中老年居民进行流行病学调查。
结果 高血压组血清 HCY 水平和 SBP、DBP 水平均显著高于对照组(P<0.01)；线性相关分析表明 SBP、DBP 水平与 HCY 水平呈明显正相关(r=0.563, 0.678，均 P<0.01)；危险因素单因素分析结果显示 HCY、BMI、冠心病家族史、糖尿病病史、高脂血症史、吸烟史和饮酒史等与高血压发病相关(P<0.05)，性别、年龄等与高血压发病无关(P>0.05)。Logistic 多因素分析结果显示 HCY、吸烟史和饮酒史是高血压发病的主要危险因素(P<0.05)(OR 值分别为 3.128、2.379 和 2.524)，
结论 HCY 水平和 SBP、DBP 水平在高血压发生发展过程中可能起重要作用，HCY、吸烟史和饮酒史可能是高血压的独立危险因素，对高血压发生有预测价值。

PU-1909

探讨肌酸激酶同工酶（CK-MB）活性高于肌酸激酶（CK）总活性的机制

高海翟
吉林大学第一医院

目的 分析血清肌酸激酶同工酶（CK-MB）活性高于肌酸激酶（CK）总活性的原因。
方法 使用贝克曼库尔特 AU 生化分析检测仪，回顾性分析 1 例 CK-MB 活性高于 CK 活性的患者。同时使用强生 5600 全自动生化分析仪检测 CK-MB 质量。
结果 本例为小儿心血管疾病患者，由于免疫抑制法的方法学原因导致 CK-MB 活性高于 CK 总活性。用 5600 生化分析仪检测 CK-MB 质量结果正常。表明 CK 中另一种亚型 CK-BB 升高，导致了免疫抑制法测量 CK-MB 结果高于总 CK。
结论 当 CK-MB 活性高于总 CK 活性时，要及时与临床沟通，考虑该患者是否有其他系统相关疾病，避免出现漏诊。

PU-1910

Malaria Detection in Blood based on Surface-enhanced Raman Spectroscopy of Gold Nano-structures

王伟[1]、董瑞玲[2]、何建安[2]、易品[1]、Jacky Fong-Chuen Loo[3]、郑磊[4]、王前[4]、顾大勇[1]
1. 深圳市第二人民医院
2. 深圳市国际旅行卫生保健中心
3. 香港中文大学
4. 南方医科大学南方医院

We have developed a simple diagnostic procedure based on Surface Enhanced Raman Spectroscopy (SERS) from a substrate with gold nano-structures (AuNS). Blood samples infected with P. falciparum and P. vivax. were dispersed on the AuNS and analyzed under a Raman microscope with a 532 nm laser as the excitation source. Raman peaks at 1370 cm^{-1}, 1570 cm^{-1}, 1627 cm^{-1} were evaluated as the fingerprint markers. The AuNS-SERS substrate provided 1,000-fold enhancement of Raman signals as compared to conventional Raman spectroscopy. From

our experiments, the limit of detection was 10^{-5} dilution, which corresponds to the minimum densities of infected red blood cells (iRBC) of $2x10^4$/L, $4x10^4$/L, and $4x10^4$/L respectively for the ring phase, trophozoite phase and schizont phase.This work has provided strong validation evidence in support of using AuNS-SERS as a practical tool for highly specific in-field identification of malaria infection due to P. falciparum and P. vivax in clinical blood samples.

PU-1911

冠心病患者血清脂质成分监测的临床价值分析

周允、魏利龙、张瑞苹、曹永彤
中日友好医院

目的 探讨血清中各脂质成分水平与冠心病患者发生急性心肌梗死（AMI）的关系。
方法 采用病例-对照的研究方法，选择 2017 年 8 月至 2018 年 2 月中日友好医院住院患者，其中心绞痛组 99 例，年龄（60.4±10.4）岁，AMI 组 105 例，年龄（61.7±14.3）岁；收集健康体检者 60 名为对照组，年龄（43.6±9.5）岁。利用全自动生化分析仪检测各脂质成分水平。Logistic 回归分析总胆固醇（TC）、低密度脂蛋白胆固醇（LDL-C）、非高密度脂蛋白胆固醇（non-HDL-C）与冠心病患者发生 AMI 的相关性。受试者工作特征（ROC）曲线分析各指标的诊断效能。
结果 AMI 组血清 TC 水平[（4.99±1.14）mmol/L 比（4.01±0.98）mmol/L]、LDL-C 水平[（2.92±0.90）mmol/L 比（2.32±0.71）mmol/L]及 non-HDL-C 水平[（3.94±1.13）mmol/L 比（3.00±1.00）mmol/L]均高于心绞痛组，差异有统计学意义（*P*<0.001）。在充分调整了协变量后，Logistic 回归显示血清 TC（*OR*=6.957，*95%CI* 2.672~18.109，*P*<0.001）、LDL-C（*OR*=5.857，*95%CI* 1.993~17.217，*P*=0.001）和 non-HDL-C（*OR*=6.485，*95%CI* 2.474~17.002，*P*<0.001）与 AMI 发病呈正相关。ROC 曲线分析表明，TC 诊断 AMI 的 AUC（*95%CI*）为 0.747（0.678~0.816），LDL-C 诊断 AMI 的 AUC（*95%CI*）为 0.711（0.639~0.782），non-HDL-C 诊断 AMI 的 AUC（*95%CI*）为 0.738（0.668~0.807）（*P* 均<0.001）。
结论 血清 TC、LDL-C 和 non-HDL-C 水平在 AMI 患者中存在异常表达，且均为冠心病患者发生 AMI 的相关因素，定期监测对 AMI 患者的风险评估和临床诊断具有重要的意义。

PU-1912

补体 Cq 与阻塞性冠心病相关

郭书忍
郑州大学第一附属医院

Background Complement C1q plays a dual role in the atherosclerosis. Previous studies showed inconsistent results about the association of serum C1q levels and Coronary artery disease (CAD).
Methods We enrolled 956 CAD patients and 677 controls to evaluate the associations of serum complement C1q activity to the presence and severity of obstructive CAD and Non-obstructive CAD.
Results Serum C1q activity in Obstructive CAD and Non-Obstructive CAD groups was significantly higher than the control group (195.52±48.31 kU/L and 195.42±51.25 kU/L vs. 183.44±31.75 kU/L, P<0.05). Greater C1q activity was significantly correlated with higher total cholesterol (TC) and triglyceride (TG) levels. C1q activity was associated with an increased Odds Ratio (OR) of CAD (OR=1.322, 95%CI 1.168-1.496, P<0.05) and 1-year restenosis after revascularization (the highest OR=1.571, 95% CI 1.281-2.802, P<0.05). Complement C1q activity was not correlated with Gensini score in the Obstructive CAD group after adjustment for confounders. C1q activity has low value in predicting the incidence of CAD.

PU-1913

The Correlation of the Blood Lipid Level and Breast Cancer

Jing Li
The Affiliated Hospital of Qingdao University

Objective To study the relationship between serum triglyceride（TG）, cholesterol（CH） and lipoprotein levels and the occurrence and metastasis of breast cancer, to improve the role of clinical routine biochemical tests in early diagnosis and treatment monitoring of breast cancer.
Method 25000 breast cancer patients aged 20-70 were selected from the Affiliated Hospital of Qingdao University from February 2014 to February 2018, whose results of serum total cholesterol (TC), triglyceride (TG), low density lipoprotein (LDL) and high density lipoprotein (HDL) were obtained by Beckman Kurt 5800 biochemical analyzer, and the results of the same tests of the same period and the corresponding healthy people were obtained. Arrange for every 10 years as one age group, and both the patients and the healthy were divided into 5 groups. R language was used to compare the difference of the 4 tests between the same age group of healthy persons and breast cancer, the 4 indexes of different treatment were compared and the correlation between the occurrence of breast cancer and the level of these 4 lipoproteins were analyzed.
Results (1) In the same age group, the levels of TC, TG and LDL were lower in healthy person than those in the breast cancer patients (P< 0.05), while the difference in HDL level was not statistically significant. (2) R scatter plot analysis showed that the levels of TC, TG and LDL were positively correlated with the occurrence of breast cancer, with the correlation coefficient R >0.9; But serum HDL level was not significantly correlated with the occurrence of breast cancer. (3) In the same age group, the level of serum TC, TG and LDL in breast cancer patients with better therapeutic effect and over 6 months of progression-free survival were significantly lower than those with no response or less than 3 months of progression-free survival(P< 0.05). The levels of TC, TG and LDL in metastatic breast cancer patients were significantly higher than those with good therapeutic effect or over 6 months of progression-free survival(P< 0.05). There was no significant difference in serum lipid levels between metastatic breast cancer patients and those with poor treatment response (P>0.05).
Conclusion Levels of serum total cholesterol, triglyceride and low density lipoprotein are closely related to the occurrence and metastasis of breast cancer, which can be considered as an indicator for early screening, warning and treatment of breast cancer.

PU-1914

H 型高血压患者血清学指标与颈动脉粥样硬化程度的相关性探讨

刘秀敏
吉林大学第二医院

目的 分析 H 型高血压患者血清学指标与颈动脉粥样硬化程度的相关性及探讨其临床应用。
方法 选取 2018 年 5 月-2021 年 5 月本院收治的 H 型高血压患者 225 例。所有患者进行颈动脉超声检查,并根据颈动脉内中膜厚度（carotid intima media thickness,cIMT）将其分为正常组（n=75）,增厚组（n=75）及斑块形成组（n=75）。比较三组基本资料、cIMT、及各血清学指标。分析血清学指标与 cIMT 的相关性。
结果 三组性别、尿素氮、肌酐（Scr）、低密度脂蛋白胆固醇（LDL-C）、甘油三酯（TG）及总胆固醇（TC）比较,差异均无统计学意义（P>0.05）。斑块形成组高密度脂蛋白胆固醇（HDL-C）低于正常组与增厚组,且增厚组 HDL-C 低于正常组（P<0.05）。斑块形成组 cIMT、Hcy、胱抑素 C（cys C）及尿酸（UA）均高于正常组与增厚组,且增厚组 cIMT、cys C 与 UA 均高于正常组

（P<0.05）。cIMT 与 Hcy、cys C、UA 均呈正相关性（P<0.05）,其中与 Hcy 关系最密切;cIMT 与 HDL-C 呈负相关性（P<0.05）。

结论 针对 H 型高血压患者的临床检查,对其血脂、颈动脉超声以及同型半胱氨酸等相关指标进行观察较为关键,医生需把握患者上述指标的情况。颈动脉粥样硬化与机体多项血清学指标存在明显联系,其中与 Hcy 关系最密切。

PU-1915

TTDA inhibited apoptosis by regulating the p53-Bax/Bcl2 axis in glioma

Huanlan Bai
Laboratory Medicine Center, Nanfang Hospital, Southern Medical University

The trichothiodystrophy group A protein (TTDA) functions in nucleotide excision repair and basal transcription. TTDA plays a role in cancers and serves as a prognostic and predictive factor in high-grade serous ovarian cancer; however, its role in human glioma remains unknown. Here, we found that TTDA was overexpressed in glioma tissues. In vitro experiments revealed that TTDA overexpression inhibited apoptosis of glioma cells and promoted cell growth, whereas knockdown of TTDA had the opposite effect. Increased TTDA expression significantly decreased the Bax/Bcl2 ratio and the level of cleaved-caspase3. TTDA interacted with the p53 gene at the -1,959 bp and -1,530 bp region and regulated its transcription, leading to inhibition of the p53-Bax/Bcl2 mitochondrial apoptosis pathway in glioma cells. These results indicate that TTDA is an upstream regulator of p53-mediated apoptosis and acts as an oncogene, suggesting its value as a potential molecular target for the diagnosis and treatment of glioma.

PU-1916

血清钾高临界值患者临床评估及其与血同型半胱氨酸关系分析

武婧
吉林大学第二医院

目的 严重的高血钾症可导致危及生命的心律失常、心脏骤停或死亡。本研究旨在探讨住院、门诊及急诊危重高钾血症（≥6.2mmol/l）的发生率及相关因素，并对其临床结果进行分析。

方法 所有在 2018 年 1 月至 2021 年 5 月来吉林大学第二医院就诊的被报告为危急值的高血清钾患者均被纳入研究。查阅病历回顾性分析该类患者的相关临床资料、共病，并对其生化数据进行收集。筛选 135 例高血钾患者被为关键实验室值，计算 Charlson 共病评分（CCS）和肾小球滤过率（eGFR）来评估共病负荷和肾功能。同时根据高血钾患者是否合并高血同型半胱氨酸血症将患者分为两组，对血清钾、血同型半胱氨酸（Hcy）及 eGFR 进行相关性分析。

结果 在 1832 例血清钾高临界值的患者中，男性患者 1034 例，平均年龄 57 岁；女性患者 798 例，平均年龄 59 岁。住院患者发病率最高（67.41%），就诊科室主要是肾病内科（49.62%），临床诊断主要是慢性肾脏病 5 期（37.88%），平均 eGFR 为 16ml/min。1832 例高血钾患者中符合后续研究标准的重点实验组共 135 例，根据 Hcy 是否增高（＞15μmol/l）分为两组，高 Hcy 组（n=99）与正常 Hcy 组（n=36）相比，CCS、血清钾明显升高，肾小球滤过率明显降低（p＜0.05）。Hcy 与 CCS 有一定的相关性（r=0.229 0, p＜0.01））。Hcy 与高临界值的血清钾呈显著正相关（p＜0.01），与 eGFR 水平均呈显著负相关（p＜0.01）。

结论 血清钾高临界值患者的特点是高共病率、eGFR 降低和高 hcy。血钾升高更易合并高血同型半胱氨酸血症，且 Hcy 是慢性肾脏病患者动脉硬化的重要危险因素，应重点关注慢性肾脏病患者与心脑血管疾病共病风险。

PU-1917

血脂、尿酸等检验指标与抑郁症的相关性研究

潘俊希
昆明医科大学第一附属医院医学检验科
云南省检验医学重点实验室
云南省实验诊断研究所

目的 探讨抑郁症患者血脂、尿酸、血糖等检验指标水平的改变，并探讨其作为抑郁症诊断标志物的可能。
方法 共收集抑郁症患者 192 例，健康对照 97 例，比较抑郁组组与对照组是否存在血脂、尿酸、空腹血糖、PLT、MPV 等检验指标差异，再将疾病组分为不同亚组，按(HDMA17 评分)分为重度抑郁组 77 例，轻中度抑郁组 115 例；按性别分为女性抑郁组，男性抑郁组，按年龄分为＜55 岁青中年组、≥56 岁老年组；按病程长短，分为病程＜2 年短病程组及病程＞2 年长病程组；在各亚组探讨上述检验指标的差异。
结果 抑郁组 TC、FC、TG、LDL、APOE、尿酸水平明显高于对照组，而 HDL 水平显著低于健康对照组（详见图 1）。空腹血糖、APOA1、APOB、LP(a)在两组间无显著差异。二元逻辑回归分析发现 UA、TG 、HDL 与抑郁症具有显著相关性，三指标联合进行 ROC 分析，其 AUC 值为 0.915（详见图 1）。在亚组分析中，女性总胆固醇、LDL、HDL 明显高于男性，而血尿酸水平比男性低，空腹血糖、TG 无差异。老年组空腹血糖、TC、FC、HD 显著高于青中年组，老年组血尿酸较青中年组低。重度抑郁组与轻中度抑郁组中，上述检验指标均无显著差异。
结论 抑郁症患者存在血脂及血尿酸水平异常，UA、TG 、HDL 三指标联合对抑郁症有较好的诊断效能。

PU-1918

全自动生化流水线常规检验中血清 CO2 检测方法的比较研究

苏看看、张洁心
江苏省人民医院（南京医科大学第一附属医院）

目的 首次在全自动生化流水线上比较循环酶法（CEM 法）和磷酸烯醇式丙酮酸羟化酶法定量检测血清二氧化碳（CO2）浓度的时间依赖性差异研究。
方法 统计 58 份门诊和住院标本在生化流水线线上开盖等待检测时长。在此基础上，收集 10 份不同患者来源的促凝血标本，经标准化前处理操作并开盖室温静置，在指定时间点（0h，1h，3h，6h）分别检测血清 CO2 浓度；计算每种方法在 1h、3h、6h 检测结果与 0h 初始结果的偏倚。
结果 58 份标本开盖等待检测时长中位数 107 分钟。标本放置 1h 和 3h 时，CEM 法检测血清 CO2 浓度结果偏倚 3.28%— -5.21%，而 PEPC 法检测结果偏倚较大（17.86%— -11.7%）；标本放置 6h 时，PEPC 法检测血清 CO2 浓度结果偏倚在 2.21%— -30.64%，但 CEM 法的偏倚仍保持在-2.38%— -13.07%。
结论 标本放置时间相同时，相比 PEPC 法，CEM 法检测血清 CO2 浓度较稳定，CEM 法更适用于大标本量实验室全自动生化流水线上 CO2 定量检测

PU-1919

Poly(ADP-Ribose) Polymerase Activity and Coronary Artery Disease in Type 2 Diabetes: An Observational and Bidirectional Mendelian Randomization Study

Xuebin Wang
Department of Clinical Laboratory, The First Affiliated Hospital of Zhengzhou University

Objective Experimental evidence suggests a close link between poly(ADP-ribose) polymerase (PARP) activation and diabetic endothelial dysfunction. Here, we tested whether PARP activity in circulating leukocytes was associated with coronary artery disease (CAD) among patients with type 2 diabetes mellitus (T2DM).
Approach and Results We performed observational and bidirectional Mendelian randomization studies of 3149 Chinese individuals with T2DM who underwent coronary angiography, with leukocyte PARP activity, 16 tag single nucleotide polymorphisms (SNPs) in PARP1 and PARP2, and 17 CAD risk SNPs analyzed. Of 3149 participants, 1180 who further received percutaneous coronary intervention (PCI) was prospectively followed for 1 year to track major adverse cardiovascular and cerebrovascular events (MACCEs). Overall, greater PARP activity was cross-sectionally associated with an odds ratio (OR) of 1.23 for obstructive CAD, and prospectively with a hazard ratio of 1.34 for 1-year MACCEs after PCI (both $P < 0.001$). Using a genetic score of 5 screened SNPs in PARP1 and PARP2 as the instrumental variable, genetically predicted elevation in PARP activity showed a causal association with obstructive CAD (OR = 1.35, $P < 0.001$). In contrast, the genetic risk of CAD had no significant effect on PARP activity. Ex vivo and in vitro cultures of human monocytes showed that rs747657, as the lead SNP strongly associated with PARP activity, caused the differential binding of transcription factor GATA2 to an intronic regulatory region in PARP1, thus modulating PARP1 expression and PARP activity.
Conclusion Greater PARP activity may have causal roles in the development of obstructive CAD among diabetic patients.

PU-1920

石墨烯量子点调控肿瘤放射增敏作用研究

王英、陈福祥、葛盛芳
上海交通大学医学院附属第九人民医院

目的 本研究采用具有良好生物相容性和丰富含氧基团的纳米材料石墨烯量子点（GQDs），探讨其对结直肠癌细胞的放射增敏作用，并对辐射增敏的机制进行初探，为纳米材料作为放射增敏剂在临床应用中奠定研究基础。
方法 制备 GQDs 并通过 CCK8 法筛选出 GQDs 的安全浓度；应用激光共聚焦显微镜观察 GQDs 在肿瘤细胞内的分布；采用 CCK8 和克隆形成实验检测 GQDs 与辐射共同处理后细胞活性和克隆的形成；采用流式细胞技术检测各处理组细胞凋亡率；利用透射电子显微镜观察细胞损伤情况以及 GQDs 亚细胞定位情况；采用流式细胞技术检测各处理组细胞周期阻滞；利用 DCFH-DA、MITOSOX Red 探针分别检测辐照后细胞内 ROS 和线粒体 ROS 的产生；采用蛋白免疫印迹技术检测照射后反映 DNA 损伤程度的 γH2AX 的表达。
结果 CCK8 实验筛选出 GQDs 的使用浓度为 50μg/mL；透射电镜和激光共聚焦显微镜结果显示 GQDs 分布在细胞质内；GQDs 可以协同辐照抑制 SW620 和 HCT116 细胞的增殖，并促进细胞凋亡发生，增加细胞的损伤；研究发现 GQDs 可协同射线产生活性氧, 引起 DNA 双链断裂，导致细胞发生 G2/M 期细胞周期阻滞。
结论 本研究在细胞水平证明了 GQDs 具有放射增敏作用，可以协同射线杀伤肿瘤细胞，最终达到抑制肿瘤生长的目的。提示 GQDs 可作为一种新型放射增敏剂。

PU-1921

降钙素原在细菌性血流感染不同致病菌中的预测价值

宋健梅、邓德耀
云南大学附属医院

目的 探讨降钙素原（Procalcitonin，PCT）在不同致病菌所致的细菌性血流感染中的预测价值。
方法 选取 2018 年至 2019 年两年某三甲医院收治的细菌性血流感染患者 339 例，按病原菌形态分为革兰阳性菌组 108 例，革兰阴性菌组 231 例，对两组致病菌 PCT 水平的测定结果进行统计分析。
结果 细菌中以大肠埃希菌最为常见，占总菌株的 40.4%。血清 PCT 水平测定结果最高的为肺炎克雷伯菌 28.29（3.82~55.17）ng/mL，其次为鲍曼不动杆菌 8.82（3.74~24.84）ng/mL、大肠埃希菌 6.28（1.20~34.31）ng/mL，革兰阴性菌 PCT 水平 6.93（1.70~38.63）ng/mL 明显高于革兰阳性菌 PCT 水平 1.03（0.30~4.54）ng/mL，差异具有统计学意义（P<0.05）；在革兰阳性菌中，各组间均无统计学差异。
结论 PCT 水平对革兰阳性菌和革兰阴性菌所致血流感染的不同菌种的鉴别具有一定临床应用价值，可为不同菌种所致的细菌性血流感染提供一定抗感染治疗的参考。

PU-1922

生化检验在肾上腺皮质疾病诊断中的准确性及临床价值研究

钟浩宇
四川省人民医院东院

目的 研究生化检验在肾上腺皮质疾病诊断中的准确性及临床价值。
方法 将 2020 年 1 月~2021 年 5 月期间本院确诊肾上腺皮质疾病患者共 39 例纳为研究对象，取分层随机化分组法划分组别后，对照组（n=20）行常规检验，观察组（n=19）行生化检验。对照组中男 7 例，女 13 例，年龄区间 19~48 岁，平均（33.51±2.09）岁；观察组中男 6 例，女 13 例，年龄区间 18~48 岁，平均（33.29±1.98）岁。基线资料组间对比结果无统计学差异，P＞0.05，研究结果可比。常规检验项目含血糖、血清甘油三酯、总胆红素、总胆固醇、尿酸、高密度脂蛋白胆固醇及微量元素等；生化检验项目含 24h 尿-17 羟皮质类固醇、尿酮固酮及血浆醛固酮。比较两组检验结果准确性及检验有效率。
结果 （1）检验准确性、有效率：观察组检验准确性（89.47%）及检验有效率（94.74%）均高于对照组，差异显著，P＜0.05。（2）诊断价值：观察组诊断符合率（89.74%）、诊断敏感度（89.74%）及阳性预测值（100.00%）均达 80%以上，且高于对照组，差异显著，P＜0.05。
结论 生化检验在肾上腺皮质疾病诊断中的应用可在常规检验指标基础上经分析受检者 24h 尿-17 羟皮质类固醇、尿酮固酮及血浆醛固酮后，提升患者疾病临床检出效果及准确性，诊断价值显著。

PU-1923

动态监测骨折患者术后血浆 D-二聚体和 FDP 水平的临床价值

朱爱民
娄底市中心医院

目的 通过动态监测骨折患者术后血浆 D-二聚体和纤维蛋白降解产物（FDP）浓度水平，研究其临床应用价值。
方法 采用胶乳免疫比浊法对 215 例骨折患者术后第 3 天、第 7 天及第 10 天进行血浆 D-二聚体和 FDP 的定量检测，观察浓度水平变化。

结果 215 例患者中有 13 例并发深静脉栓塞（DVT），并发 DVT 组术后血浆 D-二聚体和 FDP 浓度水平呈进行性增高，与未并发 DVT 组相比较，有显著性差异（P＜0.05）。
结论 动态监测骨折患者术后血浆 D-二聚体和 FDP 水平对并发深静脉栓塞具有早期诊断价值。

PU-1924

全血 CRP 对小儿败血症的诊断价值

梁巧、王玲
中南大学湘雅二医院

目的 探讨全血 CRP 在小儿败血症中的诊断价值。
方法 选取我院 2019 年 4 月至 2021 年 1 月儿科、新生儿科住院的败血症患儿为研究组，选取同期的肺炎患儿以及非炎症疾病患儿为疾病对照组和阴性对照组，检测各组全血 CRP、PCT、WBC 和 NLR，分析三组各指标之间的差异，绘制各指标的 ROC 曲线，分析其对小儿败血症的诊断以及鉴别诊断价值；并分析败血症组不同病原菌之间各指标的差异以及患儿各指标与其病情严重程度的相关性。
结果 败血症患儿的全血 CRP、PCT 高于疾病对照组和阴性对照组（P<0.05），NLR 高于疾病对照组（P<0.05），而三组的 WBC 不存在统计学差异；小儿败血症诊断的 ROC 曲线显示：全血 CRP、PCT、NLR、WBC 的 AUC 分别是 0.956、0.747、0.567 和 0.421；小儿败血症与肺炎鉴别诊断的 ROC 曲线表明：全血 CRP、PCT、NLR、WBC 的 AUC 是 0.915、0.779、0.648、0.490；全血 CRP 和 NLR 与 PITT 评分和住院时长呈正相关（r=0.303-0.375，P<0.05）；G^-杆菌感染患儿的全血 CRP、PCT 和 PITT 评分高于 G^+球菌感染患儿（P<0.05）。
结论 全血 CRP 可以用于小儿败血症的诊断、鉴别诊断以及病情严重程度的判断，并且还可用于初步判断败血症患儿感染的菌种类型。

PU-1925

血清同型半胱氨酸与脂蛋白 a 联合检测在诊断脑梗中的价值

杨婷
德州市人民医院

目的 研究同型半胱氨酸(Hcy)与脂蛋白（Lpa)联合检测在诊断脑梗中的临床价值。
方法 选择 2018 年 1 月至 2019 年 12 月期间我院收治的脑梗死住院患者 136 例按不同病情严重程度分为轻、中、重三组，选择同期体检正常人员 50 例作为对照组，采集静脉血浆检测 Hcy 和 Lpa 水平。
结果 脑梗患者血清 Hcy、Lpa 水平分别为 (14.25±4.10)μmol/L，(28.25±18.25)mg/dL 与正常对照组 (7.91±2.05)μmol/L、(18.50±9.28)mg/dL 相较均显著增高 (P<0.05)。三种不同严重程度的患者两两比较显示，重型患者血清 Hcy 水平显著高于中，轻型患者(P<0.05)；重型患者血清 Lpa 水平显著高于中、轻型(P<0.001)，且中型显著高于轻型(P<0.05)。
结论 血浆 Lpa 和 Hcy 水平与脑梗死的发生、发展密切相关，两项指标的联合监测对判断病情具有重要指导意义。

PU-1926

HPLC-FLD 法用于检测色氨酸代谢物的研究

吴妍茜
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 探究血浆中吲哚类物质对 PCOS（polycystic ovary syndrome，多囊卵巢综合征）患者抑郁的影响。
方法 采用高效液相色谱-荧光检测(HPLC-FLD)方法同时测定血浆中吲哚类物质，包括吲哚基硫酸盐(3-INDS)、吲哚-3-乙酸(IAA)、吲哚-3-丙酸(IPA)、吲哚(IND)和 3-甲基吲哚(3-MI)。选用乙醚和乙酸乙酯作为萃取剂制备样品。色谱柱为 shimm - pack VP-ODS (4.6 × 150 mm i.d.，4.6μm，岛津)，流动相为 10 mmol/L 磷酸二氢钠/甲醇(40:60,v/v)。荧光检测的激发波长和发射波长分别为 280 nm 和 355 nm。
结果 3-INDS、IAA、IPA、IND 和 3-MI 在 1.56 ~ 400.00 μmol/L、312.50 ~ 1000.00 nmol/L、125.00 ~ 600.00 nmol/L、6.25 ~ 400.00 nmol/L 和 1.56 ~ 400.00 nmol/L 血浆中线性关系良好。日内和日间精密度的变异系数(cv)分别在 4.0%和 5.2%以内。加标回收率为 90.1% ~ 109.3%，CV 为 1.6% ~ 8.2%。该方法简便、灵敏、准确。使用该方法对 PCOS 伴抑郁和不伴抑郁患者的血浆吲哚进行分析。
结论 IND 是 PCOS 患者抑郁的一个危险因素，这为 PCOS 患者抑郁的病理生理学机制提供了思路。

PU-1927

抗 CCP 抗体在类风湿关节炎诊断中的临床价值

崔嘉玥
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 研究类风湿关节炎(Rheumatic Arthritis，RA)患者血清中的抗环瓜氨酸肽抗体(ACPA)对 RA 诊断的敏感性和特异性及其在 RA 中的临床应用价值。
方法 选取 2018 年 2 月至 2020 年 1 月在北京 301 医院的 RA 患者（RA 组）、其他自身免疫性疾病患者（非 RA 组）及健康体检者（对照组）为研究对象，采用手工酶联免疫吸附法（ELISA）检测抗环瓜氨酸肽（CCP）抗体水平，采用速率散射比浊法检测类风湿因子（RF），采用日本 SYSMEX 全自动血液细胞分析仪检测超敏 C 反应蛋白（hs-CRP），采用 greiner bio-one 全自动血沉分析仪检测红细胞沉降率（ESR），所有收集得到的数据采用 SPSS20.0 软件包进行处理。
结果抗 CCP 抗体诊断 RA 的敏感性和特异性分别为 86.1%和 97.3%，与 RF（敏感性 87.5%，特异性 94.6%）相比，具有较高特异性；抗 CCP 抗体和 RF 两者联合检测，敏感性和特异性分别为 97.3%和 88.9%；受试者工作特征曲线（ROC）显示抗 CCP 抗体检测对 RA 诊断具有较高的特异性，抗 CCP 抗体和 RF 两者联合检测对 RA 诊断具有较高的敏感性。
结论 抗 CCP 抗体在类风湿关节炎早期的诊断中具有较高的特异性和敏感性，是理想的血清学指标，对类风湿关节炎的预测和诊断具有一定临床价值，值得在临床检验中推广应用。

PU-1928

MiR-495 Inhibits Fibroblast-Like Synoviocyte Proliferation and Inflammation in Rheumatoid Arthritis Rats via Wnt Signaling Pathway

hongmei yang
yantaishan hospital

As an immunological disease triggered by autoantigen, rheumatoid arthritis (RA) is manifested as redness, swelling and pain of joints, with the cardiovascular system, lungs and other organs beyond joints involved.1 Studies have shown that both inheritance and environment are risk factors of RA, but the mechanism needs an indepth exploration.1 Micro ribonucleic acids (miRNAs) are a kind of short and small non-coding RNAs.2 Increasingly more evidence has proved that miRNAs play a vital role in autoimmune diseases. In a study of Mallinson et al3 regarding response of RA patients to mesenchymal stem cell treatment, it was found that miR-495 expression is up-regulated in the response group, indicating that miR-495 is implicated in the pathogenesis of RA. The pathogenesis of RA involves multiple signaling pathways, among which the Wnt signaling pathway artificially promotes the fibroblast-like synoviocyte (FLS) proliferation in RA. Even though miR-495 has been verified to be related to RA, no report has pointed out whether miR-495 participates in the pathogenesis of RA via the Wnt signaling pathway. Given this, the rat model of RA was used to study the effects of miR-495 on the FLS proliferation, and its action mechanism was discussed.

PU-1929

全自动生化分析仪平台检测 CKMBmass 的临床应用评价

邓克廷、丁莹、徐小华、李斌
西安医学院第一附属医院

目的 探讨利用全自动生化分析仪平台检测 CKMBmass 的准确性及可靠性。采取随机抽样的方式以及检测临床标本中 CKMB（活性法）大于 CK 的样本，验证该测量程序与化学发光平台测定 CKMB(质量法)的一致性，再用超敏肌钙蛋白 I 阳性的样本验证该方法测量的准确性。
方法 使用 Beckman AU5800 全自动生化分析仪测定 CKMBmass, CKMB（活性法）； Beckman DXI800 化学发光分析仪检测 CKMB（质量法），超敏肌钙蛋白 I（hs-cTnI）。收集 40 例 CKMBmass 与 CK-MB 同时检测的倒置样本， 验证测量值一致性; 随机抽取 60 例 CKMBmass 与 CK-MB 同时检测的血清样本， 验证相关性; CKMBmass 与 hs-cTnI 同时测定心肌损伤组样本与非心肌损伤组样本， 使用 ROC 曲线进行分析， 验证 CKMBmass 准确性。
结果 40 例倒置样本， CKMBmass 测量值与 Beckman DXI800 CK-MB 测量值相同， 阴阳性一致; 60 例随机样本， CKMBmass 与 Beckman DXI800 CK-MB 测值的回归方程为 Y = 1．015X +0．185; 心肌损伤组与非心肌损伤组比较差异有统计学意义(P ＜ 0.05)。
结论 Beckman AU5800 全自动生化分析仪测定 CKMB mass 的准确性和可靠性能良好，抗干扰能力及相关性与化学发光法检测 CK-MB 一致， 满足临床诊疗需求。

PU-1930

NSE、SCC、Cyfra21-1、CEA 和 CK-19 联合检测对肺癌诊断价值的临床验证

陶亚、易斌
中南大学湘雅医院

目的 通过临床病例分析，验证神经元特异性烯醇化酶(NSE)、鳞状上皮抗原(SCC) 、细胞角蛋白 19 片段(Cyfra21-1)、癌胚抗原(CEA) 、角蛋白 19 (CK-19)五项血清肿瘤标志物联合检测对肺癌诊断、病理分型和临床分期的价值。
方法 回顾性分析从 2019 年 9 月至 2020 年 9 月中南大学湘雅医院 156 例确诊肺癌患者和 108 例良性肺病患者肺癌五项临床检验结果，血清 NSE、SCC、Cyfra21-1、CEA 和 CK-19 水平均采用化学发光法测定。
结果 肺癌组血清 NSE、Nsclc21-1、CEA 水平显著高于良性肺部疾病组 (P<0.05)，肺癌组血清 SCC、和 CK-19 水平良性肺部疾病组无明显差异(P＞0.05)；血清 NSE 水平在小细胞癌患者中明显升高(P<0.05)，血清 SCC、Cyfra21-1、CK-19 水平在肺鳞癌患者中明显升高(P<0.05)，血清 CEA 血清水平在肺腺癌患者中显著升高(P<0.05)，结合肺癌患者临床资料分析显示：男性患者血清 SCC、Cyfra21-1、CK-19 水平明显高于女性患者(P<0.05)；血清 Cyfra21-1 水平在大于 50 岁年龄组患者中明显升高 (P<0.05)；血清 NSE、Cyfra21-1、CEA、CK-19 水平与肿瘤大小成正相关(P<0.05)；血清 SCC、Cyfra21-1、CK-19 水平与淋巴结转移相关(P<0.05)；血清 CEA 水平与远处转移相关(P<0.05)；血清 NSE、Cyfra21-1、CEA、CK-19 水平与临床分期相关(P<0.05)。五项血清标志物联合检测敏感性为 71.53%，显著高于单项检测(P<0.05)，特异性为 90.21%，未显著下降(P>0.05)。
结论 1，NSE、Cyfra21-1、CEA 水平升高与肺癌发生密切相关，与文献报道相符，对肺癌早期诊断有重要的临床意义；2，NSE、SCC、Cyfra21-1、CEA、CK-19 在不同病理类型，TNM 分期，临床分期中各有特点，与文献报道相符，可为肺癌临床病理分型和临床进展提供依据；3，五项肿瘤标志物单项检测在肺癌诊断中敏感性较低，易漏检，但其联合检测可有效提高肺癌诊断准确率。

PU-1931

Effect of dry-heat inactivation on biochemical tests related to diagnosis and treatment of novel coronavirus in 2019

Tingting Ji
Nanfang Hospital, Southern Medical University

Background The World Health Organization (WHO) declared novel coronavirus disease as a pandemic disease. To reduce the risk of transmission in the laboratory and protect medical staff, dry-heat inactivation at 56 ℃ for 30 minutes for SARS-CoV-2 has been suggested. We evaluated the impact of venous blood heating on biochemical tests related to diagnosis and treatment of novel coronavirus.
Methods 150 intravenous serum specimens (of which 30 liver function tests, 30 renal function samples, 30 blood glucose samples, 30 inflammation tests and 30 myocardial injury tests) on Roche Cobas c8000 were obtained, and detected again after dry-heat treatment at 56 ℃ for 30 minutes on the day. The difference of the results before and after the inactivation was compared.
Results A total of 17 biochemical tests were assessed. Nine tests (C-reactive protein, amyloid A, albumin, total bilirubin, total carbon dioxide, uric acid, urea, lactate dehydrogenase and a hydroxybutyrate dehydrogenase were not significantly different affected by the heat treatment and accepted clinically. The differences of detection results of before and after inactivation for

aspartate aminotransferase, total protein, and creatinine was within 1/3TEA and clinically acceptable. Regression equation could correcte the detection of blood glucose, alanine aminotransferase, direct bilirubin, creatine kinase, and creatine kinase isoenzyme after inactivation to the pre-inactivation results and clinically interpreted.

Conclusion Dry-heat inactivation at 56 ℃ for 30 minutes causes no significant change in inflammation tests and renal function tests, but results in a obvious bias for many analytes. Statistical procedure could correct the affected results according to the relationship between before and after inactivation, accepted clinically. Dry-heat inactivation at 56 ℃ for 30 minutes should be recommended to reduce the risk of laboratory workers infecting novel coronavirus.

PU-1932

糖化血红蛋白与血糖相关性的研究现状分析

吴孟娜、冯磊、罗旋、邵聪
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

了解糖化血红蛋白与血糖间相关性的研究现状，为临床更精准运用糖化血红蛋白提供参考依据。本文通过收集、整理国内外有关糖化血红蛋白与空腹血糖、餐后血糖、平均血糖间相关性文献，了解糖化血红蛋白与血糖间相关性的研究现状，并分析可能引起结果间差异的影响因素。通过分析发现糖化血红蛋白与血糖相关性的研究结果间仍存在争议，两者间线性关系或模型也存在问题，因此还需统一标本类型、检测方法等因素后，针对不同种族、不同患病类型的患者进行更大的流行病学研究。

PU-1933

Beckman Coulter AU5821 全自动生化分析仪检测 SAA 的性能验证分析及其在糖尿病肾病中的临床应用研究

陶亚
中南大学湘雅医院

目的 对血清淀粉样蛋白 A（SAA）试剂盒在 Beckman Coulter AU5821 全自动生化分析仪上的检测性能进行评价，并探讨其在糖尿病肾病中的应用价值。

方法 通过实验计算 AU5821 全自动生化分析仪检测 SAA 的正确度，精密度，最低检测限，线性范围，可报告范围，生物参考区间，与厂家说明书提供的参考值比较，评估 SAA 试剂在 AU5821 生化分析仪上的检测性能。选取临床明确诊断的单纯糖尿病患者 34 例、早期糖尿病肾病患者 21 例、临床糖尿病肾病患者 30 例，体检健康者（正常对照组）30 名，检测血清 SAA 水平。

结果 SAA 的高、低水平相对偏差分别为-4.78%和-4.25%，均≤10%，符合厂家试剂正确度要求；新鲜混合血清标本高、低水平的批内精密度的变异系数（CV）分别为 1.38%、1.85%，批间精密度的变异系数（CV）分别为 2.74%、4.41%，均满足厂家说明书的要求；最低检测限为 1.37mg/L，不高于 5mg/L，符合要求。SAA 线性回归方程 Y＝1.0248x-0.9715，决定系数（R2）＝0.998，斜率 b=1.0248（在 1.00±0.03 范围内），p>0.05，R2=0.998＞0.95，SAA 可接受线性范围为 3-175.82 mg/L。结合线性范围结果，得出该试剂临床可报告范围为 3.00- 2813.12mg/L。检测的 20 份体检标本中只有 1 例标本测定结果超出厂家该项目的参考值（≤10mg/L），厂家提供的参考值（≤10mg/L）可用。单纯糖尿病组血清 SAA 水平高于健康对照组 (P<0.01)，且随着肾病的加重而升高。

结论 SAA 试剂盒在 AU5821 生化分析仪上检测性能能满足厂家和卫生行业标准要求，且其正确度好、重复性好，结果可靠，能较好地满足临床工作。血清 SAA 水平升高是糖尿病肾病重要危险因素。

PU-1934

Exploring the correlation between glycosylated hemoglobin and fasting blood glucose based on chemical reaction theory

Lei Feng 、Shiyan Nian、Ying Li、Xuejing Bai、Xuan Luo、Mengna Wu、Zefeng Yan
Department of Laboratory, People's Hospital of Yuxi City (Department of Laboratory, The Sixth Affiliated Hospital of Kunming Medical University)

Objective To explore the correlation between HbA1c and fasting blood glucose (FPG) by analyzing the HbA1c formation process and its influence factors.
Methods Natural population consist of 14266 cases in Yuxi City,Yunnan Province were collected, aged from 18 to 93 years old, including 8832 males (45.87±13.16) and 5434 females (43.46±12.07), testing their HbA1c, FPG, red blood cell distribution width (RDW) and hemoglobin (Hb) levels. 1) Compare the level differences of HbA1c and FPG between distinct sexual group; 2) analyze the trend of each index along with age changing after age stratification ; 3) divide all the subjects into 5 groups, as FPG＜5.0mmol/L、5.0-5.9 mmol/L、6.0-6.9 mmol/L、7.0-11.0 mmol/L 和≥11.1 mmol/L, calculate the correlation between FPG and HbA1c in each group, then analyze the variation trend of correlation coefficient; 4) divide all the subjects into 4 groups, as HbA1c＜5.7%、5.7-6.4%、6.5-7.4%、≥7.5%, and also calculate the correlation between FPG and HbA1c in each group, then analyze the variation trend of correlation coefficient.
Results 1) This study found that gender differences existed in HbA1c and FPG levels. 2) HbA1c, FPG and RDW varied very sharply with age, while Hb level showed a narrower fluctuation; and the changing trend of these indexes in different gender differed either; 3) The correlation between FPG and HbA1c was lower within the group which FPG below 7.0mmol/L or HbA1c below 6.5%, but with the increasing of their respective levels,the correlation increased , and it turned out similar results in both male and female.
Conclusion The correlation between FPG and HbA1c are influenced by age and FPG level. HbA1c's representativeness of blood glucose vary under different conditions.

PU-1935

糖化血红蛋白异常峰图的临床应用

万雅芳
重庆市人民医院（重庆市临床检验中心）

目的 通过利用高效液相色谱法（HPLC）检测样本的糖化血红蛋白值，对其所出现的异常峰图进行分析，确定其与地中海贫血和（或）异常血红蛋白病是否存在相关性。
方法 采用高效液相色谱法对样本进行检测，测其糖化血红蛋白值，将所出现异常峰图的 39 例（包括 HbF>1.5 或者出现了 P00 峰）样本选出。采用 PCR+导流杂交的方法对样本进行检测，确定其是否为中国人中最常见的三种缺失型 α-地贫：--SEA,-α3.7，-α4.2 和三种突变型 α-地贫：CS,QS,WS 以及 17 个位点的 19 种突变型 β-地贫。若 α，β 地贫均为阴性，还需用测序仪用双脱氧链终止法(Sanger 法) 对血红蛋白基因测序。回顾性分析血常规，肝功，血红蛋白电泳等结果。利用统计学分析法对以上结果进行总结。

结论 通过对 39 例重庆地区糖化血红蛋白异常结果的进一步检测，其中已有 11 例确定为 α 或 β 地中海贫血，其余标本由于 HbF 值均为增高状态可通过对其他检测结果的分析以及对相关文献的研究可证实其余为地贫阴性的样本还有很大一部分是存在其他基因点突变，是可以通过双脱氧链终止法(Sanger 法)对血红蛋白基因测序，并确定其具体为哪种位点突变的异常血红蛋白病。

PU-1936

联合检测 ADA 和 PCT 在结核性胸膜炎诊断中的价值

王晓芳
丹东市第一医院

目的 研究并分析检验 ADA 与 PCT 在结核性胸膜炎诊断中的临床价值。
方法 选取我院在 2017 年 3 月-2017 年 10 月期间收治并确诊的结核性胸膜炎患者 30 例组成研究组，选取我院同期收治住院非结核性胸膜炎患者 30 例为对照组。两组患者均采用酶偶联谷氨酸脱氨酶反应连续监测法检测血清 ADA，再采用干式免疫荧光法对血清 PCT 进行检测，对比分析两组患者的血清 ADA 以及血清 PCT 的含量。
结果 研究组患者的胸水 ADA 值（51.34 ±3.19）U/L 显著高于对照组（20.31 ±1.34）U/L，而且研究组血清 ADA 值（23.31 ±3.14）U/L 也明显高于对照组（20.15 ±2.10）U/L；研究组中患者血清中 PCT 含量为（1.31±0.14）ng/ml，显著高于对照组（0.01±0.003）ng/ml（P＜0.05），差异具有统计学意义。
结论 ADA 以及 PCT 对于诊断结核性胸膜炎以及非结核性胸膜炎具有诊断性意义，临床应用价值较高。

PU-1937

生化免疫流水线使用初期平诊生化标本 TAT 延长的改进措施

卢婷
南京大学医学院附属鼓楼医院

通过分析生化免疫流水线（贝克曼公司，PowerProcessor）使用初期生化平诊标本检验结果汇报时间（turnaround time,TAT）延长的原因，制定改进措施，包括优化管理制度和工作流程、培训人员、维护仪器、更换真空采血管和改变离心时间、加强和临床的沟通、制定发生故障应急预案等措施，经过上述措施，使得平诊 TAT 时间符合科室的质量指标，以供准备引入和使用贝克曼生化免疫流水线的医院作为参考。

PU-1938

酒依赖患者血浆同型半胱氨酸含量的变化

董丽梅、李琳
哈尔滨医科大学附属第一医院

目的 探讨酒依赖患者血浆同型半胱氨酸(Ｈｃｙ)含量的变化，及Ｈｃｙ相关的某些因素。
研究与方法 酒依赖患者 20 人,对照组 20 人进行血Ｈｃｙ的测定,同时测定血叶酸(叶酸)、维生素Ｂ12(ＶｉｔＢ12)的浓度。
结果 ①酒依赖患者血Ｈｃｙ显著高于对照组(Ｐ<0.01)②酒依赖患者叶酸及ＶｉｔＢ12 水平低于对照组(Ｐ<0.05)。③Ｈｃｙ浓度与叶酸、ＶｉｔＢ12 水平之间存在相关性(Ｐ<0.05)。

结论 酒依赖患者Ｈｃｙ浓度明显升高,血清叶酸、ＶｉｔＢ12 水平降低，Ｈｃｙ浓度的升高可能与患者叶酸、ＶｉｔＢ12 代谢障碍有关。

PU-1939

探讨血清 CRP 和 CER 在肝癌和肝硬化鉴别诊断中的价值

蔡桂君
南方医科大学珠江医院

目的 比较肝硬化和肝癌患者的血清 CER,CRP 含量的差异，观察这些指标对疾病的诊断和鉴别诊断是否具有临床意义。
方法 选取标本来自 2016 年 10 月~12 月间门诊及住院的肝癌与肝硬化患者，对其进行超敏反应蛋白及铜蓝蛋白的检测。
结果 血清中铜蓝蛋白浓度的比较中肝癌组明显高于肝硬化组和健康对照组(P<0.05)，但肝硬化组和正常对照组之间无显著性差异（P=0.785）。血清中 C 反应蛋白浓度的比较中肝癌组和肝硬化组均明显高于正常对照组(P<0.05)而肝癌与肝硬化组之间则无显著差异(P=0.272)。其中两项指标同时增高中，肝癌组中比例为 73%，远大于肝硬化组 47%。只有 C 反应蛋白增高，铜蓝蛋白无明显增高的样本，肝硬化组占 22%。远大于肝癌组 4%。
结论 当两项指标均显著升高时，应该多考虑患肝癌的可能性，而只有 C 反应蛋白升高，铜蓝蛋白无明显升高时，则患肝硬化的几率增加。两项指标在肝癌和肝硬化中升高程度不同，有互补性。

PU-1940

PCT、SAA、hs-CRP 和 WBC 检测对婴幼儿感染性疾病的临床诊断价值分析

黄凯
江西省儿童医院

目的 探究血清降钙素原（PCT）、淀粉样蛋白 A(SAA）、超敏 C 反应蛋白（hs-CRP）、和白细胞计数（WBC）对婴幼儿感染性疾病的早期诊断价值。
方法 选取 2020 年 1-6 月在江西省儿童医院门、急诊就诊的 177 例婴幼儿感染性疾病患者作为研究对象，将其分为非细菌性感染组（87 例）和细菌性感染组（54 例）。另选取同期该院体检科 50 例健康体检者作为对照组。检测 3 组血清 PCT、SAA、hs-CRP 和 WBC 水平，并应用受试者工作曲线（ROC 曲线）评价临床诊断价值。
结果 细菌性感染组 PCT、SAA、hs-CRP、Neu%和 WBC 水平均高于非细菌感染组和对照组，差异均有统计学意义（P<0.05）；非细菌性感染组 PCT、SAA、hs-CRP 和 Neu%水平均高于对照组，但低于细菌性感染组，差异均有统计学意义（P <0.05）。PCT、SAA、hs-CRP 和 WBC 用于诊断细菌性感染疾病的 ROC 曲线下面积分别为 0.911、0.922、0.861、0.895、0.921。PCT、SAA、hs-CRP 和 WBC 用于诊断非细菌性感染疾病的 ROC 曲线下面积分别为 0.870、0.830、0.751、0.736、0.537。PCT、SAA、hs-CRP 和 WBC 用于鉴别诊断细菌性和非细菌性感染的 ROC 曲线下面积分别为 0.625、0.632、0.693、0.728、0.915。
结论 PCT、SAA、hs-CRP、Neu%和 WBC 检测对感染性疾病有相应的早期诊断价值，同时可用于感染性疾病的鉴别诊断，从而指导临床合理用药。

PU-1941

同型半胱氨酸和脂蛋白（a）联合检测与冠心病的相关性研究

刘家汝、关秀茹
哈尔滨医科大学附属第一医院

近年来，随着人们生活水平的提升，心脏病的发病率也越来越高。冠状动脉硬化性心脏病（冠心病） 作为临床常见的心血管疾病，其高发病率和死亡率已经严重威胁到人类的健康和生命安全[1]。若在临床中无法通过相关手段早期发现冠心病患者的症状进行并实施治疗，会对患者造成极其严重的影响[2]。随着医学领域对冠心病的研究日益深入，在冠心病的临床诊断方面取得了巨大的进展[3]。许多研究表明，血浆中同型半胱氨酸和脂蛋白的水平与冠心病患者的血管功能和动脉粥样硬化的发生与发展有着密切联系，对以上两项血清生化指标进行联合检测在冠心病的早期诊断中具有重要的意义。现从 Hcy、Lp(a)对冠心病病变的作用机制及其诊断的临床意义进行综述。

PU-1942

血清乳酸脱氢酶和 β2-微球蛋白检测在非霍奇金淋巴瘤中的应用

王加
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨血清乳酸脱氢酶（LDH）及 β2-微球蛋白(β2-MG)水平在非霍奇金淋巴瘤(NHL)诊断、治疗中的变化及临床意义。
方法 回顾性分析非霍奇金淋巴瘤（NHL）患者在治疗前后血清 LDH、β2-MG 动态水平，并进行随访，判断血清 LDH、β2-MG 水平与 NHL 临床特征及治疗疗效之间的关系。
结果 NHL 患者血清 LDH、β2-MG 水平明显升高，Ⅲ-Ⅳ期患者 LDH、β2-MG 水平均显著高于Ⅰ-Ⅱ期（P<0.05）。治疗完全缓解组 LDH、β2-MG 水平均显著下降，并且 LDH 和 β2-MG 升高组的生存率低于正常组（P<0.05）。
结论 LDH 和 β2-MG 的联合检测可提高 NHL 检出率，并对评价 NHL 临床分期、治疗疗效及预后判断方面有重要的临床价值。

PU-1943

抑郁症与血浆同型半胱氨酸水平的相关性研究

付璐、李洁
哈尔滨医科大学附属第一医院

目的 探讨同型半胱氨酸(Homocysteine，Hcy)在抑郁症发病中的作用。
方法 收集 30 例抑郁症及 30 名健康者血液标本，采用高效液相层析法测定血浆 Hcy,比较两组间差异。
结果 抑郁症组血浆 Hcy 水平高于对照组[(20.31±5.9)umol/L 比(10.96±4.51)umol／1，P<0.01]。
结论 抑郁症患者的血浆 Hcy 水平升高，提示 Hcy 与抑郁症的发病具有相关性。

PU-1944

血氨检测在临床中的应用价值

赵宇、董莉芹
哈尔滨医科大学附属第一医院

氨对于人体是一种有害的物质，它主要的代谢场所在肝脏，正常人血内有少量游离氨存在。血液中氨的来源主要为体内蛋白质在代谢过程中产生的氨基酸，以及经脱氨作用分解而来的内源性氨；另一来源是蛋白质类食物在肠道内经细菌分解而成的外源性氨。在正常情况下，肝脏能将氨通过鸟氨酸循环的特殊酶系，鸟氨酸氨基甲酰转移酶，氨基甲酰磷酸合成酶等，合成尿素，再经过肾脏排出。此外，脑和肾脏等器官的氨与谷氨酸作用生成谷氨酰胺后被运输到肝脏，在肝脏转变成尿素或其它含氮化合物后由肾脏排出体外，或形成铵盐随尿排出。因此正常人血氨含量较低，这个过程不仅可以解毒，同时在此过程中消耗了 CO2，故在维持酸碱平衡中也具有重要作用。

PU-1945

LDH 与 α-HBDH 检测在评估消化道肿瘤患者病情中的临床价值

解秀梅
徐州医科大学附属医院

目的 探讨血清乳酸脱氢酶（LDH）与 α-羟丁酸脱氢酶（α-HBDH）检测在评估消化道肿瘤患者病情中的的临床价值。
方法 回顾性分析 2017.11~2018.4 本院肿瘤科收治的 282 例消化道肿瘤患者（食道癌、胃癌、结肠癌、直肠癌）的病历资料（已排除患有或疑似患有心脏疾病的患者）,其中肿瘤非转移组 158 例、肿瘤转移组 124 例，比较转移性与非转移性肿瘤、不同转移组织、不同肿瘤分期之间患者血清乳酸脱氢酶(LDH)与 α-羟丁酸脱氢酶（α-HBDH）的水平。
结果 消化道肿瘤转移组 LDH 水平升高者明显高于消化道肿瘤非转移组,且 LDH 升高的水平高于消化道肿瘤非转移组，差异有统计学意义(P<0.05);肺脏和肝脏等多处转移组的 LDH 水平明显高于腹膜和周围淋巴结转移组,差异有统计学意义(P<0.05)；消化道肿瘤转移组 α-HBDH 的平均水平高于消化道肿瘤非转移组, 但差异未达到统计学意义； 肺脏和肝脏等多处转移组的 α-HBDH 平均水平高于腹膜和周围淋巴结转组，但差异也未达到统计学意义。
结论 消化道肿瘤发生转移的患者血清 LDH 水平明显升高,且与肿瘤的转移情况相关,故，当患者血清 LDH 水平明显升高时多数预示者患者病情的恶化，为临床医生评估肿瘤患者病情及治疗提供重要的参考价值，而血清 α-HBDH 在这方面的价值较小。

PU-1946

EB 病毒抗体及异型淋巴细胞比例单独或联合检测在儿童传染性单核细胞增多症诊疗中的应用价值研究

黄亚光、秦诗睿
三峡大学附属仁和医院

目的 探讨血清 EB 病毒（EBV）抗体与外周血中异型淋巴细胞比例单独或联合检测在儿童传染性单核细胞增多症（IM）诊断治疗过程中的应用价值。
方法 选取 237 例于 2020 年 3 月至 2021 年 4 月之间在我院儿科门诊及住院就诊的儿童作为研究对象纳入实验研究。实验共分为两组，其中观察组 107 例，均为临床确诊为 IM 的儿童；对照组 130 例，均为同期在儿童保健科进行健康体检的正常儿童。分别对两组儿童血清中 EBV 抗体及外周血

中异型淋巴细胞的比例的实验结果进行统计分析，比较两者单独及联合检测时诊断结果的特异性及灵敏度。
结果 单项分析异型淋巴细胞比例时，观察组阳性为 69 例，即诊断灵敏度为 64.49%，对照组阴性 103 例，即诊断特异性为 79.23% ；EBV 抗体单项分析，其观察组阳性 88 例，诊断灵敏度为 82.24%；对照组阴性 118 例，即诊断特异性为 90.77%；而两者联合检测结果分析显示，阳性为 101 例，即诊断灵敏度可提高至 94.39%，且与两项目单项检测的灵敏度相比，差异具有统计学意义（P<0.05）。
结论 血清 EBV 抗体及外周血异型淋巴细胞比例联合检测比两者单独检测可大大提高儿童 IM 诊断的灵敏度，联合可以作为临床辅助诊断儿童 IM 较为快速可靠的实验室方法，在儿童 IM 鉴别诊断中具有重要的临床价值。

PU-1947

蛋白质组学技术在糖尿病肾病中的研究进展

张炎
郑州大学第一附属医院

随着糖尿病肾病发病率的增加，糖尿病肾病已成为慢性肾脏疾病的最常见病因，甚至成为终末期肾病的首要病因。早期识别和诊断糖尿病肾病成为临床关注重点，估计肾小球滤过率和尿白蛋白缺乏敏感性和特异性，复杂性较低、稳定性更好的尿液蛋白质组学技术成为肾脏标志物研究的重要技术。目前已识别出与糖尿病肾病相关的蛋白质组学标志物主要是尿液中的胶原片段、蛋白片段、多肽小分子等，将多种标志物联合生成高维分类器（如 CKD273 等）在疾病的早期诊断和进展预测方面发挥重要作用。

PU-1948

孕妇口服葡萄糖耐量结果分析

吴佳梅
资阳市第一人民医院

目的 通过统计分析我院孕妇口服葡萄糖耐量试验（OGTT）结果，为临床诊治 GDM 提供依据。
方法 回顾性统计我院 2018 年 12 月-2020 年 12 月共计 4383 例孕中期（24-30 周）口服葡萄糖耐量的结果，分析不同年龄组孕妇的口服葡萄糖耐量的试验结果。
结果 A 组（≤20 岁）和 B 组（21-25 岁）的空腹血糖比较 P 值为 0.208，D 组（31-35 岁）和 E 组（≥36 岁）的空腹血糖比较 P 值为 0.269，P>0.05，差异无统计学意义，其余组之间两两比较 P 值均小于 0.05，差异有统计学意义。
结论 随着年龄的增长，GDM 确诊率明显增加，及时进行规范的 OGTT 试验在 GDM 的筛查和诊治中起到很大的作用。

PU-1949

基于血清 CHE、PA、TBA 水平测定对肝硬化评估的临床价值研究

王华国
四川省资阳市第一人民医院

目的 基于生化检测中血清胆碱酯酶（CHE）、前白蛋白（PA）和总胆汁酸（TBA）水平测定探求对肝硬化评估及诊断的临床价值。
方法 收集 2020 年 4 月至 2021 年 4 月间四川大学华西医院资阳医院.资阳市第一人民医院肝硬化住院患者和体检中心进行健康查体的健康人的临床资料，筛选 195 例肝硬化患者为实验组，已通过肝功能 Child-Pugh 分级为 78 例 A 级、60 例 B 级和 57 例 C 级；65 例健康查体的健康人为对照组，对以上患者生化检验中血清胆碱酯酶（CHE）、前白蛋白（PA）和总胆汁酸（TBA）水平检测结果进行回顾性分析。
结果 与对照组做比，实验组的 A 级、B 级和 C 级中血清 TBA 检测结果均偏高，血清 CHE 和 PA 检测结果均偏低，比较差异存在统计学意义（P<0.05）。实验组中随着肝功能分级等级的递增，TBA 水平检测结果随之升高，CHE 和 PA 水平检测结果随之降低，比较差异存在统计学意义（P<0.05）。实验组按肝功能 Child-Pugh 分级即患者疾病严重程度与患者血清 CHE、PA 测定水平与实验组肝功能 Child-Pugh 分级呈现负性相关，与 TBA 测定水平呈现正性相关，且 PA 相关性最大，CHE 次之，TBA 最小。三项指标在实验组 A 级中，与对照组比较，单项检测和联合检测的阳性检出率均高；与单项检测指标比较，联合检测的阳性检出率高，比较差异存在统计学意义（P<0.05）。
结论 血清 CHE、PA、TBA 检测水平与肝脏肝细胞损害有紧密的相关性，可在一定程度上反映肝脏实质性损伤，是重要的生化指标，对肝硬化评估有积极的临床价值；提高早期肝硬化评估诊断的阳性检出率，可通过生化指标的联合检测来实现，值得临床推广应用。

PU-1950

2 型糖尿病视网膜病变患者 NLR、PLR 与病变程度及血脂的相关性研究

刘泽江
资阳市第一人民医院

目的 探讨中性粒细胞与淋巴细胞比值（Neutrophil-to- lymphocyte ratio,NLR）、血小板与淋巴细胞比值(Platelet-to- lymphocyte ratio,PLR)与 2 型糖尿病视网膜病变（DR）患者不同病变程度和血脂指标的相关性。
方法 选取 2 型糖尿病 DR 患者 200 例，根据病变程度分无明显 DR、轻度 NPDR、中度 NPDR、高度 NPDR、PDR 五组，各 40 例，组内根据是否合并高血压分为 DR 合并高血压和单纯性 DR。测定中性粒细胞计数、淋巴细胞计数、血小板计数、TC、TG、HDL-C、LDL-C、等指标水平并收集相关临床资料，对结果进行分析。
结果 NLR、PLR 变化方向与 DR 病变程度一致，无明显 DR 和轻度 NPDR 比较，差别无统计学意义。无明显 DR、轻度 NPDR<中度 NPDR<高度 NPDR<PDR,差别具有统计学意义（p<0.05）。组内比较 NLR、PLR，DR 合并高血压>单纯性 DR，差别具有统计学意义(P<0.05)。NLR、PLR 与糖尿病病程、BMI、TC、TG、TC/TG、LDL-C、HbA1c 成正相关，与 HDL-C、总胆红素、直接胆红素、间接胆红素成负相关。
结论 NLR、PLR 在 2 型糖尿病视网膜病变的进展有重要临床意义，可作为 DR 患者不同病变程度分级分期指标，对治疗有效性的评估需进一步验证。

PU-1951

评价分析常规检验与生化检验在临床糖尿病诊断中的价值

丁燕
武城县人民医院

目的 对常规检验与生化检验在临床糖尿病诊断中的价值进行评价分析。
方法 在我院选取 2020 年 1 月至 2021 年 1 月确诊的糖尿病人 120 例。随机均分为常规组和生化组，生化组采用生化检验，常规组使用常规检验，比较两组检验结果准确率。常规组患者进行常规检验：检测前保证常规组患者排空膀胱，在 30min 后，由检验人员取每位患者的 10ml 中段尿，收集后用干净容器承装，送至检验科，使用全自动尿液分析仪检验，检验内容为尿葡萄糖。使用时严格对照说明书。生化组患者进行生化检验：采血前一日，对生化组所有患者进行健康宣教，禁止饮酒，禁止饮用咖啡，浓茶等饮品，禁止使用任何有降血糖效果的药物，在保持空腹 8 小时后方可进行检验。清晨每位患者采集 3 至 5 毫升静脉血，置入 EDTA 抗凝管中，在 60min 内送至检验科，用全自动血液分析仪检测，使用时严格对照说明书。另外，对空腹血糖水平，使用氧化酶法检测；还原法检测果糖胺水平；亲和层分析法检测糖化血红蛋白，并在层析柱上增加测量水平[2]。检验完成后对各项指标进行记录。
结果 生化检验组检验结果准确率明显高于常规检验组。两组结果具有对比意义(P<0.05)。
结论 在临床糖尿病检验中，生化检验准确率更高，值得在临床检验中推广。

PU-1952

Quantified correlations between alanine aminotransferase and lipid levels in given interval ranges: A cross-sectional study

Lei Feng 、Shiyan Nian、Dan Ye、Chunting Zhang、Ying Zhu、Xuejing Bai、Mengna Wu、Zefeng Yan、Cong Shao、Qixin Ma、Qianye Bi
Department of Laboratory, People's Hospital of Yuxi City（Department of Laboratory, The Sixth Affiliated Hospital of Kunming Medical University）

Background & Aims To learn whether and how serum lipid levels are associated with alanine aminotransferase (ALT) levels in the general Chinese population.
Methods A cross-sectional study of 184,398 subjects with ALT≤40 IU/L and no medical history or treatment that affected lipid metabolism.
Results The HDL-C levels of 95.9% males and 92.1% females were ≤2.0 mmol/L. Under this classification, 60.7% of males and 63.2% of females were 2.0<LDL-C<4.5 and logarithm transformed VLDL-C (LnVLDL-C)≤0.1 mmol/L; HDL-C was negatively associated and LDL-C and LnVLDL-C was positively associated with ALT level in both genders. In addition, 11.1% of males and 20.9% of females were LDL-C≤2.0 and LnVLDL-C≤0.1 mmol/L; HDL-C and LDL-C were negatively associated and LnVLDL-C was positively associated with ALT levels in both genders. Furthermore, 17.6% of males and 5.9% of females were 2.0<LDL-C<4.5 and 0.1<LnVLDL-C<1.0 (0.5 for females) mmol/L; again, HDL-C was negatively associated and LDL-C and LnVLDL-C were positively associated with ALT level in both genders. Finally, 6.5% of males and 2.1% of females were LDL-C≤2.0 and 0.1<LnVLDL-C<1.0 mmol/L; HDL-C and LnVLDL-C were negatively and positively associated with ALT levels in both genders; LDL-C was positively associated with ALT levels only in females..
Conclusion ALT levels and lipid levels are extensively associated, with unique patterns in each given interval range of lipids; these interval-specific correlation modes might suggest differentiated pathophysiological roles of lipids in subclinical hepatocyte damage and protection in a given population.

PU-1953

一种新的可避免羟苯磺酸钙对肌酐检测负干扰的检测方法的试探

谌海兰
重庆医科大学附属第一医院

目的 探讨一种新的酶法肌酐检测试剂盒抵抗羟苯磺酸钙对肌酐检测负干扰的效果。
方法 收集 2019 年 10 月至 2020 年 7 月重庆医科大学附属第一医院收治的未服用羟苯磺酸钙患者的 12 个浓度范围的混合血清并配置成含不同浓度羟苯磺酸钙的标本，在 5 个检测系统上分别用配套系统自身酶法试剂、新的酶法试剂、苦味酸试剂进行体外干扰试验。
结果 当样本中含有不同浓度羟苯磺酸钙时，系统自身酶法试剂检测结果受到明显的负干扰，当羟苯磺酸钙浓度达到 16μg/mL 时偏倚可达到-10%，且随着干扰物浓度的增加，受到的负干扰增加。当样本中不含干扰物时，新酶法试剂与系统配套试剂检测结果的偏倚均在±12%，罗氏 cobas c701、贝克曼 AU5800、迈瑞 BS2000M 三种检测系统的偏倚控制在±4%，新酶法试剂与临床常用酶法试剂检测结果具有较高一致性。运用新酶法试剂时，除了当干扰物浓度在 32—64mg/L 且肌酐浓度较低时存在最大-16.7%的干扰，对于所有浓度范围的肌酐，在受到不同浓度羟苯磺酸钙干扰时，偏倚均维持在±4%，在临床可接受的偏倚范围内。
结论 新酶法试剂与临床在用肌酐检测试剂的检测结果符合率高，且能够有效抵抗羟苯磺酸钙对肌酐检测的负干扰，有望应用于临床实验室解决肌酐检测结果假性偏低的问题。

PU-1954

血清 GPI 在类风湿性关节炎诊断中的意义

康霜
资阳市第一人民医院

目的 探讨血清中葡萄糖-6-磷酸异构酶（ (Glucose-6-phosphate isomerase ,GPI)抗原升高对类风湿关节炎(rheumatoid arthritis，RA)患者的临床诊断价值。
方法 用酶联免疫吸附试验(ELISA)检测 72 例 RA 患者，47 例其他自身免疫性疾病患者和 30 例健康对照者血清中 GPI 抗原的浓度，同时还检测了类风湿因子(RF)，抗环瓜氨酸肽（CCP）抗体。
结果 72 例 RA 组的 GPI 浓度为（2.16±2.42 mg / L）和阳性率（80.6%）都显著高于 47 例非 RA 组 GPI 浓度为（0.23±0.41 mg / L 、21.3%）和 30 例健康对照组为（0.059±0.032 mg / L、0%）(P<0.05) ，RA 患者血清中 GPI 浓度显著高于其他自身免疫性疾病组和健康对照组(P <0.05)； GPI、抗 CCP 抗体及 RF 对 RA 诊断的灵敏度、特异度的卡方检验显示：GPI 与抗 CCP 抗体的灵敏度差异有统计学意义（P<0.05），GPI 与 RF 的灵敏度及特异度差异均无统计学意义（P>0．25）；这三个指标联合检测诊断 RA 的灵敏度为 95.8%，特异度为 97.4%；Spearman 等级相关分析显示单测检验 RA 患者 GPI 值与 RF、抗 CCP 抗体均具有显著相关性。
结论 GPI 升高对诊断类风湿关节炎有显著意义，与抗 CCP 抗体及 IgM-RF 联合检测可显著提高对 RA 的鉴别诊断价值。

PU-1955

胆红素水平对酶法测定总胆固醇结果的影响和校正

蒋叶
江苏省人民医院（南京医科大学第一附属医院）

目的 评价不同浓度胆红素水平对酶法测定总胆固醇（TC）的影响，并建立有效的校正方法。
方法 将胆红素标准品配制成系列浓度梯度的胆红素溶液，分别按 10%体积加入无黄疸患者血清中，检测各样本总胆红素（TB）和 TC 浓度，分析高胆红素水平对胆固醇检测结果的影响及二者的相关性。利用多元回归分析建立校正公式，用于临床黄疸患者标本的胆固醇测定值的数学纠正。
结果 高 TB 水平降低 TC 的酶法测定结果（$P<0.05$），两者呈负相关（$R^2=0.9894$）；以无黄疸血清标本的 TC 浓度为 Y，其对应人工黄疸标本的 TB 实测值为 X，TC 实测浓度为 Z，对变量 Z 与因变量 X、Y 进行回归分析，计算得多元回归式：Y = -0.01334+ 0.002353*X + 0.9730*Z+ 0.0003370*X*Z；经公式校正后 92.67%的黄疸标本 TC 浓度偏倚小于±10%。
结论 黄疸患者血清样本中高胆红素水平可导致其 TC 的检测结果偏低，偏倚大小与 TB 浓度以及初始 TC 浓度相关，运用纠正公式可有效校正黄疸对 TC 测定的干扰，符合临床要求。

PU-1956

血脂、Hcy、hs-CRP 及 CysC 在 ICP 中的水平变化研究

向满林
中南大学湘雅医院

目的 探究血脂、同型半胱氨酸（Hcy）、超敏 C 反应蛋白（hs-CRP）及胱抑素 C（CysC）在妊娠期肝内胆汁淤积症（Intrahepatic cholestasis of pregnancy，ICP）患者体内的代谢变化和其临床意义。
方法 选取某三甲医院产科收治的 30 例 ICP 患者血清作为实验组，另选取同期正常待产孕妇血清 30 例作为对照组，分别留取空腹血清 3ml，测定 TG、TC、LDL、HDL、NEFA、Apo-A1、Apo-B、Hcy、hs-CRP 及 CysC 等指标，分析各指标在 ICP 患者与正常孕妇之间表达情况。
结果 实验组与对照组基本情况（年龄、性别等）无明显差异；实验组 TG、TC、NEFA 与对照组差异均不明显（$p>0.05$）；LDL、HDL、HDL/TC、Apo-A1、Apo-B、Apo-A1/Apo-B、HDL/LDL、及 CysC 在两组中表达具有显著差异（$p<0.05$），且实验组 HDL/TC、Apo-A1/Apo-B、HDL/LDL 较对照组明显下降，LDL、Apo-B 及 CysC 较对照组升高；秩和检验结果显示两组 Hcy、hs-CRP 具有显著性差异（$p<0.05$）。
结论 ICP 患者存在血脂代谢异常，可能与高、低密度脂蛋白比例失衡有关；Hcy、hs-CRP 及 CysC 水平升高可能为监测和辅助诊断 ICP 提供新的参考依据。

PU-1957

高通量自动化液相色谱串联质谱法检测血清胰岛素样生长因子 1 的方法研究

赵蓓蓓[1,2]、赖丽嫦[1]、董衡[1,2]、禤学怡[1,2]、李鑫[1]、佘旭辉[1,2]、李卓阳[1,2]
1. 广州金域医学检验中心有限公司
2. 广州医科大学金域检验学院

目的 液相色谱串联质谱法（LC-MS/MS）检测血清胰岛素样生长因子 1（IGF-1）具有灵敏度更高、特异性更强、定量更准确、一致性更好、可同时监测 IGF-1 序列多态性信息的特色，较好地克服了

免疫学方法的不足。针对传统手工前处理方法存在过程复杂、处理周期长，工作效率低等问题，提出了基于质谱法的血清 IGF-1 自动化前处理平台整体设计方案，以提高检测效率，同时降低手工操作带来的质量风险。
方法 通过采用 QC STORY 适用判定和计划进度甘特图质量工具，对本研究进行了背景调研，现状数据分析，目标设定，原因和要因分析，对策制定及方案实施等一系列 PDCA 活动程序。平台以引入自动取样系统、自动化移液系统和高通量的在线固相萃取净化系统，对血清样品进行简单的净化处理后，进一步实现复杂基质样品的在线净化，并完成实时的液相色谱系统进样。此外，通过将液相系统升级为多通道液相系统的措施来达到检测效率的提升。
结果 与传统手工法比较，平台通过引入自动取样系统，取样步骤的检测效率可提升 64%；引入自动化移液系统和高通量的在线固相萃取净化系统，前处理步骤的检测效率可提升 83%；升级多通道液相系统，液相分离步骤的检测效率可提升 74%；总体检测效率提升约 71%。
结论 本研究通过使用质量管理工具，对 LC-MS/MS 检测血清 IGF-1 引入高通量自动化前处理平台，总体检测效率可提升约 71%，为 LC-MS/MS 检测方法的自动化探索提供了一种科学、有效的可行性方案。

PU-1958

微流控和细胞外囊泡：精准医学

巫杰、李智洋
南京市鼓楼医院

细胞外囊泡几乎在所有体液中都可见，如血液，尿液，乳汁等，是一种脂质双分子层囊泡，包含蛋白质，DNA、RNA、脂质等。细胞外囊泡可以将囊泡内的货物运送到目标细胞，免除其他物质的水解，因此已经成为细胞间通信的关键参与者。它们作为诊断和预后生物标志物或治疗性药物传递系统的潜力近年来引起了学者相当大的兴趣。然而，用于研究细胞外囊泡的传统方法仍然有显著的局限性，包括所需的时间长和低吞吐量技术，方法不够标准化等，因此对更好的细胞外囊泡研究工具的需求越来越强烈。在过去的几年中，基于微流控的技术逐渐出现，并在细胞外囊泡的分离中发挥了重要作用。这些技术具有几个优点，包括低成本、低样本量、高吞吐量和精度。本文综述了基于微流体的技术的最新进展，包括一体化的微流控分离，检测，分析细胞外囊泡内容物，并比较了基于传统和微流体的技术的优缺点，应用于临床护理点和临床实验室，有望促进精准医学进一步的发展。

PU-1959

液相色谱串联质谱法（LC-MS/MS）和化学发光法（CL）在测定 14 岁以下儿童血清 17-羟基孕酮的结果比较研究

赵蓓蓓[1,2]、陈秀如[1]、韦兰清[1]、董衡[1,2]、佘旭辉[1,2]、李卓阳[1,2]
1. 广州金域医学检验中心有限公司
2. 广州医科大学金域检验学院

目的 比较评价液相色谱串联质谱法（LC-MS/MS）和化学发光法（CL）测定 14 岁以下儿童血清 17-羟基孕酮（17OHP）的检测结果。
方法 收集 212 例临床送检儿童血清标本，其中新生儿（3d~1m）76 例，婴幼儿（1m~1y）83 例，儿童（1y~13y）53 例，分别使用 LC-MS/MS 法与 CL 法测定血清标本中的 17OHP 含量，并将两种方法的检测结果分别采用 Passing-Bablok 检验、Bland-Altman 和 Wilcoxon test 统计学方法进行结果比较分析。

结果 LC-MS/MS 法测定 212 例血清 17OHP 的均数为 35.80±107.26 nmol/L，CL 法测定的结果为 71.60±144.66 nmol/L。Passing-Bablok 回归分析结果显示，两种检测方法检测得到的血清 17OHP 结果之间线性相关性较差（Cusum test 显示 P<0.01)，表明两种检测方法间一致性较差。Bland-Altman 一致性分析显示，LC-MS/MS 法与 CL 法检测结果相比，差值的绝对值最大为 387.63 nmol/L，差值平均值为 35.80 nmol/L。Wilcoxon test 双尾配对检验结果显示，两种血清 17OHP 的检测结果存在显著性差异（P<0.0001）。使用各自方法学的参考区间回顾数据，LC-MS/MS 法与 CL 法测定新生儿标本异常检出率分别为 13.16%、38.16%；婴幼儿异常检出率分别为 14.46%、25.30%；儿童异常检出率分别为 45.28%、52.83%；CL 法结果异常检出率明显高于 LC-MS/MS 法。

结论 LC-MS/MS 和 CL 测定新生儿及婴幼儿血清 17OHP 的结果相关性差，但前者结果显著偏低，血清 17OHP 的准确定量对先天性肾上腺皮质增生症的筛查、确诊及分型诊断、治疗效果评估非常重要，使用 CL 测定 14 岁以下儿童血清 17-羟基孕酮可能存在异常检出率高估的风险，特别针对新生儿的检测。

PU-1960

体检人群中同型半胱氨酸与高脂血症的相关系分析

刘森
宁津县人民医院

在过去十年中，同型半胱氨酸（homocysteine, Hcy）被称为是心血管疾病的标志，并被美国心脏协会确定为中风和心脏病发作的危险因素。有文献报道，Hcy 可通过影响脂质代谢促进血管粥样斑块的形成 、导致心血管疾病的发生[14]。查阅大量文献发现 Hcy 可通过氧化应激、内质网应激、促进相关炎症因子释放促使高脂血症的发生，为探讨 Hcy 与高脂血症的相关性，本次试验选取 200 个体检人群标本，根据血脂指标将其分为两组，分别进行组内和组间分析。

PU-1961

Potential role of liver enzymes for predicting elevated blood glucose levels

Mengna Wu、Shiyan Nian、Lei Feng、Xuejing Bai、Dan Ye、Chunting Zhang、Zefeng Yan、Qixin Ma、Cong Shao、Qianye Bi、Beibei Luo
Department of Laboratory, People's Hospital of Yuxi City (Department of Laboratory, The Sixth Affiliated Hospital of Kunming Medical University)

Background This study was to explore the potential effect of different liver enzymes on elevated blood glucose with the use of a more detailed blood glucose grouping.
Methods This cross-sectional study enrolled 144,135 participants who had biochemical examinations from 2014-2018. Participants were classified by sex and different blood glucose levels (< 5.0 mmol/L, 5.0-5.5 mmol/L, 5.6-6.2 mmol/L, 6.3-6.9 mmol/L, and ≥ 7.0 mmol/L). The associations between liver function indicators and occurrence of type 2 diabetes (T2DM) were analyzed through multivariate linear regression and multiple logistic regression.
Results There was a significant difference among the biochemical indices between different blood glucose groups in males and females. Liver enzymes such as alanine aminotransferase (ALT), aspartate transaminase (AST), alkaline phosphatase (ALP), and γ-glutamyl transpeptidase (GGT) were independent risk factors for raised blood glucose, and there were gender differences in the predictive performance of each liver enzyme to elevated blood glucose levels. In men, GGT was the most appropriate to predict progressive elevation of blood glucose or T2DM risk, and ALT and ALP may only be applicable to the prediction of impaired fasting glucose (IFG). By

contrast, ALT and ALP were the most appropriate enzymes for the prediction of the risk of elevated blood glucose or T2DM in women, and AST and GGT may only be appropriate for the prediction of IFG.
Conclusions Liver enzymes were independent risk factors for elevated blood glucose. There were gender differences in the role of each liver enzyme for elevated blood glucose. GGT was more suitable as a predictor for dynastic elevated blood glucose in men, whereas for women, ALT and ALP were more suitable.

PU-1962

影响生化检验结果的分析和探讨

武雅茹
宁津县人民医院

目的 了解影响检验结果的相关因素，控制影响生化检验结果的因素，继而提高生化检验结果的精密度与准确性，从而帮助临床能及时有效的对患者的病情进行判断和治疗。
方法 利用调查统计的方法对影响生化检验质量的生理因素、检验前因素、检验中因素进行逐一的调查与分析，并提出相应的解决方案。
结果 影响生化检验结果的有各种因素，其中最重要的影响因素包括溶血，标本的采集方式，标本的处理和储存等因素，需要针对性的提出解决方案，制定有效的措施，减少检验结果的误差。
结论 影响生化检验结果的因素出现在检验过程中的各个环节中，且都会对检验结果产生重要影响，医务人员应积极控制各种影响因素，做好对生化检验的质量监控工作，提高责任意识，从而减少生化检验结果的错误率，提高检测结果的准确性。

PU-1963

宫颈癌患者联合检测血清糖类抗原 125、癌胚抗原的临床价值

陈春杰
宁津县人民医院

目的 探讨联合检测血清糖类抗原 125、癌胚抗原对于宫颈癌诊断的价值。
方法 选取我院 2017 年 4 月至 2019 年 6 月收治的 60 例宫颈癌患者设为宫颈癌组，同期选取 60 例健康体检者设为对照组，采用电化学发光法测定 CA125、CEA 水平，并对 CA125、CEA 阳性与宫颈癌病理类型的相关性进行分析。
结果 宫颈癌组 CA125、CEA 水平高于对照组，差异对比有统计学意义
结论 肿瘤标志物 CA125、CEA 检测可为宫颈癌的临床诊断及病理鉴别提供一定依据。

PU-1964

Liver Function Indicators may Outperform Lipids in Type 2 Diabetes Mellitus Prediction

Mengna Wu、Lei Feng、Shiyan Nian、Wenbo Xu、Dan Ye、Chunting Zhang、Yanjun Wan、Zefeng Yan、Qixin Ma、Cong Shao
Department of Laboratory, People's Hospital of Yuxi City (Department of laboratory, The Sixth Affiliated Hospital of Kunming Medical University)

Objective The aim of this study was to explore the potential role of serum liver function indicators in evaluating type 2 diabetes mellitus (T2DM) risk, and to compare them with traditional blood lipid indicators in predicting the risk of T2DM.
RESEARCH DESIGN AND METHODS This cross-sectional study enrolled 8076 patients with T2DM and 113164 controls who received biochemical examinations in 2014-2018. Participants were classified according to sex and age (<25, 35-34, 35-44, 45-54, 55-64, and ≥65 years). The associations between liver function indicators or lipid indicators and the occurrence of T2DM were analyzed through logistic regression, and their discriminatory capacity for T2DM was assessed with receiver operating characteristic (ROC) analysis. Comparison of the area under curve values between the ROC curves obtained by DeLong's method was used to assess T2DM risk predictive performance.
Results A significant difference among biochemical indexes was observed between T2DM and controls in both males and females. In different groups, observed differences in liver function and/or lipid variables were included in the logistic regression Results Alanine aminotransferase (ALT)/aspartate aminotransferase (AST) ratio and α-L-fucosidase (AFU) were independent risk factors for T2DM, and total bilirubin and the albumin to globulin ratio were independent protective factors, whereas the predictive effects of alkaline phosphatase (ALP) and gamma-glutamyltransferase (GGT) differed across sex and age groups. In all groups, liver function indicators and lipid indicators had ideal performance in T2DM prediction, but the liver function indicators performed better than lipid indicators. The predictive performance of the two combined indicators for T2DM was significantly better than that of either indicator alone (P<0.01).
Conclusions Adding liver function indicators to the traditional predictive model may further improve the predictive performance for T2DM. In the future, large sample case-control and prospective studies will be needed to further explore the T2DM predictive model to improve predictive performance for specific sex and age groups.

PU-1965

一种超灵敏的用于肿瘤 tsRNA 杂交链式反应扩增的 CRISPR-Cas12a 适配体传感器

巫杰、李智洋
南京市鼓楼医院

目的 tRNA-derived small RNAs（tsRNA）是近年来发现的、存在于多种生物体内的一类非编码小 RNA，来源于成熟 tRNA 或 tRNA 前体，其表达和修饰具有组织和细胞特异性。肿瘤来源的 tsRNA 生物标记物有助于癌症诊断和预后评估。然而，由于缺乏可靠、简便的定量方法，阻碍了 tsRNA 的临床应用。
方法 本实验在杂交链式反应(HCR)和成簇规则间隔短回文重复序列（Clustered regularly interspaced short palin-dromic repeats (CRISPR)/Cas12a 双重扩增的基础上，建立了直接高灵敏度检测 tsRNA 的 APTA-HCR-CRISPR 方法。用 HCR 扩增 tsRNA 靶向适配体，产生包含多个

CRISPR RNA(CrRNA)靶向条形码的长重复序列，并通过 CRISPR-Cas12a 侧枝切割活性进一步扩增信号，产生荧光信号。
结果 通过检测荧光信号的量，即为 tsRNA 的量，验证了所建立的策略，有较低的检测限，比其他方法更灵敏。同时揭示了 tsRNA 在癌症诊断中的潜在应用，以及在治疗监测中的潜在应用。
结论 该平台简单易行，可用于临床标本中 tsRNA 的高灵敏度和通用性检测，为癌症早期诊断提供非侵袭性、精准和智能的辅助诊断工具。

PU-1966

血清高敏肌钙蛋白 T 在糖尿病肾病中升高的临床价值分析

韩忠海
资阳市第一人民医院

目的 探讨心肌标志物血清高敏肌钙蛋白 T（hs-STAT）在糖尿病肾病中异常升高的临床价值。
方法 将符合要求的 2 型糖尿病（DM）患者 86 例按肾功能分级分为普通 2 型糖尿病组（DM 组）51 例和糖尿病肾病组（DN 组）35 例，分别检测两组患者血清中 hs-STAT 水平，并加以分析比较。
结果 DN 组患者中血清 hs-STAT 水平明显高于 DM 组患者。
结论 血清 hs-STAT 水平在糖尿病肾病患者中异常升高，不仅提示亚临床心肌损伤，还可以作为 2 型糖尿病进展为糖尿病肾病的早期诊断指标，有助于识别糖尿病肾病人群中肾功能显著恶化的高危患者，指导临床医生及早做出针对性决策。

PU-1967

血清胱抑素 C 对糖尿病肾病诊断的临床价值研究

王华国
四川省资阳市第一人民医院

目的 了解血清胱抑素 C（Cys C）在糖尿病肾病（DN）患者肾功能检测中的应用效果。
方法 选取资阳市第一人民医院 2017 年至 2021 年入院治疗的 II 型糖尿病（T2DM）病人 183 例，根据是否合并肾病分为单纯糖尿病组（T2DM 组，100 例）和糖尿病肾病组（DN 组，83 例），选择同期在资阳市第一人民医院行健康查体者 100 例作为对照组。3 组均进行血清 Cys C.血肌酐（Scr）及尿素氮（BUN）指标检测，比较 3 组研究对象的三项检测指标水平，对 DN 组各项指标的阳性检出率进行统计，并采用受试者工作特征曲线（ROC 曲线）分析血清 Cys C.BUN 和 Scr 对 DN 的诊断效能。
结果 DN 组和 T2DM 组患者的血清 Cys C.BUN 和 Scr 水平均显著高于对照组，并且 DN 组患者的三项检测指标水平均显著高于 T2DN 组水平，对比差异具有统计学意义（P<0.05）；DN 组三项检测指标阳性检出率对比，血清 Cys C 的检出率最高，均显著高于另外两项指标，对比差异存在统计学意义（P<0.05）；血清 Cys C.BUN 和 Scr 单独诊断 DN 的曲线下面积分别为 0.938、0.825 和 0.917，血清 Cys C 的诊断价值最高；BUN、Scr 与血清 Cys C 联合检测和三项指标联合检测的曲线下面积分别为 0.947、0.972 和 0.983，其中血清 Cys C.BUN、Scr 三项指标联合检测的诊断价值最高。
结论 血清 Cys C 是评价 DN 患者肾功能变化的有效指标，对于监测 DN 的发生和发展具有重要价值，临床可将其用于 DN 的辅助诊断和病情评估。

PU-1968

利用基因敲除技术研究 GABAB1 受体与抑郁症关系

李泽林
南方医科大学珠江医院

早期研究表明抑郁症与 GABA 系统关系密切，在药理上，人们发现给予小鼠 GABA B 受体拮抗剂能够降低小鼠在强迫游泳实验 中的不动时间；在基因水平上，GABA B1 敲除小鼠在强迫游泳实验中的不动时间也显著降低，然而小鼠哪些神经细胞上的 GABAB1 受体参与了抑郁样行为的调控，目前尚无定论。我们利用 cre-loxp 系统，特异性敲低小鼠海马星形胶质细胞、CAMKⅡ阳性的神经元和 GAD 阳性神经元，发现只有敲低星形胶质细胞细胞上的 GABAB1 受体，小鼠的强迫游泳时间才会降低，表明小鼠大脑海马星形胶质细胞 GABAB1 受体参与了小鼠抑郁样行为的调节。

PU-1969

探讨 α-L-岩藻糖苷酶（AFU）在 2 型糖尿病患者早期肾损害中的应用

蔡建
资阳市第一人民医院

目的 探讨 α-L-岩藻糖苷酶（AFU）在 2 型糖尿病患者早期肾损害中的应用。
方法 选取我院 2018 年至 2020 年诊断的 2 型糖尿病患者 150 例，根据尿蛋白排泄率(UAER)水平分为三组:A 组：单纯糖尿病组(SDM)50 例，24h 尿蛋白排泄率<30mg；B 组：早期糖尿病肾病组(EDKD)50 例，24h 尿蛋白排泄率 30-300mg；C 组：临床糖尿病肾病组(CDKD)50 例，24h 尿蛋白排泄率>300mg。分别测定三组患者血清 AFU 水平，并研究其与尿微量白蛋白的相关性。
结果 早期糖尿病肾病组与单纯糖尿病组及临床糖尿病肾病组比较，血清 AFU 水平显著升高(P＜0.05)，且尿微量白蛋白与 AFU 呈负相关(P＜0.05)。
结论 2 型糖尿病患者出现糖尿病早期肾损害时血清中 AFU 水平可出现不同程度的升高；血清 AFU 测定在预测糖尿病早期肾损害时有重要的临床价值。

PU-1970

血清 AFP、AFP/AFP-L3、PIVKA-Ⅱ联合检测在肝癌中的诊断价值研究

赵宗晨
山东第一医科大学附属省立医院

目的 探讨 AFP、AFP/AFP-L3、PIVKA-Ⅱ联合检测在肝癌中的诊断价值。
方法 选取 2016 年 9 月~2017 年 9 月于山东省立医院就诊的肝病患者 174 例，其中肝细胞肝癌的患者 89 例作为研究组，年龄为 35~81 岁，肝硬化未合并肝癌患者 85 例作为对照组，年龄为 30~77 岁。另外选取 80 例体检健康者作为健康对照组，年龄为 34~83 岁，三组分别进行 AFP、AFP/AFP-L3、PIVKA-Ⅱ及 GGT 的检测，分别比较四组 AFP、AFP/AFP-L3、PIVKA-Ⅱ的结果及与其他病理参数的关系。

结果 肝细胞肝癌患者外周血 AFP、AFP/AFP-L3、PIVKA-Ⅱ三项指标均高于肝硬化患者组及健康对照组， ROC 曲线分析 AFP、AFP/AFP-L3、PIVKA-Ⅱ曲线下面积（AUC）分别为：0.854、0.713、0.922、0.85。灵敏度分别为：73.25%、43.02%、82.56%、82.56%。特异度分别为：93.75%、98.75%、98.75%、71.25%。AFP 阳性患者与阴性患者在脉管内癌栓差异有统计学意义（P<0.05）,在性别、年龄、肿瘤直径、HBsAg 差异均无统计学意义（P>0.05）。AFP/AFP-L3 阳性患者与阴性患者在肿瘤直径、脉管内癌栓、HBsAg 差异有统计学意义（P<0.05），在性别、年龄差异均无统计学意义（P>0.05）。PIVKA-Ⅱ阳性患者与阴性患者在性别、肿瘤直径、脉管内癌栓、HBsAg 差异有统计学意义（P<0.05），与年龄无统计学意义（P>0.05）。

结论 联合检测 AFP、AFP/AFP-L3、PIVKA-Ⅱ可以明显提高肝脏肿瘤的诊断率。

PU-1971

精神分裂症患者血清同型半胱氯酸测定分析

张明华
资阳市精神病院

目的 分析精神分裂症患者前、治疗后 4 周测定同型半胱氨酸（Hcy）水平。

方法 对 100 例住院的精神分裂症患者（实验组）使用 Vit B12、叶酸治疗其高同型半胱氨酸血症前、治疗后 4 周分别测定血清同型半胱氨酸水平，并与未治疗高同型半胱氨酸血症对照组比较（对照组）。

结果 精神分裂症患者使用 Vit B12、叶酸治疗前、治疗后 4 周血清 Hcy 低于对照组（P<0.05）；患者组使用治疗前、治疗后 4 周血清 Hcy 比较有显著变化（P>0.05）。

结论 精神分裂症血清同型半胱氨酸明显升高。使用 Vit B12、叶酸治疗后同型半胱氨酸水平有所下降，说明精神分裂症患者血清 Hcy 水平下降对其预防心脑血管疾病有临床意义。

PU-1972

基于适配体和血红素/G-四聚体 DNA 酶的细胞传感器用于电化学、光学双重检测研究

谭婷婷
南京大学医学院附属鼓楼医院

目的 同时采取电化学、光学两种传感方法实现白血病细胞的灵敏检测。

方法 利用适配体的特异性靶向识别作用、血红素/G-四聚体 DNA 酶的类过氧化物酶催化作用、以及细胞的竞争性结合作用，选取 CCRF-CEM 急性白血病细胞作为模型细胞，构建基于适配体和血红素/G-四聚体 DNA 酶的竞争型细胞传感器。

结果 通过示差脉冲伏安法（DPV）对不同浓度的 CCRF-CEM 细胞进行电化学检测。由于 CCRF-CEM 细胞能与 cDNA 竞争而优先结合探针上的 aptamer，导致细胞被探针捕获、cDNA 从探针上解缔而释放出富 G 序列。CCRF-CEM 细胞的浓度越高，探针上释放出来的富 G 序列就越多，则形成具有类过氧化物酶催化活性的 hemin/G-四聚体 DNAzyme 就会越多，最终导致电极上催化 H2O2 氧化 TMB 所产生的还原峰电流信号就会越大。在 CCRF-CEM 细胞浓度为 1.0×102 至 1.0×107 cells mL–1 的范围内，峰电流与细胞浓度的对数值呈线性相关，其相关系数为 0.9993。采用比色法进一步验证本实验所构建传感器的检测性能。由于未被竞争下来的 cDNA 与探针保持的双螺旋结构可被限制性内切酶识别切割，从而导致富 G 序列从探针上脱落游离。CCRF-CEM 细胞的浓度越高，未被竞争下来的 cDNA 就会越少，则被切割而脱落游离的富 G 序列就会越少，于是

形成具有类过氧化物酶催化活性的 hemin/G-四聚体 DNAzyme 就会越少，最终导致酶催化 H2O2 氧化 TMB 所产生的显色反应越弱。被氧化的 TMB 在硫酸环境下呈黄色，随着 CCRF-CEM 细胞浓度的增大，反应溶液的颜色逐渐减弱。通过分光光度计检测可得出同样的**结果** 吸光度与细胞的浓度呈负相关。在最佳实验条件下，本实验的检测范围是 1.0×102-1.0×107 cells mL-1，检测限是 1.0×102 cells mL-1。

讨论 急性白血病的临床进展非常迅速，白血病细胞的早期快速准确鉴别和定量分析直接关系到白血病的确诊，并成为疾病治疗的基础和评估治疗效果的一种有效方式。我们成功构建新型基于适配体和 hemin/G-四聚体 DNAzyme 的竞争型细胞传感器，可同时采取电化学、光学两种传感方法实现白血病细胞的灵敏检测。该传感器结合了适配体的特异性靶向识别能力和 hemin/G-四聚体 DNAzyme 的类过氧化物酶催化能力，具有良好的特异性和灵敏度，将为白血病细胞的检测提供新的途径，为白血病的早期诊断和治疗提供有效帮助。

PU-1973

血糖检验和尿糖检验在糖尿病患者中的确诊率分析

张潇月
乐至县人民医院

目的 探讨血糖检验和尿糖检验在糖尿病患者中的确诊率分析。

方法 选取糖尿病患者 70 例，均为我院 2018 年 6 月至 2020 年 1 月收治，随机分组，对 78 例患者行以血糖检验和尿糖检验，对两项指标在血糖检验和尿糖检验中的价值进行分析研究。

结果 糖尿病患者的尿糖检验结果与其空腹血糖和餐后 2 小时血糖的诊断结果呈正相关，研究结果表明，糖尿病患者的尿糖检验结果、空腹血糖、餐后 2 小时血糖关系密切。尿糖检验结果阳性率为 81.4%，阴性率经检验呈 18.6%。本组 70 例患者尿糖检验结果和血糖检验结果呈正相关，即是在患者的尿糖含量提高同时，患者的空腹血糖水平以及餐后的 2 小时血糖水平均呈增高的趋势。

结论 糖尿病患者在血糖检验和尿糖检验两项指标的检验过程中呈正相关，尿糖检验可作为初次筛选的诊断之法，在进行明确的病情诊断时，仍需要结合血糖检验进行诊断，确保其有效诊断。

PU-1974

六种肿瘤标志物检测对结肠癌的诊断价值及其临床意义

赵宗晨
山东第一医科大学附属省立医院

目的 探讨血清癌胚抗原（CEA）、糖链抗原 125（CA125）、糖链抗原 199(CA199)、糖链抗原 724(CA724)、糖链抗原 211(CY211)和血清胃泌素释放肽前体（Pro-GRP）六种肿瘤标志物检测对结肠癌的诊断价值及其临床意义。

方法 选取 2016 年 6 月~2018 年 1 月于山东省立医院就诊的结肠患者 25 例（结肠癌组），45 例结肠息肉良性疾病患者（息肉组），70 例体检健康者（健康对照组）的上述指标及其对应的阳性检出率，分析 6 项指标单个检测的灵敏度和特异度。

结果 结肠癌组的血清 CEA、CA125、CA199、CA724、CY211 及 Pro-GRP 水平明显高于息肉组和健康对照组（P<0.05），ROC 曲线分析 CEA、CA125、CA199、CA724、CY211 及 Pro-GRP 曲线下面积（AUC）分别为：0.856、0.719、0.87、0.823、0.871、0.734。阳性检出率分别为：60%、28%、52%、44%、60%、48%。六种肿瘤标志物联合检测阳性率可达 84%。

结论 六种肿瘤标志物联合检测能为结肠癌的早期诊断提供有力的依据。

PU-1975

血清纤维蛋白原、C 反应蛋白与血常规联合检测在细菌性肺炎诊断中的价值

宋晓君
乐至县人民医院

目的 分析血清纤维蛋白原、C 反应蛋白与血常规联合检测在细菌性肺炎诊断中的价值。
方法 本次研究的对象为我院 2018 年 4 月至 2019 年 4 月间收治的疑似细菌性肺炎的患者 210 例，对其采取血清纤维蛋白原、C 反应蛋白以及血常规联合检测，分析不同检测方法的阳性检出率以及准确度、灵敏度与特异度。
结果 本次研究的 220 例受检人员中，经过病理诊断出细菌性肺炎者 192 例。血清纤维蛋白原检测阳性率为 69.52%（146/210）、C 反应蛋白检测阳性率为 64.76%（136/210）、血常规检测阳性率为 63.81%（134/210）、联合检测的阳性率为 87.62%（184/210）；血清纤维蛋白原、C 反应蛋白以及血常规检测的灵敏度、特异度以及准确度与联合检测相比，差异显著（p<0.05）。
结论 血清纤维蛋白原、C 反应蛋白以及血常规联合可有效检测出细菌性肺炎，并为临床诊断提供可靠依据。

PU-1976

血清 LDH、CK 在新生儿胆红素脑病中的表达和意义

陈阳
资阳市乐至县人民医院

目的 探讨血清 LDH、CK 在新生儿胆红素脑病中的表达以及临床意义。
方法 抽取 112 例患儿，均在 2019 年 10 月至 2020 年 10 月期间到我院接受治疗。通过对病情的诊断，将抽取的 112 例患儿分为对照组（非胆红素脑病，60 例）和观察组（胆红素脑病，52 例）。将纳入研究的患儿均进行血清检测，对其血清 LDH、CK 水平及相关性进行分析。
结果 经过对两组的观测，观察组患儿的血清 CK、LDH 的数值较对照组相比，呈现出更高的趋势（P<0.05）；在观测中，胆红素脑病患儿的血清 CK、LDH 水平与 TBIL、BAEP 的水平为正相关（P<0.001）。
结论 在对患儿的检测中，胆红素脑病患儿血清水平中 LDH 和 CK 指标有着明显的上升，为新生儿胆红素脑病的危险因素之一，可作为临床对疾病诊断的重要参考指标，为病情的诊断提供可靠的数据依据。

PU-1977

D-二聚体在胰腺癌诊断中的应用价值

赵宗晨
山东第一医科大学附属省立医院

目的 探讨 D-二聚体对胰腺癌的诊断价值。
方法 选取 2014 年 6 月~2018 年 1 月于山东省立医院就诊的胰腺癌患者 111 例作为研究组，年龄为 30~81 岁，同时随机选取 70 例健康体检者作为对照组，年龄为 28~80 岁。比较两组 D-二聚体、CEA、CA125 及 CA199 水平。并比较不同 D-二聚体水平患者肿瘤标志物（CEA、CA125、CA199）、性别、年龄、肿瘤直径、是否转移、分化程度。

结果 胰腺癌患者组的 CEA、CA125、CA199 及 D-二聚体均显著高于对照组，差异有统计学意义（均 P<0.05）。根据 D-二聚体水平的不同绘制 ROC 曲线，曲线下面积为：0.756，确定最佳截点后，将 111 例胰腺癌患者组分为低 D-二聚体组（≤395，52 例）和高 D-二聚体组（>395，59 例），高 D-二聚体组的 CEA、CA199 水平均高于低 D-二聚体组，差异有统计学意义[4.36(1.85,8.89)ng/ml 比 2.6（1.84,5.14）ng/ml、193(55.75,1000)u/ml 比 108.4（17.23,620.3）u/ml]（均 P<0.05）。高 D-二聚体组与低 D-二聚体组患者性别、年龄、肿瘤直径及是否转移差异有统计学意义（均 P<0.05）。在肿瘤分化程度差异无统计学意义（P>0.05）。
结论 胰腺癌 D-二聚体水平显著升高，为区分癌症和正常人提供了重要的参考价值，并且 D-二聚体还可作为胰腺癌患者病情评估的指标。

PU-1978

心肌肌钙蛋白 T、超敏 C 反应蛋白联合心脏型脂肪酸结合蛋白用于早期诊断心肌梗死的临床价值

刘可
乐至县人民医院

目的 探索心肌肌钙蛋白 T、超敏 C 反应蛋白联合心脏型脂肪酸结合蛋白用于早期诊断心肌梗死的临床价值。
方法 选择 100 例心肌梗死患者为试验对象（实验组），另选择同时间段的 100 例健康体检者（对照组），此次试验均在 2018 年 01 月至 2020 年 12 月期间完成；两组均接受心肌肌钙蛋白 T、超敏 C 反应蛋白联合心脏型脂肪酸结合蛋白检测方法，分析两组的临床价值。
结果 实验组的入院时各项指标均高于对照组（P＜0.05）；实验组的三项检测阳性预测值为 100.00%，特异性为 100.00%，敏感性为 98.00%，阳性预测值为 98.00%。
结论 诊断心肌梗死实施心肌肌钙蛋白 T、超敏 C 反应蛋白联合心脏型脂肪酸结合蛋白检测的早期诊断价值确切。

PU-1979

血尿胱抑素 C 水平在急性有机磷农药中毒患者中的变化及意义

宋丽婷、杜柏岩
哈尔滨医科大学附属第一医院

目的 研究急性有机磷农药中毒（AOPP）患者血、尿胱抑素 C（Cystatin C，Cys C）的变化及临床意义。
方法 对 41 例 AOPP 患者轻度 AOPP 组 12 例、中度 AOPP 组 18 例、重度 AOPP 组 11 例和对照组 50 例健康人做血、尿胱抑素 C（Cys C）、血尿素氮(BUN)、血肌酐(SCr)、尿蛋白半定量(PRO)的检测，并对照分析。
结果 轻度 AOPP 患者的血、尿 Cys C 含量高于对照组，差异有统计学意义(P<0.05)；中、重度 AOPP 患者的血、尿 Cys C、血 BUN、SCr 均高于对照组，差异有显著统计学意义(P<0.01)；41 例 AOPP 患者尿 Cys C 检测阳性率为 100%，尿蛋白半定量检测阳性率轻度 AOPP 患者为 16.7%、中度 AOPP 患者为 66.7%。
结论 血、尿 Cys C 可作为判断急性有机磷农药中毒肾小球和肾小管早期受损的指标，较血 BUN、SCr、尿蛋白半定量敏感。对 AOPP 早期肾损伤诊断及治疗有重要意义。

PU-1980

生化检验在肾上腺皮质疾病诊断中的应用效果分析

凌燕
资阳市乐至县人民医院

目的 分析在肾上腺皮质疾病诊断中采取生化检验的应用效果。
方法 本次研究共选取 88 例肾上腺皮质疾病患者作为观察对象，选取时间为 2017 年 9 月-2019 年 4 月间，并根据随机数字表法将其进行平均分组，给予其中 44 例患者常规检验，并将其设为对照组，给予其余 44 例患者生化检验，并将其设为实验组，分析这两组的总有效率。
结果 实验组 44 例肾上腺皮质疾病患者的检验总有效率为 95.45%，对照组 44 例肾上腺皮质疾病患者的检验总有效率为 77.27%，通过统计学处理后可得出结果，（$p<0.05$），证明差异对比具有统计学意义。
结论 对肾上腺皮质疾病患者采取生化检验进行诊断，可有效提高诊断准确率，并为临床治疗提供可靠依据，具有较高的临床应用价值。

PU-1981

浅谈进行生化检验对诊断小儿支原体肺炎合并肝损伤、心肌损伤的价值

周毅君
资阳市乐至县人民医院

目的 分析生化检验对诊断小儿支原体肺炎合并肝损伤、心肌损伤的价值。
方法 本次研究选取 2017 年 4 月-2019 年 4 月间在我院进行治疗的支原体肺炎合并肝损伤、心肌损伤的患儿 38 例作为观察组，再选择同期进行体检的 38 例健康儿童作为参照组，对所以参与研究的人员均采取生化检验，并分析生化检验的结果。
结果 观察组患儿的血沉水平、C 反应蛋白水平、α 羟丁酸脱氢酶指标、天门冬氨酸氨基转移酶指标以及总胆红素水平的检验结果均优于参照组，差异显著（$p<0.05$）。
结论 在诊断小儿支原体肺炎合并肝损伤、心肌损伤中采取生化检验具有较高的临床应用价值，可为临床治疗提供可靠依据。

PU-1982

临床血脂生化检验中采用分级检验对提高检验阳性率的价值

刘婉
资阳市乐至县人民医院

目的 讨论临床血脂生化检验中采用分级检验对提高检验阳性率的价值。
方法 将 160 例于 2019 年 6 月-2020 年 3 月期间在本院接受血脂生化检验的患者作为研究对象，以随机法分为对照组（拉网式检验）与研究组（分级检验）各 80 例，评判标准：血脂检验水平。
结果 研究组患者实施分级检验后的载脂蛋白 A 以及载脂蛋白 B 水平均明显高于对照组实施拉网式检验后载脂蛋白 A 以及载脂蛋白 B 水平，$P<0.05$；其余血脂指标水平在这两种血脂检验方式下并无明显差异，$P>0.05$。
结论 相对于拉网式检验，分级检验在血脂生化检验中的检验阳性率更高，值得推广。

PU-1983

临床检验生化指标在病毒性肝病患者诊断中的应用对提高肝功能指标阳性检出率的意义

陈静
资阳市乐至县人民医院

目的 研究临床生化指标检验运用在病毒性肝病患者诊断中对提高肝功能指标阳性检出率的意义。
方法 以 2019 年 1 月—2019 年 12 月在我院体检的 60 例健康者作为对照组，并以同期 60 例病毒性肝病患者为实验组，比较两组的生化指标、血常规指标、肝功能指标阳性检出率。
结果 （1）实验组白球比（A/G）、白蛋白（ALB）水平低于对照组，且总胆红素（TBIL）、谷丙转氨酶（ALT）水平高于对照组，P<0.05；（2）实验组中性粒细胞、血小板、白细胞（WBC）水平低于对照组，且淋巴细胞水平高于对照组，P<0.05；（3）实验组胆碱酯酶（CHE）、TBIL、谷草转氨酶（AST）、ALT 阳性率均高于对照组，P<0.05。
结论 为病毒性肝病患者实施生化指标检验，肝功能指标阳性检出率较高，可辅助临床诊疗，值得推广。

PU-1984

肝切除术后乳酸脱氢酶结果异常升高的原因分析

王连明、于文竹
哈尔滨医科大学附属第一医院

目的 本院收治一例因“右上腹隆起一周入院”，确定诊断“肝脓肿” 患儿。但首次手术后临床医生咨询检验科一个问题“术后乳酸脱氢酶异常增高的原因是什么？”即“哪个器官或组织引起的乳酸脱氢酶异常升高？”为了回答临床科室的这个疑问，我们通过分析乳酸脱氢酶以及其它检验指标的动态变化，分析手术可能产生的影响，比对了输血及有创操作可能引起的变化，最后为临床的治疗观察提供有价值的检验信息。
方法 收集患者门诊及住院期间的血常规、尿常规、凝血、生化等常用指标及肿瘤系列和降钙素原等诊断指标。收集患者手术前后的所有可能影响乳酸脱氢酶浓度变化的操作及治疗等，包括输血、有创操作、手术及抢救以及病情变化记录。以检验结果时间点及临床主要操作和病情变化进行动态分析。
结果 1.从 AST、ALT、LDH、CK 的动态变化比较及相关因子，排除了肝脏因素引起 LDH 增高；2.通过尿液分析和肾脏疾病的指标不支持肾脏损伤，排除肾脏导致 LDH 升高的可能；3.从 AST 与 CKMB 的相关系数（0.534）以及 CK 和 CKMB 的数值升高程度及比值变化也可以排除心机细胞损伤的原因；4.从两次手术及 4 次输血的时间点及 LDH 动态变化，确定输血也不是引起第一次术后 LDH 持续异常升高的主要原因。5.结合凝血指标变化及输注冷沉淀凝血因子后 LDH 的变化，确定 LDH 第一次术后显著增高是由于肝脏手术+术后的凝血因子减少引起的渗出所致。
结论 患者 LDH 第一次术后显著增高是由于肝脏手术+术后的凝血因子减少引起的（凝血因子未测定，表现为 PT 延长）渗出，输注冷沉淀凝血因子后得到明显改善可以证实此结论。

PU-1985

急诊检验血糖中快速血糖仪和常规生化仪两种方法的临床应用

陈义波
资阳市乐至县人民医院

目的 探究在急诊血糖的检验中采用快速血糖仪和常规生化仪的不同临床效果。
方法 随机抽取 2018 年 1 月～2019 年 1 月期间来我院进行血糖检测的 100 例患者，运用快速血糖仪和常规生化仪分别进行检测，并针对两组的血糖指标及检测时间进行统计分析。
结果 两组的血糖指标的检测结果并无显著性差异（P＞0.05）；快速血糖仪组的检测时间远低于常规生化仪组（P＜0.05），具有统计学意义。
结论 两组检测设备均能准确的实现血糖测量的有效目的，快速血糖仪相比常规生化仪拥有更为明显的测量优势，值得临床积极采纳。

PU-1986

肝功能生化检验用于肝炎肝硬化患者中的效果观察及检出率影响

刘芳芳
资阳市乐至县人民医院

目的 研究肝功能生化检验指标在肝炎肝硬化患者中的检验效果。
方法 筛选 2020 年 1 月~12 月在我院接受救治的肝炎肝硬化患者 90 例为甲组，同期体检健康对象 90 例为乙组，两组对象均接受肝功能生化检验，比较两组患者检验结果差异，统计甲组肝功能生化检验指标阳性检出率。
结果 甲组 ALB、CHE、CHO 水平均低于乙组，但甲组 TBA 水平高于乙组（P＜0.05）。肝功能等级为 A 级患者对 CHE 指标的阳性检出率为 100%，B 级患者对 CHE 指标的阳性检出率为 100%，C 级患者对 ALB 和 CHE 指标的阳性检出率最高，均为 92.50%。
结论 肝功能生化检验（ALB、CHE、CHO、TBA）对辅助肝炎肝硬化患者确诊具有积极效果。同时除 CHO 外，肝炎肝炎化患者对 ALB、CHE、TBA 均有较高的阳性检出率。

PU-1987

肝功能联合血糖、血脂检测用于非酒精性脂肪肝的诊断价值

刘可
乐至县人民医院

目的 探究肝功能联合血糖、血脂检测诊断非酒精性脂肪肝的效果。
方法 随机选取 2017 年 12 月至 2019 年 12 月本院接收非酒精性脂肪肝患者 50 例作为观察组，并择取同期前来本院体检的健康人士 50 例作为对照组。均行肝功能联合血糖、血脂检测。比较两组肝功能指标[谷丙转氨酶（ALT）、谷草转氨酶（AST）、谷酰转肽酶（GGT）]、血糖（FBG）、血脂[甘油三酯（TG）、总胆固醇（TC）、高密度脂蛋白（HDL-C）、低密度脂蛋白（LDL-C）]水平。
结果 观察组 ALT、AST、GGT 水平高于对照组（P<0.05）。观察组 FBG、TG、TC、LDL-C 水平高于对照组，HDL-C 水平低于对照组（P<0.05）。
结论 在非酒精性脂肪肝患者诊断中，应用肝功能联合血糖、血脂检测效果显著，可有效反映患者紊乱的血脂、血糖、肝功能状态，为临床诊治提供依据。

PU-1988

肝功能检测对肝炎肝硬化的诊断价值评价

刘芳芳
资阳市乐至县人民医院

目的 分析肝功能检测对肝炎肝硬化的诊断价值。
方法 选取肝炎肝硬化患者 80 例作观察组，依据肝硬化 Child-Pugh 分级标准，将患者分为 A 级 30 例，B 级 31 例，C 级 19 例，选取时间 2018 年 1 月-2019 年 5 月，同时期选取于我院行健康体检的健康人员 80 例作参照组，对 2 组患者及观察组不同分级患者的清蛋白、总胆汁酸、血清胆碱酯酶、血清胆固醇水平进行比较。
结果 观察组的清蛋白、血清胆碱酯酶、血清胆固醇水平均低于参照组，总胆汁酸水平高于参照组，统计学差异均有意义（$p<0.05$）；A 级患者的清蛋白、血清胆碱酯酶、血清胆固醇水平高于 B、C 级，B 级高于 C 级；A 级患者的总胆汁酸水平低于 B、C 级，B 级低于 C 级，统计学差异均有意义（$p<0.05$）。
结论 肝功能检测对肝炎肝硬化的诊断价值较高，可提供准确的肝损伤程度参考依据给临床医师。

PU-1989

肝功能对肝炎肝硬化诊断的临床意义

宋晓君
乐至县人民医院

目的 探究肝功能检查对肝炎肝硬化诊断的价值。
方法 随机选取 2017 年 12 月至 2019 年 12 月本院接收肝炎肝硬化患者 60 例作为观察组，并择取同期前来本院体检的健康人士 60 例作为对照组，两组纳入对象均行肝功能检查，比较两组肝功能指标水平，并分析不同程度肝炎肝硬化患者肝功能指标水平差异。
结果 观察组患者血清胆固醇、白蛋白、血清胆碱酯酶水平低于对照组，总胆汁酸水平高于对照组（$P<0.05$）。Child A 级、Child B 级、Child C 级患者血清总胆固醇、白蛋白、血清胆碱酯酶呈递减态势，总胆汁酸呈递增态势（$P<0.05$）。
结论 对肝炎肝硬化患者应用肝功能检查诊断效果显著，可有效反映患者肝功能状态，鉴别病症严重程度，为临床诊治提供依据，值得推广。

PU-1990

病毒性肝炎诊断时采用血常规和生化检验项目的效果分析

熊杨
资阳市乐至县人民医院

目的 分析在病毒性肝炎诊断时采取血常规以及生化检验项目的效果。
方法 选取我院 2017 年 7 月-2019 年 3 月间收治的病毒性肝炎患者 40 例作为实验组，再将同一时间进行健康体检的 40 例人员作为参照组，同时对两组实施血常规与生化项目的检验，并对检查结果进行对比分析。
结果 实验组的中性粒细胞数量、血小板数量、白细胞计数等均低于参照组，差异显著；实验组患者的淋巴细胞、总胆红素以及谷丙转氨酶等均高于参照组，差异具体统计学意义，（$p<0.05$）。
结论 血常规以及生化检验的结果均可作为诊断病毒性肝炎的主要标准，可为临床诊断提供有效的参考建议，值得临床推广。

PU-1991

TP、GLU、24hUCFP、mALB 联合检测用于糖尿病肾损害诊断的临床价值

张潇月
乐至县人民医院

目的 探究 TP（血清总蛋白）、GLU（空腹血糖）、24hUCFP（24 小时尿液/脑脊液蛋白）、mALB（尿微量白蛋白）联合检测在糖尿病肾损害诊断中的临床价值。
方法 于我院 2019 年 10 月-2020 年 10 月收治的 39 例糖尿病肾损害患者为研究主体，将纳入研究组，选择我院同期健康体检的 39 例健康体检者为对照组，均给予两组 TP、GLU、24hUCFP、mALB 联合检测，记录并对比检查结果。
结果 对比研究结果显示，研究组 TP、GLU、24hUCFP、mALB 水平均显著高于对照组，P＜0.05。
结论 在糖尿病肾损害的临床诊断中，实施 TP、GLU、24hUCFP、mALB 联合检测可有效发现糖尿病肾病损害情况，可为疾病治疗提供重要的参考依据，具有应用价值。

PU-1992

无明显临床指征的单独 AST 异常增高：警惕巨-AST 存在

王连明、鲁平
哈尔滨医科大学附属第一医院

目的 患者无症状 AST 单独升高，证实活性增高的原因是患者维生素 B6(吡哆醛)缺乏还是巨-AST 存在。
方法 通过稀释试验初筛，利用比对试验和纠正试验验证是否为维生素 B6(吡哆醛)缺乏；利用聚乙二醇(PEG)沉淀活性测定和冷藏法确证巨-AST 的存在。
结果 试验证实在不同的检测系统，AST 存在明显差异，而且不同仪器上的测定结果显示含有磷酸吡哆醛的试剂 AST 的测定值较高，如西门子的 Dimension 和强生的 VITROS 5600，而不含磷酸吡哆醛的试剂其测定值则较低甚至在参考范围内。但纠正试验无法进行纠正。聚乙二醇(PEG)沉淀活性测定和冷藏法确证巨-AST 的存在。证实为室温不稳定的 IgG 型复合物形成。
结论 对于无任何器官/组织功能异常的临床及生物化学指征出现的高 AST 情况，应怀疑巨-AST 存在并进行证实，保证测定结果对临床的诊断意义。

PU-1993

小儿肺炎支原体感染全血 CRP 变化以及意义

康钦松
资阳市安岳县中医医院

目的 研究小儿肺炎支原体感染全血 CRP 的变化以及意义。
方法 安岳县中医医院儿科呼吸道感染患儿 510 例，采用肺炎支原体 IgM 抗体检测试剂盒检测肺炎支原体 IgM 抗体，全血 CRP 测定仪测定患儿全血 CRP 值。100 例肺炎支原体 IgM 抗体阳性与 100 例肺炎支原体 IgM 抗体阴性为实验组，其中 43 例确诊为细菌性肺炎。选取 50 例健康儿童为对照组，分别测定全血 CRP 值。
结果 510 例患儿全血 CRP 均值 9.60±9.85mg/l，肺炎支原体 IgM 抗体阳性组患儿全血 CRP 为 8.64±9.68mg/l，肺炎支原体 IgM 抗体阴性组患儿全血 CRP 为 12.96±9.89mg/l，13 例确证为细菌

性肺炎全血 CRP 为 20.23±14.25mg/l，对照组健康儿童全血 CRP 值为 1.37±0.67mg/l。三组比较，差异具有统计学意义（P<0.05）
结论 肺炎支原体 IgM 抗体阳性组全血 CRP 稍有增高，增高程度低于肺炎支原体 IgM 抗体阴性组。并且其全血 CRP 阳性率低于肺炎支原体 IgM 抗体阴性组，肺炎支原体感染检测全血 CRP 的值对于临床早起鉴别诊和指导用药有一定的意义

PU-1994

安岳地区健康人群尿素、肌酐、钙和总胆红素参考范围调查

王维
安岳县中医医院

目的 近年来，随着人们生活水平的提高，生活方式的有所改变，人体的各生化检测值也发生了一些变化。而环境及地理因素、不同地域人群的营养状况、生活习惯等的不同也是影响因素之一。为此，我们对本地区不同年龄、不同性别的健康人群进行了调查，建立安岳地区健康人群尿素（Urea）, 肌酐（Cr）, 钙（Ca）和总胆红素（TBIL）生化正常参考值范围。
方法 筛选在我院体检的健康人群共 143 人，其中成年男性 70 人,成年女性 73 人,年龄 20-70 岁.被调查人群选择条件为:B 超、心电图、胸透、内外科及其他化验结果均正常，试验前未服用过任何药物，非孕妇。按年龄段分为 20-30 岁 55 例，31-50 岁 55 例，51-70 岁 33 例；按性别分组为男性 70 例，女性 73 例。应用日立 7600 全自动生化分析仪对生化相关指标进行检测，剔除离群点后，采用 SPSS17 软件进行统计分析，建立其参考范围，并与本实验室现行相应参考范围比较，143 名献血员按性别、年龄分组，观察其差异。检测项目包括：Urea,Cr,Ca 和 TBIL。
结果（1）本调查结果 Urea 与本实验室现行参考值有较大差异；（2）按性别分组后，Cr 和 Ca 的性别差异有统计学意义 (P<0.01), 其结果分别为 :Cr(umol/L) 男： 76.82-110.72, 女： 64.25-93.89;Ca(mmol/L)男: 2.31-2.73,女: 2.31-2.63;(3)按年龄段分组后, Urea 和 Ca 在 51-70 岁和 20-30 岁,31-50 岁之间差异有统计学意义(P<0.05)。Urea 升高, Ca 降低。
结论 从本次试验所得的结果看来，不同地区，不同性别和不同年龄间的生化相关指标确实存在一定差异。这就要求我们在今后的工作中，对与生化检测相关疾病的诊断治疗中，应考虑到地区、性别和年龄的因素。因此，各个地区各实验室应该建立自己的参考范围。

PU-1995

血清肌红蛋白检验在急性心肌梗塞临床检验中的应用价值研究

邹航
安岳县人民医院

目的 急性心肌梗塞(AMI)是临床上较为常见的心血管疾病，该病的死亡率较高，影响患者的生活。该病是因冠状动脉粥样硬化导致患者血肌细胞缺血性坏死。症状体现为心力衰竭、休克以及心律失常等.本次研究对急性心肌梗塞患者予以血清肌红蛋白检验，对其在临床检验中的应用价值进行探究。
方法 41 例急性心肌梗塞患者以及 41 例健康受检者选自 2018 年 5 月-2019 年 5 月期间，急性心肌梗塞患者为实验组；健康受检者为参照组。
结果 实验组血清肌红蛋(124.83±35.78）；高敏 C 反应蛋白(17.32±2.87）；心肌肌钙蛋白(5.67±2.98）。参照组血清肌红蛋(68.94±12.24）；高敏 C 反应蛋白(5.82±2.43）；心肌肌钙蛋白(0.42±0.13）。实验组血清肌红蛋白、超敏 C 反应蛋白、心肌肌钙蛋白指标高于参照组，对比创意具备统计学含义 P<0.05。

结论 本次研究中对急性心肌梗塞患者予以血清肌红蛋白检验，可成为该疾病确诊的有利指标，该检测方法可在急性心肌梗塞临床检验中予以推广。

PU-1996

糖尿病及其并发症的临床检验研究

赵川岚
资阳市安岳县人民医院

目的 此次研究对糖尿病及其并发症进行临床检验，对其检验价值予以探究。
方法 68 例糖尿病患者及 68 例糖尿病并发症患者和 68 例 健康检查者选自 2018 年 3 月-2019 年 3 月期间，将糖尿病患者设为 A 组，并发症患者设为 B 组， 健康检查者设为 C 组。 3 组采取临床检验，对比各组空腹血糖（FBG）、糖化血红蛋白（HbA1c）、D-二聚体（ D-Dimer）、胰岛素（ Insulin）指标。
结果 FBG（7.67±0.57）mmol/L、HbA1c（8.43±4.32）%、 D-Dimer（0.43±0.07）mg/L、Insulin（3.27±0.86）μU/mL。B 组临床指标：FBG（14.67±1.25）mmol/L、HbA1c（9.68±1.32）%、D-Dimer（0.79±0.13）mg/L、Insulin （2.17±0.92）μU/mL。C 组临床指标：FBG（5.25±0.37）mmol/L、HbA1c（5.24±0.58）%、 D-Dimer（0.33±0.06）mg/L、Insulin （4.89±0.84）μU/mL。A 组在空腹血糖、糖化血红蛋白、D-二聚体、胰岛素指标与 B 组对比差异具备统计学含义 P<0.05，且 A、B 组与 C 组的空腹血糖、糖化血红蛋白、D-二聚体、胰岛素指标对比具备统计学含义 P<0.05。
结论 本次研究对糖尿病及其并发症进行临床检验，空腹血糖、糖化血红蛋白、D-二聚体、胰岛素指标可作为糖尿病及并发症的诊断指标，该方法可推广应用。

PU-1997

生化检验中标本溶血对结果准确性的影响

张兴红
安岳县人民医院

目的 本次研究中对生化检验中标本溶血对结果准确性的影响予以探究。
方法 在 2019 年 4 月-2020 年 4 月期间收治的 64 例患者为本次研究对象，将其分为实验 A 组（32 例）采取人工溶血处理；实验 B 组（32 例）采取常规自然分离处理。对 2 组检测结果予以分析研究。
结果 实验 A 组 天门冬氩酸氨基转移酶（AST）、谷丙转氨酶（ALT）、乳酸人脱氢酶（LDH）均高于实验 B 组（P<0.05），碱性磷酸酶（ALP）低于实验 B 组（P<0.05）。2 组数据分析后差异较为明显，具备统计学意义。实验 A 组血尿酸（BUN）、血尿酸（UA）血清肌酐（Cr）、甘油三酯（TG）与实验 B 组对比，数据输入到统计学软件中分析后差异较小（P＞0.05），不具备统计学意义。
结论 在本次研究中，采取人工溶血处理在生化检验中可具有显著的效果，可提高检验结果的准确性。

PU-1998

肾功能指标联合检测应用于诊断糖尿病肾病早期的价值分析

张兴红
安岳县人民医院

目的 研究肾功能指标联合检测应用于早期糖尿病肾病临床诊断价值。
方法 随机择选我院收治 72 例糖尿病患者作为 RCT 研究对象，根据有无发生早期肾脏病变划分为管理组和常规组。两组患者接受肾功能指标检测，比较两组患者肾功能指标水平和阳性检出率。
结果 管理组各项生化指标数值均高于常规组，（P＜0.05）；管理组 Cys-C、β2-MG、Hcy 以及 Cr 阳性检出率高于常规组，（P＜0.05）。
结论 糖尿病患者肾病早期临床诊断可根据 Cys-C、β2-MG、Hcy 以及 Cr 等指标进行临床诊断。

PU-1999

自建检测尿微量白蛋白钩状效应的确认方法

陈灿星[1]、张春凤[1]、郑骁云[1]、巫海婷[1]、姚少濠[1,2]、胡志峰[1,2]、李玲[1,2]、刘勇[1,2]、陶然[1,2]
1. 广州金域医学检验中心有限公司
2. 广州医科大学金域检验学院

目的 采用微米微量白蛋白（mALB）检测试剂盒在贝克曼库尔特 AU5800 全自动生化分析仪上进行尿微量白蛋白的测定，在通过性能验证后，建立检查钩状效应的方法及处理方法。
方法 采用微米微量白蛋白检测试剂盒在 AU5800 上进行线性验证。选取 5 例在厂家声明的线性浓度范围内的样本和 5 例超过厂家的线性浓度范围内的样本检测，绘制 Heidel-berger 曲线，吸光度-反应点曲线，观察曲线找出线性范围内最大吸光度（OD）值，将此 OD 值作为检测最后超线性 OD 值，并设为报警参数。通过已知浓度的 20 例线性范围内和 20 例超线性范围内的样本原倍和预稀释 4 倍上机检测，比观察反应曲线，及结果差异，验证最大 OD 值的正确。根据 CNAS-GL037《临床化学定量检验程序性能验证指南》的要求对微米微量白蛋白检测试剂检测下限和最大稀释倍数进行验证。
结果 微米微量白蛋白检测试剂盒在 AU5800 上浓度 5.0-200.0mg/L 线性验证通过，将 0.3226 作为作为线性范围内最大 OD 值，且经评估可成功识别超过分析测量范围的浓度。验证试剂检测下限 5mg/L 及最大稀释倍数为 25 倍。
结论 设置 OD 值 0.3226 作为超线性报警参数，有助于识别高浓度尿微量白蛋白引起的钩状效应。当遇到超过检测线性或者超过最大 OD 值的结果，则采用预稀释 25 倍再进行检测，满足临床预期需求。做自建分析体系的抗原抗体项目，实验室需进行钩状效应评估，并结合线性范围确定报警下的处理方法和临床报告方案。

PU-2000

同型半胱安酸(Hcy)、脂蛋白（a）、高敏 D-二聚体在高血压以及冠心病患者中相关性研究

何昊
安岳县人民医院

目的 此次研究中，探究同型半胱安酸(hcy)、脂蛋白（a）、高敏 D-二聚体在高血压以及冠心病患者中相关性。

方法 将 2019 年 4 月至 2020 年 4 月期间 100 例冠心病患者设为研究 A 组，100 例高血压患者为研究 B 组，将同期来我院进行健康体检的 100 例健康人群为对照组。观察 3 组的检测结果，比较 3 组同型半胱安酸（Hcy）、脂蛋白 a（Lp(A)）、高敏 D-二聚体（高敏 D-D）指标。
结果 研究 A 组 Hcy、Lp(A)、高敏 D-D 指标均高于研究 B 组和对照组（P<0.05），3 组数据输入到统计学软件中分析后差异明显，具备统计学意义。
结论 本次研究得知，血清中 Hcy、Lp(a)、高敏 D-D 对高血压以及冠心病的预测有着重要的意义。

PU-2001

POCT 血糖仪与全自动生化分析仪血糖测定结果对比分析

李燕、黄茜北、杨小美、马琳琳
新疆生产建设兵团第四师医院

目的 评价 POCT 血糖仪与全自动生化分析仪血糖测定结果并进行分析。
方法 选取就诊于本院体检中心患者 40 例，进行血液样本采集，分别采用护士手持 POCT 血糖仪和贝克曼 DXC800 全自动生化分析仪进行血糖检测，并比较分析两种方法检测结果的一致性。
结果 POCT 血糖仪的结果为 9.7±3.2mmol/L，全自动生化分析仪对血糖检测的结果为 9.0±3.1mmol/L 差异无统计学意义（P>0.05）。
结论 POCT 血糖仪与全自动生化分析仪在临床上具有极高的血糖检测准确性，在已确诊的糖尿病患者的血糖测定中具有极高的选择性，值得推广。

PU-2002

新生儿低血糖症的病因分析

李燕、黄茜北、李新霞、马琳琳
新疆生产建设兵团第四师医院

目的 分析引起新生儿出现低血糖症的影响因素，为临床治疗和预防新生儿低血糖提供理论依据。
方法 选取本院 2018 年 3 月~2021 年 3 月有新生儿低血糖高风险患儿 286 例，进行血糖等项目的检测，分析出现低血糖症状患儿的临床资料并进行数据统计。
结果 150 例新生儿低血糖患儿中，胎龄为 27-36 周的患儿出现低血糖者为 25 例，低血糖的发生率为 44.6%；胎龄为 37-41 周的患儿出现低血糖者为 27 例，低血糖的发生率为 30.0%；胎龄为>42 周的患儿出现低血糖者为 5 例，低血糖的发生率为 33.4%。新生儿低血糖患儿中体重为<2500g 的患儿出现低血糖者为 19 例，低血糖的发生率为 46.3%；体重为 2500g-4000g 的患儿出现低血糖者为 23 例，低血糖的发生率为 22.0%；体重为>4000g 的患儿出现低血糖者为 1 例，低血糖的发生率为 25.0%。新生儿低血糖患儿中治愈为 100%，有效为 100%，无效率为 0%。其中早产儿、低体重儿、围产期缺氧、母妊高症、母妊娠期糖尿病、喂养困难等因素是新生儿出现低血糖症的高危因素。
结论 导致新生儿出现低血糖发生的高危因素较多，对出现低血糖症状的新生儿需要密切观察血糖水平变化，及时进行治疗，降低低血糖对患儿中枢神经伤害，提高患儿生存质量。

PU-2003

2 型糖尿病病人 HbA1c 与颈动脉增厚和斑块形成的相关性

刘运双
绵阳市中心医院

目的 探讨 2 型糖尿病病人 HbA1c 与颈动脉增厚和斑块形成的相关性。
方法 回顾性分析纳入观察对象 1460 例（41～88 岁，男性 690 例，女性 770 例）。高效液相色谱法测定 HbA1c，B 型超声仪评估颈动脉增厚和斑块形成。依据 HbA1c 水平将观察对象分为非糖尿病组（HbA1c≤5.6%，630 例）、糖尿病前期组（6.5%＞HbA1c＞5.6%,512 例）和糖尿病组（HbA1c≥6.5%，318 例）。比较各组颈动脉增厚率和斑块阳性率，使用相关性分析（Spearman 相关系数）和二元 Logistic 回归分析评价 HbA1c 水平与颈动脉增厚和斑块形成的相关性。
结果 糖尿病组的颈动脉增厚率（57.2%）、斑块阳性率（69.2）高于非糖尿病组（43.5%，60.9%）和糖尿病前期组（45.7%，67.2%），差异有统计学意义（P<0.017）。糖尿病病人 HbA1c 水平与颈动脉增厚(r=0.105, P=0.008)、斑块形成（r=0.106, P=0.008）和斑块数量（r=0.143, P=<0.001）具有相关性。校正性别、年龄、吸烟、饮酒、血压、血糖、三酰甘油、总胆固醇、高密度脂蛋白胆固醇、低密度脂蛋白胆固醇和同型半胱氨酸后，糖尿病病人 HbA1c 水平升高是颈动脉增厚（OR=2.210; 95%CI 1.178～4.146; P=0.014）、斑块形成（OR=1.071; 95%CI 0.943～1.216; P=0.004）和斑块数量超过 1 个（OR=2.722; 95% CI 1.130～6.559; P= 0.026）的独立危险因素。
结论 2 型糖尿病病人 HbA1c 升高与颈动脉增厚、斑块形成和斑块数量相关。

PU-2004

LIS 双向通讯技术在临床自动生化分析仪中的应用

陈亚秀
资阳市雁江区妇幼保健院

目的 将双向通讯技术与 LIS 信息系统结合，运用于临床自动生化分析仪检验中，缩短检验时间，提高检验质量。
方法 在临床生化检验工作中，运用双向通讯技术和 LIS 信息系统，简化工作流程完成标本检测。
结果 简化了工作流程，缩短检验时间，有效地提高了工作效率，减少了分析误差，提高了医院医疗服务水平和检验工作，保证了检验质量。
结论 使用 LIS 双向通讯技术，代替了传统工作流程，实现临床生化检验的自动化，避免不必要的人为差错，提高了检验工作效率和质量管理水平。

PU-2005

溶血对临床生化检验影响及对策

朱洁
资阳市雁江区中医医院

目的 分析溶血对临床生化检验结果的影响及预防对策。
方法 抽取 2019 年 1 月至 12 月间在我院进行体检的健康体检者 44 例作为此次的观察对象，并采集其血液标本 2 份进行分析，其中 44 份接受常规护理的血液标本设为对照组，另外 44 份接受溶血处理的血液标本设为研究组，并对这两组的相关指标进行对比分析。

结果 研究组的总胆固醇、钾离子、门冬氨酸氨基转移酶、丙氨酸氨基转移酶以及乳酸脱氢酶水平均高于对照组，对比结果（p<0.05），差异具有统计学意义；而研究组的碱性磷酸酶水平则较低，与对照组相比差异明显（p<0.05）。
结论 在生化检验中，部分检验结果与溶血密切相关，因此，临床检验应重视溶血情况。

PU-2006

两种方法检测尿蛋白的结果对比分析

张明亮[1]、王波[1]、刘小凤[2]
1. 合肥金域医学检验实验室有限公司
2. 宣城华信健康体检中心

目的 对比分析优利特 500B 全自动尿液分析仪检测尿蛋白性能，提高尿液检验结果质量。
方法 采用优利特 500B 全自动尿液分析仪及磺基水杨酸法检测 1500 例来院体检正常人群尿蛋白，对两种检测方法检测尿蛋白结果进行比较。
结果 优利特 500B 全自动尿液分析仪与磺基水杨酸法检测阳性率分别为 88%与 83%，两者间结果比较差异无统计学意义（p>0.05），两种法法联合检测的阳性率为 98%。
结论 两种检测方法其方法学不同导致检验结果存在差异，应联合应用，以提供检验结果德准确性与可靠性。

PU-2007

合肥地区体检人群糖化血红蛋白结果分析

王波、张明亮
合肥金域医学检验实验室有限公司

目的 分析合肥地区糖化血红蛋白检测结果，为该地区糖尿病早期诊断提供多方面依据。
方法 对 2019 年 4 月~2019 年 5 月合肥地区送检 1470 例糖化血红蛋白标本，标本检测采用东曹 HLC-723G8 糖化血红蛋白分析仪检测 HbA1c（%）分别按性别、年龄等对检测结果进行统计学分析。
结果 糖化血红蛋白（HbA1c）在男女之间的差异均具有统计学意义（p<0.01）；1470 例标本中糖化血红蛋白总体水平男性高于女性，且伴随年龄上升有明显增长趋势。
结论 定期进行糖化血红蛋白检测，可为糖尿病早期诊断提供依据。

PU-2008

安徽地区正常孕妇不同孕期甘胆酸参考值研究

张明亮、王波
合肥金域医学检验实验室有限公司

目的 分析安徽地区正常孕妇甘胆酸（CG）结果水平，为该地区甘胆酸建立医学参考值。
方法 选取 2020 年 1 月~2020 年 12 月送检合肥金域医学检验实验室有限公司正常孕妇甘胆酸样本 928 例，采用 Beckman Coulter AU5800 全自动生化分析仪检测（该项目参加卫生部及安徽省临床检验中心室间质评，成绩为优秀）。分析 928 例正常孕妇甘胆酸（CG）检测结果情况，建立其医学参考值。参考值范围用（P50）及双侧限值（P2.5，P7.5）表示。
结果 928 例正常孕妇甘胆酸检测结果具有统计学意义（p<0.05），孕期参考值为：（0.00-4.60）μg/mL。

结论 本次回顾性分析初步研究 CG 医学参考值水平，建立本省甘胆酸（CG）参考值水平能更好的辅助临床疾病诊疗工作。

PU-2009

血清蛋白电泳组分定量参考范围的建立及临床应用

殷杏、童妙春、吴炯
上海嘉会国际医院有限公司

目的 血清蛋白电泳技术是临床筛查单克隆免疫球蛋白血症最常用的方法之一。传统的血清蛋白电泳报告结果为蛋白组分百分比，未纳入总蛋白定量结果的考量，故可能存在筛查漏检。本研究通过纳入总蛋白定量结果，统计健康人群中血清蛋白组分定量结果，建立定量的血清蛋白电泳组分参考范围，并研究其在多发性骨髓瘤诊断中的意义。
方法 收集表观健康人群，检测血清蛋白电泳及总蛋白定量结果，建立血清蛋白电泳组分定量参考范围；分别建立多发性骨髓瘤疾病及正常对照组，使用并比较血清蛋白电泳组分定量参考范围的临床适用性。
结果 共收集表观健康人群 196 名，其中男性 101 名，女性 95 名。以百分位数法（P2.5～P97.5）建立表观健康成人血清蛋白电泳组分定量的参考范围，ALB：38.61~48.56 g/L；α1：1.79~2.90 g/L；α2：4.08~7.08 g/L；β：5.69~16.07 g/L；γ：7.77~16.07 g/L。收集多发性骨髓瘤患者 113 名及正常对照组 122 名，使用定量参考范围进行判断（任意组分定量结果高于参考范围即为异常），正常对照组异常率为 8.20%，疾病组人群异常率为 58.41%。多发性骨髓瘤患者通过 M 蛋白定量进行分级，M 蛋白浓度越高，血清蛋白电泳组分定量结果异常率越高（M 蛋白<1g/l，阳性率 36.67%；M 蛋白 1~10g/l，阳性率 54.10%；M 蛋白 10~30g/l，阳性率 100%；M 蛋白>30g/l，阳性率 100%）。
结论 本研究通过引入总蛋白定量结果，建立成人血清蛋白电泳组分定量参考范围。此定量参考范围可为多发性骨髓瘤及“前骨髓瘤”过渡期患者进行疾病早期筛查提供了可靠的实验室诊断依据。

PU-2010

液质联用检测血及 24 小时尿儿茶酚胺及其代谢物助力精准诊断异位嗜铬细胞瘤一例

栾芳
山东第一医科大学附属省立医院

患者，女，29 岁，主诉“不规则阴道流血 1+月”，门诊以“血管内平滑肌瘤、高血压病”收入院入住山东第一医科大学附属省立医院妇科。入院后化验及影像学检查结果肾素:32.05 pg/ml、醛固酮:138.70 pg/ml、醛固酮/肾素浓度比值:4.33;血管紧张素 II:113.43 pg/ml;2021-05-25 COR（8 点）皮质醇(8 点):504.00 nmol/L;肾动脉 CTA+肾上腺 CT 增强+成像（双源）示:右肾上腺 CT 扫描未见明显异常； 左侧肾上腺略显增粗； 肾动脉 CTA 未见明显异常； 腹腔肠系膜、腹膜后脂肪间隙稍浑浊。泌尿外科、心内科、内分泌科多科室会诊建议：1、先行妇科手术，泌尿外科随诊监测；2.复查血浆儿茶酚胺及其代谢产物、血糖、糖化血红蛋白；3.行腹主动脉旁、膀胱周围 B 超，完善心脏彩超、心动检测；4.继续监测血压，调整降压药物。可疑嗜铬细胞瘤？!患者随后因“1.异位嗜铬细胞瘤？ 2.高血压病（3 级 极高危）3.慢性盆腔炎”于气管插管全麻下行腹膜后病灶活检+盆腔粘连松解术，术中快速病理回示：（血管内平滑肌瘤）送检组织内见小圆细胞团增生，细胞形态温和，较一致，可疑神经内分泌源性肿瘤。结合病史结合病史、术中所见及病理考虑异位嗜铬细胞瘤可能性大，转入泌尿外科进行治疗。留取 24 小时尿和血浆检测儿茶酚胺及其代谢物：尿游离肾上腺素 676.7μg/24h，尿甲氧基去甲肾上腺素 2701.95μg/24h，尿香草扁桃酸 20.91μg/24h；血游离肾上

腺素 7070pg/ml，血多巴胺 108pg/ml，三甲氧基酪胺 28.6pg/ml，甲氧基去甲肾上腺素 2600pg/ml，定性确诊为异位嗜铬细胞瘤。进一步择日手术治疗。

PU-2011

心肌酶谱组套中 α-羟丁酸脱氢酶存在的必要性探讨

倪军
南京大学医学院附属鼓楼医院

目的 评价 α-羟丁酸脱氢酶（α-HBDH）在心肌酶谱组套内存在的必要性，配合临床路径及单病种付费政策推进，避免检验项目过度使用，降低医疗成本。
方法 按照正常体检（乳酸脱氢酶正常）组、疾病组、肝脏病组、心脏病组、心肌梗塞（心梗）组、肌钙蛋白 T（TNT）升高组分组，回顾我院实验室信息系统（LIS）中历史数据，分析 α-HBDH、乳酸脱氢酶(LDH)在不同病种中的变化趋势，并用单因素方差分析比较不同病种间两者比值差异；用正常体检（LDH 正常）对照者及心梗患者的 α-HBDH 与 LDH 比值描绘接受者操作特性曲线（receiver operating characteristic curve，ROC 曲线）并分析其结果。
结果 正常体检（乳酸脱氢酶正常）组、疾病组、肝脏病组、心脏病组、心梗组、肌钙蛋白 T（TNT）升高组中 α-HBDH 与 LDH 的线性相关斜率分别为：0.76、0.79、0.60、0.90、0.98、0.83。 各组线性相关 R 值分别为：0.90、0.98、0.93、0.98、0.98、0.97。各组 α-HBDH 与 LDH 比值为 0.80、0.79、0.75、0.80、0.83、0.82。用正常体检（LDH 正常）对照者及心梗患者的 α-HBDH 与 LDH 比值描绘的 ROC 曲线下面积为 0.61($p<0.05$)
结论 各分组中 α-HBDH 与 LDH 均呈现较好线性相关；除肝脏病组外，其他各组 α-HBDH 与 LDH 比值无差异；ROC 曲线结果显示 α-HBDH 诊断心梗的效果差，在心肌酶谱组套中无不可替代的价值，建议从该检验套餐中剔除。

PU-2012

等离子体质谱仪 7900 检测血铅的性能测定

栾芳
山东第一医科大学附属省立医院

目的 等离子体质谱仪 7900（以下简称“ICP-MS 7900”）检测血铅的性能。
方法 评估 ICP-MS 7900 检测血液标本中铅的准确度、精密度、线性范围、临床可报告范围、参考范围、携带污染率，评价血铅试剂在 ICP-MS 7900 上的分析性能。
结果 ICP-MS 7900 测定血液标本中铅的浓度，通过卫生部临检中心室间质评验证准确度，偏倚为 <5%；批内精密度为 3.3%（低值）、3.7%（高值），批间精密度为 1.7%（低值）、4.2%（高值）；线性范围为 0-800μg/L；LOD 为 0.03μg/L，LOQ 为 0.13μg/L；最大稀释倍数为 50 倍，可报告范围为 0.13~41000.0 μg/L；参考范围是<100.00μg/L；携带污染率为 0.03%，符合仪器要求。
结论 ICP-MS 7900 测定血液标本中重金属铅的准确度高、重复性好，线性范围能满足临床所需，携带污染率极低，检测快速方便，结果可靠，特别适用于中毒与职业病科、小儿科等对早期铅中毒的筛查，是临床测定血铅的理想分析仪器。

PU-2013

肌酸激酶同工酶 CKMB 免疫抑制法与质量法在标本检测中的应用及与临床疾病关系分析

徐伟
泰安市中心医院

目的 通过肌酸激酶同工酶 CKMB 免疫抑制法与质量法在心肌损伤、恶性肿瘤、神经损伤相关疾病中的检测，探讨 CKMB 结果出现假性升高的影响因素及分析与相关疾病的关系。
方法 选取 2021 年 1 月——2021 年 5 月随机选取标本为入院诊断心肌损伤、恶性肿瘤、神经损伤的标本各 30 例，以临床诊断存在心肌损伤为观察组，恶性肿瘤、神经损伤为对照组。分析 CKMB 免疫抑制法和质量法检测结果，根据参考区间确定阳性标本，使用 ROC 曲线进行分析。
结果 观察组 CKMB 两种方法线性相关性较好（R2=0.88）;对照组 CKMB 两种方法线性相关性较差，ROC 曲线分析质量法在检测心肌损伤灵敏性和特异性上均优于免疫抑制法。
结论 肌酸激酶同工酶 CKMB 在心肌损伤的检测中具有重要意义，有高度的特异性，且受到临床的广泛关注。目前，肌酸激酶同工酶 CKMB 的检测方法有免疫抑制法、电泳法、质量法等。其中免疫抑制法最为常用，但由于生理性、病理性等因素的影响，常使 CKMB 出现活性假性增高或 CK/CKMB 结果的倒置，干扰临床对心肌损伤的诊断；质量法是建立在单克隆抗体直接识别 CKMB 抗体的实验原理上的，抗体的特异性不受 CKMM、CKBB、巨 CK 的干扰，降低了心肌损害诊断的假阳性率。但有研究表明，CKMB 的免疫抑制法诊断疾病已经不局限于心肌损伤或者心肌梗死疾患上了，通过免疫抑制法检测 CK/CKMB 倒置大于 50%可以为恶性肿瘤诊断提供帮助，CKMB 质量法检测可作为心肌炎特异和可靠的诊断依据。

PU-2014

大理地区儿童 25 羟基维生素 D 水平分析

王晓君
大理州人民医院

目的 了解大理地区健康体检儿童维生素 D 状况,为临床合理补充维生素 D 提供理论依据。
方法 回顾性分析 2019 年 11 月 1 日-2020 年 10 月 31 日在大理州人民医院体检并进行常规血清 25 羟基维生素 D 检测的儿童,采用 sysmens ADVIA2400 生化分析仪以方法分析不同年龄、性别及不同民族健康体检儿童的血清 25 基生素 D 水平。结果本次调查共计 1012 名儿童 25 羟基维生素 D 水平进入研究，平均水平为（27.69±8.56）mmol/L,其中 36 名儿童缺乏（7.52±1.34）mmol/L，610 名儿童不足（21.94±4.51）mmol/L，366 名儿童充足（38.79±6.12）mmol/L；446 名女童，平均水平为（26.06±8.2）mmol/L,其中 18 名儿童缺乏（7.61±1.5）mmol/L，294 名儿童不足（21.52±4.7）mmol/L，134 名儿童充足（38.5±6.25）mmol/L；566 名男童，平均水平为（28.98±8.82）mmol/L,其中 18 名儿童缺乏（7.44±1.21）mmol/L，316 名儿童不足（22.33±4.26）mmol/L，232 名儿童充足（38.95±6.05）mmol/L。不同年龄儿童的 25 羟基维生素 D 缺乏率随着年龄的增加而增加，<1 岁龄儿童 25 羟基维生素 D 不足、缺乏率最低,>6 岁儿童 25 羟基维生素 D 不足、缺乏率最高,差异有统计学意义(P<0.05)，不同性别，相同年龄生素 D 不足、缺乏无差异无统计学意义(P>0.05) ,不同民族，相同年龄生素 D 不足、缺乏无差异无统计学意义(P>0.05),建议家长、学校都提高相关的意识，医务工作者做好科普宣传及指导用药工作，合理补充维生素 D,促进青少年儿童健康发育。

PU-2015

四川地区非高密度脂蛋白胆固醇（Non-HDL-C）水平分析

蒙立业[1]、张禾[2]、干伟[1]、贺勇[2]
1. 四川大学华西医院实验医学科
2. 四川大学华西医院实验医学科

目的 研究四川地区表观正常健康人群中非高密度脂蛋白胆固醇（Non-CHOL-C）水平的情况，探讨其与血脂等冠心病高风险因素的相关关系。
方法 收集 2021 年 1 月至 2021 年 4 月四川大学华西医院健康体检人群血脂实验室检测结果。非高密度脂蛋白胆固醇计算方法为：Non-CHOL-C=总胆固醇（CHOL） -高密度脂蛋白胆固醇（HDL-C）。分析纳入人群血脂实验室检测的数据分布情况，分析各年龄段、性别之间血脂水平的差异。
结果 总计纳入 4417 名健康体检者，男性 3423 名，女性 994 名。男性组年龄 41（33~52）岁；甘油三酯（TG）浓度 1.10（0.84~1.39）mmol/L；总胆固醇(CHOL)浓度为 4.60（4.14~5.05）mmol/L；高密度脂蛋白胆固醇(HDL-C)浓度 1.27（1.12~1.45）mmol/L；低密度脂蛋白胆固醇(LDL-C)浓度为 2.86（2.45~3.28）mmol/L；非高密度脂蛋白胆固醇(Non-CHOL-C)浓度 3.28（2.84~3.73）mmol/L。女性组年龄 45（34~55）岁；甘油三酯（TG）浓度 0.99（0.74~1.28）mmol/L；总胆固醇(CHOL)浓度为 4.75（4.26~5.19）mmol/L；高密度脂蛋白胆固醇(HDL-C)浓度 1.55（1.34~1.79）mmol/L；低密度脂蛋白胆固醇(LDL-C)浓度为 2.75（2.30~3.18）mmol/L；非高密度脂蛋白胆固醇(Non-CHOL-C)浓度 3.13（2.63~3.60）mmol/L。单因素方差分析显示男女性别之间存在统计学差异（P<0.001,F=55.38）。Pearson 相关性分析结果显示 Non-CHOL-C 与 CHOL 和 LDL-C 具有较好的相关性，相关性系数分别为 0.885 和 0.971，P 值均小于 0.001；与 TG 和 HDL-C 具有较弱相关性，相关性系数分别为 0.443 和-0.255，P 值均小于 0.001。
结论 四川地区健康人群中非高密度脂蛋白胆固醇存在性别和年龄段的分布差异，可根据性别和年龄建立相应的参考范围。

PU-2016

化学发光免疫分析技术及放射免疫测定的临床价值对比研究

赵倩雯
山东大学第二医院

目的 通过数据对比分析研究化学发光免疫分析技术与放射免疫测定对甲状腺肿瘤的诊断效果，探讨其科研价值与临床应用价值。
方法 选取某一时间段内本院所有的甲状腺肿瘤患者作为试验组，然后选取相同人数的健康人士作为对照组。对两组样本使用化学发光免疫分析，通过对照，分析该技术的误诊率。除此之外，还要对所有的甲状腺肿瘤患者（试验组）进行放射免疫测定，对比两种检验技术，分析使用不同检验技术的甲状腺肿瘤的误诊率，从而得出哪一种方法更适用于诊断甲状腺肿瘤。研究过程应尽量减小样本其他身体因素对于试验结果的影响，如样本的性别、体型、年龄、是否患有其他疾病等等。
结果 在进行化学发光免疫分析后，发现试验组与对照组的两组样本的误诊率均低于 5%，且两组间的差异很小。具体指标方面，试验组样本的游离三碘甲状腺原氨酸、血清游离甲状腺素、甘油三酯明显高于对照组样本，促甲状腺激素明显低于对照组，化学发光免疫分析技术与放射免疫测定技术对于试验组样本的误诊率存在明显差异。
结论 根据临床研究可知，甲状腺肿瘤患者有着十分明显的临床症状，通过影像学检查，可以较为容易地确定病灶位置。影像检查后，还需要对患者进行生化检验（免疫测定），结合测定结果与影像学结果对患者进行最终确诊。研究结果表明，生化免疫检验的误诊率很低，并且化学发光免疫分析技术对于确诊甲状腺肿瘤来说是优于放射免疫测定法的，因此，在临床上对于疑似患有甲状腺肿瘤的患者，除了进行影像学检查，最好还要进行化学发光免疫分析，保证不误诊患者。

PU-2017

甲状旁腺激素检测方法的优化研究

罗永彬
昆明市第一人民医院

甲状旁腺激素是甲状腺细胞分泌的一种含有 84 个氨基酸的多肽，由甲状旁腺产生、肝脏代谢、肾脏排出，半衰期大约 4min。PTH 分泌入血液循环后，迅速降解为氨基端和羧基端片段，PTH 的所有分子形式在肾脏进一步降解，排出体外，这也是羧基端片段排出体内的唯一已知途径，因此在循环中羧基端片段的浓度远超过整分子。第二代全段甲状旁腺素检测试剂盒可以检测到非全段 PTH（如 7-84），并且这些片段的半衰期更长。在肾功能异常的特别是肾移植患者中，不能仅依据全段 PTH 的检测结果制定治疗方案。第三代 PTH 检测试剂盒仍然无法区分第 8 和 18 位的亮氨酸是否被氧化。本课题探索 PTH 的前处理不同稀释液对 PTH 检测结果的影响，结果表明生理盐水、去离子水稀释对结果有明显影响，应采用复合稀释液稀释。在-20℃、4℃、室温保存对 PTH 的稳定向无明显差异。在 EDTA-K2 抗凝剂条件下保存最稳定，在促凝剂条件下、肝素抗凝条件下保存较不稳定。

PU-2018

急性冠脉综合征患者血清 hs-CRP、sST2、IL-6 的表达及其意义

相莲
西安医学院第一附属医院

目的 观察血清超敏 C 反应蛋白（hs-CRP）、可溶性生长刺激表达基因 2 蛋白（sST2）、白介素-6（IL-6）在急性综合征中（ACS）的表达水平及临床意义。
方法 选取 2018 年 7 月至 2020 年 6 月于本院就诊的 78 例 ACS 患者为研究对象。根据患者冠状动脉造影结果、病史及临床表现分为不稳定型心绞痛（UAP 组 25 例）、急性心肌梗死（AMI 组 28 例）、稳定型心绞痛（SAP 组 25 例）。同时选取健康体检者 24 例为对照组。采用酶联免疫法（ELISA）检测 IL-6 水平。采用自动生化分析仪检测 hs-CRP、sST2 水平。对比各组 hs-CRP、sST2、IL-6 表达水平。
结果 AMI 组、UAP 组、SAP 组患者血清 hs-CRP、IL-6、sST2 水平显著高于对照组（P<0.05），AMI 组、UAP 组 hs-CRP、IL-6、sST2 水平较高于 SAP 组，差异具有统计学意义（P<0.05），AMI 组血清 sST2、hs-CRP、IL-6 水平显著高于 UAP 组（P<0.05）；3 支病变组的 hs-CRP、IL-6、sST2 水平显著高于单支病变、双支病变组（P<0.05）。
结论 hs-CRP、IL-6、sST2 水平在 AMI 组患者中显著上升，可能参与了 AMI 的病理过程，hs-CRP、IL-6、sST2 水平会随着病情加重而上升。

PU-2019

糖化白蛋白在终末期糖尿病肾病患者血糖监测中的应用价值

黄勤烽
联勤保障部队第九〇〇医院

目的 探究糖化白蛋白在终末期糖尿病肾病患者血糖筛查中的应用价值。

方法 本次研究共选取 131 例糖尿病患者，其中 100 例为单纯糖尿病患者，31 例为终末期糖尿病肾病伴贫血患者，所有对象均检测 FPG，Alb，Hb，HbA1c，GA，并对结果进行统计学分析。
结果 1.终末期糖尿病肾病伴贫血组的 HbA1c 明显低于单纯糖尿病组（6.91±1.68、8.08±1.96，P<0.001）。2.终末期糖尿病肾病组中 64.51%的患者存在低蛋白血症（Alb＜35g/L）。在单纯糖尿病组中 Alb（g/L）与 GA（mmol/L）无显著性差异，终末期糖尿病肾病组低蛋白血症的患者中 Alb（g/L）与 GA（mmol/L）呈线性相关（R=0.501，P<0.05）。而 Alb（g/L）与 GA（%）无显著性差异（P=0.75>0.05）。3.各组 FPG 均与 HbA1c 呈线性相关（单纯糖尿病肾病组:R=0.701；终末期糖尿病肾病组:R=0.613）；各组 FPG 均与 GA 呈线性相关（单纯糖尿病组:R=0.668；终末期糖尿病肾病组:R=0.539）。4.单纯糖尿病组和终末期糖尿病肾病组的 HbA1c 与 GA 均显著相关（单纯糖尿病组:R=0.813；终末期糖尿病肾病组:R=0.736）。
结论 1.低蛋白血症会使 GA 的含量被低估，而以 GA/Alb 来表示 GA（%）能显著降低这种影响。2.与同期单纯糖尿病患者相比，在终末期糖尿病肾病患者中，HbA1c 会被显著低估，GA 能更准确地反应患者近期的血糖平均水平。3.HbA1c，GA 在终末期糖尿病肾病患者中与 FPG 的相关性均比单纯糖尿病患者低。

PU-2020

液体活检在肺癌诊断中的研究进展

夏艳艳
南京大学医学院附属鼓楼医院

肺癌仍是世界范围内发病率和致死率最高的疾病之一。早期诊断对提高肺癌生存率，改善预后至关重要。液体活检作为一种新型的生物标志物已成为近年来临床关注的热点。液体活检的研究内容包括循环肿瘤细胞（Circulating Tumor Cell, CTC）、循环肿瘤 DNA（circulating tumour DNA, ctDNA）和外泌体，具有操作方便快捷、能反复获取、易于实时监控等优点。全文就以上标志物在肺癌早期诊断中的应用价值以及存在的优势和局限性进行综述，以期为肺癌患者早期诊断提供新方法。

PU-2021

尿胱抑素 C、尿 β2-微球蛋白单项及其联合检测对慢性肾脏疾病肾损伤的诊断价值

韩敬华[1]、马笑也[2]、赵立杰[1]、温学红[1]
1. 天津中医药大学第二附属医院
2. 天津医科大学

目的 分析尿胱抑素 C、尿 β2-微球蛋白单项及它们联合检测对慢性肾脏疾病肾损伤的诊断价值。
方法 选取天津市某医院 2020 年 11 月-2021 年 1 月收治的慢性肾病患者 90 例，按血清肌酐浓度分组，分为慢性肾病一组（正常检测值上限＜血清肌酐≤133μmol/L）30 例，慢性肾病二组（133μmol/L＜血清肌酐≤442μmol/L）30 例，慢性肾病三组（血清肌酐＞442μmol/L）30 例。另选取同一时间段健康体检者 30 例作为健康对照组。对比尿胱抑素 C、尿 β2-微球蛋白的单项及它们的联合检测诊断对每组慢性肾病患者的敏感度的差异。
结果 慢性肾脏疾病的各组尿胱抑素 C、尿 β2-微球蛋白的水平比对照组水平高，肾病组与对照组两两进行对比，存在一定统计学意义；尿胱抑素 C、尿 β2-微球蛋白在尿中的含量水平会随着肾损害加重而升高；慢性肾病一组、二组、三组之间两两进行对比，尿胱抑素 C 的临床检测结果水平存在显著的差异，有统计学意义；慢性肾病一组与慢性肾病二组相比，尿 β2-微球蛋白水平呈明显的差异，有统计学意义；慢性肾病二组与慢性肾病三组相比，尿 β2-微球蛋白水平无显著性差异，无统

计学意义；尿胱抑素 C 和尿 β2-微球蛋白的两个指标联合检测的 ROC 曲线下的面积最大，面积是 0.924，对于慢性肾脏疾病患者的临床诊断，尿胱抑素 C 和尿 β2-微球蛋白的两个指标的联合检测的诊断价值最大。
结论 尿胱抑素 C、尿 β2-微球蛋白可作为临床早期诊断慢性肾脏疾病的重要指标，通过对尿胱抑素 C 和 β2-微生物的综合分析，即可提高对慢性肾脏疾病早期临床诊断的灵敏度。

PU-2022

在不同系统间进行糖化结果比对的评估

黄树华
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨不同糖化检测系统间结果的可比性和临床可接受性。
方法 运用 NCCLS 的 EP9-A 方案，采用临床患者新鲜标本，与本地区同级医院已通过 NGSP 认证的罗氏 C501 自动生化分析仪进行比对。将罗氏 C501 作为标准检测系统，我科国产 MQ-2000PT 糖化血红蛋白分析仪作为待检测系统。用罗氏 C501 和 MQ-2000PT 同时测定 HbA1c，进行室间比对并采用配对 t 检验和回归分析的方法进行检测结果的方法比对及偏倚评估。
结果 MQ-2000PT 的仪器根据回归方程系数经校准和调整，结果偏倚可接受，基本能得到具有一致临床意义的检测结果。
结论 实验室比对可以对检测能力进行有效的质量监控。

PU-2023

心型脂肪酸结合蛋白定量试剂盒分析性能的验证

徐文波、丁怡文、毛星星、叶丹、张春婷、黄奕然、陈剑
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 验证心型脂肪酸结合蛋白定量试剂盒的主要分析性能。
方法 依据《临床实验室对商品定量试剂盒》WS/T 420-2013 的性能验证方案[1]，对心型脂肪酸结合蛋白试剂盒进行精密度、正确度、线性范围、临床可报告范围、生物参考区间进行验证。
结果 心型脂肪酸结合蛋白试剂盒的批内、批间精密度 CV 值分别为 3.55% -2.35%、2.92% -4.42% 最大允许误差≤1/3 CLIA'88 规定的允许误差；正确度验证，高值偏倚 0.15%，低值偏倚 7.69%；项目的可报告范围试验测定值结果与预测值接近，相关系数 r ＞ 0.975，线性理想(斜率 b 接近 1) 。
结论 心型脂肪酸结合蛋白商品定量试剂盒的精密度、正确度和线性范围、临床可报告范围、参考区间性能验证均达到了临床应用的实验要求。

PU-2024

可溶性 ST2 和 ProBNP、TNT-HS 在冠状动脉粥样硬化引起的心力衰竭患者的诊断及价值

陈晓忠
广东省人民医院

目的 测定由于冠状动脉粥样硬化导致的心力衰竭（heart failure,HF）患者和其他因素导致的心力衰竭患者血清可溶性生长刺激表达基因 2 蛋白（soluble growth stimulating express 2,ST2）、血浆

中脑利钠肽前体（ProBNP）和高敏肌钙蛋白 T（TNT-HS）的水平，分析其在各种 HF 的患者中的诊断及治疗价值。
方法 连续收集 2019 年 1 月到 12 月期间在广东省人民医院心血管研究所住院的 HF 患者 244 例，诊断为由于冠状动脉硬化引起的 HF 组 118 例和其他原因引起的 HF 组 126 例。收集同时期的由于冠状动脉粥样硬化心脏病的患者 115 例为疾病对照组，健康人群 73 名为健康对照组。比较冠状动脉粥样硬化引起的 HF 组和其他原因引起的 HF 组的资料及不同射血分数分组中的血清可溶性 ST2 和血浆 ProBNP、TNT-HS 水平。可溶性 ST2 采用酶联免疫法测定，ProBNP 和 TNT-HS 采用电发光测定。采用非参数检验及 Spearman 相关性分析等统计方法进行分析。采用受试者工作曲线（ROC）分析 ST2、ProBNP 和 TNT-HS 在两组 HF 中的诊断价值。
结果 HF 患者的血清可溶性 ST2 水平［50.2(40-60)］ng/ml。高于疾病对照组［24（10.2-30.5）］和健康对照组［16.3（6.2-25.3）］ng/ml（P < 0.001）。冠状动脉粥样硬化导致的 HF 组和其他原因引起的 HF 组血清的可溶性 ST2 水平和 ProBNP 水平无统计学差异，TNT-HS 水平有统计学差异。Spearman 相关性分析，HF 组可溶性 ST2 与 ProBNP、TNT-HS 呈正相关（r>0,P<0.05）。可溶性 ST2 诊断冠状动脉粥样硬化导致 HF 的 ROC 曲线下面积（AUC）为 0.852，（95%CI：0.795~0.945，P<0.001），最佳临界值为 45.23ng/mL 在此临界值下的敏感度为 80.4%，特异度为 89.6%。可溶性 ST2 诊断其他因素导致 HF 的 ROC 的 AUC 为 0.725（95%CI：0.670~0.851，P<0.001），最佳临界值为 33.24ng/mL，在此临界值下的敏感度为 75.4%，特异度为 87.5%。ProBNP 和可溶性 ST2 在鉴别诊断冠状动脉粥样硬化导致的 HF 和其他原因导致的 HF 的 ROC 的 AUC 分别为 0.714、0.799，可溶性 ST2 高于 ProBNP。
结论 HF 组的可溶性 ST2 和 ProBNP 水平明显高于疾病对照组和健康对照组。在鉴别诊断冠状动脉粥样硬化导致的 HF 和其他原因导致的 HF 时可溶性 ST2 价值高于 ProBNP

PU-2025

痛风与高尿酸血症关联的分析

马骋赟
山东省立医院

目的 痛风是一种古老的疾病，近些年来随着生活水平的提高，我国高尿酸血症的患病率已高达 13.3%，患者规模达 1.8 亿，痛风患者人群也悄然超过 1500 万，但他们对疾病的认识仍然存在不足，此研究主要探讨痛风和高尿酸血症之间的关系，以期助力痛风的防治。
方法 选择在山东省立医院 2019 年 1 月至 2021 年 6 月门诊及住院 300 例病人结果进行分析。根据尿酸的高低分为 2 类， 按本院尿酸参考范围空腹状态下男 420umol/L、女 360umo1/L 为界，分为大于正常值和小于正常值进行比较分析看是否符合作为临界参考、年龄性别对其影响的意义，在选择正常对照组 100 例来自随机抽样的体检健康志愿者。分两组尿酸等进行比较分析。
结果 总体进行分析发现，经过统计来看尿酸高于正常值时，患者有患有高尿酸血症，但只有 10%会患有痛风症，且有 5%发生痛风症的患者其尿酸值处于正常值范围内，差异之间有统计学意义（P<0.05）。Logistic 回归分析尿酸值与痛风的发生率呈负相关。
结论 一般来讲，高尿酸血症的人中约有 10%会发生痛风，可以肯定，没有高尿酸血症就没有痛风，但高尿酸并不一定出现痛风。痛风时血尿酸水平不一定升高。虽然痛风是在高尿酸血症的基础上，但在痛风急性发作时，大量尿酸从血液中析出，中性粒细胞会对尿酸结晶进行吞噬，相比来说，此时血中尿酸含量反而降低，若此时检测血尿酸水平，多低于平常水平。但体内整体尿酸含量并没有减少。

PU-2026

急性心肌梗死预警中行心型脂肪酸结合蛋白、微小 RNA-499 检测的价值分析

郑川
成都市双流区第一人民医院（四川大学华西空港医院）

目的 探究急性心肌梗死预警中行心型脂肪酸结合蛋白、微小 RNA-499 联合检测价值。
方法 筛选我院 2018 年 1 月~2020 年 10 月收治的 150 例因胸痛急性发作来院就诊的急性心肌梗死疑似患者，所有患者在胸痛发作后 3 小时内入院，其中确诊 65 例急性心肌梗死，85 例非急性心肌梗死，入院后、4h、8h、12h 检测心型脂肪酸结合蛋白、微小 RNA-499 含量，比较单独检测和联合检测灵敏度和特异度。
结果 （1）心型脂肪酸结合蛋白含量和微小 RNA-499 含量于 4~8h 开始升高，于 8~12h 达到峰值后逐渐回落，两项指标均在 12h 后回归下降。（2）AMI 的心型脂肪酸结合蛋白、微小 RNA-499 单独检测灵敏度分别是：69.23%、69.23%，联合检测的灵敏度是 76.92%。（3）对比心型脂肪酸结合蛋白、miRNA-499 的检验结果来看，相较于单独检测，联合检测的敏感度明显更高，P＜0.05。
结论 在急性心肌梗死的早期诊断中采用血清脂肪酸结合蛋白、微小 RNA-499 联合检查，可充分提高诊断的灵敏度。

PU-2027

血清淀粉样蛋白 A 的临床运用新进展

槐以啟、年士艳
玉溪市人民医院重症医学科（昆明医科大学第六附属医院重症医学科）

血清淀粉样蛋白 A(Serum Amyloid A，SAA)是一种参与机体多种炎症反应的急性期蛋白，在炎症反应早期即可高度表达。由于其具有极高的敏感性，使得他作为炎症标志物而得到广泛运用。SAA 参与多种临床疾病的发生与发展，最近的研究发现 SAA 在指导临床疾病的诊断、动态监测疗效、预后评估等方面具有较高的研究价值。本文通过阅读相关的国内外文献，总结 SAA 与临床有关疾病的最新研究成果，为 SAA 在临床疾病的诊治及预后判断等方面提供理论参考。

PU-2028

使用临床实验室现有真实数据建立老年人肾功能干化学相关指标参考区间的可行性分析

吴佳莺
上海市第一人民医院嘉定分院

目的 参考区间的研究很多都是通过实验室现有数据进行回顾性研究及分析建立的。然而，临床实验室建立老年人肾功能尿素（Urea）、肌酐（Crea）、尿酸（UA）干化学参考区间用这种方法的可行性尚未评估。因此，本研究旨在评估仅使用来自临床实验室的现有真实数据建立老年人肾功能干化学的参考区间，并提供根据年龄、性别因素调整后建立参考区间的理论依据。
方法 使用强生 VITROS 4600 全自动干式生化分析仪，根据性别、年龄组段进行分组。建立两个衍生数据库：衍生数据库 A 和衍生数据库 B。使用严格的排除标准选择衍生数据库 A 中的参考个体，并将数据库建立的参考区间作为标准参考区间。衍生数据库 B 中的个体为直接从实验室信息系统（LIS）中导出的体检人群的数据，并对该数据库基于数据挖掘方法建立的参考区间进行评估。采

用比较置信区间（CI）的方法同时利用基于外部数据库的决策结果的一致性来比较 A 组参考区间和 B 组参考区间。
结果 老年人肾功能干化学的 B 组参考区间与 A 组参考区间结果相似。大多数肾功能干化学的参考区间上限和下限的 90%置信区间在 A 组与 B 组之间存在重叠，并且 B 组的限值在 A 组的 90%置信区间内。老年人肾功能干化学参考区间 A 组和 B 组的一致性大于 0.95。
结论 采用适当的方法剔除离群值后，利用临床实验室现有的数据建立老年人肾功能干化学参考区间是可行的。

PU-2029

肺癌患者血清乳酸脱氢酶水平及临床意义

赵欣然
中国医科大学附属盛京医院

目的 探讨肺癌患者血清乳酸脱氢酶同工酶水平变化及临床意义
方法 2019 年 1 月-2020 年 1 月收治肺癌患者 200 例作为实验组，同时选取同期体检健康者 200 例作为对照组。检测两组血清 LDH 水平，并进行分析。
结果 肺癌患者血清 LDH 水平显著高于健康人，差异有统计学意义(P<0.05)。各种病理类型非小细胞癌患者血清 LDH 水平比较，差异无统计学意义(P>0.05)。
结论 连续监测患者血清 LDH 水平对肺癌患者临床诊断有一定意义。

PU-2030

冠心病患者发病机制及不同性别危险因素概述

李琼、冯磊
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

冠状动脉粥样硬化性心脏病(CHD)是由于心脏冠状动脉存在粥样硬化斑块,导致冠状动脉管腔狭窄，进而引起心肌缺血缺氧的临床症状。不同性别 CHD 患者的危险因素可能存在差异，早期识别并积极防治，对二级预防至关重要。本研究旨在阐述 CHD 发病机制及不同性别之间危险因素的差异性，为 CHD 患者的防治措施提供重要的理论依据。

PU-2031

ACS 患者髓过氧化物酶 MPO 水平变化与病变程度的相关性

徐文青
山西省心血管病医院

目的 探讨急性冠状动脉综合征(acute coronary syndrome,ACS)患者血清中髓过氧化物酶(myeloperoxidase,MPO)水平变化同其病变程度之间的相关性。
方法 选取本院 2020 年 12 月至 2021 年 2 月收治的 130 例患者按冠脉造影结果和临床诊断分为 ACS 患者 50 例(ACS 组)、稳定型心绞痛患者 50 例(SAP 组)和健康者 30 例(对照组)同期冠状动脉造影阴性作为观察对象,分别对其血浆 MPO、高敏 C 反应蛋白(hs-CRP)、高敏肌钙蛋白 I（hs-cTnI）水平进行测定,通过冠状动脉造影检查对患者冠脉狭窄程度和病变血管支数进行回顾性分析。
结果 ACS 组 MPO 2.50±0.84 ng/ml, hs-cTnI 35.5±1.28 ng/ml, hs-CRP 10.01±1.25 mg/L；SAP 组 MPO 0.95±0.14 ng/ml, hs-cTnI 5.08±1.08 ng/ml, hs-CRP 1.08±0.25 mg/L.对照组 MPO 0.60±0.44 ng/ml, hs-cTnI 0.18±0.03 ng/ml, hs-CRP 0.58±0.15 mg/L。ACS 患者的血浆 MPO、hs-cTnI、hs-

CRP 均明显高于 SAP 组和对照组,SAP 组患者血浆 MPO、hs-cTnI、hs-CRP 水平明显高于对照组,差异有显著性(P<0.05);采用血管造影对三组受检者冠状动脉狭窄程度进行检测，不同冠脉狭窄支数的 MPO 水平差异无显著性(P>0.05);重度冠脉狭窄患者血浆 MPO 浓度明显高于中度、轻度患者,从高到低依次为重度、中度、轻度,差异有显著性(P<0.05)。

结论 血浆中 MPO 的表达水平同急性冠状动脉综合征患者的病情进展之间存在明显相关性,其中随着患者冠状动脉斑块稳定性的变差及冠状动脉阻塞程度的增加,其血浆 MPO 浓度显著上升,提示血浆 MPO 可作为急性冠状动脉综合征患者病情评估的有效生化检验指标。

PU-2032

磷脂酶 A2 与肿瘤疾病相关性的研究

周广飞、冯强
泰安市中心医院

肿瘤是机体细胞在各种内外致瘤因素长期协同作用下导致基因水平的突变和功能调控的异常，从而促使细胞持续过度增殖并导致发生转化而形成的新生物。病理和影像学的检查并辅以特异性肿瘤标志物检测是目前诊断其的金标准。但是往往要到肿瘤晚期才能有明显的指征，然而对最近肿瘤的相关性论文的研究回顾中磷脂酶 a2 作为一种新型的肿瘤相关性指标越来越受到研究者的重视。他可以在肿瘤早期起到极好的预警作用。人血浆脂蛋白相关磷脂酶 A2 是一类具有磷脂分解活性的超家族酶类。由血管内膜中的巨噬细胞、 T 细胞和肥大细胞分泌，它广泛的存在于动物的细胞和体液中，可以催化水解磷酸甘油脂 sn-2 位置的脂键，产生游离脂肪酸和溶血磷脂，参与细胞内外信号的传递、炎症及炎症相关疾病等病理反应。主要分为四大类：分泌型 PLA2（secretory PLA2，SPLA2）、胞浆型 PLA2（cytosolic PLA2，cPLA2）、钙离子非依赖型（Ca2+-independent PLA2，iPLA2 ）和脂蛋白 PLA2（Lipoprotein-associated PLA2，Lp-PLA2）.近几年肿瘤疾病与磷脂酶 a2 相关性论文研究发现，大部分选取本院住院患者的实验室免疫组织化学法或者血清学检测血清中磷脂酶 a2 的水平资料，根据不同肿瘤的组织学分级和 TNM 分期，用统计学的方法分析不同类型肿瘤磷脂酶 a2 结果异常程度的相关性和差异性。对照组为正常人群或健康查体人群。本文对磷脂酶 a2 的作用机理和对肿瘤相关疾病的影响及研究方法进行总结分析，希望对后续不同肿瘤中磷脂酶 a2 的表达水平研究提供参考。

PU-2033

西宁地区缺铁和缺铁性贫血对 HbA1c 结果的影响

马继登[1]、阿祥仁[2]、李子安[2]、刘兰民[2]、李德琴[2]
1. 青海省人民医院检验科
2. 青海省人民医院检验科

目的 研究西宁地区糖尿病和非糖尿病人群缺铁和缺铁性贫血时，对 HbA1c 检测值的影响。

方法 纳入 2018 年 1 月 1 日到 2020 年 8 月 25 日来青海省人民医院就诊的患有缺铁性贫血和潜在缺铁的患者，以及与 IDA 组年龄和性别相匹配的健康体检患者。在医院的 LIS 中采集铁蛋白(FER)、Fe(血清铁)、HbAlc、RBC（红细胞）、血红蛋白（Hb）、平均红细胞体积（MCV）、MCH（平均血红蛋白含量）、MCHC（平均血红蛋白浓度）、C 反应蛋白（CRP）、肌酐（CREA）、空腹血糖（FPG）、餐后血糖、果糖胺（FMN）等实验室数据。将非糖尿病人群分为缺铁性贫血非糖尿病组 63 例、潜在缺铁非糖尿病组 95 例、非糖尿病对照组 126 例，将糖尿病患者分为缺铁性贫血糖尿病组 22 例、潜在缺铁糖尿病组 34 例、糖尿病对照组 44 例。并对两类人群的数据分别进行方差分析。

结果 非糖尿病人群中，NDM-IDA 组、NDM-ID 组、NDM-CON 组 3 组的平均年龄、FPG、FMN 水平比较，差异无统计学意义（P>0.05）。3 组间 Fe、FER、RBC、Hb、MCV、MCH、MCHC、HbAlc 比较,差异均有统计学意义（P<0.05）。NDM-CON 组的 HbA1c 水平与 NDM-IDA 组、NDM-ID 组比较，差异均有统计学意义（P<0.05）；NDM-IDA 组与 NDM-ID 组比较，差异无统计学意义（P>0.05）。糖尿病人群中，DM-IDA 组、DM-ID 组、DM-CON 组 3 组的平均年龄、FPG、FMN 水平差异无统计学意义（P>0.05）。3 组间 Fe、FER、RBC、Hb、MCV、MCH、MCHC、HbAlc 比较,差异均有统计学意义（P<0.05）。DM-CON 组的 HbA1c 水平与 DM-IDA 组比较，差异均有统计学意义（P<0.05）；DM-ID 组与 DM-CON 组、DM-IDA 组比较，差异均无统计学意义（P>0.05）。

结论 西宁地区的非糖尿病患者，在潜在缺铁和缺铁性贫血时 HbAlc 水平都会假性升高。西宁地区的糖尿病患者若同时患缺铁性贫血时，HbAlc 水平会假性升高。

PU-2034

肌酐、甘油三酯、空腹血糖与糖化血红蛋白的关系研究

缪林君
上海市第一人民医院嘉定分院

目的 探究糖化血红蛋白与空腹血糖及肌酐 Cr、总甘油三酯 TG、高密度胆固醇 HDL 的相关性。

方法 将 2020 年 8 月-2021 年 4 月收治的确诊 2 型糖尿病患者 56 例，分为糖化血红蛋白理想范围组（<7%）52 例，糖化血红蛋白控制欠佳组（＞7%范围）4 例。以 72 例健康体检者为对照组。对比其空腹血糖、肌酐、甘油三酯，观察其差异性。结果与糖化血红蛋控制欠佳组相比，糖化血红蛋白理想范围组空腹血糖明显下降（P＜0.05），甘油三酯明显升高（P＜0.05），肌酐明显升高（P＜0.05）。与对照组相比，糖化血红蛋白理想范围组及糖化血红蛋白控制欠佳组的空腹血糖、TG、Cr 明显升高，HDL 降低（P＜0.05）。

结论 糖化血红蛋白可作为糖尿病的诊断和监控指标。糖尿病患者血脂和肾功能水平与血糖控制相关，应加强对血糖与血脂和肾功能的管理。

PU-2035

高血压检测中容易被忽略的血管紧张素 II

王慧、杨国青
贵州金域医学检验中心有限公司

目的 为了让医生更好认识血管紧张素 II 的作用机理，以及参照血管紧张素 II 的检验结果，给临床提供用药指导。

方法 ①结合血管紧张素 II 在贵州金域医学检验中心项目检测标准操作规程，阐述血管紧张素 II 在高血压乃至内分泌性疾病中的检测必要性。 ②统计分析贵州金域医学检验中心有限公司自 2018 年 05 月至 2021 年 04 月送检样本情况。

结果 ①血管紧张素 II 是由肾素作用于血管紧张素原形成的血管紧张 I 在血管紧张素转换酶的作用下形成的，是一种能够收缩血管升高血压的 8 肽。它在肾素-血管紧张素-醛固酮系统中具有重要作用。首先，血管紧张素 II 能引起小动脉血管收缩，引发血压升高；其次，血管紧张素 II 能刺激肾上腺皮质分泌醛固酮，使钠重吸收增强，从而影响人体内电解质的平衡；第三，血管紧张素 II 可以使儿茶芬胺上升，从而引起去甲肾上腺素增加，促使血管内皮细胞的增生，亦可使用血管紧张素 II 的受体拮抗剂阻断反应，来治疗高血压及肾脏疾病。

②贵州金域医学检验中心有限公司自 2018 年 05 月至 2021 年 04 月送检样本情况如下：2018 年 05 月至 2019 年 04 月间血管紧张素 II 占送检高血压总样本数的 14.97%；2019 年 05 月至 2020 年 04 月间血管紧张素 II 占送检高血压总样本数的 21.32%；2020 年 05 月至 2021 年 04 月间血管紧张素 II 占送检高血压总样本数的 30.16%。

结论 ①从贵州金域医学检验中心有限公司接收的送检样本情况分析，目前血管紧张素 II 的检验占比逐年递增，说明临床对血管紧张素 II 结果对高血压结果的综合判读逐渐增强，但仍然有很大的缺口。②根据血管紧张素 II 具有强烈收缩血管的能力，可协助医生判断是否需要进行肾动脉的影像学研究。③根据血管紧张素 II 检验结果，结合醛固酮检测结果及影像学 CT，可对高血压及肾脏疾病进行分型。④根据血管紧张素 II 在肾素-血管紧张素-醛固酮系统中的作用，可指导临床使用拮抗剂对高血压疾病进行治疗，并评估治疗效果。

PU-2036

深圳市罗湖地区女性不同年龄段 CA125、CEA 和 CA125/CEA 参考区间的建立和验证

吕康琪、陈大洋、李敏、姚恒、郭非凡、承宝贵、张秀明
深圳市罗湖医院集团医学检验实验室

目的 间接法建立深圳罗湖地区健康成年女性人群血清 CA125、CEA 和 CA125/CEA 水平的参考区间，并进行验证。

方法 对 2019 年 7 月至 2020 年 7 月健康体检人群数据分析，通过偏度-峰度值检验数据正态性，对非正态数据使用 BOX-COX 转换，四分位间距法剔除离群值后计算 95%百分位获得参考区间；分析 2020 年 8 月的健康体检成年女性数据对参考区间进行验证。

结果 深圳罗湖地区健康成年女性按年龄组分为 A 组（20-29 岁），B 组（30-39 岁），C 组（40-49 岁），D 组（50-59 岁），E 组（≧60 岁）；CA125：AB 组参考上限是 32U/mL，C 组 31.09U/mL，DE 组 20.58U/mL；CEA：A 组参考区间上限是 2.58pmol/ml、B 组 2.60pmol/ml、C 组 3.22pmol/ml、D 组 3.96pmol/ml、E 组 5.76pmol/ml；CA125/CEA：AB 组参考上限为 43.30，C 组 34.51、D 组 18.70、E 组 13.72。经验证检测结果 90.03%以上符合新建参考区间，验证均通过。

结论 间接法建立参考区间适用于临床实验室。CA125 和 CEA 参考区间存在年龄组差异，为临床不同年龄的妇科疾病诊断提供参考依据。

PU-2037

添加抗人线粒体型 CK 单克隆抗体的试剂检测肌酸激酶同工酶 MB 的临床应用评价

李振国[1]、张龙英[1]、杨银凤[2]
1. 大连医科大学附属第二医院
2. 大连医科大学

目的 研究新型免疫抑制法 CK-MB 检测试剂在检测中的临床应用。

方法 对新试剂（添加抗人线粒体型 CK 单克隆抗体的试剂）的纠正结果进行分析，并验证其抗溶血干扰能力。收集本医院 CK-MB 检测结果为阳性且非心肌损伤患者的血清样本，分别用传统试剂（未添加抗人线粒体型 CK 单克隆抗体的试剂）和新型试剂重新测定后记录结果。先初筛一周内

95 例样本计算纠正率，初步得到新试剂的总体纠正效果。再对 3 个月内收集的样本按照不同疾病分类分析，计算新检测试剂对不同疾病假阳性样本的纠正率，计算每个样本用两种方法检测的结果与对应检测方法参考范围上限的差值并做图。随机选择 50 例疑似假阳性样本测定其质量作为参照，计算新试剂检测结果与质量法检测结果的符合率。从 CK-MB 酶活性正常的样本中随机选取 8 例进行溶血，计算溶血后与溶血前酶活性比值。

结果 初筛 95 例样本的纠正率为 74.73%。不同疾病的纠正率分别为：急性白血病 83.3%；再生障碍性贫血 88.8%；扁桃体炎 90%；支气管炎 88.8%；肺癌 86.6%；胃癌 90%。50 例假性样本与质量法相比较的符合率为 78%。在溶血样本中，溶血前后传统试剂测定的 CK-MB 酶活性变化幅度显著高于新试剂。

结论 新试剂对每种所研究疾病的假阳性样本的纠正率均在 80%以上，且阴性结果与质量法的符合率为 100%，抗溶血干扰能力较强。因此新试剂测定 CK-MB 酶活性的部分性能优于传统试剂。

PU-2038

淄博地区健康人群肌酐参考区间建立的研究

类承斌、张文
淄博市中心医院

目的 调查淄博地区健康人群血清肌酐的正常参考范围，建立该地区血清肌酐的参考区间。

方法 采用酶法及贝克曼 AU5831 自动生化分析仪对该地区 1500 例健康成年人（年龄范围 18-72，其中男 676 例，女 824 例）进行血清肌酐的测定，并按性别和年龄组分别比较。

结果 男性体检者的肌酐浓度明显高于女性（P<0.001），其 95％参考区间为 56.3～91.0μmol/L（18～30 岁）、56.2～95.6μmol/L（＞30～70 岁）、60.1～112.7μmol/L（＞70 岁）；女性体检者肌酐的 95％参考区间为：41.0～65.4μmol/L（≤60 岁）、44.7～86.1μmol/L（＞60 岁）。

结论以酶法建立了淄博地区健康人群血清肌酐的参考区间供检验人员参考。

PU-2039

传统肿瘤标志物联合新兴标志物检测在乳腺癌诊断中的意义与应用

赵志红
天津医科大学肿瘤医院检验科

目的 探讨传统肿瘤标志物糖类抗原 153（CA153），糖类抗原 125(CA125)，癌胚抗原（CEA），神经元特异性烯醇化酶（NSE），糖类抗原 242（CA242）联合新兴肿瘤标志物细胞角蛋白 19 片段抗原（Cyfra21-1），肿瘤特异性生长因子 (TSGF)，鳞状上皮抗原（SCC）对乳腺癌的临床诊断价值。

方法 用电化学发光法和酶化学发光法对乳腺癌组，乳腺良性疾病组和健康对照组的临床资料进行分析。

结果 乳腺癌组八种肿瘤标志物含量明显高于对照组，单独检测 CA153，CA125，CEA, NSE ，CA242，Cyfra21-1,TSGF,SCC 阳性率分别为 44.1%，25.3%，35.6%，39.2%,38.5%，35.3%，39.0%,35.7%,联合检测率达到 71.5%。

结论 此八种肿瘤标志物联合检测可明显提高乳腺癌诊断的阳性率，弥补单项检测的缺陷和不足，有重要的临床应用价值。

PU-2040

ICP-MS 法测定全血中 15 种微量元素的方法学建立

廖倩、余羊羊
重庆金域医学检验所有限公司

目的 采用电感耦合等离子体质谱（ICP - MS）建立快速测定全血中 15 种微量元素的方法。
方法 采用 0.1％Triton X-100+0.1％HNO3 对全血样品稀释 20 倍后直接用 ICP - MS 分析，对镁、锰、铁、铜、锌、铅、钙、钒、铬、钴、镍、硒、钼、镉、铷的检测低限、精密度和正确度（加标回收）进行验证。
结果 测定全血质控品，检测值均在可接受范围，其标准曲线的相关系数均＞0.995，方法检出限的测定铜、镍等 10 种微量元素为 0.00-0.15 ug/L，锌、钙等 5 种常量元素为 0.01-1.50mg/L，重复精密度均＜6.20%，中间精密度均＜6.09%，15 种元素的加标回收率在 86.59%-113.30%。
结论 用 ICP - MS 同时测定稀释后全血中 15 种元素的方法学性能满意，结果可靠，可满足日常大量标本的快速检测要求。

PU-2041

同型半胱氨酸测定对妊娠期糖尿病意义的探讨

谢婷彦、钟白云
中南大学湘雅医院

目的 研究妊娠期糖尿病（GDM）患者中血清同型半胱氨酸（Hcy）的水平及其与妊娠结局的关系，探讨同型半胱氨酸的测定对妊娠期糖尿病的意义。
方法 选取中南大学湘雅医院 2016 年 4 月-2017 年 4 月期间收治入院的孕妇 70 例，其中 35 例妊娠期糖尿病患者纳为病例组，35 例血糖正常者纳为对照组。检测两组孕妇血清同型半胱氨酸的水平，追踪并收集两组孕妇的妊娠结局，进行比较分析。
结果 GDM 组血清同型半胱氨酸水平（7.36±1.60）较正常对照组 （6.58±1.36）升高，差异具有统计学意义（P<0.05）；GDM 组妊娠不良结局的发生率明显高于对照组（P<0.05）； 且两组妊娠不良结局的同型半胱氨酸水平较正常分娩组水平均有升高。
结论 血清同型半胱氨酸水平可能与妊娠期糖尿病的发生发展和妊娠结局相关，监测 GDM 患者的血清 Hcy 水平，对患者妊娠结局有一定的预判作用。

PU-2042

胱抑素 C 同位素稀释质谱法检测条件的优化

王建新[1]、李亚男[2]
1. 南通大学附属医院
2. 南通市第一人民医院（南通大学第二附属医院）

目的 优化胱抑素 C 蛋白同位素稀释液相色谱串联质谱法检测条件，为精准测量奠定基础。
方法 研究胱抑素 C 纯蛋白酸水解条件、色谱及质谱条件，建立同位素稀释质谱法测量蛋白水解产物亮氨酸（ Leu）、脯氨酸（Pro）、缬氨酸（Val）和苯丙氨酸（Phe）四种氨基酸。再换算出胱抑素 C 的含量，并对纯蛋白不确定度进行评定。
结果 胱抑素 C 纯蛋白在 8 M 盐酸、130℃高温下 4 h 完全水解为氨基酸；添加保护剂苯可以防止氨基酸氧化、降解，提高检测灵敏度。本法回收率 95.75%～105.60%，不精密度为 1.02%，符合 FDA 生物样本分析方法导则标准。 CysC 含量（1.29±0.07）mg/g（k=2）。

结论 建立同位素稀释液相色谱串联质谱法定量 CysC 的方法，本法无需衍生化，操作简单、结果准确，可溯源至 SI 单位。根据 GUM 原则进行各分量不确定度分析，合理评估扩展不确定度，检测结果可信。

PU-2043

不同高密度脂蛋白水平与心血管疾病终点事件的研究

钱净
昆明市第一人民医院

目的 调查不同 HDL 水平与心血管疾病终点事件。
方法 选取我院 2018 年 1 月至 4 月 1036 名具有心血管事件疾病的患者，收集所有研究对象 HDL-C、TG、CH、LDL-C 以及患者血压，饮酒史，吸烟史。比较不同 HDL-C 水平下心血管事件的发生情况。
结果 所有研究对象年龄、饮酒史、CH、TG 统计差异均无统计学意义（P>0.05）；性别、吸烟史、收缩压、舒张压、HDL-C、LDL-C 统计差异均具有统计学意义（P<0.05）；HDL-C<1.0mmol/L 下心血管事件发生率中急性心肌梗死、冠心病、急性冠脉综合征、高血压、脑梗死、短暂性脑缺血、心力衰竭分别为 14.47%、 4.68%、 7.23%、42.98%、23.83%、0%、 6.80%；HDL-C1.0-1.49mmol/L 下分别为 14.21%、6.14%、17.87%49.76%、17.45%、0.8%、4.85%；HDL-C1.5-1.99mmol/L 分别为 7.28%、 3.94%、 3.31%、52.98%、 21.19%、 0.6%、10.6%；HDL≥2.0mmol/L 冠心病、急性冠脉综合征、高血压、脑梗死、心力衰竭 0%、9.6%、3.22%、70.97%、 9.68%、0%、 6.45%；HDL-C <1.0mmol/L 下，急性心肌梗死，脑梗死，心力衰竭相关危险度＞1； HDL-C 1.5-1.99mmol/L 下，高血压，脑梗死，心力衰竭相关危险度＞1；HDL≥2.0mmol/L 下，冠心病，高血压，心力衰竭相关危险度＞1
结论 1.不同 HDL-C 水平下不同心血管疾病之间的发生情况是不同的；2.低 HDL-C 下更容易发生急性心肌梗死、脑梗死、心力衰竭；高 HDL-C 下更容易发生高血压、脑梗死、心力衰竭；极高 HDL-C 下更容易发生冠心病、高血压、心力衰竭。

PU-2044

幽门螺杆菌检测方法及应用进展

张炳峰、毕礼鑫
江苏省人民医院（南京医科大学第一附属医院）

幽门螺杆菌（H.pylor）是一种微需氧螺旋形革兰阴性螺杆菌，因其致病性和致癌性备受关注。其临床实验室检测方法多种多样，并且各有其优劣性，主要分为侵入性和非侵入性检测方法。侵入性检测方法均需先进行内镜检查，有一定的创伤性，方法有：分离培养和涂片、组织学染色和组化染色、特殊染色、快速尿素酶试验；非侵入方法无创快捷，但准确性差异较大，方法有：尿素呼气试验(UBT)、胶体金法、环介导等温扩增方法(LAMP)、酶联免疫吸附试验(ELISA)及胶乳免疫比浊法。在临床检测时，应根据相应的目的等因素选择合适的方法，特别是要考虑到 Hp 在各地的流行菌株的不同，各种检测技术方法的优缺点及其试验的可操作性。

PU-2045

血清高值肌酸激酶(CK)测定计算法与稀释法结果的比较分析

张炳峰、蒋叶、颜承靖
江苏省人民医院（南京医科大学第一附属医院）

目的 为了解决标本抽血量少而需要复检的样本，探讨血清高值肌酸激酶(CK)测定中的计算法与稀释法的差异。
方法 选择 20 例超出检测线性范围高值肌酸激酶(CK)血清标本，用稀释法和反应进程曲线计算法得出 CK 活性值。
结果 20 例高值（无结果显示） CK 通过反应进程曲线计算结果与标本稀释后测定的结果无显著差异（$P > 0.05$）。
结论 在高值血清肌酸激酶检测时，反应进程曲线计算方法可代替稀释法。

PU-2046

临床生化定量检测项目自动审核规则的建立应用

蔡永梅
宁夏医科大学总医院

目的 基于本实验室患者人群特点，建立适合自身需求的临床生化定量检测项目自动审核规则，如差异判断（Delta Check Severity DS）、结果与判断范围（Normal Range Severity NS）、临床信息（Clinical information Severity CS）、样本状态（Sample Status Severity SS）、仪器状态 Instrument Status Severity IS）、逻辑判断（Logical Judgement Severity LS）、报告与申请医嘱一致性检查等（Other Severity OS）规则实现自动审核，保证自动审核通过率有效稳定。
方法 1 依据 CNAS-CL02《医学实验室通过质量和能力认可准则》（ISO 15189：2012，IDT））、CLSI AUTO15《临床实验室特定专业领域检测结果自动审核》、CLSI AUTO-10A《临床实验室检测结果自动审核-批准指南》和中华人民共和国卫生行业标准《临床实验室定量检验结果的自动审核》（WS/T 616-2018）等标准，结合本实验室特点和要求，建立和设置项目的个性化自动审核规则并验证。设置的规则主要有固定规则、个性化规则等；将建立好的规则设置在西门子 APTIO 流水线中间体软件 Cetralink 上，验证所有规则的有效性，再通过 1 万个样本验证规则的适宜性和可行性。2 统计分析各项目自动审核不通过时违反 NS 和 DS 所占比率。
结果 1 共计 40 个生化检测项目建立、设置 400 多条有效规则。2 各项目检测结果自动审核不通过违反规则主要是 DS 和 NS，占设置规则的 95%以上。优化 DS、NS 规则后，自动审核通过率由 58%提高到 66%。
结论 NS 和 DS 规则是自动审核通过率稳定及自动审核结果准确可靠主要规则，其设置既要有科学性又要有可行性和适宜性。

PU-2047

血清淀粉样蛋白 A 和载脂蛋白 B/载脂蛋白 A1 比值在糖尿病足中的变化及意义

陈键
湖南省人民医院马王堆院区

目的 分析血清淀粉样蛋白 A（SAA）和载脂蛋白 B/载脂蛋白 A1 比值（ApoB / ApoA1）在糖尿病足（DF）中的变化及意义。

方法 选取 262 例 2 型糖尿病（DM）患者作为研究对象，按是否并发 DF 分为 DF 组（n=128）和 DM 组（n=134），另选取同期体检并无高血脂、肥胖等 DM 高危因素的健康者作为对照组（n=135），比较三组受试者周血 SAA 和 ApoB/ApoA1 指标的变化，分析 SAA 和 ApoB/ApoA1 与 DM 病程、HbA1c、FGB 等指标是否是 DF 发生的独立危险因素，并探讨 SAA 和 ApoB/ApoA1 间相关性及其对 DF 发生的预测价值。
结果 DF 组 DM 病程明显长于 DM 组，两组间比较具有统计学意义（P<0.05）；DF 组外周血 ApoB、FBG、HbA1c、SAA 和 ApoB/ApoA1 水平明显高于 DM 组和对照组，三组间比较具有统计学差异（P<0.05）。Logistic 线性回归分析：病程、FBG、HbA1c、SAA 和 ApoB/ApoA1 是 DF 发生的独立危险因素。Pearson 直线相关性分析结果显示：SAA 与 ApoB/ApoA1 呈正相关（r=0.486，P<0.001）。外周血 SAA 和 ApoB/ApoA1 二者联合对 DF 的预测敏感性（85.52%）和特异性（89.30%）高于 SAA 或 ApoB/ApoA1 单独预测效能（P<0.05）。
结论 外周血 SAA 和 ApoB/ApoA1 水平是 DF 发生的独立危险因素，对 DF 具有较好的预测价值，值得临床推广应用。

PU-2048

血液透析对尿毒症患者生化指标的影响

陈灿星[1]、姚少濠[1,2]、胡志峰[1,2]、张玲[1,2]、刘勇[1,2]、谭天畅[1]、吴嘉濠[1]、劳康文[1]、陶然[1,2]
1. 广州金域医学检验中心有限公司
2. .广州医科大学金域检验学院

目的 研究尿毒症患者经血液透析治疗后各项生化指标水平的变化，及时发现及治疗透析后并发症。
方法 400 例在独立血透中心进行透析治疗并采血送检中心实验室检测的患者作为研究对象，开展回顾性分析。统计生化指标包括二氧化碳结合力（CO2-CP）、肌酐（CREA）、甲状旁腺激素（PTH）、尿素（UREA）、尿酸（UA），血钾（K）、血钠（NA）、血氯（CL）、血磷（P）、血总钙（CA）水平，比较血液透析前后的各生化指标的变化。
结果 透析后的 CREA（409±163）μmol/L、PTH（90.72±98.41）pmol/L、UREA（8.27±3.88）mmol/L、UA（138±67）μmol/L、K（3.68±0.59）mmol/L、P（0.87±0.30）mmol/L、CA（2.41±0.22）mmol/L，与透析前 CO2-CP（17.08±3.66）mmol/L、CREA（1059±274）μmol/L、PTH（45.10±51.30）pmol/L、UREA（25.57±7.54）mmol/L、UA（502±117）μmol/L、K（5.06±0.74）mmol/L、P（2.34±0.72）mmol/L、CA（2.23±0.27）mmol/L，差异有统计学意义（P＜0.05）。透析后的 NA（137.4±2.83）mmol/L、CL（97.31±2.75）mmol/L，与透析前 NA（138.13±3.52）mmol/L、CL（97.62±4.32）mmol/L 差异无统计学意义（P＞0.05）。透析后出现低钙血症的患者较透析前的 36.7%下降到 8.6%，出现高钾血症的患者较透析前的 39.2%下降到 1.9%，但是 40.2%的人出现低钾血症。
讨论 对尿毒症患者给予血液透析治疗可改善患者的各项生化指标水平，且关注透后 PTH、CA、K 等重要指标，及时对症处理，提高患者透后的生存质量。

PU-2049

血清维生素 B12 水平与精子质量的相关性研究

刘俊鹏、宋金莉
中国医科大学附属盛京医院

目的 探讨男性血清中维生素 B12 水平对精子活动力，精子浓度的影响。

方法 根据纳入标准选择研究对象，测出研究对象的血清维生素 B12 水平和相关精子参数，将研究对象分为少弱精子症病例组和对照组，分析两组之间的血清维生素 B12 水平是否有统计学差异。分析血清维生素 B12 水平与精子前向运动力（PR），精子总活力(PR+NP)，精子浓度的相关性。
结果 少弱精子症病例组和健康对照组的血清维生素水平存在显著性差异（p<0.05）,少弱精子症病例组的血清维生素 B12 水平明显低于对照组;血清维生素水平与精子前向运动力存在正相关（r=0.519,p<0.05）;血清维生素 B12 水平与精子总活力存在正相关（r=0.531,p<0.05）;血清维生素 B12 水平与精子浓度存在正相关（r=0.491,p<0.05）。
结论 血清维生素 B12 水平对精子前向运动力，精子总活力，精子浓度有影响，血清维生素 B12 水平低的男性精子质量差。

PU-2050

血清小而密低密度脂蛋白胆固醇与短暂性脑缺血发作及再发卒中风险的相关性研究

王冬梅
滨州医学院烟台附属医院

目的 研究血清当中小而密低密度脂蛋白胆固醇(sdLDL-C)的含量与短暂性脑缺血发作及再发卒中风险的相关性。
方法 选取滨州医学院附属医院 2019 年 6 月到 12 月的 38 名因短暂性脑缺血发作来院救治患者作为患病组，同时选取相同时间的 44 名体检健康人群作为健康对照组，应用相关仪器分别测量两组人群与血脂相关的指标,并展开比较，分析其相关性。
结果 检测结果如下，患病组的总胆固醇，甘油三脂，脂蛋白 α，低密度脂蛋白胆固醇，小而密低密度脂蛋白胆固醇的浓度与健康对照组相比呈明显的升高状态；而高密度脂蛋白的浓度是降低的，并且以 P<0.05 差异有统计学意义。实验过程中，经过使用 ABCD3-Ⅰ评分方法，发现患病组 38 名患者中,有 18 例低危组患者，13 例中危组患者以及 7 例高危组患者。将 3 组相关血脂指标进行比较,发现除 sdLDL-C 的水平以外,其他血脂指标差异均无统计学意义(P>0.05),其中高危组 sdLDL-C 水平最高，与另外两组相比差异有统计学意义(P<0.05)； 并且还发现 sdLDL-C 与 TC、TG、LDL-C、Lpα 及 ABCD3-Ⅰ水平呈明显正相关(P<0.05)。
结论血清小而密低密度脂蛋白胆固醇水平与短暂性脑缺血发作具有相关性，且小而密低密度脂蛋白胆固醇水平与再发卒中风险呈正相关。

PU-2051

BNP/NT-proBNP 及心肌酶谱联合检测在新生儿肺炎诊断中的价值研究

许子贤[1]、王丹[2]、侯敏[1]
1. 天津市胸科医院
2. 陕西省延安市中医医院

目的 探究脑利钠肽（brain natriuretic peptide，BNP）/N 末端 B 型利钠肽原（N-terminal pro-B-type natriuretic peptide，NT-ProBNP）及心肌酶谱联合检测在新生儿肺炎（neonatal pneumonia，NP）诊断中的价值。
方法 选取 2019 年 6 月~2020 年 6 月出生于我院的 141 例 NP 患儿，根据感染类型分为细菌组 60 例、病毒组 51 例和其他组 30 例，另选取同期出生于我院的 30 例健康新生儿作为对照组。检测并

比较各组 BNP/NT-proBNP、心肌酶谱水平；受试者工作特征（receiver operating characteristic，ROC）曲线分析 BNP/NT-proBNP 及心肌酶谱联合检测对 NP 的诊断和鉴别价值。
结果 与对照组比较，NP 患儿 BNP/NT-proBNP 显著降低，细菌组 BNP/NT-proBNP 显著低于病毒组、其他组，病毒组显著低于其他组；NP 患儿心肌酶谱水平显著升高，病毒组显著高于细菌组、其他组，细菌组显著高于其他组，差异有统计学意义（P<0.05）。BNP/NT-proBNP 对 NP 细菌感染的诊断效能较高；心肌酶谱对 NP 病毒感染的诊断效能较高；BNP/NT-proBNP 及心肌酶谱联合检测诊断 NP 的灵敏度、特异性、准确度、阳性预测值、阴性预测值、ROC 曲线下面积（area under curve，AUC）显著高于单一指标检测的值，差异有统计学意义（P<0.05）。
结论 BNP/NT-proBNP 及心肌酶谱联合检测能够有效诊断 NP 及指导临床合理使用抗菌药物，值得临床参考。

PU-2052

尿微量白蛋白和胱抑素 C 联合检测在 2 型糖尿病肾病早期诊断中的临床意义

李江博
西安市第一医院

目的 探讨血清胱抑素 C(Cystatin C，CysC)及尿微量白蛋白(microalbu-minuria,mALB)联合检测在 2 型糖尿病患者(Diabetes，DM)早期肾损伤中的意义。
方法 以 59 例 2 型糖尿病肾病患者为糖尿病肾病组，62 例 2 型糖尿病患者为糖尿病组,64 例健康体检者为对照组，采用免疫散射比浊法检测尿液中 mALB,两点终点法测定 CysC，观察 3 组 CysC 和 mALB 变化，及两者的联合检测。
结果 糖尿病组患者的血清 CysC 及尿 mALB 高于对照组,糖尿病肾病组患者的血清 CysC 及尿 mALB 比对照组和糖尿病组患者的血清 CysC 及尿 mALB 升高更明显，差异具有统计学意义(P<O.05)。
结论 在患者出现大量蛋白尿之前，血清 CysC 和尿 mALB 可作为早期诊断糖尿病肾病较敏感的指标；联合检测能大大提高检测阳性率，对于监测早期糖尿病肾病的发生和病情发展程度有重要意义。

PU-2053

肝功能指标联合肝纤四项在肝硬化 Child-Pugh 分级中的应用

刘琼
湖南省人民医院

目的 探讨肝功能指标 CHE、TBA、ALT、AST、PA、ALP、GGT 和肝纤四项 HA、LN、PCIII 和 IV-C 在肝硬化 Child-Pugh 分级中的应用。
方法 收集 289 例 Child-Pugh A 级、B 级和 C 级肝硬化患者和 50 例健康者血清，检测 CHE、TBA、ALT、AST、PA、ALP、GGT、HA、LN、PCIII 和 IV-C 的含量，分析以上指标在肝硬化 Child-Pugh 分级中的应用价值。
结果 11 项指标整体比较均有差异，成对比较 TBA、AST、CHE、PA、LN 和 IV-C 四组间均有差异；ALT、GGT 和 ALP Child-Pugh A 级、B 级和 C 级肝硬化与对照组比较有差异；ALP C 级和 A 级比较有差异；HA 除了 A 级和对照组，余均有差异；PCIII 除了 A 级和对照组、B 级和 A 级比较外，余均有差异。有序 logistic 回归显示 ALP、CHE、PA、LN 和 IV-C 对肝硬化的 Child-Pugh 分级有意义，模型的预测准确率为 64%。
结论 联合检测 ALP、CHE、PA、LN 和 IV-C 对于肝硬化 Child-Pugh 分级的诊断有一定的参考价值。

PU-2054

UniCel DxI800 全自动化学发光免疫分析仪

暴旭广
南方医科大学珠江医院

目的 研究 UniCel DxI800 全自动免疫分析仪缓冲液国产化的课题，以代替昂贵的进口原装缓冲液。
方法 用进口随机缓冲液和国产缓冲液在 UniCel DxI800 全自动免疫分析仪上对收集的临床血清标本进行准确度分析及精密度分析。测得数据由 SPSS 10.0 统计软件进行配对 t 检验和相关分析比较。
结果 两种缓冲液分别检测 T3、fT3、fT4、PRL、FSH、LH、Testo 共 7 个项目各 30 份血清，检测重复性较好（CV<3%），结果均具有高度的线性相关性（r>0.95）。项目 T3、fT3、FSH 由两种试剂测得的结果差异无统计学意义（P>0.05）。而项目 fT4、PRL、LH、Testo 测得的结果差异有统计学意义（P<0.05）。
结论 在 UniCel DxI800 全自动免疫分析仪上，国产缓冲液不可以代替贝克曼原装缓冲液进行检测。

PU-2055

Cys C 与 NT-proBNP 的测定在慢性心力衰竭中的临床价值

王乐乐
西安市第一医院

目的 探讨血清胱抑素 C(Cystatin C，Cys C)与 N 端脑钠肽前体（NT-proBNP）水平的变化对慢性心力衰竭(CHF)患者的诊断价值。
方法 选取 CHF 组 90 例，健康体检正常者(对照组)36 名。心力衰竭程度按美国纽约心脏病学会心功能分级标准(NYHA)分为Ⅱ、Ⅲ、Ⅳ级，分别测定 CysC、NT-proBNP 等指标，并进行相关性分析。
结果 CHF 组 CysC、NT-proBNP 水平与对照组比较差异有统计学意义(P< 0.05)。CHF 组患者中血清 CysC 与 NT-proBNP 水平显著高于对照组(P< 0.05)，且随着心功能分级的增高，血清 CysC 与 NT-proBNP 水平也逐渐升高(P< 0.05)。
结论 慢性心力衰竭患者血清 CysC 与 NT-proBNP 水平明显高于非心力衰竭者；血清 CysC 与 NT-proBNP 水平随慢性心力衰竭患者心功能分级的升高而升高；血清 CysC 与 NT-proBNP 水平呈正相关，二者的联合测定有利于慢性心力衰竭的诊断，且 CysC 和 NT-proBNP 对于评价 CHF 患者临床心功能变化具有一定意义。

PU-2056

消化道恶性肿瘤患者血清 P-cadherin 变化及预测价值

宋佳音、贾丽、董冬、任丽
天津医科大学肿瘤医院

目的 探讨 P-cadherin 在消化道恶性肿瘤发生发展过程中的作用，并分析该蛋白与临床治疗的相关性从而预测患者的疗效。
方法 研究 141 消化道恶性肿瘤患者血清标本 P-cadherin 的表达。探讨其表达与消化道恶性肿瘤患者的临床病理特征是否存在关联，分析其表达水平在晚期消化道恶性肿瘤患者的治疗监测中的临床价值。
结果 ELISA 结果显示晚期消化道恶性肿瘤患者血清 P-cadherin 表达水平相对于早期消化道恶性肿瘤患者血清表达水平有显著差异（P=0.000）。54 例结直肠癌患者血清 P-Cadherin 表达水平与

CA199（r = 0.18,P = 0.19）、CA724（r = 0.39，P = 0.0045）、CA242（r = 0.12，P = 0.42）、CEA（r = 0.45，P = 0.0007）表达水平均呈正相关。43 例食管癌患者血清 P-Cadherin 表达水平与 CA724（r = 0.08，P = 0.63）表达水平呈正相关，而与 CA199（r = -0.16，P = 0.35）、CEA（r = -0.02，P = 0.91）表达水平呈负相关。44 例胃癌患者血清 P-Cadherin 表达水平与 CA199（r = 0.35，P = 0.02）、CA724（r = 0.002，P = 0.98）、CA242（r = 0.02，P = 0.88）、CEA（r = 0.12，P = 0.94）表达水平呈正相关。在消化道恶性肿瘤患者化疗疗效监测中发现患者血清 P-Cadherin 与其他肿瘤标志物水平变化一致率无明显差异，平均变化率与 CA199、CA242、CEA 存在明显差异。

结论 本研究显示血清 P-Cadherin 在消化道恶性肿瘤的发生发展过程中起到重要作用，同时 P-Cadherin 可能作为消化道恶性肿瘤一个新的肿瘤标志物并且与可以作为消化道恶性肿瘤化疗监测的指标。

PU-2057

首发抑郁症患者血清 TRPM2 与 CD38 的浓度变化

唐亚梅[1]、康涛[2]
1. 中南大学湘雅二医院
2. 中南大学湘雅医学院检验专业

目的 研究首发抑郁症患者血清中的 TRPM2 与 CD38 的浓度及铁代谢相关指标血清 TRF、NGAL、Fe 和 HCY 的水平变化，探讨上述指标与抑郁症发生的关系及在抑郁症诊疗中的临床意义。

方法 收集 2020 年 10 月至 2021 年 4 月于湘雅二医院精神科门诊就诊的 40 例首发抑郁症患者的血清和汉密尔顿量表资料；同时收集 20 例于湘雅二医院体检中心体检的正常人血清，采用 ELISA 法测定血清样本中的 TRPM2 和 CD38 水平，应用 IMMAGE800 和 HITACHI7600-DDP 仪器检测血清转铁蛋白（TRF）、NGAL、铁（Fe）和 HCY 的水平。

结果 抑郁症患者血清 TRPM2（134.27±27.56ng/ml）和 CD38（1044.88±90.41 ng/ml）浓度较健康对照组（49.78±18.62ng/ml）和（812.99±188.57 ng/ml）均显著升高（P＜0.01），差异有统计学意义；抑郁症患者 NGAL（106.96±39.66 ng/mL）水平较对照组（154.31±62.98 ng/mL）显著降低（P＜0.01），差异有统计学意义；Pearson 相关分析显示汉密尔顿量表总分与各项指标均无相关性（P>0.05）。

结论 首发抑郁症患者血清 TRPM2、CD38 和 NGAL 水平异常，三者与抑郁症的发生有关，可能涉及共同的氧化应激机制。

PU-2058

血清 KL-6 水平在间质性肺疾病中的辅助诊断价值

任亚萍
中南大学湘雅二医院检验科

目的 探讨血清涎液化糖链抗原（KL-6）水平在间质性肺疾病中的辅助诊断价值。

方法 回顾性分析 2019 年 12 月～2020 年 12 月中南大学湘雅二医院收治的 277 例间质性肺疾病患者为实验组，选取同期该院收治的 263 例非间质性肺疾病患者为疾病对照组，140 例体检健康者作为健康对照组。用化学发光法检测三组研究对象的血清 KL-6，LDH 水平；分析血清 KL-6，LDH 水平与性别，年龄，吸烟史及肺功能的相关性；比较血清 KL-6,LDH 对于间质性肺疾病的诊断价值。

结果 实验组血清 KL-6 水平[（815.700(412.450，1824.900)U/ml）]高于非肺间质疾病组[（209.300(152.700，311.300)U/ml）]和阴性对照组[（145.900(122.600，176.725)U/ml）],P 均＜0.05。KL-6 辅助诊断 ILD 的 ROC 曲线下面积（0.902，95%CI:0.878-0.926）优于 LDH(0.763，

95%CI: 0.728-0.799)；两者联合诊断间质性肺疾病的 ROC 曲线下面积为 0.902（95%CI: 0.879-0.926）。KL-6 的 cut-off 值为 305.15U/ml,敏感性和特异性分别为 84.8%和 83.1%。血清 KL-6，LDH 水平与吸烟史呈正相关（r=43.499 和 1.233，P 均<0.05）；血清 KL-6 水平与肺部弥散功能，通气功能严重程度呈负相关（r=-0.01 和-0.006，P 均<0.05）。
结论 血清 KL-6 可辅助诊断间质性肺疾病，且诊断价值高于 LDH。

PU-2059

HBV 感染患者血清 CG、ALT、AST 检测的临床意义

张春娇
连云港市中医院

目的 探讨血清甘胆酸（CG）、丙氨酸氨基转移酶（ALT）、天门冬氨酸氨基转移酶（AST）水平检测对 HBV 感染患者的临床意义，并比较甘胆酸相对于常规肝功能的优越性。
方法 搜集连云港市中医院 2018 年 5 月 1 日至 2018 年 9 月 30 日 HBsAg 阳性标本 289 例，根据 PCR 结果分为 HBV-DNA 阳性（HBV-DNA 含量>1.0E+2IU/ML）组 142 例和 HBV-DNA 阴性（HBV-DNA 含量<1.0E+2IU/ML）组 147 例，同时选取 150 名健康人作为对照组。采用酶法测定丙氨酸氨基转移酶（ALT）、天门冬氨酸氨基转移酶（AST）,均相酶免疫法测定甘胆酸（CG）。比较 HBV-DNA 阳性组与对照组及 HBV-DNA 阴性组与对照组间各指标有无统计学意义。
结果 HBV-DNA 阳性组 CG、ALT、AST 水平均明显高于对照组 CG、ALT、AST 水平，差异有统计学意义（P<0.05）；HBV-DNA 阴性组 CG 水平高于对照组 CG 水平，差异具有统计学意义（P<0.05），ALT、AST 水平和对照组无统计学意义（P>0.05）,HBV-DNA 阳性组各指标水平均高于 HBV-DNA 阴性组。
讨论 中国是 HBV 感染的高发地区，HBV-DNA 是乙肝病毒在体内复制的最直接指标，HBV-DNA 阳性患者肝细胞在病毒复制的过程中都有不同程度的炎症和损伤，ALT、AST 等酶学可较好地反映肝细胞的病理状态。但我国大多数是慢性无临床症状和体征的感染者，此类感染者虽然 HBV-DNA 阴性，可能是由于病毒含量低于检测限，也可能由于病毒在肝细胞内复制，其实肝细胞的超微结构已发生了变化,这些改变不能被常规肝功能所测出，但 CG 的水平高于对照组，表明 CG 能敏感地反映肝细胞早期受损的变化。因此对于 HBV 感染者，在测定常规肝功能的同时检测 CG,更能早期、敏感地反映乙肝患者的肝细胞的损害程度,在临床应用中更具有实用性。

PU-2060

血清小而密低密度脂蛋白胆固醇与妊娠期糖尿病患者胰岛素抵抗的相关性分析

殷雪瑞
成都市双流区第一人民医院

目的 探讨小而密低密度脂蛋白胆固醇与妊娠期糖尿病患者脂代谢情况及胰岛素抵抗的相关性。
方法 选取 2019 年 1 月-2020 年 6 月我院收治的 103 例处于孕中期的妊娠期糖尿病患者为试验组，同期匹配 61 名健康妊娠妇女为对照组，分别测定两组研究对象的总胆固醇（TC）、甘油三酯（TG）、sdLDL-C、LDL-C、HDL-C、HbA1c、空腹血糖（FBG）、空腹胰岛素（FINS），并计算胰岛素抵抗指数（HOMA-IR），比较两组研究对象的上述各指标水平，并分析 sdLDL-C 与糖脂代谢的相关性。
结果 试验组 TC、TG、LDL-C、sdLDL-C、HbA1c、FBG、FINS 以及 HOMA-IR 明显高于对照组，而 HDL-C 水平明显低于对照组（P<0.05）；sdLDL-C 与 TG、LDL-C、FBG、HbA1c 及 HOMA-

IR 呈正相关（r 分别为 0.322、0.531、0.604、0.577、0.582，P<0.05）；HOMA-IR 与 TG 呈正相关（r=0.336，P=0.023）。
结论 妊娠期糖尿病患者血清 sdLDL-C 升高与胰岛素抵抗及脂代谢异常有关，应重视 sdLDL-C 在妊娠期糖尿病中的作用。

PU-2061

C 反应蛋白与血清淀粉样蛋白 A 在急性主动脉夹层临床诊断中的临床价值

史清梅、孟繁君、岳晋巍、王利新
宁夏医科大学总医院

目的 探讨 C-反应蛋白(CRP)和血清淀粉样蛋白 A (SAA)在急性主动脉夹层(AAD)患者临床诊断中的临床价值。
方法 采用回顾性分析方法，选取 2018 年 1 月到 2020 年 6 月在宁夏医科大学总医院入院治疗的 175 例 AAD 患者、160 例急性冠脉综合征患者（疾病对照组）和同期健康体检的 148 名健康者（健康对照组）作为研究对象，采用胶乳增强免疫比浊法和胶乳免疫比浊法测定所有对象的血清 SAA 和 CRP 水平，并收集、分析相关临床资料。采用单因素及多因素 logistic 回归分析其独立危险因素，通过受试者工作特征 (ROC) 曲线分析 SAA 和 CRP 对急性主动脉夹层的诊断价值。
结果 AAD 患者组 SAA 和 CRP 水平[(165.7±7.4)mg/L、(76.0±4.0)mg/L]明显高于健康对照组和疾病对照组，差异均有统计学意义(均 P<0.05)；年龄超过 60 岁的 AAD 患者的 SAA 和 CRP 降低[(150.6±12.7)mg/L、(73.9±7.3)mg/L]，差异均有统计学意义(均 P<0.05)；具有超过 6 h 的高危疼痛特征的 AAD 患者的 SAA 水平升高，差异有统计学意义(P<0.05)； SAA 与 CRP 呈正相关(r=0.0534，P<0.05)，ROC 分析提示 SAA 和 CRP 水平与 AAD 风险独立相关(P=0.001)，其中 SAA 诊断 AAD 疾病的 ROC 曲线显示 TAAD 和 TBAD 的 AUC 分别为 0.997 和 0.995 (均 P<0.001)；CRP 诊断 AAD 疾病的 ROC 曲线显示 TAAD 和 TBAD 的 AUC 分别为 0.998 和 0.991 (均 P<0.001)。 SAA 和 CRP 的最佳临界值分别为 175.17 mg/L 和 72.96 mg/L。
结论 SAA 和 CRP 水平升高对 AAD 具有较高的预测价值，SAA 联合 CRP 有望作为辅助诊断 AAD 的实验室检测指标。

PU-2062

首发精神分裂症与抗 NMDAR 脑炎血液学指标的比较

唐亚梅
中南大学湘雅二医院

目的 首发精神分裂症(FES)和抗 NMDAR 脑炎两种疾病具有相似的精神症状，且两者与炎症系统关系密切。在本研究中，我们比较了 FES、抗 NMDAR 脑炎和健康对照组相关血液学指标和炎症指标，探索其涉及可能的机制。
方法 我们纳入来自中南大学湘雅二医院的 106 例患者(53 例 FES 患者和 53 例抗 NMDAR 脑炎患者)和健康体检中心的 59 例健康对照。采用中性粒细胞-淋巴细胞比值(NLR)、血小板-淋巴细胞比值(PLR)、单核细胞-淋巴细胞比值(MLR)、全身免疫-炎症指数(SII)评价炎症评分。其他血液学指标，如白细胞(WBC)、血小板(PLT)、尿酸(UA)和总胆红素(TBIL)、总胆汁酸(TBA)和血清白蛋白也用于比较两种疾病之间的炎症评分。
结果 FES、抗 NMDAR 及健康对照组中 SII、NLR、PLR、MLR、白蛋白差异均有统计学意义(p<0.05)。其中，抗 NMDAR 脑炎组 SII、NLR、PLR 和 MLR 值显著高于 FES 组(p<0.05)，且两种疾病组 SII、NLR、PLR 和 MLR 值均高于健康对照组(p<0.05)。抗 NMDAR 脑炎组血清白蛋白水

平明显低于 FES 组(p<0.05)。两组 WBC、中性粒细胞、淋巴细胞和单核细胞计数显著升高(p<0.05)。其他指标如 TBA、TBIL、UA 组间无差异。

结论 这是一项比较新的研究，通过比较 FES 和抗 NMDAR 脑炎两种疾病的血液炎症标志物与临床精神病性症状的关系。这两种疾病在炎症指标上呈现相同的上升趋势，但两者之间的变化幅度具有统计学差异。作者认为这两种疾病都与功能低下的 NMDAR 有关，但 SCZ 的机制似乎比抗 NMDAR 脑炎复杂得多；这两种疾病都与炎症系统和氧化应激有关，这可能证明 NMDAR 功能低下与精神病性症状有关。此外，NLR、PLR、MLR 和血清白蛋白可能会作为鉴别两种疾病的生物标志物。

PU-2063

结肠腺癌中 RNA 结合蛋白的预后模型的开发和验证

朱丹丹、陈杰荣、张喜钦
广东省人民医院

以前的研究报告指出，RNA 结合蛋白（RBPs）的失调与癌症的发展有明显的关系。然而，到目前为止，关于 RBPs 在结肠腺癌（COAD）中的作用的研究还很少。从 The Cancer Genome Atlas（TCGA）数据库中下载了 COAD 患者的 RNA 测序和临床数据，以确定 COAD 组织和正常结肠组织之间差异表达（DE）的 RBPs，然后通过系统的生物信息学分析详细研究这些 RBPs 的表达和预后意义。通过一系列的回归分析，7 个 RBPs（RPL10L、ERI1、POP1、CAPRIN2、TDRD7、SNIP1 和 PPARGC1A）被确定为与预后相关的枢纽基因；然后被用来构建预后模型。基于该模型的进一步分析表明，高危组的总生存期（OS）低于低危组。在这个预后模型中，TCGA 队列的时间依赖性接受者特征（ROC）曲线下面积为 0.697，GSE17538 队列为 0.581，表明该模型具有良好的预测能力。我们还根据 TCGA 队列中的 7 个 RBPs 建立了一个提名图，该模型对 COAD 显示出良好的鉴别能力。

PU-2064

非糖尿病学龄前儿童糖化白蛋白的调查及分析

何谦、常倩楠
西安交通大学第二附属医院

目的 通过测定 700 例非糖尿病学龄前儿童糖化白蛋白数值（glycated albumin,GA），探究学龄前儿童在不同年龄段糖化白蛋白的水平。

方法 利用全自动生化分析仪检测自 2019 年 1 月 1 日至 2021 年 4 月 1 日来西安交通大学第二附属医院就诊或体检符合研究标准的 700 名非糖尿病学龄前儿童的糖化白蛋白。

结果 婴儿组的 GA 参考范围为 5.103%-12.837%，幼儿组为 8.130%-13.890%，学龄前组为 9.550%-14.830%，各组间相互比较发现，非糖尿病学龄前儿童在不同年龄段的糖化白蛋白的组间差异具有显著统计学意义（P 值均＜0.01）。按性别分组得到学龄前男童组与女童组的参考范围分别为 6.209%-13.891%、6.210%-14.162%，两组相互比较发现，组间差异无统计学意义（P=0.466＞0.05）。

结论 婴儿组、幼儿组、学龄前组的糖化白蛋白宜分别采用不同的参考范围，学龄前儿童参考范围值与性别无关。

PU-2065

常规血脂检验诊断冠心病的临床意义分析

郑家辉
滨州医学院烟台附属医院

目的 分析在临床工作中，常规血脂检验对诊断冠心病的意义。
方法 以在院住院的 50 例冠心病患者作为观察组，以同期在查体中心进行健康查体的 50 例人员作为参照组，两组研究对象共计 100 例同时实施常规血清脂质检测。对两组检验结果进行统计、回顾性分析。
结果 检测结果如下:观察组的血清脂质检测指标(LDL-C、TG 和 TC)的数值明显高于参照组（P<0.05）；而观察组的 HDL-C 水平明显低于参照组（P<0.05）；观察组患者的高 TC 血症、高 TG 血症、高 LDL-C 血症和低 HDL-C 血症所占的比例均明显高于参照组（P<0.05）。
结论 血脂水平异常可导致冠心病发作。分析患者血脂检验指标，了解其血脂水平的变化，对冠心病的早期预防和后续确诊后的治疗具有非常重要的指导意义。

PU-2066

分离胶真空采血管样本保存时间对血糖测定结果的影响

孙学伟
滨州医学院烟台附属医院

目的讨论分离胶真空采血管原管保存样本加盖与否对其血糖检测后果的变动能否在临床容许误差范围内。
方法分离胶真空采血管原管保留血清 (3500 rpm· min-1 离心 10min)原管上机测定血清葡萄糖(葡萄糖氧化酶法), 加盖或不加盖 2 ~ 8℃冰箱冷藏保存, 各自于 2、 4、8、 24、48、72 h 反复检测血清葡萄糖程度。
结果 未加盖原管血清保存时间不同血糖测定结果不同，变化率在-2.4%~7.9%之间，血糖值与未加盖样本放置时间无相关性(P>0.05)；加盖原管血清保存时间不同血糖测定结果有高有低，变化率在-1.5%~0.6%之间，血糖值与加盖样本放置时间无相关性(P>0.05)。加盖与否,4d 内原管保存样本其血糖检测结果的变动均无统计学意义(P>0.05)且在临床允许误差领域之内<10%。
结论在不加盖保存的情况下，分离胶原管内保留 3d 内的样本可以用于血糖的检测。

PU-2067

临床生化检验项目危急值的建立与应用

苗田田
滨州医学院烟台附属医院

目的 分析并比较患者的致命死亡率和致命死亡率之间的差异。
方法 选择某院 2017 年 5 月至 2019 年 5 月接受治疗的 100 例已达危急值的患者，计算具有致命价值的患者的死亡人数，并对危急值项目的死亡率差异进行比较分析。
结果 100 例危重患者中有 12 例死亡，男女死亡比为 7：5，60 岁以上的患者高于 60 岁以下的患者。生化危急值患者死亡率与电解质危急值、血气分析危急值者之间无统计学差异(P>0.05);血气分析危急值患者死亡率高于电解质危急值者。

结论 建立危急值对提高医院的诊疗水平非常重要，能够迅速抢救患者的生命，对提高医院的治疗水平和社会形象有重要作用。 我们将努力对重要价值的管理进行标准化，信息化和综合化。

PU-2068

妊娠期糖尿病血清唾液酸的相关研究

蒋雨晴
滨州医学院烟台附属医院

目的 探寻血清唾液酸（SA）在妊娠期糖尿病患者及血糖正常孕妇体内的变化。
方法 选取 2019 年 5 月至 8 月本院就诊的 35 岁以上妊娠期糖尿病患者 30 例以及 35 岁以下妊娠期糖尿病患者 30 例为观察组；35 岁以上以及 35 岁以下血糖正常孕妇各 30 例为对照组，测定其血清唾液酸（SA）、空腹血糖值和口服糖耐量试验 1h 及 2h 血糖值。
结果 35 岁以上妊娠期糖尿病患者血清唾液酸水平为(673.33±86.42)mg/L, 35 岁以上血糖正常孕妇血清唾液酸水平为(662.03±82.04)mg/L， 35 岁以下妊娠期糖尿病患者血清唾液酸水平为(651.40±86.02)mg/L， 35 岁以下血糖正常孕妇血清唾液酸水平为(651.13±64.42)mg/L 。
结论 妊娠期糖尿病孕妇血清唾液酸水平与血糖正常孕妇无显著差异。

PU-2069

原发性肾病综合征高脂血症患者与肾功能指标的检查分析

李钊
滨州医学院烟台附属医院

目的 调查研究原发性肾病综合征（PNS)患者高脂血症与肾功能指标的关联。
方法 比较 PNS 组与其他肾病对照组,健康对照组的血脂水平，以及甘油三酯，高密度脂蛋白，低密度脂蛋白，载脂蛋白等。 线性分析 PNS 组内各项血脂指标与肾功能指标的关系。
结果 显示 PNS 患者组各项血脂指标明显高于疾病对照组和健康对照组，有统计学有意义（P<0.05);发现 ALB,eGFR,SCr 与血脂指标存在相关性
结论 PNS 患者血脂指标存在差异，且存在血脂指标与肾功能指标相互促进关系。

PU-2070

Consistency evaluation of elements in human whole blood between two ICP-MS systems

Xiang Ji、Yue Li、Xiaowen Dou、Dan Xiong、Xiuming Zhang
Shen Zhen Luohu Hospital Group

Elementals are essential to maintain the body’s metabolism and support a variety of biological functions. It is wildly accepted that imbalance of elements may serve as an indicator of illness，and increasing research interests of understanding their biological functions have arisen. Inductively coupled plasma mass spectrometry (ICP-MS) is commonly accessible in most research institutes; however its application in routine clinical analysis is still in development, as the CFDA approved instrument and reagent was not available. In the past few months, although several CFDA approved ICP-MS have been launched, their capability in blood sample analysis has not been systematically compared. In this work, the analytical performance of a novel CFDA

approved ICP-MS and a research instrument were compared to evaluate their consistency of analyzing 6 elements in human whole blood quantitatively.

PU-2071

多项生化检测指标对早期糖尿病肾病的诊断分析

刘立轩
南京医科大学第一附属医院（江苏省人民医院）

目的 评价早期糖尿病肾病使用多项生化检测指标的诊断价值。
方法 选择我院 2019 年 2 月至 2020 年 3 月期间接诊的 53 例糖尿病肾病患者作为观察组，选择同时期我院接诊的 53 例健康体检者作为对照组，两组均接受多项生化检测指标，比较两组的数据差异性。
结果 观察组的 CRP、Cys-c、HbAlc、FFA、Hcy、β2-MG、UA、PRO、Cr、BUN、RBP 均高于对照组，（P＜0.05）具有统计学意义。
结论 早期糖尿病肾病的诊断中应用多项生化检验指标可以为患者的早期诊断与治疗提供有效依据。

PU-2072

唐氏筛查中假阳性率相关因素分析

王玲
山东大学第二医院

目的 探讨母体血清中 HCG 指标在中期妊娠中的变化规律，及在唐氏筛查中假阳性率的相关性。
方法 检测 500 例唐氏筛查母体血清 AFP、HCG、uE3 水平，结合年龄、体重，用相应软件对唐氏风险度进行评估，根据结果进行统计学分析。
结果 正常血清 AFP、uE3 随孕周增加而增加，血清 HCG 随孕周增加而降低，血清 HCG 同孕周中阳性组明显高于阴性组，差异有统计学意义(P<0.01)，且假阳性率随血清 HCG、年龄及体重的增加而增加。
结论 唐氏筛查在临床检验过程中发现存在许多假阳性结果，对孕妇及家人带来很大的心里负担，国内外学者一直致力于研究导致假阳性率的相关因素，以降低产前筛查假阳性率，但目前仍没有定论。在本研究中，发现在唐氏筛查中，孕中期妇女血清 HCG 高值、高龄、肥胖者，会导致假阳性率的增加。

PU-2073

CA125 在伪膜性肠炎中的临床诊断价值

王玲
山东大学第二医院

目的 CA125 作为最重要的卵巢癌肿瘤标志物，广泛应用于临床，指导临床诊治，本研究旨在分析 CA125 在伪膜性肠炎中的临床诊断价值
方法 收集本院伪膜性肠炎病例，对其 CA125 阳性率进行分析
结果 收集的 109 例患者中 CA125 的阳性率为 80.7%，且阳性值大都<300U/mL。
结论 CA125 在良恶性肿瘤病变、非肿瘤性病变及生理性情况中，均有不同程度升高。本研究在分析临床案例中发现 CA125 在伪膜性肠炎中的阳性率很高，具有较高的诊断价值，但其具体机制有待进一步深入研究。

PU-2074

糖化血红蛋白 A1c 诊断妊娠糖尿病标准的初步探讨

徐志晔
南京大学医学院附属鼓楼医院

目的 初步评估使用糖化血红蛋白 A1c（HbA1c）诊断妊娠糖尿病的最佳切点。
方法 2019 年 6 月-2019 年 10 月在南京鼓楼医院门诊进行妊娠糖耐量筛查的妊娠者，同时测定其 HbA1c。以世界卫生组织（WHO）的标准诊断妊娠糖尿病，用受试者工作特征曲线（ROC）分析 HbA1c 诊断 DM 的能力。
结果 以非 DM 组为对照组，用 HbA1c 来诊断妊娠糖尿病，ROC 曲线下面积（AUCROC）为 0.931，最佳切点为 6.1%，敏感性为 90.6%，特异性为 88.9%。当切点为 5.9%时，敏感性下降为 81.8%，特异性为 93.7%。
结论 本次研究中 HbA1c 诊断妊娠糖尿病的最佳切点为 6.1%，但本次调查人群范围较小，诊断标准仍有待大范围调查后确定。

PU-2075

探讨迈瑞 CL-2000i 化学发光免疫分析法和罗氏 cobas E602 电化学发光免疫分析法检测甲胎蛋白与前列腺特异抗原结

俞欢欢
中国人民解放军北部战区总医院

目的 探讨迈瑞 CL-2000i 化学发光分析仪与罗氏 cobas E602 电化学发光分析仪两个检测统检测甲胎蛋白（AFP）和前列腺特异抗原（TPSA）结果的相关性。
方法 选取 2019 年 1 月--2019 年 2 月来本院就诊的门诊及体检患者的新鲜标本，其浓度范围涵盖低、中、高值,并且尽可能分布均匀，以罗氏 cobas 602 为目标检测系统，迈瑞 CL-2000i 为实验检测系统，选用伯乐第三方三个水平的质控物，同时检测血清样本中甲胎蛋白（AFP）、前列腺特异抗原（TPSA）血清浓度，并对数据进行相关统计学分析。
结果 两个系统检测 AFP、TPSA 质控物显示日间精密度、准确度符合临床要求，检测结果差距无统计学意义 （P＞0.05），实验组与目标组数据存在良好的线性关系 （r2＝0.9975 ＞0.99），迈瑞检测系统与罗氏检测系统的相关回归方程和相关系数为：TPSA (y=1.3083x -1.4526,r=0.9843），AFP(y=1.0748x - 0.8004,r=0.9924,)。预期偏倚和相对偏倚均可接受。
结论 迈瑞 CL-2000i 全自动化学发光免疫分析系统与罗氏 cobas E602 电化学发光系统检测中 AFP、TPSA 相关性良好。

PU-2076

假性高血钾原因简析

曹雅威
雅安市人民医院检验科

钾是机体不可缺少的电解质之一，对维持细胞新陈代谢、调节渗透压与酸碱平衡、维持神经肌肉的兴奋性具有重要的生理作用。在生理状态下，98％的钾分布于细胞内，2％分布于细胞外液，其中血钾仅占 0.3％；人体血钾浓度为 3.3-3.5mmol/L。当血清钾浓度 >5.5mmol/L 时，称之为高血钾症。①高血钾症是一种常见的电解质紊乱，严重时危及生命，早期发现并及时给予降钾治疗可以

避免发生不良临床后果。临床上钾离子紊乱可表现为高血钾症和低血钾症。假性高血钾症是一种检测血钾浓度时发生的体外现象，常由于钾离子外溢引起。检验科应该在注意滋生实验室质量控制的同时，及时排除假性高血钾，避免给临床医生造成困惑，从而怀疑检验室的诊断水平。因此，本文结合近些年国内外报道的假性高血钾症的病例，总结发生假性高血钾症的原因，提出早期识别假性高血钾症的建议，从而避免不必要的降钾危险治疗。

PU-2077

2 型糖尿病视网膜病变合并高尿酸血症的危险因素分析

程静茹
武汉大学人民医院

目的 探究 2 型糖尿病视网膜病变合并高尿酸血症的危险因素。
方法 选取 2018 年 1 月至 2018 年 12 月武汉大学人民医院收治的 2 型糖尿病视网膜病变患者 120 例为研究对象,根据患者尿酸水平分为 2 型糖尿病视网膜病变组和 2 型糖尿病视网膜病变合并高尿酸血症组,每组各 60 例。比较两组患者基本资料、生化指标。
结果 合并高尿酸血症组患者体重指数、收缩压、舒张压显著高于 2 型糖尿病视网膜病变组（P<0.05）,总胆固醇、甘油三酯、低密度脂蛋白胆固醇值显著高于 2 型糖尿病视网膜病变组（P<0.05）,高密度脂蛋白胆固醇、血清肌酐、血尿素氮值低于 2 型糖尿病视网膜病变组（P<0.05）。
结论 2 型糖尿病视网膜病变合并高尿酸血症的患者肥胖、高血压发生率高，且伴有代谢紊乱可导致病情进一步发展。

PU-2078

重症新冠肺炎患者的临床指标特点

刘静
中国人民解放军北部战区总医院

目的 探讨新型冠状病毒肺炎患者实验室检测指标在普通型和重症型中的差异性，从而提供更完善的诊疗依据。
研究方法 根据患者病情严重程度，连续纳入 2020 年 1 月至 3 月武汉市医院收治的普通型和重症型新冠肺炎患者共 234 例，其中普通型 142 例，重症型 92 例。收集所有患者的基本信息，临床症状，生化指标（Ca 离子，白蛋白，球蛋白，白球比，谷草转氨酶，谷丙转氨酶，肌酸激酶及其同工酶，C 反应蛋白）血细胞分析指标（中性粒细胞百分比，淋巴细胞百分比，中性粒细胞/淋巴细胞比值，血小板，红细胞分布宽度，红细胞分布宽度/血小板比值，血小板/淋巴细胞比值）等资料进行对比分析。另将患者出现的发热、咳嗽、咳痰、等症状分别赋值为 1 分，即分值越高症状越重，从而研究血分指标与其严重程度的相关性。
结果 与普通型相比，重症组患者白球比、AST、ALT、CK、NEUT、NLR、RDW、PLT/LYM 水平较高，RBC、HGB、Ca 离子、ALB、Ur、LYM、RDW/PLT 水平较低，差异均有统计学意义（均 P＜0.05）。
结论 普通型与重症型对比发现该病毒对心脏，肝脏，肺部等器官损害严重，实验室相关指标为靶向治疗，预后评估提供可靠依据。

PU-2079

吉林省 0~＜18 岁健康儿童淀粉酶及脂肪酶参考区间的建立

徐攀洋、何冰、许建成
吉林大学第一医院

目的 我国目前所使用的参考区间大多来自行业手册、教科书，制造商或试剂说明书等，而这些参考区间往往会有一些局限性。研究发现，同一检验项目，由于检测系统或检测人群的性别、年龄、种族、地域、饮食、生活习惯等情况不同，参考区间可能存在差异。例如在某项研究中发现发现，儿童的血清碱性磷酸酶浓度比成人高得多，而且这些浓度与骨生长速度有关。碱性磷酸酶(ALP)水平在生命的前 3 个月相对于成人水平略有升高，在青春期增加 2-3 倍，并在 1 到 2 年内保持在成人水平以上。同时发现在儿童的不同年龄组之间也存在显著差异，这表明，建立适宜的儿科参考区间是十分必要的。本研究的目的是采用直接取样方法，建立血清淀粉酶和脂肪酶的年龄和性别特异性儿科参考区间。目前并没有关于此方面的报道。
方法 经父母知情同意，在吉林省五个行政区的社区和学校共招募了 6466 名 1m~＜18y 的健康汉族儿童。 在 VITROS 5600 生化分析仪上测定血清淀粉酶(AMY)和脂肪酶(LPS)水平。 年龄和性别特异性参考区间采用 Harris 和 Boyd 检验或非参数 Mann-Whitney U 检验进行划分，为避免假阳性采用 Bonferroni 法校正 P 值，然后采用非参数秩法计算参考区间，用 Lambda-Mu-Sigma(LMS)方法评价参考区间的动态变化。
结果 淀粉酶的参考区间分为 4 个分区，1~＜5 岁之间迅速上升，5~＜12 岁之间略呈下降趋势，12~＜18 岁缓慢上升。脂肪酶水平在 1 岁之后表现出性别差异，无论男女均呈上升趋势，且女性脂肪酶水平高于男性。
结论 本研究结果建立了中国健康儿童淀粉酶及脂肪酶的参考区间，为临床儿科疾病的诊断和预后评估提供了更准确的解释。

PU-2080

血清 HCY、CysC 与中老年冠心病的相关性及临床价值

方林兰
中国人民解放军联勤保障部队第九二一医院

目的 分析血清同型半胱氨酸（HCY）、胱抑素 C（CysC）联合检测对中老年冠心病的临床意义。
方法 回顾性分析 100 例中老年冠心病患者临床资料作为研究组，另取 100 例健康体检者为对照组。比较各组 HCY、CysC 水平，比较联合检测结果与单项检测结果的敏感度、特异度和准确度。
结果 研究组血清 HCY 和 CysC 水平明显高于对照组，差异均有统计学意义（P<0.05）；联合检测的敏感度、特异度和准确度明显高于单项检测，且差异具有统计学意义（P<0.05）。
结论 联合检测血液中的 HCY 与 CysC 能提高冠心病检查的准确率，具有较高临床价值。

PU-2081

SAA，CRP，PCT 在呼吸道病毒感染的临床诊断中的应用

赵宇佳
中国人民解放军联勤保障部队第九二一医院

目的 分析血清淀粉样蛋白 A（SAA）、C-反应蛋白（CRP）、降钙素原（PCT）在呼吸道病毒感染的临床诊断中的应用。

方法 选取 2020 年 7 月-2020 年 12 月于联勤保障部队第 921 医院诊断为呼吸道病毒感染阳性患者血清 30 例和正常人血清 20 例分为感染组及未感染组，并检测其 SAA、CRP、PCT。
结果 未感染组 SAA（6.012±1.487）mg/L，CRP（4.034±1.977）mg/L，PCT（0.102±0.055）μg/L；感染组 SAA（13.770±1.389）mg/L，CRP（4.898±1.366）mg/L，PCT（0.168±0.088）μg/L。未感染组 PCT 与感染组 PCT 差异无统计学意义（p>0.05）。诊断呼吸道病毒感染时血清 SAA、CRP、PCT 的 AUG 分别为 0.822、0.752、0.589，检测临界值分别为 5.71mg/L、1.18mg/L、0.052μg/L。
结论 SAA、CRP 和 PCT 均能为临床呼吸道病毒感染提供一定的诊断参考，但 SAA 的效能最佳。

PU-2082

RBP、Cys-C 及 hs-CRP 联合检测在Ⅱ型糖尿病肾病早期诊断中的临床价值

张雅涵
中国人民解放军联勤保障部队第九二一医院

目的 研究视黄醇结合蛋白（RBP）、胱抑素 C（Cys-C）及超敏 C 反应蛋白（hs-CRP）联合检测对糖尿病肾病患者早期诊断的临床价值。
方法 收集中国人民解放军联勤保障部队第九二一医院神经内科、肾病内科等科室 2017 年 12 月至 2020 年 12 月收治的 100 例Ⅱ型糖尿病确诊患者为研究对象，根据患者尿白蛋白肌酐比值（UACR）将患者分为单纯糖尿病组和早期糖尿病肾病组，另收集同时期排除Ⅱ型糖尿病的健康体检者 50 例为健康对照组，记录三组对象 RBP、Cys-C 及 hs-CRP 三项指标水平，采用 SPSS20.0 软件对数据进行分析处理。
结果 早期糖尿病肾病组 RBP、Cys-C 及 hs-CRP 检测值均高于单纯糖尿病组，差异具有统计学意义，P<0.05。较年轻糖尿病肾病患者 RBP、Cys-C 及 hs-CRP 检测值均低于较老年患者，差异具有统计学意义，P<0.05。RBP、Cys-C 及 hs-CRP 联合检测对早期糖尿病肾病敏感度为 92.1%，特异度为 84.24%，显著高于单项指标单独检测。
结论 血清 RBP、Cys-C 及 hs-CRP 联合检测可显著提高对Ⅱ型糖尿病肾病患者早期诊断的灵敏度。

PU-2083

不同年龄段孕妇体重、孕周因素对唐氏筛查的影响探究

甘慧泉
广东省人民医院
广东省医学科学院

目的 研究不同年龄段孕妇孕早期和孕中期唐氏筛查阳性率与其体重和孕周的关系，为临床诊疗提供更加细化的指导建议。
方法 回顾性分析广东省人民医院 2017 年 1 月至 2018 年 12 月进行孕早期和孕中期产前筛查孕妇共 7338 例。根据筛查结果，采用方差分析和调节效应分析统计数据。
结果 孕早期和孕中期唐氏筛查阳性率和年龄呈正相关。年龄 30 周岁以上和 30 周岁以下各组的孕妇，唐氏综合征筛查阳性率存在统计学差异。对不同年龄段孕妇，在孕早期和孕中期，孕周与年龄的交互作用对唐氏筛查阳性结果的影响都是显著的。但是孕周对不同年龄段孕妇的唐氏筛查阳性不起调节作用；体重与年龄的交互作用对唐氏筛查阳性结果的影响不显著，但是体重在孕中期对不同

年龄段的唐氏筛查起调节作用。单就孕周因素而言，孕早期和孕中期唐氏筛查阳性率与孕周均不存在相关关系；单就体重因素而言，孕早期和孕中期唐氏筛查阳性与体重均呈正相关。
结论 对于唐氏综合征的筛查结果，年龄，体重，孕周等因素都有影响。对于孕周和体重的调节效应，孕早期和孕中期孕妇年龄和孕周的交互作用对唐氏筛查阳性的作用是显著的；和体重的交互作用对唐氏筛查阳性的作用是不显著的。孕早期和孕中期唐氏筛查阳性率与体重均呈正相关。

PU-2084

老年高血压合并冠心病患者经氨氯地平联合阿托伐他汀钙片治疗后小而密低密度脂蛋白的变化及临床意义

杨晓东、杨华、饶丽华
三峡大学附属仁和医院

目的 探讨老年高血压合并冠心病患者经氨氯地平联合阿托伐他汀钙片治疗后血清小而密低密脂蛋白胆固醇（sdLDL-C）的变化及临床意义。
方法 选择 2019 年 1 月至 12 月在本院就诊的 150 例老年高血压合并冠心病患者，采用随机数字表法平均分成 2 组。其中对照组 75 例给予氨氯地平口服治疗，观察组 75 例在此基础上联合阿托伐他汀钙片口服。治疗后，比较两组患者的临床疗效，同时比较 2 组患者治疗前后血脂相关指标，分析比较 sdLDL-C 水平和 sdLDL-C/LDL-C 比值的变化。
结果 观察组 DBP、SBP、TC、TG、LDL-C、sdLDL-C 水平低于对照组，HDL-C 水平高于对照组，差异均有统计学意义（P<0.05）；观察组 sdLDL-C 水平低于对照组，且 sdLDL-C/LDL-C 比值高于对照组，差异均有统计学意义（P<0.05）
结论 老年高血压合并冠心病患者经氨氯地平联合阿托伐他汀钙片治疗后血清小而密低密脂蛋白胆固醇降低，sdLDL-C/LDL-C 比值升高，从而避免动脉粥样硬化的风险。

PU-2085

尿轻链比值结合免疫固定电泳初步筛查以肾脏损伤为首发症状的老年多发性骨髓瘤患者的研究

衣鲁江
江苏省人民医院（南京医科大学第一附属医院）

目的 近年来老年人中 MM 发病率逐渐升高，由于 MM 早期无明显体征，早期症状常以肾损伤形式体现，为能早期明确诊断，探索用尿轻链比值结合免疫固定电泳初步筛查以肾脏损伤为首发症状的老年 MM 患者。
方法 回顾性分析我院 2017 年 1 月至 2019 年 2 月门诊初诊为“肾脏疾病”的老年患者共 981 例，根据免疫固定电泳结果分为 M 蛋白组和非 M 蛋白组，分析各组相关实验室检测数据。
结果 981 例入组病例中，M 蛋白组 84 例，占 8.6%，M 蛋白组患者与非 M 蛋白组患者间比较，Crea 以及 eGFR 检测结果差异均无统计学意义。以 KAP 型轻链表达为主的 M 蛋白组，KAP/LAM 比值高于非 M 蛋白组；以 LAM 型轻链表达为主的 M 蛋白组 KAP/LAM 比值低于非 M 蛋白组(P<0.01)。比较不同 M 蛋白类型间的肾功能指标，IgG 组、IgA 组和 IgM 组间没有统计学差异（P>0.05），单纯轻链组与 IgG 组、IgA 组和 IgM 组比较，Crea、u-mALB/Crea 增高，而 eGFR 降低（P<0.05）。897 例非 M 蛋白组中不同原因引起的肾脏疾病其肾功能指标（Crea、eGFR、u-mALB/Crea）差异显著。而血、尿 KAP/LAM 比值差异没有统计学意义，且各组比值与正常范围相比较，差异也没有统计学意义。

结论 尿 KAP/LAM 比值用于初步筛查以肾脏损伤为首发症状的老年 MM 患者有较好的特异性，可以反应单克隆增殖程度，且留样便捷无创，易于被患者接受，适合用于体检或疑似 MM 患者的初步筛查。

PU-2086

GATA-4/HCC-1 途径对内皮细胞衰老和动脉粥样硬化的影响及机制研究

黄瑞莹
南方医科大学南方医院

研究背景与目的 年龄增长引起的血管内皮细胞衰老是动脉粥样硬化的独立危险因素，内皮细胞衰老在 AS 早期起着重要作用。有研究发现，GATA-4 对人成纤维细胞的衰老过程起着重要的调控作用，而血液滤过 CC 趋化因子 1（HCC-1）可通过影响炎症过程参与各种疾病的发生发展，但能否影响内皮细胞的衰老过程和 AS 尚不清楚。本研究通过探究 GATA-4 对内皮细胞衰老及动脉粥样硬化的影响，观察细胞衰老对动脉粥样硬化的影响及相关机制。
方法 通过小鼠主动脉瓣组织免疫组化染色观察 GATA-4 在 AS 斑块中的表达情况；通过构建 GATA-4 小干扰片段转染原代人脐静脉内皮细胞（HUVEC）敲减 GATA-4，通过细胞衰老相关 β 半乳糖苷酶化学染色探究 GATA-4 对内皮细胞衰老的影响；通过单核巨噬细胞粘附实验探究 GATA-4 对细胞粘附能力的影响，通过 WB 实验进行初步机制研究，最后收集不同年龄层 AS 患者及健康体检者的血清样本，探究 HCC-1 在血清中的表达量和其与 AS 临床指标的相关性，分析 HCC-1 作为临床风险预测指标的可能性。
结果 1、与正常小鼠主动脉瓣组织相比，在小鼠主动脉瓣 AS 斑块中，GATA-4 表达上调。
2、si-GATA4 可显著抑制 H2O2 诱导的原代 HUVEC 衰老。
3、si-GATA-4 可下调细胞表面粘附能力
4、敲减 GATA-4 后，可显著下调 HCC-1 及 p16 表达，而使用 HCC-1 重组蛋白处理 HUVEC 后可上调 p16 表达，且同时敲减 GATA-4 后，HCC-1 可回复部分 GATA-4 对 p16 上调作用。
5、HCC-1 在 AS 及衰老患者血清中显著高表达。
结论 1、在小鼠主动脉瓣 AS 斑块中，GATA-4 表达显著上调。
2、GATA-4 可促进原代 HUVEC 衰老级单核巨噬细胞粘附原代 HUVEC。
3、HCC-1 可能介导 GATA-4 促进 p16 表达，进而促进内皮细胞衰老。
4、HCC-1 有作为年龄相关性 AS 的新的风险预测指标的潜能。

PU-2087

探讨检测孕中期血清 β-HCG、ACA 和孕后期尿酸浓度对先兆子痫的预测价值

张懿
南方医科大学珠江医院

目的 通过比较先兆子痫患者和正常孕妇孕中期 β-HCG、抗心磷抗体 ACA 和孕后期尿酸的浓度变化，探讨这三项指标对该疾病的预测价值。
方法 回顾性分析 2012.1-2016.8 在南方医科大学珠江医院接受孕中期筛查并成功随访直至分娩的 65 例单胎妊娠孕妇，其中 30 例经诊断为子痫前期患者，对照组有 35 例血压正常的孕妇。比较两组孕妇的 BMI 指数，孕中期（15-20 周）血清的 β-HCG 浓度，β-HCG MoM 值和抗心磷脂抗体 ACA 水平，以及孕妇孕后期（20 周以后）尿酸浓度，分析这些指标与孕妇发生子痫前期的相关性。

结果（1）子痫前期组孕妇 BMI 指数、β-HCG MoM 值、尿酸均显著高于正常对照组(P<0．05)。(2)多因素 Logistic 回归分析显示 BMI 指数、血清尿酸浓度都是子痫前期的预测指标，其中尿酸水平的预测能力最强 ,BMI 次之。
结论 抗心磷脂抗体 ACA 对孕妇患子痫前期的预测意义不明显，先兆子痫患者组的 BMI 值、尿酸水平均显著高于正常对照组，与疾病具有一定的相关性。子痫前期患者孕中期的 β-HCG 水平显著升高，可作为预测子痫前期的一个指标，经修正的 β-HCG MoM 值诊断效能更强。

PU-2088

探究颈动脉粥样硬化患者血清中 sdLDL-C/ LDL-C、hs-CRP 表达水平的变化

闵媛婷、杨婕、刘曼舒、林文源
宜昌市第二人民医院

目的 探讨颈动脉粥样硬化(CAS)患者血清中小而密低密度脂蛋白胆固醇/低密度脂蛋白胆固醇（sdLDL-C/ LDL-C）、超敏感 C 反应蛋白（hs-CRP）表达水平的变化，分析其与 CAS 病变程度的相关性。
方法 选取行颈血管彩超检查的患者 279 例，根据颈动脉内中膜厚度(IMT)将患者分为斑块组（118 例）、内膜增厚组（48 例）、正常组（113 例）。测定各组间 sdLDL-C/ LDL-C、hs-CRP 水平，以 Pearson 相关性分析、多因素 Logistic 回归分析等统计学方法探讨 sdLDL-C、sdLDL-C/ LDL-C、hs-CRP 与颈动脉粥样硬化程度的相关性及其诊断价值。
结果 斑块组血清 sdLDL-C、LDL-C、sdLDL-C/ LDL-C、hs-CRP 表达水平较正常组升高（P<0.05），与内膜增厚组相比无统计学意义（P>0.05）。Pearson 相关性分析提示 hs-CRP 与 sdLDL-C（r=0.3043）、sdLDL-C/ LDL-C（r=0.3804）呈正相关（P<0.05），与 LDL-C 不具有相关性（P>0.05）；IMT 与 sdLDL-C（r= 0.4142）、sdLDL-C/ LDL-C（r=0.4915）、hs-CRP（r= 0.4528）呈正相关（P<0.05），与 LDL-C 不具有相关性（P>0.05）。多因素 Logistic 回归分析提示 sdLDL-C、hs-CRP 可能为患者产生颈动脉粥样硬化斑块的独立影响因素。
结论 随着 CAS 疾病的进展，sdLDL-C、LDL-C、sdLDL-C/ LDL-C、hs-CRP 表达水平升高。sdLDL-C、sdLDL-C/ LDL-C、hs-CRP 与颈动脉粥样硬化斑块大小呈正相关，sdLDL-C、hs-CRP 可能相互作用，共同促进 CAS 的发展。

PU-2089

自建检测系统检测风湿三项的性能评价

来金欣、陈杰荣、周茂华、甘慧泉
广东省人民医院（广东省医学科学院） 检验科

目的 评估自建检测系统检测风湿三项的分析性能。
方法 应用美国临床和实验室标准化协会（CLSI)EP5-A2、EP15-A2、EP6-A、EP17-A、C28-A2 方法评价自建检测系统检测风湿三项试剂即抗链球菌溶血素 O(ASO)、类风湿因子（RF）、C 反应蛋白（CRP）的精密度、准确度、分析测量范围、临床可报告范围、生物参考区间。自建检测系统(1-3)由罗氏 cobas c702 生化分析仪、第三方检测试剂、校准品和质控品组成。
结果 自建检测系统的批内精密度小于 1/4 TEa，批间精密度≤1/3TEa，符合《医学实验室质量和能力认可准则在临床化学检验领域的应用说明》中对分析性能的要求；对卫生部室间质控品进行检测，测定结果与统计的靶值进行比对，偏差符合要求；线性范围与厂商提供的性能指标相符；可报告范围符合临床需求；生物参考区间验证显示：本研究选择的参考个体水平符合厂家试剂说明书给定参考区间。

结论 自建检测系统的精密度、准确度、线性范围（可报告范围）、生物参考区间在可接受范围内，可满足临床需求。

PU-2090

肝酶、平均血小板体积和红细胞分布宽度值对于预测妊娠期糖尿病发生发展的临床应用价值

杨璐、蒋叶
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨测定肝酶、红细胞分布宽度(RDW)和平均血小板体积(MPV)数值对于预测妊娠期糖尿病(GDM)发生发展的临床应用价值。
方法 收集 368 例 2016 年 1 月至 2016 年 12 月在江苏省妇幼保健院确诊为妊娠期糖尿病孕妇的病例资料，记录相关实验室检查参数结果。同时收集同期 368 例健康体检者作为对照组，比较不同组间所有参数差异。
结果 在所有参数中，GDM 组的血小板分布宽度(PDW)、转氨酶(ALT)和 γ-glutamyl 转移酶（GGT）明显高于健康对照组（P＜0.05）；GDM 组的血小板压积 (PCT)水平显著降低(P＜0.01)；而在平均血小板体积（MPV）、红细胞分布宽度（RDW）、血小板计数（PLT）和天冬氨酸转氨酶（AST）水平上，组间无显著差异。
结论 我们的研究结果表明，ALT、GGT、PCT 和 PDW 可以作为预测 GDM 发展的预测指标，为临床诊断妊娠期糖尿病开拓了新的思路。

PU-2091

Roche 电化学发光 E602 检测白介素 6 的方法学评价

卫丽[1]、刁晓艳[1]、梁涯[2]
1. 青海省人民医院
2. 广州市中医医院同德围分院

目的 验证和评价罗氏 E602 模块定量检测白介素 6（IL-6）的分析性能。
方法 对罗氏 E602 分析仪定量检测 IL-6 的准确度、精密度、线性进行验证、交叉污染率评估实验，
结果 准确度、精密度均符合罗氏 E602 性能标准；IL-6 检测呈一次线性（R^2=0.99996 ,p<0.05），罗氏 E602 分析仪交叉污染率为 0.077%。
结论 罗氏 E602 检测 IL-6 的主要分析性能验证结果与厂商声明的基本一致，符合质量目标要求，可应用于临床标本检测。

PU-2092

血清酶类指标联合血清总胆汁酸检测分析肝脏功能的临床意义

周觅
山东大学第二医院

目的 研究血清酶类指标联合血清总胆汁酸(TBA)检测分析肝脏功能的临床意义,为临床提供参考.
方法 选择我院 2011 年 9 月~2012 年 9 月 89 例肝病患者作为观察组,对其进行血清酶类指标联合血清总胆汁酸检测,同时选择同期 89 例健康体检者作为对照组,作相同项目的检查,比较两组患者 TBA

与血清酶类指标天门冬氨酸转移酶(AST)、γ-谷氨酰转肽酶(γ-GT)、丙氨酸氨基转移酶(ALT)、碱性磷酸酶(AKP).
结果 89 例患者按肝病类型分组,其中急性肝炎 29 例,慢性活动性肝炎 22 例,肝硬化 22 例、肝癌 16 例,所有肝病患者血清酶类指标与 TBA 值均显著高于对照组,其中以急性肝炎组 TBA 升高最明显,其次是肝硬化、肝癌和慢性活动性肝炎;肝癌组 γ-GT、AKP、ALT 值明显高于对照组及其它肝病组,组间比较差异具有统计学意义,P＜0.05.
结论 血清总胆汁酸与血清酶类指标联合检测在肝脏性疾病中有显著的临床意义.

PU-2093

陕西省 2020 年 21861 例儿童血铅的检测结果分析

郑金磊
西安金域医学检验所有限公司

目的 铅是一种严重危害人体健康的重金属元素，会对儿童造成神经系统、造血系统、免疫系统等的损害，影响儿童智力和体格发育。本研究讨论 2020 年陕西省≤12 岁儿童血铅的超标率，为预防儿童慢性铅中毒提供数据支持及指导。
方法 选取 2020 年西安金域检测的 21861 例≤12 岁儿童的血铅检测数据，按照年龄分为 3 组：分别为 0-3 岁共 10884 例、3-6 岁共 6308 例、6-12 岁共 4669 例。按照性别分为 2 组：分别为男童 12311 例、女童 9550 例。样品采集：用肝素抗凝管采取空腹静脉全血 1-2ml 或加有肝素抗凝的 EP 管采取末梢血 100μl。试剂与仪器：采用 0.1%TritonX-100 和 0.1%HNO3 对样本稀释 20 倍混匀后，使用电感耦合等离子体质谱法(ICP－MS)直接测定血铅的含量，数据采用 SPSS22.0 统计学软件分析，以 P＜0.05 为差异有统计学意义。
结果 1、以 1991 年美国 CDC 的分级标准作为参考，儿童血铅的整体超标率为 0.33%，分析不同年龄段儿童血铅的超标率差异显著，具有统计学意义(P＜0.05)；2、分析不同性别儿童间的差异无统计学意义(P>0.05)；3、其中 0-3 岁血铅的超标率为 0.48%，3-6 岁血铅的超标率为 0.21%，6-12 岁血铅的超标率为 0.13%，其中 1 例复查血铅的含量≥700μg/L。
结论 0-3 岁儿童血铅超标率远高于其他年龄段儿童，此年龄段儿童应作为重点筛查对象，定时监测儿童血铅的含量预防慢性铅中毒，铅污染来源除了工业污染外，有很大一部分来自于生活污染，儿童主要通过消化道吸收铅，应对儿童及其监护人开展健康教育，教导儿童勤洗手，避免儿童啃咬手指、玩具、文具等经常接触或含铅量较高的物品，降低儿童高含铅量食物的摄入。

PU-2094

脂代谢异常与胰腺炎的诊断及预后评估

李伯宣
昆明医科大学第二附属医院

目的 急性胰腺炎是常见的消化系统疾病之一,我国的发病率约 1%,而 20～30%的 AP 可发展成为重症急性胰腺炎(severe acute pancreatitis，SAP),常出现局部和全身并发症,预后差 1，2。淀粉酶脂肪酶相关性不高，所以通过研究脂代谢变化来探究与 AP 的诊断和预后的评估相关。
方法 回顾性分析 2020 年 9 月至 2021 年 6 月期间昆明医科大学第二附属医院收治的胰腺炎患者 80 例临床资料，根据血脂水平、并发症、临床分为正常、轻度、中度、重度和临床结果的比较。将患者分为轻度组、中度组、重度组、慢性组、正常组（对照组）。收集患者一般资料、病死率、病情严重程度及并发症情况。不符合正态分布的计量资料多组间比较采用 Kruskal-Wallis H 检验，进一步两两比较采用 Dunn -Bonferroni 检验。计数资料无序分类变量多组间及两两比较采用 χ2 检验，有序多分类变量多组间比较采用 Kruskal-Wallis H 检验，进一步两两比较采用 Mann-Whitney U 秩

和检验。患者发生脂代谢异常影响因素采用多因素 logistic 回归分析。绘制 ROC 曲线评价不同指标对 AP 的预测价值。
结果 根据 ROC 曲线得出脂肪酶诊断效能最高，其次是 TG、淀粉酶、NONHDL、LDL。表明在脂代谢中相关度最高的指标是 NONHDL。
结论 胰腺炎与脂代谢存在一定相关性，两者互相影响。对于胰腺炎诊断及预后来说可以在胰腺功能测定中增加胆固醇项目。在治疗疾病时应积极控制血脂水平，降低疾病严重程度。

PU-2095

血清胆红素组分对梗阻性黄疸的鉴别及预后判断的价值

白艳
昆明医科大学第二附属医院

目的 探讨血清胆红素组分在梗阻性黄疸鉴别及预后判断中的临床价值。
方法 测定 133 例梗阻性黄疸患者治疗前后的血清 Tbil、ALT、AST、GGT，根据诊断将患者分为梗阻性黄疸组，分析血清胆红素组分对梗阻性黄疸良恶性的鉴别意义。
结果 ①DBil、IBil、IB/DB、ALT、GGT 可鉴别梗阻性黄疸与其他两类黄疸，但对于溶血性黄疸与肝细胞性黄疸的鉴别中无明显统计学差异。在梗阻性黄疸良恶性鉴别中，TB、DB、DB/TB 的曲线下面积（AUC）的值都很显著。

PU-2096

环形 RNA circRNA_0036167 促进心肌肥厚作用机制研究

李晖
广东省人民医院

目的 环形 RNA circRNA_0036167 在心肌肥厚中的作用及其机制。
方法 1、通过 RT-qPCR 检测 Ang-Ⅱ诱导心肌肥厚模型小鼠 circRNA_0036167 的表达水平；
2、利用腺病毒介导在小鼠原代心肌细胞中过表达 circRNA_0036167，并通过鬼笔环肽染色、RT-qPCR 和 Western blot 检测 circRNA_0036167 在体外对心肌细胞肥大表型的影响；
3、利用心肌特异过表达 circRNA_0036167 转基因小鼠（Tg-circ36167），建立 Ang-Ⅱ诱导的心肌肥厚模型，并通过超声心动图、WGA 染色、RT-qPCR 和 Western blot 检测过表达 circRNA_0036167 对心肌肥厚表型的影响；
4、通过 RT-qPCR 检测心力衰竭患者心肌组织和外周血浆中 circRNA_0036167 的表达水平。
结果 1、circRNA_0036167 在肥厚的小鼠心肌和心力衰竭患者心肌组织中表达均明显升高；
2、在原代小鼠心肌细胞中过表达 circRNA_0036167，心肌细胞明显肥大、肥厚相关基因 β-MHC 和 ANP 的表达显著增加；
3、Ang-Ⅱ诱导 Tg-circ36167 小鼠心肌肥厚模型，Tg-circ36167 小鼠心功能明显降低、心肌细胞明显肥大、β-MHC 和 ANP 水平显著增加；
4、circRNA_0036167 在心力衰竭患者心肌组织和血浆中表达均明显升高。
结论 circRNA_0036167 可在体内外发挥促进心肌肥厚作用，并作为心力衰竭新型循环标志物。

PU-2097

单核细胞/高密度脂蛋白胆固醇比值与合并高同型半胱氨酸血症的冠心病患者的冠脉狭窄程度的关系研究

邓倩昀[1]、陈科[2]、顾兵[1]
1. 广东省人民医院
2. 广州医科大学

目的 分析单核细胞与高密度脂蛋白胆固醇比值（MHR）在冠心病合并高同型半胱氨酸血症患者中的变化，并探讨其与冠状动脉狭窄程度的关系。
方法 选取 2020 年 7 月-2021 年 1 月于广东省人民医院经冠状动脉造影确诊冠心病 285 例，根据同型半胱氨酸（HCY）水平分为同型半胱氨酸正常组（223 例）和高同型半胱氨酸血症组（62 例）；根据冠状动脉造影的结果分为轻度狭窄组（97 例）、中度狭窄组（97 例）和重度狭窄组（91 例）。选取同期于本院健康查体 254 例正常人为对照；分别比较对照组与同型半胱氨酸正常组和高同型半胱氨酸血症组以及与轻度狭窄组、中度狭窄组和重度狭窄组受试者一般资料和实验室检查指标。
结果 对照组、HCY 正常组和 HHCY 组受试者中性粒细胞/淋巴细胞比值（NLR）、MHR 比较，差异有统计学意义（P<0.05）；同型半胱氨酸正常组（HCY 正常组）和高同型半胱氨酸血症组（HHCY 组）患者年龄和高血压史比较，存在差异有统计学意义（P<0.05）。其中对照组受试者 MHR、NLR 低于 HCY 正常组和 HHCY 组，差异有统计学意义（P<0.05）；HCY 正常组患者 MHR 低于 HHCY 组，差异有统计学意义（P<0.01）；对照组、轻度狭窄组和中度狭窄组受试者 HCY、NLR 及 MHR 比较，差异有统计学意义（P<0.05）。对照受试者 HCY、NLR 及 MHR 低于轻度狭窄组、中度狭窄组和重度狭窄组，差异有统计学意义（P<0.05）。
结论 MHR 在冠心病合并高同型半胱氨酸血症患者中显著升高，与冠心病患者冠状动脉狭窄程度呈正相关。

PU-2098

一步法制备双功能碳纳米管用于 AFP 电化学免疫分析

陈梦园[2]、宁振强[1]、沈艳飞[1,3,4]
1. 东南大学医学院
2. 东南大学医学院
3. 东南大学中大医院，临床检验医学中心
4. 东南大学江苏省重症重点实验室

功能性碳纳米材料，例如多壁碳纳米管（MWCNT），因其独特的光、电、热和力学性能使其在生物传感领域受到极大的关注[1-2]。在基于 MWCNT 电化学生物传感器的制备过程中，生物分子的界面偶联和电化学探针的附着是影响传感性能的两大关键因素。由于两者反应条件不同，一般只能通过分步实现。然而由于 MWCNT 的反应活性低，要想在连续反应条件下精确控制两种改性剂在 MWCNT 表面的用量仍具有较大的挑战性。为此，我们课题组以自由基聚合为基础开发了一步电接枝法，该法以乙烯基二茂铁（VFc）和 N-羟基琥珀酰亚胺丙烯酸酯(NSA)分别作为电化学探针和生物分子偶联剂，二者因反应类型相似，可以一步电接枝到 MWCNT 上，增强二茂铁和琥珀酰亚胺基团的附着，促进氧化还原信号和抗体捕获，解决了影响此类生物传感灵敏度的两大关键问题。在此过程中，调节两种修饰剂的比例来平衡电化学信号强度和生物分子连接程度，对传感器性能的提高起着至关重要的作用。我们将此方法成功运用到以甲胎蛋白(AFP)作为模型分析物的定量检测上。通过实验条件优化，基于双功能化 MWCNT 的生物传感器显示出 10 $ng \cdot mL^{-1}$ 到 50 $\mu g \cdot mL^{-1}$ 的检测范围，能较好满足肝癌诊断的实际需要。本工作为生物传感和临床诊断领域构建具有信号放大增强作用的电化学生物传感器开辟了新途径。

PU-2099

高糖环境下 GATA4 通过调节 RUNX2 影响成骨细胞增殖分化的研究

陈妍汶
绵阳市中心医院

目的 探讨高糖环境下 GATA 锌指转录因子蛋白 4（GATA4）对成骨细胞增殖分化的影响，及对转录因子蛋白 2（Runx2）的调控作用。
方法 取 MC3T3-E1 成骨细胞，在高糖（25mmoL/L）的条件下分别培养 1、4、7、14d，免疫印迹法（Western blot）法检测 GATA4、Runx2 蛋白表达水平。将 MC3T3-E1 成骨细胞分为空白对照组、高糖诱导组、GATA4 过表达腺病毒（Ad-GATA4）组、GATA4 空载腺病毒组（Ad-eGFP）组，CCK-8 法检测各组细胞的存活率，碱性磷酸酶（ALP）染色法及茜素红染色法检测细胞分化能力；Western blot 法检测各组细胞 GATA4、Runx2、成骨细胞特异性转录因子(OSX)、骨唾液蛋白（BSP）蛋白表达水平。共转染 Ad-GATA4 及 Runx2 干扰腺病毒（Ad-si-Runx2），将 MC3T3-E1 成骨细胞分为 Ad-GATA4-si-Runx2 组、Ad-GATA4-eGFP2 组、Ad-eGFP-si-Runx2 组、Ad-eGFP-eGFP2 组及未转染组（高糖组），高糖条件下培养 7d 后检测 GATA4、Runx2、OSX、BSP 蛋白表达水平。
结果 随着高糖培养时间延长，细胞中 GATA4、Runx2 蛋白表达持续降低，在第 7d 降低至最低，选取高糖培养 7d 为后续培养条件。转染 Ad-GATA4 后，与空白对照组比较，高糖诱导组细胞矿化结节形成较少，细胞存活率、ALP 活性、GATA4、Runx2 蛋白表达、OSX、BSP 蛋白表达降低（P<0.05）；与高糖组相比，Ad-GATA4 组细胞矿化结节形成较多，细胞存活率、ALP 活性、GATA4、Runx2 蛋白表达、OSX、BSP 蛋白表达升高（P<0.05），Ad-eGFP 组与高糖诱导组相比上述指标差异无统计学意义（P>0.05）。Ad-GATA4 与 Ad-si-Runx2 共转染后，与高糖诱导组相比，Ad-GATA4-eGFP2 组细胞 GATA4、Runx2、OSX 及 BSP 蛋白表达升高（P<0.05）；Ad-eGFP-si-Runx2 细胞 Runx2、OSX 及 BSP 蛋白表达降低（P<0.05），GATA4 蛋白表达变化差异无统计学意义（P>0.05）。与 Ad-GATA4-eGFP2 组比较，Ad-GATA4-si-Runx2 细胞 Runx2、OSX 及 BSP 蛋白表达降低（P<0.05），GATA4 蛋白表达变化差异无统计学意义（P>0.05）。
结论 高糖可抑制成骨细胞增殖分化，伴随 GATA4、Runx2 蛋白表达降低，过表达 GATA4 则可促进成骨细胞在高糖环境中的增殖、分化，其可能与激活 Runx2 表达有关。

PU-2100

四氮唑蓝法检测血清果糖胺及其临床应用

王永松[2]、林穗雄[1]、李建华[1]、邓穗德[2]、吕灼荣[1]、陈爱贤[2]、李晓莹[2]
1. 广州市从化区妇幼保健院
2. 广州金域医学检验中心

目的 建立四氮唑蓝法检测血清果糖胺的方法，并初步应用于临床。
方法 根据血清中果糖胺在碱性条件下能还原四氮唑蓝为甲臜，与经过同样处理的果糖胺校准品进行比较，即可计算出样本中果糖胺含量的方法，同时作方法学评价，并临床检测与分析 20 例糖尿病患者血清中果糖胺水平。
结果 批内及批间变异系数 1.77%和 2.46%，回收率为 98.7%，不同浓度的测定值与理论值比较，线性范围：R2=0.9994＞0.95，b=1.0297，25 份标本与另一三甲医院结果比对，回归方程为 Y=0.03835+1.0225X，糖尿病患者血清中的果糖胺浓度显著高于对照组（P ＜0.01）。
结论 此法简单、快速，适用于自动生化分析仪，线性范围能满足需要，在标准操作下，可在临床中推广应用。

PU-2101

清热利湿方对脂肪肝细胞磷脂肌醇-3 激酶/肾上腺受体激酶表达的调节作用研究

张巍、邵明亮、苗同国、侯桂英、戴二黑
河北医科大学附属石家庄第五医院

目的 观察清热利湿方对氧化损伤脂肪肝大鼠磷脂肌醇-3 激酶(PI3K) /肾上腺受体激酶(ARK)通路调节作用。
方法 选取大鼠 60 只，分为正常对照组、高脂模型组、多烯磷脂酰胆碱组及清热利湿方高、中、低剂量组 6 组，采用高脂饲料复制大鼠脂肪肝实验动物模型，从第 6 周开始，清热利湿高、中、低剂量组分别给予 0. 3、0. 1、0. 05 g/(100 g·d)清热利湿方汤剂灌胃，多烯磷脂酰胆碱组给予 25 mg/(100 g·d)灌胃，12 周后取材。病理检查各组脂肪肝程度，ELISA 检测血清高敏 C 反应蛋白(hs-CRP)含量及三磷酸腺苷酶(ATPase)活性，生化分析仪检测各实验组血脂及肝功能指标。Western blot 检测脂肪变肝细胞 PI3K/ARK 表达。
结果 高脂模型组 hs-CRP 明显升高，与清热高剂量组比较差异具有统计学意义(P =0. 0331)。各实验组 ATPase 呈现不同程度降低，清热高剂量组血清 ATPase 水平明显提高，与高脂模型组比较差异具有统计学意义(P =0. 0401); western blot 实验结果可见，各实验组大鼠肝细胞 PI3K/ARK 表达存在明显差异，清热利湿方治疗后，PI3K/ARK 水平明显降低。
结论 清热利湿方通过调节 ATPase、hs-CRP、PI3K/ARK 而降低肝细胞氧化应激炎症介质，改善肝细胞由于脂类代谢异常形成的过氧化损伤，促进肝细胞功能的恢复，具有一定的改善脂肪变性效果。

PU-2102

清热利湿方对脂肪肝细胞 PI3K/Ark 表达调节研究

张巍、邵明亮、苗同国、侯桂英、戴二黑
河北医科大学附属石家庄第五医院

目的观察清热利湿方对脂肪肝细胞酸肌醇 3-激酶（PI3K/Ark）通路调节作用。
方法 选取大鼠 60 只，随机数字表法将大鼠分为 6 组：正常对照组、高脂模型组、多烯磷脂酰胆碱组、清热高剂量组、清热中剂量组、清热低剂量组，采用高脂饲料复制大鼠脂肪肝实验动物模型，6 周开始清热利湿组分别给与给予 0.3 g/ （100 g·d）（清热高剂量组）0.1 g/ （100 g·d）（清热中剂量组），0.05 g/ （100 g·d）（清热低剂量组）灌胃，多烯组给予 25 mg/ （100 g·d）灌胃，12 周后取材。 病理检查各组脂肪肝程度，ELISA 检测血清急性时相反应蛋白（hs-CRP）含量及 ATP 酶活性，生化分析仪检测脂肪肝各实验组血脂（TC/TG）、肝功能（ALT/AST/GGT）。Western-blot 检测脂肪变肝细胞磷脂酰肌醇-3 激酶（PI3K）/Ark 表达。
结果 高脂模型组 hs-CRP 明显升高，与清热高剂量组比较具有明显差异（P<0.05）。 各实验组 ATPase 呈现不同程度降低，清热高剂量组血清 ATPase 水平与高脂模型组比较具有明显差异（P<0.05）；Western blot 实验结果可见，各实验组大鼠肝细胞 PI3K/Ark 表达存在明显差异，清热利湿方治疗后，明显降低表达 PI3K/Ark 水平。
结论 清热利湿方通过调节 ATPase、hs-CRP、PI3K/Ark 肝细胞氧化应激炎症介质，改善肝细胞由于脂类代谢异常形成的过氧化损伤，促进肝细胞功能的恢复，具备一定的改善脂肪变性效果。

PU-2103

血清 α-羟基丁酸脱氢酶表达水平与卵巢癌辅助诊断的相关性研究

陆昭锦
滨州医学院烟台附属医院

目的 分析卵巢癌患者的血清 α-羟基丁酸脱氢酶（α-HBDH）的水平，为临床诊断提供参考。
方法 回顾性收集 2017 年 1 月至 2019 年 12 月在本院确诊治疗的卵巢癌病人 28 名作为 A 组,同时选取在本院确诊治疗的卵巢良性病变病人 29 名作为 B 组,还有正常健康查体 35 名女性为 C 组。统计并且分析所有研究对象血清中的 α-羟基丁酸脱氢酶和糖类抗原 125(CA125)的表达水平。方法学：采用 SPSS17.0 统计处理数据，率的比较采用 X2 检验，数据为偏态分布，采用中位数（四分位数间距）[M(P25~P75)]表示，多组间比较采用 Kruskal-Wallis H 检验，以 P<0.05 为差异有统计学意义。
结果 A 组血清 α-HBDH 中位数为 172.63U/L， B 组为 151.33U/L， C 组为 110.35U/L。A 组高于 B 组，B 组高于 C 组，三组间差异有统计学意义；A 组血清 α-HBDH，CA125 及联合检测阳性率都高于 B 组和 C 组，三组间差异有统计学意义。
结论 血清 α-HBDH 和 CA125 水平在卵巢癌患者中表达都升高，其两者的联合检测对于卵巢癌的诊断具有参考意义。

PU-2104

血清脂蛋白（a）检测在肾脏疾病诊断中的应用

杨翌明
滨州医学院烟台附属医院

目的 诊断肾疾病的应用价值时，研究与血清脂蛋白(a)的水平的关系。
方法 制定病例组和健康组两组，在健康组的存在下，对比罗氏 702 全自动生化分析仪上测量出病例组患者的结果，最后得出结论。对象为在乳山市人民医院住院的肾脏疾病患者，共选取肾脏疾病病例 102 例，其中用 30 例肾病综合征组，40 例肾早期损害组以及 32 例尿毒症组作为研究的对象，另外选取 50 名经过健康查体的健康人作对照组与之对照。采用免疫透射比浊的方法进行检测血清脂蛋白(a)水平，分析肾脏疾病的病变程度和不同肾疾病患者血液中的 LP(a)水平的关系和 LP（a)在临床里的应用价值。
结果 肾病综合征组，尿毒症组和肾早期损害组的病人，与健康对照组的相比,他们血液里的 LP(a)水平升高,差异有统计学意义(P< 0.05);肾病综合征组的结果和尿毒症组测出的 LP(a)明显高于肾早期损害组，差异有统计学意义(P< 0.05)。
结论 检测脂蛋白(a)的水平在观察肾疾病患者病程发展上有重大意义，它水平可以作为肾脏疾病病变程度诊断的一项有效指标之一。

PU-2105

血清Ⅳ型胶原水平在结直肠癌肝转移中的应用价值

李佳、高佳、崔婵娟、崔巍
中国医学科学院肿瘤医院

目的 通过检测结直肠癌患者血清中Ⅳ型胶原的水平，探讨血清Ⅳ型胶原水平在结直肠癌肝转移中的应用价值。

方法 收集在中国医学科学院肿瘤医院就诊的 220 例结直肠癌患者(其中发生肝转移的 145 例，未发生肝转移的 75 例)以及 80 例健康体检人群的血清样本，检测血清中Ⅳ型胶原的水平，检测方法为乳胶免疫比浊法。

结果 结直肠癌组血清Ⅳ型胶原水平明显高于健康对照组($p<0.05$)，结直肠癌肝转移组血清Ⅳ型胶原水平明显高于结直肠癌组($p<0.05$)和健康对照组($p<0.05$)。结直肠癌肝转移组治疗前血清Ⅳ型胶原水平明显高于结直肠癌组($p<0.05$)。结直肠癌肝转移组治疗后患者与治疗前患者相比，血清Ⅳ型胶原水平明显降低($p<0.05$)。经历肝转移瘤切除术的结直肠癌肝转移患者，术后 30 天内的血清Ⅳ型胶原水平明显高于术后 30 天以上($p<0.05$)。

结论 血清Ⅳ型胶原水平在结直肠癌肝转移患者的辅助诊断及治疗监测方面具有一定的应用价值，可以作为结直肠癌患者治疗监测的检测指标之一。

PU-2106

血浆 D-二聚体、血清 LDL-C、Non-HDL-C、HDL-C、TG、TC 的联合检测在 2 型糖尿病患者合并冠状动脉粥样硬化性心脏病时的临床价值

李丽莉、邓德耀、薛云松、李宜铮、顾津伊
云南大学附属医院

目的 对 2 型糖尿病患者合并冠状动脉粥样硬化性心脏病时进行 D-二聚体、LDL-C、Non-HDL-C、HDL-C、TG、TC 等指标检测，分析检测结果的临床价值，为临床诊疗提供客观依据。

方法 收集我院 2017 年 3 月至 2020 年 9 月心血管内科收治住院的 180 名 2 型糖尿病合并冠状动脉粥样硬化性心脏病的患者为观察组，根据糖化血红蛋白结果分为Ⅰ组（HbA1c<7.0%）86 例，Ⅱ组（HbA1c>7.0%）94 例，再择同期健康体检人群 80 例作为对照组。比较观察组、对照组、以及观察组中组间的 D-二聚体、LDL-C、Non-HDL-C、HDL-C、TG、TC 等各项指标检测结果。

结果 观察组 D-二聚体、LDL-C、Non-HDL-C、TG、TC 等检测指标结果均高于对照组（P<0.05），而 HDL-C 结果则低于对照组（P<0.05），差异有统计学意义；观察组组间比较 D-二聚体、LDL-C、Non-HDL-C、TG、TC 等检测指标结果，Ⅱ组高于Ⅰ组（P<0.05），而 HDL-C 结果则是Ⅰ组高于Ⅱ组（P<0.05），差异有统计学意义。

结论 2 型糖尿病患者合并冠状动脉粥样硬化性心脏病时可联合检测 D-二聚体、LDL-C、Non-HDL-C、HDL-C、TG、TC 等指标，对临床诊疗有重要价值。

PU-2107

Identification of the miRNA signature and key genes in colorectal cancer lymph node metastasis

Haifang Zhang、Hong Du
Department of Clinical Laboratory, The Second Affiliated Hospital of Soochow University, Suzhou, Jiangsu, 215004, China.

Background Because its metastasis to the lymph nodes are closely related to poor prognosis, miRNAs and mRNAs can serve as biomarkers for the diagnosis, prognosis, and therapy of colorectal cancer (CRC). This study aimed to identify novel gene signatures in the lymph node metastasis of CRC.

Methods GSE56350, GSE70574 and GSE95109 datasets were downloaded from the Gene Expression Omnibus (GEO) database, while data from 569 colorectal cancer cases were also downloaded from The Cancer Genome Atlas (TCGA) database. Differentially expressed miRNAs (DE-miRNAs) were calculated using R, while gene ontology and enrichment analysis of target mRNAs were performed using FunRich. Furthermore, the mRNA-miRNA network was constructed using Cytoscape. Gene expression levels were verified using the GEO datasets. Similarly, quantitative real-time PCR (qPCR) was used to examine expression profiles from 40 paired non-metastatic and metastatic lymph node tissue samples obtained from patients with CRC.
Results In total, five DE-miRNAs were selected, and 34 mRNAs were identified after filtering the Results Moreover, two key miRNAs (hsa-miR-99a, has-miR-100) and one gene (heparan sulfate-glucosamine 3-sulfotransferase 2 [HS3ST2]). The GEO datasets analysis and qPCR results showed that the expression of key miRNA and genes were consistent with that obtained from the bioinformatic analysis. A novel miRNA-mRNA network capable of predicting the prognosis and confirmed experimentally, hsa-miR-99a-HS3ST2-has-miR-100, was found after expression analysis in metastasized lymph node tissue from CRC samples.
Conclusions In summary, miRNAs and genes with potential as biomarkers were found and a novel miRNA-mRNA network was established for CRC lymph node metastasis by systematic bioinformatic analysis and experimental validation. This network may be used as a potential biomarker in the development of lymph node metastatic CRC.

PU-2108

肾病综合征患者血清 25 羟基维生素 D 的测定及相关因素分析

龚慧、林冰纯、李一凡、杜冀晖、罗迪贤
华中科技大学协和深圳医院

目的 分析肾病综合征（Nephrotic Syndrome，NS）患者血清 25 羟维生素 D（ 25-hydroxyvitamin D，25 (OH) D ）的水平及其与相关临床检验指标、NS 病理分型之间相关性，以探究 25 羟维生素 D 在肾病综合征发生发展和治疗过程中的临床意义。
方法 收集患者临床资料及相关临床检验指标（其中健康对照者 80 例，初次确诊为 NS 患者 155 例）。应用 SPSS19.0 统计软件回顾性分析比较两组间 25 羟维生素 D 均值的差异性。分析 25 羟维生素 D 与相关临床检验指标的相关性，再以 25 羟维生素 D 水平的中位数划分为高值组和低值组，分析两组间相关指标差异，并分析不同病理类型及临床分期的患者 25 羟维生素 D 水平的差异。
结果 NS 患者的平均 25 羟维生素 D 水平显著低于健康组患者（P<0.05）。25 羟维生素 D 与血清总蛋白、白蛋白、估算肾小球滤过率均呈正相关，与 24 小时尿蛋白、血清肌酐、甘油三酯均呈负相关。25 羟维生素 D 低值组的总蛋白、白蛋白、估算肾小球滤过率均显著低于高值组，24 小时尿蛋白显著高于高值组。四种不同 NS 病理类型患者的 25 羟维生素 D 水平比较并无统计学差异（P>0.05）。而在膜性肾病不同分期中，相对于Ⅰ期患者，Ⅱ、Ⅲ期患者的 25 羟维生素 D 显著下降（P<0.05）。
结论 25 羟维生素 D 水平与肾病综合征密切相关，25 羟维生素 D 有望用于肾病综合征患者的病情监测、预后评估和临床治疗。

PU-2109

VITROS 5600 全自动生化免疫分析仪性能验证

王参军
东南大学附属中大医院

目的 从准确度、精密度、线性范围、临床可报告范围及比对试验对奥森多 VITROS 5600 全自动生化免疫分析仪检测的 20 个项目进行性能验证。
方法 依据 CNAS-CL02：2012《医学实验室质量和能力认可准则》和 CNAS-GL037：2019《临床化学定量检验程序性能验证指南》,使用奥森多 VITROS 5600 全自动生化免疫分析仪原装配套试剂及校准品，从准确度、精密度、线性范围、临床可报告范围及比对试验对 20 个项目进行性能验证。
结果 奥森多 VITROS 5600 全自动生化免疫分析仪检测 20 个生化项目的 2 个质控水平的准确度验证偏倚均小于 1/2TEa，表明该仪器检测结果准确。批内精密度均小于 1/4TEa，批间精密度均小于 1/3TEa，表明仪器检测结果重复性良好。20 个生化项目的回归方程 a 值均在 1.00±0.05 范围内，相关系数 r≥0.975，表明仪器线性范围良好。本研究针对临床不同项目高值的需要，选用仪器线性范围内的高值患者标本及其相应的稀释液进行不同稀释倍数的验证。临床可报告范围可报告范围验证结果 20 个生化项目的 R＜1/2TEa，表明该仪器稀释后的结果准确可靠。选择 20 份体检合格的健康人标本,在检测系统上进行测定,对结果进行统计并对仪器说明书提供的参考区间进行验证,结果显示参考区间验证通过率均≥90%,验证通过;比对试验中各项目相对偏倚小于实验室允许的偏倚或相对偏倚验证值,比对试验通过。
结论 奥森多 VITROS 5600 全自动生化免疫分析仪检测项目的准确度、精密度、线性范围、临床可报告范围及比对试验均验证通过，完全能够满足临床应用的需求。

PU-2110

The association between hyperuricemia and obesity phenotypes in Chinese General Population: A retrospective analysis

Haoneng Tang、Xiaojing Feng、Huiqi Xie、Yanyi Yang、Lingli Tang
Department of Laboratory Medicine，The Second Xiangya Hospital，Central South University

Purpose Obesity has been related to many chronic metabolic diseases, and may be influenced by several inflammation factors, including uric acid. This retrospective study investigated relationship between serum uric acid and the metabolic phenotypes of obesity.
Methods The demographic, hematological and biochemical data were collected for 11,922 patients undergoing routine physical examination and 7463 participants were enrolled in our study. Participants were classified into four obesity phenotypes according to their BMI and the presence of metabolic syndrome: metabolically healthy overweighted/obese (MHOO), metabolically healthy and normal weighted (MHNW), metabolically abnormal overweighted/obese (MAOO) and metabolically abnormal but normal weighted (MANW). Univariate and multivariate linear regression analyses, stratified analyses and interaction analyses, and multiple logistic regression were conducted to analyze the relationship between serum uric acid and obesity phenotypes.
Results The prevalence of MAOO and MHOO phenotype were significantly higher ($p<0.001$) among hyperuricemia subjects (41.39% vs 18.66%; 22.81% vs 17.39%, $p<0.001$), while the percentage of MHNW were significantly lower(22.23% vs 50.20%, $p<0.001$). However, the prevalence of MANW phenotype was similar between subjects with hyperuricemia and those with normal uric acid level. Multivariable logistic regression analysis showed that hyperuricemia was positively associated with MHOO, MANW and MAOO phenotype relative to MANW. After

adjusting for the co-variants, the odds ratios (OR) for individuals with hyperuricemia to be MHOO, MANW and MAOO phenotype were 2.14(1.71-2.67), 1.63 (1.23-2.15) and 3.19(2.54-4.01) respectively. The ORs for having MHOO, MANW and MAOO increases 6% [OR: 1.06(1.05-1.08), P<0.0001], 4% [OR:1.04(1.02-1.05), P<0.0001] and 10%[OR:1.10(1.09-1.12), P<0.0001] for each 10 unit of increase in serum uric acid level. Stratification analysis as well as interaction test showed that sex and age did not interfere with the association of hyperuricemia and each obesity phenotype.Among the components of metabolic syndrome, hyperuricemia was positively associated with increased BMI [OR: 1.84 (1.55–2.19), P <0.0001]. After adjusting for other co-variants hyperuricemia had no significant association with hyperglycemia and decreased HDL-C (all P >0.05) while hypertension [OR: 1.20 (1.02-1.41), P=0.0023] and hypertriglyceride[OR: 1.41 (1.11-1.80), P=0.0052] was positively associated with hyperuricemia.

Conclusions In our study, we discovered that hyperuricemia was positively associated with MHOO, MANW and MAOO phenotypes. The increase in serum uric acid level also positively correlated with these obesity phenotypes. Sex and age did not significantly modify this relationship. To sum up, our research provided evidence on the important role of uric acid for the different metabolic status among both obese and non-obese subjects.

PU-2111

双胎妊娠合并甲状腺功能减退症的研究进展

韦金伶
柳州市妇幼保健院

妊娠期合并甲状腺功能减退症会增加母体及不良妊娠结局风险，如贫血、妊娠期高血压、妊娠期糖尿病、流产、早产、胎儿生长发育迟缓、死胎和新生儿神经发育畸形等。目前的研究多是单胎妊娠合并甲减，关于双胎妊娠合并甲减的相对较少。随着国内辅助生殖技术的不断提高，双胎妊娠的发生率逐年上升。通过检索涉及双胎妊娠合并甲状腺功能减退症的病因及发病机制、母婴结局、甲状腺功能指标参考区间的建立等相关文献，综合分析后，得出结论双胎妊娠孕妇有较高的甲减发生率，主要病因有桥本氏甲状腺炎、糖尿病等。妊娠期甲状腺功能减退会影响妊娠结局与新生儿预后，增加产科并发症的发生率。双胎妊娠孕妇的促甲状腺激素（TSH）孕期变化趋势与单胎相同，但双胎孕妇 TSH 水平更低以及持续时间更长。若使用基于单胎孕妇所建立的甲状腺功能参考范围来评估双胎孕妇的甲状腺功能状态，会增加甲减的漏诊率。建立双胎孕妇各妊娠期甲状腺功能筛查指标的参考范围显得尤为重要，以期能早期筛查出双胎妊娠孕妇甲状腺功能减退症患者，及时控制孕妇甲状腺激素水平，改善母婴结局。

PU-2112

Structural basis for the recognition of MucA by MucB and AlgU in Pseudomonas aeruginosa

Shanshan Li
The First Affiliated Hospital of Zhengzhou University

Alginate production in Pseudomonas aeruginosa is regulated by the alter-nater factor AlgU,which in turn is regulated by the MucABCD system.The anti-sigma factor MucA binds AlgU in the cytoplasm and prevents AlgU from binding to the RNA polymerase for transcription.MucB binds MucA in the periplasm and inhibits proteolysis of MucA and subsequent release of AlgU.In this work,we report crystal structures of MucA incomplex with AlgU and MucB. A structure of MucB alone reveals the structural changes required for MucA recognition. A unique disulfide bond is identi-fied in MucB, and mutation of this disulfide bond results in a shift from monomer to MucB dimers or tetramers. As MucB tetramers have previ- ously been shown to be unable to bind

MucA, this suggests a redox-sensi-tive stress response mechanism in MucB.The AlgU–MucA structure reveals a conserved sigma factor/anti-sigma factor complex, but AlgU lacks a disul-fide bond conserved in many other sigma factors. Our structures reveal the molecular basis for MucA recognition by MucB in the periplasm and AlgU in the cytoplasm,thus providing an important step in understanding the mechanisms that regulate a key signal transduction pathway involved in P.aeruginosa pathogenesis.

PU-2113

脂血对生化检验结果的影响研究

王永涛
山东大学第二医院

目的 研究脂血对生化检验结果的影响，透彻分析不同程度脂血对常用生化检测指标（谷丙转氨酶、谷草转氨酶、总蛋白、白蛋白、前白蛋白、钾离子、钠离子）的干扰情况，以此发现生化检测的常见问题，对此进行分析以指导临床诊疗工作。
方法 脂血前后的标本至少 15 份，通过生化检测进行对比分析。使用本实验室罗氏 e702 全自动化分析仪进行检测。
结果 通过检测结果得出由于乳糜颗粒增多而引起脂浊脂血是对生化检测结果产生影响的关键因素，脂浊会干扰到生化检测常用的比色（谷丙转氨酶、谷草转氨酶、总蛋白、白蛋白）或比浊方法（前白蛋白）。另一方面，脂浊还会造成光线散射的问题，使血清的透光度降低，吸光度增加，最终使检测结果高于正常值。但对于离子选择性电极法检测的钾、钠离子的结果没有影响。
结论 脂血对部分生化检验结果影响有较大的影响，要想提高生化检测结果的准确率，就必须减少因人为原因而造成的影响。

PU-2114

为缩短标本 TAT 时间的实验室工作流程的研究

王永涛
山东大学第二医院

目的 通过从各方面优化生化流水线来缩短病人标本的 TAT 时间和减少标本采集的数量。
方法 随着实验室信息化和自动化的快速发展，对于大型医院来说，自动化流水线已经从“花瓶”转变为“实用品”和“必需品”。自动化流水线能够有效整合资源、加快检测速度、节省人力、缩短 TAT、减少生物危险、减少实验室差错等优点已经深入人心，越来越多的实验室即将或者已经购置了流水线系统，对它充满期望。然而，天下没有免费的午餐，要充分挖掘流水线的功能，使它发挥最大的功效，需要我们付出时间和努力。本文就山东大学第二医院临床生化科的生化免疫检测的优化进行简单阐述，并通过样本在实验室的 TAT 时间的缩短来证明优化的效果。1.检测项目的合理组合。2.实验室流程的改进。3.辅助设备的使用问题及解决。4.非线上仪器的使用。5.信息系统的问题及改进。6.多台仪器间标本的分配问题。7.线上离心和线下离心的合理搭配和使用。8.自动审核功能的建立和使用。比较优化前后实验室内的 TAT 时间和平均病人采血管数量。
结果 经过优化后，实验室内的 TAT 时间较大幅度的缩短，平均病人采血管数量也有所减少。
结论 检验科各类流水线越来越多，只有通过合理的优化，才能充分发挥其功能，从而更好地服务于临床和病人。

PU-2115

外周血白细胞参数及高敏 CRP 与非高龄妊娠晚期 GDM 孕妇发生不良妊娠结局的相关性研究

梅宇峰
武汉大学人民医院

目的 探讨外周血白细胞参数:白细胞总数 WBC、中性粒细胞数 NEU、淋巴细胞数 LYM、单核细胞数 MONO、中性粒淋巴细胞比值 NLR，及高敏 C 反应蛋白（hsCRP）与孕晚期妊娠糖尿病（GDM）发生不良妊娠结局相关性。
方法 选取 2017 年 8 月至 2020 年 9 月武汉大学附属人民医院确诊的 198 例非高龄妊娠糖尿病患者为实验对象，根据有无不良妊娠结局分为合并不良妊娠结局 GDM 组(GDM 组)和无不良妊娠结局 GDM 组（NGDM 组），用 logistic 回归模型评价指标与 GDM 不良妊娠结局的相关性。
结果 GDM 组外周血白细胞参数 WBC[8.42±0.23x109 比 8.73(7.03,10) x109]、NEU[6.15±0.21x109 比 6.43(5.1,7.33)x109]、LYM[1.51（1.19，1.74）x109 比 1.5（1.25，1.79）x109]、MONO[0.59±0.02x109 比 0.6±0.02x109]、NLR[4.07(3.14,5.14) 比 4.14(3.24,5.49)] 与 NGDM 组无明显差异，差异无统计学意义（P>0.05）; GDM 组 hsCRP[5.35(2.99,10.33)mg/L 比 2.51(1.3,4.59)mg/L]高于 NGDM 组，差异有统计学意义（P<0.05）。对 hsCRP 进行 logistic 回归结果显示：标准误:0.054，P 值<0.01，优势比（OR）：1.282，OR 的 95%CI：1.154~1.424。当 hsCRP 临界值为 3.39mg/L 时，约登指数最大 （95%CI ：0.680~0.816，标准误：0.035，P<0.01），此时 ROC 曲线下面积为 0.748，特异度为 0.656，灵敏度为 0.713。
结论 血清中高敏 CRP 与非高龄晚期 GDM 孕妇发生不良妊娠结局存在相关性，hsCRP 升高可能提示有不良妊娠结局。

PU-2116

糖化血红蛋白和空腹血糖筛查体检人群血糖状态的差异性分析

唐浩能、冯晓晶、杨燕贻、唐玲丽
中南大学湘雅二医院

目的 探讨糖化血红蛋白（HbA1c）和空腹血糖（FPG）在体检人群中筛查糖代谢异常的一致性并分析导致两种指标定义血糖状态不一致的影响因素。
方法 本研究为横断面研究，收集 2019 年 1 月至 12 月在中南大学湘雅二医院健康管理中心进行健康体检的 11 922 名体检者的一般资料、血常规、肝肾功能、糖代谢和脂代谢等指标。根据 HbA1c 和 FPG 两种指标，对其血糖状态进行分类，通过多因素 logistic 回归模型分析影响筛查结果不一致的主要因素。
结果 采用 HbA1c 筛查糖尿病和糖尿病前期的人群比例（分别为 8.13%，34.79%）均明显高于 FPG（分别为 4.70%，8.97%）（χ^2 值=2635.940；P<0.001），两种指标筛查糖代谢异常不一致的人群比例为 35.65%，并主要集中于 HbA1c 为 5.7%~6.0%且 FPG<5.6mmol/L 的人群，其次为 HbA1c 为 6.1%~6.4%且 FPG <5.6mmol/L 的人群,不一致人群比例在男性和女性中均随年龄的增加而增加。导致不一致现象的主要因素包括年长、超重或肥胖、低白蛋白血症、血脂紊乱和高尿酸血症等，其中 45 岁以上人群（OR=3.525, 95%CI: 3.216~3.863, P<0.001）相比 45 岁以下人群，超重（OR=1.474, 95%CI: 1.341~1.620, P<0.001）或肥胖人群（OR=1.856, 95%CI: 1.633~2.110, P<0.001）相比于体重正常人群，均更容易出现筛查不一致的现象。
结论 本研究表明采用 HbA1c 和 FPG 两种指标筛查体检人群糖代谢紊乱时存在差异，主要集中于 HbA1c 定义的糖尿病前期人群，且受到年龄、肥胖等多种因素影响。

PU-2117

Circular RNA circRNA_000203 aggravates cardiac hypertrophy and its role as novel circulating biomarker for heart failure

Hui Li
Guangdong Provincial People's Hospital

Objectives The present study aimed to investigate the effect of circRNA_000203 in cardiac hypertrophy and the potential clinical value involved.
Methods 1. The expression of circRNA_000203 in the Ang-II-induced myocardial hypertrophy mice and neonatal mouse ventricular cardiomyocytes (NMVCs) and its characteristics.
2. Study on the biological function of circRNA_000203 in cardiac hypertrophy in vitro and in vivo.
3. Clinical value of CircRNA_000203 as novel circulating biomarker for heart failure.
Results 1. Up-regulation of circRNA_000203 in the Ang-II-induced myocardial hypertrophy mice and NMVCs.
2. CircRNA_000203 enhances hypertrophy of NMVCs. Enforced expression of circRNA_000203 enhances cell size and expression of atrial natriuretic peptide (ANP) and β-myosin heavy chain (β-MHC) in NMVCs.
3. Overexpression of circRNA_000203 exacerbates Ang-II-induced cardiac hypertrophy in vivo.
In vivo, heart function was impaired and cardiac hypertrophy was aggravated in Ang-II-infused myocardium-specific circRNA_000203 transgenic mice (Tg-circ36167).
4. Up-regulation of circRNA_000203 in the cardiac tissue and peripheral blood plasma of patients with heart failure.
Conclusions Our data demonstrated that circRNA_000203 exacerbates cardiac hypertrophy and the clinical translational value of circRNA_000203 as biomarkers for early diagnosis and prognosis of heart failure.

PU-2118

蛋白质组学在肝细胞癌诊断研究中的进展

黄强
郴州市第一人民医院

近几年研究发现，对于肝细胞癌（hepatocellularcarcinoma,HCC）进行蛋白质组学的研究有利于发现能够更早期、更直接、更准确地反映 HCC 临床分期病情的蛋白质类肿瘤标志物或者蛋白质组模式。笔者分别从血清、组织两方面阐述本领域的最新研究进展。

PU-2119

2 型糖尿病患者估算肾小球滤过率与糖尿病视网膜病变的相关性研究

陶俊
武汉大学人民医院

目的 探讨 2 型糖尿病患者估算肾小球滤过率（eGFR）与糖尿病视网膜病变(DR)的相关性。
方法 2018 年 10 月至 2019 年 4 月在武汉大学人民医院收治的 204 例 2 型糖尿病患者，根据其是否并发糖尿病视网膜病变，将其分为无视网膜病变（NDR）组 88 例，视网膜病变（DR）组 116

例。比较分析各组间预估肾小球滤过率（eGFR）、糖化血红蛋白（HbA1c）、空腹血糖（FPG）、谷丙转氨酶（ALT）、谷草转氨酶（AST）、碱性磷酸酶（ALP）、总蛋白（TP）、白蛋白(ALB)、尿素（urea）、肌酐（Scr）、尿酸(UA)、总胆固醇（TC）、甘油三酯（TG）、低密度脂蛋白胆固醇（LDL-C）、高密度脂蛋白胆固醇（HDL-C）、收缩压（SBP）、舒张压（DBP）水平的差异以及 eGFR 与上述指标的相关性。
结果 与 NDR 组比较，DR 组 HbA1c、urea、Scr、UA、SBP 水平显著升高，ALB、eGFR 水平显著降低，差异均有统计学意义（P<0.05）。Spearman 相关性分析显示，eGFR 与年龄(rs=-0.422)、HbA1c(rs=-0.336)、urea(rs=-0.441)、Scr(rs=-0.733)、UA(rs=-0.348)、SBP(rs=-01.90)呈显著的负相关（P<0.05）。多因素非条件 Logistic 回归分析显示 eGFR、HbA1c、ALB、urea、UA 是 DR 发生的危险因素（P<0.05）。
结论 DR 患者 eGFR 水平显著降低。

PU-2120

2 型糖尿病患者血清糖化白蛋白/白蛋白与肝功、肾功、血糖、血脂、血压的相关性分析

陶俊、李艳
武汉大学人民医院

目的 探讨 2 型糖尿病患者血清糖化白蛋白与肝功、肾功、血脂、血糖的相关性。
方法 2019 年 3 月至 2019 年 7 月在武汉大学人民医院收治的 193 例 2 型糖尿病患者，按其糖化白蛋白/白蛋白（GA/ALB）是否高于 0.17 分为组分为 GA 异常组 135 例和正常组 58 例，。比较分析两组间空腹血糖（FPG）、糖化血红蛋白（HbA1c）、C 肽（CP）、谷丙转氨酶（ALT）、谷草转氨酶（AST）、碱性磷酸酶（ALP）、总蛋白（TP）、尿素（urea）、肌酐（Scr）、尿酸(UA)、预估肾小球滤过率（eGFR）、总胆固醇（TC）、甘油三酯（TG）、低密度脂蛋白胆固醇（LDL-C）、高密度脂蛋白胆固醇（HDL-C）、收缩压（SBP）、舒张压（DBP）水平的差异以及 GA/ALB 与上述指标的相关性。
结果 GA 异常组 FPG、HbA1c、ALP 水平显著高于 GA 正常组，CP、TP、UA 水平显著低于 GA 正常组，两组间差异有统计学意义（P<0.05）。相关性分析显示，GA/ALB 与 FPG、HbA1c、ALP 呈显著的正相关（P<0.01）,与 CP、UA 呈显著的负相关（P<0.01）。
结论 2 型糖尿病患者 GA/ALB 异常者血清 FPG、HbA1c、ALP 水平增高，CP、TP、 UA 水平降低。

PU-2121

血清胆碱酯酶、总胆汁酸检测在肝脏疾病诊断中的作用分析

周宏
昆明市中医医院

目的 观察血清胆碱酯酶、总胆汁酸检测在肝脏疾病诊断中的作用。
方法 我院 2019 年 2 月-2020 年 2 月收治的 32 例肝脏疾病确诊患者（即为观察组）以及同期入院行常规体检的 62 例个体（即为对照组）为本次研究对象，比较两组血清胆碱酯酶、总胆汁酸检测结果。
结果 观察组血清胆碱酯酶低于对照组、总胆汁酸检测结果高于对照组,数据差异明显（P<0.05）。
结论 肝脏疾病患者肝功能可出现不同程度的损伤，血清胆碱酯酶显著低于正常水平、总胆汁酸显著高于正常水平。

PU-2122

1454 名体检者血脂检测分析

赵若莲
昆明市中医医院

目的 调查区域内一般人群的血脂水平及其特点，为相关人群的血脂异常防治打下一定基础。
方法 对 1454 名体检者血脂水平进行检测，按性别和年龄分组进行分析。
结果 男性组 TG、TC、LDL 均高于女性组（P<0.01）。中老年组 TC、LDL_C 水平高于青年组（P<0.05）。
结论 本区域一般人群血脂水平逐年升高，男性高于女性，中老年高于青年，需加强重点人群的监测及健康指导。

PU-2123

减重手术前后患者肝肾功能和血脂水平变化研究

宋为娟
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨肥胖患者减重手术后一年内血清肝肾功能指标和血脂水平的变化。
方法 对江苏省人民医院 119 例实行减重手术的患者进行回顾性分析。采集患者术前、术后即刻及 1、3、6、12 个月静脉血，分别进行血清肝肾功能指标和血脂水平检测。
结果 术前血清 ALT、AST、ALP、GGT、TG 和 UA 水平与 BMI 呈正相关（r 值分别为 0.289、0.309、0.285、0.245、0.125 和 0.360，P < 0.05），HDL 水平与 BMI 呈负相关（r = -0.284，P < 0.05）。血清 ALT、AST、GGT、TG、UA 水平分别于术后不同时间显著下降（ALT：3 个月；AST：6 个月；GGT、TG、UA：1 个月），至术后 1 年，水平均明显低于术前（P < 0.0001）。HDL 水平于术后逐渐升高，6 个月时显著升高（P = 0.002）。
结论 BS 可在短期内改变多数生化指标，有效改善肥胖患者肝功能和降低血脂。

PU-2124

标本放置时间对凝血测定结果的影响

孙函丽
昆明市中医医院

目的 观察标本放置时间对凝血指标测定结果的影响。
方法 采集 10 例血液标本即时测定凝血指标，分别 2 h 和 4 h 后再测定凝血指标，与即时测定结果进行比较。
结果 室温 2 h 或 4 h 后测定结果与即时测定结果进行比较，凝血酶原时间结果缩短，而活化部分凝血活酶时间测定结果延长。
结论 为避免放置时间对测定结果的影响，凝血指标测定应在采血后 2 h 内完成。

PU-2125

用糖化血红蛋白作为糖尿病前期筛查指标的探讨

刘荣均
昆明市中医医院

对 2433 例糖化血红蛋白 HbA1c 检测结果进行回顾性分析，共检出糖尿病前期（PDM）病例共 471 例。其中以单纯糖耐量受损（IGT）占比最高，其次为空腹血糖受损（IFG）合并糖耐量受损，空腹血糖受损（IFG）占比最低。各类型糖尿病前期病例糖化血红蛋白均不同程度升高，尤其以空腹血糖受损合并糖耐量受损病例升高更为明显。糖化血红蛋白作为一种快速简便的检测项目，代替餐后 2 小时血糖作为对糖尿病的筛查指标，可提高糖尿病前期病例的诊断率，对糖尿病的防治有较大意义。

PU-2126

探讨重度脂血的凝血酶原时间检测的影响

李紫春
昆明市中医医院

目的 探讨重度脂血对凝血酶原时间的检测是否存在影响。
方法 从 2020 年 1 月至 2020 年 10 月中记录 10 列，因第一次采血未对饮食进行控制造成脂血，在检测凝血酶原时间时因结果异常导致需进行第二次采血复查，并在同一仪器 sysmes CS-5100 全自动血凝仪和相同试剂的条件下进行凝血酶原时间检测的患者结果进行分析对比。
结论 轻度脂血对凝血酶原时间的检测无太明显影响,而重度脂血对凝血酶原时间的检测存在明显的影响。

PU-2127

凝血检测前的质量控制

李曦
昆明市中医医院

目的 探讨凝血检测前对检验结果的影响因素。
方法 收集我院三个院区（东风院区、呈贡院区、关上院区）从检验科退回的溶血标本 20 份、血量不足标本 26 份、有凝块样本 12 份、认为有问题的标本 10 份, 对以上标本均进行患者的再次采血, 并将两组标本的检测结果进行比较。
结果 溶血、血量不足、已凝固等问题标本与重新采血后标本的 凝血酶原时间 PT、凝血酶时间 TT、活化部分凝血酶时间 APTT 检测结果均有统计学差异($P<0.05$) 。
结论 凝血检测项目对采血技术要求比较高, 应严格规范操作方法; 如出现溶血、血量不足、有凝块等样本, 均应及时重新采血, 以保证检测结果的准确性和可靠性。

PU-2128

肺心病患者测定血浆 B 型钠尿肽中的临床应用

李伟
昆明市中医医院

目的 探讨血浆中 B 型钠尿肽在肺心病患者中的应用。
方法 利用双抗体夹心法测定 57 例肺心病患者血浆中的 B 型钠尿肽的浓度，同时测定 50 例健康体检者为对照组。
结果 肺心病组的 B 型钠尿肽为 2435.33 ± 197.32ng/ml，正常对照组为 68.71 ±23. 11 ng/ 。肺心病组和对照组相比有显著性差异。
结论 B 型钠尿肽浓度的检测对肺心病的病情判断、疗效、以及预后具有重要的价值。

PU-2129

血清同型半胱氨酸、高密度脂蛋白胆固醇与失眠中医证型的关系

黄亚玫
昆明市中医医院

目的 探讨血清同型半胱氨酸（HCY）、高密度脂蛋白胆固醇（HDL-C）与失眠中医症型的关系。
方法 选择 2019 年 1 月 1 日至 2020 年 3 月 1 日昆明市中医医院治未病专科就诊的失眠患者 80 例，根据患者一般资料进行辨证分型。检测血清 HCY 和 HDL-C 水平。
结果 失眠常见的中医证型有痰热内扰证，阴虚火旺证，心脾两虚证，肝郁化火证。不同证型失眠患者血清 HCY、HDL-C 水平比较差异有统计学意义（P<0.05）。心脾两虚、肝郁化火型患者血清 HCY 水平高于阴虚火旺（P<0.05），痰热内扰型高于心脾两虚、肝郁化火型（P<0.05），痰热内扰型患者血清 HDL-C 水平低于阴火虚旺、肝郁化火组（P<0.05）心脾两虚组。失眠中医证型与 HCY，HDL-C 水平具有相关性。
结论 不同证型失眠患者血清 HCY、HDL-C 水平存在差异。

PU-2130

吸入性糖皮质激素药物布地奈德治疗 AECOPD 的研究进展

张毅、陈剑、周利、张继华
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

慢性阻塞性肺疾病（Chronic Obstructive Pulmonary Disease，COPD）是一种临床常见的呼吸系统多发病，其主要特征是持续的气道受限，且不完全可逆和持续性进行，因其高患病率和病死率受到世界各国的普遍重视[1]。COPD 急性加重（AECOPD）是一种以患者的呼吸道症状急性加重为特征的临床事件，需改变药物治疗方案[2]。AECOPD 是 COPD 的重要组成部分，COPD 患者长期反复的急性加重可导致病情进展，肺功能及生活质量的不断下降[3]。一项前瞻性研究证实了 AECOPD 患者的高住院费用、高病死率及高复发率[4]。而吸入糖皮质激素治疗 AECOPD 患者能有效缓解患者临床表现，改善检测指标[5,6]。该文综述了糖皮质激素在 COPD 急性加重时的应用进展，以期为 AECOPD 患者寻找安全有效的治疗方法提供理论依据。

PU-2131

蛋白酶与抗蛋白酶失衡在 COPD 中的研究进展

张毅、陈剑、周利、张继华
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

COPD 的主要特征为肺血管、肺实质、气道慢性炎症性病变。大量研究表明，引起 COPD 的致病因素主要有氧化应激和炎症，而蛋白酶与抗蛋白酶失衡也是其重要的发病机制。早有学术假说指出，蛋白酶（巨噬细胞与中细粒细胞生成）和抗蛋白酶（从血浆渗出）失衡能够造成 COPD 组织损伤，而且在 COPD 急性加重期还会表现出更加严重的失衡。蛋白酶能够将弹性蛋白以及其他蛋白结构（肺泡壁上）消化，其中，MMPs（matrix metallo proteinases）基质金属蛋白酶、NE（Neutrophil Elastase）中性粒细胞弹性蛋白酶等都比较重要；蛋白酶的这种作用会受到抗蛋白酶系统的对抗，其中，SLPI（secretory leucocyte protease inhibitor）分泌性白细胞蛋白酶抑制物、α1-AT（alpha-1 antitrypsin deficiency）α1 抗胰蛋白酶、TIMPs（tissue inhibitor of metallo proteinases）组织金属蛋白酶抑制物等比较重要。本文着重对 COPD 中蛋白酶与抗蛋白酶以及二者失衡相关的研究情况进行论述。

PU-2132

IL-35 通过诱导乳腺肿瘤微环境中淋巴细胞的转化促进肿瘤进展

刘佳、李宁
山东大学第二医院

乳腺肿瘤细胞及乳腺肿瘤微环境（Tumor microenvironment，TME）中的 Treg 均可表达和分泌免疫抑制性细胞因子 IL-35。乳腺肿瘤细胞分泌的 IL-35 可通过介导 T 细胞向 iTR35 细胞的转化。另一方面，IL-35 也可抑制 B 细胞的增殖，并介导 B 细胞转化为可分泌 IL-10 和 IL-35 的 Breg 细胞亚群，即 IL-35+Breg。本研究通过建立小鼠荷瘤模型，模拟高 IL-35 的肿瘤微环境，通过体内实验探索 IL-35 对乳腺 TME 中浸润淋巴细胞分化的诱导作用，以及 IL-35 对 TME 血管生成、肿瘤局部进展及远处转移的影响。结果显示，IL-35 可通过直接刺激肿瘤细胞增殖、诱导肿瘤局部免疫抑制性淋巴细胞的转化,以及间接促进肿瘤血管的生成,形成有利于肿瘤生长的微环境,为肿瘤细胞的发展和转移创造有利条件。

PU-2133

南京地区体检人群血糖水平分析

马亮、黎青
江苏省人民医院（南京医科大学第一附属医院）

目的 调查南京地区体检人群血糖水平的性别和年龄分布特征，了解本地区人群血糖水平的变化趋势，为糖尿病的防治提供参考。
方法 对 2021 年 1 至 4 月间前往本院进行常规体检的 8466 例体检者（男 6620 例，女 1846 例），通过己糖激酶法测得的空腹血糖结果进行分析。
结果 8466 名体检者空腹血糖均值为（5.41±1.45）mmol/L，结果不符合正态分布。男女均值分别为（5.48±1.52）mmol/L 和（5.14±1.09）mmol/L。高血糖（≥7.0mmol/L）检出率 6.7%，低血糖（＜3.9mmol/L） 检出率 0.38%。男性空腹血糖水平高于女性，差异有统计学意义（P＜0.05）。不同年龄组之间，小于 45 岁人群空腹血糖均值为（5.06±0.95）mmol/L，高血糖检出率 1.96%；45 至 60 岁人群空腹血糖均值为（5.74±1.74）mmol/L，高血糖检出率 11.08%；大于 60 岁人群空

腹血糖均值为（5.92±1.81）mmol/L，高血糖检出率 14.78%。大于 45 岁人群与小于 45 岁人群的空腹血糖水平间的差异有统计学意义（P＜0.05）。

结论 空腹血糖水平随年龄的增长呈升高趋势，高血糖的检出率也随年龄增加。建议定期检测血糖水平，并向不同年龄段人群有针对性的加强宣传教育，预防糖尿病的发生。

PU-2134

肌酐白蛋白比对重症急性胰腺炎的预后价值

陈颖、马亮
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨 CREA / ALB 对急性重症胰腺炎患者的预后价值。

方法 回顾性分析 2015 年 1 月至 2019 年 12 月南京医科大学附属第一医院 ICU 收治的 167 位急性重症胰腺炎患者。根据 30 天的预后，将急性重症胰腺炎患者分为 135 例生存组和 32 例院内死亡组。从生化结果中计算 CREA / ALB。记录两组急性生理和慢性健康评估 II（APACHE II）评分和顺序器官衰竭评估（SOFA）评分和 CREA / ALB 并进行比较。构建特征曲线（ROC），并绘制生存曲线以研究 CREA / ALB 对 SAP 患者的预后价值。

结果 生存组和院内死亡组之间的基线参数相当。院内死亡组的肌酐白蛋白比率， APACHE II 评分和 SOFA 评分显着高于存活组（P <0.05）。 CREA / ALB 分别与 APACHE II 评分和 SOFA 评分显着相关。CREA / ALB 的 ROC 曲线下面积（AUC）均大于 APACHE II 得分和 SOFA 得分。结果表明，CREA / ALB 对预测急性重症胰腺炎患者的死亡率具有更好的预后价值。曲线表明，CREA / ALB 预测非存活组患者的敏感性为 70.1％，特异性为 88.2％（AUC，0.831； 95％CI 0.658–0.843）。在多元逻辑回归分析中，CREA / ALB 可作为独立的危险因素来预测 SAP 患者的死亡率。此外，Kaplan–Meier 生存分析表示，当 CREA / ALB> 2.476 时，院内死亡率更高（p = 0.001）。

结论 院内死亡组 SAP 患者的 CREA / ALB 比存活组患者高。 CREA / ALB 与 APACHE II 和 SOFA 得分显着相关。 CREA / ALB 对 SAP 患者的预后价值高于 APACHE II 和 SOFA 评分，临床医生可以将其用于治疗 SAP 患者。

PU-2135

AMY、NLR、GP-2α 在急性胰腺炎病情评估中的价值及对预后的影响

陈印宜
南华大学附属第一医院

目的 探讨淀粉酶（AMY）、中性粒细胞/淋巴细胞比值（NLR）、糖蛋白-2α（GP-2α）在急性胰腺炎病情评估中的价值及对预后的影响。

方法 选取 92 例 AP 患者作为研究对象，根据严重程度不同分为 MAP 组（n=44）、MSAP 组（n=30）和 SAP 组（n=18）；同期选取 50 例健康体检者作为对照组，对比各组 AMY、NLR 和 GP-2α 差异，用 Pearson 相关分析 AMY 与 NLR 和 GP-2α 之间的关系；绘制受试者工作曲线（ROC）探讨 AMY、NLR 和 GP-2α 各单项指标及联合指标在 AP 病情评估中价值；用 COX 回归分析探讨 AMY、NLR 和 GP-2α 对 SAP 预后的影响。

结果 对照组、MAP 组、MSAP 组和 SAP 组四组 NLR、AMY 和 GP-2α 比较，差异有统计学意义（P<0.05）；其中 SAP 组高于 MSAP 组（P<0.05），MSAP 组高于 MAP 组（P<0.05），MAP 组高于对照组（P<0.05）。经 Pearson 相关分析，AMY 与 NLR 和 GP-2α 均呈明显正相关（P<0.001）。绘制 ROC 曲线发现，NLR 和 AMY 单项指标在鉴别 MAP 组、MSAP 组和 SAP 组时差异无统计学意义（P>0.05），而 GP-2α 单项指标可鉴别 MAP 组、MSAP 组和 SAP 组

（P<0.05）；联合检测均可鉴别 MAP 组、MSAP 组和 SAP 组（P<0.05），以 AMY+NLR+GP-2α 效果最佳，其灵敏度和特异度分别为 86.3%和 82.5%。经 COX 回归分析，AMY、NLR 和 GP-2α 升高，SAP 死亡风险增加(P<0.05)。
结论 AMY、NLR、GP-2α 在评估 AP 病情严重程度中具有一定价值，且可影响 SAP 患者预后。

PU-2136

“全时段采血”在妊娠早期甲状腺疾病诊断中的应用评价

宋宏庆、刘栋、周莉莉
陕西省铜川市人民医院

目的 评价“全时段采血”是否适用于本地区妊娠早期甲状腺疾病的筛查与诊断。
方法 选取铜川市人民医院 2017 年 6 月 1 日至 2020 年 10 月 31 日门诊检测甲状腺功能的妊娠早期女性共 6761 例。从 LIS 中根据采血时间排序分为 6 组：A 组（6:00-8:00）628 例、B 组（8:00-10:00）1722 例、C 组（10:00-12:00）1428 例、D 组（12:00-14:00）953 例、E 组（14:00-16:00）1399 例和 F 组（16:00-18:00）631 例，比较每组三碘甲状腺原氨酸(Triiodothyronine，T3)、甲状腺素（Tetraiodothyronine，T4）、游离三碘甲状腺原氨酸(Free triiodothyronine，FT3)、游离甲状腺素(Free thyroxine，FT4)和促甲状腺激素(Thyroid-stimulating hormone ，TSH)水平；比较每组妊娠期低甲状腺素血症、亚临床甲状腺功能减退、临床甲状腺功能减退和妊娠期甲状腺毒症的检出率。
结果 各组间 T3，T4，FT3，FT4 和 TSH 水平差异有统计学意义，P 均<0.05；各组间妊娠期单纯低甲状腺素血症和妊娠期亚临床甲减检出率差异有统计学意义，P 均<0.05；妊娠期临床甲减和妊娠期甲状腺毒症各组检出率无统计学差异（χ2 值分别为 5.447 和 0.741，P 均>0.05）。
结论 “全时段采血”模式不宜用于本地区妊娠早期甲状腺疾病的筛查与诊断。

PU-2137

血清铁蛋白影响新发 2 型糖尿病患者肾功能早期变化的研究

叶桂云
福建省南平市第一医院

目的 探讨血清铁蛋白(SF)水平影响新发 2 型糖尿病(T2DM)患者肾功能的早期变化。
方法 入选 2019 年 8 月至 2020 年 5 月就诊的新发 T2DM 患者 340 例，另选取同期体检的正常体检者 95 例为对照组。研究对象均进行一般情况调查，测量颈动脉内膜中层厚度(IMT)，检测血糖、糖化血红蛋白(HbA1c)、血清铁蛋白(SF)、载脂蛋白 B(ApoB)、载脂蛋白 A1(ApoA1)、尿白蛋白、肌酐(Crea)以及脂类项目等，计算 ApoB/A1、尿白蛋白/肌酐比值(UACR)。Pearson 相关分析法分析 SF 与各指标的相关性；多元逐步回归法分析 UACR 的主要影响因素。
结果 T2DM 的三酰甘油(TG)、高密度脂蛋白胆固醇(HDL-C)、ApoB/A1、空腹血糖(FPG)、餐后 2 小时血糖(2hPG)、HbA1c、IMT、SF、UACR 均显著高于正常对照组(P＜0.05)；Pearson 相关分析显示，SF 与 TG、HDL-C、FPG、2hPG、HbA1c、IMT、ApoB/A1、UACR 相关(P＜0.05)；多元逐步回归分析得出 SF 是 UACR 最强影响因素；治疗后的降糖药联合升铁调素药组 SF、UACR 均明显低于降糖药组(P＜0.05)。
结论 新发 T2DM 中 SF 水平影响肾功能的早期变化，是糖尿病并发症监测的重要项目。

PU-2138

同型半胱氨酸水平与动脉粥样硬化性心血管疾病的分析

王永辉
宝鸡高新医院

目的 探讨同型半胱氨酸水平检测在临床动脉粥样硬化诊断中的价值，以及同型半胱氨酸水平在不同类型动脉粥样硬化疾病中的差异。
方法 选取宝鸡高新人民医院心血管内科、外科 2019 年 1 月 1 日——2019 年 12 月 31 日，已出院确诊的动脉粥样硬化性心血管疾病患者 110 例，将其作为病例组，其中稳定型心绞痛 17 例，不稳定型心绞痛 39 例，心肌梗死 54 例。另外随机选取同时期来我院做健康体检的 110 例作为对照组。
结果 病例组和对照组在性别方面无统计学差异（P>0.05）；病例组与对照组在年龄方面具有统计学差异（P<0.05）；病例组较对照组同型半胱氨酸水平升高，差异有统计学意义（P<0.05）；心肌梗死组同型半胱氨酸水平高于不稳定型心绞痛（P<0.05），差异具有统计学意义；不稳定型心绞痛同型半胱氨酸水平高于稳定型心绞痛（P<0.05），差异具有统计学意义。
结论 同型半胱氨酸水平检测对临床动脉粥样硬化诊断具有一定的价值。高同型半胱氨酸水平对于动脉粥样硬化性心血管疾病的分类判别具有重要参考价值。

PU-2139

尿微量白蛋白与肌酐比值在 2 型糖尿病早期肾损伤中的临床意义

赵多祥
宝鸡高新医院

目的 探讨尿微量白蛋白与肌酐比值在诊断糖尿病早期肾损伤的临床意义。
方法 选取 2019 年 1 月-12 月宝鸡高新人民医院内分泌科 2 型糖尿病患者 95 例，按照尿蛋白定性分为尿蛋白阳性组和尿蛋白阴性组，同期健康体检者 30 例做为对照组，应用日立 LABOSPECT 008AS 型全自动生化分析仪测定其尿微量白蛋白（Malb）与肌酐（Cr），并计算尿微量白蛋白与肌酐比值（Malb/Cr），进行统计学处理。
结果 糖尿病患者 Malb/Cr 的值明显高于健康人群，尿蛋白阳性组的 Malb/Cr 的值也高于尿蛋白阴性组的值，三组分别比较差异均具有统计学意义（P<0.001）。
结论 Malb/Cr 的升高提示早期肾损伤，可以作为发现尿蛋白阴性的早期糖尿病肾病患者的一项敏感而可靠地诊断指标，值得临床推广应用。

PU-2140

用霍乱弧菌二核苷酸环化酶高效制备克级别的 c-di-AMP

吕云、孙启超
山东大学趵突泉校区

Purpose prepare c-di-AMP on a gram scale with Vibrio cholerae dinucleotide cyclase DncV
Methods The method mainly includes four steps: preparation of DncV-immobilized resin, enzymatic synthesis of c-di-AMP, purification using macroporous absorption resin SP207, and desiccation using rotary evaporation and lyophilization.
Results After purification, up to 1 g of the diammonium salt of c-di-AMP with weight purity of ≥98% was obtained as white powder.
Conclusion we report a practical and economical enzymatic method for gram-scale preparation of c-di-AMP using an immobilized Vibrio cholerae dinucleotide cyclase DncV.

PU-2141

福建省糖化血红蛋白一致性计划研究

戴婉如、黄建刚、陈发林
福建省立医院

目的 本文旨在福建省糖化血红蛋白室间质评的基础上，提升福建省参加实验室 HbA1c 检测结果的一致性。

方法 选定 1 家 NGSP Level Ⅰ级实验室（福建省立医院）和 2 家 SHGHP Level Ⅱ级实验室（福建医科大学附属协和医院；福建医科大学附属第一医院）组成定值检测系统，向参加实验室分发赋值的新鲜全血样本和校准品，比对各临床实验室 HbA1c 检测结果的一致性。

结果 三家定值实验室高水平和低水平全血标本的 HbA1c 检测结果总 CV 值分别为 0.59%和 1.06%；参加实验室校准前平均 CV 值为 2.24%，校准后平均 CV 值为 1.63%；FJGHP 通过率 2020 年和 2021 年分别为 81.58%和 89.74%；全血质控品的平均 CV 为 2.15%，干粉质控品的平均 CV 为 2.81%。

结论 该计划通过应用新鲜全血标本，进行不同检测系统的校准和比对，有效提高了福建省糖化血红蛋白 HbA1c 检测结果的一致性，提高了各实验室检测结果的可比性。

PU-2142

不同厂家试剂检测同型半胱氨酸的结果分析

彭晓建、缪丽华、黄颖琪、杨红英
昆明金域医学检验所有限公司

目的 探讨分析不同厂家试剂在同型半胱氨酸检测中的应用,并对检测结果进行比较。

方法 2021 年 1 月随机挑选样本 70 例，分别以罗氏和迈克试剂对同型半胱氨酸进行检测，比较分析不同检测方法以及不同年龄标本所获得检测结果的差异。

结果 罗氏和迈克对血清同型半胱氨酸检测结果差异无统计学意义(P＞0.05)，但对于年龄大于 60 岁的受检者，两个厂家的参考值有所不同，其血清同型半胱氨酸水平的差异具有统计学意义(P＜0.05)。

结论 不同厂家试剂对同型半胱氨酸的检测结果无明显影响。但对年龄大于 60 岁的受检者其检测结果的阴阳性判断不同，罗氏试剂应制定相应的参考值。

PU-2143

冠心病患者血清同型半胱氨酸和脂蛋白相关磷脂酶 A2 的水平变化及临床意义

王参军
东南大学附属中大医院

目的 探讨血清同型半胱氨酸（Hcy）、脂蛋白相关磷脂酶 A2（LP-PLA2）检测对冠心病的诊断价值。

方法 选择 2018 年 01 月～2020 年 12 月本院收治的冠心病患者 240 例为观察组,其中 98 例急性心肌梗死患者（A 组）,75 例稳定型心绞痛患者（B 组）,67 例不稳定型心绞痛患者（C 组）;同时选取同期住院的无冠心病患者 160 例为对照组。分别检测各组患者的血清 Hcy、LP-PLA2 水平,并进行比较;对比单项指标与联合检测的阳性率,同时比较各组血清 Hcy、LP-PLA2 指标测定值范围。

结果 A、B、C 组单纯血清 Hcy、LP-PLA2 检测及联合检测阳性率均高于对照组,差异有统计学意义（P<0.05）;A、C 组单纯血清 Hcy、LP-PLA2 检测及联合检测阳性率高于 B 组,差异有统计学意义（P<0.05）;A、B、C 组血清 Hcy、LP-PLA2 联合检测阳性率高于单纯血清 Hcy、LP-PLA2 检测,差异有统计学意义（P<0.05）;A 组血清 Hcy 水平高于 B 组、对照组,差异有统计学意义（P<0.05）;A、B、C 组 LP-PLA2 水平均高于对照组,差异有统计学意义（P<0.05）;B、C 组的 LP-PLA2 水平存在明显界线。Logistic 回归分析显示 Lp-PLA2>197 ng/ml、Hcy>17.5 μmol/L 是急性缺血性脑卒中发生的独立风险因素（P<0.05）。
结论 血清 Hcy、LP-PLA2 水平联合检测对冠心病诊断具有应用价值。

PU-2144

Assessment of serum a-hydroxybutyrate as an indicator of insulin resistance in patients with type 2 diabetes mellitus and non-alcoholic fatty liver disease

Ming Zong[1]、ZHONGGAN JIN[2]、SHANSHAN YU[1]、QI TAN[1]、LIEYING FAN[1]
1. Shanghai east hospital
2. 上海市临床检验中心

Objective Numerous studies have shown that insulin resistance (IR) is involved in the pathophysiology of metabolic disorders such as non-alcoholic fatty liver disease (NAFLD) and Type 2 Diabetes (T2DM). The a-hydroxybutyrate (α-HB) molecule is thought to be the most sensitive biological indicator that could distinguish IR subjects from insulin-sensitive subjects. The purpose of this study was to establish an ultra-high-performance liquid chromatography-tandem mass spectrometry (UHPLC-MS/MS) method for detecting α-HB in serum and to investigate its association with IR in T2DM and NAFLD.
Method Electrospray ionization (ESI) negative ion mode and multiple reaction monitoring (MRM) were used to detect serum α-HB. We evaluated the linearity, low limits of quantification, precision, and recovery of UHPLC-MS/MS. Serum samples were collected from 50 healthy controls, 72 T2DM subjects, and 100 NAFLD patients. Serum levels of α-HB, fasting serum insulin, and others were measured; a homeostasis model assessed insulin resistance (HOMA-IR).
Results The UHPLC-MS/MS method for measuring α-HB was performed with a run time of 4 min. It had a good linear relationship from 0.5 to 40 μg/mL (r = 0.9994); the limit of quantification was 0.5 μg/mL, and the within and between run precision values were less than 4.1% and 6.3%, respectively. The recovery ranged between 95.8% and 103.8%. We found that the serum α-HB levels in T2DM and NAFLD patients were significantly higher (P< 0.001) than the control group. For α-HB, the area under curve (AUC) was 0.737 with a 95% confidence interval (0.655, 0.819) in the diagnosis of NAFLD. The levels of serum α-HB were significantly different between patients with severity of NAFLD.
Conclusion A serum α-HB UHPLC-MS/MS detection method was established in this study. This simple and rapid method meets the needs of clinical detection and can evaluate IR in T2DM and NAFLD. Although additional studies are needed, our data suggest that the analysis of α-HB can be useful in the differentiation of NAFLD severity.

PU-2145

Externalized Histone H4: A Novel Target that Orchestrates Chronic Inflammation by Inducing Lytic Cell Death

Yao Zhang
The First People's Hospital of Changde City

Cardiovascular diseases (CVDs) such as hypertension, coronary artery disease (CAD), and atherosclerosis (AS), are characterized by lipid deposits (atheromatous plaque), thrombosis, inflammatory response, and smooth muscle cell (SMC) activation and death. Despite the common use of lipid-lowering medications, CVDs remain a serious global health issue due to the high mortality and morbidity rates. AS, one of the most frequent causes of cardiovascular morbidity, involves extensive inflammatory activity and remodeling of the vascular endothelium. Chronic inflammation is found to be an important patho-physiological factor in the global medical burden, possibly caused by non-programmed cell death. Chronic inflammation induces monocytes to adhere to activated endothelial cells, infiltrate into the subendothelial space of the arterial wall, and transform into macrophages. Foamy macrophages secrete various inflammatory cytokines that stimulate SMC proliferation and migration, thus leading to plaque rupture, forming atherosclerotic plaque.

PU-2146

Neu-P11 Reduces Rat's Intraocular Pressure in the Hypertensive Condition

Yao Zhang
The First People's Hospital of Changde City

In the search for new compounds to reduce intraocular pressure (IOP), with fewer side effects, we have found that Piromelatine (Neu-P11), a novel melatonin agonist, can reduce IOP being, therefore, interesting for the treatment of ocular hypertension and glaucoma. The objective of this study was to investigate effects of Neu-P11 on IOP in high intraocular pressure rats. Hypertension model was established by Trendelenburg position(prone -80° head down). Vehicle or different concentrations of Neu-P11or melatonin was administrated by local or systemic method for a week. IOP raised to 302.9% compared to normols in a hypertensive condition ($p<0.05$). The results showed that Neu-P11 was able to reduce IOP in a hypertensive condition by local and intraperitoneal administration. On local administration, Neu-P11 (100μM and 200μM) and melatonin(100μM) had no effect on MDA level, SOD and GSH-Px activities. However, on intraperitoneal administration, Neu-P11 (20mg/kg and 50mg/kg) as well as melatonin(10mg/kg) produced a decrease on MDA level and a increase on SOD and GSH-Px activities ($P<0.01$; Neu-P11 or Mel vs. control). Neu-P11 could effectively improve oxidative stress to reduce IOP on intraperitoneal administration. These results may suggest the use of this novel melatonin agonist for the treatment of those ocular conditions, which involve an abnormal raise of intraocular pressure.

PU-2147

Neu-P11 对眼内压的影响

张瑶
常德市第一人民医院

目的 研究 Neu-P11 对急性高眼压大鼠眼内压的影响及其相关机制。
方法 采用 Trendelenburg 卧位（头低脚高 80°位置）建立急性高眼压模型。建模后用不同浓度 Neu-P11/Mel 进行局部或全身给药。给药后水平位置休息 2 h，再次置于 Trendelenburg 卧位 45 min，放于平面后每小时测量一次眼内压，连续监测 6 小时，重复实验一周。连续给药一周后注射过量戊巴比妥处死 SD 大鼠，心脏取血检测急性高眼压大鼠血清中 MDA 含量、SOD 和 GSH-Px 活性；留取各组大鼠眼球常规组织学切片观察 SD 大鼠视网膜形态学变化；免疫组化检测 SD 大鼠视网膜 AQP4、GFAP 和 TNF-α 表达水平的变化。
结果 通过 Trendelenburg 卧位法，我们成功建立 SD 大鼠急性高眼压模型，与正常组相比，模型组大鼠眼内压值升高了约 202.9%（P < 0.01），且视网膜增厚，层次不清，相关蛋白 AQP4、GFAP 和 TNF-α 的表达呈强阳性。而经 Neu-P11/Mel 局部或腹腔注射治疗后，各项指标均有不同程度的改善。另外，Trendelenburg 卧位诱导大鼠氧化应激水平升高，经 Neu-P11/Mel 全身治疗可显著降低 SD 大鼠 MDA 含量，增加 SOD 和 GSH-Px 酶活性，而局部治疗无明显疗效。
结论 Neu-P11 有降低高眼压大鼠眼内压的作用，其机制可能与降低相关蛋白 AQP4、GFAP 和 TNF-α 的表达和抑制机体氧化应激水相关。

PU-2148

血清 TSH、超声与增强 CT 对甲状腺乳头癌及淋巴结转移的诊断价值

岳潇潇
中国医科大学附属盛京医院

目的 探讨血清 TSH 联合超声与增强 CT 对甲状腺乳头状癌，及其淋巴结转移的诊断价值，为甲状腺结节的治疗方案提供依据。
方法 调查 2018 年 1 月至 2020 年 10 月就诊于中国医科大学附属盛京医院并在普通外科病房进行甲状腺手术治疗的患者，收集患者的性别、年龄、病程等数据及术前甲状腺功能血清检测指标（包括 FT3、FT4、TSH、anti-TPO、anti-Tg）、甲状腺超声、颈部增强 CT 和术后病理等结果，排除不合格数据后得到良性结节 30 例和甲状腺乳头状癌 122 例，根据癌灶直径是否大于 1cm 及是否伴淋巴结转移，将乳头状癌病例细分为微小癌组（65 例）、非微小癌组（57 例）、淋巴结转移组（76 例）、非淋巴结转移组（46 例）。对数据进行整理，进行正态性检验后，再分析各组数据特征有无差别，将相关因素（P＜0.05）纳入 logistic 回归模型。并通过绘制 ROC 曲线比较 TSH、超声、增强 CT 单独应用及联合诊断的诊断效果。
结果 组间比较中，TSH、超声 TR 分级、超声最大淋巴结直径以及超声提示淋巴结异常为甲状腺乳头状癌的危险因素；超声最大结节直径的差异在非微小癌和微小癌中有统计学意义（P＜0.05）。结节数量、超声提示甲状腺异常是甲状腺乳头状癌转移的独立危险因素（P＜0.05）。超声、增强 CT 与它们联合诊断有无甲状腺癌淋巴结转移时 AUC 分别为 0.666、0.590、0.637、0.612，其中只有单独增强 CT 诊断时 P >0.05。
结论 TSH、超声 TR 分级对于判断结节性质有较好的诊断价值，但它们联合并不能增加诊断效果；甲状腺功能检测指标的水平与甲状腺乳头状癌病灶大小不相关,但超声最大结节直径可用于判断甲状腺乳头状癌病灶大小。甲状腺功能检测指标的水平与甲状腺乳头状癌是否有淋巴结转移不相关；

PU-2149

肾综合征出血热患者 α-淀粉酶、脂肪酶变换分析

郑秀丽
齐齐哈尔市第七医院(原:齐齐哈尔市传染病防治院)

目的 观察肾综合征出血热患者血清 α-淀粉酶、脂肪酶变化
方法 回顾性分析 2020 年 1 月 1 日至 2021 年 5 月 31 日确诊的 51 例肾综合征出血热住院病人检验数据。
样本 血清样本，避免溶血。
原理 汉坦病毒检测采用胶体金免疫层析技术，在玻璃纤维纸上预包被胶体金标记的汉坦病毒重组抗原（Au-NP-Ag），在硝酸纤维膜的检测线和对照线处分别包被抗人 IgGγ 链单克隆抗体、抗人 IgMμ 链单克隆抗体和兔抗汉坦病毒抗体。检测阳性标本时，血清中汉坦病毒抗体（IgG 或 IgM）与 Au-NP-Ag 结合形成复合物，由于层析作用复合物沿纸条向前移动，经过检测线时与预包被的抗人 IgGγ 链单克隆抗体或抗人 IgMμ 链单克隆抗体形成“Au-NP-Ag-汉坦病毒抗体-抗人 IgGγ（或抗人 IgMμ）-固相材料”夹心物而凝聚显色，游离金标抗原则在对照线处与兔抗汉坦病毒抗体结合显色。阴性标本仅对照线处显色。
α-淀粉酶与 α-葡萄糖苷酶偶联，水解特异性底物 4,6-亚乙基-4-硝基苯酚-α-庚糖，产生对-硝基苯酚，对-硝基苯酚生成速率与 α-淀粉酶的活性成正比，在 405nm 波长下用速率法检测。
1,2-邻-二月桂宗甘油-3-戊二酸-（6´-甲基试卤灵）-酯在脂肪酶/OH^-作用下生成 1,2-邻-二月桂宗甘油、戊二酸和 6´-甲基试卤灵，在 570nm 波长下，根据产物红色的甲基试卤灵生成速率测定脂肪酶的活性。
结果 住院肾综合征出血热 51 例患者 α-淀粉酶、脂肪酶均出现不同程度增高，通过每日检测血清样本，发现 α-淀粉酶、脂肪酶逐步增高，有的甚至可达到正常参考范围的 10 倍以上，经过对症治疗，再逐步下降直至正常。
结论 通过回顾性分析，肾综合征出血热患者随着病情进展，α-淀粉酶、脂肪酶出现增高现象，α-淀粉酶、脂肪酶是胰腺疾病监测的重要项目，监测 α-淀粉酶、脂肪酶可以及时发现肾综合征出血热病人是否合并胰腺疾病，及时进行有效治疗。

PU-2150

UPLC-MS-MS 同时检测人血清中 5-羟色胺和褪黑素水平及性能验证

戴锦娜
中国医科大学附属第一医院

目的 5-羟色胺和褪黑素作为人体内重要的吲哚胺类神经递质，具有调节生物节律、情绪、认知、清除自由基、促进炎信号传导等多种生物活性，同时还对骨代谢有着重要的影响。本研究采用 UPLC-MS/MS 法建立人血清中 5-羟色胺和褪黑素的定量检测方法并进行方法学验证，为考察人体中 5-羟色胺和褪黑素水平与骨质疏松症状的相关性奠定基础。。
方法 以 5-羟色胺-d4 和褪黑素-d4 为内标，采用 SCIEX 6500 QTRAP 超高效液相色谱串联质谱仪建立血清中 5-羟色胺和褪黑素的 LC-MS/MS 方法，采用 Waters BEH C18 (2.1×100 mm, 1.7μm) 色谱柱，柱温 40℃，梯度洗脱，进样量为 2 微升，前处理采用液液萃取法，并自制高、中、低质控品进行方法学验证，包括特异性、基质效应、精密度、准确度、分析测量范围等。
结果 5-羟色胺和褪黑素的分析测量范围分别为：1ng/ml~500ng/ml、0.001ng/ml~0.5ng/ml，线性关系良好；采用加标回收率试验评估方法的准确性，结果显示，5-羟色胺和褪黑素的加标回收率在

97.45%-108.06%之间，其批内、批间精密度分别为 0.75%~3.00%、1.57%~2.86%。收集了绝经期骨质酥松妇女患者 80 例，对其血清 5-羟色胺和褪黑素进行检测。
结论 本研究建立了 ID-UPLC-MS/MS 同时测定人体血清中 5-羟色胺和褪黑素的方法。血清用量少（仅需 200 μL），前处理简单，且一针分析多种物质只需 3.5 分钟，简单快速。利用超高效液相色谱串联质谱技术检测血清中 5-羟色胺和褪黑素浓度，可以通过外周 5-羟色胺和褪黑素水平来反应人体骨量和骨结构变化，为临床诊治提供科学依据。

PU-2151

转录因子 Twist 1 和 PPARγ 在 3T3-L1 脂肪细胞中可能的基因调控关系

任瑞
山东大学第二医院

背景 过氧化物酶体增殖物激活受体 γ（PPARγ）是调节机体脂肪细胞功能的重要基因。因此，研究 PPARγ 的分子调控机制有助于了解脂肪组织功能。Twist 1 是脂肪组织中另一个重要的功能基因，数百个基因受 Twist 1 调控。本研究的目的是探讨的 Twist 1 和 PPARγ 在 3T3-L1 脂肪细胞表达调控。
方法 体外诱导 3T3-L1 前脂肪细胞分化，检测 Twist 1 和 PPARγ 的表达变化。用 PPARγ 激动剂吡格列酮和 PPARγ 拮抗剂 T0070907 研究 PPARγ 对 Twist 1 表达的影响。此外，利用逆转录病毒干扰和过表达的 Twist 1 观察 Twist 1 对 PPARγ 表达的影响。
结果 在 3T3-L1 脂肪细胞诱导分化过程中，Twist 1 和 PPARγ 表达。PPARγ 激动剂（吡格列酮）或拮抗剂（T0070907）可影响 Twist 1 的表达，吡格列酮（1μm，24 h）作用下 Twist 1 上调，T0070907（100μM，24h）时 Twist 1 下调。此外，逆转录病毒干扰 Twist 1 下调 PPARγ 的蛋白质和 mRNA 的表达水平，而过表达 Twist 1 有截然相反效果。
结论 在 3T3-L1 脂肪细胞中，Twist 1 和 PPARγ 之间可能存在的调控关系。这调节联系增强 PPARγ 的调节，可能是 Twist 1 调节脂肪细胞生理病理的功能机制。

PU-2152

HPLC 法测定非那西丁和扑热息痛浓度评估肝脏储备功能

任瑞
山东大学第二医院

目的 对非那西丁和扑热息痛含量分析进行方法学研究，并进行应用性验证，以评估肝脏储备功能。
方法 建立高效液相色谱技术（HPLC）测定非那西丁与扑热息痛含量，进行标准曲线建立、精密度试验及方法回收率试验，并用健康血浆进行应用性验证。
结果 非那西丁与扑热息痛在浓度 0.8-40μg/ml 的范围内均呈现良好的线性关系；在 5、15、25μg/ml 的样品浓度下，非那西丁测定的日内精密度分别为 0.84、1.09 和 0.53，日间精密度分别为 1.51、1.10 和 1.38，回收率分别为 99.81%、100.09%和 99.75%。扑热息痛测定的日内精密度分别为 0.76、0.89 和 0.67，日间精密度分别为 1.02、1.46 和 1.21，回收率分别为 100.76%、99.19%和 100.97%。
结论 HPLC 分析方法简便快捷、灵敏度和准确度高，为评估肝脏储备功能提供了一种快捷、准确的方法。

PU-2153

Cystatin C level is associated with the recovery of renal function in cancer patients after onset of acute kidney injury

Rui Li
Laboratory of the Fifth People's Hospital of Shenyang

Purpose The objectiveis to study the prognostic value of cystatin C (Cys C) in cancer patients with AKI.
Methods According to the inclusion and exclusion criteria, cancer patients diagnosed and treated in the oncology department of Shenyang fifth hospital from April 2014 to March 2019 were included. The relationship between the baseline level of Cys C and the occurrence of AKI and the changes of renal function during the follow-up period after AKI was analyzed. The cancer patients with AKI were divided into two groups according to the changes of renal function during the follow-up period, the renal function recovery group and the non recovery group. The differences of baseline data between the two groups were compared, and the risk factors related to the non recovery of renal function were analyzed by logistic single factor and multi factor regression.
Results A total of 3127 patients were included. Among them, 659 cases (21.1%) had AKI and 2468 cases had no AKI. Among the patients with AKI, 473 cases recovered, 186 cases did not. Univariate and multivariate logistic regression analysis showed that age (or = 1.133, 95% CI: 1.064-1.219), diabetes mellitus (or = 1.226, 95% CI: 1.093-1.385), chronic kidney disease (or = 1.347, 95% CI: 1.108-1.624), hematological malignancy (or = 1.174, 95% CI: 1.063-1.311), chemotherapy (or = 1.119, 95% CI: 1.055-1.304), systolic blood pressure (or = 1.108, 95% CI: 1.062-1.267), serum creatinine (or = 1.262, 95% CI: 1.063-1.311), chemotherapy (or = 1.119, 95% CI: 1.055-1.304), 95% CI: 1.105-1.446) and CysC (or = 1.416, 95% CI: 1.251-1.739) were associated with renal failure after AKI.
Conclusion Baseline CysC is associated with AKI in cancer patients, and with no recovery of renal function during follow-up.

PU-2154

住院病人低钙血症的病因分析

童开、张莹、虢瑾、刘家云
空军军医大学西京医院

目的 研究住院病人发生低钙血症的原因，为临床诊断和治疗提供依据。
方法 回顾性分析 2020 年 1 月至 2020 年 12 月空军军医大学第一附属医院住院患者中血钙水平小于 1.6mmol/L 患者的临床资料，共 342 例，分析患者的相关实验室指标，分析每位患者发生高钙血症的病因，按病因进行分类分析。
结果 342 例有低钙血症的住院患者中，肾功能衰竭 119 例（占 34%），甲状旁腺功能减退 43 例（占 12%），吸收不良维生素 D 代谢障碍 63 例（占 18%），恶性肿瘤 21 例（占 7%），其他 96 例（占 29%）各病因的患者间血钙水平比较，差异无统计学意义。
结论 低钙血症的主要原因为肾功能衰竭、甲状旁腺功能减退、维生素 D 缺乏、恶性肿瘤等。临床中应结合病史具体分析并采取正确的治疗方案。

PU-2155

西北地区健康人群胆固醇参考区间的初步探讨

童开、张莹、杨小云、虢瑾、刘家云
空军军医大学西京医院

目的 建立西北地区健康人群血清胆固醇(CHOL)的参考区间。
方法 参照 IFCC 多中心酶学研究参考人群筛选标准，募集 18－79 岁健康参考人群 722 人，其中男性 357 人和女性 365 人，分别用和光试剂检测系统和罗氏试剂检测系统建立西安地区健康人群胆固醇的参考区间。
结果 两个系统间检测结果无统计学意义（P=0.483>0.05）。农村与城市人群检测结果无差异（P=0.398>0.05）。各年龄段间结果有明显差异，18-29 岁与 30-39 岁两组检测结果间有显著差异（P=0）；30-39 岁与 40-49 岁两组检测结果间有显著差异（P=0）；40-49 岁与 50-59 岁两组检测结果间有显著差异（P=0）；50-59 岁与 60-79 岁两组检测结果间无统计学差异（P=0.116>0.05）。各年龄段间男性和女性结果无差异。
结论 西北地区健康人群胆固醇检测结果在两种检测方法间无显著差异，城市人群和农村人群间检测结果也无明显差异，不同年龄段间检测结果存在显著差异，男性和女性检测结果无差异。随着年龄的增长，胆固醇的检测结果逐渐增大。本次研究表明，西北地区胆固醇参考区间有所提高，本文实验结果高于目前我们临床所用的参考区间，高于我国血脂异常防治建议提出的合适水平。

PU-2156

西安地区健康人群胆碱酯酶参考区间的建立

童开、张莹、杨小云、刘家云
空军军医大学西京医院

目的 建立西安地区健康人群血清胆碱酯酶实验室参考区间。
方法 采用日立 7600 全自动生化分析仪进行检测，选择西安地区 1017 例健康体检人群，男 540 例、女 477 例，按照年龄及性别将健康人群分为男、女青年（18-39 岁）组，男、女中年（40-59 岁）组和男、女老年(60-79 岁)组。采用 SPSS18.0 统计软件对数据进行分析，绘制胆碱酯酶直方图，应用线性回归分析，计量资料组间比较采用 t 检验，对偏态分布数据用百分位数得出双侧 95%置信区间作为正常参考范围。
结果 西安地区健康人群胆碱酯酶参考值，按照性别分组为男性胆碱酯酶参考值 5500-13500 U/L；女性胆碱酯酶参考值 5500-12500 U/L。按照性别和年龄分组为男性青年 5500-13500 U/L、男性中年 6500-13500 U/L、男性老年 4500-10500 U/L；女性青年 5500-12500 U/L、女性中年 4500-12500 U/L、女性老年 4500-10500 U/L。
结论 西安市地区健康人群胆碱酯酶正常参考值为 5500-13500 U/L，男性和女性胆碱酯酶正常参考值分别为 5500-13500 U/L 和 5500-12500 U/L。每个地区的人群特点不同应建立适合本地区人群的正常参考值范围。

PU-2157

青年职业女性无症状高尿酸血症合并代谢性疾病的现状分析

单梦雅、蒋理
江苏省人民医院（南京医科大学第一附属医院）

目的 分析高尿酸血症（HUA）与血糖、血脂等代谢性共病及肾功能之间的关系，发现易患高尿酸及其相关的代谢性共病和肾功能异常的人群，讨论其控制血尿酸水平的重要性。
方法 选取 2020 年 5 月至 2021 年 4 月在我院参加体检的 20-44 岁青年职业女性共 29987 人，比较不同年龄段的高尿酸血症患病率；根据尿酸水平分组，比较不同等级尿酸水平者空腹血糖、总胆固醇、三酰甘油，高密度脂蛋白胆固醇（HDL-C）、低密度脂蛋白胆固醇（LDL-C）、血肌酐、血尿素异常的比例。
结果 无症状 HUA 总体患病率为 7.69%，20-24 岁年龄段患病率为 9.35%，25-29 岁年龄段患病率为 9.03%，30-34 岁年龄段患病率为 7.93%，35-39 岁年龄段患病率为 7.40%，40-44 岁年龄段患病率为 5.78%；在所有研究对象中随着尿酸水平升高，其合并空腹血糖、总胆固醇、三酰甘油、高密度脂蛋白胆固醇（HDL-C）、低密度脂蛋白胆固醇（IDL-C）、血肌酐、血尿素异常的比例增高。
结论 高尿酸血症 20-24 岁年龄段高尿酸血症患病率最高。在所有研究对象中随着血尿酸水平升高，其各分析指标异常比例升高，且其合并异常指标的组成成分越多，异常程度越严重；不仅是患有高尿酸血症的人需要提高警惕，血尿酸水平高于平均水平未达诊断 HUA 标准的人同样要足够重视其代谢异常及肾功能的风险已大大增加

PU-2158

血清神经丝轻链蛋白 NfL 在急性缺血性脑卒中诊疗中的临床应用价值

权文强、王旭、常文婧、孙祖俊、李冬
上海市同济医院(同济大学附属同济医院)

目的 检测急性缺血性脑卒中患者（Acute ischemic stroke，AIS)血清神经丝轻链蛋白 NfL（Neurofilament light，NfL）水平，探究其与血清总胆固醇（Total cholesterol，TC），甘油三酯（Triglyceride，TG），同型半胱氨酸（Homocysteine，HCY），葡萄糖（Glucose，GLU），降钙素原（Procalcitonin，PCT），C-反应蛋白（C-reaction protein，CRP）等指标的相关性，明确 NfL 在 AIS 诊疗中的临床价值。
方法 收集同济大学附属同济医院神经内科经明确诊断的急性缺血性脑卒中患者 111 例，同期健康体检者 50 例作为对照组。ELISA 法检测 AIS 患者和健康体检者血清 NfL 水平，比较两组间差异；检测患者 TC、TG、HCY、GLU、PCT、CRP 等血清学指标水平，观察血清 NfL 与血清学指标之间的相关性。比较不同严重程度（NIHSS 评分）分级的 AIS 患者血清 NfL 水平，同时绘制受试者工作特征曲线（ROC 曲线）评价其诊断效能。
结果 相对于健康对照组，AIS 患者组血清 NfL 水平明显升高，且差异具有统计学意义（$p<0.001$)；血清 NfL 水平与血清 PCT 和 CRP 水平呈明显正相关（$r=0.537$，$p<0.001$ 和 $r=0.376$，$p<0.001$），与血清 TC 水平呈轻度正相关（$r=0.265$，$p<0.01$）；不同严重程度的急性缺血性脑卒中患者中血清 NfL 表达水平存在明显差异（单因素 ANOVA；$F=8.467$，$p<0.001$）；血清 NfL 对于急性缺血性脑卒中诊断 ROC 曲线下面积（AUC）为 0.840，特异性和敏感度均优于 PCT（AUC=0.666）和 CRP（AUC=0.591）。
结论 血清 NfL 是较好的急性缺血性脑卒中的诊断标志物，且与 AIS 的严重程度相关，具有一定的临床诊疗应用前景。

PU-2159

心肌型脂肪酸结合蛋白的临床应用进展

任真、凌芸
江苏省人民医院（南京医科大学第一附属医院）

心肌型脂肪酸结合蛋白（H-FABP）是一种低分子量的可溶性蛋白，主要存在于心肌细胞胞浆中，具有组织特异度。H-FABP 作为诊断早期心肌缺血性疾病特别是急性心肌梗死（AMI）的生化标志物，近年来受到广泛关注。在这篇综述中，我们介绍了 H-FABP 的生物学特性、常用检测方法，以及 H-FABP 在急性冠脉综合征(ACS)、缺血再灌注损伤（ISI）、严重脓毒血症中的应用。

PU-2160

多种肿瘤标志物联合检测在肺癌诊断中的价值研究

季孝
丽水市中心医院

目的 探讨血清糖类抗原 125（CA125）、癌胚抗原（CEA）、细胞角蛋白 19（CYFRA21-1）、铁蛋白（FER）、神经元特异性烯醇化酶（NSE）、胃泌素释放前体（ProGRP）、鳞状细胞癌抗原（SCCA）联合检测在肺癌诊断中的价值。
方法 选择 2020 年 4 月-2021 年 4 月在我院住院的肺癌患者（肺癌组）283 例、同期肺部良性病变患者（良性对照组）306 例、健康体检者（健康组）37 例为研究对象，所有受拭者均行 CA125、CEA 、CYFRA21-1、FER 、NSE ProGRP、SCCA 电化学发光法检测，比较各组之间肿瘤标志物水平差异。用 Logistic 回归分析确定肺癌的独立预测因素，并组建联合检测组合。运用受试者工作特征曲线（ROC）及曲线下面积（AUC）评价单一肿瘤标志物及联合检测的诊断价值。
结果 ①肺癌组 CA125、CEA、CYFRA21-1、FER、NSE、SCCA 水平显著高于其它各组（均 P<0.05），Logistic 回归分析 CA125、CEA、CYFRA21-1、FER 是肺癌的独立预测指标。②4 种肿瘤生物标志物联合检测（CA125+CEA+CYFRA21-1+FER）诊断肺癌的 AUC 为 0.863，显著高于 CA125、CEA、CYFRA21-1、FER 单独诊断肺癌时的 AUC(分别为 0.703、0.739、0.742、0.778）（均 P<0.01）。③联合检测（CA125+CEA+CYFRA21-1+FER）诊断肺癌的敏感度、特异度（分别为 81.6、80.1)，均优于单一肿瘤标志物。
结论 CA125、CEA、CYFRA21-1、FER 可独立预测诊断肺癌,（CA125+CEA+CYFRA21-1+FER）联合检测可以有效提高对肺癌的诊断效能，对临床确立治疗方案有积极意义。

PU-2161

六西格玛质量管理方法在医学实验室中应用

牛爱军
山东大学第二医院

六西格玛（6σ）质量管理方法最早起源于美国摩托罗拉公司，之后广泛应用于企业管理中，并取得令人瞩目成绩，Nevalainen 等于二十世纪九十年代首次将六西格玛质量管理引入到实验室质量管理中，我国在 2000 年左右开始在医院管理领域进行应用，近年来随着 ISO15189 实验室认可工作的逐渐展开，越来越多的国内临床实验室将六西格玛管理方法应用到实验室的质量管理体系中，本研究应用六西格玛质量管理方法对我实验室中临床化学检测项目进行质量评价，计算各项目的西

格玛水平及质量目标指数，指导实验室的质量改进，为六西格玛质量管理方法在临床实验室的逐步推广应用提供实验数据支持。

PU-2162

生化危急值结果复检的符合性及必要性探讨

牛爱军
山东大学第二医院

目的 探讨生化危急值结果复检的符合性及必要性。
方法 对 330 份生化危急值标本的钾、钠、钙、葡萄糖等危急值结果进行复检，并计算复检结果与初检结果的偏倚及复检符合率，以偏倚（%）≤1/2 CLIA'88 或国家卫健委临检中心室间质评最大允许误差，作为判断危急值复检结果与初检结果是否一致的标准。
结果 330 份危急值标本中满足判断标准，即复检结果与初检结果一致的标本为 303 份，整体复检符合率为 91.8%，复检不一致标本为 27 份，均为低于危急值下限的极低值结果。
结论 生化危急值不符合结果主要集中在一些项目的极低值结果上，而极低值复检结果的存在的偏倚并不影响临床决策和治疗效果，因此复检并不能有效提高检测准确性，危急值结果复检并不都是必要的。

PU-2163

肿瘤标志物在不同检测系统间的应用现状及建议

牛爱军
山东大学第二医院

化学发光免疫分析（chemiluminescence immunoassay, CLIA ）是目前国内肿瘤标志物检测的主流方法，但由于不同检测系统间在针对抗原位点、抗体来源、包被方式以及发光原理等方面存在差异，导致肿瘤标志物在不同系统间的检测结果不尽相同。如何正确评价哪一种品牌设备更具有优势，目前尚缺乏统一判断标准，单纯将国产设备检测结果数值与进口品牌进行比对并不科学，也不客观。本文就目前主要进口设备及国产设备检测肿瘤标志物的现状及在不同检测系统间的方法学比对建议做一综述。

PU-2164

临床血脂生化检验中运用分级检验方法的检验效果观察

黄瑶楠
空军军医大学西京医院

目的 分级检验方法应用在血脂生化检验过程中，观察该种检验方法效果。
方法 将我科 2020 年 4 月--2020 年 8 月的血脂生化检验者 102 例作为观察对象，并且分成试验组与常规组，分别采用分级检验法和拉网式检验法，观察两种检验方法效果。
结果 （1）试验组和常规组 TC、TG、HDL-C 阳性率中，试验组分别是 54.90%、37.25%、14.70%，常规组分别是 53.92%、38.23%、15.68%，（x2=0.348,p=0.661），结果有差异。（2）试验组和常规组 LDL-C、Apo AI、Apo B 阳性率对照中，试验组分别是 75.49%、4.90%、48.03%，常规组分别是 50.00%、0.98%、19.60%，（x2=22.627,p=0.023），结果有差异。
结论 分级检验方法应用在血脂生化检验过程中效果优良，该方法值得在临床上推广。

PU-2165

液相色谱串联质谱衍生化法与电化学发光法检测 25-羟基维生素 D 的比较

胡玉皎、张莹、胡娟娟、冯玉洁、和昱辰、王昊、刘家云
空军军医大学西京医院

目的 通过比较血清维生素 D(Vitamin D,VD)电化学发光(ECLI)法和高效液相色谱-串联质谱(LC-MS/MS)法的相关性，并探讨体内 25-羟基维生素 D2 和固醇类物质对二者结果的影响，评估 ECLI 和 LC-MS/MS 法检测 VD 的应用价值。
方法 回顾性分析 ECLI 法和 LC-MS/MS 法测定血清 VD 的相关性，并分析总胆固醇(Total cholesterol, TCho)、高密度脂蛋白胆固醇（High density liptein cholesterol，HDL-C）、低密度脂蛋白胆固醇（Low density lipoprotein cholesterol，LDL-C）、总胆汁酸（Total bile acid，TBA）、孕酮（Progesterone, P）、睾酮（Testosterone, T）、雌二醇(Estradiol， E2)对检测方法的影响。
结果 不同年龄段、性别 LC-MS/MS 法测定血清 25-OHD 平均值分布存在差异，VD 缺乏症和不足发生率不同，P<0.01；ECLI 法和 LC-MS/MS 法测定血清 25-OHD 结果具有相关性，ECLI 法较 LC-MS/MS 法结果偏高（2.04±18.43）ng/mL，P<0.01；ECLI 法结果与 LC-MS/MS 法相关性随 25-OHD2 水平升高而降低，P<0.01；ECLI 法结果受 TCho、HDL-C、LDL-C、TBA、P、T、E2 水平影响，调整后 R2 为 0.846，且与 LDL-C、TBA、P、E2 水平相关，P<0.05。
结论 ECLI 法与 LC-MS/MS 法检测 25-OHD 结果差异大，随 25-OHD2 水平升高相关性降低，且受体内 LDL-C、TBA、P、E2 水平影响，查体筛检及疾病诊疗监测中应合理结合 ECLI 和 LC-MS/MS 法的特点做到科学配置医疗资源。

PU-2166

多项实验指标检测在早期诊断多发性骨髓瘤中的综合研究

胡娟娟
空军军医大学西京医院

目的 分析血清蛋白电泳、游离轻链 κ、λ 及其比值和免疫球蛋白系列联合检测在早期诊断多发性骨髓瘤（MM）中的临床价值。
方法 对空军军医大学第一附属医院 784 例 MM 患者的血清、蛋白电泳、游离轻链 κ、λ 及其比值和免疫球蛋白系列的检测结果进行回顾性分析。
结果 血清蛋白电泳显示,784 例 MM 患者中有 673 例检出 M 带，阳性检出率为 85.84%。游离轻链 κ、λ 及其 κ/λ 显示,740 例游离轻链有不同程度的升高或者比值异常，阳性检出率为 94.39%，与对照组比差异具有统计学意义（P<0.05)。免疫球蛋白系列结果显示, 各型 MM 患者中有 603 例结果异常,阳性检出率为 76.92%，与正常组比差异具有统计学意义（P<0.05)。通过对三种方法单独和联合检测数据做 ROC 曲线，血清蛋白电泳曲线下面积 AUC=0.867，游离轻链比值曲线下面积 AUC=0.940，免疫球蛋白系列曲线下面积 AUC=0.737，联合检测曲线下面积 AUC=0.987，联合检测是大于三个指标单独检测，可见联合诊断效果更佳。
结论 血清蛋白电泳、游离轻链 κ、λ 及其 κ/λ 和免疫球蛋白系列联合检测对 MM 早期诊断有重要临床价值。

PU-2167

血清一氧化氮水平检测在肝脏疾病诊断中的临床意义

和昱辰
空军军医大学西京医院

目的 探讨一氧化氮（NO）在不同肝脏疾病中的动态变化规律及其临床意义。
方法 检测对象为临床诊断为肝损伤的 42 例、肝硬化 41 例、病毒性肝炎 48 例、免疫性肝病 33 例、肝癌 46 例和无肝脏疾病的健康对照 42 例，总计 252 例。对上述各组的血清 NO 水平进行检测，同时检测血清丙氨酸氨基转移酶（ALT）、天门冬氨酸氨基转移酶（AST）、谷氨酰转肽酶(GGT)。
结果 肝损伤组与健康对照组有显著差异（P <0.01）；病毒性肝炎组与健康对照组有显著差异（P <0.05）；肝硬化组与健康对照组有显著差异（P <0.01）；肝癌组与健康对照组有显著差异（P <0.05）。肝硬化组血清 NO 水平与 ALT 呈显著正相关(r=0.594，P<0.01);与 AST 呈正相关(r=0.389，P<0.05)；与 GGT 呈显著正相关(r=0.578，P<0.01)病毒性肝炎组血清 NO 水平与 ALT 呈正相关(r=0.301，P<0.05)；与 AST 呈正相关(r=0.326，P<0.05)；与 GGT 呈正相关(r=0.367，P<0.05)。**结论** 病毒性肝炎、肝硬化、肝癌时血清 NO 浓度的变化与肝内炎症程度、肝病严重程度及病程的演变方向密切相关，同时也是反映肝脏疾病的一个敏感指标。
结论 血清 NO 水平与肝脏疾病严重程度及病程的演变有关。

PU-2168

不同疾病类型所引起低血糖与白细胞数量之间的相关性研究

虢瑾、张莹、肖鹏涛、童开
空军军医大学西京医院

目的 分析我院门急诊和住院病人低血糖发生情况，探讨其不同的疾病类型导致的低血糖和白细胞数量之间的统计学意义。
方法 选取我院 2019 年 1 月到 2020 年 12 月血糖测定值<2.8mmol/L 的 449 例病例作为研究对象，根据临床诊断分为糖尿病与内分泌疾病组、胰腺病变组、肝病组、营养不良与恶病质组、胃相关疾病组和其他疾病组。分析其与白细胞数量之间的统计学关系。
结果 在 449 例血糖危急值中，糖尿病与内分泌疾病组 47 例（10.5％ ）白细胞计数大于 10 的 5 例占比 10.86%，胰腺病变组 34 例（8％ ）白细胞计数大于 10 的 17 例占比 50%，肝病组 66 例（14.7％ ）白细胞计数大于 10 的 35 例占比 53%，营养不良和恶病质组 59 例（13.14％ ）白细胞计数大于 10 的 44 例占比 73%，胃相关疾病组 57 例（12.69％ ）白细胞计数大于 10 的 32 例占比 55.17%，其他病组 183 例（40.76％ ）白细胞计数大于 10 的 94 例占比 51.37%。通过 SPSS23 数据分析，除外糖尿病所导致的低血糖外，其他类疾病与白细胞数量升高具有有统计学意义（P<0.05）。
结论 遇到低血糖危急值时，有部分疾病导致的低血糖与白细胞计数的升高具有直接关系。从而可以判断其是否为真实的低血糖血症。

PU-2169

基于患者样品不确定度应用的探索

冯玉洁、张莹、胡玉皎、胡娟娟、王昊、刘家云
空军军医大学西京医院

目的 使用多浓度患者样品，评估 4 项实验室常规生化项目测量不 50 份患者样本确定度的应用。
方法 采用速率法测定碱性磷酸酶（ALP）、谷氨酰转肽酶（GGT）、丙氨酸转氨酶（ALT）和天门冬氨酸转氨酶（AST）水平；每个项目的 50 份患者样本分为 5 个水平，重复检测两遍后合成 A 类不确定度，使用校准品引入的分量作为 B 类不确定度最终评估相对不确定度和绝对不确定度在临床中的异同。
结果 以待检样本的浓度为横坐标，合成不确定度为纵坐标绘制曲线图，每个图中都出现一个交点。在此交点上，小于这个浓度使用绝对不确定度大于这个浓度用相对不确定度。
结论 目前评估不确定度大多使用质控作为 A 类的分量，由于只有两浓度水平，有一定的局限性。若使用多浓度患者的样本绘制多浓度曲线作为不确定度的一种评估，有助于最大程度的减少误差，确定合理的检测不确定度范围。

PU-2170

动脉硬化相关因子在亚临床甲状腺功能减退患者血中的表达及临床意义

周萱军
山东大学第二医院

目的 亚临床甲状腺功能减退症是指无症状或者症状轻微，血清促甲状腺激素水平高于参考值上限，而血清游离甲状腺激素水平以及血清游离三碘甲状腺原氨酸水平处在参考范围内为特点的甲状腺功能紊乱。亚临床甲状腺功能减退对动脉硬化的影响一直存在争议。本研究旨在通过检测动脉硬化相关因子在亚临床甲状腺功能减退患者血中的表达，多角度探讨亚临床甲状腺功能减退与动脉硬化的相关性，为亚临床甲状腺功能减退患者的防治工作提供理论依据。
方法 选取新近诊断为亚临床甲状腺功能减退患者 100 例作为观察组，同期健康志愿者 100 例作为对照组，两组研究对象之间性别年龄无显著差异。分别测定并比较两组研究对象的甲状腺功能，血脂，血白介素-6 ，C 反应蛋白，血沉以及颈动脉内膜中层厚度。
结果 1. 观察组血清促甲状腺激素水平(TSH)显著高于对照组(P<0.05)，而两组间血清游离甲状腺激素(FT4)以及游离三碘甲状腺原氨酸(FT3)水平无显著差异(P 均>0.05)。
2. 观察组血总胆固醇(TC)、甘油三酯(TG)、低密度脂蛋白胆固醇(LDL-C)、血白介素-6 ，C 反应蛋白以及血沉水平均显著高于对照组(P 均<0.05)，而血高密度脂蛋白胆固醇(HDL-C)水平显著低于对照组(P <0.05)。观察组颈动脉内膜中层增厚程度显著高于对照组(P <0.05)。
3. 血总胆固醇(TC)、甘油三酯(TG)以及低密度脂蛋白胆固醇(LDL-C) 、血白介素-6 ，C 反应蛋白以及血沉水平与促甲状腺激素水平(TSH)水平呈正相关。血总胆固醇(TC)、甘油三酯(TG)以及低密度脂蛋白胆固醇(LDL-C)水平与颈动脉内膜中层厚度呈正相关。
结论 亚临床甲状腺功能减退患者血中动脉硬化危险因素水平显著升高，增加了患者发生动脉硬化甚至发展成心血管疾病的机率，有必要对亚临床甲状腺功能减退患者采取适当的干预措施或者定期随访以减少心血管事件发生的危险。

PU-2171

一个同时检测尿草酸、枸橼酸的超高效液相色谱-串联质谱方法

李霖[2]、传良敏[1]、蒋黎[1]
1. 电子科技大学附属医院·四川省人民医院
2. 电子科技大学附属医院·四川省人民医院

目的 草酸、枸橼酸是亚洲人群尿路结石的主要成分，当尿草酸、枸橼酸盐的排泄增加，可使尿草酸钙、枸橼酸钙过饱和，从而导致结晶聚集、尿石病和/或肾钙沉着病。同时这些结晶也可沉积于肾间质和肾小管细胞内，反复的尿石病可以导致肾实质炎症及纤维化，如果持续存在，还可以导致终末期肾病。因此，本研究的目的是开发一个同时检测尿草酸、枸橼酸的超高效液相色谱-串联质谱方法。
方法 校准液及尿液样本（50 μL）与混合内标液（草酸-13C2、枸橼酸-d4）及 5%甲酸水溶液混合后经 Waters OASIS WAX 固相萃取柱，使用 5%NH3 甲醇溶液洗脱，洗脱液复溶于 100μL 超纯水进样到质谱系统。质谱采用 Waters Acquity H-class 串联 Xevo TQD 系统，采用 ESI 负模式扫描，草酸、枸橼酸及其对应内标的 MRM 检测离子对分别为 m/z 88.6/60.5、m/z 90.5/61.5；m/z 191.1/110.9、m/z 195.1/112/9。色谱分离在 Waters HSS T3（2.1 × 100 mm，1.8 μm）色谱柱上进行，0.1%甲酸水和 0.1%甲酸乙腈为流动相，流速为 0.4 mL/min。
结果 在优化的色谱条件下，草酸和枸橼酸的保留时间分别为 0.35 min、0.67 min。草酸和枸橼酸的平均回收率分别为 95.6%、102.5%，最低定量限分别为 45.00 μmol/L、40.00 μmol/L。草酸的线性范围为 45.00-1500.00 μmol/L，枸橼酸的线性范围为 40.00-4000.00 μmol/L。草酸和枸橼酸检测的日间精密度均小于 10%。
结论 我们建立了一个新的可同时快速测定尿液中草酸和枸橼酸的超高效液相色谱-串联质谱方法。

PU-2172

Development of an ultra-high performance liquid chromatography-mass spectrometry method for the rapid quantification of serum total homocysteine, folate and vitamin B12 levels in senile cataract patient

Lin Li[2]、Wenna Liu[1]、Honglang Huang[1]、Kecheng Li[1]、Liangmin Chuan[1]、Li Jiang[1]
1. Sichuan Academy of Medical Sciences & Sichuan Provincial People's Hospital
2. 电子科技大学附属医院·四川省人民医院

Objective Senile cataract is a multifactorial disease which affect more than one hundred million people with age over 60 years-old in China. It was reported that elevated homocysteine (Hcy) is involved in the pathogenesis of cataract, while folate (VB9) and vitamin B12 (VB12) are involved in the metabolism of Hcy. The objective of this study was to develop a rapid ultra-high performance liquid chromatography-mass spectrometry (UPLC-MS/MS) method for the quantification of serum Hcy, VB9 and VB12 levels in senile cataract patient.
Methods A Waters Acquity H-class UPLC coupled with Xevo TQD MS/MS system was used for the method development. All MS investigations were carried out with electron spray ionization source operated in positive mode under multiple reaction monitoring (MRM) conditions. MRM transitions of m/z 136.1/90.1 and m/z 140.1/94.1, m/z 460.1/313.1 and m/z 464.2/317.2, as well as m/z 678.4/147.2 were monitored for Hcy, Hcy-d4, VB9, VB9-d4, and VB12, respectively. The chromatographic separation was carried out on a reversed-phase C18 column (Phenomenex, Kinetex C18, 100×4.6 mm, 2.6 μm).The mobile phases were 0.1% formic acid in H2O (A) and 0.1% formic acid in methanol (B). The gradient elution program were as follows: 0-3.0 min, 3%B; 3.0-4.5 min, 90%B; 4.5-5.5 min, 3%B.

Results The assays were linear within the concentration ranges of 4.0-800.0 ng/mL for Hcy, 5.0-500.0 ng/mL for VB9 and 5.0-200.0 ng/mL for VB12, respectively. The recovery was between 94.42% and 108.05%. The intra-assay coefficient of variations (CVs) ranged from 2.6% to 7.3% (n=20), and the inter-assay CVs ranged from 3.7% to 10.6% (n=20). Reference intervals were established and verified (n=125). The serum Hcy, VB9 and VB12 levels of 415 senile cataract patients were successfully confirmed.
Conclusion A rapid and sensitive UPLC/MS/MS method was successfully developed for the simultaneous quantification of serum Hcy, VB9 and VB12 in senile cataract patients.

PU-2173

汉藏人群维生素 D 水平、血清钙水平和骨密度的相关性研究

李霖[2]、李科成[1]、黄红浪[1]、宋天歌[1]、张婷[1]、蒋黎[1]
1. 电子科技大学附属医院·四川省人民医院
2. 电子科技大学附属医院·四川省人民医院

目的 维生素 D 是一种重要的类固醇激素，在肝脏中可被羟化形成稳定的 25(OH)D 形式，随后在肾脏中转化为生物活性代谢物 1,25-二羟基维生素 D (1,25(OH)2D)。1,25(OH)2D 在钙磷代谢中起着重要作用，而钙磷代谢被认为是骨密度的影响因素。在前期研究中，我们发现汉藏人群的 25(OH)D 水平存在显著差异。因此，我们进行了横断面研究，探讨汉藏人群的血清钙和骨密度是否存在差异。
方法 我们于 2019 年 9 月至 2020 年 12 月在阿坝藏族羌族自治州人民医院招募了 40 名汉族成年人和 80 名藏族成年人，年龄在 18-43 岁之间。空腹时从肘部前静脉抽 4 mL 血。LC-MS/MS 检测血清 25(OH)D2、25(OH)D3、1α、25(OH)2D3 水平。采用酶联免疫吸附法测定游离维生素 D。免疫分析法检测血清 PTH、P1NP 和 β-CTX。分光光度法测定血清钙、磷含量。采用双能 X 线骨密度仪测量骨密度。采用学生 t 检验和非参数检验探讨汉藏成人差异。
结果 汉族人群维生素 D3 浓度显著高于藏族人群(26.20 ng/ml vs. 16.99 ng/ml, P < 0.001)，藏族人群 1α，25(OH)2D3 浓度略低于汉族人群(36.73 pg/ml vs. 43.55 pg/ml, P = 0.06)。然而，与维生素 D 水平相反，藏族人群血清钙浓度显著高于汉族人群(3.12 mmol/L vs. 2.59 mmol/L, P < 0.001)。此外，藏族人群股骨骨干和第四腰椎关节的骨密度显著高于汉族人群(P = 0.031 和 P = 0.029)。
结论 我们的研究结果表明，维生素 D 代谢和钙代谢在汉藏人群中存在潜在的差异。为揭示汉藏人群维生素 D 代谢和钙代谢的分子机制差异，有必要开展进一步的遗传流行病学研究和功能研究。

PU-2174

A Protein Standard Addition Method for Absolute Quantitation of Cystatin C in human serum by LC-MS/MS

Hewei Sun、qing li、gan jin
上海市临床检验中心

Objective To established an LC-MS/MS approach based on the standard addition method for the absolute quantification of Cys C in human serum.
Methods In Sample preparation, we used the streamlined method without the use of chemical denaturants, reduction, and alkylation. Due to reduce of preparation steps, it can avoid the loss of protein before proteolysis. Varying concentrations of recombinant Human Cys C in PBS was added to serum for calibrations, and the same volume of PBS solution was added to the serum samples, so that the calibrations and samples were digested in the same matrix to achieve the same digestion efficiency. Peptides labeled in 13C and 15N atoms (A [13C615N] LDFAVGEYNK)

served as an internal standard are added to the serum samples just before proteolysis. After SPE steps of purification, the sample is measured by selected reaction monitoring using LC–MS/MS.
Results The calibration range was from 0.7 mg/L to 14 mg/L with LLOQ of 0.15 mg/L and LOD of 0.05mg/L, respectively. The certified reference material (ERM-DA471) was determined at 5.43 mg/L with bias of -0.9%. Imprecision was assessed by analyzing three replicates of each QC level on five different days (Table 1): the intra assay imprecision values ranged from 0.8% to 2.8% (QC1), from 0.8% to 2.1% (QC2), and from 1.5% to 2.5% (QC3); the inter assay imprecision values were 2.8% (QC1), 3.3% (QC2), 3.8% (QC3). Reference Material ERM®-DA471/IFCC (certified value 5.48±0.15 mg/mL) was used to validate the accuracy of the assay with three replicates on each day for five days (Table 1). The reference material was determined at 5.43 mg/L with a bias of -0.9%
Conclusion This work established an ID-LC-MS/MS procedure for the absolute quantification of Cys C in human serum samples which using protein standard addition method coupled with streamlining sample preparation. The design of such method aims to create a calibration system which has a matrix as similar as possible to the testable samples in serum Cys C quantification. In summary, this method demonstrates excellent accuracy and imprecision, may be used in the development of reference measurement procedures for serum Cys C.

PU-2175

Metabolomic Analysis of Synovial Fluids from Rheumatoid Arthritis Patients Using Quasi-Targeted Liquid Chromatography-Mass Spectrometry/Mass Spectrometry

Hongxing Wang
Qilu Hospital, Shandong University

Objectives Synovial fluid (SF) accumulates extensively in joints of individuals with rheumatoid arthritis (RA), which reflects the pathological state of the synovium and disease activity. This study applied quasi-targeted liquid chromatography-mass spectrometry/mass spectrometry, an advanced metabolomics technique, to find characteristic metabolism in RA.
Methods SF samples from the patients (n=20) were collected and examined using the metabolomic technique. SF samples from patients with osteoarthritis (OA) (n=20) were used as controls.
Results Four hundred seventy nine variable metabolites were detected, and 250 of these metabolites were identified by searching the Human Metabolome Database (HMDB) and a self-constructed information list of possible metabolites. S-plot and volcano plot analysis detected 22 metabolites with differential levels in RA SF compared with those in OA SF. With these 22 candidate metabolites, pathway analysis using the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway database detected upregulation of pyrimidine metabolism and purine metabolism, and downregulation of fatty acid biosynthesis and unsaturated fatty acid biosynthesis in RA SF. Receiver operating characteristic (ROC) analysis and logistic regression models detected increased levels of guaiacol, naringenin, phenylpropanolamine and vanillylmandelic acid in RA SF. Furthermore, the naringenin level showed positive correlation with rheumatic factor (RF) and anti-cyclic citrillinated peptides (anti-CCP) levels.
Discussion Our study suggests disturbed pyrimidine metabolism, purine metabolism, fatty acid biosynthesis and unsaturated fatty acid biosynthesis as well as increased naringenin level are characteristic metabolism in RA.

PU-2176

Polymorphism and plasma levels of apolipoprotein E and the risk of aneurysmal subarachnoid hemorrhage in a Chinese population: a case-control study

Xiaofeng Liu、Qishui Ou
Department of Laboratory Medicine, The First Affiliated Hospital of Fujian Medical University, Fuzhou 350005, China

Background Aneurysmal subarachnoid hemorrhage (aSAH) is the most common types of subarachnoid hemorrhage, which is a critical clinical problem with high morbidity, mortality, and economic impact. Recent studies have shown that APOE was a genetic risk factor of aSAH, however, the studies lack consistent conclusions and the evidence from Chinese Han population is rare.
Objective To determine the relationship between APOE polymorphism and the incidence of aSAH in Chinese Fujian Han population and explore the possible mechanism of ApoE in the pathogenesis of aSAH.
Methods A total of 131 patients newly diagnosed with aSAH were selected as aSAH group and 137 healthy subjects were selected as the control group. All the samples were analyzed for blood lipids and serum ApoE levels, and ApoE genotype was determined by a commercial chip and further confirmed with Sanger sequencing. An adjusted multivariate logistic regression analysis was carried out to estimate the effects of APOE polymorphism on the risk of aSAH.
Results Compared with the controls, the serum TC, HDL-C and ApoA1 levels in aSAH were significantly lower: TC (4.52 ± 1.38 vs. 5.11 ± 0.86 mmol/L, P < 0.001), HDL-C (1.23 ± 0.46 vs. 1.44 ± 0.32 mmol/L, P < 0.001) and ApoA1 (1.20 ± 0.32 vs. 1.38 ± 0.25 g/L, P < 0.001). The distribution of ε2/ε3 genotype (19.08% vs. 9.49%, P = 0.038) and ε2 allele frequency (11.07% vs. 5.84%, P = 0.039) was significantly higher in aSAH than the healthy controls. The multivariate logistic regression identified that ApoE ε2 allele was independently associated with aSAH (OR = 2.083; and 95% CI = 1.045-4.153, P = 0.037). The serum ApoE in aSAH were significantly higher than controls (53.03 ± 24.64 vs. 45.06 ± 12.84 mg/L, P = 0.010).
Conclusion APOE polymorphism might be associated with the incidence of aSAH in Chinese Fujian Han population. ApoE ε2 may be a risk factor for the incidence of aSAH, which may be related with the impacts of ApoE genotypes for the serum lipids, especially for the plasma levels of ApoE.

PU-2177

血清内毒素水平与各级肾脏疾病肌酐水平的相关性研究

王彩娥
西安市第一医院

目的 探讨血清内毒素水平与不同严重程度肾脏病患者肌酐水平的关系。
方法 根据肌酐水平选取四级肾脏病患者各 40 例，选取 40 例健康者作为正常对照组，检测受试者的血清内毒素，对比各组血清内毒素水平差异进行水平相关性分析。
结果 不同分级肾脏病患者的血清内毒素水平较正常对照组均明显升高,且组间两两比较差异均有统计学意义（P＜0.05）。
结论 慢性肾脏病患者存在高内毒素血症，高内毒素水平可能是慢性肾脏病发生发展的影响因素。

PU-2178

Prognostic value of prealbumin in liver cancer: A systematic review and meta-analysis

Weizhou Qiao、Feng Leng、Tong Liu、Yueying Wang、Dongjie Chen、Jinlong Wei
Dalian Municipal Central Hospital

Accumulated studies have reported the prognostic significance of prealbumin in liver cancer, but the results were not conclusive. The aim of this study was to evaluate the association between pretreatment serum prealbumin and clinical outcome of liver cancer patients through a meta-analysis. We comprehensively searched EMBASE, PubMed, Web of Science and the Cochrane library to identify eligible studies. The pooled hazard ratios (HRs) and their 95% confidence intervals (CIs) were utilized to evaluate the prognostic value of pretreatment serum prealbumin in overall survival (OS) and recurrence-free survival (RFS) of liver cancer patients. A total of 3470 patients from 10 eligible studies were finally included for analysis. The combined effects of prealbumin on liver cancer patients' OS and RFS were HR = 1.83, 95% CI: 1.46–2.30, p =0.000 and HR = 1.62; HR=1.47, 95%CI: 1.01–2.14, p =0.045 respectively. Sensitivity and subgroup analysis showed that the pooled HR of prealbumin on liver cancer patients' OS was stable. Since potential publication bias was identified in the OS studies, the trim-and-fill method therefore was performed to explore publication bias, and the results showed reliability. This meta-analysis shows that low pretreatment serum prealbumin is significantly associated with poor prognosis of liver cancer patients.

PU-2179

The short-term prognostic value of lactic dehydrogenase toalbumin ratio in patients with heart failure

Yiling Huang 、Jun Zhou
The First Affiliated Hospital of Nanjing Medical University

Purpose Heart failure (HF) has a worldwide diffusion.Heart failure is not a separate disease, but an end stage in the development of heart disease .Heart failure is a syndrome with symptoms and signs caused by cardiac dysfunction, resulting in reduced longevity. The aim of this study was to assess the value of lactic dehydrogenase toalbumin ratio(LAR) in patients with heart failure.
MethodsA total of 156 patients with heart failure were included in this retrospective investigation from January 2017 to December 2019. Admission blood routine parameters and biochemical data were gathered and LAR was computed.Independent prognostic factors were determined by multivariate Cox regression analysis.
ResultsThe average levels of serum LAR were significant lower in survivor group than those in non-survivor group (19.64±17.94 vs8.54±6.35, p<0.001) and serum LAR was an independent factor associated with in-hospital mortality (odds ratio(OR): 8.91; 95% confidence interval (CI):4.01-19.77; p<0.001). The area under the ROC curve (AUC) was 0.768 (95% CI 0.675–0.861, p<0.001).
ConclusionThese results show that the LAR at admission is associated with in-hospital mortality among patients.Thus, admission serum LAR can be used as an independent predictor of in-hospital mortality in patients with heart failure.

PU-2180

串联质谱法检测胆汁酸谱的性能评估及孕妇参考区间建立

陈辰、陈亚军
南京市妇幼保健院

目的 建立基于串联质谱(LC-MS/MS)技术检测胆汁酸谱的方法并进行性能评估；建立适用于本地区孕妇的胆汁酸亚型参考区间。
方法 用 LC-MS／MS 方法检测孕中期孕妇血清 15 种胆汁酸亚型，根据（CLSI）C62-A 和 FDA 的生物分析方法验证导则标准从定量检出限、准确度、精密度、线性、携带污染率等几个方面进行性能评估，并根据（CLSI）EP28-A3c 推荐的方法和程序建立本地区孕妇孕中期 15 种胆汁酸亚型的参考区间，用小样本验证法（20 例）对新建立的参考区间进行验证。
结果 1. LC-MS／MS 方法可同时检测孕妇血清中 15 种胆汁酸亚组分，最低定量限（LLMI）为标准曲线最低浓度点（S1）的浓度，最低检测限（LoD）为 1/4S1；2. 各亚型均呈现良好线性关系，相关系数 r2 均大于 0.99；3.准确度：各亚型加标回收试验回收率均在 80%-120%之间，偏倚<15%；4.批内精密度和批间精密度 CV 均小于 15%；5.携带污染率小于最低定量限的 25%。6.以石胆酸（LCA）为例，新的参考区间为：0.07-13.46ng/ml，验证结果 95%落于新的参考区间内。
结论 1.该方法可以精准快速地检测胆汁酸谱 15 种亚型，评估结果符合性能验证各项要求。2.新建立的胆汁酸谱 15 种亚型的参考区间适用于本地区孕中期孕妇。

PU-2181

脂蛋白相关磷脂酶 A2 增加无症状高尿酸血症风险

马琳琳[1]、杨琼[2]、龚美亮[3]、于金星[2]、周洲[2]、蔺亚晖[2]、丛玉隆[3]
1. 北华大学附属医院
2. 中国医学科学院阜外医院
3. 解放军总医院第二医学中心

目的 探寻脂蛋白相关磷脂酶 A2(Lp-PLA2)与无症状高尿酸血症两者之间的相关性。
方法 回顾性分析中国医学科学院阜外医院就诊的 174 例表观健康老年患者的年龄、性别、体重指数（BMI）等一般资料，以及血常规、尿酸、肌酐、尿素氮、血脂、Lp-PLA2 等实验室资料。高尿酸血症（hyperuricemia，HUA）是指正常饮食状态下，不同时间 2 次空腹血尿酸水平男性>420 μmol/L (7 mg/dl)， 女性>360 μmol/L(6 mg/dl)。当不伴有痛风、尿结石或肾病等症状时，称为无症状高尿酸血症。依据高尿酸血症（HUA）诊断标准将患者分为尿酸正常组和高尿酸组，进行病例对照研究。通过回归分析探究无症状高尿酸血症的独立危险因素。
结果 所有研究对象中男：女=1：1，平均年龄（63.76±8.48）岁，高尿酸组患者的体重指数（BMI）、甘油三酯（TG）、低密度脂蛋白胆固醇（LDL-C）、Lp-PLA2 及高血压发病率明显高于尿酸正常组患者。女性 HUA 的发病率高于男性。Lp-PLA2 的升高可独立导致血尿酸水平升高，对 Lp-PLA2 浓度进行三分位分组后，与低浓度相比高浓度 Lp-PLA2 组增加无症状高尿酸血症风险的 OR 值为 4.61(95%CI:1.807~11.76；P<0.05)。
结论 脂蛋白相关磷脂酶 A2 是无症状高尿酸血症的独立危险因素。

PU-2182

乳酸在结直肠癌患者外周血清中的表达及其临床应用价值

孙祖俊
上海市同济医院(同济大学附属同济医院)

目的 探讨乳酸在结直肠癌患者外周血清中的表达水平及其对结直肠癌早期诊断的临床应用价值，为结直肠癌的早期临床诊断及治疗决策提供依据。
方法 回顾性分析 2019 年 1 月至 2021 年 4 月期间收治的 120 例结直肠癌患者的临床资料，另选取 120 例肠息肉或其他良性消化道疾病患者作为疾病对照组和 100 例健康体检人群作为正常对照组。采用干式生化检测血清中乳酸表达水平并使用 ROC 曲线评估其在结直肠癌早期诊断中的价值。另外，将乳酸与目前临床常用结直肠癌诊断血清学标志物 CEA 和 CA19-9 进行比较及联合分析，综合评估其临床应用价值。
结果 与正常对照组和消化道良性疾病患者组比较，结直肠癌组患者血清乳酸水平均显著升高（P<0.001）；血清乳酸与 CEA、CA19-9 联合检测诊断结直肠癌的灵敏度和诊断符合率均显著高于单项检测，ROC 曲线下面积最大为 0.767，其灵敏度为 88%，特异度为 70%；血清乳酸与 CEA、CA19-9 联合检测鉴别诊断结直肠癌的灵敏度和诊断符合率均显著高于单项检测，ROC 曲线下面积最大为 0.729，其灵敏度为 70%，特异度为 66%。
结论 血清乳酸水平增高可能是结直肠肿瘤发生的一个早期事件，乳酸、CEA 和 CA19-9 联合检测可明显提高结直肠癌检出灵敏度和诊断符合率，有助于结直肠癌的早期诊断和鉴别诊断，让临床尽早采取最佳治疗方案，从而提高患者的生存率和预后生活质量。

PU-2183

过程能力指数在临床实验室质量控制评估中的应用

董苹[1]、陶然[2,3]、李会[1]、彭德志[1]、王佳佳[1]、邓小燕[2,3]、程雅婷[2,3]
1. 济南金域医学检验中心有限公司
2. 广州金域医学检验中心有限公司
3. 广州医科大学金域检验学院

目的 通过不同实验室间质控数据过程能力指数的对比分析，帮助实验室监控项目分析性能。
方法 统计 2020 年 5 月 25 家实验室 23 个项目的最小 *Cp* 和 *Cpk*，与绝对标准进行对比分析。同时以本组自上而下排名第 20%实验室的结果为相对标准，两者结合可确定项目需改善的重点（精密度还是正确度）及原因。
结果 共获得 575 组质控数据，绝对标准分析：*Cp* 优秀 305 个（53.0%）、良好 202 个（35.1%）、一般 55 个（9.6%）、较差 13 个（2.3%）。*Cpk* 优秀 256 个（44.5%）、良好 220 个（38.3%）、一般 72 个（12.5%）、较差 27 个（4.7%）。所有实验室 *Cp* 和 *Cpk* 结果均表现为优秀或良好的项目分别有 6 项和 4 项。济南金域项目分析：孕酮（P）和 N 端-B 型钠尿肽前体(NT-proBNP)分别表现为个别改善精密度和个别改善正确度，其余项目均为稳定。
结论 使用过程能力指数进行质控数据分析，可从精密度和正确度两个方面帮助实验室发现质控隐患，并提供各项目的性能改进建议，确保报告结果的准确可靠。

PU-2184

探讨肝脏疾病患者凝血功能指标与肝脏损伤严重程度的相关性及临床意义

贺元
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 肝脏疾病患者凝血功能大多会出现明显异常，而不同肝脏疾病患者出现的凝血功能紊乱各有差异。本研究的目的是探讨各肝脏疾病患者凝血功能指标与肝脏损伤严重程度的相关性及临床意义。
方法 随机抽取 2019 年在本院体检的健康人群 100 例为对照组及被诊断患有肝脏疾病的住院患者 100 例为实验组。使用全自动凝血功能分析仪（SYSMEX CS5100）及其配套校准品、质控品及试剂检测两组的凝血指标（PT、APTT、FIB、TT）并对其结果进行 t 检验统计学分析。
结果 肝硬化组、肝癌组和肝炎组的 PT 检测值分别为 15.29±1.99、15.93±2.70、15.69±3.51，P<0.05；APTT 检测值分别为 44.47±6.29、 42.43±11.13、 46.97±14.21，P<0.05；FIB 检测值分别为 1.73±0.61 、 2.76±1.01、 1.74±0.58 ，P<0.05；TT 检测值分别为 18.72±2.25 、17.39±1.48、20.22±3.20，P<0.05。PT 和 APTT 值在肝脏疾病患者中较健康人水平普遍偏高，且 PT 和 APTT 值同健康人群相比有显著性差异。肝癌患者 FIB 值同健康人群检测结果相比基本无差异，而肝硬化和肝炎患者的 FIB 值同健康人群检测水平相比有显著性差异；TT 检测结果与健康人群相比仅有肝炎患者差异明显，肝癌和肝硬化患者虽存在差异但均不是特别显著。
结论 肝脏疾病患者出现的凝血功能损伤程度各有不同，其损伤程度与肝脏损伤严重程度成正相关。凝血功能检测可辅助临床对肝病严重程度的判断与治疗，肝病越严重患者凝血功能越差。凝血功能检测对临床加强预防肝病患者出血有重大意义。

PU-2185

血清 PCT、CRP 和 WBC 对感染性心内膜炎患者的临床意义

于晓洁
吉林大学第一医院

目的 探讨降钙素原（PCT）、C 反应蛋白（CRP）及白细胞（WBC）联合检测在感染性心内膜炎诊治中的应用价值。
方法 研究对象为我院 2019 年 5 月至 2021 年 5 月诊治的 20 名感染性心内膜炎患者（观察组）以及同期健康体检的 20 例健康者（对照组）。比较两组 PCT、CRP 及 WBC 的检测结果、三者指标单独检测与联合检测的阳性率以及评价它们的灵敏度和特异度。
结果 观察组患者的 PCT、CRP 及 WBC 的检测结果均高于对照组（P<0.05）;观察组中 PCT、CRP 及 WBC 三项联合检测阳性率、灵敏度以及特异度比单独检测高（P<0.05）；观察组患者行赘生物清除术后，规律应用抗生素治疗 7d 后,PCT 及 WBC 结果均与对照组无明显的差异（P>0.05），CRP 高于对照组（P<0.05），但低于术前（P<0.05）。
结论 PCT、CRP 及 WBC 联合检测能提升早期辅助诊断感染性心内膜炎的阳性率,以及其有较高的灵敏度和特异度,同时对于治疗效果的判断有一定的指导意义。

PU-2186

Normal Reference Intervals of Prognostic Nutritional Index in Healthy Adults: A Large Multi-center Observational Study from Western China

guishu yang、huaichao luo
Sichuan Cancer Hospital & Institute, Sichuan Cancer Center, School of Medicine, University of Electronic Science and Technology of China

Background It has been widely reported that the prognostic nutritional index (PNI) played a pivotal role in nutritional assessment of surgical patients and tumor prognosis. In order to improve the accuracy of evaluation in western China, we established reference intervals (RIs) of PNI in healthy controls.
Methods A retrospective cohort study on healthy ethnic Han adults (18-79 years) was conducted to explore the influences of age, gender, study centers, and instruments on PNI and to establish RIs. The data came from a healthy routine examination center database and laboratory information system (LIS) of four centers in western China, and there were 200 persons selected randomly for verification of RIs.
Results 5,839 healthy candidates were enrolled. PNI showed a marked gender dependence, and males had significantly higher PNI than females across all ages (P<0.01). We found that PNI is significantly different between age groups (P<0.01), the value of PNI tended to decrease with age increasing. There is also an obvious influence of centers and instruments on PNI (P<0.01).
Conclusions We established reference intervals of PNI in healthy Han Chinese population in Western China, and validated successfully. Further established RIs will lead to better standardizations of PNI for clinical applications.

PU-2187

老年骨质疏松伴病理性骨折患者血清铁蛋白与炎症因子的水平变化及相关性分析

钟剑
杭州余杭邦尔医院

目的 分析老年骨质疏松伴病理性骨折患者血清铁蛋白与炎症因子的水平变化及相关性。
方法 选取 2017 年 9 月 1 日～2021 年 1 月 31 日期间杭州余杭邦尔医院骨质疏松伴病理性骨折患者（81 例）及健康体检者（30 例）作为实验组及对照组,分别检测骨密度（BMD）、FERR、血清淀粉样蛋白 A（SAA）、超敏 C 反应蛋白（h-CRP）、白细胞介素 6（IL-6）、免疫球蛋白 IgA（IgA）、白细胞计数（WBC）、中性粒细胞百分比（Neu%）、淋巴细胞百分比（Lym%），比较两组检测结果并对血清铁蛋白水平与炎症因子等检测指标进行 spearman 相关性分析。
结果 实验组 BMD、Lym%低于对照组，差异有统计学意义（P<0.05)，实验组 FERR、SAA、h-CRP、IL-6、IgA、Neu%高于对照组，差异有统计学意义（P<0.05)；实验组 FERR 水平与骨密度呈负相关（r=-0.406,P<0.05)，与 SAA、h-CRP、IL-6、IgA 等炎症因子呈正相关(r=0.331,r=0.385,r=0.371,r=0.288，P<0.05)。
结论 老年骨质疏松伴病理性骨折患者血清 FERR 水平与 SAA、h-CRP、IL-6、IgA 等炎症因子水平有正相关关系，对该病的预防、诊断及治疗有一定临床参考价值。

PU-2188

长链非编码 RNA AC020891.2 在结直肠癌中的功能及临床价值研究

孔雪、王传新
山东大学第二医院

目的 结直肠癌（CRC）是世界上最常见的肿瘤之一。越来越多的研究表明，长链非编码 RNA（lncRNA）在结直肠癌的发生发展中发挥着至关重要的作用。本研究旨在探讨 lncRNA AC020891.2 在结直肠癌中的功能及临床价值。
方法 运用 TCGA 数据库评估 lncRNA AC020891.2 在结直肠癌中的预后价值，并利用 qRT-PCR 技术检测 AC020891.2 在结直肠癌细胞系及血清样本中的表达水平。通过 CCK8 增殖试验检测 AC020891.2 对结直肠癌细胞增殖能力的影响。采用受试者工作曲线（ROC）分析血清 AC020891.2 对结直肠癌的诊断效能。
结果 lncRNA AC020891.2 在结直肠癌样本中的表达高于癌旁正常组织，并且其高表达与结直肠癌患者的不良预后显著相关。qRT-PCR 结果显示，结直肠癌细胞株 AC020891.2 的表达水平明显高于正常结直肠上皮细胞。在结直肠癌细胞系 HCT116 中敲低 AC020891.2，细胞增殖能力明显减弱。另外，与健康对照相比，结直肠癌患者血清中 AC020891.2 的表达显著升高，ROC 曲线曲线下面积 AUC=0.767，表明其对乳腺癌具有较好的诊断价值。
结论 研究表明 lncRNA AC020891.2 在结直肠癌中高表达并可促进结直肠癌的增殖，且与患者预后不良相关，可作为结直肠癌患者潜在预后及诊断的分子标志物。
关键词：结直肠癌，长链非编码 RNA，标志物，增殖

PU-2189

A novel long non-coding RNA AC073352.1 promotes breast cancer metastasis by YBX1

Xue Kong、Juan Li、Chuanxin Wang
The second hospital of Shandong university

Purpose Breast cancer (BC) is the most common malignancy and the second leading cause of cancer death in women worldwide. Long non-coding RNAs (lncRNAs) have been found to play a crucial role in the development of BC. The purpose of this study was to investigate the functions and molecular mechanisms of lncRNA AC073352.1 in BC.
Method The lncRNA microarray and TCGA database analysis were used to screen the target lncRNA AC073352.1, and its expression levels and clinical features were further investigated in a cohort of BC in situ hybridzation. We detected its expression in BC cell lines and normal breast cell by qRT-PCR. The stable knockdown or overexpressed BC cell lines of AC073352.1 were built by Lentivirus infection techniques, and the effects of lncRNA AC073352.1 on migration and invasion were determined by in vitro and in vivo experiments. The regulatory mechanism of AC073352.1 was studied by Western blot, RNA pull-down, mass spectrometry (MS) and RIP analysis. Co-culture and exsome labeling experiments were performed to assess exosomal AC073352.1 transfer from BC cells to endothelial cells. The role of exosomal AC073352.1 in angiogenesis was further investigated in vitro.
Results The expression of AC073352.1 in the BC tissues was significantly upregulated, and high expression of AC073352.1 was associated with a poorer overall survival and lymph node (LN) metastasis. Knockdown of AC073352.1 inhibited cells migration and invasion in MDA-MB-468 and MCF-7, and overexpression of AC073352.1 promoted cells migration and invasion in MDA-MB-231 and BT549. And knockdown of AC073352.1 decreased pulmonary metastases of BC in vivo. And interestingly, RNA pull-down, MS, RIP and subsequent Western blot experiments

showed that AC073352.1 directly binds to YBX1. Rescue experiments confirmed that AC073352.1 regulated BC metastasis by YBX1. Furthermore,we found BC-derived exosomes transferred AC073352.1 to human umbilical vein endothelial cells (HUVECs) to promote in vitro angiogenesis.
Conclusions Taken together, the results suggest that the expression level of lncRNA AC073352.1 is closely related to the prognosis of BC patients, and it acts as an oncogene in BC, which can promote the ability of metastasis by binding to YBX1.

PU-2190

脂浊对西门子 ADVIA2400 免疫透射比浊法测定血清前白蛋白等 6 个项目的干扰及纠正分析

倪莉、池嘉豪、徐晓杰、朱丽丹
温州医科大学附属第二医院（温州医科大学附属育英儿童医院）

目的 研究脂浊对免疫透射比浊法测定血清前白蛋白等 6 个项目的干扰。
方法 按照 NCCLS 推荐的 EP7-A2 和 EP9-A2 方案，选取 40 份无脂浊、无溶血、无黄疸患者血清样本，分别以低速离心(3500 r/min*7min)与高速离心（16000 r/min*10min）测定血清前白蛋白（PA）、脂蛋白 a(Lp(a))、载脂蛋白 A1(Apo AI)、载脂蛋白 B(Apo B）、胱抑素 C（CysC)、超敏 C 反应蛋白(hsCRP）；再选取 40 份不同脂浊指数（脂浊指数分别为+、++、+++和++++各 10 份）患者血清样本，分别以高速与低速离心获得血清，低速离心后的血清分为三份，其中一份不做处理、另外两份分别用生理盐水进行 2 倍稀释与 3 倍稀释后与高速离心后的血清同时测定 PA 、Lp(a)、Apo AI、Apo B、CysC、hsCRP 6 个项目。
结果 无脂浊血清标本 PA、Lp(a)、Apo AI、Apo B、CysC、hsCRP 低速与高速离心检测结果均无显著性差别（P＞0.05）；不同程度脂浊标本低速离心后 LPa、APOA1、APOB、Cys-C、hsCRP 检测结果与高速离心后的检测结果均无明显偏倚；脂浊指数＜55.8 时，对 PA 检测无明显干扰，当脂浊指数≥55.8 时，低速离心检测 PA 存在明显负干扰；脂浊指数≥63.9 时，标本二倍稀释 PA 还存在负干扰；脂浊指数≥93.3 时，标本三倍稀释 PA 也还存在负干扰。
结论 脂浊对免疫透射比浊法测定血清 LPa、APOA1、APOB、Cys-C、hsCRP 无明显干扰；轻度脂浊对透射比浊法测定 PA 无明显干扰，当脂浊指数≥55.8 时，对 PA 测定存在明显负干扰，需经高速离心后重新检测或标本稀释后再检测。

PU-2191

高敏心肌肌钙蛋白在急性冠脉综合征诊断中的应用价值

乔理华、贾玉芝、娄加陶
上海市胸科医院

随着日常生活和工作压力的不断升高，以及作息和饮食习惯的改变，心血管疾病的发病率和死亡率呈不断上升趋势，且正朝着年轻化的趋势发展。在我国，冠状动脉疾病也已成为城市人群的主要疾病和死亡原因之一。急性冠脉综合征(ACS)作为心血管内科发病率较高的疾病之一，具有发病较急且病情变化快，同时临床表现较复杂的特点，若得不到早期精准的诊断常会致死，该疾病目前正严重威胁人类的生命健康。随着医学水平的快速进步，血浆肌钙蛋白凭借其组织特异性强、灵敏度高的优势，成为诊断 ACS 的重要指标，经过不断地更新换代，高敏心肌肌钙蛋白检测法(hs-cTn)横空出世，较普通肌钙蛋白检测灵敏度、精密度更高，并已被广泛应用于临床。本文就 hs-cTn 在 ACS 中的诊断应用与价值进行综述。

PU-2192

肿瘤标志物 D-2-羟基戊二酸的快速灵敏检测

张文
山东大学第二医院

近年来在急性髓细胞样白血病、神经胶质瘤、肉瘤等多种肿瘤中检测到异柠檬酸脱氢酶（IDH）突变，IDH 突变可导致该蛋白产生催化 2-酮戊二酸还原生成 D-2-羟基戊二酸（D-2-HG）的活力，造成 D-2-HG 积累。D-2-HG 是 IDH 突变肿瘤的发生诱因及小分子标志物，在急性髓性细胞白血病、胶质瘤中作为诊断、预后及治疗监测性指标等，具有较大的临床应用价值。目前主要通过质谱等进行检测。本文旨在建立一种 D-2-HG 酶学检测方法。基于前期发现的无色杆菌来源的 D-2-羟基戊二酸脱氢酶（D2HGDH）专一性催化 D-2-HG 并能直接传递电子给刃天青的特性，研究者构建了一步法检测方案，通过荧光酶标仪进行检测。反应体系仅包含 PBS 缓冲液、D2HGDH 及刃天青。通过优化，实现定量限 0.1μM 级别，检测比较稳定。血清、尿液、脑脊液等样本经过去蛋白处理后可应用此方案。该检测方法组成成分更加简单，干扰小，成本更低，操作更为简便快速，易于构建试剂盒。

PU-2193

白介素-6 与慢阻肺急性加重期患者病情及预后存在相关性的研究

李露
郴州市第一人民医院中心医院

目的 探讨某院 2018-2019 年因慢性阻塞性肺疾病急性加重期入住我院呼吸与危重病科-1 的患者其静脉血血清中白介素-6 水平与其病情及预后的相关性分析。
方法 随机收取 2018 到 2019 年由于慢阻肺疾病急性加重期入住我院呼吸与危重病科-1 的 100 例病例。同时随机收集由于普通慢阻肺疾病入住我院呼吸与危重病科-2 的 100 例病例。及同期于我院耳鼻喉科检查但非炎症的 100 例病例。且将收集到的慢性阻塞性肺疾病急性加重期 100 例患者中经临床干预治疗后转变为普通慢性阻塞性肺疾病或其他轻症肺部疾病或痊愈等好转情况的 25 例病例。收集的共 300 例病例的患者在入院时都抽取外周静脉血离心后用血清标本采用双抗体夹心免疫层析法，在上转发光免疫分析仪检测白介素-6 水平，经治疗后有好转的 25 例病例患者转归后也应用上述方法进行了血清白介素-6 水平的检测。
对加重期实验组，普通对照组，健康对照组和预后判断前后组共五组数据分别进行正态性检验，其均完全符合正态性分布，用直方图描述，后进行方差齐性分布检验，如果方差齐；随后将前三组数据进行单因素方差分析，比较两两样本间的均数，有差异是 $P<0.05$，具有统计学意义。在急性加重期患者经过治疗后其前后两次白介素水平之间对两两数据进行比较，使用独立的样本 t 进行检验，有差异是 $P<0.05$，具有统计学意义。以上数据是在 SPSS23.0 统计软件进行处理及分析的。
结果 普通慢阻肺疾病对照组和健康对照组其血清中白介素-6 水平明显低于慢性阻塞性肺疾病急性加重期实验组，三者间具有差异表明具有统计学意义（$F=49.41,P<0.01$）。
在慢性阻塞性肺疾病急性加重患者中，经过临床干预治疗后其前后两次白介素水平之间比较，治疗前白介素-6 水平明显高于治疗后水平，具有差异有统计学意义（$t=4.11,P<0.01$）。
结论 慢阻肺急性加重患者的病情及预后与外周静脉血血清中白介素-6 水平具有相关性。

PU-2194

恶性肿瘤患者血清 Hcy 检测的临床意义

李亚琴、丁世凯
甘肃省肿瘤医院

目的 检测恶性肿瘤患者、健康体检者血清同型半胱氨酸，对比分析血清同型半胱氨酸检测与恶性肿瘤相关性。
方法 选取我院 2020 年 1 月-12 月住院乳腺癌、胃癌（81 例）为病例组，同时间段健康体检者（71 例）为对照组，检测两组血清同型半胱氨酸。
结果 病例组血清同型半胱氨酸平均浓度（9.35-27.41umol/L）显著高于对照组（6.41-15.71umol/L），两组差异有统计学意义。
结论 乳腺癌、胃癌患者检测血清同型半胱氨酸有临床意义。

PU-2195

子痫前期 ACR 与 24 小时尿蛋白定量的相关性研究

王兰芳、张倩
安徽省妇幼保健院

目的 探讨子痫前期孕妇尿微量白蛋白/肌酐（ACR）与 24 h 尿蛋白定量的关系，子痫前期（preeclampsia，PE）是怀孕 20 周以后，孕妇尿液中出现少量蛋白、水肿和血压升高三联症状，如不及时治疗会发展为子痫。
方法 收集子痫前期 72 例孕妇尿液，从早上 8：00 到第二天早上 8:00 的 24 小时尿液，加二甲苯防腐剂。随机留取中段尿作为尿微量白蛋白/肌酐的标本。年龄在 22-44 岁，孕 35-42 周，根据病情分重度组 44 例，轻度组 28 例；同期抽取 20 名正常孕妇作为对照组，两组孕妇的年龄、胎次和入院时孕周等一般资料无明显差异（p>0.05），所有孕妇孕前无肾脏疾病，实验前未服用任何药物。24 小时尿蛋白采用贝克曼生化仪检测，使用原装配套试剂；尿微量白蛋白/肌酐使用的是自动尿液微量白蛋白肌酐分析仪，采用免疫比浊法，定量检测尿液微量白蛋白(mALB)和尿肌酐(Cr)的浓度并计算出二者的比值(ACR)，用配套试剂检测。参考范围随机尿样的 ACR<30mg/mmol 正常，ACR30-300mg/mmol 为微量白蛋白尿，ACR>300mg/mmol 为临床白蛋白尿。
结果 实验组与对照组比较 ACR 及 24 h 尿蛋白定量有明显的差异（P＜0.05）；子痫前期组和正常对照组单一比较中 ACR 及 24 h 尿蛋白定量呈线性升高；在轻度组及重度组间比较 ACR 及 24 h 尿蛋白定量有明显的差异（P＜0.05）；轻度组及重度组 ACR 及 24 h 尿蛋白定量单一比较呈线性关系。
结论 ACR 与 24h 尿蛋白定量在判断子痫前期的严重程度上有高度相关性，对子痫前期孕妇检测尿白蛋白/肌酐（ACR）比检测 24h 尿蛋白定量更具有优越性。ACR 的检测方便快速，随机尿即可检验，它的检测结果不论是在产前子痫、妊娠高血压，还是在糖尿病肾病等的诊断方面都有很高的临床价值，将来会比 24 小时尿蛋白定量更受临床医生的青睐。

PU-2196

重氮法和钒酸盐法检测胆红素结果比对分析

解春宝
电子科技大学附属医院•四川省人民医院

目的 探讨某实验室重氮法和钒酸盐法检测胆红素结果的可比性，为实现胆红素测定结果的一致性提供依据。
方法 以 Abbott C16000 全自动生化分析仪及重氮法试剂组成的检测系统为参比系统（X），以 Olympus AU 5800 全自动生化分析仪及钒酸盐法试剂组成的检测系统为待评系统（Y）。测定患者新鲜血清中总胆红素（TBIL）和直接胆红素（DBIL）的准确度和精密度。对 X 和 Y 两种系统的胆红素结果进行比较并进行计算其相对偏差（SE%）。以《WS/T 403-2012 临床生物化学检验常规项目分析质量指标》文件规定的允许误差或根据生物学变异确定的偏倚为判断依据，研究两套系统测定胆红素结果的可比性和一致性。
结果 Olympus AU 5800 和 Abbott C16000 全自动生化分析仪测定 TBIL、DBIL 结果的准确度和精密度符合要求，参比系统和待评系统间的误差或相对偏差在临床可接受水平内。
结论 两套生化分析仪检测胆红素结果具有较好的可比性和一致性，可满足临床需求。

PU-2197

肝指数与肝癌侵袭性指数

江秀娟、杨银芳、苏海翔
甘肃省肿瘤医院

目的 寻找肝脏指数与肝癌侵袭性指数的关系。
方法 优化建立肝细胞癌（HCC）侵袭性指数，包括最大肿瘤的大小、多灶性、门静脉血栓和血甲胎蛋白水平 4 个临床参数总分。选择与肝癌侵袭性相关的具有最高危险比的血液总胆红素、γ-谷氨酰转肽酶、白蛋白和血小板水平 4 个参数构成肝脏指数。
结果 肝脏指数得分与肝细胞癌患者的生存率显著相关，也与侵袭性指数及其单个参数显著相关。
结论 肝脏功能不仅是肝癌患者重要的预后因素，而且可能与肝癌的生物学和侵袭性有关。血总胆红素、γ-谷氨酰转肽酶、白蛋白和血小板水平是可以被用来构建与 HCC 侵袭性参数显著相关的肝脏指数。

PU-2198

An LC/MS/MS method for analyzing the steroid metabolome with high accuracy and from small serum samples

tengfei yuan、yan li
Department of Clinical Laboratory, Renmin Hospital, Wuhan University

n and liquid-liquid extraction. The organic phase was dried by evaporation, and isonicotinoyl chloride was added for steroid derivatization, followed by evaporation under nitrogen and redissolution in 50% methanol. Chromatographic separation was performed on a reverse-phase PFP column, and analytes were detected on a triple quadrupole mass spectrometer with ESI. The lower limits of quantification ranged from 0.005 ng/ml for estradiol to 1 ng/ml for cortisol. Apparent recoveries of steroids at high, medium, and low concentrations in quality control samples were between 86.4% and 115.0%. There were limited biases (10.7% to 10.5%) between the

measured values and the authentic values, indicating that the method has excellent reliability. An analysis of the steroid metabolome in pregnant women highlighted the applicability of the method in clinical serum samples. We conclude that the LC/MS/MS method reported here enables steroid metabolome analysis with high accuracy and reduced serum consumption, indicating that it may be a useful tool in both clinical and scientific laboratory research.

PU-2199

Steroid profile analysis by liquid chromatography-tandem mass spectrometry in second-trimester pregnant women for trisomy 21 screening

tengfei yuan、yan li
Department of Clinical Laboratory, Renmin Hospital, Wuhan University

Background Trisomy 21 is a serious chromosome abnormality. The conventional Down's screening test is the most widely used for trisomy 21 screening. However, this method could lead to a higher false positive rate. Therefore, we aim to analyze steroid profile in second-trimester pregnant women and identify novel serum biomarkers of trisomy 21.
Methods We employed an LC–MS/MS method to measure the steroid profile. The concentrations and product-to-substrate ratios in 71 second-trimester pregnant women were determined and statistically analyzed to identify novel biomarkers for trisomy 21 screening.
Results We found that there were significant differences in levels of E3, 11-deoxycortisol, and 11deoxycortisol /17-hydroxyprogesterone between two groups. The OPLS-DA plots revealed obvious separation between two groups. Combining VIP analysis (VIP > 1.0) with volcano plot (P < 0.05 and fold change >1.2 or < 0.83), 11-deoxycortisol was identified as a novel biomarker for trisomy 21. After controlling for confounders, we found 11-deoxycortisol was associated with trisomy 21 (adjusted P = 0.009), and the fully adjusted OR (95 % CI) was 0.098 (0.016−0.593) in highest quartile versus lowest quartile of 11-deoxycortisol (P = 0.011).
Conclusions Steroid profile analysis for the first time showed that steroid hormones perturbations occurred in pregnant women carrying a fetus affected by trisomy 21 and decreased 11-deoxycortisol levels were associated with trisomy 21.

PU-2200

血清簇集蛋白、肽素与抵抗素联合检测对 2 型糖尿病急性脑梗死临床治疗的指导意义

陈良
郑州人民医院

目的 评价 2 型糖尿病急性脑梗死患者应用血清簇集蛋白、肽素与抵抗素联合检测临床价值以及对其产生的指导意义。
方法 病例选取时间为 2019 年 11 月至 2020 年 11 月，对本医院收治的 47 例 2 型糖尿病急性脑梗死患者作为 A 组，另选取同时期接收的 47 例 2 型糖尿病患者以及 47 例急性脑梗死患者分为分为 B 组和 C 组。对比各组之间和肽素、血清簇集蛋白、抵抗素检测结果以及对预后所产生的影响。

PU-2201

Prognostic value of platelet to platelet distribution width ratio in postoperative patients with type A acute aortic dissection

Yaman Wang、jun zhou
Jiangsu Provincial People's Hospital (First Affiliated Hospital of Nanjing Medical University)

Objective Acute type A aortic dissection is a serious life-threatening cardiovascular emergency with high in-hospital mortality without aggressive clinical treatment. The study aims to evaluate the relationship between platelets (PLT) to platelet distribution width (PDW) ratio (PPR) with in-hospital mortality in postoperative patients with type A acute aortic dissection (AAD).
Methods 171 type A AAD patients were recruited in this retrospective study from January 2017 to December 2019. Receiver operating characteristics (ROC) were used to determine the optimal cut-off values for PPR, then patients were divided into low-PPR group and high-PPR group by the optimal cut-off value of PPR. Finally, univariate and multivariate analysis were performed to analyze the prognostic value of PPR.
Results The cut-off value of PPR was 9.76 and the mortality was statistically higher in low-PPR group than that in high-PPR group (29.1% vs 6.0%, p<0.01). The area under the ROC curve (AUC) of PPR was 0.724 (95% CI, 0.633-0.815; p <0.001) with a 56.4% sensitivity and 80.6% specificity. Multivariate analysis showed that serum PPR was an independent factor associated with in-hospital mortality (hazard ratio (HR): 1.151; 95% confidence interval (CI): 1.035-1.297; p=0.010).
Conclusion Serum PPR can be used as an independent predictor of in-hospital mortality in postoperative patients with type A AAD.

PU-2202

尿总蛋白与肌酐的比值可用于判断尿蛋白异常的初筛

贾宇
郑州大学第一附属医院

目的 比较尿总蛋白与肌酐的比值（TCR）与 24h 尿总蛋白结果的一致性及差异性。
方法 回顾性分析 803 名患者尿蛋白数据，患者同时进行了 24h 尿蛋白量及尿 TCR 检测且检测时间不超过 24h。根据尿蛋白含量值（g）分为六组：≤0.15、0.151-0.20、0.21-1.5、1.51-2.0、2.01-3.5、>3.5。采用 Kappa 分析比较两种方法结果的一致性，配对秩和检验比较两组定量结果的差异性，并评价 TCR 法的敏感度、特异性、阳性预测值（PVP）、阴性预测值（PVN）。
结果 按照阴阳性分组，Kappa=0.483，一致性中等；按照阳性程度分组，Kappa=0.345，一致性一般。根据均值±标准差，TCR 及 24h 尿蛋白量分别为 1.99±2.76g 及 3.10±3.82g，两组差异有显著性意义（p=0.000）。结果显示 TCR 小于 24h 尿蛋白量有 671 例（其中相差≥1 倍有 341 例，占 50.82%），TCR 大于 24h 尿蛋白量有 124 例（其中相差≥1 倍有 31 例，占 25%），两者相差≥1 倍共计 372 例，占总例数的 46.32%。此外，TCR 的灵敏度及特异性分别为 87.2%和 85.1%，PVP 及 PVN 分别为 98.3%和 40.4%。
结论 1. TCR 可用于判断尿蛋白异常的初筛；2. TCR 无法替代 24h 尿蛋白量进行尿蛋白含量的评估；3. TCR 用于患者尿蛋白含量评估，可能会低估患者的病情。

PU-2203

Meta-analysis: Association of homocysteine with recurrent spontaneous abortion

juan li[1]、danqin feng[2]、shiwei he[3]、qichang wu[4]、zhiying su[5]、huiming ye[6]
1. Women and Children's Hospital, School of Medicine, Xiamen University
2. Women and Children's Hospital, School of Medicine, Xiamen University
3. School of Public Health, Xiamen University
4. Women and Children's Hospital, School of Medicine, Xiamen University
5. Women and Children's Hospital, School of Medicine, Xiamen University
6. Women and Children's Hospital, School of Medicine, Xiamen University

Objectives The differences in serum homocysteine (Hcy) levels in patients with a history of recurrent spontaneous abortion (RSA) and those who had not experienced pregnancy-related complications were assessed through a meta-analysis, which provided a reference for the diagnosis and treatment of recurrent abortion.
Methods Literature and data on recurrent spontaneous abortion and homocysteine levels that were published before September 2019 were retrieved from the PubMed, EMBASE, CNKI, and Wanfang databases. The quality of the included literature was assessed using the Newcastle Ottawa Scale (NOS), using Stata 12.0 for the combined statistical analysis of data.
Results Patients with recurrent spontaneous abortion had higher Hcy levels than the controls, with statistically significant difference ($p < 0.05$).
Conclusion Hcy levels in patients with recurrent spontaneous abortion were significantly higher than those in healthy controls were. High homocysteine levels may be an important risk factor for recurrent spontaneous abortion, which may be a non-invasive marker for the diagnosis of recurrent abortion.

PU-2204

乙肝表面抗原(0.01-0.05) IU/ml 存疑区间的复查分析

孙宁
沈阳金域医学检验所有限公司

目的 随着对 HBV 研究的逐渐深入，为了加大预防肝癌的力度，进行 HBsAg 的检测需求已经逐渐遍布于各行各业。检测量的日益加大，介于 0.05IU/ml 及以下的、不便判读的检测结果也引起了检测者足够的重视。为确定其真实检测值选取 10 日内的目标样本再一次进行了复查，通过对复查结果分析，探究导致结果介于(0.01-0.05) IU/ml 存疑区间的原因。
方法 记录标本初始数据，再运用控制变量法用高速离心机对标本离心复查，记录数据并与初始数据比对。观察标本是否存在黄疸、溶血、脂血并标注。回忆实验过程中那些操作可能导致标本出现误差并分析初次检测与复查不想符合的原因，得出结论，并结合生化肝功及两对半的结果对结论进行验证。
结果 在 200 例 10 日内 HBsAg 检测结果介于(0.01-0.05) IU/ml 区间标本中，初始数据和此次初查数值与复查数值有细微差值的为 139 例(占 69.5%)，完全一致的为 81 例(40.5%）。
回忆实验过程中那些操作可能导致标本出现误差，并分析原因，得出结果
根据变量（离心速度）的改变，导致了两次检测结果的微小差异。高速离心排除了血细胞、纤维蛋白原和其他蛋白的干扰，使表面抗原的检测更为准确。
通过生化肝功及两对半的检测，也确实证明了两次复查均接近 0.05IU/ml 确实存在肝脏检测项目的异常，而初次检测为 0.05-0.04IU/ml 复查结果与初查不一致且为阴性的，是受到血清中异常细胞和蛋白的干扰所致，其肝功项目数值相对正常。

结论 面临 HBsAg 检测结果介于(0.01-0.05) IU/ml 区间时，高速离心复查能排除血细胞、纤维蛋白原和其他蛋白的干扰，使表面抗原的检测更为准确。再结合标本的历史结果、生化肝功和两对半等进行多方面佐证，再发出报告。

PU-2205

血液透析患者实验室生化发光相关检测指标的分析

苏圣
沈阳金域医学检验所有限公司

目的 血液透析（ hemodialysis）患者的实验室生化指标变化情况，为监测患者的病程进展提供实验室依据。
方法 收集 2021 年 1 月至 2021 年 3 月 沈阳金域医学检验所有限公司接收血液透析患者检测者共 186 例(男 116 例，女 70 例)，测定患者血液透析前相关实验室指标，采用非参数检验及 Pearson 相关分析对尿素（BUN）、血肌酐 (Scr)、血钙(Ca)、血磷(P)、甲状旁腺激素、等指标进行统计。
结果 93.2%的患者甲状旁腺激素(PTH)高于 500pg/mL，PTH 与血清无机磷 （P）的升高呈显著正相关(r=0.362,P<0.001)。56%患者呈现低钙(Ca)血症， 尿素(BUN)与肌酐(Scr)呈显著正相关(r=0.538,P<0.001)
结论 血液透析患者存在不同程度的继发性甲状旁腺功能亢进、低钙血症，等慢性并发症，实验室检测指标对于评估血液透析患者的整体状况具有重要意义。

PU-2206

糖化血红蛋白与血清 C 肽联合检测在糖尿病诊断中的应用价值

闫悦闻
沈阳金域医学检验所有限公司

目的 探讨糖化血红蛋白与血清 C 肽联合检测在糖尿病诊断中的应用价值。
方法 选取 2020 年经我公司检测的 100 例 2 型糖尿病（T2DM）患者作为研究对象，其中轻症 58 例，重症 42 例，选取同期健康体检者 100 例为对照组。分别采用己糖激酶法检测其空腹血糖值和餐后 2 小时血糖值，电化学发光法检测其空腹血清 C 肽和餐后 2 小时血清 C 肽水平，高效液相色谱法检测其糖化血红蛋白结果，比较 3 组各指标之间的差异，并进行相关性分析。纳入标准：（1）研究组患者诊断均符合世界卫生组织制定的 2 型糖尿病诊断标准，其中按糖化血红蛋白检测结果将糖化血红蛋白≤10%者纳入轻症组，糖化血红蛋白>10%者纳入重症组。对照组均为我公司健康体检者。排除标准：（1）合并肝肾功能不全、自身免疫性疫病或急慢性感染疾病患者；（2）近期服用可能影响血糖相关指标药物的患者。采用 SPSS20.0 进行统计学数据处理，计量资料采用 t 检验，计数资料采用卡方检验，相关性采用 Person 相关分析。
结果 糖尿病重症患者空腹血糖值、餐后 2 小时血糖值、糖化血红蛋白值水平显著高于轻症组（P<0.05），且二者均显著高于健康对照组（P<0.05）；轻症组患者空腹血清 C 肽和餐后 2 小时血清 C 肽水平显著高于健康对照组和重症组（P<0.05）。其中轻症组、健康对照组的糖化血红蛋白与血清 C 肽呈显著正相关（r=0.835，r=0.798，P 均<0.05），而重症组、健康对照组的糖化血红蛋白与血清 C 肽呈显著负相关（r=-0.804，r=-0.746，P 均<0.05）.
结论 糖化血红蛋白与血清 C 肽联合检测可对糖尿病诊断提供可靠数据，并反映糖尿病患者血糖水平及病情严重程度，值得推广。

PU-2207

时间、溶血对神经元烯醇化酶（NSE）影响的探究

苏圣
沈阳金域医学检验所有限公司

目的 排除时间、溶血对神经元烯醇化酶（NSE）影响，给予临床准确可靠的结果，在肺癌领域能够更好的结合其他标志物更精确的分析病情。
方法 收集 2021 年 4 月至 2021 年 5 月 沈阳金域医学检验所有限公司接收 NSE 在 0-16ng/ml 范围内未见溶血血液样本，258。在相同温度、相同仪器上，进行两组实验，第一组（原管组）将带有血细胞的原管震荡搅匀（使其溶血）离心上机检测，根据肉眼观测可分为：溶血“+/-”66 例、溶血“1+”131 例、溶血“2+”49、未溶血 12 例；第二组（分血组）将血液标本离心后上机检测。
将第二组样本，室温放置 4 小时，放置 8 小时，分别进行检测。
结果 当样本溶血时溶血程度与检测结果呈正相关；当样本未见溶血时，放置时间与检测结果成正相关，时间越长检测结果越高。
结论 NSE 测定会因溶血、测定时间的延长的增加而使结果偏高。

PU-2208

溶血血标本对血钾值的影响及其相应措施

郝广运
沈阳金域医学检验所有限公司

目的 探讨溶血血标本对于血钾值的影响及相应措施，为临床提供应用价值。
方法 本人通过日常在工作中随机选取了 10 例低血钾麻痹病人患者部分溶血和非溶血标本，还有 15 例慢性肾功能不全病人部分溶血与非溶血标本，通过诊断学标准确诊后，又及时采集了一份非溶血标本送检过来并通过离子选择电极法检测并作比较。
结果 非溶血标本血钾值小于 3.5mmol/L 为低血钾症；血钾值介于 3.5mmol/L~5.5mmol/L 之间为体内平衡；血钾值大于 5.5mmol/L 时为高血钾症。部分溶血者血标本值均比同时送检的非溶血血钾值明显偏高。
结论 标本溶血测得的血钾值会显著增高，这是由于红细胞内钾的含量大大高于血清中的含量，约为血清中血钾含量的 20 倍。标本放置时间过长，也会使测得的血清钾结果偏高，这是因为标本放置过久，血清与血细胞凝块接触，钾离子从血细胞内向血清转移，从而使得测得的结果偏高。造成标本溶血的原因有:抽血速度过快；试管针管潮湿不干燥；抽血部位皮肤消毒液不干；向试管内注血过猛，注入泡沫血；采集好的血标本剧烈震荡，采集后标本放置过久等。具体相关措施如下：1、加强责任心，端正采血态度，尊重患者要对每一个患者负责。2、应用一次性针管，并保证试管针管务必干燥，注意待皮肤消毒液干燥后采血。3、注血时不要只求速度，应该拔掉针头缓慢匀速沿试管壁注入，以免红细胞破裂影响检测结果。4、注血前应将注射器内空气排空，注入后切勿剧烈震荡。

PU-2209

镁检测试剂盒的性能评价

王晓
沈阳金域医学检验所有限公司

目的 对使用终点比色法测定的镁检测试剂盒进行实验室验证和评价,以确定该试剂盒分析性能的可靠性,评价其是否符合临床应用需要。
方法 取接近厂家线性的低值和高值标本各一例，按照低值、低值与高值 4：1、3:2、2:3、1:4、高值配比成 6 例标本，重复测定三次，通过 SPSS 软件计算得出最适方程，同时计算测定浓度均值并与理论值进行相关性分析，计算出 r 值及均值偏差，要求 r≥0.98，均值|偏倚＜2.50%。经 SPSS 软件计算得出最适方程为 y=1.932x+0.080 不精密度：1.05%
结果 血镁（Mg）浓度在 0.08-2.02mmol/L 范围内相关性良好，定值准确，测定浓值与理论值|偏倚|＜2.50%，相关系数 r=0.9998，与理论值呈显著的相关性，故本次线性验证判定为通过。厂家提供的线性范围是 0.10-2.00mmol/L，实验室验证范围小于厂家提供的线性范围。经验证血镁（Mg）在 0.08-2.02mmol/L 范围内呈线性。
结论 该试验使用的镁检测试剂盒在准确度、精密度、可报告范围、参考区间等方面分析性能可靠,能满足临床应用需要。

PU-2210

梗阻性黄疸患者脂蛋白代谢异常的原因及临床意义

旋瑀
沈阳金域医学检验所有限公司

目的 部分梗阻性黄疸患者的脂蛋白代谢存在异常，本次实验探讨这类患者的实验室指标特点及临床意义。
方法 以 2020 年我公司检测的 200 例梗阻性黄疸患者作为研究对象，检测肝功、肾功、血糖、血脂等实验室指标，筛选出（HDL-c+LDL-c）/TC 小于参考范围的 120 例患者。分析梗阻性黄疸伴（HDL-c+LDL-c）/TC 异常组（n=120），单纯性梗阻性黄疸组（n=80）和正常对照组（n=100）肝功、肾功、血糖、血脂等实验室指标的差异，分析梗阻性黄疸伴（HDL-c+LDL-c）/TC 异常组（HDL-c+LDL-c）/TC 比值与其他指标的相关性。
结果 部分梗阻性黄疸患者的（HDL-c+LDL-c）/TC 比值存在异常，表现为极低浓度的高密度脂蛋白胆固醇和低密度脂蛋白胆固醇，（高密度脂蛋白胆固醇+低密度脂蛋白胆固醇）/总胆固醇比值降低，载脂蛋白 B（ApoB）浓度与低密度脂蛋白胆固醇（LDL-c）浓度不匹配。梗阻性黄疸伴（HDL-c+LDL-c）/TC 异常患者的各项肝功能指标如总胆红素（TBIL）、直接胆红素（DBIL）、丙氨酸氨基转移酶（ALT）、天冬氨酸氨基转移酶（AST）、碱性磷酸酶（ALP）、γ-谷氨酰转肽酶（GGT）高于健康对照组与单纯性梗阻性黄疸患者（P<0.05），而总蛋白（TP）和白蛋白（ALB）)低于健康对照组与单纯性梗阻性黄疸患者（P<0.05）。梗阻性黄疸伴（HDL-c+LDL-c）/TC 异常患者（HDL-c+LDL-c）/TC 比值与总胆红素（TBIL）、直接胆红素（DBIL）呈负相关，相关系数为-0.621 和-0.659（P<0.05）。
结论 部分梗阻性黄疸患者的高密度脂蛋白胆固醇和低密度脂蛋白胆固醇浓度极低，造成（高密度脂蛋白胆固醇+低密度脂蛋白胆固醇）/总胆固醇比值显著降低，该比值降低可能与肝功能异常有关，提示这类患者病情加重的可能。

PU-2211

电化学发光分析仪测定促甲状腺激素的分析性能评价

王明然
沈阳金域医学检验所有限公司

目的 对在罗氏 Cobas 8000 e602 电化学发光分析仪上用电化学发光免疫分析法检测促甲状腺激素[TSH]的分析性能进行评价，判断其是否能满足实验室及临床需求。
方法 参考国家卫健委、美国临床和实验室标准化协会（CLSI）发布的行业标准和相关文件，结合工作实际从精密度、线性、正确度、临床可报告范围、以及生物参考区间几个方面进行评价。
结果 TSH 重复性不精密度 CV（%）、中间精密度 CV（%）两个水平均小于室间质评允许总误差的要求。取接近厂家线性的低值和高值标本各一例，按照低值、低值与高值 4:1、3:2、2:3、1:4、高值配比成 6 例标本，重复测定三次，通过 SPSS 软件计算得出最适方程，同时计算测定浓度均值并与理论值进行相关性分析，计算出 r 值及均值偏差，要求 r≥0.98,均值|偏倚<12.5%，最适方程为 y=0.261x+100.472，不精密度：1.19%，回归线相关系数 r=1.0051，r^2=0.9997
回归线斜率 b=1.0051，回归线截距 a=0.2281，测定浓值与理论值|偏倚|<12.5%，相关系数 r=1.0051，与理论值呈显著的相关性。最大稀释倍数为 10 倍，临床可报告范围是 0.005-996.90μIU/mL。胆红素 41mg/dL 以下、溶血 1000mg/dL 以下、脂血 1500mg/dL 以下对 TSH 测定结果检测干扰的偏移量都小于等于 10%。以健康人群 20 例样本验证实验室引用的参考区间，1/3 规则无离群值，不需补充数据，无超出情况，均在正态-95%置信区间内。
结论 根据以上方法精密度、线性范围、临床可报告范围、参考区间验证等，以此对促甲状腺激素[TSH]检测项目作出方法性能评价，在此次评价过程中未发现性能不可接受的状况，说明该检测方法的分析性能被接受，满足我室临床标本检测的要求。

PU-2212

Current understanding and management of plasma cell mastitis: Can we benefit from what we know?

Jiexin Zhang、Shichang Zhang
Department of Laboratory Medicine, The First Affiliated Hospital of Nanjing Medical University

Background Plasma cell mastitis (PCM), also known as mammary duct ectasia, is a chronic nonbacterial breast inflammation characterized by duct expansion and plasma cell infiltration. The severe and intense clinical manifestations profoundly affect the quality of life of female patients. Although the pathological process of PCM is known to include four stages (duct dilatation, inflammation, abscess and fistula), there is still lack of imaging techniques and serum markers with high specificity in clinical practice. Due to recurrent acute attacks and the prolonged healing process of the disease, most patients choose to accept mastectomy.
Methods We searched for studies, reports and reviews referring to PCM in the past 20 years; more than half of the results were related to animal studies, and little attention has been paid to human beings, which may explain the frequent misdiagnosis of PCM as breast cancer and the limited treatment options.
Results This review focuses on the current diagnostic Methods and markers for PCM and hierarchically discusses the typical clinical features, etiological causes and relevant molecular mechanisms of PCM.
Conclusion We herein highlight the urgent need to develop more specific and sensitive biomarkers in clinical laboratory. It will help to establish a standardized flowchart for the diagnosis and treatment of PCM in order to improve recovery for female patients.

PU-2213

碱性磷酸酶、同型半胱氨酸和游离脂肪酸在急性脑梗死预后评估中的应用价值

李齐光、梁雅茹
广州医科大学附属第六医院/清远市人民医院

目的 探讨碱性磷酸酶、同型半胱氨酸和游离脂肪酸对急性脑梗死患者预后的评估价值.
方法 选取 435 例急性脑梗死患者作为研究对象,根据患者脑梗死发作后第 30 天 Rankin 量表评分的结果将患者分为预后良好组和预后不良组,比较分析两组患者的临床资料和各项实验室指标.
结果 多变量 Logistic 模型得出碱性磷酸酶(alkaline phosphatase,ALP)、同型半胱氨酸(homocysteine,Hcy)、游离脂肪酸(free fatty acid,FFA)与急性脑梗死患者的预后不良密切相关,3 种指标的优势比和 95%的可信区间分别为:ALP(1.091;1.058～1.124),Hcy(0.923:0.872～0.978),FFA(0.930,0.889～0.974).
结论 碱性磷酸酶、同型半胱氨酸和游离脂肪酸的检测对急性脑梗死的预后评估有重要意义,值得临床参考应用.

PU-2214

血清同型半胱氨酸、超敏 C 反应蛋白及血脂相关指标在下肢动脉硬化闭塞症患者中的临床意义

薛枭
吉林大学第一医院

目的 探讨血清同型半胱氨酸（HCY）、超敏 C 反应蛋白（CRP）及血脂相关指标在下肢动脉硬化闭塞症（ASO）患者中的临床应用价值。
方法 收集本院 100 例 ASO 患者作为实验组，其中男 62 例，女 38 例；选取同期健康体检者 80 例作为正常对照组，其中男 46 例，女 34 例。检测所有受试对象空腹血的 HCY、CRP、总胆固醇（TC）、甘油三酯（TG）、高密度脂蛋白胆固醇（HDL-C）、低密度脂蛋白胆固醇（LDL-C）水平；HCY 采用循环酶法，CRP 采用免疫比浊法，TC 采用 CHOD-PAP 法，TG 采用采用 GPO-PAP 法，HDL-C 和 LDL-C 采用直接法-过氧化物酶清除法；采用统计学方法分析比较 ASO 组和对照组各指标之间的水平差异。
结果 ASO 组血清 HCY、CRP、TC、TG 和 LDL-C 的水平均高于对照组，差异有统计学意义（P<0.05）。
结论 HCY、CRP 等指标在下肢动脉硬化闭塞症的诊断中有一定的临床价值。

PU-2215

餐后血糖代谢过程动力学建模与体外血糖调控优化设计

张婉
中日友好医院

目的 本项研究通过给予大鼠三种不同的膳食研究，探究不同营养成分食物摄入后在体内的代谢及胰岛素和胰高血糖素分泌的互作模式，建立合适的数据公式模型，模拟体外血糖调节的规律，为 1 型糖尿病治疗提供新的可参考方案。

方法 将实验大鼠随机平均分配，设计三种膳食所含能量总量相同的不同营养成分的膳食，包括高碳水化合物饮食、高蛋白饮食和高脂饮食，按照制定的技术路线进行饲养，饲养结束后受试采集血液标本进行血糖，胰岛素，胰高血糖素及 c 肽检测，根据实验数据模拟体外血糖分泌及抑制规律，实现 1 型糖尿病血糖的体外调节。
结果 大鼠摄入相同碳水化合物含量但不同营养成分比例的食物餐后血浆葡萄糖、胰岛素、胰高糖素浓度时间序列与基于动态葡萄糖监控传感器的血糖测量数据序列相比有一定相关性，体外建立血浆胰岛素和胰高糖素浓度随血浆葡萄糖浓度和时间变化的动态生理学模型具有可行性。
结论 根据体外建立大鼠摄入不同餐食模型，采集基础数据，利用驱动建模方法建立描述皮下葡萄糖浓度、血浆胰岛素和胰高糖素浓度间动态耦合关系的状态空间模型可以为 1 型糖尿病体外精准控制血糖提供参考依据。

PU-2216

血清脂蛋白(a)与同型半胱氨酸联合检测在冠状动脉粥样硬化性心脏病诊断中的应用

陈则金、龚嫄圆、魏建威
福建省第二人民医院

目的 总结血清脂蛋白(a)与同型半胱氨酸联合检测方法在冠状动脉粥样硬化心脏病诊断中的可行性。
方法 选择我院于 2018 年 12 月—2020 年 7 月间收治的 130 例患者，并选择同一时期的 130 例健康体检者，分别对两组受试者进行血清脂蛋白(a)、同型半胱氨酸检测，比较两组受试者的临床指标差异，并总结单一指标检测与联合检测方法的临床价值。
结果 比较两组受试者的血清脂蛋白(a)与同型半胱氨酸水平，冠状动脉粥样硬化性心脏病组分别为（319.52±19.53）mg/L、（18.56±3.19）μmol/L，显著高于健康体检者，数据差异具有统计学意义（P＜0.05）。比较单一指标与联合检测在诊断冠状动脉粥样硬化性心脏病中的敏感度、特异度、准确率等数据，联合检测方法显著高于血清脂蛋白(a)与同型半胱氨酸的单一检测，数据差异具有统计学意义（P＜0.05）。比较联合检测方法与冠状动脉造影检查结果的数据差异，数据差异不显著（P＞0.05）。
结论 在本病症临床诊断，血清脂蛋白(a)与同型半胱氨酸联合检测方法能够取得更满意效果，与单一诊断方法相比具有更高检出率，因此应该成为临床诊断的首选方法。

PU-2217

估计白蛋白排泄率指标与尿白蛋白/肌酐相比是否能提高对肾脏病患者 24h 尿微量白蛋白量的评估能力？

贾宇、张弓达
郑州大学第一附属医院

目的 探讨估计白蛋白排泄率（Estimated Albumin Excretion Rate, eAER）与尿白蛋白/肌酐（ACR）相比较是否能提高评估肾脏患者 24h 尿微量白蛋白含量的准确度。
方法 回顾性分析 1721 例肾脏病患者的 24h 尿微量白蛋白定量及 ACR 的结果，其中男性 1027 例，年龄 10-86（44.12±16.08）岁；女性 694 例，年龄 9-93（46.19±15.60）岁。两种方法检测结果的间隔时间不超过 24h，且 ACR 均为晨尿。根据患者的年龄和性别计算出各自的尿肌酐排泄率，通过尿肌酐排泄率计算出每位患者的 eAER 值。以 24h 尿微量白蛋白量为金标准，分析 ACR 和 eAER 的结果，通过偏倚及四分位间距来评价两种方法的准确度，若 eAER 偏倚程度比 ACR 超出 5%及以上视为准确度提高无效，反之有效。

结果 对于评估肾脏病患者 24h 尿微量白蛋白的含量，eAER 指标比 ACR 的准确度更高。在 1721 例患者中，采用 eAER 指标计算后可有效提高的患者为 1221 例，占 70.95%。对有效提高的患者组进行分析可得，ACR 的偏倚结果在 15%及 30%以内的分别占 6.63%及 20.48%，而 eAER 的偏倚结果得到明显提升，分别为 25.39%及 48.89%。ACR 的偏倚中位数为 48.40%，而 eAER 的偏倚中位数为-26.31%。
结论 eAER 可能是一个有效提高临床评估尿微量白蛋白能力的指标。

PU-2218

糖化血红蛋白年个体内变异对糖尿病诊断的价值

张世昌
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨糖化血红蛋白(HbA1c)浓度的长期个体内生物学变异特征对糖尿病诊断的价值。
方法 收集 2011 年至 2015 年连续 5 年在本院进行健康体检的 1075 名志愿者的静脉血，进行 HbA1c 浓度测定。根据第 1 年 HbA1c 浓度分为正常组（< 5.7%）641 例、糖尿病前期组（5.7%-6.5%）310 例、糖尿病组（> 6.5%）124 例。分析不同人群 HbA1c 浓度的个体内变异。
结果 HbA1c 正常组、糖尿病前期组、糖尿病组的 HbA1c 浓度均值在男性与女性之间无显著差异（P > 0.05）；三组 2015 年 HbA1c 浓度均显著高于 2011 年（P < 0.05）; HbA1c 浓度个体内变异在糖尿病前期组中男性与女性之间均有显著差异（P < 0.05）; HbA1c 正常组、糖尿病前期组、糖尿病组的 HbA1c 浓度个体内变异分别为 3.44%、4.08%、7.40%，有统计学意义（P < 0.05）。
结论 HbA1c 浓度随着年龄增加而逐渐上升，个体内变异能更准确反映血糖控制效果，有助于糖尿病的诊断与治疗。

PU-2219

ICP-MS 法测定陕西省儿童微量元素锌的检测结果分析

郑金磊
西安金域医学检验所有限公司

目的 锌是人体内不可或缺的微量元素之一，对于儿童身体生长发育有重要作用，锌还有维持人体正常食欲、增强人体免疫力等功能。本研究讨论本地区 2020 年陕西省儿童微量元素锌的缺乏情况并更好的提供营养指导。
方法 选取 2020 年西安金域检测的 16576 例≤6 岁儿童的微量元素锌检测数据，按照年龄分为 3 组：分别为＜6 个月共 1281 例、6 个月-2 岁共 6275 例，2-6 岁共 9020 例。样品采集：用肝素抗凝管采取空腹静脉全血 1-2ml 或加有肝素抗凝的 EP 管采取末梢血 100μl。试剂与仪器：采用 0.1%TritonX-100 和 0.1%HNO3 对样本稀释 20 倍混匀后，使用电感耦合等离子体质谱法(ICP－MS)直接测定微量元素锌的含量，数据采用 SPSS22.0 统计学软件分析，以 P＜0.05 为差异有统计学意义。
结果 1、对比参考标准值，儿童微量元素锌的整体缺乏率为 30.47%，分析不同年龄段儿童微量元素锌的含量，发现不同年龄段儿童微量元素锌的平均值之间差异显著，且有统计学意义(P＜0.05)；2、其中＜6 个月微量元素锌的缺乏率为 83.61%，且平均值过低，6 个月-2 岁微量元素锌的缺乏率为 48.40%，2-6 岁微量元素锌的缺乏率为 10.45%；3、在不同性别儿童间的差异无统计学意义（P>0.05）。
结论 在儿童生长发育过程中，不同年龄段的儿童消耗微量元素锌的水平不同，＜6 个月的儿童微量元素锌的缺乏情况十分严峻，6 个月-2 岁儿童的微量元素锌的缺乏情况也十分明显，应当引起家长

和社会的重视，在各个年龄阶段都需要定期监测体内微量元素锌的含量，合理应用膳食来补充微量元素锌，维持人体内微量元素锌的平衡，以保证身体的正常生长发育。

PU-2220

Evaluation of the effect of haemolysis on quantitative chemiluminescent immunoassay results for 10 analytes

Xuejun Qin
The Affiliated People's Hospital of Fujian University of Traditional Chinese Medicine

BACKGROUND To evaluate the effect of haemolysis on the quantitative chemiluminescent immunoassay results of 10 analytes and to provide a basis for formulating specific sample rejection criteria and reviewing report Results
METHODS Haemolysis based on the clinical haemolysis index, haemolysis 1+, 2+ and 3+ samples and matched normal samples were collected. The quantitative chemiluminescent immunoassay results of 10 analytes from the two samples (haemolysis and normal) were determined and differences between the results obtained from samples with different degrees of haemolysis and those obtained from normal samples were evaluated.
RESULTS A total of 34 pairs of samples were collected, including 10 pairs of 1+ haemolysis samples, 10 pairs of 2+ haemolysis samples and 14 pairs of 3+ haemolysis samples. The quantitative chemiluminescence immunoassay detection results for the 10 analytes showed that regardless of the degree of haemolysis, the differences in Alpha fetoprotein(AFP), Carcinoembryonic antigen(CEA), Carbohydrate antigen(CA19-9), Luteinizing hormone(LH), Follicle-stimulating hormone(FSH), Ferritin(FER) between the haemolysis and normal samples were all lower than the total allowable error (TEa) based on biological variation; there were no statistically significant differences between the samples. However, the results for Insulin (INS) began to decrease significantly at a haemolytic index of 1+; Folic acid (FOL) showed an increase at a haemolytic index of 2+ and there was a significant difference at a haemolytic index of 3+.
CONCLUSIONS This research identified the analytes that are susceptible to haemolysis interference in chemiluminescent immunoassays. The influence of haemolysis on Haemolytclinical laboratory tests was closely related to the assay system used; thus, laboratories should evaluate the effect of haemolysis on their own analysis systems and define assay-specific haemolysis warning indices.

PU-2221

可溶性 ST2 的临床评估与心力衰竭的关联

陈禾惠、郭玮、王蓓丽
复旦大学附属中山医院

目的 研究可溶性 ST2 的临床评估及其与心力衰竭的关联。
方法 围绕可溶性 ST2 的生物学特性、目前主要检测手段及其在急、慢性心力衰竭诊断与预后评估中的作用作一综述。
结果 心力衰竭作为心脏疾病发展的终末阶段，具有可进展性、高发病率及病死率的特点。可溶性 ST2 作为心脏肥大、心肌纤维化的标志物，其不受年龄、性别、体重等生理学因素的影响，对心力衰竭的危险分层与预后评估都具有一定价值，尚不能替代 N 末端 B 型利钠肽原和 B 型利钠肽对心力衰竭的诊断作用，但与两者结合使用时对心衰患者发生不良心血管事件具有较高的预测价值。
结论 可溶性 ST2 对心力衰竭的诊断缺乏特异性，但其对心衰患者的危险分层及预后评估都有较好的应用前景，与传统心衰标志物联合应用能更有效地在心力衰竭患者诊断、分层、预后判断与疗效检测中起作用。

PU-2222

半定量干化学法测尿白蛋白/肌酐比值的检测性能和临床应用评价

张水检[1]、周琰[2]、邵文琦[2]、张春燕[1,2]、潘柏申[2]、王蓓丽[2]、郭玮[2]
1. 复旦大学附属中山医院厦门医院
2. 复旦大学附属中山医院

目的 对 Sysmex UC-3500 全自动尿液分析仪半定量干化学方法检测尿白蛋白/肌酐比值（ACR）的检测性能进行验证，并探讨其在肾脏疾病诊断中的应用价值。
方法 选取 2020 年 5 月-8 月，复旦大学附属中山医院厦门医院就诊的不同 ACR 等级（半定量结果 1 级-5 级）的患者新鲜尿液 170 份，分别通过全自动生化分析仪和半定量试纸条法检测尿白蛋白和肌酐，通过仪器设定计算 ACR，比较两种方法检测结果一致性。参照厂商和相关文件的验证要求，对半定量干化学法测尿 ACR 的正确度、精密度、检测下限和参考范围进行验证。同时收集 40 例表观健康者（对照组）和 40 例肾脏病患者（实验组），分别检测两组血清肌酐、尿素、尿 N-乙酰-β-D-葡萄糖苷酶、尿转铁蛋白、尿 β2-微球蛋白、尿免疫球蛋白 G、尿 α1-微球蛋白和尿 ACR，比较两组间各项参数结果是否有差异。
结果 半定量干化学法检测尿 ACR 的正确度验证均在标示浓度范围内（低值：半定量结果 1 级；高值：半定量结果 4 级-5 级）；批内 CV 为 0%，批间 CV 为 5.6%，均符合厂家声明的要求（CV < 10%）；待测标本均在参考范围内；重复检测 20 次 ACR 半定量结果为 1 级的标本，20 次测试均全部检出，且结果符合厂家声明的检测限（半定量结果 1 级）；实验组血清肌酐、尿素、尿 N-乙酰-β-D-葡萄糖苷酶、尿转铁蛋白、尿 β2-微球蛋白、尿免疫球蛋白 G、尿 α1-微球蛋白、尿 ACR 值均高于对照组，差异有统计学意义（P < 0.05）。Pearson 检验相关性分析显示，半定量试纸条检测尿 ACR 与全自动生化分析仪定量检测尿 ACR 结果具有良好相关性（r=0.943，P < 0.01）。
结论 采用半定量干化学法检测尿白蛋白/肌酐比值（ACR）检测性能可靠，可用作为对肾脏疾病诊断、筛查的有效补充，值得推广普及。

PU-2223

CKMBmass/CK 比值在心血管疾病的诊断价值探讨

田亚玲、张维贞
永州市中心医院

目的 通过检测血清肌酸激酶（CK），肌酸激酶同工酶质量（CKMBmass）水平及 CKMBmass/CK 比值，探讨 CKMBmass/CK 比值在心血管疾病中的诊断价值。
方法 选择 2019 年 8 月~2020 年 9 月在永州市中心医院住院的急性冠脉综合征（ACS）和心力衰竭患者，其中 ACS 组分为不稳定性心绞痛组 60 例、急性心肌梗死组 60 例；心力衰竭组分别为急性心衰组 60 例、慢性心衰组 66 例；对照组 60 例，检测各组患者 CKMBmass、CK 的血清学水平，并计算 CKMBmass/CK 比值，分别绘制 ROC 曲线，计算敏感性、特异性，评估其对心血管疾病的诊断价值。
结果 ACS 组血清 CK 水平、CKMBmass 水平以及 CKMBmass/CK 比值明显高于对照组以及心力衰竭组，差异有统计学意义（P<0.05）；心力衰竭组与对照组在 CK 水平上无统计学差异（P>0.05），而 CKMBmass 水平以及 CKMBmass/CK 比值与对照组相比，差异有统计学意义（P<0.05）。病例组各亚组中不稳定心绞痛组、急性心肌梗死组与对照组相比，各生化指标均有统计学差异（P<0.05）；而急性心衰组、慢性心衰组与对照组进行比较，其中除急性心衰组与对照组的 CKMBmass、CK 水平及 CKMBmass/CK 比值、慢性心衰组与对照组血清 CK 水平无统计学意义外（P>0.05），其余各组间比较均有统计学差异（P<0.05）。CKMBmass/CK 比值诊断心

血管疾病的 ROC 曲线下面积、灵敏度、特异度分别为 0.918、81.7%、96.7%，均高于 CKMBmass(0.807、79.2%、75.0%)。
结论 CKMBmass/CK 比值在心血管疾病中有一定的诊断价值，其敏感度和特异度相对较高。

PU-2224

血清 HE4、CA125 和 ROMA 指数对盆腔妇科恶性肿瘤的风险评估

罗盈
广东省人民

目的 探讨血清 HE4、CA125 和 ROMA 指数对盆腔妇科恶性肿瘤的风险评估。
方法 收集 2018 年 11 月-2019 年 8 月在广东省人民医院的妇科病区住院女性患者 495 例，根据最终病理学结果分为卵巢癌组、宫颈癌组、子宫内膜癌组、卵巢良性肿瘤组、宫颈良性肿瘤组、子宫良性疾病组。并把卵巢癌组根据不同组织学分类、FIGO 分期。选择健康体检人群 121 例为对照组。采用电化学发光法检测对照组以及不同组间的血清中 HE4、CA125 的水平，并联合患者的绝经状态计算 ROMA 值。
结果（1）卵巢癌组血清 HE4 水平和 ROMA 指数显著高于除子宫内膜癌组的其他各组（P<0.01），差异有统计学意义；（2）卵巢良性肿瘤组血清 HE4 水平和 ROMA 指数与对照组相比（P>0.05），差异并无统计学意义；（3）子宫内膜癌组血清 HE4 水平和 ROMA 指数显著高于卵巢良性肿瘤组、子宫良性疾病组、对照组，有统计学意义。（4）卵巢癌诊断效能依次为，ROMA（0.929）>HE4（0.916）>CA125（0.839），子宫内膜癌诊断效能依次为，ROMA（0.808）>HE4（0.750）>CA125（0.653）。（5）将卵巢癌组按组织学分类，上皮性癌与恶性生殖细胞肿瘤的血清 HE4 和 ROMA 比较差异有统计学意义。（6）将卵巢癌组按 FIGO 分期分组统计，患者血清 CA125、HE4 水平和 ROMA 指数在四个分期之间的差异无统计学意义，进一步分为早期（I、Ⅱ）和晚期（III、IV），两两比较，差异有统计学意义，表明 HE4 水平和 ROMA 指数与 FIGO 分期呈正相关关系。
结论 血清 HE4 水平和 ROMA 指数对卵巢癌和子宫内膜癌有较高的诊断价值，且其鉴别诊断效能高于 CA125；ROMA 指数的引入有助于提高血清 HE4 水平对卵巢癌和子宫内膜癌的诊断效能。而且，HE4、ROMA 与卵巢癌的组织学分类和临床分期显著相关，随着病情进展而水平升高。

PU-2225

Beckman Coulter AU5800 全自动生化分析仪检测血管紧张素转化酶的性能验证分析

王参军
东南大学附属中大医院

目的 对 ACE 试剂盒在 AU5800 全自动生化分析仪上的检测性能进行评价。
方法 1.正确度：参考 WS/T492-2016，选用室间质评质控品为参考物质，选择 2 个浓度水平，每批次重复测定 10 次，计算均值、SD 及偏倚，判断偏倚是否<1/2Tea。2.精密度：参考 WS/T492-2016，取配套高、中、低水平质控品各 1 支（1）批内精密度：分别连续检测 20 次，计算检测结果的均值、SD 和 CV。（2）批间精密度：每天检测 1 次，连续测定 20 天，计算均值、SD 与 CV，是否<1/3Tea。3.线性范围：参考 WS/T420-2013，取接近线性范围上限的高值血清 H（252.87），低值样本 L（去离子水）,分 L、4L+H、3L+2H、2L+3H、L+4H、H 六个浓度梯度，依次测定，重复 3 次，将实测均值与理论值进行线性回归分析，计算线性相关系数（r）。4.临床可报告范围：用

接近线性范围上限的高值血清（250U/L），按 1、1:1、1:2、1:4、1:8、1:16 稀释成 5 个稀释度，每个稀释水平分别检测 3 次，计算测定均值与理论测量值之间的偏离程度 R。以 R 在 80%~120%之间为可接受限。5.参考区间：依据 WS/T420-2013，选择体检健康者新鲜血清标本 20 例进行验证，检测结果在厂家说明书规定的参考值范围 20~68U/L 的符合率应>90%。

结果 ACE 的高、低水平的正确度的 CV 分别为 2.75%、0.78%。ACE 的高、中、低水平质控品的批内、批间精密度的 CV 分别为 5.44%、5.21%、3.73%，5.68%、5.53%、3.84%，均满足厂家说明书的要求。线性范围区间为 5~250U/L，其 R2=0.995。临床可报告范围为 5~4000U/L。参考区间为 20~68U/L,20 份标本中有 1 份标本超出范围，符合要求。

结论 ACE 试剂盒在 AU5800 生化分析仪上准确度好、重复性好，结果可靠，能满足临床工作。

PU-2226

Gender differences in the efficacy of pioglitazone treatment in nonalcoholic fatty liver disease patients with abnormal glucose metabolism

Weiyun Wu、HONG-MEI YAN
Department of Laboratory Medicine, Zhongshan Hospital, Fudan University

Background Pioglitazone is a promising therapeutic method for nonalcoholic fatty liver disease (NAFLD) patients with or without type 2 diabetes. However, there is remarkable variability in treatment response. We analyzed our previous randomized controlled trial to examine the effects of gender and other factors on the efficacy of pioglitazone in treating Chinese nonalcoholic fatty liver disease (NAFLD) patients with abnormal glucose metabolism.

Methods This is a post hoc analysis of a previous randomized, parallel controlled, open-label clinical trial (RCT) with an original purpose of evaluating the efficacy of berberine and pioglitazone on NAFLD. The total population (n = 185) was randomly divided into three groups: lifestyle intervention (LSI), LSI + pioglitazone (PGZ) 15 mg qd, and LSI + berberine (BBR) 0.5 g tid, respectively, for 16 weeks. The study used proton magnetic resonance spectroscopy (1HMRS) to assess liver fat content.

Results As compared with LSI, PGZ + LSI treatment further decreased liver fat content in women (- 15.24% ± 14.54% vs. - 8.76% ± 13.49%, p = 0.025), but less decreased liver fat content in men (- 9.95% ± 15.18% vs. - 12.64% ± 17.78%, p = 0.046). There was a significant interaction between gender and efficacy of pioglitazone before and after adjustment for age, smoking, drinking, baseline BMI, BMI change, treatment adherence, baseline liver fat content, and glucose metabolism.

Conclusion The study recommends pioglitazone plus lifestyle intervention for Chinese NAFLD female patients with abnormal glucose metabolism.

PU-2227

重组人 PD-L1 全长蛋白在巴斯德毕赤酵母中的分泌表达

战映璇、王清
青岛大学附属医院

目的 利用酵母表达系统获得重组 PD-L1,并对其生物活性进行验证。

方法 参照巴斯德毕赤酵母表达系统的密码子偏好对 PD-L1 基因序列进行优化并人工合成，构建 pPIC9k-PDL1 质粒并利用电转化方法将其插入毕赤酵母基因组中，经无组氨酸的 MD 平板初筛、不同浓度梯度的遗传霉素（G418）筛选多拷贝后，利用甲醇诱导阳性重组酵母表达，通过 SDS-PAGE 和 western blot 检测表达产物及其生物活性。

结果 成功获得稳定表达 PD-L1 的多拷贝酵母菌株，其表达的 PD-L1 相对分子质量约为 46kDa。
结论 成功获得有生物学活性的重组人 PD-L1 蛋白，可用于进一步研究。

PU-2228

免疫球蛋白及补体在矽肺中的含量及作用分析

贺腊姑
湖南省职业病防治院

目的 研究矽肺患者血清中的免疫球蛋白及补体的含量变化，为矽肺病的诊断、分期以及防治工作提供帮助。
方法 根据《职业性尘肺病的诊断》(GBZ70－2015)诊断标准选取湖南省职业病防治院 300 例不同期别的矽肺病人以及职业健康体检者 100 例,检测血清中的免疫球蛋白和补体的含量。
结果 矽肺病人组与对照组相比，矽肺患者血清中的免疫球蛋白增高，尤其是 IgG 和 IgA 的含量升高最明显，且 IgG 和 IgA 随着矽肺分期的增高而增高，而补体 C4 含量下降，差异均有统计学意义(P ＜0.05)。IgG 和 IgA 含量与患病时间呈正相关，补体含量与患病时间呈负相关(P ＜0.05)。
结论 矽肺患者血清中免疫球蛋白含量升高及补体含量下降，尤其是 IgG 和 IgA 的含量升高及补体 C4 含量下降对矽肺患者临床诊断、分期、预后以及矽肺病发病机制的探讨有一定的意义。

PU-2229

TOSOH HLC-723 G11 高效液相色谱法检测糖化血红蛋白的性能评价

黄亚萍、黎春宝、徐玉兵
上海金域医学检验所有限公司

目的 对 TOSOH HLC-723 G11 高效液相色谱法检测糖化血红蛋白的性能进行验证，评价其性能是否满足实验室质量及临床诊疗的要求。
方法 按 CNAS-GL037:2019 文件的方法对糖化血红蛋白进行正确度、精密度和线性验证；按 WS/T 402 2012 的方法对参考区间进行验证；携带污染采用连续进样高、低值样本各三次的方法进行验证，计算携带污染率。
结果 与参考仪器（TOSOH HLC-723 G8）20 例样本的比对结果偏差不超过 0.2，正确度验证通过；糖化血红蛋白浓度为 5.05%的实验室重复性精密度标准差为 0.035，期间精密度标准差为 0.05，批内 CV 为 0.69%，总 CV 为 1.06%，糖化血红蛋白浓度为 10.34%的实验室重复性精密度标准差为 0.035，期间精密度标准差为 0.05，批内 CV 为 0.34%，总 CV 为 0.51%，均小于厂家声明的精密度，精密度验证通过；糖化血红蛋白线性校准品的实测值和目标值的线性回归方程为 Y = 1.0011X +0.0228，相关系数指数 r 2 为 0.9998，线性良好；20 份健康成人标本的 糖化血红蛋白检测结果均落在生物参考区间 4.0%~6.0%范围内，参考区间验证通过；无携带污染（k =0）。
结论 TOSOH HLC-723 G11 精密度高，正确度、线性良好，携带污染率低，可用于临床检测糖化血红蛋白。

PU-2230

类固醇激素 LC-MS/MS 检测用于亚临床库欣综合征患者早期筛查研究

彭颖斐、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 亚临床库欣综合征(subclinical Cushing's syndrome，SCS) 是肾上腺意外瘤中最常见的一种内分泌综合征，因缺乏典型的库欣综合征临床表现而常被漏诊和误诊。研究表明 SCS 的发生发展与类固醇激素代谢异常所导致的内分泌紊乱密切相关。
方法 采用基于前期开发的液相色谱串联质谱的靶向类固醇激素定量技术，对孕烯醇酮及其下游的 20 项类固醇激素包括孕激素、盐皮质激素、糖皮质激素、雄激素和雌激素进行系统检测。
结果 定量结果明确了 SCS 患者的血浆类固醇激素动态变化规律。17-羟孕烯醇酮（17-hydroxypregnenolone， 17-OH-PR ）、睾酮（ Testosterone， T ）和二氢睾酮（Dihydrotestosterone， DHT）等类固醇激素水平在 SCS 患者中中存在显著差异。
结论 SCS 患者外周血中 17-OH-PR/T/DHT 通路活性异常，是导致 SCS 发病的一个潜在因素。基于质谱技术的类固醇激素检测是 SCS 早期诊断和预后评估的一条新途径，并为研发治疗 SCS 新药提供理论指导。

PU-2231

20 项类固醇激素在多囊卵巢综合征患者中的差异性表达

程子韵、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 通过液相色谱串联质谱(Liquid chromatography tandem mass spectrometry, LC-MS/MS)检测多囊卵巢综合征(Polycystic Ovarian Syndrome, PCOS)患者体内 20 项类固醇激素表达情况，探讨类固醇激素检测对提高 PCOS 诊断准确性的意义。
方法 选取 2019 年 1 月至 2019 年 12 月于复旦大学附属中山医院确诊的 PCOS 患者 34 例，另外选取 80 例健康女性作为对照。PCOS 患者的诊断依据 2018 年中国多囊卵巢综合征诊疗指南中的相关标准。采用 LC-MS/MS 对受试者血清中的 T、DHEA-S、DHT、A4 和 17α-OHP 等 20 项类固醇激素进行测定及分析。
结果 LC-MS/MS 法检测 PCOS 组患者的 T、DHEA-S 和 A4 水平较对照组升高，差异存在统计学意义。对比两组患者间的 DHT、17α-OHP、17α-OHPR、孕酮及孕烯醇酮水平无统计学差异。绘制 ROC 曲线并计算曲线下面积，发现 T 和 DHEAS 两项指标诊断生化高雄激素血症的价值较高，曲线下面积分别为 0.812 和 0.785。
结论 PCOS 患者存在类固醇激素合成异常，采用 LC-MS/MS 法检测的 T 和 DHEAS 对诊断生化高雄激素血症具有一定价值。

PU-2232

慢性完全堵塞患者外周血脂质代谢标志物 LC-MS/MS 临床检测方法的建立

王真昕、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 慢性完全冠状动脉堵塞(CTO)的发生发展与脂质代谢异常所导致的脂质沉积密切相关。我们在前期研究中已阐明，CTO 患者外周血中的二酰基甘油激酶/二酰基甘油/磷脂酸（DGK/DAG/PA）通路活性异常，是导致 CTO 发病的一个潜在因素。
方法 基于非靶向脂质组学和靶向脂质组学策略相结合，系统描述 CTO 患者的脂质代谢动态变化。
结果 CTO 患者外周血磷脂酸如 PA 28:1 等生成异常，致使下游产物二酰甘油如 DAG34：5 等显著下调并最终诱发脂质代谢紊乱。
结论 为开发基于组学技术定量脂质分子用于 CTO 早期诊断和预后评估提供一条新途径。同时，该成果也为研发治疗 CTO 新药提供理论指导。

PU-2233

液相色谱-串联质谱检测血浆血管紧张素 II 方法的建立

秦嘉倩、胡玉懿、王真昕、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 建立液相色谱-串联质谱（Liquid chromatography-tandem mass spectrometry，LC-MS/MS）检测高血压患者血浆血管紧张素 II（Angiotensin II）浓度的检测方法，用于辅助临床医生进行高血压分型在诊断及高血压严重程度评估。
方法 13C15N 标记的血管紧张素 II 作为内标，采用 Phenomenex Kinetex C18（2.6μm，100mm×3mm）色谱柱进行分离。分离色谱柱温 55℃，流动相为 0.2%甲醇水溶液和 0.2%甲酸甲醇溶液，流速为 0.5mL/min 梯度洗脱。对该检测方法进行预验证，内容包括：特异性和选择性、基质效应、携带污染、重复性。预验证结果满足条件后，对该检测方法进行性能验证，内容包括：定量下限（lower limit of measuring interval，LLMI）、线性、精密度、回收率、稀释一致性和血浆标本稳定性等。采用液相色谱-串联质谱检测方法对 279 名表面健康人群（男性 146 名，女性 133 名，平均年龄 46 岁）的血浆血管紧张素 II 浓度进行检测。采用 SPSS17.0 软件进行检测结果的统计学分析。
结果 该检测方法通过了特异性和选择性、基质效应、携带污染、重复性的预验证性能评价。血管紧张素 II 的 LLMI 为 2.83pg/mL，血管紧张素 II 的检测线性范围为 2.83 pg/mL-1000 pg/mL。日间和批内不精密度的变异系数（coefficient of variation，CV）均符合要求小于 15%，准确度偏差均小于 15%，回收率结果为 94.24%-108.15%。建立的血浆血管紧张素 II 生物参考区间为 4.42 pg/mL-45.52 pg/mL。
结论 我们建立了准确检测血浆血管紧张素 II 浓度的液相色谱-串联质谱的检测方法，可用于辅助临床医生进行高血压分型诊断及高血压严重程度评估。

PU-2234

液相色谱-串联质谱检测血浆 17- 羟基孕酮在先天性肾上腺增生疾病中的应用

彭颖斐、秦嘉倩、陈方俊、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 建立一种稳定的血浆 17-a 羟基孕酮的液相色谱-串联质谱（LC-MS/MS）检测方法，并应用于先天性肾上腺增生疾病。
方法 使用 Waters 公司 UPLC XevoTQs 液质联用仪建立方法，并对该方法的定量下限、线性范围、准确度、干扰、稀释一致性、精密度和稳定性进行评价。并与免疫法进行比对。
结果 以同位素氘 8 作为内标，采用 BEH C8 色谱柱进行分离。流动相为 NH4F 和甲醇，梯度洗脱；柱温为 35℃。LC-MS/MS 检测 17-a 羟基孕酮的线性范围为 0.025～25ng/mL，定量检出限为 0.0125pg/mL，天间和批间 CV 均＜4%，回收率为 100.83%～106.8%。与免疫法进行比对，相关性较差，结合临床案例，质谱检测方法能更好的对疾病进行诊断。
结论 建立了可靠的检测 17-a 羟基孕酮的 LC-MS/MS 方法，能够灵敏、准确地检测血浆 17-a 羟基孕酮水平，并将其应用于先天性肾上腺增生疾病。

PU-2235

高效液相色谱-质谱联用法同时检测血浆中 8 种抗癫痫药物血药浓度及其在治疗药物监测中的应用

秦嘉倩、胡玉懿、王真昕、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

背景 癫痫是一种具有多种危险因素的综合性疾病，具有很强的遗传易感性。抗癫痫药治疗浓度监测的广泛运用可以达到最佳治疗效果并且避免不良反应。
方法 通过用含有内标的溶液稀释血浆样品进行样品制备。使用三重四极杆质谱仪在具有质谱检测的超高压液相系统上完成分离。该方法已根据临床和实验室标准协会的 C62-A 进行了生物分析方法验证并通过《中国液相色谱和质谱法临床指南》的验证。
结果 所有分析物在 3.5 分钟内分离并定量。该方法已通过线性验证（八种分析物的 r2 > 0.9），定量检测下限均为 50ng / ml，除了丙戊酸和奥卡西平的定量检测下限分别为 500ng / ml 和 1ng / ml。八种分析物的变异系数为 4.34％至 6.69％。批内和批间不精度均低于 15％，符合指南的要求。通过回收实验来评估准确性发现所有偏差均在目标值的±15％以内。背景峰面积/ 定量检测下限峰面积与背景峰面积/内标峰面积之比在 1％以内，表明该方法具有优异的特异性。黄疸，溶血和血脂对样品检测没有影响。
结论 我们开发了一种灵敏且稳定的方法，可以同时定量检测 8 种抗癫痫药，并将其成功应用于临床实践中。

PU-2236

缺血修饰蛋白对急性心肌梗死早期诊断的 Meta 分析

廖生俊
武汉大学中南医院

目的 采用 meta 分析系统评价缺血修饰蛋白在胸痛发生 6h 内对急性心肌梗死诊断的临床价值。
方法 检索 PubMed、Embase、中国知网、万方等中英文数据库，筛选建库以来至 2020 年 2 月关于缺血修饰蛋白在 AMI 早期诊断中的研究，采用 STATA 14.0 软件进行分析。
结果 13 个研究，共 1463 例受试者纳入 meta 分析。结果显示血清缺血修饰蛋白检测诊断 AMI 的灵敏度为 85%(95CI:0.82-0.88)，特异度为 86%(95CI:0.79-0.92)，阳性似然比为 6.3(95CI:3.9-10.1)，阴性似然比为 0.17(95 CI:0.13-0.22)，诊断比值比为 37(95CI:20-68)，SROC 曲线下的面积(AUC)为 0.90。
结论 缺血修饰蛋白对 AMI 的具有较高的诊断性能，可作为临床上早期诊断 AMI 的重要指标。

PU-2237

肝纤四项联合细胞因子在肝脏疾病中的诊断意义

周逸雯、朱晶、邵文琦、王蓓丽、郭玮
复旦大学附属中山医院

目的 本研究旨在从 AFP、PIVKA-II、AFP-L3、AFU、肝纤四项、细胞因子筛选出 HCC 早期诊断特异性的血清标志物，并创建和验证出最佳的诊断计算模型以预测 HCC 患者。
方法 本研究选取了复旦大学附属中山医院 2019 年 9 月-2020 年 9 月住院患者中 100 例乙肝并发肝癌、20 例慢性乙型肝炎、20 例乙肝相关肝硬化和 20 例良性肝肿瘤患者；同时入组 100 例健康对照组。收集了基础的流行病学资料并对其术前血清异常凝血酶原、甲胎蛋白、甲胎蛋白异质体和 a-L-岩藻糖苷酶、肝纤维四项（透明质酸、层粘连蛋白、III 型胶原、IV 型胶原）以及细胞因子等指标采用逐步 logistic 回归法评估进行回顾性分析。
结果 结果显示除 B、C 期肝癌无显著性差异外，血清 PIVKA-II 和肝纤四项水平随 BCLC 分期显著升高（P<0.05），而 AFP 水平无明显升高、细胞因子随 BCLC 分期无显著升高。血清 PIVKA-II 水平联合肝纤维四项可作为 HCC 患者预测微血管侵犯的独立风险因子。
结论 HBV-HCC 组患者血清血清 PIVKA-II 水平、肝纤四项水平明显高于良性疾病组和健康对照组患者。二者联合可作为 HCC 患者预测微血管侵犯的独立风险因子。

PU-2238

急诊实验室不合格标本原因分析及对策

杨静、周佳烨、周琰、邵文琦、朱晶、王扣琼、郭玮、王蓓丽
复旦大学附属中山医院

目的 分析急诊不合格标本产生的原因并制定相应对策，提高急诊标本分析前环节的标本质量。
方法 回顾性分析复旦大学附属中山医院急诊实验室 2018 年 1 月 1 日至 12 月 31 日记录的所有不合格标本共 501 份。根据 WS/T496-2017 中国卫生行业标准-临床实验室质量指标中的检验前质量指标进行急诊标本不合格率的统计，并分别对病人类型、日间夜间不合格情况进行统计分析，以了解急诊不合格主要原因、病人类型和采血时间对不合格原因的影响。

结果 2018 年急诊实验室标本不合格率为 6.67/万标本，其中 66%来自住院患者，22%为急诊患者，12%为监护室患者。在病区不合格标本中有 77%来自内科病房，23%来自外科病房。不合格标本最多的三种标本类型分别是血常规（EDTA 抗凝管）标本、出凝血标本（枸橼酸钠抗凝管）和生化标本（促凝胶管），分别占所有不合格标本的 31.5%、27.5%和 21.56%；其中血常规和出凝血标本的共同主要不合格原因为抗凝标本有凝块，分别占 47.1%和 47.8%，其次是标本量少，分别占 11.6%和 4.5%。生化标本最主要的不合格原因是溶血，占 21.56%。日间标本不合格标本量（占 71%）高于夜间（占 29%）。
结论 通过对不合格标本的记录和分析，积极主动与护理部和临床部门进行沟通，一同寻找原因并制定改进措施，同时我们要不断提高分析前自动化程度，希望以此能降低标本不合格率，提高急诊实验室的整体质量管理水平，保证病人诊疗安全。

PU-2239

血清一氧化氮检测与在判断血管健康状况中的应用价值

沈逸枫、邵文琦、王蓓丽、郭玮
复旦大学附属中山医院

目的 本研究旨在探讨血清一氧化氮检测在判断血管健康状况中的价值。
方法 本研究收集了临床诊断高血压患者 224 例，冠心病 PCI 术后患者 56 例，糖尿病周围血管病变患者 272 例，以及表面健康人群 60 例。收集基础的流行病学资料并采集空腹血清样本进行一氧化氮检测。比较疾病组与健康对照组的血清一氧化氮水平。根据试剂盒给定的参考范围对三个疾病组的患者进行划分，统计其人数及所占该疾病组的百分比。
结果 疾病组的血清一氧化氮水平均值（18.4μmol/L）低于健康对照组（42.7μmol/L）（P<0.05）。高血压组中有 67%（150 例）的患者 NO 低于参考范围，冠心病组中有 67.8%（56 例）的患者 NO 低于参考范围，糖尿病组中有 69.9%（190 例）的患者 NO 低于参考范围，健康对照组 NO 水平全部在参考范围内或高于参考范围。
结论 一氧化氮偏低可能提示血管内皮受损。

PU-2240

谷胱甘肽还原酶在原发性肝癌中临床应用评估

张爱伦、邵文琦、王蓓丽、郭玮
复旦大学附属中山医院

目的 对紫外酶法检测谷胱甘肽还原酶（GR）的分析性能进行评价，并探讨其在肝病中的临床应用价值。
方法 收集 120 例表观健康标本、70 例乙肝肝炎患者标本、70 例肝硬化患者标本及 70 例原发性肝癌患者标本，检测血清 GR 活性水平及其他肝功能标志物水平。对紫外酶法检测谷胱甘肽还原酶的性能（正确度、精密度、线性范围、临床可报告范围和参考区间）进行验证。采用组间单因素分析、多重线性回归分析和受试者工作特征曲线分析评估 GR 活性水平与肝损伤的相关性。
结果 紫外酶法检测 GR 定值校准品的相对偏移为-3.28%~0.51%，低于厂商声明的偏移（<10.0%）。批内变异系数（CV）为 0.93%～1.13%、批间 CV 为 0.92%～1.69%，均符合厂商声明的要求（<5%）。线性范围为 0～157.12 U/L。20 名表观健康者的血清 GR 检测结果均落在厂商声明的参考区间（33~73 U/L）内，参考区间验证通过。临床可报告范围为 0~1472U/L。对照组、肝炎患者、肝硬化患者以及肝癌患者的 GR 水平分别为 51、67、70、89U/L，差异存在统计学意义（P<0.001)。TNM 分期为 III~IV 期的原发性肝癌患者 GR 水平显著高于 I~II 期患者(P<0.01)。多因素线性回归分析结果显示，肝损伤患者 GR 活性水平与年龄、丙氨酸氨基转移酶（ALT）、天门

冬氨酸氨基转移酶（AST）和碱性磷酸酶（AKP）、透明质酸（HA）均呈正相关（r=0.095、0.335、0.370、0.356，P<0.001）。血清 GR 活性水平对慢性乙肝患者、肝硬化患者及肝癌患者的诊断切点分别为 61.4、57.8、80.8U/L，曲线下面积（AUC）分别为 0.881、0.812、0.991（P<0.001)。

结论 血清 GR 活性水平升高是肝损伤的独立危险因子，可作为临床诊断、评估肝损伤的辅助指标。

PU-2241

纤维连接蛋白在结直肠癌中的应用评估

张祎弛、邵文琦、王蓓丽、郭玮
复旦大学附属中山医院

目的 评估九强金斯尔的纤维连接蛋白(FN)试剂盒日立 HITACHI 7600 化学发光分析仪的性能。

方法 根据美国临床实验室标准化研究所(CLSI)系列文件(EP15-A2、EP6-A2、C28-A2)，对 FN 试剂盒在 HITACHI 7600 化学发光分析仪上性能进行验证。

结果 FN 批内精密度低水平为 0.74％；高水平为 0.65％。批间精密度低水平为 1.39％；高水平为 2.49％。FN 检测值与 CAP 目标值的相关系数≥0.99，FN 线性方程为 y = 1.00354x - 3.86230，r2=0.982。FN 的参考范围符合率为 100％。

结论 FN 试剂盒在日立 HITACHI 7600 化学发光分析仪上性能符合临床要求。

PU-2242

2018-2019 年血清蛋白电泳数据分析回顾

邵文琦、朱丽娜、王蓓丽、郭玮
复旦大学附属中山医院

目的 本研究对复旦大学附属中山医院 2018-2019 年所有血清蛋白电泳数据进行回顾性分析，旨在研究不同人群血清蛋白电泳区间与异常条带的分布规律，以及比较电泳法与溴甲酚绿法对白蛋白的检测性能。

方法 本研究选取复旦大学附属中山医院 2018-2019 年所有血清蛋白电泳数据，使用统计学方法，分析血清蛋白电泳各区间以及异常条带在不同性别、不同年龄人群中的分布差异情况，以及比较电泳法与溴甲酚绿法检测白蛋白结果的相关性。

结果 除 β1 区间外，其余各区间占比均存在性别差异：男性的白蛋白、α1、α2、β2 区间占比均高于女性，而女性的 γ 区间所占比例比男性更高；按照年龄以 10 岁间隔为一组进行分组，统计学结果表示各区间占比在年龄组之间均有差异：其中白蛋白区间占比随年龄的增长呈下降趋势；α1、α2、β2 以及 γ 区间占比随年龄的增长呈上升趋势，而 β1 区间随年龄变化差异未呈明显趋势；随着年龄的上升，异常条带出现的频率增高，且男性高于女性。电泳法与溴甲酚绿法检测白蛋白结果有差异，且有显著相关性。

结论 血清蛋白电泳可以根据人群的性别与年龄建立不同的参考区间，而电泳法与溴甲酚绿法检测白蛋白具有显著相关性，进一步证明了血清蛋白电泳价格低廉却在临床诊断中有不小的价值。

PU-2243

经皮冠状动脉介入治疗术后脂联素临床应用评估

倪铭晨、邵文琦、朱晶、王蓓丽、郭玮
复旦大学附属中山医院

目的 对脂联素测定试剂盒进行评价，研究经皮冠状动脉介入术（PCI）手术患者血清脂联素的浓度水平变化。
方法 评估脂联素试剂盒的基础性能指标（精密度、正确度、线性范围、参考区间、最大稀释比）；选取药物洗脱支架置入术的冠心病患者和 PCI 术的急性心肌梗死患者各 50 名，分别测定术前及术后的血清脂联素，并与 CK、CK-MB、cTnT、BNP 等指标分析相关性。
结果 试剂盒性能符合要求；冠心病患者 PCI 术前术后的脂联素水平变化不显著，急性心肌梗死患者 PCI 术后脂联素水平显著降低，与 cTnT、BNP 呈负相关（P＜0.05），与 CK、CKMB 不相关（P＞0.05）。
结论 脂联素的浓度水平变化可反映急性心梗患者 PCI 手术的心肌损伤及预后情况。

PU-2244

经皮冠状动脉介入治疗术后 AST、m-AST、m-AST/AST 的临床应用评估

邵文琦、张茜林、沈逸枫、朱晶、王蓓丽、郭玮
复旦大学附属中山医院

目的 对血清天冬氨酸氨基转移酶线粒体同工酶（m-AST）测定试剂盒进行评价，研究经皮冠状动脉介入术（PCI）手术患者血清天冬氨酸氨基转移酶（AST）、m-AST、m-AST/AST 等的变化。
方法 对 m-AST 测定试剂盒的性能（精密度、正确度、线性范围、参考区间、最大稀释比）进行评估；选取进行药物洗脱支架置入术的冠心病患者和 PCI 术的急性心肌梗死患者各 44 例，分别测定术前及术后的血清 AST、m-AST 等水平，计算 m-AST/AST 的比值，并分析与 Gensini 积分的相关性。
结果 精密度、正确度、线性范围、参考区间均通过验证，最大稀释比为 1:10；冠心病患者 PCI 术前术后血清 AST、m-AST 水平和 m-AST/AST 比值无变化，与 Gensini 积分不相关；急性心肌梗死患者 PCI 术后 AST、m-AST 水平显著升高，m-AST/AST 比值显著下降，与 Gensini 积分不相关。
结论 m-AST 测定试剂盒性能验证通过，血清 AST、m-AST 水平和 m-AST/AST 比值的变化可反映急性心肌梗死患者 PCI 手术的心肌损伤及恢复。

PU-2245

尿 NAG、NGAL 及血清 CysC 联合检测在肾病急性肾损伤诊断中的价值

董宝军[1]、曹海南[2]、王毅[1]
1. 天津市天津医院
2. 天津医科大学 医学检验学院

目的 评价尿 NAG、NGAL 及血清 CysC 联合检测在肾病急性肾损伤（AKI）诊断中的价值。
方法 选择天津医院 2020 年 5 月至 2021 年 2 月期间收治的肾病患者发生 AKI 者为研究组，总患者 100 例，其中男性 51 例，女性 49 例；另选同期非 AKI 肾病患者作为对照组，总患者 40 例，其中

男性 22 例，女性 18 例，采用 ADVIA ®2400 全自动生化仪检测所有受试者的尿 NAG、NGAL 和血清 CysC 的含量，采用 ROC 曲线比较 uNAG、uNGAL 和血清 CysC 对肾病急性肾损伤的诊断效能。

结果 ①肾病急性肾损伤组的尿 NAG、NGAL 和血清 CysC 水平明显高于肾病非急性肾损伤组（P 值均小于 0.05）。②尿 NAG、NGAL 和血清 CysC 对肾病急性肾损伤诊断的灵敏度分别为 76%、83%和 86%，三种指标联合检测的灵敏度为 93%；尿 NAG、NGAL 和血清 CysC 对肾病急性肾损伤诊断的特异性分别为 70%、80%和 82.5%，三种指标联合检测的特异性为 67.5%。uNAG、uNGAL 和血清 CysC 对肾病急性肾损伤诊断的 ROC 曲线下面积分别是 0.833、0.908 和 0.931，三种指标联合检测时 ROC 曲线下面积为 0.960。

结论 血清胱抑素 C（CysC）对肾病急性肾损伤诊断灵敏度最高，其与尿 NAG 和 NGAL 联合检测，可提高对肾病早期肾损伤的阳性诊断率，有利于患者及时的诊断和治疗。

PU-2246

不同生化检测系统丙氨酸氨基转移酶检测结果的差异评估及其临床价值

张世昌、梁婷婷
江苏省人民医院（南京医科大学第一附属医院）

目的 对比分析 2 种生化检测系统检测丙氨酸氨基转移酶(ALT)结果的差异，并明确造成结果差异的原因和探讨其潜在的临床应用价值。

方法 收集健康对照组和肾功能衰竭患者血清各 25 例，标本中添加磷酸吡哆醛(PLP) 浓度至 0.1 mmol/L，分别采用贝克曼库尔特 AU5800(试剂中不含 PLP)和强生 Vitros 5600(试剂中含 PLP)全自动生化分析仪检测各组血清中 ALT 浓度。

结果 分析仪 Vitros 5600 和 AU5800 检测质控品 ALT 结果分别为 36.9±1.7 U/L vs 33.6±1.9 U/L 和 102.9±3.0 U/L vs 100.2±3.7 U/L，相对 Vitros 5600 分析仪的检测结果偏倚分别为 8.9%和 2.6%;对照组中分析仪 Vitros 5600 与 AU5800 检测 ALT 结果无显著差异，相对偏倚为 7.7±2.2%；肾功能衰竭组中分析仪 Vitros 5600 检测 ALT 结果显著高于 AU5800 检测结果($P < 0.01$)，相对偏倚为 58.5±14.6%；添加 PLP 可显著提高肾功能衰竭组 AU5800 的 ALT 检测结果，将相对偏倚降低至 5.1±3.6%，但对 Vitros 5600 检测结果无显著影响。

结论 在健康人群中 2 种生化检测系统的 ALT 检测结果有较好的一致性，在肾功能衰竭患者中 2 种检测系统 ALT 检测结果的差异性是 PLP 缺乏造成，可用于初步判断患者维生素 B6 缺乏程度。

PU-2247

Recent advancements of human iPSC derived cardiomyocytes in drug screening and tissue regeneration

Ting Wang
The First Affiliated Hospital of Nanjing Medical University

Myocardial infarction together with subsequent heart failures are among the main reasons for death related to cardiovascular diseases (CVD). Restoring cardiac function and replacing scar tissue with healthy regenerated cardiomyocytes (CMs) is a hopeful therapy for heart failure. Human-induced pluripotent stem cell (hiPSC) derived CMs (hiPSC-CMs) offer the advantages of not having significant ethical issues and having negligible immunological rejection compared to other myocardial regeneration Methods hiPSCs can also produce an unlimited number of human CMs, another advantage they have compared with other cell sources for cardiac regeneration.

Numerous researchers have focused their work on promoting the functional maturity of hiPSC-CMs, as well as finding out the precise regulatory mechanisms of each differentiation stage together with the economical and practical Methods of acquisition and purification. However, the clinical applications of hiPSC-CMs in drug discovery and cardiac regeneration therapy have yet to be achieved. In this review, we present an overview of various Methods for improving the differentiation efficiency of hiPSC-CMs and discuss the differences of electrophysiological characteristics between hiPSC-CMs and matured native CMs. We also introduce approaches for obtaining a large quantity of iPSC-CMs, which are needed to achieve biomanufacturing strategies for building biomimetic three-dimensional tissue constructs using combinations of biomaterials and advanced microfabrication techniques. Recent advances in specific iPSC technology-based drug screening platforms and regeneration therapies can suggest future directions for personalized medicine in biomedical applications.

PU-2248

移植患者 25 羟基维生素 D 水平检测及维生素 D 营养状态

潘永圣、蒲丹、汪佳婕、孟国艳、徐宏忍、许小靓
昆明市第一人民医院

目的 维生素 D 除促进骨骼和肌肉发育外，还具有免疫调节作用。了解移植患者血清 25 羟基维生素 D [25（OH）D]水平及营养状态，为移植患者合理补充维生素 D 提供科学依据。
方法 选取昆明市第一人民医院 148 例移植患者为研究对象，采用吖啶酯化学发光法检测血清 25（OH）D 水平，分析移植患者血清 25（OH）D 水平及营养状态。
结果 148 例移植患者血清 25（OH）D 水平为 22.10±8.32 ng/ml。血清 25（OH）D 缺乏率为 43.92%（65/148），不足率为 40.54%（60/148），充足率为 15.54%（23/148）。男性患者血清 25（OH）D 水平高于女性，不同性别血清 25（OH）D 水平差异有统计学意义（t=3.314，P<0.01）；女性患者的缺乏率（52.86%）高于男性（35.90%），血清 25（OH）D 的缺乏、不足和充足率在男女性患者间差异有统计学意义（χ^2=10.694，P<0.01）。
结论 移植患者维生素 D 充足率仅为 15%左右，维生素 D 作为移植术后预后指标之一，应确定移植患者补充维生素 D 的有效和安全剂量，并给予补充。

PU-2249

ICP-MS 法检测微量元素内标元素的选择应用解析

陈振朋
西安金域医学检验所有限公司

目的 电感耦合等离子体质谱仪（ICP-MS）是无机元素分析的尖端仪器之一。ICP-MS 法在应用过程中，为了减少样液的基体效应，使 ICP-MS 法的测定结果准确，通常会使用内标法。内标的工作原理是以假定分析元素与内标元素在等离子体中的行为相似为前提的，因此选择合理的内标非常重要。
方法 内标的确定一般从以下两个方面考虑：
1.内标元素选择原则：1)待检样本中不含该元素；2）通过质量数选择，一般内标元素质量数应与待测元素接近；3）依据电离能的匹配性进行选择，如高电离能一般匹配高电离能的内标元素；4）化学性质相近。
2. 内标元素浓度的确定：内标的浓度是由基体的复杂性决定的，一般基体的 TDS 越大，内标的浓度应越大，如干净的机体（TDS＜0.01%）时基体基本不会存在污染，内标浓度在 1-10ppb，中度基体（TDS＜0.1%），基体存在轻微污染，内标浓度在（10-50ppb），对于更高的 TDS 基体，根据实际情况选择更高浓度的内标。在考虑基体 TDS 外，内标浓度落在标准品中间浓度附近为宜。

结果 内标不仅可以矫正检测结果，每天还可以根据内标的响应值来判断仪器的状态，内标回收率要求在 70%-130%。若发现内标响应不在范围内，考虑检测系统污染、内标引入问题、内标溶液问题、样品机体影响以及样本中含有内标元素等；内标 RSD 过大时应考虑进样管否破损、进样管松弛无法提升样品、泵管夹松紧程度是否合适、管路中是否有气泡。排除以上问题后可能是仪器预热时间不够引起，可重新定标。
结论 使用 ICP-MS 检测微量元素，选择合适的内标元素不仅可以提高检测的准确性，同时还可通过内标回收率、内标 RSD 的变化监测仪器的状态。

PU-2250

β2 微球蛋白、胱抑素 C 及尿微量白蛋白联合检测在糖尿病肾病诊断中的应用价值

崔思洋
吉林金域医学检验所有限公司

目的 探讨 β2 微球蛋白，胱抑素 C 及尿微量白蛋白联合检测在糖尿病肾病诊断中的应用价值。
方法 选取 2020 年-2021 年确诊为糖尿病肾病患者 180 例，其中单纯糖尿病患者 60 例为对照组，早期糖尿病肾病患者 60 例为 A 组，中晚期糖尿病肾病患者 60 例为 B 组，这三组均使用罗氏 cobas c702 全自动生化分析仪及其原装试剂对 β2 微球蛋白，胱抑素 C 及尿微量白蛋白进行检测，对这三组 β2 微球蛋白，胱抑素 C 及尿微量白蛋白的结果及其阳性率进行比对，并行相关性分析。
结果 B 组 β2 微球蛋白，胱抑素 C 及尿微量白蛋白的结果明显高于对照组与 A 组，A 组 β2 微球蛋白，胱抑素 C 及尿微量白蛋白的结果明显高于对照组，差异均具有统计学意义（P＜0.05），三者联合检测各组患者阳性率均高于 β2 微球蛋白，胱抑素 C 及尿微量白蛋白单独检测，差异具有统计学意义（P＜0.05），经分析，β2 微球蛋白，胱抑素 C 及尿微量白蛋白水平与糖尿病肾病发展进程呈正相关。
结论 β2 微球蛋白，胱抑素 C 及尿微量白蛋白三者联合检测可提高糖尿病肾病的阳性检出率，有助于诊断早期糖尿病肾病，为治疗方案的确定提供参考依据。

PU-2251

慢性乙肝患者 Q-HBsAg、HBV-DNA（内标法）与 ALT 联合的临床价值

陈敏静
广东省人民医院

目的 回顾性分析慢性乙型肝炎（CHB）患者乙肝表面抗原定量监测（HBsAg quant，Q-HBsAg）、乙肝病毒核酸检测 HBVDNA（内标法）、乙肝 e 抗原（HBeAg）和丙氨酸氨基转移酶（ALT）的相关性及其应用价值。
方法 收集 89 例慢性乙型肝炎患者的 Q-HBsAg、HBeAg、HBVDNA（内标法）和 ALT 共 4 个检测指标，根据 HBeAg 结果其分为 HBeAg 阳性组和 HBeAg 阴性组。采用 Spearman 秩相关分析对 Q-HBsAg、HBVDNA（内标法）和 ALT 进行相关性分析；采用 Wilcoxon 秩和检验对 HBeAg 阳性组和 HBeAg 阴性组的 Q-HBsAg、HBVDNA（内标法）和 ALT 进行对比分析；再将 HBeAg 阳性组的 HBVDNA（内标法）数据分为 HBVDNA＜20000IU/ml 和 HBVDNA≥20000IU/ml，HBeAg 阴性组的 HBVDNA（内标法）数据分为 HBVDNA＜2000IU/ml 和 HBVDNA≥2000IU/ml 进行比较，并作 ROC 曲线进行分析。

结果 通过分析得出 Q-HBsAg、HBVDNA（内标法）和 ALT 之间存在正相关性；在 HBeAg 分组比较中只有 Q-HBsAg 在 HBeAg 阳性和阴性组中有显著差异，其余无显著差异；而 HBeAg 阳性组的 ALT 在 HBVDNA 分组比较中有显著差异，HBeAg 阴性组的 Q-HBsAg 在 HBVDNA 分组比较中有显著差异。

结论 CHB 患者的 Q-HBsAg、HBVDNA（内标法）和 ALT 均有一定的相关性，在 HBeAg 阳性的患者中，ALT 能一定程度反映 HBVDNA 载量，适用于无核酸检测时，对患者病情的判断。Q-HbsAg 对判断 HBeAg 阴性的患者 HBVDNA 的载量会相对准确。

PU-2252

Electrochemical detection of methotrexate in serum sample based on the modified acetylene black sensor

Ziwen Deng、Hui Li、Qingwu Tian、Yusun Zhou、Xiaomin Yang、Yang Yu、Bing Jiang、Yinghua Xu、Tingting Zhou
The Affiliated Hospital of Qingdao University

A novel acetylene black (AB) sensor modified with stearyltrimethylammoniumbromide (STAB) was fabricated and applied to the determination of methotrexate (MTX) in serum. For the strong adsorption of STAB and the high catalytic capacity of AB, the prepared sensor performed better adsorption and electrochemical catalysis capacity compared with acetylene black paste electrode (ABPE). Several factors affecting the performance of the sensor, such as the construction of the sensor and the parameters affect the electrochemical catalysis were optimized carefully on sequences in this study. The prepared sensor showed favorable performance in the determination of MTX with the linear range of 0.005 μM to 7.0 μM and the detection limit of 3.07 nM. Furthermore, the fabricated sensor exhibited good stability and repeatability, which was of importance in the electrochemical detection. Finally, the established electrode was employed in the detection of MTX in real sample of serum, which demonstrated the reliable and accurate of the prepared method. It is obvious that the prepared sensor existed great potential in the determination of MTX, which could provide a new approach for the fast and low-coat detection for MTX.

PU-2253

Comparison of MPL-ANN and PLS-DA models for predicting the severity of patients with acute pancreatitis: an exploratory study

Xinrui Jin[1]、Zixuan Ding[1]、Tao Li[1]、Jie Xiong[2,3]、Gang Tian[1]、Jinbo Liu[1]
1. Affiliated Hospital of Southwest Medical University
2. 西南医科大学
3. 成都军区总医院

Objective Acute pancreatitis (AP) is a common inflammatory disorder that may develop into severe AP (SAP), resulting in life-threatening complications and even death. The purpose of this study was to explore two different machine learning models of multilayer perception-artificial neural network (MPL-ANN) and partial least squares-discrimination (PLS-DA) to diagnose and predict AP patients' severity.

Methods The MPL-ANN and PLS-DA models were established using candidate markers from 15 blood routine parameters and five serum biochemical indexes of 133 mild acute pancreatitis (MAP) patients, 167 SAP (including 88 moderately SAP) patients, and 69 healthy controls (HCs). The independent parameters and combined model's diagnostic efficiency in AP severity

differentiation were analyzed using the area under the receiver operating characteristic curve (AUC).
Results The neutrophil to lymphocyte ratio (NLR) is the most useful marker in 20 parameters for screening AP patients [AUC = 0.990, 95% confidence interval (CI): 0.984–0.997, sensitivity 94.3%, specificity 98.6%]. The MPL-ANN model based on six optimal parameters exhibited better diagnostic and predict performance (AUC = 0.984, 95% CI: 0.960–1.00, sensitivity 92.7%, specificity 93.3%, accuracy 93.0%) than the PLS-DA model based on five optimal parameters (AUC = 0.912, 95% CI: 0.853–0.971, sensitivity 87.8%, specificity 84.4%, accuracy 84.8%) in discriminating MAP patients from SAP patients.
Conclusion The results demonstrated that the MPL-ANN model based on routine blood and serum biochemical indexes provides a reliable and straightforward daily clinical practice tool to predict AP patients' severity.

PU-2254

79 例 2 型糖尿病新发患者检测 HbA1c 和血脂四项水平分析

黄继伟
自贡市第一人民医院

目的 探究糖化血红蛋白（HbA1c）联合血脂四项检测水平，在 2 型糖尿病（T2DM）新发患者病情评估中的应用价值。
方法 选取四川省自贡市第一人民医院在 2020 年 1 月～12 月治疗住院的 79 例 T2DM 新发患者（实验组），以及 79 例同期在本院体检的健康志愿者（对照组）作为研究对象。两组均予以 HbA1c 和血脂四项检测，采用独立样本 t 检验比较组间差异，Pearson 双变量回归分析实验组 HbA1c 与血脂四项指标的相关性，并计算单独与联合检测的阳性率。
结果 实验组 HbA1C、CHOL、TG 和 LDL-C 检测水平均高于对照组，HDL-C 检测水平低于对照组，组间差异均有有统计学意义（P＜0.05）。CHOL、TG 和 LDL-C 检测水平与 HbA1C 检测水平呈正相关（r 值分别为 0.65，0.72，0.49，P 值分别为 0.027，0.011，0.039），HDL-C 检测水平与 HbA1C 检测水平呈负相关（r 值为-0.51，P 值为 0.032）。单独检测 HbA1C 和血脂四项的阳性率分别为 69.62%（55/79）和 60.76%（48/79），均低于 HbA1c 联合血脂四项检测的阳性率 94.94%（75/79）,比较差异有统计学意义（P＜0.05）。
结论 T2DM 新发患者显示出 HbA1c 和血脂四项血清水平的改变。T2DM 患者中 HbAlc 水平与血脂各项指标具有一定的相关性。联合检测 T2DM 新发患者的 HbAlc 及血脂四项水平，对 T2DM 患者的病情诊断和控制、疗效观察等方面、临床诊治方案的制定提供可靠支持依据，具有非常重要的意义。

PU-2255

一例异常微量元素铜检测结果分析

陈振朋
西安金域医学检验所有限公司

目的 铜是人体必需微量元素之一，其主要的生物学功能为将肠上皮细胞吸收的二价铁转化为三价铁，从而实现铁在血液里的运输。但是，体内铜含量过高也会对机体产生危害，甚至危及生命。因此监测体内铜含量，尤其是铜相关行业从业人员体内铜含量，及时发现及时干预非常重要。
方法 本患者送检样本为全血五元素(包括铜、锌、钙、镁、铁)，使用检测方法为电感耦合等离子体质谱法。
结果 结果显示该患者铜含量为 20000ug/L（参考范围：720-1750ug/L），其他元素未见异常。患者年龄 55 岁，性别男性。对原样本进行复查后，结果符合。与临床沟通，该患者从事铜冶炼工作

30 年，临床表现有肺部造影，神经炎，神经衰弱，咯绿色痰，轻微发热，细菌培养未检出致病菌。首先患者有肺部造影，可以判断患者体内过多的铜是通过呼吸道吸收，若是胃肠道，则有胃肠道表现，比如食欲不振、腹痛腹泻，同时大量的铜从肠上皮细胞被动扩散进入体内，会导致肠上皮破坏，其他元素吸收障碍，含量减低。其次金属元素经呼吸道吸收时会有类流感样发热表现，称之为金属热。结合以上分析结果及患者从事行业，判断该患者为慢性职业性铜中毒。

结论 慢性职业性铜中毒因患者呼吸道铜屏障已破坏，因此治疗前首先需脱离目前从事行业。服用铜螯合剂治疗，同时可使用可的松加速肾对铜的清楚。另外金属元素中毒时，在治疗之前，首先需要确定中毒的来源，只要及时脱离污染源，治疗方可有效。

PU-2256

福州地区人群血清游离脂肪酸参考区间的建立

石安然
福建医科大学附属协和医院

目的 建立福州地区人群血清游离脂肪酸的参考区间，并比较不同性别之间、不同年龄层之间血清游离脂肪酸浓度有无差异性。

方法 收集选取 2016 年 1～9 月于福建医科大学附属协和医院检验科体检中心体检的健康人群血清游离脂肪酸浓度资料共 1212 例进行统计分析。

结果 福州地区健康人群血清游离脂肪酸 95%参考区间为 0.12～0.80mmol/L,性别因素对于血清游离脂肪酸浓度差异有统计学意义（$p<0.05$），男性 95%参考区间为 0.10～0.80mmol/L，女性 95%参考区间为 0.14～0.83mmol/L，女性血清游离脂肪酸浓度较男性高；而年龄层分布在男性或者女性皆对血清游离脂肪酸浓度差异没有统计学意义（$p>0.05$）。

结论 已建立福州地区血清游离脂肪酸浓度参考区间。本研究表明性别因素对于血清游离脂肪酸浓度差异有统计学意义，而年龄层分布在男性或者女性皆对血清游离脂肪酸浓度差异没有统计学意义。

PU-2257

POCT 血糖仪与全自动生化分析仪检测血糖结果的比对分析

刘杭敏
福建医科大学附属协和医院

目的 通过福建医科大学附属协和医院各个病区 POCT 血糖仪和全自动生化分析仪检测血糖浓度的差异，以评估临床 POCT 血糖仪的可靠性以及纵向分析近三年血糖仪比对结果从而明晰床旁检验管理制度的完善程度。

方法 2018 年 3 月 7 日及 2018 年 4 月 4 号利用医院 LIS 系统收集五份 EDTA 抗凝全血（分别覆盖高、中、低三个浓度水平）用 40 台 POCT 血糖仪测定其浓度，设为试验组，随后用全自动生化分析仪测定其血糖浓度，为对照组。用 SPSS 软件比较两种测定血糖方法的差异。

结果 各个病区 POCT 血糖仪和全自动生化分析仪检测结果相关性良好，部分结果略低，二者比较的结果差异有统计学意义，但符合 ISO15179:2013 比对要求。

结论 临床各个病区 POCT 血糖仪和全自动生化分析仪相关性较好，可用于临床血糖监测和糖尿病患者筛查，但不可完全替代全自动生化分析仪对血糖的检测；近四年临床 POCT 血糖仪管理呈现出较大的上下波动形势，提示临床 POCT 血糖仪规范化管理有待加强。

PU-2258

New Method for the Diagnosis of Pheochromocytomas and Paragangliomas by Spot Urinary Free Metanephrines and 3-Methoxytyramine with Internal Reference Correction

Haoran Wang
Suzhou Dushu Lake Hospital
重庆医科大学

Background Quantification of urinary free normetanephrine (NMN), metanephrine (MN) and 3-methoxytyramine (3-MT) could be used to diagnose pheochromocytomas and paragangliomas (PPGLs). Our aim is to develop a simple and specific method for the detection of spot urinary free NMN, MN and 3-MT and its application in the diagnosis of PPGLs.
Methods Spot urinary free normetanephrine (NMN), metanephrine (MN), 3-methoxytyramine (3-MT) were detected by HPLC with fluorescence and combined with simultaneous detection creatinine (Cr) by ultraviolet detection. This assay enrolled 37 patients with PPGLs and 164 control subjects without PPGLs. The peak area ratios of NMN, MN, and 3-MT to Cr were established innovatively in the diagnosis of PPGLs. The chromatograms of spot urine sample from a patient with PPGLs and a healthy volunteer are shown in Figure 1.
Results The intra-day and inter-day coefficient variations for the spot urinary analytes were within 4.5% and 5.8%, respectively. The results are summarized in Table 1. For all analytes, the average recoveries were in the range of 90.7–118.0% with CVs ranging from 1.9% to 4.9%, as shown in Table 2. Using peak area ratios in the diagnosis of PPGLs, the sensitivities of NMN/Cr, MN/Cr and 3-MT/Cr were 94.6%, 91.9% and 86.5%, and the specificities were 96.3%, 93.9% and 82.3%, respectively. ROC curves are shown in Figure 2.
Conclusions The novel method using peak area ratios of spot urinary free NMN, MN and 3-MT to Cr is simple, sensitive and specific for the diagnosis of PPGLs.

PU-2259

Combination of serum biochemical indices for predicting early renal injury in patients with T2DM

Zhenqiang Huang[1]、Chunsheng Qu[1]、Wei Wang[1]、Haiya Zheng[1]、Yaping Ma[2]
1. Department of Clinical Laboratory, the Sixth Affiliated Hospital, Wenzhou Medical University, Zhejiang Province, China
2. 丽水市疾控中心

Aims Diabetic nephropathy (DN) is a common long-term microvascular complication in type 2 diabetes mellitus (T2DM) patients, and is easily ignored because of inconspicuous clinical symptoms, leading to irreversible renal function failure. Individual urine/serum marker has limitations and some combinational models have been proposed in recent years to predict early renal injury of T2DM patients. This study aims to find a new model based on serum biochemical indices for predicting early renal injury in T2DM.
Materials and Methods 588 T2DM patients were recruited in the present study and were divided into two groups based on urinary albumin/creatinine ratio (UACR): 294 T2DM patients had normal-dose albuminuria (Normal group, UACR<30mg/g) and the others had micro-dose albuminuria (Micro group, 30mg/g≤UACR≤300mg/g). The two groups had similar age- and gender- distribution. Serum biochemical indices were measured with AU5800 automated bio-analyzer. In addition, 142 T2DM patients (89 cases for Normal group and 53 cases for Micro group) were enrolled for further diagnostic test.
Results GLB (serum globulin), TP (serum total protein), TG (triglycerides), BUN (blood urea nitrogen), Scr (serum creatinine), ADA (adenosine deaminase) and MAO (monoamine oxidase)

were significantly increased in Micro group compared with that of Normal group, but ALT (alanine transaminase) and GPDA (glycylproline dipeptidyl aminopeptidase) were statistically decreased. GLB (r=0.278, p<0.001), TP (r=0.175, p<0.001), TG (r=0.094, p=0.022), BUN (r=0.099, p=0.016), Scr (r=0.115, p=0.005) and ADA (r=0.221, p<0.001) had positive correlations with UACR, and GPDA (r=-0.116, p=0.005) had a negative relationship, however, MAO (p=0.181) and ALT (p=0.061) had no statistical significant correlations. Binary logistic regression showed that the predictive probability of early renal injury (P) could be calculated by the regression equation Ln (P/(1-P)) = -4.403 + 0.113 GLB + 0.023 Scr + 0.083 ADA - 0.018 GPDA. The AUC of the equation was 0.715 (p<0.001, 95% CI: 0.674-0.756), and the optimal critical value of that was 0.454, with 72.7% predictive sensitivity and 60.5% predictive specificity, showing highest AUC and the optimal sensitivity and specificity, compared with individual serum biochemical markers. This optimal critical value got 71.7% actual sensitivity and 59.6% actual specificity for the equation with diagnostic test.
Conclusions The new model could be used for predicting early renal injury of T2DM patients to prevent clinicians from misdiagnosis.

PU-2260

Relationships between TyG and liver enzymes in MAFLD: a retrospective cross-sectional study

Zhi Liu、He He、Yuzhao Dai、Lidan Yang、Shenling Liao、Zhenmei An、Shuangqing Li
West China Hospital of Sichuan University

Background The triglyceride and glucose index (TyG) was a new combination of fasting plasma glucose (FPG) and triglyceride (TG), which was found to be a substitude marker of insulin resistance. We aimed to investigate the relationship between TyG and liver enzymes in order to recognize individuals at risk for MAFLD and better diagnose it.
Methods A retrospective cross-sectional study was carried out in West China hospital of Sichuan University and 248 people (109 Metabolic-Associated Fatty Liver Disease (MAFLD) and 139 Non-MAFLD) were included. Biochemical indexes from blood were measured. MAFLD was diagnosed by Ultrasound.
Results Serum ALT, AST, GGT and TyG were higher in MAFLD group than Non-MAFLD. The correlation coefficients of TyG and ALT, AST, GGT were 0.556, 0.509 and 0.555 respectively (all p<0.01). Through binary logistics regression analysis, the odds ratio of ALT and TyG were 1.146 (95%CI: 1.090-1.205) and 17.389 (95% CI: 4.133-73.158) after adjusting age and gender. In addition, the combination of age, gender, BMI, ALT and TyG had a greater diagnostic efficiency for MAFLD. MAFLD with diabetes mellitus (DM) or Hyperlipidemia (HPL) expressed a higher level of TyG than MAFLD alone, both of them differed from the control group in TyG.
Conclusions TyG has moderate relationship with liver enzymes and is a potential risk factor for MAFLD. The combination of age, gender, BMI, ALT and TyG improves the diagnostic capability of MAFLD.

PU-2261

高海拔地区居民红细胞代谢相关血清学指标分析

刘治娟[2]、邹雨桶[1]、刘小星[3]、田丽萍[4]、李洪雷[1]、侯立安[1]、马超超[1]、王丹晨[1]、羊红燕[2]、邱玲[1]
1. 中国医学科学院北京协和医院检验科
2. 西藏自治区人民医院检验科
3. 西藏阿里地区人民医院检验科
4. 西藏林芝地区妇幼医院检验科

目的 探讨西藏地区居民红细胞代谢相关血清学指标分布及主要的影响因素，建立西藏地区相关指标的参考区间。
方法 2016 年 9 月至 2018 年 8 月，采用标准调查问卷整群随机抽取西藏阿里地区、拉萨市、日喀则市和林芝市人群 1615 名，测定血常规、血清铁(Serum Iron ,SI)、未饱和铁(Unsaturated iron binding capacity,UIBC)、铁蛋白(Ferritin, FER)、转铁蛋白(Transferrin ,TRF)、叶酸(folic acid ,FA)、维生素 B12(Vitamin B12,Vit B12)，换算转铁蛋白饱和度(Transferrin saturation, TSAT)等指标。
结果 西藏地区男性 SI、TSAT、FER 水平显著高于女性，而 TRF、FA、,UIBC 水平则显著低于女性。SI、TRF、FER 和 Vit B12 呈现随海拔降低而降低的趋势，TRF 和 UIBC 在拉萨和日喀则地区中呈现最高分布水平。TRF 和 UIBC 呈现出随年龄升高而降低的趋势，而 FER 则呈现随年龄升高而升高的趋势，Vit B12 在 30-39 岁的年龄组中呈现最高分布水平。FA、Vit B12 和 SI 的分布与饮食密切相关。与行业标准相比，西藏地区男性 SI 的参考区间明显偏低，女性 SI 的参考区间分布更宽。
结论 高海拔地区居民铁代谢指标存在生理性差异，与平原地区分布也存在不同，应针对西藏地区建立铁代谢指标的参考区间。

PU-2262

血脂与糖化血红蛋白检测应用于糖尿病诊断的意义研究

吴萍萍
上海迪安医学检验所有限公司

目的 对糖尿病诊断中的血脂与糖化血红蛋白检测应用价值进行分析，为糖尿病的临床诊断实践提供参考。
方法 对 2019 年 1 月到 2019 年 12 月期间的 60 例糖尿病患者及 60 例健康体检人群的血液样本进行血脂与糖化血红蛋白检测，对比两组人群的血脂与糖化血红蛋白检测结果。
结果 与健康体检人群相比较，糖尿病患者的糖化血红蛋白及甘油三脂、血清总胆固醇、低密度脂蛋白胆固醇明显更高，而高密度脂蛋白胆固醇则显著更低，各项指标对比差异均具有统计学意义。
结论 在糖尿病的诊断中，血脂与糖化血红蛋白联合检测具有较高的应用价值，能够辅助准确筛查、诊断糖尿病患者，值得加强推广。

PU-2263

大庆市 603 例孕妇血清维生素 A 与 25- 羟基维生素 D 水平调查分析

谢曙光、李玲
广州金域医学检验中心

目的 分析大庆市孕妇血清维生素 A（VitA）、 25- 羟基维生素 D（25-OH-D）水平，为大庆地区孕妇孕期合理补充维生素提供科学依据。
方法 通过分析 2019 年 1 月-12 月大庆市 603 例孕妇血清样本送往本中心实验室用质谱方法检测维生素 A、25- 羟基维生素 D（25-OH-D）的实验数据。
结果 603 例调查对象中，维生素 A、D 在不同年龄、不同孕期、不同季节均有不足及缺乏。VitA 在 30 岁以下与 30 岁以上两组平均水平差异有统计学意义（P=0.003），其中 30 岁以下 VitA 不足及缺乏占比 19.94%，30 岁以上不足及缺乏占比 2.83%。VitA 在孕早期、孕中期、孕晚期进行两两比较，孕中期与孕晚期孕妇 VitA 平均水平差异有统计学意义（P=0.032），在孕晚期平均水平最低，其他组间无差异。VitA 不同季节进行比较，组间差异无统计学意义（P＞0.05），夏季 VitA 平均水平最低，冬季平均水平最高；25-OH-D 平均水平在 30 岁以下与 30 岁以上两组差异无统计学意义（P＞0.05），不同年龄组 25-OH-D 不足及缺乏差异无统计学意义（P＞0.05）。不同孕期 25-OH-D 平均水平进行比较，组间差异均有统计学意义(P＜0.05)，其中孕早期平均水平（11.21±5.81ng/mL）最低，孕中期平均水（19.65±10.07ng/mL）平其次，孕晚期平均水平（23.22±10.78ng/mL）最高。25-OH-D 平均水平在不同季节进行比较，春季与秋季组间差异有统计学意义（P＜0.05），春季平均水平（16.64±10.33ng/mL）最低，秋季平均水平（21.02±17.96ng/mL）最高，其他组间差异无统计学意义（P＞0.05）。
结论 大庆市孕妇维生素 A、D 平均水平存在不同程度的缺乏，应加强对维生素 A、D 的监测，合理补充维生素 A、D。

PU-2264

帕金森病血清标志物的研究进展

胡元慧
武汉大学人民医院

帕金森病(Parkinson’s disease，PD)是一种复杂的神经退行性疾病，目前无治愈手段。该病面临无法早期诊断和难以预测疾病进展等困难。目前为 PD 早期诊断和治疗寻找可靠生物标志物受到人们关注，本文就 PD 生物标志物综述最新进展。

PU-2265

基于随机森林的空腹血糖受损诊断模型建立及验证

李迪
武汉大学人民医院

目的 构建并验证糖尿病预测模型。
方法 收集信息化数据库中空腹血糖小于 7.00 mmol/L 的患者，排除信息不全或 BMI 极度异常(BMI<15 kg/m2 或 >55 kg/m2) 的患者。最终纳入训练集 9045 例，同时纳入临床特征与之匹配的验证集 3562 例。用随机森林在训练集数据中对变量进行重要性排序，筛选变量并构建糖尿病预测模型同时进行验证。

结果 训练集与验证集的临床特征中各个变量均匹配良好（P>0.05）。训练集中，随访时间跨度为2.00-5.71 年，随访期间糖尿病共发生 61 例（6.74‰）；验证集中，随访时间跨度为 2.00-5.65 年，随访期间糖尿病共发生 20 例(5.61‰)。根据平均准确度下降程度（Mean Decrease Accuracy）对自变量重要性进行排序，用赤池信息量(AIC)准则和贝叶斯信息量(BIC)准则对模型进行筛选得出模型包含是 Change in FPG, FPG 和 Age 三个变量。在内部验证中，模型的 C 指数为 0.921，Brier Score 为 0.006，十折交叉验证平均 AUC 为 0.915；在外部验证中，模型总 C 指数为 0.921，按照预测概率分组后随着样本量下降 C 指数有所降低，但总体上仍较高。模型的 Brier Score 为 0.005。十折交叉验证平均 AUC 为 0.960。反应了本研究模型有极高的准确性。
结论 本研究建立的预测模型对糖尿病患病风险有很好的预测能力。

PU-2266

老年脓毒症患者血清降钙素原、前白蛋白和乳酸检测及临床价值

胡元慧
武汉大学人民医院

目的 探讨降钙素原（PCT）、前白蛋白（PA）和乳酸（Lac）对老年脓毒症的临床价值。
方法 回顾性研究 2019 年 1 月 1 日至 2019 年 11 月 1 日在武汉大学人民医院诊治的脓毒症患者共 81 例，按照疾病程度分为脓毒症组（28 例），严重脓毒症组（35 例）及脓毒症休克组（18 例），和同期 67 例健康人做对照，分别测定 PCT、PA 和 Lac 水平，对其临床价值进行分析。计量资料采用单样本 Kolmogorov-Smirnov 法检验各组数据是否符合正态性，正态资料多组间比较采用方差分析，进一步两两比较采用 LSD-t 检验；非正态分布资料多组间比较采用 Kruskal-Wallis H 检验，两两比较采用 Mann-Whitney U 检验。
结果 脓毒症组 PCT 和 Lac 组检测结果水平明显高于对照组，脓毒症组 PA 检测水平明显低于对照组；脓毒症组 PCT、PA 和 Lac 水平和对照组相比，差异具有显著统计意义（P<0.05）；不同指标 PCT、PA 和 Lac 水平变化情况相关性分析，PCT 和 Lac 水平与 PA 水平均呈负相关（r=-0.666、-0.489），PCT 和 Lac 水平成正相关（r=0.492）；严重脓毒症及脓毒症休克组 PCT、Lac 水平高于脓毒症组，差异有统计学意义（P<0.05）；严重脓毒症及脓毒症休克组 PA 水平低于脓毒症组，差异有统计学意义（P<0.05）。
结论 PCT、PA 和 Lac 水平有助于评估脓毒症病情危重程度。

PU-2267

酒精性肝病患者血睾酮和雌二醇水平的变化观察

谭扬
宜宾市第一人民医院

目的 观察酒精性肝病（alcoholic liver disease ALD）患者血清中睾酮（testosterone，T）和雌二醇（estradiol，E2）水平的变化。
方法 对长期嗜酒者、正常健康者进血清睾酮（T）和雌二醇（E2）、丙氨酸氨基转移酶(ALT)、天门冬氨酸氨基转移酶(AST)、γ-谷氨酰转肽酶(GGT)、外周血白细胞（WBC）和红细胞平均体积(MCV)进行检测。
结果 在 269 例嗜酒者中符合诊断 ALD（A 组）者 75 例，占 27.9%；其余者为嗜酒组（B 组）。A 组的血清 T（12.8±6.57 ）较 B 组（23.8±9.62 ）和对照组的 T（29.7±10.52 ）都降低（p＜0.001）；B 组的血清 T（23.8±9.62 ）较对照组的 T（29.7±10.52 ）水平低(p＜0.001）。A 组的血清 E2 水平（237.4±109.46）较 B 组的血清 E2 水平（133.5±66.15）和对照组的 E2 水平（128.30±54.77）明显增高(p＜0.001），B 组的 E2 水平高于对照组（p＞0.05）。

结论 嗜酒者和酒精性肝病患者血清睾酮（T）均水平降低，而在酒精性肝病患者中血清雌二醇（E2）水平增加高，嗜酒者和对照组血清雌二醇（E2）水平变化无显著差异，说明慢性酒精中毒对男性睾丸功能有一定的影响。

PU-2268

急性呼吸窘迫综合征伴严重乳酸酸中毒 1 例并文献复习

路尧、刘辰庚、王培昌
首都医科大学宣武医院

急性呼吸窘迫综合征（ARDS）和严重乳酸酸中毒（LA）都是临床上较常见的极危重症，病死率为 35%~50%[1-2]。ARDS 一旦合并 LA，其病死率将成倍增加，且预后与乳酸水平呈负相关[3]。乳酸酸中毒多数被报道为糖尿病的并发症，病死率高。国内关于 ARDS 合并 LA 的病例报道比较罕见，本例患者是本院收治的一位无既往糖尿病史，ARDS 合并 LA 的急重症患者。

PU-2269

一例使用体外膜肺氧合的重症肺炎患者乳酸变化的分析

褚怡铭、刘辰庚、王培昌
首都医科大学宣武医院检验科

在我国重症肺炎（severe pneumonia，SP）和是临床上比较常见的及危重症[1]。血乳酸是血气分析的一个重要指标，乳酸持续升高与病死率有明显的相关性。国内关于重症肺炎合并乳酸酸中毒的病例报道较少，本文分析我院一例使用体外膜肺氧合的重症肺炎合并乳酸酸中毒患者的乳酸变化情况。肌肉溶解使乳酸升高，抑制糖异生，减少肝和肌肉对乳酸的摄取，减少胃排酸功能，而减少乳酸的去路，因而乳酸堆积[5]；pO2 和 O2Sat 两个指标下降，提示机体处于低氧状态，组织细胞糖酵解增强，导致乳酸浓度升高 [6] ；体外膜肺氧合（extracorporeal membrane oxygenation，ECMO）的介入可使血气分析结果中仅 pO2 和乳酸结果异常，应予以重视。
本病例提示，使用 ECMO 的重症肺炎患者可因肌肉溶解、组织细胞糖酵解等原因出现乳酸酸中毒。ECMO 在肌溶解时纠正乳酸酸中毒的效果有限，临床应结合病情作合理的判断与处理。

PU-2270

High Level of ACE in Serum May be an Indicator for Abnormal Glucose Metabolism and Diabetic Nephropathy Progression

Kangkang Huang、Yunlai Liang、Yating Ma、jiahui Wu、Bin Yi
中南大学湘雅医院检验科

Aim Diabetic nephropathy (DN) is one of the most common complication of type 2 diabetes mellitus (T2DM), renin-angiotensin-aldosterone system (RAAS) plays a vital role in the development of DN. Moreover, AngiotensinⅡ is the most functional material of RAAS and angiotensin converting enzyme (ACE) is the key enzyme in the process from AngiotensinI to AngiotensinⅡ. Therefore, we were interested in the variation of ACE concentration in DN patients' plasma.

Methods A total of 155 participators were enrolled in this study, including 44 T2DM patients and 75 DN patients and 36 normal glycogen metabolism individuals in Xiangya Hospital of Central South University from August 2018 to February 2019. Serum levels of ACE, glycosylated hemoglobinA1c (HbA1c) and other indexes were detected with corresponding kits, and the data was analyzed with appropriate statistical Methods

Results ACE level in DN patients were significantly higher than T2DM patients and control. ACE also significantly correlates with Urine microalbumin (UmALB), blood urea nitrogen (BUN), HbA1c, urinary albumin-to-creatinine ratio (uACR), albumin (ALB), estimated glomerular filtration rate (eGFR). Meanwhile, BUN, HbA1c, UmALB, gender, ALB, eGFR were introduced into regression equation Y=2.839+0.648X1+2.001X2+0.003X3-6.637X4+0.416X5-0.134X6 (X1: BUN; X2: HbA1c; X3: UmALB; X4: gender; X5: ALB, X6: eGFR, R2=0.655). When divided DN group into subgroup, we found ACE level of advanced-stage DN patients elevated compared with early-stage DN patients.

Conclusion Higher serum ACE level could partly reflect abnormal glucose metabolism and renal dysfunction. Furthermore, high ACE serum level of T2DM patients may be an indicator for diabetic nephropathy progression.

PU-2271

Characterization of the chromatin accessibility in mouse Alzheimer's models

Yaqi Wang、Xiaomin zhang、Qiao Song、Yuli Hou、Jing Liu、Yu Sun、Peichang Wang
Xuanwu Hospital，Capital Medicine University

Background Previous studies showed that the pathological hallmarks of Alzheimer's disease (AD) are characterized by β-amyloid (Aβ) deposition, neurofibrillary tangles induced by phosphorylation of tau protein, the upregulation of inflammation and neuronal apoptosis, which involves the alteration of numerous genes. However, the molecular mechanisms of most genes participated in the pathways above remained unclear. Gene expression is associated with the transcriptional level which is decided by the chromatin accessibility. In this study, the landscape of chromatin accessibility was described to disclose the outline of the transcriptions of AD-associated metabolism and gene expression in an AD model mice.

Methods The assay for transposase-accessible chromatin by sequencing (ATAC-seq) was utilized to investigate the AD-associated chromatin reshaping in APPswe/PS1dE9 AD mouse model. The ATAC-seq data in the hippocampus of 8-month-old APP/PS1 mice was generated and the relationship between the chromatin accessibility and the gene expressions was analyzed in combination with RNA-seq. Gene ontology (GO) analysis was applied to facilitate elucidating the alteration of biological process and signaling pathways. In addition, critical transcription factors were identified and, the alteration of the chromatin accessibility was further confirmed using ChIP assays.

Results 1690 AD-associated chromatin accessible regions in the hippocampal tissues of APP/PS1 mice were identified. These regions were enriched in the signaling pathways included PI3K-Akt signaling pathway, Hippo signaling pathway, TGF-β signaling pathway and Jak-Stat signaling pathway which play essential roles in regulating of cell proliferation, cell apoptosis and inflammatory. GO analysis showed that many AD-associated biological processes declined including cellular response to hyperoxia and insulin stimulus, synaptic transmission, and positive regulation of autophagy. 1090 genes were found to be up-regulated, and 1081 genes were found to be down-regulated in the hippocampus of the AD model mice. Interestingly, enhanced ATAC-seq signal were found around 740 genes, of which 43 genes exhibited up-regulated mRNA level. Several most significantly increased genes were also identified, including Sele, Clec7a, Cst7 and Ccr6 which critically involved in the development of AD. In addition, numerous of transcription factors, including Olig2, NeuroD1, TCF4, NeuroG2 were found to enrich in the AD-associated accessible chromatin regions. Besides, the transcription-activating marks of H3K4me3 and

H3K27ac were increased in the promoters of Sele, Clec7a, Cst7 and Ccr6 gene. These results above indicated that the mechanism for the up-regulation genes could attribute to the enrichment of open chromatin regions by transcription factors and histone marks H3K4me3 and H3K27ac.
Conclusion Altogether, our study reveals that the alterations of chromatin accessibility might be an initial mechanism in AD pathogenesis.

PU-2272

脂毒性应激诱导 Bcl-2 蛋白失调致胰岛 β 细胞凋亡作用的研究

丘创华、钟丽红、彭紫元
深圳市第二人民医院

目的 探究脂毒性应激诱导 Bcl-2 蛋白失调致胰岛 β 细胞凋亡作用机制。
方法 利用 C57BL/6 小鼠构建 PUMA-/-（p53 upregulated modulator of apoptosis）小鼠，喂食高脂肪饮食。使用胶原酶 P 分离朗格汉斯小鼠胰岛，MIN6 细胞在补充有 10%FCS 的 DMEM 培养基中培养。将小鼠胰岛和 MIN6 细胞进行 FFA 或 MG132 处理，随后检测蛋白酶体活性，实时定量 PCR 和 Western Blot 检测 ATF4，Bip，Chop，Bcl-2，Bcl-XL 和 Mcl-1 表达水平，流式细胞术检测细胞死亡。
结果 FFA 棕榈酸酯可阻断泛素-蛋白酶体系统（UPS），并通过诱导 ER 应激和 Bcl-2 蛋白失调进而引起 β 细胞凋亡。棕榈酸酯和蛋白酶体抑制剂 MG132 在 β 细胞中诱导内质网应激，从而导致生存蛋白 Bcl-2，Mcl-1 和 Bcl-XL 的表达降低，且前体仅 BH3 的蛋白 PUMA 上调；萝卜硫素对 UPS 的药理作用减轻了 ER 的压力，上调了 Bcl-2 生存蛋白，保护 β 细胞免于 FFA 诱导的细胞死亡。
结论 靶向 UPS 和 Bcl-2 蛋白表达能有效预防 2 型糖尿病中 β 细胞死亡。

PU-2273

SAA 联合 CRP 在幼儿呼吸道感染疾病辅助诊断中的应用与分析

唐春进[1]、杨淑雅[2]、杨宇[3]
1. 靖江市妇幼保健院
2. 靖江市中医院
3. 常州市新北区三井人民医院

目的 分析 SAA 和 CRP 水平与幼儿呼吸道感染性疾病的相关性，探讨其在幼儿呼吸道感染性疾病诊断中的价值。
方法 选取靖江市中医院 2020 年 1 月~2020 年 12 月诊治的 134 例呼吸道感染患儿为研究对象，按照感染类型的不同将患儿分为细菌感染组（60 例）和病毒感染组（74 例）；选择 40 例健康儿童为对照组。检测并对比三组研究对象 SAA 和 CRP 的水平，分析其与幼儿呼吸道感染性疾病的相关性。
结果 细菌感染组 SAA 水平为 235.47±23.72、CRP 水平为 22.33±5.08、两者比值为 10.05±2.28；病毒感染组 SAA 水平为 298.63±29.88、CRP 水平为 10.97±1.37、两者比值为 27.21±5.36；非感染组 SAA 水平为 5.01±0.39、CRP 水平为 6.52±1.058、两者比值为 0.83±0.12。三组研究对象 SAA、CRP 水平及两者比值比较 ，细菌感染组和病毒感染组水平显著高于非感染组（$P<0.05$），数据差异具有统计学意义；病毒感染组的 SAA 水平及两者比值水平高于细菌感染组（$P<0.05$），数据差异具有统计学意义。
结论 SAA、CRP 水平及两者比值水平在幼儿呼吸道感染性疾病的鉴别诊断中具有重要的价值。

PU-2274

2000 例成年女性全血微量元素铁和铜结果分析

陈振朋、张维
西安金域医学检验所有限公司

目的 铜和铁同为人体必需微量元素，在维持人体健康方面发挥着无可替代的作用，了解人体内铜和铁的含量水平，为微量元素缺乏的补充提供重要依据。
方法 统计了 2000 例成年女性的微量元素铜和铁的结果，年龄段在 17 岁-40 岁之间，并对统计结果进行分类分析。
结果 2000 例成年女性其中，处于孕期的女性为 880 例，占比为 44.4%，非孕期的女性为 1120 例，占比为 56%。通过计算，处于孕期女性铁结果均值为 451.45mg/L，铜结果均值为 1225.52μg/L。处于非孕期女性铁结果均值为 483.97mg/L，铜结果均值为 897.35mh/L。处于孕期的女性铁元素结果明显低于非孕期女性，而铜元素明显高于非孕期女性。血液中，铁主要存在红细胞内，组成血红蛋白，参与氧气和二氧化碳的运输。在女性孕期，血容量增加，随着孕期延长，血容量呈递增式变化，最多时可增加总血容量的 20%，而血液红细胞增加无法与之匹配，导致单位体积内红细胞数减少，机体处于相对贫血状态。此时机体通过负反馈调节一方面刺激铁的吸收，促进骨髓造血，同时加强体内铁的运输。肠粘膜上皮细胞吸收的铁为二价铁，在血液中被转运必须转化为三价铁，而铜蓝蛋白是人体内唯一的亚铁氧化酶，可将二价铁氧化为三价铁，进而转运至骨髓造血，铜是铜蓝蛋白的功能成分。因此孕期女性铁水平相对降低，而铜水平相对偏高。
结论当机体铁缺乏时，在进行铁元素补充时，还应适当的增加铜元素的补充，以增强体内铁元素的转化运输作用。

PU-2275

血清 GP73、CXCL13 与肝纤维化指标联合检测对原发性肝癌的诊断价值

李章勇
郴州市第一人民医院

目的 探讨血清高尔基体蛋白 73（GP73）、趋化因子 13（CXCL13）与肝纤维化指标联合检测在原发性肝癌疾病诊断中的意义。
方法 选择 2018 年 1 月至 2019 年 12 月在我院接受肝胆外科手术治疗的 79 例原发性肝癌患者作为观察组，选择 70 例同期在本院体检中心接受体检的健康人群为对照组。检测并比较两组患者的血清 GP73、CXCL13 和肝纤维化指标，并使用 ROC 曲线确定各指标对肝癌诊断的临界值。
结果 观察组患者血清 GP73、CXCL13、III 型前胶原（PCIII）、层粘蛋白（LN）、IV 型胶原（IV-C）及透明质酸（HA）水平均明显高于对照组，差异有统计学意义（P＜0.05）。血清 GP73、CXCL13 对原发性肝癌诊断的临界值分别为 64 ng/ml 和 124.02 pg/ml。血清 PCIII、LN、IV-C、和 HA 对原发性肝癌诊断的临界值分别为 103.4 μg/L、121.8μg/L、97.9μg/L、和 105.2μg/L。联合检测血清 GP73、CXCL13 与肝纤维化指标（PCIII、LN、IV-C、和 HA）对早期原发性肝癌诊断的敏感度、特异度、准确率分别为 0.978、0.851 和 0.969。
结论 联合检测血清 GP73、CXCL13 与肝纤维化指标对早期原发性肝癌诊断的敏感度、特异度和准确度率均较高，具有较好的临床应用价值。

PU-2276

微量元素在弥漫性系统硬化症患者中的变化研究

刘征[2]、李霞[1]、王秀娟[2]、李锦[2]、刘姗姗[1]
1. 桂林医学院附属医院检验科
2. 桂林医学院

Objective The current study measure the serum K, Na, Cl, Ca, P, Fe, Cu, and Mg in patients with diffuse systemic sclerosis (dSSc).
Methods 51 dSSc patients were enrolled in this study, and healthy 106 participants with similar age and gender were used as control. We examined the serum trace elements in dSSc patients with or without pulmonary fibrosis.
Results The results demonstrated that serum K, Ca, P, and Mg were significantly increased in dSSc patients, while Cu was decreased. Serum Cu in dSSc patients with pulmonary fibrosis was significantly lower than that without pulmonary fibrosis.
Conclusion Our study provided evidence that serum K, Ca, P, Cu, and Mg were changed significantly in dSSc patients, and lower Cu was associated with patients with pulmonary fibrosis.

PU-2277

ICP-MS 检测全血硒元素的方法学建立与评价

陈振朋、赵婷
西安金域医学检验所有限公司

目的 本研究拟利用电感耦合等离子体质谱建立全血硒元素的精确检测方法，并对该方法进行多方面评价，以保证该方法的可行性与检测结果的准确性，为临床诊疗提供客观准确的依据。
方法 本研究所用样本来自金域医学检验中心，共 20 例样本。应用校准品为国家有色金属及电子材料分析中心硒单元素标准品。采用 Agilent ICP-MS7900 对硒元素进行分析。Agilent ICP-MS79 检测硒元素的方法有外标法和标准加入法两种方法。
结果 外标法验证硒重复性精密度时发现，重复性精密度 CV＞22.3％，检测回收率小于 70％，对仪器性能参数进行调整，未见改善。而采用标准加入法，即在配制标准溶液时，标准溶液中引入一定本底的全血样本，仪器性能参数同外标法，测试重复性精密度，CV＜3.33％。 使用加标回收法测试该方法的正确度，回收率可达到：99.68%，满足定量项目要求的 85％-115％；携带污染：分别选取一份高值和一份低值病人样本进行检测，求出所有低-低值的标准差 SD1，平均值 X1 以及所有高-低值平均值 X2，结果为 X2-X1＜3SD1，即携带污染不予考虑。检测限：空白样本连续测量 21 次，计算均值和标准差，以 3 倍的标准差和 10 倍的标准差作为该项目的检出限和检测低限，分别为 0.24 ug/L 和 0.81ug/L，检测的全血样本是经 20 倍稀释后测试，故将标准曲线最高浓度点作为该项目的检测上限，其检测限为 0.81-800 ug/L，满足临床需求。
结论 综上所述，硒元素测试不稳定，全血样本基质复杂，产生的基质效应对检测结果的准确性影响较大，使用标准加入法在标准溶液内引入一定体积的全血，可消除基质效应带来的影响，提高检测结果准确性。通过对建立的标准加入法方法学评价可知，该方法的准确度、精密度、检测限及携带污染均满足要求，表明本研究建立的全血硒检测方法具有优良的全血硒检测性能，可在临床硒元素的检测中大范围推广。

PU-2278

简述糖化血红蛋白检测的临床影响因素

岳耀玲
莘县第三人民医院

我国糖尿病发病率逐年增高。HbAlc 的水平与糖尿病的血糖控制情况及并发症有着密切的关系，是糖尿病监检测的重要指标。检测 HbAlc 的结果能够对糖尿病患者检测前 3 个月的血糖情况进一步了解，能够为糖尿病的诊断提供一定的数据参考及指导临床医师应用降糖药物。HbAlc 在糖尿病的诊断、治疗以及病情监测中起着不容忽视的作用。通过临床观察和查阅相关文献，对糖化血红蛋白检测的影响因素和临床探究进行分析，简述如下。

PU-2279

中枢性尿崩症合并高渗高血糖综合征病例的实验室分析

郭迎雪
吉林大学第二医院

目的 研究探讨中枢性尿崩症合并高渗高血糖综合征的临床特点，并与单纯的高渗高血糖综合征进行对比。
方法 回顾性分析我院 2018 年 9 月到 2019 年 9 月收治的单纯性高渗高血糖综合征的患者 12 例作为单纯组，分析中枢性尿崩症合并高渗高血糖综合征的患者 4 例作为合并组，分析两组患者的血压、年龄、性别及 BMI 等一般资料，分析比较两组患者治疗前后的血钠、血糖、渗透压及尿比重等指标。
结果 两组患者的性别、BMI、血 BUN/Cr、收缩压及舒张压等比较，差异无统计学意义（P＞0.05），单纯组患者的年龄显著高于合并组患者，差异具有统计学意义（P＜0.05）。两组患者治疗前，血糖、血钠、尿比重、血渗透压以及尿渗透压等比较，差异无统计学意义（P＞0.05）。经过扩容等对症治疗后，两组患者的血渗透压、血糖及尿渗透压均得到一定程度的改善，显著优于治疗前，差异具有统计学意义（P＜0.05），但是合并组患者的尿渗透压及尿比重显著低于单纯组患者，差异具有统计学意义（P＜0.05），合并组患者的血渗透压及血钠显著高于单纯组患者，差异具有统计学意义（P＜0.05）。
结论 中枢性尿崩症与高渗高血糖综合征在实验室检查以及临床表现上存在相似之处，但是高渗高血糖综合征的患者经过降血糖等治疗后，高血钠未被及时纠正，应该考虑高渗高血糖综合征合并中枢性尿崩症的可能。

PU-2280

中性粒细胞/淋巴细胞比值与 CysC、mAlb 联合检测对 2 型糖尿病肾病的诊断价值

程霏
徐州医科大学附属医院

目的 研究中性粒细胞与淋巴细胞的比值(NLR)在 2 型糖尿病肾病(T2DN)中的变化,探讨 NLR 与 T2DN 之间的关系。
方法 选择 2017 年 3 月至 2017 年 6 月在徐州医科大学附属医院就诊的 113 例 2 型糖尿病患者进行回顾性分析，按临床诊断分为单纯 2 型糖尿病组(DM)51 例，2 型糖尿病肾病组(DN）62 例，选取

同期健康体检者 22 例作为对照组，检测各组的中性粒细胞，淋巴细胞，NLR、尿微量白蛋白（mAlb）、血清胱抑素 C（CysC）。
结果 DM 组和 DN 组淋巴细胞水平低于对照组(P<0.01)，NLR、mAlb、CysC 水平明显高于对照组(P<0.01)；DN 组 NLR、mAlb、CysC 水平明显高于 DM 组(P<0.05)。
结论 中性粒细胞与淋巴细胞的比值可作为糖尿病肾病的参考指标，与 CysC、mAlb 联合检测对 2 型糖尿病肾病的诊断具有重要临床意义。

PU-2281

FOXC2 Attenuates LPS-Induced Cell Adhesion via Suppression of ICAM-1 Expression in HUVECs

Pan Li
Laboratory Medicine Center, Nanfang Hospital, Southern Medical University, Guangzhou, Guangdong, China.

Atherosclerosis is a chronic vascular inflammatory disease that involves diverse cell types and circulating regulatory factors, including intercellular adhesion molecule (ICAM)-1, a proinflammatory cytokine. Lipopolysaccharides (LPS) increase ICAM-1 expression and promote cell adhesion, but the mechanism is not clear. We found that LPS induced time- and dose-regulated upregulation of ICAM-1 expression and downregulation of forkhead box protein C2 (Foxc2) expression in human umbilical vein endothelial cells (HUVECs). Overexpression of Foxc2 significantly inhibited both LPS-induced ICAM-1 expression in HUVECs and LPS-induced adhesion of THP-1 cells to HUVECs. Foxc2 siRNA dramatically increased both LPS-induced ICAM-1 expression and LPS-induced adhesion of THP-1 human monocytes cells to HUVECs. We conclude that Foxc2 inhibited LPS-induced adhesion of THP-1 cells to HUVECs by suppressing ICAM-1 expression in HUVECs.

PU-2282

PIVKA-II Serves as a Potential Biomarker that Complements AFP for the Diagnosis of Hepatocellular Carcinoma

Honglei Feng、Ze Li、Qian Wei、Li Ren
Tianjin Medical University Cancer Institute and Hospital

Background Hepatocellular carcinoma (HCC) is one of the most common malignant tumors of the digestive system and has high morbidity and mortality rates. It is essential to search new biomarkers to improve the accuracy of early HCC diagnosis. Therefore, we evaluated the diagnostic value of prothrombin induced by vitamin K deficiency or antagonist- II (PIVKA-II) as a potential biomarker that complements α-fetoprotein (AFP) in HCC by detecting the serum PIVKA-II levels.
Methods Serum PIVKA-II levels were compared in 168 HCC patients, 150 benign liver disease patients and 153 healthy controls to investigate the PIVKA-II potential to be a HCC biomarker. Receiver operating characteristic curve (ROC) analysis was used to evaluate the value of PIVKA-II in the diagnosis of HCC and its complementary role of AFP. The correlation between serum PIVKA-II levels and clinicopathological characteristics was analyzed to study the value of PIVKA-II in assessing HCC progression and prognosis. Finally, the ability of PIVKA-II in assessing the surgical treatment effects of HCC was studied by comparing the pre- and post-operative serum PIVKA-II levels in 89 HCC patients.
Results Serum PIVKA-II levels in HCC patients were significantly higher than that in patients with benign liver disease and healthy controls. The PIVKA-II performance in the diagnosing HCC as

an individual biomarker was remarkable. The combined detection of PIVKA-II and AFP improved the diagnostic efficiency of HCC. PIVKA-II retained significant diagnosis capabilities for AFP-negative HCC patients. Significant correlations were found between PIVKA-II expression levels and some clinicopathological characteristics, including tumor size, tumor stage, tumor metastasis, differentiation degree and complications. PIVKA-II expression obviously decreased after surgical resection.
Conclusions PIVKA-II is a promising serum biomarker for the HCC diagnosis that can be used as a supplement for AFP. The combined diagnosis of the two markers greatly improved the diagnostic efficiency of HCC. The PIVKA-II levels in HCC patients were widely associated with clinicopathological characteristics representing tumor cell dissemination and/or poor prognosis. PIVKA-II can be used to evaluate the curative effects of HCC resection.

PU-2283

探索脂肪肝新型诊断标志物

赵艳华、夏君香、干伟
四川大学华西医院

目的 探索脂肪肝的危险因素，评价其作为脂肪肝新型诊断标志物的价值。
方法 纳入四川大学华西医院 2016 年 5 月至 2020 年 5 月期间明确诊断为脂肪肝的患者 2900 例，同期间健康对照患者 2700 例。收集患者一般资料、临床病理信息、血常规与生化等实验室检查结果。并计算 TG/HDL-C、RC（残余胆固醇）、Non-HDL-C、NLR(中性淋巴比）、PLR（血小板淋巴比）、LMR（淋巴单核比）、MHR（单核高密脂蛋白比）。采用两样本 Mann-Whitney U 检验、二元 logistic 回归分析 TG/HDL-C、MHR、NLR、PLR、LMR 比值与脂肪关系，利用 ROC 曲线评价作为脂肪肝新型诊断标准物的价值。
结果 脂肪肝患者 BMI 指数、ALT、AST、ALB、WBC、PLT 等实验指标与健康对照有显著差异（P＜0.05）。在调整性别、年龄、BMI 等混杂因素后，两组之间 TG/HDL-C、LMR 有明显差异（P＜0.001）；单多因素分析发现 TG/HDL-C、LMR 是脂肪肝的危险因素，OR 值分别为 3.375（3.002，3.795）、1.225（1.176，1.275）。ROC 曲线分析 TG/HDL-C、MHR、NLR、PLR、LMR 联合诊断脂肪肝的 AUC 面积为 90%。
结论 TG/HDL-C、LMR 是脂肪肝的独立危险因素，联合指标 TG/HDL-C、MHR、NLR、PLR、LMR 可作为脂肪肝新型诊断标准物。

PU-2284

外周血 SAA、Hs-CRP、CD64 指数联合检测在感染性疾病中的诊断价值

曾磊
南方医科大学珠江医院

目的 探讨联合血清淀粉样蛋白（SAA）、超敏 C 反应蛋白（HsCRP）和外周血中性粒细胞 CD64 指数检测在感染性疾病中的意义。
方法 选取 2019 年 1 月-5 月份，广州市珠江医院门诊和病房诊断为感染性疾病的患者，依据病原体不同分为病毒性感染感染（30 例），细菌性感染（30 例），选取同期健康体检人群作为对照组（30 例），分别检测各组的 SAA、HsCRP、CD64 指数的水平，分析在感染性疾病患者中 3 项指标水平变化及其在诊断感染性疾病中的效率。
结果 显示研究组患者 CD64 指数，SAA,hs-CRP 均明显高于对照组。

结论 1.CD64 指数、CRP、SAA 联合联测对细菌感染有良好的临床诊断价值，对诊断病毒感染的准确性低。2.SAA 和 hs-CRP 一起可以诊断细菌感染，但 SAA 在病毒感染时会升高，CD64 诊断细菌感染的特异性比其它两个指标好，但是敏感性欠佳，因此，以上三个指标联合检测，可以更好地辅助诊断感染性疾病。

PU-2285

毛细管电泳 HbA1c 检测系统在 HbE 病中的应用

林子沛
南方医科大学珠江医院

目的 探讨毛细管电泳与高效液相色谱法 HbA1c 系统相比的优势以及对诊断 HbE 病的应用价值。
方法 选取正常健康人静脉血标本 20 例，作为正常组。HbE 患者静脉血样本 10 例作为异常组。分别用毛细管电泳仪和高效液相色谱仪进行血红蛋白检测，记录数据并进行分析，运用统计学方法处理数据。
结果 正常组毛细管电泳法和高效液相色谱对于 HbA1c 检测相关性良好。异常组检测 HbA1c 两种方法存在差异，毛细管电泳法结果与实际血糖相符。毛细管电泳法能将 HbE 分离并定量。
结论 毛细管电泳不仅能满足日常糖化血红蛋白的检测，且与高效液相色谱法相比具有一定的优势，前者不受血红蛋白变异体的干扰，HbA1c 结果能与临床诊断相符，并且对 HbE 的诊断有一定的价值。

PU-2286

纯水机反渗透膜更换对生化结果的检测影响研究

梁少聪
南方医科大学珠江医院

目的 探究纯水机中反渗透膜更换对生化项目检测结果的影响
方法 在本院纯水机反渗透膜更换前后进行电阻率的记录，进行两个浓度生化质控物检测，分析电阻率的变化及生化项目检测是否受到影响。
结果 反渗透膜更换前后电阻率差异无统计学意义（$p>0.05$）。生化项目在更换反渗透膜前后的结果除外甘油三脂，均符合实验室质量目标。其中更换反渗透膜后甘油三脂结果升高，经分析与新反渗透膜携带干扰性物质相关。
结论 纯水机反渗透膜更换后应先进行持续制水排水，减少干扰性物质对检测结果的影响。

PU-2287

床旁即时检测 C 反应蛋白与特定蛋白检测比较及影响因素分析

欧锦霞、谢晓灵、陈恩中、吕亚梅、周韶松、潘沅
南方医科大学珠江医院

目的 评估床旁即时检测(Point of Care Testing，POCT)的 QR-1000 免疫比浊仪测定全血 C 反应蛋白（C-reactiveprotein,CRP）的可靠性，与常规方法全自动特定蛋白分析仪 BN ProSpec 检测血清比较，为 POCT 检测 CRP 质控提供依据。
方法 参照 EP15-A2、EP9-A2 文件，测定 QR-1000 仪（POCT）检测精密度；收集同时送检全血（POCT）和血清（常规方法）检测 CRP 的患者资料，比较两系统检测的差别、对临床判断的影响以及红细胞压积（HCT）、CRP 浓度及标本放置时间的影响。

结果 对于模拟样本，POCT 全血检测 CRP 精密度较血清差，CV 值随 CRP 浓度升高而降低；POCT 和常规方法测定血清 CRP 相关性好（r2=0.9844, P <0.001），结果具可比性；对于患者实测数据，HCT 为 0.42～0.46 时全血（POCT）与血清（常规方法）CRP 测定无显著性差异，患者 HCT 越接近设定值，两系统测定值越相近，校正后更具可比性；无论校正与否，POCT 法与常规法测定值均相关，但结果有显著性差异，且超出临床允许误差，POCT 高于常规**方法** (P<0.05)，结果不具可比性；如果用于临床炎症定性，两系统一致率较好（Kappa 值均≥0.75)，用于心血管事件风险定性评估，两系统临床判断一致率一般（0.4≤Kappa<0.75）。标本放置时间、CRP 浓度对结果影响小。

结论 POCT 全血与常规方法血清检测 CRP 结果不具可比性，当 HCT 偏离最佳理论值时 POCT 全血测定值必须校正；POCT 全血检测 CRP 适于临床炎症定性；POCT 全血 CRP 检测应严格遵循操作规程，建议与常规方法定期比对。

PU-2288

脑心清片对急性心肌梗死患者血清炎性因子水平影响

吕亚梅
南方医科大学珠江医院

目的 观察脑心清片对急性心肌梗死（AMI）后患者血清高敏 C 反应蛋白（hs-CRP）、肿瘤坏死因子-α（TNF-α）和白细胞介素 6（IL-6）的影响。

方法 将 66 例急性心肌梗死患者随机分为治疗组和对照组各 33 例，2 组均经常规治疗，治疗组在此基础上给予脑心清片治疗，1 个月后观察 2 组治疗前后血清 hs-CRP、TNF-α、IL-6 的水平。

结果 经过治疗后，治疗组可明显降低血清 hs-CRP 、TNF-α、IL-6 水平，差异有统计学意义（P<0.05）。

结论 在常规治疗基础上加用脑心清片治疗急性心肌梗死可以使血清 hs-CRP、TNF-α、IL-6 的水平显著降低，炎症反应减轻，从而改善心功能。

PU-2289

血清淀粉样蛋白 A 及 C 反应蛋白在痛风性关节炎中的临床价值

赖伟波
南方医科大学珠江医院

目的 探讨血清淀粉样蛋白 A 及 C 反应蛋白浓度在痛风性关节炎中的临床价值。

方法 选取 2018 年 9 月至 2019 年 2 月间住院风湿免疫科患者 90 例，其中 21 例诊断为类风湿性关节炎患者，14 例诊断为痛风性关节炎，13 例诊断为风湿性关节炎患者，22 例诊断为系统性红斑狼疮患者。比较各组患者血清 SAA、CRP 的浓度，并分析两项指标对该疾病诊断的相关性，对其疾病活动程度进行评估并比较其相关性。采用便利抽样法选取年龄性别成组匹配的健康体检成人 20 例作为对照组。

结果 急性期中，痛风组血清 SAA、CRP 表达水平显著高于对照组，且二者在活动期痛风组的水平均显著高于风湿组和 SLE 组；类风湿组中 SAA 和 CRP 水平虽高于对照组但低于痛风组，SAA 联合 CRP 的检测结果的灵敏度会高于单一项血清 SAA 或 CRP 检测的结果。

结论 1）痛风组血清 SAA、CRP 表达水平显著高于高于风湿组和 SLE 组；2），SAA 联合 CRP 的检测结果的灵敏度会高于单一项血清 SAA 或 CRP 检测的结果；3）SAA 联合 CRP 的检测表达水平可作为痛风性关节炎和类风湿性关节炎临床上的灵敏的检测指标

PU-2290

新型衰老标志物的发现及其与相关疾病的关联研究

韦钊
山东大学齐鲁医院

目的 目前的细胞衰老标志物均存在或多或少的局限性，这些衰老标志物虽然可以一定程度上指示衰老发生，但并不具有指示所有细胞衰老模式的普遍性和只存在于衰老细胞中的特异性。此外，可作为常规检测的衰老标志物更是匮乏。探索血液体液中的衰老标志物并研究其与衰老相关疾病的联系可为衰老相关疾病的检测和治疗提供新的思路和依据。
方法 有文献报导小鼠体内存在某一因子可激活 Wnt 信号通路并促进衰老相关表型。而人类中是否存在血液或体液中便于检测的类似指标有待我们进一步研究。我们将利用健康年轻个体及年老个体的血液或体液进行相关检测。
结果 我们发现多种细胞类型的复制衰老模式中存在共同上调的基因，通过对人体组织基因表达数据库的分析证实该基因在人体皮肤和皮下脂肪组织中的表达随年龄增长也显著升高。我们将进一步检测其在血液中是否表达并且与个体老化或某种衰老相关疾病是否存在相关性。与此同时，我们将对人类血液进行 RNA-Seq 检测，探索更多可能的检测指标。
结论 可能存在某些基因与个体老化或某种衰老相关疾病存在密切相关性。通过分析验证发现血液中的衰老标志物并研究其与衰老相关疾病的联系，将为老年性疾病提供尽早发现并提前缓解的可能性，将为人类生存质量的提高提供更好的理论基础及实际应用价值。

PU-2291

E3 泛素连接酶 CUL4B 减缓细胞早衰的机制研究

韦钊
山东大学齐鲁医院

目的 细胞衰老对于个体健康而言是一把双刃剑，既有利也有弊。活性氧（ROS）在多种类型的衰老模式中广泛上调，并促进细胞衰老进程，揭示细胞衰老进程中 ROS 的调控机制对于细胞衰老相关疾病的治疗具有重要潜在价值。我们的前期研究论证了 CUL4B 对 ROS 的调控作用，以及 CUL4B 减缓压力诱导细胞衰老的作用机制。进一步研究揭示细胞早衰进程中 CUL4B 的上游调控机制以及其中存在的反馈环仍非常重要。
方法 我们用 NHF 细胞构建衰老模型，通过病毒包装技术构建低表达和过表达 CUL4B 的细胞系，并使用多种细胞系进一步验证。检测 CUL4B 对 p53 蛋白及其靶基因的调控作用；通过 IP 检测 CUL4B 与 p53 蛋白的结合。预测 CUL4B 上游调控元件，通过 RT-PCR 初步验证上游调控元件是否影响 CUL4B 的转录水平，并通过 ChIP 实验以及荧光素酶报告基因实验验证上游转录因子对 CUL4B 的转录结合。
结果 CUL4B 在压力诱导的细胞衰老中显著下调。CUL4B 低表达强化压力诱导的细胞衰老，且该过程依赖于 ROS 水平的升高。压力刺激下，CUL4B 低表达促进 p53 磷酸化和靶基因表达。压力刺激后 CUL4B 与 p53 蛋白相互结合，并且 CUL4B 低表达减少了 p53 的泛素化。预测到有重要转录因子结合在 CUL4B 转录起始区域，并进一步验证了表达相关性。可能存在 p53-CUL4B 负反馈环。CUL4B 调控一系列 ROS 相关基因，这种调控的具体机制仍有待研究。
结论 前期研究已证实压力刺激后 CUL4B 介导 p53 泛素化，促进 p53 蛋白降解。进一步研究结果表明，CUL4B 受重要转录因子调控，且两者间存在重要反馈环。CUL4B 调控一系列抗氧化基因及促氧化基因的转录水平，预测存在共同的靶点，CUL4B 通过调控这一靶点影响一系列 ROS 相关基因。

PU-2292

胃泌素释放肽前体对小细胞肺癌的诊断效率

丁新
南方医学科大学珠江医院

目的 研究胃泌素释放肽前体(ProGRP) 在小细胞肺癌患者中辅助诊断、疗效评价和预测复发的价值。
方法 选择 50 例肺部良性病变患者，68 例非小细胞肺癌患者，74 例小细胞肺癌患者。收集所有患者血清胃泌素释放肽前体 (ProGRP)、鳞状细胞癌抗原(SCC-Ag)、神经元特异性烯醇化酶(NSE)、癌胚抗原(CEA)、细胞角蛋白 19 片段(CYFRA21-1)的测定结果。同时查阅所有患者病情变化情况，分析针对小细胞肺癌早期诊断、疗效评断以及预测复发的最佳指标。
结果 小细胞肺癌与肺部良性疾病血清 ProGRP 水平差异有统计学意义(P＜ 0.05) ,小细胞肺癌与非小细胞肺癌血清 ProGRP 水平差异有统计学意义（P＜ 0.05）。 ProGRP 在诊断小细胞肺癌中的 ROC 曲线下面积为 0.872 ，在疗效判断与预测复发方面，血清 ProGRP 水平与影像学检查结果提示病情变化相符率为 74.29%。
结论 血清 proGRP 水平对于小细胞肺癌辅助诊断、疗效评价和预测复发有重要意义。

PU-2293

中性粒细胞明胶酶相关脂质运载蛋白（NGAL）项目在 Cobas C702 生化分析仪的性能验证

邹梦雪
南方医科大学珠江医院检验医学部

目的 利用罗氏 Roche Cobas C702 全自动生化分析仪对中性粒细胞明胶酶相关脂质运载蛋白（NGAL）的性能指标进行验证。
方法 参考 CNAS-GL：2019，CNAS-GL037：2019 等文件，使用北京世纪沃德试剂，校准品及质控品对中性粒细胞明胶酶相关脂质运载蛋白的精密度，正确度，线性范围，参考区间，可报告范围进行数据统计分析验证。
结果 中性粒细胞明胶酶相关脂质运载蛋白（NGAL）两个水平精密度检测结果的批内变异系数与批间变异系数均低于 5%，精密度通过验证；正确度通过与外院奥林巴斯 AU5821 进行比对，两系统间结果偏倚小于声明的偏倚，偏倚可接受；线性通过验证，最大稀释倍数可稀释至 10 倍。
结论 罗氏 Cobas C702 全自动生化分析仪对中性粒细胞明胶酶相关脂质运载蛋白（NGAL）项目检测的精密度、正确度、参考区间及可报告等性能验证评价良好，符合临床需求。

PU-2294

探讨血清 CRP 和 CER 在肝癌和肝硬化鉴别诊断中的价值

蔡桂君
南方医科大学珠江医院

目的 比较肝硬化和肝癌患者的血清 CER,CRP 含量的差异，观察这些指标对疾病的诊断和鉴别诊断是否具有临床意义。
方法 选取标本来自 2016 年 10 月~12 月间门诊及住院的肝癌与肝硬化患者，对其进行超敏反应蛋白及铜蓝蛋白的检测。

结果 血清中铜蓝蛋白浓度的比较中肝癌组明显高于肝硬化组和健康对照组(P<0.05)，但肝硬化组和正常对照组之间无显著性差异（P=0.785）。血清中 C 反应蛋白浓度的比较中肝癌组和肝硬化组均明显高于正常对照组(P<0.05)而肝癌与肝硬化组之间则无显著差异(P=0.272)。其中两项指标同时增高中，肝癌组中比例为 73%，远大于肝硬化组 47%。只有 C 反应蛋白增高，铜蓝蛋白无明显增高的样本，肝硬化组占 22%。远大于肝癌组 4%。
结论 当两项指标均显著升高时，应该多考虑患肝癌的可能性，而只有 C 反应蛋白升高，铜蓝蛋白无明显升高时，则患肝硬化的几率增加。两项指标在肝癌和肝硬化中升高程度不同，有互补性。

PU-2295

罗氏 cobas E801 全自动免疫分析仪检测甲胎蛋白的性能验证

吴华仙
南方医科大学珠江医院

目的 验证罗氏 E801 全自动免疫分析仪电化学发光法检测血清甲胎蛋白的性能验证。
方法 参考美国临床和实验室标准化协会（NCCLS）系列文件和相关的国内行业标准等要求对 AFP 的精密度、正确度、分析测量范围和参考区间进行验证及评价。
结果 甲胎蛋白在浓度为 11.4μg/L 的批内和批间精密度分别为 0.75%和 0.97%，在浓度为 135μg/L 的批内和批间精密度分别为 0.6%和 0.1%，均小于标准要求；正确度验证达到行标文件要求，线性范围在 1.17-1132μg/L，a 值为 0.993 在 0.97-1.03 内，R2=0.9998;生物参考区间复合要求。
结论 罗氏 E801 全自动免疫分析仪电化学发光法检测 AFP 分析性能符合标准，适用于临床。

PU-2296

成都地区表面健康藏族人群N末端脑钠肽前体（NT-proBNP）水平调查

宋昊岚[1]、向生平[2]、潘柯宇[1]、李贵星[1]、秦莉[1]
1. 四川大学华西医院
2. 西藏自治区人民政府驻成都办事处医院（四川大学华西医院西藏成办分院）

目的 调查成都地区表面健康藏族体检人群 N 末端脑钠肽前体(NT-proBNP)水平。
方法 以 2019 年 9 月至 12 月成都市表面健康藏族体检者 425 名，汉族体检者 422 名为研究对象，应用秩和检验比较[1] 不同性别、年龄的藏汉两族人群 NT-proBNP 水平，并分析其影响因素。
结果 NT-proBNP 在人群中呈偏态分布，①表面健康藏族人群 NT-proBNP 水平为 65.23ng/L(35.39,118.6)，显著高于表面健康汉族人群 NT-proBNP 水平 26.52ng/L（10.44,52.85)，差异有统计学意义（P＜0.05）；[2] [SH3] ②成都地区表面健康藏族女性 NT-proBNP 水平显著高于男性，分别为 86.13ng/L（53.04，155.7），及 45.21 ng/L（22.21，75.92），差异有统计学意义（P＜0.05）。
结论 成都地区表面健康藏族人群 NT-proBNP 水平明显高于汉族人群，女性水平高于男性。建议对此特殊人群建立合适的参考区间，如使用厂家推荐参考区间评估心脏功能时，应注意结合其临床表现及影像学资料。
应该出统计学分析的方法
两组受试者年龄有统计学差异，这样比出来的结果不能说明问题 [SH3]补充对照组（汉族体检者）数据后，两组年龄无差异

PU-2297

肾素、醛固酮化学发光免疫法的性能验证及筛查原发性醛固酮增多症的价值

刘稚、任艳、陈涛、高洪蛟、何訸、阿衣李桂、刘英、安振梅、张玫
四川大学华西医院

目的 验证化学发光免疫法（CLIA）检测肾素、醛固酮的性能及筛查原发性醛固酮增多症（原醛症）的价值。
方法 根据美国临床实验室标准化协会相关文件验证 CLIA 检测肾素、醛固酮的精密度、线性范围和携带污染率。纳入 115 例疑似原醛症的患者，均采用 CLIA、放射免疫法（RIA）检测肾素和醛固酮，比较两种方法的相关性和对原醛症的筛查价值。
结果 CLIA 法检测肾素、醛固酮的精密度、线性范围和携带污染率均符合要求。在疑似原醛症患者中，CLIA 法和 RIA 法检测肾素、醛固酮和醛固酮/肾素（ARR）的相关系数分别为 0.904、0.858、0.845（P 均<0.001）。患者立位状态，ARR 为 5.635（ng/dL）/（ng/L）时，CLIA 法筛查原醛症灵敏度为 78.8%，特异度为 94.4%；ARR 为 14.085（ng/dL）/[ng/（mL·h）]时，RIA 法 ARR 灵敏度为 90.4%，特异度为 81.5%。卧位状态，ARR 为 5.64（ng/dL）/（ng/L）时，CLIA 法筛查原醛症灵敏度为 96.1%，特异度为 82.8%；ARR 为 38.976（ng/dL）/[ng/（mL· h）]时，RIA 法灵敏度为 92.2%，特异度为 75.9%。
结论 CLIA 法检测肾素、醛固酮的性能均满足临床要求，立位 ARR 初筛原醛症的特异性相比卧位 ARR 更高，敏感性较低。

PU-2298

降钙素原在儿童急性淋巴细胞白血病化疗后感染中的应用价值

周泽杰
南方医科大学珠江医院

目的 研究降钙素原（PCT）在儿童急性淋巴细胞白血病化疗后感染的诊断价值。
方法 选取在南方医科大学珠江医院出院诊断为急性淋巴细胞白血病（ALL）的儿童 113 例，分为 3 组，分别为重症细菌感染组 27 例、局部细菌感染组 69 例，非细菌感染组 17 例为对照组。采用固相免疫层析技术测定各组降钙素原（PCT）水平。
结果 重症细菌感染组、局部细菌感染组及非细菌感染组之间患儿降钙素原不全相等，具有统计学意义（P<0.05）。根据尤登指数， PCT>0.19 时为早期细菌感染的最佳诊断阈值，敏感度 62.5%, 特异度 100%。
结论 在儿童急性淋巴细胞白血病化疗后细菌感染诊断中，降钙素原较 CRP 特异度高，是一种具有较高特异性新型诊断指标；严重细菌感染时，降钙素原水平异常升高，且与感染的严重程度及预后有关。

PU-2299

基于激活型核酸适体探针用于外泌体的无标记检测

陈娟、邢金芳、石瑛、张琳琳、袁恩武
郑州大学第三附属医院（河南省妇幼保健院）

外泌体作为细胞外囊泡的一个重要亚群，携带蛋白质、脂质、核酸等重要的生物分子。同时其在细胞间信息交流中发挥着重要作用，并与肿瘤的发生和发展密切相关。因此，高灵敏、高选择性

的检测外泌体对肿瘤的早期诊断及治疗具有重要的指导意义。基于核酸适体对外泌体膜蛋白的特异性识别能力和 DNA 链置换反应，本文构建了一种构型转换的可激活核酸探针用于外泌体的无标记检测。在优化的实验条件下，线性范围为 5×10^5 到 5×10^7 particles/μL，最低检测限为 3.4×10^5 particles/μL。最后，该探针成功用于实际血液样品中外泌体的高灵敏和高选择性检测。

PU-2300

估算的肾小球滤过率在痛风分型中的诊断价值

苏镜
广州中医药大学第三附属医院

目的 探讨估算的肾小球滤过率（eGFR）在痛风分型中的诊断价值。
方法 根据纳入标准和排除标准选取原发性痛风性关节炎患者尿酸排泄减少型 204 例、尿酸生成增多型 80 例、尿酸代谢混合型 106 例、尿酸代谢其他型 32 例及健康对照组 107 例，收集其临床资料、实验室检查指标、血清标本及 24 小时尿液标本，AU5800 全自动生化分析仪检测患者的生化指标。方差分析 eGFR 在痛风分型组间差异，Pearson 回归分析 eGFR 与临床资料、生化指标关联性，线性相关分析 eGFR 与痛风分型诊断指标相关性，ROC 分析 eGFR 在痛风分型中的诊断价值。
结果 ①方差分析发现 eGFR 在尿酸排泄减少型组及尿酸代谢其他型组明显低于正常对照组，在尿酸代谢混合型中明显高于正常对照组；eGFR 在尿酸代谢混合型组、尿酸生成增多型组、尿酸排泄减少型组、尿酸代谢其他型组呈依次减低趋势。②Pearson 回归分析发现 eGFR 与 UUE 呈正相关性。③线性相关分析发现尿酸代谢混合型组、尿酸生成增多型组、尿酸排泄减少型组、尿酸代谢其他型组中 eGFR 与 UUE 呈正相关。④ROC 分析发现尿酸排泄减少型组与正常对照组 eGFR（AUC 为 0.606）；尿酸代谢混合型组与正常对照组 eGFR（AUC 为 0.755）；尿酸代谢其他型组与正常对照组 eGFR（AUC 为 0.890）。尿酸排泄减少型组与尿酸生成增多型组 eGFR（AUC 为 0.625）；尿酸排泄减少型组与尿酸代谢混合型组 eGFR（AUC 为 0.878）；尿酸排泄减少型组与尿酸代谢其他型组 eGFR（AUC 为 0.891）；尿酸生成增多型组与尿酸代谢混合型 eGFR（AUC 为 0.727）；尿酸生成增多型组与尿酸代谢其他型组 eGFR（AUC 为 0.901）；尿酸代谢混合型组与尿酸代谢其他型组 eGFR（AUC 为 0.978）。
结论 eGFR 可以作为痛风分型的辅助诊断指标，可以提高痛风分型诊断准确率，有效的减少痛风分型归类错误概率。

PU-2301

血糖与尿糖相关性分析

周芳宇
吉林金域医学检验所有限公司

目的 血糖指的是血液中葡萄糖的浓度，尿糖是指尿液中葡萄糖的含量。本文旨在研究血糖与尿糖的相关性。
方法 选取 2021 年 3 月 1 日到 2021 年 3 月 7 日同时检测血糖及尿糖的患者结果数据进行研究。血糖检测采用罗氏全自动生化分析仪 C702，尿糖检测采用迪瑞尿液分析仪 H-800。筛选出所有血糖阳性的患者，分为三组，A 组为当血糖>10mmol/L，B 组为当血糖为<10mmol/L 且>9mmol/L，C 组为低于肾糖阈且血糖>6.11mmol/L；观察每组患者的尿糖是否为阳性且阳性程度的情况。

结果 其中在 A 组，83%的尿糖为两个加号(++)，少部分会出现一个加号(+)甚至阴性(-)；B 组，80%的尿糖为一个加号(+)，少部分为两个加号(++)或阴性(-)；C 组尿糖为阳性几乎不存在，大约为 1%。最终显示血糖和尿糖的阳性符合率占血糖阳性的 83.3%。
结论 当血浆葡萄糖浓度超过 8.96～10.08mmol/L 时，近端小管对葡萄糖的重吸收达到极限，尿中开始出现葡萄糖，此时的血糖浓度即为肾糖阈。由于肾糖域的存在且每个人的肾糖域随个人体质的波动，血糖和尿糖没有达到 100%的符合率，因此在疾病诊断时要综合患者的个人情况选择对糖的检测方法，以及对结果的分析。

PU-2302

血流感染患者肝功能指标相关分析

刘武征、徐东江
北京积水潭医院

目的 本研究的目的是评估常规肝功能生化检测作为血流感染诊断的潜在指标。
方法 我们收集了 115 例血培养阳性并实验室证实的血流感染患者(实验组)和 120 例血培养阴性并细菌感染患者(对照组)。两组患者均无潜在肝胆疾病。对于实验组的患者，我们分析了第一次血培养阳性当天的肝功能检查结果。对于对照组，在两对血培养瓶阴性血培养的第一天获得相同的数据。分别收集两组的肝功能指标 ALT、AST、TBIL、DBIL、γ-GT、ALP、ChE 及感染指标 CRP 并比较两组数据的相关性。
结果 经 t 检验，实验组血清 ALT、AST、TBIL、DBIL、γ-GT、ALP 水平显著高于对照组，而 ChE 水平显著低于对照组（P<0.05），作为感染指标的 CRP 两组却没明显差异（P >0.05）。多变量分析发现 ChE 是一个独立的因素,血清胆碱酯酶在 ROC 曲线下的面积（AUC）为 0.748，而 ALT、AST、TBIL、DBIL、γ-GT、ALP 在 ROC 曲线下的面积（AUC）分别为：0.59、0.67、0.71、0.72、0.69、0.63。当血流感染时血清 ALT、AST、TBIL、DBIL、 γ-GT、ALP、ChE 水平变化明显比非血流感染患者更快。
结论 血流感染患者的 ChE 活性水平明显降低。我们的结果表明，ChE 活性可用于诊断血流感染。有必要进行长期的随访研究，以确定其在临床实践中的确切作用。

PU-2303

尿碘水平检测与甲状腺癌的相关性研究

高海锋
陕西省宝鸡市中心医院

目的 探讨尿碘水平检测与甲状腺癌的相关性，为甲状腺癌的诊断提供实验室依据。
方法 选取 2019 年 4 月至 2020 年 8 月宝鸡市中心医院内分泌科收治的 323 例甲状腺结节患者为研究对象，后经 B 超及组织病理确诊为甲状腺癌患者 114 例，甲状腺良性结节患者 209 例，同时选择同期体检健康者 100 例作为对照组。采用比色法测定尿碘水平，并对结果进行统计学分析。
结果 甲状腺癌组、甲状腺良性结节组和对照组尿碘水平存在显著性差异（H=21.140，P=0.000），且随着疾病进展，尿碘水平逐渐升高；甲状腺癌组中碘缺乏、碘超量和碘过量的比率显著高于其它组（c2=5.614，P=0.022）；各组 TSH、TT3、TT4、TGAb 和 TPOAb 存在显著性差异（FTSH=7.83,P=0.012；FTT3=5.41，P=0.038；FTT4=4.93，P=0.032；FTGAb=14.127，P=0.001；FTPOAb=13.262，P=0.001）；尿碘水平与各组的 TSH 水平均具有相关性，而尿碘水平只与甲状腺癌组的 TGAb 和 TPOAb 具有相关性，与甲状腺良性结节组和对照组无明显相关性，尿碘水平与各组的 TT3 和 TT4 均无明显的相关性。

结论 尿碘水平检测对甲状腺癌的诊断具有很高的临床诊断价值，可能成为诊断甲状腺癌的一种快速、无创的检查手段，值得在临床上推广。

PU-2304

万万没想到，这种疾病竟会导致玻片“变蓝”？

何永建[1]、庄鸿鑫[2]
1. 南方医科大学南方医院
2. 南方医科大学

多发性骨髓瘤（multiple myeloma, MM）是由于单克隆浆细胞在骨髓内异常增生并产生大量单克隆 M 蛋白，引起溶骨性骨质破坏、贫血、肾功能损害等临床特征的一类恶性血液系统肿瘤性疾病。作为全球第二大血液系统恶性肿瘤，该疾病在临床上并不罕见，但该疾病引起血涂片异常蓝染的现象在临床上易于被忽视。本病例报道的是 1 例以血涂片染色异常为特点的 MM 患者的诊断过程，并结合文献复习，对该疾病相关临床和实验室诊断特点进行探讨分析。

PU-2305

胃癌淋巴结转移 mRNAs 预后分子标志物的识别

史爽、王传新
山东大学第二医院

目的 绘制胃癌淋巴结转移 mRNAs 差异表达图谱，并鉴定预后相关 mRNA 分子标志物，用于胃癌患者淋巴结转移的预测与患者预后评估。
方法 下载 TCGA-STAD 数据集，使用 R 语言 limma 软件包对数据集中发生淋巴结转移与未发生淋巴结转移的 mRNA 测序结果进行差异分析，以|log2 fold change|＞1 为标准，筛选差异表达的 mRNAs 分子。使用 R 语言 Survival 软件包对差异 mRNAs 分子进行预后分析，并绘制其 Kaplan-Meier 生存曲线。
结果 以|log2 fold change|＞1 为标准，共识别 480 个淋巴结转移中差异表达的 mRNAs 分子，其中 217 个 mRNAs 分子特征性上调，263 个 mRNA 分子特征性下调。单因素 Cox 回归分析和 Kaplan-Meier 生存曲线结果显示，480 个差异 mRNAs 分子中，共有 23 个 mRNAs 表达量与患者预后存在显著相关性。
结论 本研究识别了胃癌淋巴结转移相关 mRNAs，及胃癌患者预后相关 mRNAs，揭示了胃癌淋巴结转移与预后潜在分子标志物，有助于改善胃癌患者的长期预后。

PU-2306

p62 promotes lipid accumulation by regulating the mTOR-ULK1 autophagy pathway in macrophage foam cells

Ling Ding、Xiaochen Yu、Dan Liu、Hongyun Jing、Fei Yu、Xiuru Guan*
First Affiliated Hospital of Harbin Medical University

p62, a multifunctional polyubiquitin-containing protein which is the center of the intracellular signaling and degraded by autophagy, can regulate the autophagy pathway associated with mTOR to affect the proliferation and differentiation of cells. And the accumulated p62 has been found in the macrophages treated by high concentration of ox-LDL. However, the correlation of p62 with the lipid accumulation in macrophages remains obscure. Herein, we mapped that

silencing p62 with the small interference RNA (siRNA) could palliate the accumulated lipids and reduce the secretion of inflammatory cytokines IL-1β. Mechanistically, p62-silencing could downregulate the expression of mTOR and then upregulate the expression of ULK1 to promote autophagy. These results proved that macrophage foam cells play a key role in atherosclerotic plaque rupture, p62 effectively aggravates the accumulation of lipids through mTOR-ULK1 autophagy pathway, indicating p62 should be considered as a new therapeutic target to treat atherosclerosis.

PU-2307

肥厚型心肌病的分子遗传学研究进展

徐婧[1]、刘向东[2]
1. 东南大学附属中大医院
2. 东南大学生命科学研究院

目的 肥厚型心肌病（HCM）是一种常见的遗传性心脏病，有高度遗传异质性。已有研究表明肌节基因突变是导致 HCM 的最主要原因，但是仍有约 30%的 HCM 病例致病原因未明。该部分研究在遗传背景未知的 sHCM 群体中引进了大规模测序方法。结合多种最新的公共数据库和数据分析方法，从不同角度探索了 HCM 新的可能的致病基因和突变，探讨 HCM 的致病机理。
方法 本研究基于前期大规模的 HCM 患者筛查，选取了 74 位 sHCM 患者，这些患者在 8 个常见 HCM 致病肌节基因上并未发现携带有突变。应用 WES 技术，设计 WES 二代测序数据分析流程和突变筛选流程鉴定突变。再根据已知 HCM 致病基因和 HCM 风险基因之间的结构功能相似性，进行数据库挖掘和相关文献调研，探讨 HCM 新候选致病基因可能的致病机制。另外，调用相关基因的相互作用数据，构建蛋白质-蛋白质相互作用网络（PPI）。
结果 在 7/74（9.5%）的患者中鉴定出共 7 个已知 HCM 致病基因上 EMs。比较 sHCM 患者人群和中国汉族人群的 WES 突变数据，进一步分析预测出 10 个具有高优先级的 HCM 新候选致病基因，包括 TTN、RYR2、NEB、OBSCN、CMYA5、PLAC4、NES、CAP1、CFLAR 和 MYH15。组织表达谱分析显示其中 7 个基因在心血管系统中呈相对高表达。动物模型分析显示 6 个基因的斑马鱼或小鼠模型中显示出心血管系统异常表型。进一步的文献调研也揭示了其中 7 个基因与各类型心脏病致病的重要联系。这些研究结果表明预测出的 HCM 新候选致病基因在心血管系统中可能存在着重要功能，可能和 HCM 致病相关。PPI 网络还揭示了泛素蛋白酶复合体系统在 HCM 疾病调控中的重要地位，为 HCM 遗传基础的进一步研究提供了新方向。
结论 结合多种最新的公共数据库和数据分析方法，从不同角度探索了 HCM 新的可能的致病基因，探讨 HCM 的致病机制，为 HCM 的基础和临床研究提供了新的参考。

PU-2308

新城疫病毒 F 糖蛋白 HRB 连接区氨基酸突变分析

谢文艳[1]、王志玉[2]
1. 山东省千佛山医院
2. 山东大学 公共卫生学院 病毒研究室

目的 为了弄清人副流感病毒 3 型（human parainfluenza virus type 3，HPIV3）F 糖蛋白 HRB 连接区对膜融合活性的影响，探讨 HRB 连接区影响膜融合功能的机制。
方法 采用定点突变和体内同源重组相结合的方法将该连接区内的 T429、E432、I443 和 N446 位氨基酸进行单点突变，测序确定构建成功后将它们在真核瞬时表达系统内进行蛋白表达。采用吉姆萨染色法、指示基因法、染料转移法定性和定量检测各突变体蛋白对膜融合功能的影响。采用流式细胞术来检测各突变体 F 蛋白在细胞表面的表达效率。

结果 各突变株蛋白细胞表面蛋白表达效率与野毒株蛋白相比没有统计学差异，而突变株细胞融合活性表现为两种情形，E432A、I443A 和 N446S 表现为融合活性轻微升高，其中 N446S 融合活性达到野毒株的 118.6％；T429A、T429L 和 N446A 表现为融合活性的降低，其中 N446A 的融合功能只有野毒株的 15.2％。HRB 连接区的氨基酸突变对膜融合活性有重要影响，其中第 446 位天冬酰胺（N）为关键氨基酸。
结论 HPIV3 F 糖蛋白 HRB 连接区对膜融合功能有重要影响，其中第 446 位天冬酰胺（N）为关键氨基酸位点。

PU-2309

一例心脏瓣膜置换术后嗜酸性粒细胞升高的病例探讨

高倩
空军军医大学西京医院

嗜酸性粒细胞是白细胞的组成部分，来源于骨髓造血干细胞，具有杀伤细菌、寄生虫的功能，也是免疫反应和过敏反应过程中极为重要的细胞。嗜酸性粒细胞可以释放颗粒中的内容物，引起组织损伤，促进炎症进展。嗜酸性粒细胞增多一般见于寄生虫感染、变态反应、血管炎或肿瘤等疾病中，出现多系统、多器官损害的临床表现。

PU-2310

双原发肿瘤合并慢性淋巴细胞白血病一例报道

孙学青
东营市人民医院

恶性肿瘤严重危害人们的健康，实体肿瘤多见全身器官或组织转移，双原发肿瘤合并慢性淋巴细胞白血病较为少见，我们遇到一例报道如下：
结合病史、多次复查血常规血象异常、骨髓形态学检查、骨髓流式细胞学，目前诊断慢性淋巴细胞白血病明确。

PU-2311

门诊抽血处存在的常见问题及解决策略

伏广丽、史沛芹
连云港市第一人民医院

目的 三甲医院门诊抽血处是门诊检验血项目分析前质量控制的关键场所，是医院院感检查的重点科室，也是医患容易产生矛盾的地方，探讨其存在的常见问题及解决策略。
方法 建立符合医院实际的规章制度，重视抽血医务人员业务及心理伦理培训，实行人文管理。在 ISO15189 及《医院感染管理条例》要求下，规范操作程序，抽血过程无菌及消毒隔离，做好手卫生；医疗废物医疗垃圾统一处理，净化抽血处室内环境与卫生，体现人文关怀；必要的应急预设抢救措施。
结果 三甲医院门诊抽血处存在的常见问题及策略：一，LIS 数字化条码系统高效项目管理，第一时间追踪血标本抽血流程，具体环节中某个步骤，保障检验血项目分析前质量控制 ；二，抽血人员加强业务的熟练操作及心理伦理培训，对病患同理心，同时人性化管理，弹性工作时间，调动医务人员的工作热情，形成良好的医患关系。三 ，抽血处环境狭小拥挤，医疗垃圾的不当处理是医院感染问题多的主要原因：改善环境，营造舒适宽敞的空间，抽血电子叫号系统，报告单提醒系统

LED 显示屏，遵循医学伦理设置黄线隔板等尊重患者隐私。生活垃圾与医疗垃圾严格分开医院统一处理。等候区视频播放系统，免费早餐热水供应，儿童座椅等人文关怀；四，对婴幼儿和血管条件差的患者，安排专人（在新生儿病区轮转，业务娴熟心理素质好者）专门抽血通道，对行动不便的患者预约上门抽血服务等。配备必要的应急预设抢救措施，对于体弱晕针者，突发急症者，给予及时救助。

结论 抽血处每天承担门诊病人的抽血工作，是医院对外服务的“窗口”责任大工作量重，患儿哭闹环境嘈杂，从心理上容易烦躁，医患双方容易发生矛盾，对工作人员业务及心理素质和工作场所都要求非常高，所以管理上要重视细化，人文管理。抽血处的门诊标本准确及时高效的运行是检验科标本周转时间（TAT）的第一保障，也是门诊患者满意度的重要体现，应重视抽血处的日常工作，提升医院服务质量和医院综合实力。

PU-2312

1,25-(OH)2D3 protects pancreatic beta cells against H2O2-induced apoptosis through inhibiting the PERK-ATF4-CHOP Pathway

Cong Hu[2]、Xinhua Wang[1]、Xiaobo Hu[3]
1. Yi Yang Central Hospital
2. Yiyang Central Hospital
3. Hengyang Medical School, University of South China

Endoplasmic reticulum (ER) stress plays a critical role in pancreatic β cell destruction which leads to the pathogenesis of type 1 diabetes mellitus (T1DM). Vitamin D (VD) has been reported to reduce the risk of T1DM; however, it remains unknown whether VD affects ER stress in pancreatic β cells. In this study, we investigated the role of the active form of VD, 1,25-dihydroxyvitamin D3 (1,25-(OH)2D3), in ER stress-induced β cell apoptosis and explored its potential mechanism in mouse insulinoma cell line mouse insulinoma 6 (MIN6). The results of cell counting kit-8 (CCK8) and flow cytometric analyses showed that 1,25-(OH)2D3 caused a significant increase in the viability of MIN6 cells injured by H2O2. The protein kinase like ER kinase (PERK) signal pathway, one of the most conserved branches of ER stress, was found to be involved in this process. H2O2 activated the phosphorylation of PERK, upregulated the activating transcription factor 4 (ATF4) and C/EBP homologous protein (CHOP) expression, and subsequently initiated cell apoptosis, which were significantly reversed by 1,25-(OH)2D3 pretreatment. In addition, GSK2606414, a specific inhibitor of PERK, suppressed PERK phosphorylation and reduced the expressions of ATF4 and CHOP, leading to a significant decrease in β cell apoptosis induced by H2O2. Taken together, the present findings firstly demonstrated that 1,25-(OH)2D3 could prevent MIN6 cells against ER stress-associated apoptosis by inhibiting the PERK-ATF4-CHOP pathway. Therefore, our results suggested that 1,25-(OH)2D3 might serve as a potential therapeutic target for preventing pancreatic β cell destruction in T1DM.

PU-2313

ELISA 法与胶体金法联合检测乙肝表面抗原的临床应用分析

江婷、高安琦、沈竹莲、李亚楠
杭州迪安医学检验中心有限公司

目的 ELISA 法（酶联免疫吸附试验）在乙肝表面抗原（HBsAg）的检测过程中的影响因素多，探讨联合胶体金法检测 HBsAg 的临床应用分析。
方法 对本室 2020 年 12 月乙肝表面抗原 ELISA 法检测结果为阳性的 2512 例标本用胶体金法进行复检，记录不同范围 S/CO 值下两者阳性结果检测情况。
结果 2512 例 ELISA 法检测 HBsAg 阳性的标本中，胶体金法检测阳性例数为 2289，检测阴性例数 223，胶体金的阳性检出率为 91.1%。ELISA 法阳性中真阴性有 43 例，其假阳性率为 1.7%。
结论 胶体金法的阳性检测率随着 S/CO 值的增加而增加，并且用 ELISA 检测 HBsAg 存在一定的假阳性，在 S/CO 低值时假阳性的概率会逐步增高。用胶体金法复检可以减少 HBsAg 假阳性报告的发出，结合两种方法检测可以提高 HBsAg 检测的准确度。

PU-2314

卵巢癌细胞生长环境中 CD4+ Treg 细胞和 CD4+ Teff 细胞的糖代谢特征初探

吴茗[2]、徐睿[1]、刘书娜[1]、王芳[1]
1. 南京医科大学第一附属医院江苏省人民医院
2. 南京医科大学第一附属医院江苏省人民医院

目的 探究 CD4+Treg 细胞（CD4+CD25+CD127low 调节性 T 细胞）和 CD4+Teff 细胞（CD4+CD25-CD127+ 效应性 T 细胞）在卵巢癌细胞生长环境中的糖代谢特征。
方法 FACS 分选和扩增 CD4+Treg 细胞和 CD4+ Teff 细胞，建立两种细胞与 SKOV3 细胞的共培养体系，采用 RT-PCR 和 Western blot 检测 CD4+ Treg、Teff 细胞糖摄取和糖酵解水平。
结果 卵巢癌细胞生长环境中的人外周血 CD4+Treg 细胞糖代谢水平高于 CD4+ Teff 细胞，卵巢癌细胞可以促进人外周血 CD4+Treg 细胞糖代谢相关蛋白和基因表达水平上调。
讨论 研究结果发现，将 CD4+Treg 与卵巢癌细胞 SKOV3 共培养后，其糖摄取、糖酵解相关基因和蛋白表达水平均高于对照组。当细胞处于肿瘤微环境中，卵巢癌细胞的生长导致静止的 T 细胞被激活，Glut 表达的增高促进 CD4+Treg 细胞和 CD4+Teff 细胞的糖摄取，耗氧量增加，而且 T 细胞必须大量增殖以产生足够的效应细胞来对抗肿瘤，同时需要和增殖水平极快的肿瘤细胞进行营养竞争，这时细胞的代谢需求明显增加。同时研究结果发现卵巢癌细胞生长环境中 CD4 Treg 细胞的糖摄取与糖酵解水平显著高于 Teff 细胞，说明在 SKOV3 生长环境中，CD4+Treg 细胞代谢特征与效应细胞相比会消耗更多能量，抑制效应细胞发挥功能，促进肿瘤生长，这些结果都证明了肿瘤细胞的生长影响了肿瘤微环境中免疫细胞的代谢, 对抑制免疫细胞、促进肿瘤的进展具有重要的意义。因此深入理解 T 细胞尤其是 Treg 细胞糖代谢的表型、调控机制、及其动态变化将为自身免疫、肿瘤等免疫相关疾病的防治提供有效的分子靶点和潜在临床治疗新方法、新工具。

PU-2315

肝内胆管癌患者术后预后模型的建立与应用

王琳
江苏省人民医院（南京医科大学第一附属医院）

目的 建立肝内胆管癌(ICC)患者接受肝切除术后的预后模型并对其进行评估。
方法 回顾性分析 2017 年 1 月至 2020 年 1 月在南京医科大学第一附属医院确诊的 134 例 ICC 患者的资料，采用单因素和多因素 Cox 比例风险模型分析实验组的独立危险因素，建立基于术前实验室常规指标的总生存率（OS）预测模型。使用一致性指数（C-index）和校准图对模型的区分度和校准度进行评价。
结果 实验组中，中位生存期 30.2 个月，5 年生存率 36.4%。糖类抗原 199（HR=1.230，95%CI 1.059-1.334）、癌胚抗原（HR=1.156，95%CI 1.047-1.254），中性粒细胞与淋巴细胞比率（HR=1.010，95%CI 1.054-1.136）、血小板计数（PLT）（HR=1.011，95%CI 1.002-1.019），白蛋白（HR=0.767，95%CI 0.613-0.917）是与 ICC 患者术后预后相关的独立危险因素。实验组和验证组的一致性指数（C-index）分别为 0.740（95%CI：0.715-0.768）和 0.744（95%CI：0.716-0.785），校准图中校准曲线拟合良好。
结论 本研究成功建立了 ICC 患者术后预后评估模型，该模型可为临床术前决策提供依据。

PU-2316

41 例新型冠状病毒肺炎患者血清抗体检测分析

余珊
南华大学附属南华医院

目的 比较新型冠状病毒肺炎（corona virus disease 2019, COVID-19）不同临床分型患者血清中新冠病毒（SARS-CoV-2）特异性 IgM 和 IgG 抗体的差异和不同时期的浓度变化,并以抗体水平变化判断核酸复阳是否为二次感染。
方法 选取 2020 年 2—3 月南华大学附属南华医院收治的 41 例 COVID-19 患者,共收集其患病 15-65 天血清标本 126 份;作为对照,同时选取 91 例发热门诊核酸检测阴性患者采集血清各 1 份。采用化学发光免疫分析法（chemiluminescence immunoassay, CLIA）检测血清中新冠病毒 IgM 和 IgG 抗体水平,经组间 t 检验和 Mann-Whitney U 检验对抗体浓度变化进行统计学分析。
结果 无症状感染者 IgM 和 IgG 抗体平均浓度高于阴性对照组,低于普通型和重型患者,差异均具有统计学意义（P<0.05）;普通型患者 IgM 和 IgG 抗体浓度均低于重型患者,IgM 抗体差异有统计学意义（P<0.05）,但 IgG 抗体差异没有统计学意义（P=0.06）;COVID-19 患者急性期的 IgM 和 IgG 抗体浓度均高于康复期,差异均有统计学意义（P<0.05）。复阳后,患者体内 IgM 和 IgG 抗体浓度没有增加,持续下降。
结论 COVID-19 患者的 SARS-CoV-2 IgM 和 IgG 抗体浓度,依无症状感染、普通型、重症型患者临床类型逐次升高,康复期逐渐降低,但大部分体内仍存在较高水平的 IgG 抗体。核酸复阳之后的 SARS-CoV-2 IgM 和 IgG 抗体浓度并未增高,说明未发生二次感染。

PU-2317

血浆同型半胱氨酸和胱抑素 C 水平与糖尿病患者早期肾损害的关系研究

乔慧
长治医学院附属和平医院

目的 探讨血浆同型半胱氨酸（Hcy）及胱抑素 C（CYC）在 2 型糖尿病患者中的表达及与早期肾损害的关系。
方法 选取 2018 年 8 月~2020 年 11 月收治的 2 型糖尿病患者 80 例为观察组，其中肾功能正常（尿白蛋白肌酐比≤30mg/g）45 例，肾功能异常（30mg/g＜尿白蛋白肌酐比＜300mg/g）35 例，另选同期体检健康人员 77 例为对照组。所有对象均对血浆 Hcy、CYC 及其他相关生化指标予以检测，并采用 Pearson 相关性分析对血浆 Hcy、CYC 与肾功能指标的关系予以分析。
结果 观察组血浆 Hcy、CYC、FBG、UAER、Scr 水平与对照组比较，均明显较高，Hb 水平与对照组比较，明显较低，差异有统计学意义（P＜0.05）；肾功能正常组患者 Hcy、CYC、FBG、UAER、Scr 水平与肾功能异常组患者比较，均明显较低，Hb 水平与肾功能异常组患者比较，显著较高，差异有统计学意义（P＜0.05）；相关性分析显示，血浆 Hcy 与 UAER 水平呈正相关性（P＜0.05），与 Scr 水平呈正相关性（P＜0.05），与 Hb 水平呈负相关性（P＜0.05）；血浆 UA 与 UAER 水平呈正相关性（P＜0.05），与 Scr 水平呈正相关性（P＜0.05），与 Hb 水平呈负相关性（P＜0.05）。
结论 2 型糖尿病患者血浆 Hcy、CYC 表达均存在明显异常，且与早期肾损害有相关性，对血浆 Hcy、CYC 水平予以监测，可为 2 型糖尿病患者肾功能评估提供指导。

PU-2318

7 例遗传性凝血因子 XI 缺陷症患者的基因型与临床表型分析

翁妙珊
潮州市中心医院

目的 分析 7 例遗传性凝血因子 XI（FXI）缺陷症患者的基因突变类型与临床表型。
方法 采用一期法检测患者 FXI 活性（FXI：C），免疫火箭电泳法检测 FXI 抗原（FXI：Ag）水平，并抽提患者外周血 DNA，PCR 扩增患者 FXI 基因所有的外显子及其侧翼序列，DNA 直接测序进行基因分析。
结果 在 7 例遗传性 FXI 缺陷症患者中共发现 5 种基因突变，包括 3 种无义突变（p.Lys327X、p.Tyr351X、p.Gln263X），1 种移码突变（p.Leu424fsX10）和 1 种剪接位点突变（c.326-1G>A）；除患者 7 为单杂合突变，FXI：C 为 56.7%，FXI：Ag59.2%，其余患者 FXI：C 和 FXI：Ag 均明显降低（<2% 和<1%），基因型为纯合突变或复合杂合突变；患者临床出血表现轻重不一，患者 1、2 均有术后出血不止的表现，而患者 5 则无术后出血表现。
结论 所发现的 5 种基因突变是导致 7 例遗传性 FXI 缺陷症患者的分子发病机制，其中 p.Gln263X 较常见，p.Lys327X 为新发现的 FXI 基因突变类型，而 FXI：C 与患者的临床表型之间无明显相关性。

PU-2319

浅谈检验科危急值报告制度的建立

王赵梅
昆明市中医医院

不同医务人员认识和重视程度参差不齐，不能准确判定是否为假阳性危急值，危急值报告项目和范围管理缺失之处，这些因素决定了建立医学检验危急值报告制度的必要性和重要意义。所以，要加强危急值报告登记制度，建立完善的医学检验危急值文件，根据病种病因不同界定不同危急值范围，加强检验人员和医护人员的沟通，加强危急值的监督管理，及时发现、核实和处理医学检验危急值，提高报告的准确性，确保医疗质量和医疗安全。

PU-2320

2017 年-2020 年中国郴州儿童下呼吸道感染的流行病学调查

周杰英
郴州市第一人民医院

Objective This study aimed to explore the epidemiology of pathogens in children who were hospitalized with acute lower respiratory tract infections (ALRTIs) .
Methods Children aged less than 13 years who were hospitalized with ALRTIs were enrolled from January 2017 to December 2020. Respiratory specimens were collected for the detection of common respiratory viruses, atypical bacteria and other bacteria using current laboratory diagnostic tests. The epidemiological characteristics of the respiratory pathogens were analyzed by spss 20.0.
Results A median age of 12 months, 10849 (63.61%) were positive for at least 1 pathogen. Mycoplasma pneumoniae(M.pneumoniae) was the most commonly detected pathogen in the 17054 specimens (4504, 26.41%), followed by RSV (3263,19.13%), PIV (1411, 8.27%). FLU and RSV detected more often in winter. MP was the most prevalent pathogen among children ≥5 years , whereas RSV was the most common pathogen in very young children aged less than 6 months. Co-infections were found in 17.28 % of patients. Of these co-infections, viral-bacterial coinfections was the most common.
Conclusions The most common pathogens causing acute respiratory infection among children in Chenzhou of China were MP and RSV. The detection rates for pathogens displayed specifific seasonal, gender and age group variations. Coinfections with multiple respiratory pathogens were common.

PU-2321

探讨试剂耗材信息化管理的价值

黄鑫鑫
山东省千佛山医院

目的 探讨二维码和 LIS 系统联合使用对试剂耗材信息化管理的价值。
方法 引进二维码技术与 LIS 系统结合对试剂耗材进行信息化管理，并对其进行全程实时监控。
成果 试剂耗材的信息化管理，提高了管理小组的工作效率，降低了工作强度，并可对试剂耗材的有效信息及时分析判断，对近有效期的试剂耗材进行优先管理消耗，对出现的问题及时处理并采取相应措施达到持续改进的效果，保证检验质量。

结论 该方法的建立提高了试剂耗材的管理水平和工作效率，确保了试剂耗材有效性以及对供应商和生产厂家的可追溯性，降低了科室耗占比，杜绝试剂耗材的失效浪费。

PU-2322

醋甲唑胺对动脉粥样硬化血管钙化治疗作用的研究

袁琳
山东省千佛山医院

目的 本研究计划探究碳酸酐酶 1（carbonic anhydrase 1,CA1）在动脉粥样硬化（atherosclerosis，AS）血管钙化中的作用和机制以及 CA 抑制剂醋甲唑胺（methazolamide，MTZ）对 AS 的治疗作用。
方法 本研究分两部分，第一部分检测 CA1 在人主动脉 AS 组织中的表达情况，观察 CA1 表达水平与 AS 病变的关系。该研究也计划建立 ApoE-/-小鼠 AS 模型，检测 CA1 在模型小鼠主动脉组织中的表达情况，通过观察 CA1 的表达与钙盐沉积及 AS 斑块的关系，进一步探究 CA1 与 AS 钙化的相关性。同时，本研究对 AS 模型小鼠应用 CA 抑制剂 MTZ，观察 MTZ 对 AS 斑块形成的影响和对 AS 的治疗作用。血管平滑肌细胞是血管钙化的核心场所，血管平滑肌细胞向成骨细胞表型转化是血管钙化的核心环节，CA1 如何调控血管钙化尚不明确。所以本研究第二部分选择血管平滑肌细胞作为实验对象，研究 CA1 在血管平滑肌细胞钙化中的作用。通过体外诱导大鼠血管平滑肌细胞（rat VSMCs）钙化，观察细胞钙化后 CA1 的表达情况。同时，应用 anti-CA1 siRNA 和 CA 抑制剂 AZ 处理 VSMCs，抑制 CA1 的表达，分析确定 CA1 在 VSMCs 钙化中的作用。同时也通过干扰 CA1 的表达，观察 VSMCs 增殖、迁移和凋亡能力的变化情况。醋甲唑胺片是一种临床药品，但是没有无菌状态可用于细胞培养实验的 MTZ。用于细胞培养实验的无菌 AZ 可商用获得。所以本研究选择 MTZ 用于第一部分的动物实验，AZ 用于第二部分的 VSMCs 细胞实验。
结果 CA1 在人主动脉 AS 组织和 AS 模型小鼠的主动脉组织中高表达，高表达的 CA1 刺激 AS 血管钙化过程。醋甲唑胺可能通过抑制 CA1 表达及其所调控的钙化过程对 AS 发挥治疗作用。抑制 CA1 调节的钙化可能是治疗动脉粥样硬化的关键点。
结论 醋甲唑胺有望成为治疗动脉粥样硬化血管钙化的辅助药物。

PU-2323

两种荧光 RT-PCR 试剂检测肠道病毒通用型、EV71、CA16 核酸的比较

凌永基
南方医科大学珠江医院

目的 比较两种市售荧光定量 PCR 试剂（深圳太太基因公司和中大达安基因公司）检测肠道病毒 71 型(EV71)和柯萨奇病毒 A 组 16 型(CA16)特异性及通用型(EV)核酸的性能，有无差别及差别对临床诊断有无影响。
方法 收集临床疑似手足口病患儿的肛拭子标本 43 例，采用相同的方法提取核酸后分别用两种试剂同时测定 EV、EV71、CA16 核酸，配对 χ2 检验比较两者检出率；采用培养的 EV71 病毒上清液 10 倍倍比稀释后用上述方法提取核酸，分别用两种试剂检测，比较两者检测灵敏度。
结果 检出率结果太太基因公司：EV 通用型核酸检出率 58.1% (25/43)，EV71 检出率 51.2% (22/43），CA16 检出率 4.3%（1/23）；达安基因公司：EV 核酸检出率 32.6% (14/43)，EV71 检出率 16.3%（7/43），CA16 检出率 0.0%（0/23）。两种试剂 EV 通用型核酸（P=0.00）、EV71 核酸（P=0.00）、CA16 核酸（P=0.043）检出率均有显著性差异，检出率太太试剂均高于达安试剂。

灵敏度结果太太基因公司检测 10 7 、10 8 倍稀释 EV 核酸均阳性（Ct：27.5 和 31.8），达安基因公司检测 10 7 倍稀释 EV 核酸阳性（Ct：32.5），10 8 倍稀释 EV 核酸阴性；太太基因公司检测 10 7 、10 8 倍稀释 EV71 核酸均阳性（Ct：25.6 和 29.9），达安基因公司检测 10 7 、10 8 倍稀释 EV71 核酸均阴性。太太基因公司相比达安基因公司，检测 EV 通用型和 EV71 核酸的灵敏度更高。

结论 两种试剂检测临床标本结果有显著差异。实验室必须选择质量好且符合自己实验室要求、与本实验室仪器相匹配的试剂以保证检验质量。

PU-2324

Impact of COVID-19 Outbreak on the Gynecological HPV Infection Rate in Wuhan, China: a retrospective observational study

Hang Liu、yan li
Renming Hospital of wuhan university

Background The outbreak of SARS-CoV-2 has caused millions of people deaths and greatly influenced other diseases' timely diagnosis and treatment. Nevertheless, the Background of the pandemic dramatically reduced the prevalence of several sexually transmitted infections. However, the impact of this pandemic on the HPV infection has not been well investigated.
Materials and Methods We retrospectively gathered the HPV and cervical cancer screening data of outpatients in gynecological clinics from December 1, 2018 to December 31, 2020. Based on the timeline of the SARS-CoV-2 pandemic in Wuhan, we divided this period into four relatively independent stages to compare the HPV screening visit numbers and infection rates.
Results The HPV screening visits and HPV infection rates decreased dramatically during the pandemic. After the pandemic, the HPV infection rates remain lower than the baseline before the outbreak, but the HPV screening visits returned to the baseline before the outbreak.
Conclusion HPV infection rate greatly influent by the outbreak of SARS-CoV-2 in a short time. The efficient HPV and cervical screening program should immediately reinforce to prevent transmission of HPV and cervical cancer progression.

PU-2325

第三方医检联合疾控共同助力新冠病毒大筛查

陈玉辉、刘静、许友强
新疆金域医学检验所有限公司

目的 2019 年底爆发的新冠肺炎疫情是中国及世界所有国家历史以来遇到的爆发速度最快、波及范围最广、防疫难度最大的一次突发公共卫生事件，对全球每个国家而言，在救治检测服务上无疑都是一场严峻的挑战。面对前所未有的大规模人群、物表的核酸检测任务，公共医检资源有限，医检人员数量、技术水平有限，为弥补政府及医疗卫生单位检测能力短板，也为实现区域医疗诊断资源的集约化，助力政府核酸病毒检测大筛查快速、有效的完成。
方法 根据新疆各级卫健委有关文件要求，新疆金域医学检验所有限公司积极落实国家政策、响应政府号召，携手当地疾控部门联合共建核酸检测中心实验室，积极开展新冠核酸的检测工作，并承接政府委派核酸检测任务。新疆金域充分利用自身在质量管理、服务流程、医学领域专家资源、市场高效便捷的物流网络体系等方面优势，协助当地疾控中心高标准、高质量管理运行核酸检测实验室。

结果 利用社会资本和政府资源,依托 PCR 检验中心的强大的检测服务能力，该实验室目前核酸检测能力已达 10000 管/日,有效辐射了当地周边医疗机构，快速、准确地完成送检样本的检测，为当地卫健部门做好疫情防控部署，及时提供了准确有效的参考数据，并起到积极作用。
结论 此次合作共建实现了优质医疗资源的共享，促进 了当地公共卫生事业健康发展。在抗击新冠疫情、全面核酸病毒大筛查的过程中，第三方医检平台在当地打赢疫情防控阻击战中发挥了“主力军”的作用。

PU-2326

达雷妥尤单抗干扰复发性/难治性多发性骨髓瘤病实验诊断病例分析

安云飞、严琳、李壹、蔡蓓
四川大学华西医院

目的 多发性骨髓瘤(multiple myeloma，MM)是一种恶性浆细胞疾病。以浆细胞肿瘤性增殖，并产生单克隆免疫球蛋白为特征。该病不可治愈，约占血液系统恶性肿瘤死亡病例的 20%。大部分患者通过实验诊断手段均能识别与诊断疾病。
多发性骨髓瘤在疾病进程中都会出现疾病进展。其中一部分患者会发展为复发性或难治性多发性骨髓瘤。疾病的进展通常与实验诊断指标的变化同步。所以在识别患者疾病进展的方法中，实验诊断的持续性监测则显得十分重要。针对于复发性或难治性多发性骨髓瘤患者，虽然目前的治疗方案选择越来越丰富，但是大部分患者会经历多次复发，所以准确有效的识别每次复发则显得特别重要。目前越来越多的生物制剂不断的应用于临床，给患者带来了更多的治疗选择和更好的治疗效果。达雷妥尤单抗是一种人源化、抗 CD38 IgG1、kappa 型单克隆抗体，主要应用于复发和难治性多发性骨髓瘤患者。这一药物的应用对我们以免疫学方法为基础的检测提出了挑战。目前已有数据表明单克隆抗体药物将显著影响实验诊断结果，导致假阳性的结果判读。而我国引入这一类药物时间较短，我们仍未产生较为清晰的认识和认知。
方法 回顾性分析 2020 年 1 月至 6 月送检免疫固定电泳患者用药信息。通过回顾分析患者实验诊断数据和图形，判断实验诊断报告是否存在单抗药物应用的干扰。
结果 回顾性分析 2020 年 1 月至 6 月送检免疫固定电泳的临床住院患者信息。共识别出 3 例住院患者明确确认应用达雷妥尤单抗。这 3 例患者的报告均出现了一定程度的结果的错误判读和解读。影响实验诊断报告的质量以及 TAT 时间。
结论 目前随着越来越多的生物制剂应用于临床，对基于免疫学方法的实验诊断迎来了更大的挑战，提出了更高的要求。针对于复发性/难治性多发性骨髓瘤患者的动态监测和随访，患者信息的纳入不仅停留于实验诊断数据本身，还要涵盖患者的完整治疗方案。这样才能更好的提供高质量的实验诊断服务。

PU-2327

2015-2019 天津地区儿童肺炎支原体呼吸道感染的流行情况及其与环境因素的关系探讨

娜仁、沈永明
天津市儿童医院

目的 了解天津地区儿童肺炎支原体呼吸道感染的流行情况，并探讨其与环境因素的相关性。
方法 收集 2015 年 6 月至 2019 年 2 月天津市儿童医院呼吸道感染住院患儿资料共 63821 例，挑选肺炎支原体检出阳性的患儿进行病例回顾性分析，总结肺炎支原体的流行情况。同时收集同期环境

因素资料，采用 SPSS 19.0 软件进行相关性分析，探讨肺炎支原体呼吸道感染与环境因素的相关性。
结果 2015 年 6 月至 2019 年 2 月肺炎支原体总检出率为 23.62%，各季节肺炎支原体检出率分别为 22.89%（2891 / 12628）、21.55%（3295 / 15288）、25.32%(4001 / 15799)、24.31%(4888 / 20106)，比较差异有统计学意义。住院呼吸道感染患儿例数与气温、NO2 、CO、O3 呈中度相关（rs = -0.647、0.681、0.530、-0.514，P<0.05），与 AQI 指数、PM2.5、PM10、SO2 呈低度相关（rs = 0.395、0.401、0.317、0.473，P<0.05）；肺炎支原体检出率与文中分析的所有环境因素指标均无相关性。
结论 2015 年 6 月至 2019 年 2 月，住院呼吸道感染患儿中肺炎支原体总检出率为 23.62%。儿童肺炎支原体呼吸道感染全年高发，秋冬季更为常见。住院呼吸道感染患儿例数与气温、NO2 、CO、O3 呈中度相关，与 AQI 指数、PM2.5、PM10、SO2 呈低度相关；肺炎支原体检出率与文中分析的所有环境因素指标没有相关性。

PU-2328

青海省血细胞分析各项指标参考区间调查与分析

韩启福
青海省人民医院

目的 调查我省二级以上公立医院医学实验室血细胞分析项目参考区间行业标准实施情况。
方法 实验室通过基于 WEB 方式的室间质量评价(EQA)软件上报参考区间相关信息，包括参考区间上下限、来源、是否验证、分组规则等，后台将回报数据另存为 Microsoft Excel 2007 文档，对已颁布参考区间行业标准的血常规项目参考区间行业标准实施情况和适用性进行分析。
结果 参考区间来源于试剂说明书的实验室占 26.27-35.56%、来源于仪器厂家说明书的实验室占 13.87-16.91%、 来源于教科书或操作规程的实验室占 22.20-40.80%、实验室自己确定的占 3.65-8.89%、来源于行业标准的实验室占 6.4-8.64%，参考区间引用行业标准的实验室占比较少，引用与未引用行业标准实验室的参考区间上下限大部分项目差异有统计学意义(P＜0.05)，调查发现仅有少部分实验室对引用的参考区间进行了验证，且 Hb、RBC、HCT、MCV 等项目的参考区间对高海拔地区实验室不适用。
结论 血细胞分析检验项目参考区间行业标准的实施情况并不乐观，只有少部分实验室引用行业标准，且有相当一部分实验室未对参考区间进行验证，为解决我省高海拔地区医学实验室使用血细胞分析参考区间的适宜性，还需要做大量人群的统计研究。

PU-2329

1000 例女性人乳头瘤病毒筛查结果分析

姜坤宏
联勤保障部队第 970 医院

目的 近年来，宫颈癌的发病率逐年升高，成为仅次于乳腺癌的中国妇科好发恶性肿瘤的第 2 位，逐渐成为威胁女性健康最为严重的疾病之一。当代许多研究表明人乳头瘤病毒（human papilloma virus,HPV)与子宫颈癌的发生有密切的关系。为此分析了解来某医院就诊女性人乳头瘤病毒的感染情况，为临床诊疗及宫颈癌的防治提供依据。
方法 使用实时荧光 PCR 法，采用人乳头瘤病毒（HPV）核酸检测试剂盒对女性宫颈样本中 HPV-DNA 进行检测，统计 2020 年 8-10 月筛查检测的 1000 例标本结果，分析来该医院就诊女性 HPV 感染情况，统计 HPV 感染总体阳性率，高危型占比，阳性率较高的亚型，以及≤25、26-35、36-45、46-55、≥56 五个年龄组感染情况。

结果 1000 例中共有阳性 170 例，阳性率 17.0%，其中高危型 147 例（含混合感染），仅感染高危型的 134 例，所占比例为 91.16%；阳性率最高的亚型为 HPV52 型，占比 13.99%，其次为 16 型（9.88%）、58 型（8.64%）、33 型（5.76%）；1000 例标本中小于等于 25 岁女性标本数为 146 例，占比例为 14.6%，在各年龄组中阳性率最高为 29.45%，其次大于等于 56 岁阳性率为 22.54%，不同年龄段阳性率比较，差异有统计学意义（c2=69.05，P<0.05)。
结论从以上数据可以看出，HPV 在女性人群中的感染率较高，而感染人群中，高危型占有很高的比例，需密切关注有无相应的临床症状，从各年龄组比较中看出，HPV 感染有年轻化的趋势。因此早期诊断有重要意义，可定期进行妇科体检早期发现，也建议人群能够根据自己的年龄情况接种疫苗，做好个人预防。

PU-2330

两种不同检测系统肿瘤标志物参考区间的建立与分析

张磊
重庆医科大学附属第一医院

目的 应用直接法和间接法建立两种不同检测系统的血清癌胚抗原（CEA）、甲胎蛋白（AFP）、细胞角蛋白 19 片段（CYFRA21-1）、糖类抗原 19-9（CA19-9）、糖类抗原 15-3（CA15-3）、糖类抗原 125（CA125）、游离前列腺特异性抗原（fPSA）、总前列腺特异性抗原（tPSA）的参考区间并加以分析。
方法 间接法：收集 2019 年 1 月至 2020 年 6 月罗氏 E602 和 2020 年 6 月至 2021 年 3 月雅培 I2000 所做体检成人血清 CEA、AFP、CYFRA21-1、CA19-9、CA15-3、CA125、fPSA、tPSA 的检测结果，在剔除部分信息缺失样本后得到 E602 上 CEA 17968 例、AFP 18366 例、CYFRA21-1 6220 例、CA19-9 8235 例、CA15-3 3139 例、CA125 6533 例、fPSA 4747 例、tPSA 9572 例，和 I2000 上 CEA 43429 例、AFP 43638 例、CYFRA21-1 6150 例、CA19-9 9055 例、CA15-3 7020 例、CA125 11344 例、fPSA 4954 例、tPSA 21012 例。剔除各个项目离群值后，再建立各个项目参考区间。直接法：收集健康志愿者标本（不少于 120 例）作为参考个体，建立各项目参考区间。
结果 用间接法建立了 E602 和 I2000 两种不同检测系统 CEA、AFP、CYFRA21-1、CA19-9 不同性别和年龄、女性 CA15-3、CA125 不同年龄以及男性 fPSA、tPSA 不同年龄的参考区间，用直接法建立了两检测系统各项目参考区间。
结论 通过间接法和直接法建立的两种不同检测系统肿瘤标志物的参考区间，具有较好的临床应用价值，为临床对患者的诊断和治疗提供了更加准确、客观的参考依据。

PU-2331

AZD8055 Ameliorates Experimental Autoimmune Encephalomyelitis by Suppressing NLRP3-mediated Pyroptosis through mTOR/NLRP3 Pathway

Miao He
the First affliated hospital of Chengdu medical college

Objective Experimental autoimmune encephalomyelitis (EAE), a mouse model of a chronic inflammatory autoimmune disease called multiple sclerosis (MS) that has limited conventional treatments, is characterized by immune-mediated demyelination and neurodegeneration. There are multiple inflammatory demyelinating plaques in the white matter of CNS in the acute active stage, and the patients are characterized by multiple lesions, remission and recurrent course of disease. Previous studies have shown that the activation of NOD-like receptor protein 3 (NLRP3)

inflammasome can aggravate the spinal cord inflammation of EAE and affect its occurrence and development. NLRP3 inflammasome can induce a type of proinflammatory programmed cell death called pyroptosis, which is characterized by the swelling of cells when their membranes burst, large amounts of inflammatory cytokines are released and leading to dangerous inflammatory cascades. In MS, excessive inflammation can cause demyelinating lesions and axonal injuries; hence, blocking the NLRP3-mediated-pyroptosis is expected to alleviate neuroinflammation and postpone disease progression. Autophagy is a pivotal metabolic mechanism ensure cellular survival following various inflammatory injuries. Recently, it has been thought to be associated with the relief of widespread inflammation, including EAE. However, the effect of autophagy on NLRP3 in EAE and its mechanism are still unclear. In this study, we examined whether the autophagy activator AZD8055 can alleviate signs and symptoms of EAE by activating autophagy to inhibit NLRP3 activation.

Methods (1) Construction of EAE model and detection of autophagy and scorch death: the mouse model of multiple sclerosis was established, and the construction of EAE model was evaluated in terms of symptoms and body weight changes. (2) the role of AZD-8055 in reducing neuroinflammation: the changes of disease indexes related to multiple sclerosis were evaluated in terms of symptoms and body weight by intraperitoneal injection of AZD-8055, at the same time of constructing EAE model. On this model, HE staining was used to evaluate the occurrence of brain and spinal cord inflammation, LBF staining was used to evaluate spinal cord demyelination, ELISA was used to detect the secretion of IL-1 β and IL-18, and Western Blotting was used to detect inflammatory factors such as IL-6 and IL-8. (3) to detect the level of autophagy and scorch death in the model: Western Blotting, immunohistochemistry and immunofluorescence were used to detect the expression of proteins related to autophagy and scorch death, such as mTOR, LC3II / I, beclin-1, NLRP3, Caspase1 and so on.

Results The results showed that after AZD8055 treatment, the score of clinical behavior abnormality decreased and the body weight increased in EAE model mice, and the histological examination showed that the degree of inflammatory infiltration and demyelination of spinal cord was mild. At the same time, AZD8055 successfully inhibited mTOR, and the autophagy-related proteins were up-regulated, such as beclin-1,LC3 Ⅱ / Ⅰ and so on. In addition, in the EAE group treated with AZD8055, the proteins expression of NLRP3-mediated pyroptosis, such as NLRP3,Caspase-1, was decreased, and the co-localized expression of LC3 and NLRP3 was detected.

Conclusion Our research found that AZD8055 could ameliorate autoimmune myelitis in MOG-induced EAE mice by alleviating the demyelination and inflammation of spinal cord, reducing scores of clinical behaviors, and improving function behaviors. Furthermore, AZD8055 could activate autophagy and increase the co-localization of LC3 and NLRP3 in EAE mice in order to repress NLRP3-mediated pyroptosis by mTOR/NLRP3 pathway. These results revealed the relationship between autophagy and pyroptosis, and provided a new direction for the treatment of MS and the study of its pathogenesis.

PU-2332

一例 5p15.2-pter 缺失及 20p12.2-pter 重复胎儿的产前诊断

詹福寿
宁夏医科大学总医院

目的 探讨单核苷酸多态性芯片(single nucleotide polymorphisms array，SNP-array)技术在胎儿 5p15.2-pter 缺失及 20p12.2-pter 重复诊断中的应用。

方法 抽取孕妇及其丈夫外周血行常规染色体 G 显带核型分析，在 B 超引导下行羊膜腔穿刺术，抽取羊水常规细胞培养，收获、制片，G 显带处理，对胎儿进行染色体 G 显带核型分析，并采用 SNP-array 技术对胎儿全基因组拷贝数变异(copy number variants，CNVs)进行检测。

结果 胎儿及其双亲染色体 G 显带核型分析未见明显异常。胎儿 SNP-Array 检测结果为 arr[hg19] 5p15.33p15.2(113,576-13,376,497)x1,20p13p12.2(61,661-9,838,776)x3。
结论 SNP-array 技术可以诊断染色体 G 显带核型分析不能辨别的胎儿 5p15.2-pter 缺失及 20p12.2-pter 重复，并可精确定位，为基因型和表型的关联分析积累数据。

PU-2333

以机器学习算法建立 IgA 肾病与非 IgA 肾病的鉴别诊断模型

杨晗、刘记宏、张慧、刘子杰
昆明医科大学第一附属医院

目的 基于患者的流行病学资料和临床实验室常规检测结果，用机器学习算法建立 IgA 肾病与非 IgA 肾病鉴别诊断模型。
方法 本研究共纳入经肾穿刺活检确诊的患者 260 例，其中 IgA 肾病 130 例，非 IgA 肾病 130 例。收集患者的流行病学资料和临床实验室常规检测结果。将 260 例数据分为训练集(70%，182 例)和测试集(30%，78 例)。分别使用决策树、随机森林、支持向量机(SVM)、XGBOOST 算法建立鉴别诊断模型。并使用混淆矩阵，ROC 曲线评估模型效能。
结果 与决策树、随机森林和支持向量机相比，XGBOOST 模型性能最佳，其准确率为 83.33%，ROC 曲线下面积为 0.84，诊断为 IgA 肾病的敏感度、特异度、阳性预测值、阴性预测值分别为 89%、79%、78%、89%。
结论 采用 XGBOOST 方法建立的 IgA 肾病与非 IgA 肾病鉴别诊断模型具有较好的临床性能。

PU-2334

智慧标本管理与流程监控系统的建立及运行初探

张崇唯
四川大学华西医院

目的 为解决临床中由于运输和储存方式不当，引起的血液标本质量问题，规范标本送检过程，实现标本运输的实时监控。
方法 设计研发集标本储存、运输和管理为一体的智慧标本管理与流程监控系统。通过合适的内部环境、安全的运输过程，可视化的送检流程，减少标本检验前问题，增加标本可接受性，实现归责到人，提高医疗机构人力物力资源的使用效率。通过建立微信小程序、云开发程序，其特点具有学习成本小、开发门槛低、开发效率高等优点，将小程序与血液标本管理和运输有机结合，符合了移动医疗背景下的创新理念。
结果 开发标本运输及管理系统，实现了二维码生成、新标本信息生成、运输、查询、个人信息模块。而客户端小程序界面前端系统处理流程包括如下：首先，在首页可以通过点击扫一扫，扫描二维码查询获取运输信息；然后，可以点击下方导航栏进行不同页面之间的切换：中间的导航栏用于创建新的运输订单，右边导航栏用于登录以及查看用户自身的信息和系统相关信息等。后端信息管理使用了微信小程序自带的云开发服务提供的数据库。
结论 本项目针对目前我国医院中存在的血液标本质量不合格和送检不及时等问题，设计了一种可以优化标本储存环境、确保安全运输、把控送检流程的智能血液标本管理与流程监控系统，在技术支持下，实现标本运输流程可控性和透明化，合理配置医疗资源，提高医疗服务质量，促进医院信息化建设。

PU-2335

上海市宝山区 18501 例健康儿童末梢血白细胞计数及其分类参考区间的建立

张宇亮、徐灵、崔邦铨、李仁杰、董成林、吴成志
上海中冶医院

目的 建立实验室 2-6 岁健康儿童白细胞计数及其分类正常值的参考区间。
方法 选取 18501 例 2019 年 4 月至 8 月在我院进行幼托体检的 2-6 岁健康儿童白细胞计数及其分类数据按年龄段分成 5 组进行统计分析。
结果 同年龄组男女间结果比较，除白细胞计数和中性粒细胞百分率外，其他参数 P 值均＜0.05，具有统计学意义，其中淋巴细胞百分率女性明显高于男性，单核细胞百分率和嗜酸性粒细胞百分率男性明显高于女性；不同年龄组间结果比较，白细胞计数及其五分类参数间差异均有统计学意义（P＜0.05），其中中性粒细胞百分率随着年龄的增长而增长，淋巴细胞百分率随着年龄的增长而下降；
结论 实验室应根据自身的检测系统，在充分考虑性别、年龄和临床需求的基础上，建立适应自己医院临床诊断需求的白细胞计数及其分类的参考区间。

PU-2336

含冷凝集素患者输注血制品采用输液加温器必要性的探讨

吴成志、李仁杰、张宇亮、徐灵、董成林
上海中冶医院

目的 健康人或某些疾病的患者均可含有一定滴度的冷凝集素，为了防止输注血制品时因低温导致冷凝集素激活而引起输血不良反应，有必要采用输液加温器输注法。
方法 选择 64 例冷凝集素滴度为 1:16～1:32 血制品输注患者分成两组，32 例采用常规不加温输注悬浮红细胞≥2 单位，同时对输前和输后 24h 的血标本作补体 C3 浓度的测定并进行结果比对。32 例输注悬浮红细胞时采用输液加温器，输注悬浮红细胞的量也为≥2 单位，对输前和输后 24h 的血标本作补体 C3 浓度的测定并进行结果比对。另外对一例含有 1:16 效价的冷凝集素的标本做冷凝集素试验时同时加豚鼠血清，观察红细胞的形态变化情况。
结果 输悬浮红细胞时未使用输液加温器组，输注悬浮红细胞 24h 后的补体 C3 浓度低于输注前（P<0.001）。而采用输液加温器组，输注悬浮红细胞 24h 后的补体 C3 浓度与输注悬浮红细胞前无明显变化（P>0.05）。
结论 大部分人群均含有一定量的冷凝集素，某些疾病如冷凝集素综合征、非典型肺炎、支原体肺炎等冷凝集素滴度可高达 1:1024，因此输冷藏的悬浮红细胞时采用输液加温器可防止由于冷凝集素而导致的输血不良反应的发生。

PU-2337

长三角三级医疗机构输血科建设情况分析

刘志刚[1]、谢杰锋[2]、范刚[3]、王学锋[1]、张睿[4]
1. 上海交通大学医学院附属瑞金医院
2. 成都市血液中心
3. 上海市血液中心
4. 国家卫生健康委医政医管局

目的 通过对长三角三级医疗机构临床用血和输血科专职专业技术人员情况的调查、分析，为卫生健康行政部门和医疗机构对临床输血管理决策与输血科规范化建设提供依据。
方法 依据《临床用血质量控制指标（2019 年版）》， 选取长三角三级医疗机构共 435 家，进行统计分析。
结果 长三角三级医疗机构输血科组织机构与人才队伍建设有待加强与完善。
结论 加强输血科规范化建设，提高临床科学合理用血水平。

PU-2338

新型冠状病毒肺炎患者血液炎性相关标志物水平表达研究

刘婷、刘佳星、石玉如、王云、刘杨、谷妍、戚应杰
安徽省立医院感染病院

目的 探讨血液炎性相关标志物表达水平在诊断新型冠状病毒肺炎（Corona- virus Disease 2019，COVID-19）中的应用价值。
方法 回顾性分析 2020 年 1 月到 2020 年 3 月我院收治的 82 名 COVID-19 确诊病例和 89 例非 COVID-19 疑似病例的血液炎性相关标志物的检测结果和临床资料，分析其炎性相关标志物水平的表达差异及临床诊断效能。
结果 （1）COVID-19 组的淀粉样蛋白 A（SAA）、白介素 6（IL-6）中位数水平高于非 COVID-19 组，差异具有统计学意义（P<0.05）。COVID-19 组的淋巴细胞计数（L#）中位数水平低于非 COVID-19 组，差异具有统计学意义（P<0.05）。COVID-19 组的 WBC、N#、L#、SAA、CRP、IL-6 异常率分别为 20.73、26.83、35.37、89.02、65.85、26.83，均高于非 COVID-19 组。（2）重型和危重型组的白细胞计数（WBC）、中性粒细胞计数（N#）、C-反应蛋白（CRP）中位数水平高于普通型组，差异具有统计学意义（P<0.05）。重型组的降钙素原（PCT）、SAA、IL-6 中位数水平高于普通型组，差异具有统计学意义（P<0.05）。重型和危重型组的 L#中位数水平低于普通型组，差异具有统计学意义（P<0.05）。重型和危重型组的 WBC、L#、M#、CRP、IL-6 异常率均高于普通型组，危重型组 PCT、SAA 异常率高于普通型组。（3）ROC 曲线分析显示，L#、IL-6、SAA 诊断 COVID-19 的 AUC 分别为 0.779、0.790、0.823（P<0.05）。取最佳临界值时，敏感度和特异度最高的指标都是 SAA。L#联合 IL-6 的 AUC 为 0.779，L#联合 SAA 的 AUC 为 0.867，SAA 联合 IL-6 的 AUC 为 0.823，3 项指标联合检测的 AUC 均为 0.868。
结论 血液炎性相关标志物的表达水平对新型冠状病毒肺炎患者的诊断以及临床分型有重要的参考价值，其中 SAA 对 COVID-19 诊断的敏感度和特异度最高。L#、IL-6、SAA 三项指标联合检测对 COVID-19 的诊断比单项检测更准确，提供更高的价值。

PU-2339

Biochemical and Molecular characteristics of Citrin Deficiency in South China

Yanna Cai、Mizhi Peng、Yongxian Shao、Zhikun Lu、Wen Zhang
Guangzhou Women and Children's Medical Center

Objectives Neonatal intrahepatic cholestasis caused by citrin deficiency (NICCD) shows diverse metabolic abnormalities and suppressed gluconeogenesis.
Methods Here, we investigated the mutational spectrum and biochemical characteristics of NICCD patients. The genetic results and biochemical data were retrospectively analyzed.
Results A total of 174 NICCD patients were included. These patients all had abnormally high levels of liver function parameters (alanine aminotransferasese, asparlateaminotransferase, alkaline phosphatase, γ-glutamyhranspepti dase), prothrombin time, and activated partial thromboplastin time, as well as low levels of glucose, total protein, albumin, globulin, prealbumin, fibrinogen. In addition, these NICCD patients had elevation of proteinogenic amino acids, except for alanine and tryptophan, which were decreased compared with normal controls. Furthermore, the levels of methionine showed positive correlation with age. Significant correlation between genotype and some biochemical parameters was observed.
Conclusions This study showed that, some biochemical markers in c.851_854del group of NICCD patients were lower than other gene types. Patients, who had the ratio of AST/ALT>2 and decrease level of total protein and prothrombin time should be suspected with NICCD, and the elevated citrulline, methionine, threonine and tyrosine further convinced the possibility of NICCD. The NICCD children generally did not resolve at 6 to 12 months of age. Identification of the NICCD patients when they are under one years, early genetic testing would be of value.

PU-2340

143 例 Citrin 缺陷导致婴儿肝内胆汁淤积症血浆氨基酸谱分析

梅慧芬
广州市妇女儿童医疗中心

目的 本研究拟分析 Citrin 缺陷导致的婴儿肝内胆汁淤积症（NICCD）患儿血浆氨基酸谱特点，以及氨基酸谱与基因型的相关性。
方法 1.2004 年至 2019 年间在我院确诊的 143 例 NICCD 患儿，与 56 例正常对照儿童组、49 例不明原因肝内胆汁淤积症(INH)组患儿的氨基酸谱进行比较；并对上述数值进行受试者工作特征(ROC)曲线分析。2.NICCD 病人分为小于 6 个月组、6 个月至 12 月组和正常对照儿童组的血浆瓜氨酸、蛋氨酸、组氨酸、缬氨酸、亮氨酸、异亮氨酸水平比较。3.NICCD 患儿按 SLC25A13 基因突变类型分为复合杂合突变组与纯合突变组进行比较。
结果 与正常对照组、INH 组比较，NICCD 患儿血浆中天冬酰胺、组氨酸、瓜氨酸、蛋氨酸、苏氨酸、酪氨酸、甘氨酸、苯丙氨酸、鸟氨酸、赖氨酸、精氨酸、丝氨酸水平显著升高，差异均有统计学意义；谷氨酰胺和色氨酸水平显著降低，差异均有统计学意义。NICCD 组瓜氨酸、蛋氨酸、苏氨酸、酪氨酸 ROC 曲线下面积分别是 0.986[95％可信区间（CI）]：0.974－0.998、0.850 (95％CI：0.786－0.915)、0.899(95％CI：0.849－0.949)、0.700(95％CI：0.620－0.781)。NICCD 组 R 瓜氨酸/丝氨酸，R 瓜氨酸/（亮氨酸和异亮氨酸），R 苏氨酸/丝氨酸 ROC 曲线下面积分别是 0.968（95％CI：0.946－0.991）、0.984 (95％CI：0.970－0.998)、0.896 (95％CI：0.833－0.960)。NICCD 患儿纯合突变组的天冬氨酸、谷氨酸水平比复合杂合突变组高。NICCD 病人的瓜氨酸、蛋氨酸、苏氨酸、组氨酸浓度随年龄而变化。

结论 血浆氨基酸谱分析是筛查和诊断 NICCD 的一种灵敏快速的方法。最为敏感的诊断指标为瓜氨酸升高结合 R 瓜氨酸/（亮氨酸和异亮氨酸）升高，可对 95.1%的患者进行诊断。NICCD 患儿瓜氨酸浓度变化与年龄有关。

PU-2341

中性粒细胞/淋巴细胞比值及中性粒细胞群落参数在类风湿关节炎诊断中的作用

李美美[2]、殷睿映[1]
1. 郑州大学第一附属医院
2. 郑州大学第一附属医院

目的 探讨类风湿关节炎患者的外周血中性粒细胞/淋巴细胞比值（NLR）及中性粒细胞群落参数的变化及临床意义。
方法 选取郑州大学第一附属医院 2020 年 6 月至 2020 年 9 月就诊的已确诊类风湿关节炎的患者 125 例，以及 137 例健康体检者，分别为病例组和正常对照组。记录两组的性别、年龄等临床资料；使用迈瑞 BC-6800 血细胞分析仪进行全血细胞计数，收集常规报告参数和中性粒细胞群落研究参，并计算 NLR、PLR。比较两组的白细胞计数、中性粒细胞绝对值、淋巴细胞绝对值、血小板计数、NLR、PLR 及中性粒细胞群落参数（Neu-X, Neu-Y, Neu-Z）之间的差异；逐步回归分析对类风湿关节炎有显著贡献的指标，并制作 ROC 曲线分析这些指标对类风湿关节炎诊断的价值。
结果 两组的白细胞计数、中性粒细胞绝对值、淋巴细胞绝对值、血小板计数、NLR、PLR 及中性粒细胞群落参数中的 Neu-X、Neu-Z 之间都存在显著的统计学差异（$p<0.05$）。淋巴细胞绝对值和 Neu-Z 在类风湿关节炎组中显著低于正常对照组；其余指标均在类风湿关节炎组中显著增高。回归分析显示 NLR、Neu-X、Neu-Z 对区分类风湿关节炎具有显著贡献；NLR、Neu-X、Neu-Z 对类风湿关节炎诊断的曲线下面积分别为 0.678，0.592，0.614，三者联合的曲线下面积达 0.765。
结论 类风湿关节炎患者外周血 NLR、Neu-X、Neu-Z 发生显著变化，且对类风湿关节炎的临床诊断具有一定指导意义。

PU-2342

锁骨骨折切开复位内固定术后与骨不连相关的因素

王榕榕[1]、晁宝婷[1]、刘芸[1]、王勇[1]、王大伟[2]、卢志明[1]、白晓卉[1]
1. 山东第一医科大学附属省立医院临床医学检验部
2. 山东第一医科大学附属省立医院骨科

目的 切开复位内固定术后的骨不连是常见的术后并发症。本研究的目的是确定锁骨骨折切开复位内固定术后与骨不连相关的因素。
方法 我们回顾性地确认了 2010 年 1 月至 2019 年 5 月在山东省立医院接受切开复位内固定术治疗的 251 例锁骨骨折患者。所有患者接受至少一年的随访。在本研究中，我们使用了组间比较、单变量分析和多变量分析等方法来确定与切开复位内固定术后骨不连相关的因素。
结果 本研究共纳入了 251 名锁骨骨折患者，其中正常愈合的 237 名，不愈合 14 名，骨不连率为 5.6%。本研究包括男性患者 180 名，占 71.71%；女性患者 71 名，占 28.29%。251 名患者平均年龄 43.97±14.72 岁。单因素分析结果显示，受伤到手术时间、血清纤维蛋白原浓度、白细胞计数、淋巴细胞绝对值与骨不连有关($P < 0.05$)，其他变量无显著差异。将单因素分析中 $P<0.05$ 的结果纳入多变量回归分析，结果显示受伤到手术时间 ($OR = 1.25$；$P = 0.005$)、血清纤维蛋白原浓度($OR = 2.11$；$P = 0.002$)、白细胞计数 ($OR= 0.72$；$P = 0.031$)、淋巴细胞绝对值($OR = 0.29$；$P = 0.022$)与骨不连的发生独立相关。

结论 锁骨骨折患者经切开复位内固定术治疗后发生骨不连的概率为5.6%，单因素和多因素分析后显示受伤到手术时间、血清纤维蛋白原浓度、白细胞计数以及淋巴细胞绝对值与锁骨骨折切开复位内固定术后骨不连有关。这些结果对于术后骨不连有预测意义，并为临床医生及时采取措施改善患者预后提供了重要指导。

PU-2343

区分抗原抗体 HIV 检测策略的临床应用

李潇涵、罗岚、邓杰伦、王远芳、陶传敏、李冬冬
四川大学华西医院

目的 中国疾病预防控制中心于 2020 年发布最新版《全国艾滋病检测技术规范》[1]，该规范中包含了使用区分抗原抗体 HIV 检测试剂时的检测流程，本研究旨在分析 Elecsys HIV Duo 检测试剂使用过程中区分抗原抗体检测策略的临床应用情况。
方法 回顾分析我院 2020 年 HIV 确证样本的筛查试验（以 Elecsys HIV Duo 检测试剂和胶体金免疫层析试剂构成的筛查程序）结果、补充试验（HIV 抗体确证试验以及 HIV-RNA 检测）结果以及临床随访信息。
结果 我院 2020 年共检测 HIV 抗体确证样本 399 例，男性 282 例，女性 117 例；确证阳性共计 248 例，阳性率为 62.15%（248/399），抗体不确定 35 例，阴性 116 例；其中男性确证阳性 191 例，阳性率为 67.73%（191/282），女性确证阳性 57 例，阳性率为 48.71%（57/117），男女阳性比为 3.35：1；Elecsys HIV Duo 筛查结果中仅抗体阳性而胶体金复检阴性 87 例，经随访和核酸检测共确诊 2 例感染；此外 Elecsys HIV Duo 筛查结果仅抗原阳性送检确证样本 42 例，约占总确证样本数的 10%（42/399）。
结论 Elecsys HIV Duo 作为初筛试剂，当筛查结果为抗体阳性而抗原为阴性时，使用胶体金试剂复检两次均为阴性时出具 HIV 抗体阴性，HIV-1p24 抗原阴性的报告存在漏检风险，建议仍出具 HIV 感染待确定，通知患者进行 HIV-RNA 检测或随访，并结合临床表现进行诊断；同时我们还需要加强临床交流，强调 HIV 核酸检测对于急性感染的重要性，提高 HIV 核酸在可疑急性感染发生时的送检率，才能及时检出、及时治疗。

PU-2344

儿童难治性肺炎支原体肺炎发生塑型性支气管炎的临床特征及高危因素预测

崔小健
天津市儿童医院

目的 分析难治性肺炎支原体肺炎（RMPP）发生塑型性支气管炎患儿的临床特点，探讨 RMPP 患儿形成塑型性支气管炎的高危因素。
方法 回顾性分析 2019 年 1 月至 12 月在天津市儿童医院住院诊断符合 RMPP 并行纤维支气管镜治疗的 399 例患儿的临床资料,依据镜下表现分为塑型性支气管炎(PB)患儿 142 例、非塑型性支气管炎(非 PB)患儿 257 例,比较两组临床特征、实验室检查指标、影像学表现的差异,将组间存在统计学差异的指标行受试者工作特征(ROC)曲线和多因素逐步 logistic 回归分析，预测儿童 RMPP 发生塑型性支气管炎的高危因素。
结果 PB 组较非 PB 组，高热、低氧血症、肺外表现人数多，发热天数与住院天数更长，差异具有统计学意义(P<0.05)。实验室指标中，PB 组 NEUT%、LYMP%、PLT、CRP、PCT、IL-6 、AST、 ALT 、LDH、CK 、D-D 水平较非 PB 组高，差异有统计学意义(均 P<0.05)。 ROC 曲线和

多因素分析显示：最高体温＞39.8℃、肺不张、NEUT%＞72.9%、IL-6＞26.65 pg/mL、AST＞49.5 U/L 是 RMPP 发生 PB 的独立危险因素。

结论 最高体温＞39.8℃、肺不张、NEUT%＞72.9%、IL-6＞26.65 pg/mL、AST＞49.5 U/L 可能是儿童 RMPP 发生 PB 的重要预测指标，有助于早期诊断。

PU-2345

耐碳青霉烯类抗菌药物肠杆菌科细菌分布特征及耐药性分析

谢强
安徽省滁州市第一人民医院

目的 探讨耐碳青霉烯类抗菌药物肠杆菌科细菌(CRE) 的分离率、标本来源、病区分布以及耐药情况，为临床抗感染治疗提供依据。

方法 回顾性分析 2017－2019 年滁州市第一人民医院分离的 332 株 CRE 菌株，对其药物敏感实验结果、科室分布等数据进行系统分析。

结果 2017－2019 年本院共分离肠杆菌科细菌 5499 株，其中 CRE 332 株，检出率为 6.0％，近三年 CRE 的分离率呈递增趋势，排名前 3 位的分别是肺炎克雷伯菌（196 株，59.0％），大肠埃希菌（35 株，10.5％）和阴沟肠杆菌（23 株，6.9％ ）；标本来源前 3 位的分别为呼吸道标本（211 株，63.6％）、尿液标本（77 株，23.2％）和分泌物标本（17 株，5.1％）。CRE 菌株对替加环素的耐药率最低，为 9.3％，其次为阿米卡星（38.6%）、复方新诺明（46.7%）和庆大霉素（53.9%），对其余监测的抗菌药物的耐药率均大于 80%。近三年 CRE 菌株对所监测的抗菌药物（除替加环素外）的耐药率呈上升趋势。

结论 本院 CRE 菌株的分离率较低，但近三年检出率有均有增加的趋势，应引起临床的足够重视。

PU-2346

体检人群 AFP 检测情况调查与分析

王海
东南大学附属中大医院

目的 探究体检人群血浆甲胎蛋白（AFP）的年龄，性别分布情况，并进行不同年龄段和性别间 AFP 含量差异分析

方法 回顾性分析 2016 年 1 月~2021 年 5 月期间东南大学附属中大医院健康管理中心 166068 名≥17 岁体检人群中血浆 AFP 含量，采用卡方检验比较不同性别、年龄段（<60 岁和≥60 岁）AFP 阳性（>10ng/mL）发生率。

结果 166068 名检测了血浆 AFP 含量的人群的平均年龄为 44.2 岁，范围为 17~99 岁，其中年龄≥60 岁的有 27570 人（16.6%），<60 岁的有 138498 人（83.4%）；男性共 99656 人（60%），女性共 66412 人（40%）。166068 人中，AFP 均值为 2.68±14.98 ng/mL，范围为 0 ~ 4708.63 ng/mL，共 1021 人检测 AFP 阳性（>10 ng/mL）。男性 AFP 阳性发生率显著低于女性（0.4% vs 0.9%，P<0.001）；≥60 岁人群 AFP 阳性发生率显著低于<60 岁人群（0.4% vs 0.7%，P<0.001），且 AFP 阳性组平均年龄显著低于非阳性组（43.06 vs 44.43，P=0.002）。

结论 体检中心检测血浆 AFP 含量人群主要集中在 60 岁以下，且≥60 岁人群 AFP 阳性发生率显著低于<60 岁人群；男性 AFP 阳性发生率显著低于女性。

PU-2347

2017-2019 年滁州市第一人民医院医院细菌耐药性监测

谢强
安徽省滁州市第一人民医院

目的 了解 2017-2019 年滁州市第一人民医院临床分离菌对抗菌药物的耐药性。
方法 使用 VITEK2-Compact 对临床分离菌进行鉴定和药敏实验，补充药敏实验采用纸片扩散法，使用 WHONET5.6 软件对药敏结果进行统计分析。
结果 3 年共分离细菌 11540 株，其中革兰阳性菌 3025 株（26.2%），革兰阴性菌 8515 株（73.8%）。金黄色葡萄球菌和凝固酶阴性葡萄球菌中甲氧西林耐药株（MRSA 和 MRCNS）的检出率分别为 44.1%和 80.9%，三年里 MRSA 的检出率呈逐年下降趋势，MRCNS 的检出率呈逐年上升趋势。MRSA 和 MRCNS 对监测的多种抗菌药物的耐药率明显高于甲氧西林敏感株（MSSA 和 MSCNS），未见万古霉素和利奈唑胺耐药的葡萄球菌。肠球菌中粪肠球菌对所有监测药物（除四环素和高浓度的链霉素外）耐药率明显低于屎肠球菌。三年里检出的成人和儿童非脑膜炎肺炎链球菌对青霉素保持全敏感。肠杆菌科细菌对碳青霉烯类抗菌药物仍然保持较高的敏感性，耐药率均小于 15%，耐碳青霉烯类的肠杆菌科细菌（CRE）的检出率为 6.0%，其中耐碳青霉烯类抗菌药物的肺炎克雷伯菌的检出率为 11.5%。铜绿假单胞菌对所监测的抗菌药物的耐药率均不大于 25%。三年里不动杆菌属（鲍曼不动杆菌占 84.9%）对所监测的抗菌药物的耐药率呈下降趋势（除哌拉西林外），对亚胺培南和美罗培南的耐药率由 2017 年的 63.9%和 50.3%下降到 2019 年的 38.4%和 36.7%。
结论 近三年多重耐药情况仍然严重，尤其是耐碳青霉烯类的肺炎克雷伯菌检出率仍然较高，但不动杆菌属细菌对碳青霉烯类抗菌药物的耐药率呈下降趋势，应继续做好细菌耐药性监测，同时加强实验室与临床的沟通，以发挥细菌耐药监测的价值。

PU-2348

PCT 联合 CRP 和 ESR 水平检测对肺结核患者合并肺部细菌感染的诊断价值分析

刘璐
保山市人民医院

目的 探讨血清降钙素原(PCT)联合 C-反应蛋白(CRP)和红细胞沉降率(ESR)检测对肺结核(PTB)患者合并肺部细菌感染的诊断价值。
方法 2019 年 04 月—2021 年 04 月，选择我院接收的肺结核患者合并肺部细菌感染 50 例作为研究对象，分别行 PCT、CRP 和 ESR 检测，观察对比 CRP 和 ESR 检测与 PCT 联合 CRP 和 ESR 检测的特异性和差异性，同时纳入同期接收的未合并肺部细菌感染患者，采用 SPSS16.0 软件对两组资料进行统计分析，观察对比两组患者 PCT、CRP 和 ESR 水平差异和 ESR 检。
结果 PCT 联合 CRP 和 ESR 检测的敏感性和特异性分别为 94.12%、88.89%明显高于 CRP 和 ESR 检测 76.34%、54.35%，P＜0.05，差异有统计学意义；未合并肺部细菌感染患者 PCT、CRP 和 ESR 水平均明显低于合并肺部细菌感染患者，P＜0.05，差异有统计学意义。
结论 肺结核患者合并肺部细菌感染情况较多，且临床诊断难度加大，PCT 联合 CRP 和 ESR 检测诊有一定价值，具有较高的敏感性和特异性，值得广泛推广。

PU-2349

应用风险管理对某酶免分析一体机检测过程控制持续改进初探

段友斌、姚丽菊
云南昆明血液中心

目的 应用风险管理对设备使用情况进行分析，持续改进酶免分析一体机检测过程管理措施，保证血液安全。
方法 统计 2019 年 1 月 1 日-2019 年 12 月 31 日某酶免分析一体机检测情况和失效失控率，分析失效失控原因，根据统计结果，针对该设备使用过程中特有的风险点进行风险管理，制定应对措施，降低该设备使用过程中的风险。
结果 2019 年 1 月 1 日-2019 年 12 月 31 日共进行 2088 板次检测，失效失控 42 次，失效失控率 2.01%，失效失控的原因主要为仪器设备和人为因素，占 42.86%、33.33%。通过风险管理，识别和评价了 12 个设备特有的风险增加和风险不可接受的风险点，进行风险应对后，9 个风险点为可接受风险，3 个风险点从风险不可接受下降为风险增加，检测过程风险下降。
结论 使用风险管理，对某酶免分析一体机使用过程进行管理，能够有效分析处理设备潜在隐患，杜绝事故的发生，能够对设备使用过程质量管理体系进行持续改进，保障血液安全。

PU-2350

血站血液筛查实验室检测过程风险管理实施细则的验证

段友斌、杜霞、杨洪岗、张珺珂、何清、苏品璨
云南昆明血液中心

目的 应用新建的检测过程风险管理实施细则，对采供血机构血液筛查实验室 2 种 ELISA 复验标本检测方案的检测过程进行风险管理，验证采供血机构血液筛查实验室检测过程风险管理实施细则的有效性。
方法 根据血液筛查实验室质量管理特点建立血液筛查实验室检测过程风险等级表和管理措施可行性等级表，作为风险管理实施细则，对 2 种通常认为有差别的复验标本检测方案的检测过程进行风险评估、风险应对和应对措施可行性分析。对风险评估结果和管理措施可行性分析结果进行统计学分析。
结果 通过风险评估，2 种复验标本检测方案均有 8 项检测过程风险，2 种方案风险等级评分有统计学差别（$P<0.05$）。根据风险等级和应对原则各制定 15 项和 12 项管理措施，2 种方案可行性分析有统计学差别（$P<0.05$）。采用的检测过程风险管理实施细则能够对检测过程进行有效风险管理。
结论 检测过程风险管理实施细则，能够有效帮助对 2 种复验标本检测过程进行有效风险管理，为血站血液筛查实验室质量体系中的过程管理提供一种充分有效可行的方法。

PU-2351

通过生化免疫分析流水线布局改造提高标本处理效率

张丽军、覃俊龙
深圳市罗湖医院集团医学检验实验室

目的 通过实验室罗氏自动化流水线上三台 cobas 8000 生化免疫分析平台（以下简称 cobas 8000）的模块调整及优化检测项目配置，提高流水线上 cobas p612 标本前处理系统（简称 p612）以及 cobas 8000 标本处理效率。

方法 实验室于 2021 年 3 月 26 日对罗氏流水线上三台 cobas 8000 进行布局调整，增加 2 台生化分析模块，以 A 代表 C702 生化分析模块，B 代表 E602 免疫分析模块，调整前三台 cobas 8000 配置为：AAA、BBB、BBB，调整后配置为：AABB、AABB、ABB，调整后对模块中项目进行设置，前两台 AABB 开展相同的项目，第三台开展量较大的组合项目。收集分析数据：罗氏流水线模块布局调整前 7 天（3 月 10 日至 3 月 16 日）标本 16384 支，调整后 7 天（4 月 19 日至 4 月 25 日）标本 18147 支，进行数据对比分析。（1）比较 p612 调整前后标本分管率。（2）通过每支标本进入 p612 时间和进入 cobas 8000 时间计算 p612 平均处理时长，了解调整前后 p612 对标本的处理时间变化情况。（3）通过标本送达实验室时间和检验报告发送时间计算检验中 TAT，评估调整前后检验中 TAT 是否缩短。（4）按照第（1）条分管率，当标本量相同时，计算调整前后分管所带来的耗材成本对比。

结果（1）调整前 7 天标本总数 16384 支，分管 3272 支，分管率 19.97%；调整后标本总数 18147 支，分管 1437 支，分管率 7.92%，分管率下降 12.05%。（2）计算调整前后各 7 天中所有标本，从进入 p612 至进入 cobas 8000 时长，调整前平均处理时间 24.6 分钟，调整后平均处理时间 15 分钟，p612 平均处理时间缩短 9.6 分钟。（3）调整前检验中 TAT 平均为 2 小时 07 分钟，调整后检验中 TAT 平均为 1 小时 36 分钟，检验中 TAT 缩短 30 分钟。（4）按照前面调整前后的标本分管率，以每个月 8 万支标本计算，每月可少分管 10703 支，每分管一支消耗试管、吸头、后处理试管盖等耗材费用 1.11 元，每月可节省耗材费用 1 万元。

结论 实验室通过罗氏自动化流水线上三台 cobas 8000 生化和免疫模块调整及检测项目重新配置，一支标本在一台 cobas 8000 中即可完成检测，从而减少 p612 前处理系统对标本分管的可能，提高 p612 处理效率，缩短检验中 TAT 时间。分管情况减少也减少分管耗材的使用，带来经济效益，后处理系统因分管少降低了冰箱空间占有率，从而能储存更多样本。调整后有两台 cobas 8000 拥有相同的检测项目，可以实现双机备份，防止因一台 cobas 8000 故障而影响检验结果发放。

PU-2352

The associations between fasting plasma glucose levels and mortality of SFTS in patients

Yin Zhang、Yuanhong Xu、Ying Huang
Department of Clinical Laboratory, The First Affiliated Hospital of Anhui Medical University

Objective To identify the correlation between the level of at-admission fasting plasma glucose (FPG) with poor outcomes in hospitalized patients suffering from severe fever with thrombocytopenia syndrome (SFTS).

Methods Between April 1 and December 1, 2020, the list of hospitalized patients affected with SFTS infection was provided by the Infectious Disease Department at First Affiliated Hospital of Anhui Medical University, followed by the collection of information I.e., gender, age, diabetic history and the level of FPG on admission.

Results In this study, a total of 77 patients were included and were categorized into three groups (<5.6, 5.6–6.9, and ≥7.0 mmol/l) on the basis of their glucose level in the blood. The obtained results revealed that among three groups considerable variations were observed in leukocytes, FPG, D-Dimer, aspartate aminotransferase (AST), tumor necrosis factor-α (TNF-α), fibrin degradation products (FDP), and interleukin (IL)-10 level. Correlation analysis indicated a linear negative correlation between PLT and FPG ($r = -0.28$, $P = 0.01$), however, a linear positive correlation was observed between AST, IL10, D-Dimer, and FDP levels and FPG (P-value < 0.05). Multivariate statistical analysis results show that there was significant difference between group comparison ($F=17.01$, $P<0.001$) and interaction between group and time ($F=8.48$, $P<0.05$); but there was no significant difference between time point comparison ($F=0.04$, $P=0.96$). With the prolongation of time, the changes of FBG were different between survivor group and non-survivor group. The FBG in survival group shown a downward trend; The non-survivor group shown an upward trend.

Conclusions Elevated level of FPG has been correlated with hypercoagulability, inflammation, and lower PLT in SFTS patients. The measurement of FPG level can help in evaluating the inflammatory process, hypercoagulability, and prognosis of patients suffering from SFTS. FBG can predict the prognosis of SFTS. It is necessary to pay attention to the role of FBG in the process of treatment in patients with SFTS.

PU-2353

支原体培养及鉴定室间质量评价结果分析

张敏敏
上海市临床检验中心

目的 通过开展支原体培养及鉴定室间质量评价活动（简称室间质评），了解上海及部分其它地区医疗机构近两年支原体培养及鉴定项目的检测质量。
方法 收集 2019~2020 年参加上海市临床检验中心（SCCL)支原体培养及鉴定室间质评项目的反馈结果，并对鉴定符合率进行统计分析。
结果 2019~2020 年参加 SCCL 开展的支原体培养及鉴定室间质评活动的实验室数由 60+增加至 100+。其中，人型支原体项目由 60 个实验室增至 96 个实验室，合格率由 93%增加到 100%；解脲支原体项目由 65 个实验室增至 104 个实验室，合格率由 43%增加到 99%。
结论 人型支原体和解脲支原体培养及鉴定室间质评计划，是保证各临床实验室检测质量的重要手段，可以考察参评实验室对临床微生物项目的检测水平。上海及部分其它地区开展的支原体培养及鉴定室间质量评价活动，鉴定上总体检测能力和准确率较高，但个别实验室检测能力有待提高，临床实验室的质量控制对于保证检测结果的准确性具者十分重要的作用。相信随着该项的不断广泛化、检测试剂方法的不断优化、室内质量控制的不断加强、相关管理制度的不断落实、检测质量会越来高。

PU-2354

阵发性睡眠性血红蛋白尿症一例

高龙斌、和迎春
大理大学第一附属医院（云南省第四人民医院）

阵发性睡眠性蛋白尿症（paroxysmal nocturnal hemoglobinuria，PNH）是一种获得性造血干细胞基因突变引起血细胞膜缺陷所致的溶血病，其血细胞膜对补体异常敏感而破坏，导致持续性血管内溶血，常伴有血红蛋白尿、全血细胞减少或反复血栓形成，有时可出现骨髓衰竭 。鉴于该病罕见，故通过对该病例的报告能够补充病例库，同时可提高临床医生和检验人员对该病的认识及诊疗水平。

PU-2355

智慧医疗在独立医学实验室领域的发展

梁雨欣、董晓毅
杭州迪安医学检验中心有限公司

智慧医疗将大数据、人工智能和物联网等先进技术融合，实现患者与医务人员、医疗机构、医疗设备之间的信息无缝传递和有效使用。近年来，我国独立医学实验室行业在信息化、智能化和连锁化方面发展迅速，在检验前阶段，有冷链物流系统为患者样品和检测试剂保驾护航；在检验中阶

段，统一的检测系统和质控平台促进了室内质控室间化，助力实验室间检测结果互认；在检验后阶段，智能审核系统极大提升了报告审核速度，远程病理平台解决了基层医疗机构缺乏优质病理诊断资源的难题。另外，通过互联网，直接向消费者提供上门样本检测服务；以及通过对独立实验室检验大数据的深入分析，可建立多个常规医学检验项目与临床疾病的发生发展的相关性，从而指导临床决策；另外，还可通过大数据分析验证和建立实验室生物参考区间等，充分展示了智慧医疗在独立实验室领域发展的无限可能性。

PU-2356

异常凝血酶原(PIVKA-II)—肝癌检测新指标

段又心
西昌路昆明医科大学第一附属医院

肝细胞癌（Hepatocellular carcinoma，HCC）是世界范围内发病率居第五，死亡率居第二的恶性肿瘤。对 HCC 进行准确、灵敏的早期诊断是提高患者疗效和存活率的关键。异常凝血酶原也称为维生素 K 缺乏诱导的蛋白质（Protein Induced by Vitamin K Absence,PIVKA-Ⅱ），作为一种新的肿瘤标志物，对于 HCC 的诊断、治疗效果评估、预后判断及肿瘤复发监测均具有较好的临床应用价值，本文就 PIVKA-II 的生物学特性和临床应用作综述。

PU-2357

输血后基因型改变一例

王凯、冯飞雪、马艳侠
陕西中医药大学附属医院

本病例输血对患者 MTHFR-C677T 基因分型产生了影响，患者实际基因型为 MTHFR-677 CT 符合临床表现。输血后相关基因检测需结合临床综合分析结果，对可疑结果应进行后续复查。由于患者曾短时间内大量输血，且自身呈骨髓危象，后不足 48H 采血，血液中含有受血者基因成分，造成结果 MTHFR-C677T CC 分型异常。

PU-2358

输血传播感染性疾病实验室检测室内质控的研究进展

王远芳、邓杰伦、李潇涵、罗岚、李冬冬、谢轶
四川大学华西医院

室内质量控制是保证实验室结果正确的常用手段，在输血传播感染性疾病（Transfusion-Transmissible Infections，TTI）中广泛使用。随着 TTI 检测手段由定性向半定量发展，对其质量控制的要求也从判断是否符合阴/阳性预设结果，转变成在 Westgard 规则为基础的质量规则体系下，使用不同水平的质控品，判断结果是否在要求的规则范围。但由于 TTI 检测方法特点、质控品的局限性、批号更换引起的质控结果偏移等原因，现行的质控方案在 TTI 检测中的应用受到了较多的限制。针对这个问题，许多研究在更改质控规则、增加样本质控和控制批号更换等方面做了尝试性的探索。

TTI 检测的室内质量控制，目前参照现有技术水平，以定量项目的质控规范为基础建立。但由于其自身的特点，这样的质控规范对于 TTI 检测的质量控制还有各种不足，造成假失控过高，引起不必要的临床处理，且有可能忽略真正引起患者结果错误的严重失控。目前，不论是对质控规则的

更改，还是加入患者样本的质量控制，都无法较好解决这个问题。质量控制的量化评价，对于 TTI 检测的质量控制发展十分重要，还需要更多深入的研究进行完善。

PU-2359

血液病患者血培养检出蜡样芽孢杆菌，污染菌还是致病菌的案例分析一例

辛娜
西安医学院第一附属医院

蜡样芽孢杆菌是革兰阳性需氧芽孢杆菌，广泛分布于自然环境并可长期存在于 医 院 环 境 中。蜡样芽孢杆菌可引起不同程度的感染，如食物中毒、局部感染、菌血症等。尽管血标本中芽孢杆菌的分离经常考虑为污染，但蜡样芽孢杆菌对于血液病患者往往为血流感染的病原菌，甚至可伴发严重的并发症，即颅内感染，病死率高达 4 2 %。我国恶性血液病伴中性粒细胞缺乏患者中由该菌引起的菌血症报道并不多见，当血液病患者血培养检出蜡样芽孢杆菌后，临床医生往往缺乏足够的重视。本文对某院一例恶性血液病患者在粒细胞缺乏期合并蜡样芽孢杆菌菌血症病例进行总结分析如下。

PU-2360

西安市不同年龄健康儿童甲状腺功能指标正常参考范围的建立

徐晓丽、刁艳君、刘家云、何娟、胡恩亮、颜楠、荆晶
空军军医大学西京医院

目的 建立西安市不同年龄健康儿童甲状腺功能指标：促甲状腺素激素(TSH)、总三碘甲状腺原氨酸(TT3)、总甲状腺素(TT4)、游离三碘甲状腺原氨酸(FT3)、游离甲状腺素(FT4)的正常参考范围，为临床诊断、治疗提供数据支持。
方法 随机选取 2019 年 01 月—2020 年 12 月西安市 0-16 岁健康儿童 1500 名(男 750 名，女 750 名)。使用全自动化学发光免疫分析仪检测血清甲状腺功能 7 项相关指标，比较不同性别年龄段 7 组甲状腺激素水平。
结果 按不同年龄段划分参考范围为：1 组 1~28 d（含)：TSH 0.55~13.02 μIU/mL,TT3 0.70~2.78 nmol/L,TT4 66.52~167.64 nmol/L,FT3 2.35~5.77 pmol/L，FT4 9.71~24.84 pmol/L。（因字符限制，其余分组具体结果详见摘要附件）。不同性别组间 TSH、TT3、TT4、FT3、FT4 水平比较，差异无统计学意义（P>0.05)；不同年龄组间 TSH、TT3、FT3、FT4 水平比较差异有统计学意义（P<0.05)，TT4 比较差异无统计学意义（P＞0.05)。
结论 建立本市儿童甲状腺激素正常参考范围数据，为甲状腺激素测定规范化、标准化和临床应用提供了依据，为临床诊断儿童甲状腺疾病及合理用药提供了数据支持。

PU-2361

尿微量白蛋白免疫比浊法勾状效应的解决方法

马飞
天水市第四人民医院

目的 探讨尿微量白蛋白免疫比浊法定量检测时出现勾状效应的解决方法。

方法 收集我院肾病科 2018 年 4 月至 2021 年 3 月尿常规检测尿蛋白分别为+-、+、++、+++病人尿液各 50 例，按尿常规试纸条说明书提供的蛋白浓度用生理盐水稀释、对尿常规检测尿蛋白++++尿液用尿蛋白阴性尿液进行稀释；使稀释结果在线性范围 0-200mg/L 内，然后在贝克曼 AU5800 全自动生化分析上进行尿微量白蛋白免疫比浊法的定量测定。
结果 尿蛋白干化为+-尿液尿微量白蛋白最大值为 181mg/L、最小值为 101mg/L、均值为 132mg/L、中位数为 108mg/L，稀释倍数为原倍；尿蛋白干化为+尿液尿微量白蛋白最大值为 331mg/L、最小值为 121mg/L、均值为 202mg/L、中位数为 198mg/L，稀释倍数为 2 倍；尿蛋白干化为++尿液尿微量白蛋白最大值为 899mg/L、最小值为 336mg/L、均值为 660mg/L、中位数为 598mg/L，稀释倍数为 6 倍；尿蛋白干化为+++的尿液尿微量白蛋白最大值为 2601mg/L、最小值为 1331mg/L、均值为 2232mg/L、中位数为 1998mg/L，稀释倍数为 20 倍；尿蛋白干化为++++尿液尿微量白蛋白最大值为 20301mg/L、最小值为 3311mg/L、均值为 12021mg/L、中位数为 13008mg/L，稀释倍数为 130 倍。
结论 尿微量白蛋白的免疫比浊法测定出现的钩状效应可根据尿常规蛋白定性的结果对其进行盐水或者尿液进行相应倍数的稀释。

PU-2362

健康成人 NLR、PLR、SII RI、PNI 的正常参考区间研究

何林波
宜宾市第一人民医院

目的 调查健康成人 NLR、PLR、SII RI、PNI 的正常参考区间。
方法 采用回顾性队列研究方法，从健康体检中心数据库和实验室信息系统中检索 18 岁至 79 岁的健康汉族人群资料。通过遵循临床和实验室标准协会（CLSI），建立和验证每个参数的 RI。
结果 2380 名健康受试者被纳入分析。结果发现，个体性别对 PLR、PNI、SII 有显著影响（均 P<0.05），对 NLR 无显著影响（P>0.05）。令人惊讶的是，我们还发现，随着年龄的增长，PLR、PNI 和 SI 趋于降低，而 NLR 保持稳定。青年(18～64 岁)PLR、PNI、SII 值显著高于老年(65～79 岁)(P<0.001)。NLR、PLR(成人)、PLR(老年人)、PNI、SII 的 RI 分别为 0.88-4.0、49-198、42-187、2.63-9.9、142×109/L-804×109/L。
结论 本研究针对四川西部地区健康汉族成人 NLR、PLR、SII RI、PNI 的可能变异，建立共识，有助于实验设计的相关研究，让 RI 在临床中的应用更加标准化。

PU-2363

河南省儿童铁蛋白水平及检测铁蛋白的重要性

王亚龙
郑州金域临床检验中心

血清铁蛋白是体内含铁最丰富的蛋白，在铁的代谢方面起着重要的作用。血清铁蛋白广泛存在于其他组织细胞中，当人体某一系统出现疾病时，血清铁蛋白可出现异常改变。血清铁蛋白能够反应体内铁存储量及肌体的营养状态，是判断体内铁缺乏及超负荷的有效指标。

目的本文就河南省儿童检测血清铁蛋白数据的统计，来展示河南省儿童血清铁蛋白的水平，讨论儿童检测血清铁蛋白的必要性。

PU-2364

Severe fever with thrombocytopenia syndrome in Hefei: Clinical features, risk factors, and ribavirin therapeutic efficacy

Yin Zhang、Yuanhong Xu、Ying Huang
Department of Clinical Laboratory, The First Affiliated Hospital of Anhui Medical

Objectives This study described the clinical features, risk factors, factors affecting the outcome of this disease, and ribavirin therapeutic efficacy for severe fever with thrombocytopenia syndrome (SFTS) patients in Hefei.
Methods Between April 2020 and July 2020, 62 cases admitted to the First Affiliated Hospital of Anhui Medical University were included in this study. Serum samples were collected from all patients, after which diagnosis was made via reverse transcription-polymerase chain reaction and via the use of a colloidal gold immunochromatography assay approach.
Results In multivariate analysis, the following factors were determined as risk factors for SFTS: Being a farmer (odds ratio [OR], 3.033), working in areas with weeds and shrubs (OR, 2.807), and being bitten by a tick (OR, 6.64). The rates of confusion, neck stiffness, viral encephalopathy, and the presence of liver damage were higher in the patients who died than that in the surviving ones. Additionally, the median of alanine aminotransferase, aspartate aminotransferase, lactate dehy_x0002_drogenase, creatine phosphokinase, activated partial thromboplastin time, D-dimer, fibrinogen degradation products, creatinine, and urea was also higher in the patients who died. One of the 15 patients treated with ribavirin in the early stage could not survive (6.7%), whereas 11 of the 35 patients treated with ribavirin in the late stage could not survive (31.4%); this difference was statistically significant. However, there was no significant difference in mortality between the untreated group and the other two groups (i.e., patients who started antiviral treatment <5 days from the onset and those who started antiviral treatment ≥5 days from the onset). Moreover, there was no positive effect determined on clinical or laboratory parameters in SFTS patients treated with ribavirin. Also, it was observed that leukocyte levels and platelet levels took longer to return to normal.
Conclusions In Hefei, clinical features, prognostic factors, and risk factors asso_x0002_ciated with SFTS are similar to those in other areas. Patients who were given ribavirin did not have better survival rates than patients who were not given ribavirin.

PU-2365

尿蛋白不同检测方法在健康体检中的应用研究

张云
中国人民解放军总医院第六医学中心

目的 比较干化学试带法、尿总蛋白尿肌酐比值（Urinary Protein to Creatinine Ratio, PCR）和尿白蛋白尿肌酐比值（Urinary Albumin to Creatinine Ratio, ACR）三种尿蛋白筛查方法一致性，并研究其在健康体检人群的应用价值。
方法 盲法选取 2020 年 8 月 11～30 日解放军总医院第六医学中心征兵体检数据管理中心某部所有健康体检人群 936 例新鲜晨尿标本，分别进行尿蛋白试带法定性/半定量测定，尿总蛋白、尿微量白蛋白和尿肌酐定量测定，研究干化学试带法、PCR 与 ACR 的检测结果符合率，干化学试带法少量蛋白尿与 ACR 微量白蛋白尿的一致性，尿蛋白阳性样本回顾性或跟踪分析等。
结果 ACR＜30 mg/g 时，PCR 符合率 97.6%、干化学法符合率 98.9%，一致性较高；ACR 在 30～300 mg/g 之间时，PCR 假阴性占 28.7%,干化学法假阴性占 78.3%，符合性较差；ACR＞300

mg/g 时，PCR 符合率 100%，干化学法符合率 84.6%，其中 2 例假阴性均因高尿酸口服碳酸氢钠所致。36 例干化学试带法 1+（半定量 250～749 mg/L）时对应尿微量白蛋白在此区间内仅 10 例，符合率 27.8%，与研究人群年龄和代谢状态相关。118 例三种检测方法结果不一致样本，运用回顾性分析、跟踪研究、咨询经治医生等方式了解其临床特征，8 例干化学法阳性、PCR 和 ACR 均阴性样本中，临床特征包括糖尿病 3 例和高血压/高血脂 4 例，尿肌酐均＞2.5mmol/L。110 例干化学阴性、ACR 和（或）PCR 阳性样本中， 检验显示，干化学法假阴性率 67.4%，假阳性率 0.3%；ACR 假阴性率 16.2%，假阳性率 1.8%；PCR 假阴性率 20.6%，假阳性率 0.8%。
结论 尿蛋白检测应针对不同对象选择不同检测方法和评价方式，尿蛋白结果的解读应纳入患者近期饮食、口服药物和代谢状态。

PU-2366

全自动血细胞分析仪 XN20(A1)性能评价

任方芳
电子科技大学附属医院•四川省人民医院

目的 对 Sysmex XN20(A1) 全自动血细胞分析仪进行性能评价。
方法 对 Sysmex XN20(A1)全自动血细胞分析仪的本底计数、携带污染率、批内及批间精密度、线性、正确度、准确度以及仪器间的比对进行评价。
结果 Sysmex XN20（A1)全自动血细胞分析仪的批内精密度和批间精密度小于美国临床实验室改进修正法规 '88（CLIA'88）规定的总允许误差的 1/4，仪器精密度良好。携带污染率最高为 0.03%，符合厂家要求≤ 1.00%。仪器检测线性范围：WBC 为 0.03～163.64×109/L，RBC 为 0.01～8.65×1012/L，HGB 为 0.0～263 g/L，HCT 为 0.1%～77.3%，PLT 为 3～1018×109/L。本底计数均符合厂家要求。比对试验符合原卫生部关于《临床血液学检验常规项目的分析质量要求》2012 版规定的偏差范围，同时也符合 1/2 CLIA'88 要求的偏差范围。
结论 XN9000-20A1 精密度良好，携带污染率极低，空白干扰极低，线性范围宽广，正确度及准确度较高，其检测结果准确可靠，能够满足绝大多数临床实验室的工作需求。

PU-2367

绵阳地区中老年尿液阿尔茨海默相关神经丝蛋白水平及相关因素分析

张玉蓉、方堃、王芳、刘阳、杨平、吴燕、李磊、赵园宇、蔡志龙、杨佳、袁丹
四川省科学城医院

目的 探讨尿液阿尔茨海默相关神经丝蛋白（Alzheimer- associated neuronal thread protein, AD7c-NTP）在体检人群的分布及常见代谢性指标与其含量的相关性。
方法 选取四川省科学城医院体检者 1150 例，采用酶联免疫吸附法检测尿 AD7c-NTP，常规方法测定血生化指标。收集体检者人口学指标和神经系统相关检查。
结果 体检者尿液 AD7c-NTP 浓度中位值 0.60 (0.30,1.20) ng/ml，男 0.84 ng/ml，女 1.04 ng/ml，最高 9.10 ng/ml，女性高于男性，有显著性差异（z =4.202，P<0.001）。＜1.5ng/ml 者 956 例，中位值 0.50(0.30,0.90)；≥1.5ng/ml 者 194 例，中位值 2.10(1.70,2.10)；尿液 AD7c-NTP 浓度除与年龄（r=0.184, P<0.001，Y=-0.1871+0.01663X）外，与其它人口学指标及相关神经系统疾病等无相关性；AD7c-NTP 正常组和升高组的血糖 (t/z =3.506， P< 0.001)、血尿酸 (u=2.574, P<0.05)、血尿素氮 (t/z =2.891, P<0.05)、总胆红素(t/z =3.936, P< 0.001)、谷草转氨酶(t/z =0.969, P< 0.05)、总胆固醇（t=3.956, P<0.001）、低密度脂蛋白（t/z =-5.678, P<0.001）有显著差别；女性

（n=556）尿 AD7c-NTP 与血 UA 值相关性具统计学意义（r=0.148，P<0.001，Y=0.09313+0.003098X），男性未观察到。
结论 尿 AD7c-NTP 值与年龄相关，女性尿 AD7c-NTP 值和血尿酸水平相关，预防认知功能障碍，早发现阿尔茨海默病，需加强血尿酸值监控。

PU-2368

我院 2015 年~2019 年肺炎克雷伯菌临床分布特点及耐药性变迁

邓文平、罗国霞、张国欢、许涛
重庆市涪陵中心医院（重庆市微创外科研究所）

目的 分析临床标本中肺炎克雷伯菌的科室分布与耐药情况，为临床合理使用抗菌药物、降低细菌耐药率及控制医院感染提供指导依据。
方法 回顾分析 2015 年~2019 年我院临床各种标本分离出的 2296 株肺炎克雷伯菌的临床科室分布、标本来源以及耐药情况。
结果 获取非重复分离的肺炎克雷伯菌 2296 株，主要标本为痰 1697 株（73.9%）、血液 161 株（7.0%）、尿液 161 株（7.0%）、脓和分泌物 115 株（5.0%）；科室分布主要在神经外科 360 株（15.7%）、重症医学科 330 株（14.4%）、儿科 313 株（13.6%）、新生儿科 261 株（11.4%）、肝胆科 126 株（5.5%）、呼吸科 122 株（5.3%）；肺炎克雷伯菌对头孢他啶、头孢噻肟、头孢吡肟、哌拉西林、氨苄西林/舒巴坦、氨曲南、四环素等在 2015 年~2019 年各年中的最低耐药率分别为 26.51%、32.15%、28.81%、34.44%、30.89%、28.81%、23.77%，并且亚胺培南、美罗培南的耐药率逐年显著升高，2015 年为 0.98%、0.98%，2019 年为 8.14%、6.88%，重症医学科为 17.02%、14.90%，呼吸科为 30.77%、30.77%。
结论 我院肺炎克雷伯菌耐药严重并且碳青霉烯类的耐药率逐年明显上升，医院需加强对肺炎克雷伯菌感染者的目标性监测，指导临床正确且合理使用抗菌药物，有效的预防和控制耐药菌的蔓延。

PU-2369

利用电子表格设计基于风险管理指数的统计质量控制策略

张裕[1,2]、邹国英[2]、余启华[1,2]
1. 湖南省临床检验中心
2. 湖南省第二人民医院

临床实验室质量控制的新指南 CLSI C24-Ed4 结合了 EP23-A 中提出的风险管理的概念和原理，强调了实验室应评估室内质量控制策略的有效性，以最大程度地减少因检测过程中的不稳定性而产生的错误结果，导致不恰当的临床决策和医疗行动对患者造成伤害的风险。C24-Ed4 文件制定委员会主席 Parvin 为此提出了一个指标：风险管理指数（RMI），即报告的错误结果对患者伤害的预期概率与可接受的患者伤害概率之比，来确定患者伤害风险是否得到有效控制，并开发出配套的风险防控软件，但该软件不能免费使用，现有的文献中也没有简单的工具可以计算。本研究旨在梳理 RMI 计算原理，通过使用常见的办公软件 EXCEL 编辑函数，利用实例计算风险管理指数水平，并绘制示意图，在一定程度上帮助实验室进行基于风险管理指数的统计质量控制策略设计。

PU-2370

RDW、LNR 与血清 CA125 联合检测在子宫内膜癌中的应用价值

李颖[1]、蓝婷[2]
1. 徐州医科大学附属医院
2. 徐州医科大学

目的 探讨红细胞分布宽度（Red blood cell distribution width，RDW）、中性粒细胞/淋巴细胞比值（Neutrophil/lymphocyte ratio，NLR）及血清糖类抗原 125（Cancer Antigen 125，CA125）联合检测在子宫内膜癌诊断中的价值。
方法 选取 2018 年 1 月至 2021 年 5 月在徐州医科大学附属医院收治的初诊为子宫内膜癌患者 91 例作为研究组，选取同时期健康体检者 91 例作为对照组。回顾分析两组患者的 RDW、NLR 及 CA125 水平，绘制 ROC 曲线，分析 RDW、NLR 及 CA125 在子宫内膜癌患者中的诊断效能。
结果 研究组 RDW、NLR 及 CA125 水平均高于对照组（$p<0.01$），术前 RDW 水平与子宫内膜癌患者临床分期呈正相关；研究组中，患者术前 RDW、NLR 及 CA125 水平均高于术后；RDW、NLR 及 CA125 三者联合诊断子宫内膜癌的 AUC 值最大，灵敏度和特异度最高，高于单一指标检测或任意两种指标联合检测。
结论 RDW、NLR 及 CA125 三者联合检测可获得较高的诊断效能，辅助临床诊疗。

PU-2371

COPD 稳定期患者 CRP/Alb 比值、NLR、WBC 对急性加重的早期评估效能分析

黄义、黄友军、颜彦
郴州市第一人民医院

慢性阻塞性肺病（COPD）是一种常见的慢性阻塞性肺病呼吸系统疾病，一般是暴露于有毒颗粒或气体引发的气道和/或肺泡异常导致，是死亡率在全世界所有疾病居中位居第四位疾病。COPD 可分为急性加重期和稳定期，其中加重其患者的咳嗽和咳痰症状轻微且稳定，病情基本恢复到急性加重前状态，而 COPD 急性加重是疾病进展及其发病的重要事件，随着急性加重发生次数的增加，患者的病情加重，可增加相关不良预后的发生风险，影响患者的生活质量，加速疾病进展过程，增加住院率和再住院率。COPD 急性加重是疾病进展及其发病的重要事件，其频率和严重程度与患者预后密切相关。COPD 的发生发展涉及到炎症细胞和多种炎症指标。NLR 反应体内中性粒细胞和淋巴细胞水平平衡状态，较单一指标更能反应全身炎症状态，可作为 AECOPD 患者的病情评估及预后的指标。WBC 是传统的炎症标志物，与 COPD 的急性加重有关。CRP/Alb 比值结合血清炎症因子 CRP 和 Alb 浓度，已被证实与脓毒症以及肺炎等密切相关，但其与 COPD 及其急性加重关系的研究缺乏。可能通过联合检测更准确进行 COPD 稳定期患者急性加重的早期评估，但目前相关研究缺乏，因此，本项目首次分析 COPD 稳定期患者 CRP/Alb 比值、NLR、WBC 对急性加重的早期评估效能，从而指导 COPD 稳定期患者急性加重的有效防治，减少 COPD 稳定期患者急性加重的发生及其相关病情不良影响、经济支出及医疗负担，改善 COPD 预后和患者生存质量。

PU-2372

339 家实验室血清葡萄糖室内质控图基本信息完整性调查分析

张裕[1,2]、邹国英[2]、彭爱红[1,2]
1. 湖南省临床检验中心
2. 湖南省第二人民医院

目的 利用室内质控图基本信息指标，了解实验室室内质控图基本信息指标录入完整性情况，分析存在的问题。
方法 参照 CNAS-CL02-A003 中关于质控图基本信息的 17 项指标，对收集到的 339 家实验室血清葡萄糖纸张室内质控图每个指标的录入情况以及录入途径进行统计。
结果 17 项基本信息指标中，“项目名称”和“中心线和控制界线”录入率最高，达 100%；“试剂批号”、“仪器唯一标识”、“校准物批号”、“数据点时间”录入率最低，均低于 6%；只有 5 项指标达到 3σ 以上水平；无一家实验室信息录入完整率为 100%，录入了 10 项指标的实验室数量最多，占 28%。在录入途径方面，“有录入空位但未录入”的情况中，“试剂批号”、“校准物批号”、“方法学名称”占比最高，在“无录入空位但手工补录”的情况中，“质控物批号”、“质控物名称”、“仪器名称”占比最高。10 家已获得 ISO 15189 认可的实验室普遍缺失 3-7 项指标。常规化学专业室间质量评价得分随着录入指标数量的增加有上升趋势。
结论 室内质控图基本信息缺失现象比较普遍，基本信息的缺失不利于失控状态原因分析以及质控数据的回顾性分析，实验室人员应加强室内质控意识，主动记录室内质控相关基本信息，并积极完善 LIS 系统或质控软件功能。

PU-2373

同型半胱氨酸、D-二聚体与急性胰腺炎严重程度的相关性研究

曾昭伟
天津市中西医结合医院·南开医院

目的 探讨同型半胱氨酸（Hcy）、D-二聚体（D-dimer）与急性胰腺炎（AP）严重程度的相关性。
方法 选取 2018 年 10 月—2020 年 7 月天津市南开医院住院和门诊收治的 AP 患者 87 例，根据病情严重程度分为轻度 AP48 例、重度 AP 组 39 例；选取同期健康体检者 50 例为对照组，检测各组的血清 Hcy 和 D-dimer 水平并进行比较，采用受试者工作特征曲线（ROC 曲线）分析 Hcy、D-dimer 对 AP 病情严重程度的预测价值。
结果 AP 组患者的血清 Hcy、D-dmier 水平明显高与对照组，差异有统计学意义（P<0.01），87 例 AP 患者的血清 Hcy 和 D-dmier 的阳性率为 71.26%、58.62%。AP 组患者血清 Hcy、D-dimer 阳性率高于 CON 组，差异有统计学意义（P<0.001）。SAP 组与 MAP 组患者的血清 Hcy、D-dmier 阳性率差异无统计学意义。Hcy、D-dmier 的受试者工作特征曲线下面积（AUC）分别为 0.956、0.722，差异有统计学意义，Hcy 诊断 AP 的敏感度为 92.0%，特异度为 92.0%，分别高于 D-dmier 的 78.2%及 68.2%，差异有统计学意义（P<0.01）。Hcy 检测对 AP 早期预测及严重程度评估的价值优于 D-dmier 检测。
结论 AP 患者 Hcy 和 D-dmier 水平高于对照组，且随着疾病严重程度的加深而增高，Hcy 检测诊断 AP 的临床价值优于 D-dmier 检测。

PU-2374

A 7-year Retrospective Analysis of Fungal Keratitis at a University Hospital in Shandong Province, China

Xiaoli Zhang
Shandong University Qilu hospital

Background and Purpose Early diagnosis of mycotic keratitis is challenging. This retrospective study aims to analyze the demographics, risk factors, microbiology at a tertiary hospital.
Methods We reviewed medical records and microbiology reports of 96 patients of clinically suspected fungal keratitis from January 2013 to December 2019. The data included patients' history, age, gender, demographics, risk factors, seasonal variation, in vivo confocal microscopic examination and laboratory findings.
Results 67.7% of patients were males and 32.3% were females. Mean age was 54±26 years (range 7-87 years). Most of corneal scrape samples were from age group 51-60 years (30.2%). Total fungal culture positivity was 42.7%. Fusarium species (63.4%) were the most common isolates, followed by Aspergillus species (19.5%), Alternaria (9.8%), Penicillium (4.9%), and Exophiala (2.4%).
Conclusions Mycotic keratitis is the leading cause of ocular blindness. Our study investigated the spectrum and epidemiology of fungal keratitis in the southwest of Shandong province. Direct microscopic examination of corneal scrape smear is a rapid and simple diagnostic method. The use of MALDI-TOF MS with fungal culture is proved to be a fast identification approach of fungi at the species level for successful management of mycotic keratitis.

PU-2375

一项念珠菌血症的回顾性研究

张晓丽
山东大学齐鲁医院

目的 随着医学技术的不断进步，实体器官移植的发展，免疫抑制病人的增多等，临床真菌感染日益严重，逐渐出现了多重耐药的真菌菌株，威胁着广大病人的身体健康。本研究旨在分析调查既往患有念珠菌血症的病人临床特点，微生物学特征，为念珠菌血症的临床治疗提供帮助。
方法 通过回顾性研究分析 2013 年至 2019 年间的念珠菌血症的患者病例资料和实验室微生物学报告，了解最近 7 年间住院患者血流感染的念珠菌分布情况，危险因素，临床特征，抗真菌药物敏感性情况。
结果 本次研究共纳入了 123 例念珠菌血症患者，同时包含 123 株念珠菌，其中，近平滑念珠菌是念珠菌血症的最主要的分离菌株，占 31.7%，光滑念珠菌次之，占 21.1%，而白色念珠菌占念珠菌血症的 18.7%，热带念珠菌占 17.9%，而葡萄牙念珠菌、季也蒙念珠菌、克柔念珠菌分别占 4.0%，3.3%，3.3%。绝大部分分离的酵母菌属对抗真菌药物敏感。
结论 我们的研究证实非白色念珠菌导致的血流感染占了 80%，这与以往白色念珠菌感染是念珠菌血症感染的主要致病菌的结论不同，说明近些年来念珠菌血症的病原菌谱发生了改变，可为临床诊疗提供依据。

PU-2376

2 型糖尿病视网膜病变与血清 non-HDL-c、CysC 相关性分析

王前明
厦门大学附属第一医院检验科

糖尿病视网膜病变（diabetic retinopathy，DR）是糖尿病最常见的微血管并发症之一, 严重时可导致失明，因此早发现，早诊断，早治疗尤为重要。非高密度脂蛋白（non-high density lipoprotein cholesterol cholesterol，non-HDL-c）是除高密度脂蛋白胆固醇（high density lipoprotein cholesterol，HDL-c）外的其他胆固醇的总和，其在 DR 中的变化仍鲜有报道。血清胱抑素 C（Cystatin C，CysC）是肾功能损伤的早期标志物，与 DR 关系的相关报道仍较少，本研究拟分析 CysC、HbA1c 及 non-HDL-c 等血脂指标在 DR 的变化规律，为 DR 的早期诊断提供新的依据。

目的 探讨 2 型糖尿病(T2DM)患者血清非高密度脂蛋白胆固醇(non-high density lipoprotein cholesterol ,non-HDL-c)、胱抑素 C(Cystatin C ,CysC)与视网膜病变发病风险的相关性。

方法 收集 144 例 T2DM 患者的临床资料，根据眼底拍照结果分成视网膜病变组（DR 组）和单纯糖尿病组(DM 组)，比较两组 non-HDL-c 、CysC 等指标的差异并分析其与 DR 的相关性；

结果 DR 组患者病程、CysC 、CHO、HDL、LDL，ApoA、ApoB、HbA1c 和 non-HDL-c 与 DM 组比较，差异有统计学意义（P＜0.05）；Pearson 相关分析结果显示 DR 分级与 CysC 、CHO、HDL-c、LDL-c、non-HDL-c、ApoA、ApoB、HbA1c 呈正相关（P＜0.01）；多元 Logistic 回归分析显示，CysC、HbA1c、ApoA、病程为 DR 的影响因素（P＜0.05）；

结论 non-HDL-c、CysC、HbA1c 对 DR 诊断有重要价值，联合检测 non-HDL-c、CysC、HbA1c 等指标,对于 DR 的早期风险评估有重要意义。

PU-2377

山东地区健康成人超氧化物歧化酶参考区间的初步建立

曹修娥、张倡誌、潘璐、栾芳
山东第一医科大学附属省立医院

目的 分析山东地区健康成人超氧化物歧化酶（SOD）的血清含量，初步建立成人 SOD 的参考区间，并分析 SOD 与其他常用生化指标的相关性。

方法 选取 2019 年 3 月至 2020 年 10 月在山东大学附属省立医院健康体检中心体检的健康成人为研究对象，最终共纳入 2559 例，其中男 1293 例，女 1266 例，收集其血清标本，采用比色法检测血清 SOD 浓度水平，依据美国临床和实验室标准协会（CLSI）C28-A2 的要求，以非参数法建立基于性别和年龄的 SOD 参考区间。

结果 血清 SOD 水平在研究对象中呈非正态分布，男性 SOD 为 181.30（172.00～189.45）U/ml，略高于女性[174.45（165.60～184.33）U/ml]（Z= -9.67，P<0.001）。相关性分析结果显示，血清 SOD 与白蛋白（ALB）、丙氨酸氨基转移酶（ALT）、天门冬氨酸氨基转移酶（AST）、尿素氮（BUN）、肌酐（CR）、总胆红素（TBIL）、直接胆红素（DBIL）、γ-谷氨酰基转移酶（GGT）、甘油三酯（TG）、总蛋白（TP）、尿酸（UA）和肾小球滤过率（eGFR）呈正相关，与年龄和高密度脂蛋白胆固醇（HDL-C）呈负相关，与碱性磷酸酶（ALP）、胆固醇（CH）和低密度脂蛋白胆固醇（LDL-C）无相关性。男性 18～40 岁年龄组血清 SOD 水平显著高于 41～50 岁和≥51 岁年龄组，因此分为 18～40 岁、41～50 岁和≥51 岁三组；女性 18～40 岁年龄组血清 SOD 水平显著高于 41～60 岁和≥61 岁年龄组，因此分为 18～40 岁、41～60 岁和≥61 岁三组。采用百分位数法得出山东地区健康成人血清 SOD 的参考区间为男性 152.48～206.32U/ml（18～40 岁）、147.92～205.77 U/ml（41～50 岁）和 144.84～199.71 U/ml（≥51 岁），女性 142.60～

201.75 U/ml（18～40 岁）、139.86～197.65 U/ml（41～60 岁）和 135.78～190.34 U/ml（≥61 岁）。

结论 初步建立了山东地区健康成人血清 SOD 的参考区间，且血清 SOD 水平存在性别、年龄差异，更好的为 SOD 的临床应用提供依据。

PU-2378

Meta-analysis of the trend of Varicella Zoster virus seroprevalence with age in China

Xin Wang、Li Wang
The First Affiliated Hospital of Xi'an Medical University

Background Varicella-Zoster Virus (VZV) is the pathogen of human varicella and herpes zoster, its prevalence is related with the host's immune response and the seropositivity rate of VZV-immunoglobulin G (IgG) antibodies in the general population. The aim of this meta-analysis was pooled on the comprehensive information of the epidemiology of VZV infection and analyzed the seropositivity of VZV-IgG antibodies in different age groups, gender, and regions in China, so as to arouse people's attention on VZV.
Methods We performed a systematic review by searching both English and Chinese literature databases. Random or fixed effects models were used to summarize the prevalence of VZV according to statistical tests forheterogeneity. Subgroup, sensitivity, and meta-regression analyses were performed to address heterogeneity. Publication bias was evaluated using Egger's test. Results 2035 literatures were obtained by searching keywords "seroprevalence", "varicella zoster virus" and "VZV-IgG antibodies". Literatures were screened according to the inclusion criteria and 10 studies from 1997 to 2019 with a total of 9166 individuals were included. According to the results of heterogeneity test, random effect model and fixed effect model were used for system analysis. The heterogeneity was calculated using I-square statistics.
Results The overall VZV seroprevalence in the Chinese population was 57.1% (95% CI: 45.3% - 68.5%), and the peak prevalence was 93.37% (95% CI: 90.7% - 95.7%) in the age 36-45 while the VZV seroprevalence rate (84.7%, 95% CI: 48.8% - 100%) was not increased in individuals of 45 and older.
Conclusion The prevalence of VZV increases with age, and there was no significant difference between different genders or regions. This results can provide epidemiological evidence for the prevention and treatment of VZV.

PU-2379

实验室指标对于骨质破坏、腰椎压缩性骨折、多发性骨髓瘤致腰椎压缩性骨折的诊断价值

赵晓彤
石河子大学医学院第一附属医院

目的 收集并分析三种病因导致骨痛的患者的实验室检查结果，提高首发症状为腰痛、而影像学表现为骨质破坏，腰椎压缩性骨折的多发性骨髓瘤疾病与骨科疾病单纯骨质破坏、腰椎压缩性骨折疾病的诊断效率，从而进一步指导临床诊断，降低误诊率。
方法 回顾 2016 年 8 月至 2021 年 6 月石河子大学医学院第一附属医院诊治的多发性骨髓瘤 76 例，收集以腰痛为主诉的多发性骨髓瘤病例 16 例，骨科单纯骨质破坏病例 16 例，腰椎压缩性骨折病例 17 例，健康查体正常人 17 例的实验室检查指标。实验室检查观察指标：生化（总蛋白、白蛋白、球蛋白、胱抑素 C、电解质）、血凝、血常规，临床特点观察指标：性别、年龄。组间符合正态分

布、方差齐的指标采用独立样本 t 检验，不符合正态分布的指标采用独立样本秩和检验进行比较。
结果 多发性骨髓瘤组的生化检查（总蛋白、球蛋白、胱抑素 C）、血凝检查（凝血酶原时间、凝血酶时间）高于骨质破坏组、腰椎压缩性骨折组和体检组，P<0.05,差异有统计学意义；多发性骨髓瘤组的生化检查（白蛋白）、血常规检查（血红蛋白、红细胞计数、红细胞压积）、低于骨质破坏组和腰椎压缩性骨折组，P<0.05,差异有统计学意义；而多发性骨髓瘤组的血凝检查（活化部分凝血酶时间）高于腰椎压缩性骨折组，P<0.05,差异有统计学意义。
结论 对于腰痛为主诉但实验室检查生化检查（总蛋白、球蛋白、胱抑素 C）、血凝检查（凝血酶原时间、凝血酶时间、活化部分凝血酶时间）偏高；生化检查（白蛋白）、血常规检查（血红蛋白、红细胞计数、红细胞压积）偏低的骨科就诊患者，应进一步行免疫球蛋白、免疫固定电泳、血尿轻链、骨髓穿刺、免疫组化检查明确诊断，降低误诊的可能性，让病人尽早接受血液科化疗治疗，从而得到更好的预后。

PU-2380

Evaluation of a novel laboratory candiduria screening protocol in the intensive care unit

Zhengxin He 、Chang Su、Yuwang Bi、Yan Cheng、Daxin Lei、Fukun Wang
Bethune International Peace Hospital of PLA

Objectives Since the urine cultures are only guaranteed for patients with obvious urinary symptoms in most cases, most of candiduria episodes are ignored in clinic. This study aimed to design a screening protocol to improve the candiduria identifying efficiency, and to provide information of Candida species and drug susceptibility.
Methods All patients admitted to the intensive care unit (ICU) of our hospital during December 1, 2018 and October 1, 2019 were enrolled. Urinalysis was performed every three days for each subject from the first day of ICU admission. Urine samples were applied to fungal culture when: (1) yeast like cell counting (YLCC) ≥ 200; (2) positive YLCCs were observed in two consecutive tests, and at least one YLCC ≥ 100.
Results The screening protocol greatly enhanced the candiduria diagnostic efficiency by which the diagnosed ICU candiduria incidence rate was improved from 2.28% to 17.27%. However, compared to the historical control, the screening protocol has no time-saving advantage in candiduria diagnosing. Higher percentage of C. albicans in screening protocol-identified candiduria patients was observed, although there was no statistical difference. Female gender, pneumonia, diabetes and infarction/hemorrhage patients were more prone to develop candiduria. Non-candiduria patients showed a better tendency for survival and shorter ICU stay length. Multisite colonization was very common in candiduria patients we identified, and up to 70.83% of them had Candida positive cultures in sputum.
Conclusions The screening protocol established in the study was an easy and practical tool for early warning and management of candiduria and invasive candidiasis.

PU-2381

自然流产与孕妇 TORCH 感染关系的荟萃分析

王馨、王莉
西安医学院第一附属医院

目的 通过 Meta 分析评价孕妇感染 TORCH 与自然流产的相关性，为孕妇优生优育和临床治疗提供支持。

方法 利用关键词检索 CNKI、WANFANG、PubMed 等数据库获得文献 4180 篇，根据纳入标准进行筛选，纳入研究 25 篇，观察组孕妇 5852 例，对照组孕妇 19944 例。
结果 Meta 分析发现观察组（有自然流产史的孕妇）TORCH-IgM 抗阳性率分别为 TOX-IgM 14.54%、RV-IgM 8.83%、CMV-IgM 15.60%、HSV-IgM 15.70%；对照组（无自然流产史的孕妇）TORCH-IgM 抗阳性率分别为 TOX-IgM 0.58%、RV-IgM 0.59%、CMV-IgM 1.03%、HSV-IgM 0.49%。观察组 TORCH-IgM 抗阳性率显著高于对照组，p<0.00001，差异具有统计学意义。
结论 有自然流产史的孕妇 TORCH 感染率较正常孕妇高，HSV 的感染率更高一些，此结果可以为 TORCH 感染的预防和治疗提供流行病学依据，引起育龄妇女和孕妇关注和预防 TORCH 感染。

PU-2382

结核分枝杆菌检测方法的系统综述

高灿
石河子大学医学院第一附属医院

目的 目前针对结核分枝杆菌的检测方法有多种，本文旨在对结核分枝杆菌的检测方法做一个概况总结。
方法 通过检索中国学术期刊网全文数据库，输入篇名“核分枝杆菌的检测方法”进行了精确匹配搜索，共搜索到 427 条结果，然后通过选择主题词“检测方法”共检测到 170 条结果，然后通过阅读篇名、摘要和关键词选择了 33 篇文献，最后通过限定时间范围 2017-2021 年最终选择了 26 篇文献。
结果 择选出的 26 篇文献中对自己有参考价值的有 14 篇。
结论 通过对最终选出的 14 篇文献作出了总结，PCR 技术能够监测出结核分枝杆菌和非结核分枝杆菌，具有较强的敏感性和特异性，并且简单快速、不易污染，可作为实验室辅助检测结核杆菌的方法。

PU-2383

联合监测炎症因子在手术部位感染中的诊断价值

吴伶俐
东南大学附属中大医院

目的 探讨某教学医院肛肠外科手术部位感染的炎症监测指标水平，为术后感染的预防提供循证依据。
方法 回顾性分析 2017 年 1 月-2019 年 12 月肛肠外科手术患者资料 2995 份，根据患者术后是否发生手术部位感染分为感染组和未感染组，分析肛肠特征以及患者白细胞(WBC）、降钙素原(PCT）和 C-反应蛋白（CRP）水平。采用 Logistic 回归分析手术部位感染的相关危险因素，从而制定有效的预防对策。
结果 肛肠外科手术部位感染者 WBC、PCT 和 CRP 的平均水平明显高于非感染者。
结论 针对病原菌特征和独立危险因素，应加强炎症指标监测和采取积极有效的干预措施，从术前、术中、术后严格把关，降低肛肠术后病原菌感染的发生率。

PU-2384

新型冠状病毒肺炎疫情期间应急实验室标本检测管理及感染防控经验分享

苏杨
四川省医学科学院·四川省人民医院

目的 四川省人民医院检验科于 2020 年专门成立了新型冠状病毒肺炎应急实验室，旨在确保发热门诊和应急隔离病房标本的分流与高效检测。最大程度降低疑似及确诊病例患者标本可能包含病毒的气溶胶及接触性传播途径，阻断病毒在医院内的传播，以保证医患安全。笔者结合应急实验室工作经验和检验科对于疑似新冠病毒肺炎检测标本的接收、处理、检测流程，提出检验科应对疑似含有新冠病毒标本的管理及感染防控措施。
方法 制定应急实验室设立基本原则，包括研究和制定新冠肺炎疫情期间检验科标本检测相关制度、流程及预案，确保各项工作措施落实到位。按照国家标准《实验室生物安全通用要求》GB19489-2008 有关规定，建立符合生物安全防护水平为二级的医学检验实验室。应急实验室筹建及成立后，先后组织科室骨干成员及应急实验室工作人员和科室全员进行医院内部及科室内部新冠肺炎感染及防控政策、措施的相关知识培训和考核。要求全员必须熟悉及掌握疫情防控相关政策、制度及流程。依照《医疗机构内新型冠状病毒感染预防与控制技术指南（第一版）》（国卫办医函〔2020〕65 号）中的分级防护，及其他相关医疗机构的分级防护，针对本院检验科应急实验室实际情况，制定了四川省人民医院检验科医疗防护分级，并加强监督执行及管理。明确规定并实施实验室医务工作人员标本运送过程、检测前、检测中、检测后操作及防护流程。
结果 应急实验室符合医学生物安全二级实验室要求，并验收合格。科室骨干成员及应急实验室工作人员和科室全员熟练掌握手卫生流程、隔离防护用品穿戴及消毒方法和防护分级等相关知识，相关知识培训和考核均完成良好。熟悉及掌握疫情防控相关政策、制度及流程。
结论 四川省人民医院检验科作为四川省级新型冠状病毒肺炎定点诊疗医院的一线科室在疫情期间严格执行感控政策措施，做到无一名医务人员及患者发生医院内感染的好成绩。

PU-2385

Molecular epidemiology, antifungal susceptibility, and virulence evaluation of Candida isolates causing invasive infection in a tertiary care teaching hospital

Lingbing Zeng
The First Affiliated Hospital of Nanchang University

Background Despite the increasing incidence of invasive candidiasis, the epidemiology, antifungal susceptibility, and virulence of Candida spp. in most hospitals remain unclear. This study aimed to evaluate invasive candidiasis in a tertiary care hospital in Nanchang City, China.
Methods MALDI-TOF and 18s rDNA ITS sequencing were used to identify Candida strains. Randomly amplified polymorphic DNA analysis (RAPD) was used for molecular typing, and biofilm production, caseinase, and hemolysin activity were used to evaluate virulence. The SensititreTM YeastOne YO10 panel was used to examine antifungal susceptibility.
Results We obtained 110 Candida strains, which included 40 Candida albicans (36.36%), 37 C. parapsilosis (33.64%), 21 C. tropicalis (19.09%), 9 C. glabrata (8.18%), 2 C. rugose (1.82%), and 1 C. haemulonii (0.91%) isolate. RAPD was used for molecular typing. At a limiting point of 0.80, C. albicans isolates could be grouped into five clusters, C. parapsilosis and C. tropicalis into seven clusters, and C. glabrata into only one cluster that consisted of six strains. Comparison of selected virulence factors that are detectable in a laboratory environment, such as biofilm production and caseinase and hemolysin production, showed that 98.2% of Candida isolates

were caseinase and hemolysin producers with strong activity (Pz values of <0.69). Furthermore, C. parapsilosis had more total biomass (average Abs620 = 0.712) than C. albicans (average Abs620 = 0.214, $p < 0.01$) or C. tropicalis (average Abs620 = 0.450, $p < 0.05$), but all C. glabrata strains were either low- or no-biofilm formers. Antifungal susceptibility testing revealed that the isolates showed the greatest overall resistance against fluconazole (6.36%), followed by voriconazole (4.55%). All C. albicans and C. parapsilosis isolates exhibited 100% susceptibility to echinocandins (anidulafungin, caspofungin, and micafungin), whereas one strain of C. glabrata isolate was resistant to echinocandins.
Conclusion This study provides vital information on the epidemiology, pathogenicity, and antifungal susceptibility of Candida species among patients admitted to Nanchang City Hospital.

PU-2386

“5＋1”S 管理法在医学实验室中的应用

李华丽
西安医学院第一附属医院

目的 探讨“5＋1”S 管理法在医学实验室中的应用效果。
方法 自 2020 年 4 月至 2021 年 4 月在“5＋1”S 质量检查中以医技科室“5＋1”S 管理考核标准对实验室进行考核，按照检查成绩分为“5＋1”S 管理法示范实验室及“5＋1”S 管理法非示范实验室作为对比。
结果 “5＋1”S 管理法示范实验室比“5＋1”S 管理法非示范实验室“5＋1”S 管理考核标准检查成绩高出 9.4 分。
结论 “5＋1”S 管理是提升实验室管理水平不可多得的良方,同时也是改善个人工作生活素质的秘诀,这也正切合人文素质教育的发展方向，值得推广。关键词：“5＋1”S 管理法 “5＋1”S 管理考核标准 “5＋1”S 管理法示范实验室

PU-2387

维生素 D 营养状态及缺乏的研究进展

潘永圣、肖芳、蒲丹、汪佳婕
昆明市第一人民医院

维生素 D 是身体发育过程中所必需的一种脂溶性维生素，其主要生理作用是促进肠道内钙和磷的吸收。机体在缺乏维生素 D 的状态下，仅有 10~15%的膳食钙和约 60%的磷被吸收。目前维生素 D 缺乏最为普遍，全球近 10 亿人处于维生素 D 不足或缺乏状态。近年来研究发现维生素 D 除了促进骨骼和肌肉发育外，还与癌症、传染病、心血管疾病、糖尿病、自身免疫性疾病和精神系统疾病等的发生密切相关。而且维生素 D 还具有免疫调节作用，可以保护同种异体肾，维生素 D 充足可以提高肾移植术后患者移植肾的长期存活率，且使用活性维生素 D 能改善移植物预后、减少移植物丢失、防止排斥反应发生，并使人类白细胞抗原 DR 等位基因（HLA-DR）、CD28、CD86、CD40 表达均出现不同程度的下降。本综述就近几年维生素 D 缺乏或不足与相关疾病的研究进行论述。

PU-2388

小而密低密度脂蛋白与其它血脂指标的相关性研究

冯都都
长治医学院附属和平医院

目的 探讨小而密低密度脂蛋白 sd-LDL 与其它血脂指标（甘油三酯 TG、总胆固醇 TCH、低密度脂蛋白 LDL、高密度脂蛋白 HDL）的相关性。
方法 收集于本院接诊的血脂异常患者 147 例，根据血脂异常分类指标将其分为高甘油三脂组（高 TG 组）36 例、高胆固醇组（高 TCH 组）38 例、混合高血脂组（混合组）37 例、低高密度脂蛋白组（低 HDL 组）36 例，同时选取 39 例血脂正常患者作为对照组，分析 sd-LDL 的血脂水平差异及 sd-LDL 与其它血脂指标的相关性。
结果 高 TG 组、高 TCH 组、混合组、低 HDL 组的 sd-LDL 的浓度分别为（0.86±0.18）mmol/L、（1.08±0.32）mmol/L、（1.47±0.44）mmol/L、（0.67±0.26）mmol/L，均高于对照组[(0.50±0.22) mmol/L ,P<0.05)；高甘油三脂组、高胆固醇组、混合高血脂组的 sd-LDL/LDL 的比值分别为 0.30±0.04、0.28±0.07、0.33±0.08 ,均高于对照组(0.24±0.07，P<0.05)，低高密度脂蛋白组（0.27±0.06）与对照组无差异（P>0.05）；混合组、高 TCH 组的 sd-LDL、sd-LDL/LDL 均与 HDL 成负相关（P＜0.05），低 HDL 组的 sd-LDL、sd-LDL/LDL 均与 HDL 无显著相关性（P＞0.05）；混合组、高 TG 组、低 HDL 组、对照组仅 sd-LDL 均与 TCH 具有正相关（P＜0.05），高胆固醇组的 sd-LDL、sd-LDL/LDL 均与 TCH 无相关性（P＞0.05）；混合组、高 TCH 组、低 HDL 组、对照组的 sd-LDL、sd-LDL/LDL 与 TG 均成正相关（P＜0.05），高 TG 组的 sd-LDL、sd-LDL/LDL 均与 TG 无相关性（P＞0.05）；混合组、高 TCH 组、低 HDL 组、对照组、高 TG 组仅 sd-LDL 与 LDL 成正相关（P＜0.05）。
结论 sd-LDL、sd-LDL/LDL 与 HDL 成负相关；sd-LDL 均与 TCH、TG、LDL 成正相关，且仅有 TG 与 sd-LDL/LDL 成正相关。

PU-2389

外泌体在心血管疾病中的研究进展

曾灵
中南大学湘雅二医院

外泌体是直径 40-160 纳米之间的脂质双分子层囊泡，其内携带蛋白质、脂质、miRNA、crcRNA、mRNA、DNA 等信息分子。近年来，外泌体在细胞间信息交流中的作用引起关注。外泌体在机体生理稳态的维持和免疫系统的稳定等方面具有重要作用，参与多种疾病的发生发展，例如神经系统疾病、免疫系统疾病、心血管疾病等。全世界每年死于心脑血管疾病的人数高达 1500 万人。心脑血管疾病是一种 50 岁以上中老年人健康的常见病，居各种死因首位，具有高患病率、高致残率和高死亡率的特点，即使应用目前最先进、完善的治疗手段，仍可有 50%以上的脑血管意外幸存者生活不能完全自理。目前全球心血管疾病的死亡率和发病率升高，严重影响人们生活质量，是全球医疗卫生行业难题。外泌体广泛存在于机体的血液、尿液、唾液中,针对体液中外泌体的检测可以对疾病起到潜在的诊断作用；且因其具有低免疫原性和人体相容性，且具备脂质体所不具备的特性，外泌体现已成为了药物靶向治疗的良好载体；且病理生理情况下外泌体内含物成分、含量的差异可提供有益于疾病监测方面信息。外泌体在心血管疾病的研究引起广泛关注。随着外泌体分离、提纯、鉴定与检测技术日益发展，外泌体研究助力精准医学，具有较好前景。本文主要阐述外泌体在肺动脉高压、急性心肌梗死、动脉粥样硬化、心力衰竭等心血管疾病中的风险评估、疾病监测的作用，及其临床治疗潜能，为心血管疾病的诊断、治疗、预后提供新思路。

PU-2390

江西儿童地中海贫血患儿致病基因分析

刘发娣、武文韬、周红平、卢娟、柯江维
江西省儿童医院

目的 探讨江西地区 α-与 β-地中海贫血患儿的基因突变类型、频率与分布概况，为该地区地中海贫血疾病的遗传咨询与儿童未来婚育指导提供依据。
方法 纳入 2016 年 8 月 1 日至 2019 年 7 月 31 日就诊于江西省儿童医院的疑似地中海贫血患儿 1765 例，运用 PCR-反向斑点杂交法进行常规 α 和 β 地中海贫血基因检测，分析样本中地中海贫血患儿的基因类型、频率及分布特点。斑点杂交提示存在罕见突变者采用 Gap-PCR 和基因测序进行检测。
结果 共检出 932 例地中海贫血患儿，检出率为 52.80%；β-地贫共 555 例占 59.55%，含杂合子 505 例，双重杂合子和纯合子 50 例（9.01%）；α-地贫 357 例占 38.30%，含 290 例杂合子地贫患儿，65 例 HbH 病患儿；αβ-复合型地贫 20 例，占 2.15%；在 β-地贫中，IVS-II-654 位点突变是最常见的等位基因，占 50.41%，其次是 CD41-42（占 22.81%）与 CD17（占 10.41%）；α-地中海贫血突变频率最高的突变类型为--SEA，占 72.88%，其次是-α3.7（20.52%）；检出一患儿携带罕见型突变-α27.6，基因型为-α27.6/--SEA。
结论 江西地区儿童地中海贫血发病主要以 β-地中海贫血主，占 59.55%；重型 β 地贫的检出率仍然较高；地贫的防控形势仍不乐观，需要加强地贫知识的宣传和遗传咨询工作，进一步推进优生优育，提升人口质量。

PU-2391

红细胞分布宽度的升高为慢性髓细胞白血病患者的预后不良因素

李涛、方洋洋、郑晓群
温州医科大学附属第二医院

目的 红细胞分布宽度（Red blood cell Distribution Width，RDW）被认为药物治疗效果评估或各种恶性肿瘤患者预后潜在生物标志物。大多数慢性髓细胞白血病（Chronic Myelocytic Leukemia，CML）患者初次发病时处于慢性期，但仍有部分患者初发或随访阶段诊断为加速期或急变期（进展期）。但是，RDW 在 CML 中的临床价值仍处于探索阶段。
资料与方法 本研究通过收集温州医科大学附属第二医院 168 例健康成人和 153 例确诊 CML 患者资料（训练集 n=106；验证集 n=37），进一步探讨 RDW 在 CML 中的临床意义。
结果 本研究根据疾病不同阶段得出 CML 患者预后不佳的 RDW 阈值（RDW=16.8%）且该阈值与患者 OS 有明显的相关性。进一步验证该阈值临床实用性发现慢性期 CML 患者中，RDW 与患者的 OS（p=0.0008）和 EFS（p=0.0221）显著相关，但与患者 TFS 无关（p=0.0821）。此外，本研究表明 RDW 水平的下降与接受酪氨酸激酶抑制剂治疗患者的效果评估密切相关，尤其是接受治疗后的 6 月和 12 月。多因素分析表明患者年龄（OR, 1.081; 95CI％1.039~1,125; p<0.001）和初次入院时 RDW（OR, 1.469; 95CI％1.121~1.925; p=0.005）为疾病进展期的独立危险因素。
结论 对于慢性期 CML 患者，较高水平的 RDW 可作为其潜在的临床预后生物标志物。

PU-2392

痰培养样本合格性分析

陈乐
西安医学院第一附属医院

目的 探讨合格痰培养标本在诊疗中的重要性，为临床合理使用药物提供科学依据。
方法 对 200 例呼吸道疾病的痰标本进行培养，并对可疑菌株采用法国梅里埃公司的全自动微生物分析系统进行鉴定及药敏实验。
结果 痰培养合格标本的阳性率（11%）低于不合格标本的阳性率（17%）；痰培养合格标本的阳性结果与临床诊断符合率（90%)远远高于不合格标本的阳性培养结果与临床的诊断符合率（6%），两组经统计学分析（p<0.01），有显著差异，具有统计学意义；痰培养合格标本的阳性结果与临床治疗符合率（80%）远远高于不合格标本的阳性培养结果与临床的治疗符合率（3%）,两组经统计学分析（p<0.01），有显著差异，具有统计学意义。
结论 痰液合格标本的阳性培养结果能客观真实反映患者的病理状态，为临床合理使用抗菌药物提供科学依据，从而减少医疗资源浪费，减轻患者的经济负担，减少由于抗生素选择性压力的作用而产生的耐药菌株，保护微生态环境。

PU-2393

希森美康全自动血细胞分析仪不确定度评估

苏杨
四川省医学科学院·四川省人民医院

目的 评估实验室内多台 Sysmex 血细胞分析仪在量值溯源性建立之后的不确定度
方法 以配套校准物校准 Sysmex XE-2100（LJ-24）血细胞分析仪手动进样模式，建立规范操作检测系统。规范操作检测系统对一健康人新鲜全血进行定值，以定值新鲜全血对 Sysmex XE-2100（LJ-12）校准。对 Sysmex XE-2100（LJ-12）血细胞分析仪测定 WBC,RBC,HGB,HCT,PLT 的结果进行溯源，每溯源一步就产生一个不确定度分量，对各个不确定度分量进行评估，然后计算合成不确定度和扩展不确定度。
结果 实验室内 Sysmex XE-2100（LJ-12）建立了溯源性后正确评估了该仪器的不确定度。 取包含因子 k=2，该五个项目在中值质控水平上的扩展不确定度分别为 Urel（WBC 中）=0.44×10^9/L；Ure（RBC 中）=0.178×10^12；Urel（HGB 中）=2.72g/L，；Urel(HCT 中)=1.96%；Urel（PLT 中）=18.88×10^9/L。
结论 两台仪器建立溯源性后，我们通过分析寻找各项因素及运用数理统计方法，对 Sysmex XE-2100（LJ-12）血细胞分析仪测定 RBC,WBC,HB,HCT,PLT 的测量不确定度进行了较为全面和合理的评定。

PU-2394

基于能量代谢探讨蒙药三味檀香散对缺血性记忆障碍的保护作用机制

赵东[1]、何静波[2]、贾培飞[1]、雷红华[3]
1. 包头医学院第二附属医院
2. 包头医学院
3. 内蒙古科技大学包头医学院第二附属医院

目的 探讨蒙药三味檀香散是否对血管性痴呆大鼠神经功能具有保护作用，并研究其作用机制是否与调控线粒体能量代谢有关。
方法 将 72 只 SD 大鼠随机分为假手术组、缺血模型组、阳性对照组、三味檀香散大剂量组、三味檀香散中剂量组、三味檀香散小剂量组，共 6 组，12 只/组。给予普通饲料适应性喂养 1 周后，按照改良结扎颈总动脉方法建立缺血性痴呆模型，以双盲法对神经功能缺损评分，以同侧出现 Horner 征以及评分>1 分者为栓塞成功，否则被剔除。然后给予药物。连续给药 27d 后进行水迷宫实验，记录其空间记忆能力。水迷宫实验结束后，以 3%戊巴比妥钠将大鼠麻醉，腹主动脉取血后，每组中一半大鼠进行甲醛灌注后取脑组织，另一半直接断头取脑。灌注后脑组织进行切片，染色，对海马 CA1 区病理学改变进行分级，未灌注脑组织匀浆，检测脑组织中 ATP、ADP、AMP 含量，ELISA 法检测 TchE、LDH、LD 和 ATP 酶活力。
结果 与模型组比较，三味檀香散给药各组大鼠神经功能评分显著降低（P<0.05）；各剂量组均可明显改善脑缺血大鼠学习记忆能力，缩短大鼠逃避潜伏期(P ＜0. 05)，增加大鼠穿越平台次数(P ＜0. 05)，显著升高脑缺血大鼠脑组织内 ADP、ATP、ADP 含量，并使 AMP 含量下降；TchE、LDH、LD 和 ATP 酶活力明显提高；其中，三味檀香散高剂量组最为显著 (P ＜0. 05) ，三味檀香散中、低剂量组之间无显著差异(P＞0. 05)。
结论 三味檀香散可以通过调节体能量代谢从而起到神经保护作用。

PU-2395

胆道感染病原菌与药敏结果分析

张炯
四川省医学科学院·四川省人民医院

目的 了解我院胆道感染的常见病原菌及指导临床有效合理使用抗生素，也为经验用药提供依据。
方法 对我院 2 年来送检的 102 例胆汁标本有氧培养出的 53 例阳性结果进行细菌谱和药敏的回顾性分析。
结果 鉴定出的肠杆菌科细菌占 69.8%，其中以大肠埃希菌为主；非发酵菌占 13.2%；革兰阳性球菌占 17%，肠杆菌科细菌对亚胺培南，美诺培南无耐药菌株，对阿米卡星耐药率也很低。非发酵菌对阿米卡星和哌拉西林耐药率相对较低。革兰阳性球菌未发现对万古霉素耐药菌株。
结论 胆道感染以肠杆菌科细菌感染为主，并且对多种抗生素表现出耐药，胆道感染患者可能感染不同病原菌，临床应根据细菌鉴定和药敏结果，结合感染部位药物浓度及毒副作用合理用药以缩短患者病程。

PU-2396

浅谈后疫情时代医学检验管理

林花
吉林大学第一医院

质量是医学检验生存的基础、核心。后疫情时代作为一门交叉学科的医学检验，不仅更加提高应急管理能力，同时更加把控质量管理，以全新的检验理念、现代化检验技术、职业道德及业务技能，充分发挥检验医学其独特的价值。应对这次突发公共卫生事件，实验室 24 小时运转，检验人争分夺秒地准确检测新冠肺炎核酸和部分抗体的检测，在控制疫情过程中起巨大的作用。在此事件的推动下医学检验也备受关注，检验工作者也从之前的幕后工作搬到了台前，检验人精准的检测技术推动了整个医疗行业的进步。核酸检测技术、微生物检测技术、质谱技术、免疫化学技术、分子生物学技术、细胞生物学技术、各类床旁检测技术、数据信息化管理等在临床工作中发挥了越来越重要的作用。后疫情时代检验人仍然面临巨大挑战，需要完善应急管理、生物安全管理、信息管理、质量控制，同时要及时与临床有效沟通。质量是认可和权威性、检验结果的准确性以及检验与临床的科学对接。检验前质量控制直接影响到检验结果的准确性；检验中质量控制保证检测的精准；检验后质量控制直接影响到临床合理选择药物。检验工作者与临床医护人员共同配合，一切从患者利益出发，保证诊疗质量、科学管理，更好地为患者服务，共同推动医疗事业的发展

PU-2397

简析临床检验分析前质量管理

张炯
四川省医学科学院·四川省人民医院

检验科的质量目标是能否及时向临床提供准确高效可靠的高质量检验报告，使检验结果更好地符合患者的实际情况，得到患者和临床的信赖和认可［1］。自 2002 年 4 月 1 日起开始实施的《最高人民法院若干民事诉讼证据的若干规定》中，明确指出“因医疗行为引起的侵权诉讼，由医疗机构就医疗行为与损害结果之间不存在因果关系承担举证责任”，这一规定被简称为“举证倒置”，即一旦发生医疗纠纷，由患者投诉，医疗机构要拿出证据证明在诊治工作中一切医疗行为是正确无误的。检验科为达到这一报告准确的目的，进行全面质量管理，包括分析前质量管理、分析中质量管理和分析后质量管理。分析中质量管理和分析后质量管理在临床检验中心组织开展的室内质评活动、室间质评活动中，经多年的努力使报告结果的检验准确性越来越高。有关单位统计临床有关检验质量的意见，一半以上是与检测标本本身的不合格有关。

分析前阶段是指从临床医师开出医嘱起始，按时间顺序的步骤，包括提出检验要求，患者的准备，原始标本的采集，运送到实验室并在实验室内传送，至分析检验程序启动，此期终止［2］。这一环节的执行涉及面较广，包括检验科人员、临床科室医师、护士、护工以及受检者本人，任一环节的疏漏和不规范均可导致检验结果的误差。以下浅析加强检验分析前的质量管理。

PU-2398

化学发光微粒子免疫测定法检测丙型肝炎抗体的临床效果分析

苏志琳
厦门大学附属第一医院

目的 研究在检测丙型肝炎抗中应用化学发光微粒子免疫测定法的临床效果。

方法 回顾性分析我院自 2019 年 5 月至 2019 年 9 月期间收治的 63 例输血病人所有资料，选取发光免疫分析法与酶免疫测定法开展丙型肝炎抗体检查，对比两种检测的结果。
结果 对本次分析的 63 例输血病人进行丙型肝炎抗体检查，经化学发光微粒子免疫测定法与酶免疫测定法的诊断之后，阳性检出例数都为 7 例，阳性率为 11.11%。检验化学发光微粒子免疫测定法与酶免疫测定法诊断符合率之间差异不显著且 P＞0.05，无统计学意义。高值组与低值组阳性标本检出率对比差异显著且 P＜0.05，统计学意义存在。
结论 近年来丙型肝炎抗体检查中酶免疫测定法、化学发光微粒子免疫测定法都是比较常用的技术，虽然化学发光微粒子免疫测定法存在更高价值，但需要依据实际情况选择有效的诊断技术。

PU-2399

移植后感染病例分析

施丽娟
昆明市第一人民医院

目的 对一特殊的单核细胞异常增高（71%）的移植后感染病例的病例分析，来了解移植后感染的一种特殊情况。
方法 回顾分析一例经确诊移植后感染病例的各项检查和治疗。患儿，陈 XX，男，2 岁 9 个月。肝移植史，长期服用他克莫司（FK506）。患儿因”发热 4 天，右眼红肿 2 天” 患儿间断发热，最高体温 38.3℃。停用免疫抑制剂，抗感染，局部点眼等支持治疗。9 月 4 日实验室检查：血细胞分析：白细胞 6.59 x109/L，中性粒细胞 占 4 %, 单核细胞 占 71%，淋巴细胞 占 24.3%；感染标记物：超敏 C 反应蛋白 180.1mg/L，降钙素原 5.89 ng /dl。
结果 经抗感染相关治疗后，9 月 9 日 血细胞分析：白细胞 9.07 x 109/L ,中性粒细胞 占 47.2%,单核细胞 占 4.1%，淋巴细胞占 46.4%；超敏 C 反应蛋白 3.58mg/L。9 月 10 日分泌物培养结果显示铜绿假单胞菌，药敏结果哌拉西林等敏感，停用万古霉素改用哌拉西林舒巴坦抗感染治疗。9 月 14 日患儿无发热，右眼红肿消退，无肿胀，眼部相关体格检查已恢复正常，病情基本好转，复查分泌物培养阴性，达到出院标准，巩固治疗后予出院。
结论 该患者在使用免疫抑制剂后，T 细胞功能受到明显抑制，机体免疫力明显降低，导致其在病程中出现多种机会性感染，临床上对此须高度重视。 在抗感染治疗中，根据病人情况停用免疫抑制剂是合理的，注意合理应用抗菌药物，避免盲目使用大量广谱抗菌药物，以降低耐药率。

PU-2400

恶性肿瘤患者 T 淋巴细胞亚群变化及其临床意义

李石
四川省肿瘤医院

目的 探讨恶性肿瘤（肝癌、肺癌、消化道肿瘤、女性生殖系统肿瘤）患者外周血 T 淋巴细胞亚群的变化及其临床意义。
方法 应用 BD FACSCanto Ⅱ流式细胞仪对上述疾病患者外周血总 TT（CD3＋）、Th（CD4＋）、Ts（CD8＋）、Th/Ts（CD4＋/CD8＋）进行检测，同时检测健康者标本 30 例作为健康对照组，进行统计分析。
结果 肝癌患者和肺癌患者总 TT(CD3+) 细胞明显低于健康对照组(P<0.05)。四种疾病肿瘤患者 Th(CD4+)细胞、Th/Ts（CD4＋/CD8＋）均明显低于健康对照组(P<0.05)。肺癌患者和女性生殖系统肿瘤患者 Ts(CD8+)细胞高于健康对照组(P<0.05)。
结论 外周血 T 淋巴细胞亚群的检测可以作为恶性肿瘤患者临床免疫功能的初步诊断指标，辅助疾病治疗和病情观察。

PU-2401

运用品管圈构建 ISO15189 医学实验室质量管理体系

朱星成、王宁、白志瑶、高晶、施春玲
曲靖市第二人民医院

目的 探讨运用课题研究型品管圈手法构建 ISO15189 医学实验室质量管理体系。
方法 按照 QCC 活动步骤从人员、设备、设施环境、信息、检验前、检验中、检验后素等多个维度把握实验室现状水平，对攻坚点进行分析、挖掘和合并，整合为三大方策群组并加以实施：质量管理体系文件的构建；加强人员培训及管理；完善检验过程的质量管理；
结果 通过方策群组的实施，我们进行效果确认，条款知晓率提高了 50.2%、标本标签不合格率降低 6.1%、标本类型错误率降低 3.15‰、标本容器错误率降低 3.26‰、标本溶血率降低 1.1%、室内质控项目开展率提高 17%、室内质控达标率提高 15%、室间质评项目不合格率降低 4%、患者满意度提高 15%、医护满意度提高 15%。
结论 采用品管圈管理方式能够构建实验室质量管理体系，提高圈员们运用 QCC 工具解决检验科实际问题的能力。

PU-2402

Development and application of electronic document management system for clinical laboratory

Xinyuan Han
Medical Laboratory of Shenzhen Luohu Hospital Group

Objective To develop and clinically apply an information document management system based on the ISO15189 system.
Methods Browser/Server (B/S) mode and information technology such as Java and database software were used to build a Web platform. An intelligent document management system was built based on platform functions and related requirements of ISO15189. We distributed questionnaires to 184 employees in the laboratory and collected relevant results to evaluate clinical practicability.
Results An inspection knowledge base covering more than 400 external documents and more than 2,200 internal documents were established to meet the daily learning needs of staff. All internal files in the system have a unified format and unique identification code, ensuring that all files can be uniquely identified. The multi-process control mode is adopted to authorize specialized personnel to compile, review, approve and publish documents according to their types and attributes. After the file is updated and revised, the old file is automatically archived to the obsolete folder. The system automatically reminds the relevant persons in charge of the process at all levels to complete the tasks that need to be performed according to the data summary on the day, and automatically forms a complete and detailed electronic record after the operation is completed, which fully guarantees the uniqueness, traceability and security of the file. Users can access various types of files online through computers or mobile phones, and form a learning log. The system has search function, and users can quickly find the target file through fuzzy search. The recovery rate of the questionnaire reached 100%. More than 95% of the employees believed that the time for document review, revision, and approval were greatly shortened, 82.61% of the employees believed that the system was easy to operate, and 36.41% of the employees thought that the file search function needed to be improved, 7.61 % Of employees said that the speed of file update needs to be improved.
Conclusion The system fully meets the requirements of ISO15189 on document management, and realizes the Intelligent management. It is necessary to formulate detailed improvement

measures in the search and update of documents, and gradually upgrade the system to make it more convenient for employees to use.

PU-2403

Can AMH tell us more?

Taichang Tan
Department of Laboratory Medicine, Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China.

A 37-year-old Tibetan woman with infertility was referred to the outpatient clinic of the obstetrics and gynecology department of our hospital. She had experienced with a dizziness and weakness for three years. The patient said that she had sporadic menstruation and hypomenorrhea. She took no medications and had no known allergies. Now the patient lived with her husband in a mountain farm. Her mother had conceived her easily. The patient's father and two sisters were healthy; both of her sister had their own children.

On examination, the weight was 60.1 kg, the height 160.8 cm, and the body-mass index (the weight in kilograms divided by the square of the height in meters) 23.2. And she has normal female external genitalia and breast development, with sparse pubic hair and axillary hair. The remainder of the physical examination was normal. Ultrasound and pelvic computed tomography (CT) scan showed normal female external genitalia and absence of cervix and uterus with a blind vaginal; presence of dense symmetric, homogeneous enhancement of gonads structure sized 2.3×1.4 cm and 3.2×1.7 cm located in the anterior pelvis.

On the basis of the medical history and results on examination, the most likely diagnosis in this case is either mullerian aplasia or complete androgen insensitivity syndrome.

Several days later, chromosomal analysis on the peripheral blood lymphocytes revealed a 46,XY karyotype. Serum hormone measurement showed elevated levels of testosterone (17.23 nmol/L; reference range for women: 0.38–1.97 nmol/L) and anti-mullerian hormone (AMH) (695.88 ng/ml; reference range for women: 0.24–11.78 ng/ml), and inhibin B (275.49 pg/ml; reference range, <139 in premenopausal women during the follicular phase, <92 in premenopausal women during the luteal phase). These results were consistent with the diagnosis of complete androgen insensitivity syndrome. Then the patient has determined to identify her specific androgen-receptor mutation. Sequences generated from patients were compared with the published AR complementary DNA (cDNA) reference sequences from the National Center for Bio-technology Information (http://www.ncbi.nlm.nih.gov/; GenBank accession number: NM_000044.4). The gene sequencing results showed that a DNA-binding domain site mutation (c.1730G > T), resulting in a cystine to valine substitution and a histidine to phenylalanine substitution.

After four weeks of iron treatment, there were significant effects on hemoglobin, and the patient's fatigue disappeared. We recommended surgical removal of the intraabdominal gonads due to the risk of testicular cancer. But the patient would not to undergo further treatment.

Serum anti-Müllerian hormone (AMH) is a biomarker of ovarian reserve. It can be guessed from our research that AMH may provide valuable diagnostic clues, it is important to pay more attention to patients with extremely high level of AMH.

PU-2404

METTL3 介导的 CYP2B6 的 m6A 甲基化在非酒精性脂肪性肝病中的作用研究

李永清[2]、逯素梅[2]、张丹彤[2]、马万山[1,2]
1. 山东大学附属千佛山医院
2. 山东第一医科大学第一附属医院(山东省千佛山医院)

实验目的 非酒精性脂肪性肝病（Non-alcoholic fatty liver disease, NAFLD）是指除外酒精和其他明确的肝损害因素所致的、以弥漫性肝细胞大泡性脂肪变为主要特征的临床病理综合征，是一种慢性代谢性疾病。CYP2B6 基因是核受体家族成员孕烷 X 受体(pregnant X receptor, PXR)和组成型雄甾烷受体(constitutive androstane receptor, CAR)的靶基因，在糖异生、脂类代谢中扮演着重要的角色。有研究表明高脂饮食的小鼠体内，PXR 和 CAR 受体被激活，会导致其靶基因 Cyp2b10 与对照组相比表达增高，可能与 NAFLD 的产生有关。本研究探讨 CYP2B6 基因 m6A 甲基化修饰在 NAFLD 中的作用。
实验方法 构建小鼠的肝脏脂肪变模型，将肝脏组织利用基因芯片技术筛选出发生 m6A 甲基化的目的基因 Cyp2b10，检测该基因在脂肪肝中的表达情况。将人类正常肝细胞 LO2 进行脂肪酸的诱导，构建体外细胞模型，检测 CYP2B6 和甲基化酶 METTL3 的表达情况。借助 MeRIP-qPCR 技术确定 METTL3 对 CYP2B6 的 m6A 甲基化修饰作用。干扰 METTL3 或 CYP2B6 以后，用油红 O 染色，油红半定量检测 LO2 脂肪变的效果，并检测胰岛素信号通路的表达变化。
实验结果 基因芯片的结果显示小鼠肝组织中 Cyp2b10 的 m6A 甲基化水平比对照组高了 2.72 倍（$p<0.05$）。Cyp2b10 和 Mettl3 在脂肪变的小鼠肝脏中明显升高，在脂肪变的 LO2 中也显著升高。MeRIP-qPCR 的结果显示，CYP2B6 的甲基化水平受到 METTL3 的调控。但是干扰 METTL3 或 CYP2B6，LO2 的脂肪变效果和胰岛素信号通路未发生明显的变化。
实验结论 CYP2B6 的 m6A 甲基化受到甲基化酶 METTL3 的调控，但在 LO2 的脂肪变和胰岛素信号通路程中未发挥关键调控作用。

PU-2405

肝硬化门静脉高压症肝癌外科切除全程评估和管理的进展

洪源
昆明医科大学第一附属医院

我国肝硬化的发病率呈增长趋势，肝硬化所导致的门静脉高压症在我国非常常见。肝硬化和门静脉高压症患者因原发性或转移性肝癌而需要进行肝切除。然而，这类患者行扩大范围肝切除的围手术期并发症发病率，术中管理及术后效果对现代医学而言仍然是挑战。巴塞罗那临床肝癌分期建议将肝硬化肝癌患者的手术切除限定在肝硬化呈现门静脉高压症的初期。但是随着术前肝功能评估手段的增加和全面化，围手术期肝病管理的规范化，术后重症监护和肝切除技术的发展，使得肝硬化伴门静脉高压症患者行扩大范围肝切除的成为可能。因此，我们对肝硬化门静脉高压症患者行扩大范围肝切除的术前风险评估，围手术期发病率及死亡率和术后管理等进行文献综述。

PU-2406

Dietary inflammatory index and pancreatic cancer risk: a systematic review and dose–response meta-analysis

Yuan Hong
The First Affiliated Hospital of Kunming Medical University

Objective The meta-analysis was conducted to test the link between pancreatic cancer (PC) risk and dietary inflammatory index (DII®) score. Design: Systematic review and meta-analysis. Setting: We searched PubMed, Embase, Web of Science and the Cochrane Library up to 22 November 2020 to identify the relevant studies. Studies that reported the risk estimates and the corresponding 95 % CI for the DII category and PC risk were included. The effect sizes were pooled using the random-effects model. Dose– response analysis was conducted where possible. Participants: Two prospective cohort studies of 634 705 participants (3152 inci_x0002_dent cases), and four case–control studies of 2737 cases and 4861 controls.
Results Overall, the pooled risk ratio (RR) indicated that individuals in the highest category compared with the lowest category had an increased PC risk (RR = 1·45; 95 % CI 1·11, 1·90; P = 0·006). Meanwhile, significant heterogeneity was also revealed. The dose–response meta-analysis indicated that a 1-unit increase in the DII score was associated with the PC risk (RR = 1·08; 95 % CI 1·002, 1·166; P = 0·045; I2 = 94·1 %, P < 0·001). Nonlinear result showed an increased risk of moving from fewer to more inflammatory borders with increasing DII score (Pnonlinearity = 0·003; I2 = 76·5 %, P < 0·001). Subgroup analyses found that signifi_x0002_cant positive association between PC risk and DII score appeared to be in case– control studies (RR = 1·70; 95 % CI 1·16, 2·50; P = 0·007) and studies with ≤ 31 DII components (RR = 1·76; 95 % CI 1·14, 2·72; P = 0·011).
Conclusion These findings suggested dietary habits with high inflammatory fea_x0002_tures (high DII score) might increase PC risk.

PU-2407

6S 在样本前处理中的应用

陈韵同、于俊杰、陈思宇、王福权
杭州迪安医学检验中心有限公司

通过改变员工的工作习惯，提高工作素养等，来达到降本增效，质量安全保证的目的。样本前处理是样本检验的基础，样本的及时准确处理是保证患者检验结果准确性和可靠性的基础。6S 管理法的主要对象为人、事、物。实施的原则是为了提高工作效率，人性化全员遵守，管理理念适合现场管理，展示让人舒适的工作环境。

临床中越来越多的样本转送至第三方检验中心，样本的增多则需要对样本前处理进行有效的管理，保证样本检验前质量。根据 6S 内容指定相关标准，推行相关准则并实施，针对 6S 管理法的制定全员参与，制定制度和目标，明确 6S 管理中的权、责。日常针对 6S 工作进行监督、检查及效果评比。实行定期或不定期检查、考核、评定的管理模式，对评比结果进行评比，增加员工参与度。

在制度实施后用时明显减少，改进了报告时间及改善了因人员操作造成的报告发布不及时等情况，且员工对工作环境满意度上升，增加了工作积极性。对样本前处理开展 6S 管理，不仅员工本身习惯品质素养得到很大的改善，同时对患者而言也能更加及时有效的取得相关报告，有更好的就医体验；良好的工作环境，提高了员工的工作效率及工作质量；且做到降本增效，杜绝浪费， 减少公司支出成本，提高竞争力 ；确保医疗安全，降低医疗事故风险，利于和谐医患关系的构建[2]。

PU-2408

The Diagnostic Value of T-SPOT.TB and ADA in Pleural Effusion for Tuberculous Pleurisy: A Systematic Review and Meta-Analysis

xiaomei zhang
Shangrao People's Hospital, Shangrao, China.

Background Tuberculous infection of T cell spot test (T-SPOT.TB) and adenosine deaminase (ADA) have a high diagnostic value in pleural effusion for tuberculous pleurisy. However, there were major differences in existing research in regard to the clinical application of the two trials. Therefore, we conducted a meta-analysis to systematically evaluate the diagnostic value of T-SPOT.TB and ADA.
Methods Pubmed, Web of Science, EMbase, CNKI and WanFang databases were searched to compare diagnosis of tuberculous pleurisy by T-SPOT.TB and ADA. The search period was from inception to December 31, 2020. Statistical analyses were performed using Meta-disc 1.4,Revman5.4 and Stata 16.0. Pooled sensitivity, specificity, positive likelihood ratio (PLR), negative likelihood ratio (NLR), and diagnostic odds ratio (DOR) were determined. Summary receiver operating characteristic (SROC) curves and the area under the curve (AUC) were used to summarize overall diagnostic performance.
Results 17 qualified original research studies were included, of which 9 were in English and 8 in Chinese, with a total of 2453 patients. The pooled estimates of diagnostic accuracy of T-SPOT.TB were as follows: sensitivity, 0.92 (95% CI: 0.91-0.93; I2 = 87.8%); specificity, 0.76 (95% CI: 0.73-0.79; I2 = 92.1%); PLR, 4.61 (95% CI: 2.95-7.20; I2 = 92.4%); NLR, 0.11 (95% CI: 0.06-0.20; I2 = 92.3%), DOR, 53.39 (95% CI: 20.96-136.03; I2 = 88.2%). The AUC for SROC was 0.9443 (95% CI: 0.9043-0.9843). The pooled estimates of diagnostic accuracy of ADA were as follows: sensitivity, 0.60 (95% CI: 0.58-0.63; I2 = 96.2%); specificity, 0.90 (95% CI: 0.87-0.92; I2 = 69.5%); PLR, 5.77 (95% CI: 4.00-8.31; I2 = 65.1%); NLR, 0.35 (95% CI: 0.20-0.62; I2 = 98.9%), DOR, 17.75 (95% CI: 10.39-30.34; I2 = 72.6%). The AUC for SROC was 0.8916 (95% CI: 0.8382-0.9450).
Conclusion Both T-SPOT.TB and ADA had high value in the diagnosis of tuberculous pleurisy. The sensitivity of T-SPOT.TB was higher than ADA, but the specificity of ADA was higher than T-SPOT.TB. The diagnostic accuracy of T-SPOT.TB was higher than ADA, but there was no significant difference between them.

PU-2409

一例新发 DNAH1 基因移码突变分析

张慧、黄吴键、陈国勇、梅晓妍、兰风华、张朵
第 900 医院

目的 对 2 例临床表现为严重弱精子症、精子鞭毛形态多发异常（Multiple Morphological Abnormalities of the Flagella，MMAF）的原发性不育患者进行致病基因分析，探讨 DNAH1 基因新的突变位点在精子尾部多发畸形发生中的致病作用。
方法 抽取两名患者的外周血进行全外显子组测序，由于该两名患者为兄弟，父母为表亲关系，发现可疑致病位点后，在该家系内部及 100 名健康个体中针对该突变位点进行 PCR 扩增、Sanger 测序进行验证分析，利用 Mutation Taster 等软件对突变位点进行蛋白功能危害性分析。
结果 全外显子组测序结果发现该 2 名患者存在同一个纯合突变，为轴丝动力蛋白重链 1(在该家系内部及 50 名健康个体中针对该突变位点进行 PCR 扩增、Sanger 测序进行验证分析，利用 Mutation Taster 等软件对突变位点进行蛋白功能危害性分析。Dynein Axonemal Heavy Chain1，

DNAH1)第 31 号外显子上的移码突变：c. 5093delA（p.Lys1698Argfs*9），其父母、奶奶都被确定为该突变的杂合子携带者，在 100 名健康个体中未检测到上述突变。该突变位点查阅相关文献及突变数据库，未见报道。运用 Mutation Taster 对其进行预测，该突变可能造成终止密码子提前，翻译提前终止，产生截短蛋白，或其所转录的 mRNA 被无义密码子介导的 mRNA 降解机制（NMD）所降解，从而无法发挥正常功能而最终致病性。

结论 MMAF 是一种由遗传因素导致的精子严重畸形症，临床表现为男性不育，本研究通过全外显子组测序发现一个 DNAH1 基因新发可疑致病突变位点，有待后续功能分析进一步验证其致病性。

PU-2410

医学检验科门诊采血和谐医患关系的探索

黎七绮
重庆医科大学附属第一医院

医学检验科门诊采血窗口作为医院对外形象的窗口，直接为临床一线服务，不仅患者人数多、病情复杂、涉及病种多、患者停留时间短、随机性强、难以建立和谐的护患关系。患者停留在门诊采血的时间较短，而短时间的接触很有可能因为采血者的态度、言语等细微问题引起纠纷，因此，积极探讨医学检验科采血医患关系的原因并采取积极主动的预防措施十分重要且必须。医患沟通不仅应贯穿于医学教育的全程，更应积极落实于医疗服务实践中。医患沟通是提高医患交流水平的直接影响因素，同时间接地影响着医疗结果的质量和效率。静脉采血是一种常见的医疗项目，患者常因对静脉采血的认识不足和自身心理素质较差而对采血有一定的消极态度并产生不利采血顺利进行的反应。因此，医护人员要本着以人为本的沟通信念与患者进行合理的心理沟通，为患者普及基本医学常识，使采血工作顺利进行。

PU-2411

不同肾功能指标在精神疾病患者血锂浓度监测中的适用性

翟媛媛、马瑾、屈秋侠
西安市第十医院西安市精神卫生中心

目的 通过对服用碳酸锂的精神科患者血锂浓度及肾功能相关指标的测定，研究不同血锂浓度与肾小球滤过率及肾功能指标的关系，从而选择可作为个体锂盐代谢能力的指标。

方法 回顾性分析 2021 年 1 月至 2021 年 5 月在西安市精神卫生中心的就诊的 118 例服用碳酸锂缓释片 3 天以上的精神科患者的血锂浓度及肾功能相关指标，分别基于血肌酐及血胱抑素 C 估算肾小球滤过率（eGFR1；eGFR2）。采用 SPSS17.0 软件对患者的血锂浓度与各指标之间进行单因素 Pearson 相关分析。

结果 入组患者的稳态血锂浓度为 0.21-1.15 mmol/L，平均（0.64±0.23）mmol/L。

单因素 Person 相关性分析结果显示，血锂浓度与 eGFR2 显著负相关（r=0.247,P=0.01），与胱抑素 C 呈现显著的正相关（r=-0.313、,P=0.001），未发现血锂浓度与 eGFR1、尿酸、肌酐、尿素氮之间的相关性(P>0.05)。

结论 本研究结果显示血锂浓度与基于胱抑素 C 的 eGFR2 呈负相关，推测肾小球滤过功能可影响碳酸锂的代谢,。临床上可采用 eGFR2 和胱抑素 C 判断锂盐的代谢能力，有助于早期识别容易锂盐中毒的高危患者，避免锂盐中毒的发生。

PU-2412

沙黎族自治县新海南省白生儿 G6PD 缺乏症基因特征分析

晋艳婷、王洁
海南省妇女儿童医学中心

目的 寻找海南省白沙黎族自治县新生儿 G6PD 缺乏症发病情况和基因特征。
方法 以新生儿干血斑为样本，筛查使用荧光分析法，筛查阳性疑似病例使用 G6PD 基因试剂盒（PCR+导流杂交法）进行基因分型，提示有新突变的样本外送测序家系验证。
结果 ①在 2970 例新生儿当中初筛阳性样本 366 例，G6PD 缺乏症初筛阳性率约为 12.3%（366/2970）。男性阳性率 15.1%（247/1632），女性阳性率 8.9%（119/1338），男女之间疑似患病（ 2=9.610，p=0.002）有统计学意义。366 例疑似病例干血斑样本经基因分析确诊 279 例，G6PD 发病率为 9.4%（279/2970），男女之间发病（x2=6.145，p=0.013）有统计学意义。②本次确诊黎族患者 170 例，黎族发病率 9.8%（170/1742），其他民族确诊患儿 109 例，发病率 8.9%（109/1228），经统计学分析（x2=0.188，p=0.664）没有统计学差异。③基因检测到 12 种突变类型：c.1376 G>T、 c.1388 G>A、c.95 A>G、c.1311C>T、c.871 G>A、c.1024 G>T、c.392G>T、c.1360C>T、c.517T>C、c.592C>T、c.487G>A 和 c.383T>C，发现一例未知突变，经家系基因测序分析发现 c.1007C>A 新突变。
结论 海南省白沙黎族自治县新生儿 G6PD 发病率高。基因突变主要以 c.1376G>T、c.1388G>A 和 c.95 A>G 突变为主，三者突变合计 87.4%。

PU-2413

临床微生物实验室规范化管理

刘旭
郑州大学第一附属医院

研究目的 临床微生物实验室工作人员在日常工作中会密切接触患者的血液、体液及排泄物等传染源。医务工作者存在在日常工作中被锐器刺伤和传染源喷溅的事件发生，且经常进行搅拌、震荡、离心、敲打及超声波破碎等操作，这些操作均可产生大量的气溶胶播散实验室，如果管理不当，有可能引起实验室感染。因此制定科学合理的临床微生物实验室管理办法，保证医护人员安全，医疗环境安全以及实验室长期安全稳定运行的前提保证。
方法 通过对《病原微生物实验室安全管理条例》和《中华人民共和国国家操作实验室生物安全通用要求》以及《CNAS-CL02:2012 医学实验室质量和能力认可准则》和《CNAS-CL02-A005 医学实验室质量和能力认可准则在临床微生物学检验领域的应用说明》等临床微生物实验室建设管理的重要指导性文件的研究，构建实验室相应的生物安全防护工作制度、岗位职责、质量标准、安全防护、操作考核及制度差错事故登记制度等，并予以落实，保证内部生物安全，形成有效的生物安全管理体系。
结果 临床微生物实验室管理的影响因素包含了：健全的安全规章制度、良好的生物安全工作环境、发生职业暴露的紧急处理以及人员健康档案的构建以及计划免疫等。其中最重要的影响因素是人员的管理，人员管理是落实检验科全面质量管理体系的重要组成部分，也是保证实验室生物安全管理的主导者，应该有完善的准入体系，定岗定责。
结论 人员管理临床微生物学实验室最重要的组成部分，也是保证实验室生物安全管理的主导者，应该有完善的准入体系，定岗定责。面对不同的人群应有相对的管理方法，并及时开展临床微生物安全的相关宣教工作，把临床微生物实验室的规范落实到每一项工作当中，才能真正实现临床微生物实验室规范化管理。

PU-2414

ACL-TOP700CTS 全自动凝血分析仪检测系统性能验证

逯世林
山西医科大学第二医院（山西红十字医院）

目的 对沃芬公司 ACL-TOP700CTS 型全自动凝血分析仪检测系统的主要分析性能进行验证。
方法 参照美国临床与实验室标准化委员会（CLSI）制定的性能验证相关评价方案为标准进行评价，通过对该仪器主要检测项目的三项参数凝血酶原时间（PT）、活化部分凝血活酶时间（APTT）、纤维蛋白原（FIB）进行性能验证，熟悉掌握其精密度、线性范围、正确度、可比性、携带污染率（CR）及参考区间等主要性能。
结果 ACL-TOP700CTS 全自动凝血分析仪的精密度、正确度、携带污染率均符合要求。ACL-TOP700CTS 全自动凝血分析仪与对照仪器的结果相比，各检测项目测定结果比对有良好的一致性，相对偏差符合率>80%。FIB 线性验证过程中，其实测值与理论值呈线性关系，斜率 a 在（1±0.05）范围内，相关系数 r≥0.975。参考区间验证通过。
结论 本研究 PT、APTT、FIB 三个参数试验结果显示，批内精密度为 0.70%~1.92%，日间精密度为 1.50% ~6.70%，远小于 CLSI EP15-A2 判断标准，表明 ACL-TOP700CTS 全自动凝血分析仪精密度良好。
FIB 的 5 个水平实测均值与理论值之间线性关系良好，线性范围为 0.73~5.74g/L，覆盖了厂家申明的线性范围（0.80~5.0g/L），a 值为 0.9849，r 为 0.9966，表明该仪器检测参数 FIB 线性良好。
ACL-TOP700CTS 全自动凝血分析仪正确度评价是以 ACL-TOP700 全自动凝血分析仪为靶机，分别在 ACL-TOP700CTS 全自动凝血分析仪上测定并计算 PT、APTT、FIB 三项的偏倚，偏倚为-1.44%~2.93%，均满足临床血液学检验常规项目分析的质量要求。 ACL-TOP700CTS 全自动凝血分析仪的可比性验证和参考区间验证均符合判断标准要求，样本浓度污染率和项目携带污染率验证结果分别为 1.56%、2.04%，说明该仪器 PT、APTT、FIB 携带污染率极低，在测定各项目高值血浆标本时，对低值血浆标本无明显携带污染。
综合上述各项验证试验，结果表明 ACLTOP700CTS 全自动凝血分析仪精密度、正确度、线形及携带污染率评价、参考区间验证、检测系统间比对等均达到检测要求，符合 ISO 15189 的质量要求，该机性能稳定良好，检测性能适用于临床需要。

PU-2415

sST2 与 CD4+T 细胞在多器官衰竭中的相关性研究

吕宏祥、谢垚、彭启松
南京市江宁医院

目的 探讨 sST2 与 CD4+T 在组织衰竭患者疾病发展进程中的作用。
方法 纳入器官衰竭患者 100 例外周血血清标本，并收集健康体检者外周血血清标本 20 例设为对照组。采用免疫荧光干式定量法检测血清中 sST2 的表达水平，并对器官衰竭组与对照组进行比较；流式细胞仪检测 $CD4^+T$ 细胞比例；分析血清 sST2 的表达量与 $CD4^+T$ 细胞在器官衰竭患者发展进程中的相关性。
结果 器官衰竭患者外周血血清 sST2 的表达高于对照组；器官衰竭患者外周血 $CD4^+T$ 细胞比例明显低于对照组；器官衰竭患者血清 sST2 表达量与 $CD4^+T$ 细胞比例具有相关性。
结论 sST2 与 $CD4^+T$ 呈现负相关可能提示组织器官发生衰竭。

PU-2416

检验智能信息系统的设计开发与应用分析

徐宏忍
昆明市第一人民医院

目的 本研究旨在探讨临床检验智能信息系统的设计与应用分析。
方法 将检验科的工作划分为检验前，检验中，检验后，设计临床检验智能信息系统对上述三个流程所包含的工作进行模块化智能集成，探讨临床检验智能信息系统在医院的应用。
结果 临床检验智能信息系统已经实现采血叫号功能，标本容器智能识别，医嘱与采集容器关联，取报告凭证打印，标本交接功能，智能编号功能，标本检验管理，标本周转时间监控，仪器通信管理，报告智能审核，自助报告机管理。
结论 临床检验智能信息系统有效地解决了检验业务持续增长带来的排队时间过长和患者隐私保护的问题，降低了交叉感染的风险。从多个方面改善了检验科的质量指标，提高了工作效率，节约人力和时间成本，更好地服务患者。

PU-2417

自动审核在缩短患者等待时间提高报告正确率方面的应用分析

徐宏忍
昆明市第一人民医院

目的 运用自动审核，缩短生化标本的患者等待时间，提高报告正确率。
方法 对 2016 年（生化自动审核验证阶段），2017 年（生化自动审核改进阶段），2018 年（生化自动审核稳定运行阶段），总计三年的 90 余万份报告，按照急诊、平诊、门诊、住院，四个维度来分析标本的结果完整传输到 LIS 至报告审核的 50%位数和 90%位数，同时分析错误报告率。
结果 2016 年至 2018 年，生化标本量增加了 76%，标本的结果完整传输到 LIS 至报告审核的 50%位数由 3 分钟缩短至 1 分钟，标本的结果完整传输到 LIS 至报告审核的 90%位数由 40 分钟缩短至 17 分钟，错误报告由 1541 份减少至 325 份，
结论 运用自动审核缩短了生化标本的患者等待时间，提高了报告正确率。

PU-2418

转化生长因子-β 信号通路与纤维化

王晓玲
山西省中医院

转化生长因子-β (TGF-β)是一组结构相关的细胞因子超家族，在发育过程、组织稳态和疾病期间基本细胞事件中发挥着普遍作用。TGF-β 超家族由 33 个成员组成，包括 TGF-β 1-TGF-β5 亚家族、骨形态发生蛋白(BMP)亚家族、Nodal、Activins、Mullerian inhibitors (MIS)、胶质细胞系来源的神经营养因子(GDNF)亚家族等。TGF-β 信号通路在不同的时间、组织特异性模式下表达，在不同细胞过程的调节中发挥重要作用，包括增殖、分化、迁移或细胞死亡，这些过程对组织和器官的稳态至关重要，与自身免疫、炎症、肿瘤密切相关。许多结果表明，由于 TGF-β 功能的多样性和多效性，其通路的去调控导致了人类疾病，广泛靶向 TGF-β 抗纤维化策略并不可行。因此，本文综述了 TGF 各种生物学效应以及在器官纤维化的研究进展，旨在为开辟新的治疗策略提供参考。

PU-2419

血清残余脂蛋白胆固醇在冠心病中的研究进展

张壶涵、段勇
昆明医科大学第一附属医院

自 2000 年起，无论是城市居民还是农村居民，心血管病死亡率始终位于总死亡原因首位，尽管 PCI 和冠心病二级预防策略已减少和改善了冠心病患者的死亡率和预后，然而，冠心病患者出院后不良心血管事件的发生情况仍然有待改善。众所周知，LDL-C 是冠心病的独立危险因素，然而近年来的研究显示，在冠心病患者 LDL-C 治疗达标情况下仍有再次发生心血管事件的残留风险。研究表明，血清残余脂蛋白胆固醇（RLP-C） 能解释这种风险。通过回顾 RLP-C 相关的研究，从 RLP-C 的定义、分布特征、代谢及检测方法，RLP-C 与冠状动脉粥样硬化性心脏病的相关研究以及药物治疗方面做一综述。

PU-2420

Inhibition of Hepatic Fibrosis by regulating hepatic stellate cell β-catenin/TCF/FoxO1

Xiaoling Wang
Shanxi Academy of Traditional Chinese Medicine, Shanxi Traditional Chinese Medicine Hospital

Liver fibrosis is a leading and growing cause of mortality worldwide. Hepatic stellate cells (HSCs), residing in the space of Disse between the sinusoidal endothelial cells and hepatocytes, as the major fibrogenic cell type in the injured liver, exert a dominant role in liver fibrosis. Transforming growth factor Beta（TGF-β）released by multiple cell types will induce activation of HSCs during an inflammatory reaction in the liver. It is hypothesized that to redirect β-catenin/TCF and β-catenin/FoxO1 could reduce liver fibrosis by inhibiting the activation of HSC in this study. We detected the different outcomes of HSC in vitro by interfering with the transcription factor complexes β-catenin/TCF and β-catenin/Foxo1, then in the liver fibrosis models of common bile duct ligation (BDL). The results showed that the inhibition ofβ-catenin/TCF mediated transcription using ICG-001, redirected to promote β-catenin/FoxO1, resulted in cell cycle arrest, enhanced antioxidant capacity, weakened HSC activation, and reversal of liver fibrosis. In addition, we found that fibrosis levels were associated with transcription factor complexes β-catenin/TCF and β-catenin/Foxo1 in liver fibrosis tissue samples of children with congenital biliary atresia at different stages.

PU-2421

河南地区 26249 例丙型肝炎病毒五种常见亚型分布分析研究

胡正川、李利娟、任伟丹
郑州金域临床检验中心有限公司

目的 统计河南各地区丙型肝炎病毒（HCV）感染者 HCV 基因分型检测结果，分析该地区丙型肝炎患者病毒亚型分布特征，为临床用药指导以及疗效评估提供数据支持。
方法 收集 2017-2020 年郑州金域临床检验中心有限公司实验室检测的丙型肝炎病毒（HCV）基因分型 26249 例临床样本进行结果统计分析。26249 例临床样本通过 PCR-荧光探针法或基因测序法（突变和重组亚型）检测 1b、2a、3a、3b 和 6a 五种常见型别。
结果 26249 例丙型肝炎病毒分型检测结果显示，1b 亚型占比 61.63%，2a 亚型占比 34.73%，3a 亚型占比 2.01%，3b 亚型占比 1.24%，6a 亚型占比 0.39%。

结论 河南地区丙型肝炎病毒（HCV）感染者 HCV 基因分型主要以 1b 亚型和 2a 亚型为主，对临床用疗效评估和用药指导具有重要意义。

PU-2422

临床危急值管理的实践与体会

董郭枫
襄阳市第一人民医院

检验科是目前医院当中重要的组成部分，在检验科的实际工作当中，危急值十分多见，主要是指临床检验项目当中某一检验的结果严重异于正常的检验结果，且这一异常结果会给患者的身体健康与生命安全带来严重危害。伴随医疗卫生体制改革的不断深入，临床检验工作也在面临较大压力，患者等对于检验科也提出了更高的要求。临床检验科危急值以及危急值报告可以很好地降低患者风险发生几率，并确保其生命安全，但当前检验科危急值管理仍存在一些问题，本文将进行分析，并探讨一些相关改进方式。

PU-2423

1630 例河南省儿童铁蛋白水平调查

贾全胜、陈明、王亚南
郑州金域临床检验中心有限公司

血清铁蛋白是体内含铁最丰富的蛋白，在铁的代谢方面起着重要的作用。血清铁蛋白广泛存在于其他组织细胞中，当人体某一系统出现疾病时，血清铁蛋白可出现异常改变。血清铁蛋白能够反应体内铁存储量及肌体的营养状态，是判断体内铁缺乏及超负荷的有效指标。

目的本文就河南省儿童检测血清铁蛋白数据的统计，来展示河南省儿童血清铁蛋白的水平，讨论儿童检测血清铁蛋白的必要性。

PU-2424

4 种国产新型冠状病毒核酸检测试剂第三方质控品检测结果分析

王晓玲[1]、任建平[2]
1. 山西省中医院
2. 山西省中医药研究院（山西省中医院）

目的 针对现有 4 种国产新冠病毒核酸检测试剂采用可溯源的第三方质控品检测结果进行分析，探讨不同检测试剂质量是否与 SARS-CoV-2 核酸检测假阴性相关。

方法 采用第三方质控品浓度梯度稀释作为待测标本，磁珠法提取核酸，选取 4 种新冠核酸检测试剂进行平行实验，初步分析不同试剂的检测结果。

结果 A 试剂 ORF1ab 基因位点检出比例（84.38%） 与 B 试剂（87.50%）相当，N 基因位点检出比例（65.63%）高于 B 试剂（50.00%）；C 试剂 N 基因位点检出比例 18.75%（6/32），E 基因位点检出比例 9.38%（3/32）；D 试剂 N 基因位点检出比例高于 C 试剂，E 基因位点检出比例低于 C 试剂。A 试剂、B 试剂对弱阳性标本检出比例高于 C 试剂和 D 试剂，A 试剂批内批间精密度优于其它试剂。

结论 4 种 SARS-CoV-2 核酸检测试剂对于可溯源的第三方质控品不同浓度梯度的检出比例、精密度有差异。

PU-2425

细胞学检查联合人乳头状瘤病毒(HPV)检测对子宫颈癌前病变筛查的重要意义

经晶
吉林金域检验医学检验所有限公司

目的 宫颈癌是我国女性常见的恶性肿瘤之一，而宫颈癌是目前可以通过筛查提前发现、提前预防的癌症之一，故宫颈癌前病变筛查的重要手段对预防宫颈癌有着重要意义，本文探讨了细胞学检查联合人乳头状瘤病毒(HPV)检测对宫颈癌前病变筛查的意义，为临床提供参考依据。
方法 选取 2020 年 1 月至 2020 年 12 月送检我公司的宫颈癌筛查样本 982 例，年龄为 19~70 岁，有性生活史的患者病例。所有样本均接受宫颈液基细胞学检查、HPV 检查及病理学检查,以病理学检查结果作为确诊标准,分别对单纯宫颈液基细胞学检查、单纯 HPV 检查以及宫颈液基细胞学联合人乳头瘤病毒（HPV）检测的诊断价值进行结果分析。
结果 982 例患者中，179 例患者 HPV 检测为阳性，阳性率为 18.2%，81 例患者细胞学为 ASCUS 及以上病变，其中 ASCUS 为 48 例，宫颈上皮内瘤变(CIN)Ⅰ级 21 例,CIN Ⅱ 及 CINⅢ 8 例,宫颈浸润癌 1 例,非典型腺细胞 3 例，子宫颈腺癌 0 例，子宫内膜癌 0 例，细胞学阳性率总体为 8.2%，39 例患者组织学为阳性病变，组织学宫颈上皮内瘤变(CIN)Ⅰ级 17 例,CIN Ⅱ 9 例,CIN Ⅲ 8 例,宫颈浸润癌 4 例,子宫颈腺癌 1 例。而人乳头状瘤病毒(HPV)检测、细胞学检查均为阳性者共 73 例，结合组织学对照阳性率高达 90.1%。
结论 联合宫颈液基细胞学及 HPV 检查的诊断灵敏度、特异性、准确率均明显高于单纯宫颈液基细胞学检查及单纯 HPV 检测，其辅助诊断是一种十分简便易行、经济有效、便于随诊观察、患者又无痛苦且诊断性高的宫颈癌诊断方法，对女性宫颈癌防治有重要意义。因此宫颈细胞学检查联合人乳头状瘤病毒(HPV)检测对子宫颈癌前病变有着重要的诊断意义。

PU-2426

结肠癌干细胞标志物和信号通路的研究进展

马苏红
山东大学第二医院

结肠癌是一种最常见的消化道恶性肿瘤，世界范围内 其发病率位列第三。大部分的结肠癌患者死 亡由肿瘤的复发转 移和耐药性所致，而这些过程都有肿瘤干细胞的参与。因此，靶 向肿瘤干细胞将成为未 来根治结肠癌的重要研究方向，而结肠 癌干细胞标志物的发现则为其提供了新思路。同时，因结肠癌干 细 胞的生长依赖多种信号通路的作用，故其相关信号通路靶向 药物的研究也将是一大发展方向。现阶段主要的结肠癌干细胞标志物包括 CD133、 CD44、CD166、 EpCAM、CD24、CD26、ITGB1、 Lgr5、ALDH1、Oct4、Sox2 和 Nanog 等， 通 常 可 用于鉴定和分离 CCSC (表 1)[3-15]。其中， CD133、CD44、CD166、EpCAM、CD24、Lgr5、ALDH1、Sox2 和 Nanog 还可能在预测病理分期、癌症诊断 方面具有作用。CD24、CD26 和 CD29 是参与细胞间黏附的膜表面糖蛋白，并可能与肿瘤的扩散 转移有关 ；而 Oct4、Sox2 和 Nanog 是维持胚胎干细 胞特性 的转录因子，并参与肿瘤的形成过程。此外，miRNA 作为 CCSC 生物标记物的潜力也被证明，而且标志物之间的联 合检测有利于结肠癌的诊断及治疗。可用于探索新 型的靶向治疗方法。

PU-2427

滤泡辅助性 T 细胞在疫苗研究中的作用

谢婷、黄民成、陈建设、覃艳玲
邵阳市中心医院

T 滤泡辅助细胞（T follicular helper，Tfh）是一类辅助性 CD4 T 细胞，在生发中心中可诱导 B 细胞增殖，抗体类别转换和体细胞突变，从而诱导长寿命浆细胞和记忆性 B 细胞的产生。大多数成功的疫苗如抗乙型肝炎，黄热病和天花等通过诱导持久的中和抗体来清除病原体并防止靶细胞感染。在大多数疫苗研究中，Tfh 细胞频率的增加与保护性体液免疫的诱导相关。有研究表明循环 Tfh 细胞的比例，特别是具有活化表型的细胞，可以正向预测疫苗接种后抗原特异性应答水平，包括针对流感和肺炎链球菌的疫苗、活化的 cTfh 频率也可预测口服疫苗引起的粘膜抗体反应。而在 HIV、乙型肝炎病毒、流感病毒、HPV 等疫苗接种后，Tfh 细胞表型、功能及活化状态变化对保护性抗体应答的产生起重要作用。因而在病原体感染过程中，Tfh 细胞的频率、表型及功能改变可作为血液中有用的生物标志物。本文就 Tfh 细胞及其亚群在疫苗接种后，对抗体应答的产生中的作用进行总结，旨在为疫苗的研究提供新见解。

PU-2428

牙克石地区健康成年男性人群血清甘油三酯（TG）水平的调查报告

陈吉兴
牙克石市人民医院

目的 调查牙克石地区表观健康成人男性血清甘油三脂水平年龄分布特征并分析其相关危险因素。血清甘油三脂（TG）升高可能成为动脉样硬化性心血管疾病的危险因素。[1]
方法 选取 2019 年 3 月至 2019 年 8 月在我科进行健康体检的 1392 例成人男性血清甘油三脂检测数据进行统计分析。
结果 一、不同年龄人群 TG 水平情况：1392 例男性血清甘油三酯（TG）平均水平为：2.58mmol/l，分布区间：0.31-22.57mmol/l。其中，20-30 岁血清甘油三酯（TG）平均水平为：1.82mmol/l，分布区间:0.35-6.55mmol/l；31-40 岁血清甘油三酯（TG）平均水平为：2.64mmol/l，分布区间:0.42-15.59mmol/l；41-50 岁血清甘油三酯（TG）平均水平为：3.02mmol/l，分布区间:0.31-22.57mmol/l；51-60 岁血清甘油三酯（TG）平均水平为：2.3mmol/l，分布区间:0.54-14.13mmol/l。二、不同 TG 水平人群分布情况：小于 1.7mmol/l 人数为：541 人，占比 38.87%；1.7-2.25mmol/l 人数为：278 人，占比 19.97%；2.26-5.65mmol/l 人数为：475 人，占比 34.12%；大于 5.65mmol/l 人数为：98 人，占比 7.04%。
《中国成人血脂异常防治指南》（2016 修订版）意见是 TG 合适水平小于 1.7mmol/l，边缘升高：1.7-2.3mmol/l，升高：大于 2.3mmol/l。[2] 美国 NCEP-ATP-III 报告建议的血清甘油三酯（TG）评价水平：正常水平：小于 1.7mmol/l；边缘增高：1.7-2.25mmol/l；增高水平：2.26-5.65mmol/l；极高水平：大于 5.65mmol/l。[3]
结论 1、我市男性血清甘油三酯（TG）平均水平为 2.58mmol/l，明显高于《中国成人血脂异常防治指南》（2016 修订版）意见的合适水平，合适水平人群仅占 38.87%。2、我市男性血清甘油三酯（TG）水平随年龄增加而增高，41-50 岁人群组达峰值。
降低甘油三酯的方法有哪些？一是合理饮食，控制脂肪的摄入，增加膳食纤维，多吃蔬菜及保证蛋白质的摄入；二是适量运动，有规律的运动可以直接到达降低甘油三酯的效果；三是戒烟限酒，饮酒也是造成甘油三酯升高比较常见的原因，甘油三酯超过极高水平的人群应禁酒。美国 IAS 指南中

对血脂异常人群生活方式的干预应优先于药物干预[4]。当空腹甘油三酯大于等于 5.6mmol/l 时，考虑使用药物来降低甘油三酯。

PU-2429

高危型 HPV 及液基细胞学（LCT）在宫颈病变筛查的检出率比较

张鸿
吉林金域检验医学检验所有限公司

目的 高危型 HPV 及液基细胞学（LCT）在宫颈病变筛查的检出率比较
方法 选取 2019 年至 2020 年送检吉林金域医学检验所的患者各 500 例为研究对象，分别于沉降式液基细胞学（LCT）检测、HPV 病毒检测及组织病理活检，对三者结果进行比对分析。
结果 500 例宫颈沉降式液基细胞学（LCT）标本中，阳性标本共有 41 例，占 8.2%，阴性标本 459 例，占 91.8%，与宫颈活检阳性符合率为 85.3%；500 例高危型 HPV 标本中，阳性标本例 44 例，占比 8.8%，阴性 556 例，占比 91.2%，与宫颈活检阳性符合率为 79.2%；同时做高危型 HPV 及液基细胞学标本中，阳性 61 例，占 12.2%，共同阳性 43 例，占比 8.6%，与宫颈活检阳性符合率为 95.7%。宫颈癌是妇科常见的肿瘤之一，近些年来发病率日趋年轻化，严重威胁女性健康。高危型 HPV 病毒感染与宫颈上皮内病变具有关联性。高危型 HPV 检测方便快捷，特异度、灵敏度较高，符合率稍低；液基细胞的优点有特异度、敏感度较高，符合率少高等，主观判断性较强，同时因宫颈癌筛查人群多为健康妇女，随访难度大。所以高危型 HPV 及液基细胞联合筛查检出率高，二者同时阳性时与宫颈活检阳性符合率高，从而降低宫颈癌发病率。
结论 高危型 HPV 及液基细胞学联合筛查检出率较高，且二者同时阳性时与宫颈活检阳性符合率高，因此二者联合筛查是比较经济实用、有效的方法。

PU-2430

2020 年深圳市某三甲医院医学检验科员工满意度调查分析

许晓清、李佳瑜
深圳市罗湖医院集团

目的 通过员工满意度调查，获取员工工作建议和需求，评估并合理实施这些建议，促进实验室管理层与员工进行有效沟通。
方法 通过微信问卷星形式，向所有检验科员工发送电子问卷，分析 2020 年深圳市罗湖区人民医院医学检验科员工的满意度调查结果，根据 Iso15189 要求，结合检验科质量指标管理程序文件，以科室管理，管理层表现，科研、教育关注度，实验室工作环境、人员、设施配制，工作岗位安排，实验室工作流程，休假与工资待遇 7 个方向共 35 项调查问题，分析总结调查结果。
结果 调查表中各调查内容的评价意见分为“满意”、“较满意”、“一般”、“较不满意”、“不满意”共 5 个级别，各级别赋值分别为 5 分、4 分、3 分、2 分、1 分。员工满意度(%)=问卷得分/总有效问卷分数×100。经统计后深圳市罗湖区人民医院检验科共有员工 119 名，共收到 119 份问卷，员工问卷总得分为 19399 分，总有效问卷分数为 20825 分，员工满意度为:93.15%，同时筛选出有代表性的有效整改意见共 20 条，主要涉及科室文化建设，科室职能细化，个人职业发展支持，薪资休假制度改善，员工轮岗制度完善，与临床加强沟通等几个方面 。
结论 通过员工满意度调查表，逐步完善科室制度，解决员工工作需求，可提高员工的工作积极性，持续改进实验室服务和检验质量；问卷星是员工满意度调查的一种方便快捷方式。

PU-2431

检验医学中的人工智能伦理:原则与实践

马苏红
山东大学第二医院

越来越多的人工智能应用正在开发和应用于实验室医学。这些技术带来的风险和好处必须通过道德的角度进行评估和管理。人工智能(AI)正在改变社会和医疗保健。计算能力的扩大和大型数字数据集为技术和商业创新创造了工业革命以来从未见过的理想条件。人们对这些人工智能工具在改变和改善医疗保健方面的潜力抱有极大的热情这反映在检验医学专业人员努力加强检验医学的实践，并基于我们生成的数据推进医学知识。人工智能包括广泛的机器学习(ML)，深度学习，和其他分析工具从统计和计算机科学。在大多数情况下，AI 应用程序开发人员使用真实数据集来“训练”他们的应用程序生成所需的输出。理想情况下，应用程序使用独立的真实数据集进行验证，以评估 AI 输出的准确性和通用性。例如，在病理 AI 中，训练或验证数据集可能由数字化的显微镜图像以及由人类病理学专家评估的相关诊断组成。病理学家和其他实验室专业人员提供关于病理学和检验医学中医疗 AI 应用的伦理发展、验证和实施的指导。这包括但不限于以下内容:管理病人资料；软件应用程序的开发；临床应用的验证；人工智能应用的科学研究和出版；制定体制政策和程序；对外业务关系的管理。希望为与人工智能相关的组织政策和程序的发展提供信息，包括与外部业务合作伙伴有关的政策和程序。并对监管机构在考虑对这些技术进行法律监督的新方法时有用。工智能是一套日益强大的技术，有潜力推进诊断实验室医学为患者的利益。然而，人工智能带来了收益、风险和成本的复杂组合。最大化利益同时最小化风险和成本需要在道德框架内管理技术。病理学家和实验室专业人员，以及他们的临床和学术组织以及潜在的行业合作伙伴，都有义务在他们自己的组织和外部合作伙伴中促进伦理人工智能的开发、验证和实施。

PU-2432

急性血管内溶血病例分析一例

张玲
泰安市中心医院

病案经过：患者**，女，72 岁，查体发现肝大入院，既往有乳腺恶性肿瘤、高血压病史。停阿司匹林一周后拟行剖腹探查术。术前麻醉满意，开腹后患者血压骤降，休克表现，立即停止手术并进行缝合，给与输血补液等抗休克治疗血管内凝血，后转入 ICU。后患者出现刀口渗血，引流夜及尿液均为酱油色，积极治疗后效果不接，并血液循环障碍、代谢障碍，心脏骤停后死亡。

目的 分析患者死亡原因，学习急性血管内溶血，弥散性血管内凝血的病因，生理病理机制，以及探讨检验诊断在临床实际运用中的思路。

方法 研究病历，学习急性血内溶血、弥散性血管内溶血的理论知识，查阅相关文献，与临床沟通等。

结果 笔者于患者转入 ICU 后接收到其血液和尿液标本，，发现血液标本离心后血清呈酱油色，尿液亦是如此，首先考虑血管内溶血，并与临床沟通，了解病情，考虑患者出现了围手术期麻醉药物过敏，进而发生了急性血管内溶血，并极有可能进展为急性弥散性血管内凝血，建议加做 3P、乙醇胶试验，结果为阳性，结合患者症状，确证为 DIC，并立即给与抗凝、大量输注凝血因子、血浆、血小板等对症治疗，但由于患者病情进展迅速，后出现了血液循环障碍，代谢障碍，最终发生心脏骤停后死亡

结论 围术期过敏反应是一种在接触过敏原后突然出现的，严重的、危及生命的、系统性过敏反应，病死率高达 3%～9%。急性血管内溶血是指红细胞某些诱因下于血管内发生自溶，血红蛋白直接进入血浆后引起的急性反应，多表现为高热、寒战、血红蛋白降低、酱油色尿等，进展迅速极易诱发弥散性血管内凝血（DIC）。DIC 是由于在原发病基础上，致病因素损害微血管体系，导致凝血活

化，全身微血管血栓形成、凝血因子大量消化并继发纤溶亢进，引起以出血及微循环衰竭为特征的临床综合征。实验室支撑项目有 PT、APTT、Fig、D-二聚体，3P、乙醇胶试验，血常规、肝肾功、LDH 和 ADAMTS13、外周血图片镜检等，临床检验工作人员在发现疑似 DIC 的检验诊断时，要及替代支持治疗；必要时时与临床沟通，以免贻误病情；同时 DIC 病情进展迅速，治疗上关键是对基础疾病进行治疗，再有出血表现或风险时给与抗凝和抗纤溶治疗。

PU-2433

HIV 感染者/AIDS 患者合并梅毒感染对 CD4+淋巴细胞影响的研究

徐丽萍、黄山、吕松琴、施金丽、聂磊、李晓非
昆明市第三人民医院

目的 研究分析 HIV 感染者/AIDS 患者合并梅毒感染对 CD4+淋巴细胞的影响，为艾滋病的诊疗提供一定数据基础。
方法 收集 2019 年 1 月-12 月昆明市第三人医院收治的 1052 例 HIV 感染者/AIDS 患者血清样本，进行梅毒抗体和 CD4+绝对计数检测。
结果 1052 例 HIV 感染者/AIDS 患者中，梅毒感染率为 8.84％(93/1052)，合并梅毒感染患者中男性占比为 83.87%(78/93)远远高于女性 16.13%(15/93)，CD4+绝对计数小于 100 个/ml 占比 50.50%（47/93）远高于 100-500 个/ml 28.00%（26/93）和>500 个/ml21.51%（20/93），差异有统计学意义（c2=，c2=，c2=，P<0.001）。
结论 云南地区 HIV 感染者/AIDS 患者合并感染梅毒占比不低，50%的合并感染患者 CD4+绝对计数大多数低于 100 个/ml。

PU-2434

标本类型、储存时间和温度对促肾上腺皮质激素测定的影响评价

尹建洁
吉林大学第一医院

促肾上腺皮质激素测定结果随时间延长，温度的升高、测量值逐渐降低。血清和血浆在室温条件下促肾上腺皮质激素浓度测量值较 4 ℃条件下下降显著，差异有统计学意义(P<0.01)；在室温保存条件下血浆促肾上腺皮质激素浓度分别立即检测、放置 4 小时、24 小时小时检测，（4 小时、24 小时小时结果偏倚分别为-3.1 和-18.3)。血浆促肾上腺皮质激素在 4 ℃冰箱保存（4 小时、24 小时小时检测偏倚分别为-0.86 和-3.49）。

PU-2435

抗凝标本可接受样本量分析

周利艳[1,2]、陆丹[1,2]、吴晓宁[1,2]、郭宇妮[1,2]、何秋媛[1,2]
1. 广西医科大学第二附属医院
2. 广西医科大学第二临床医学院

目的 为减轻临床工作和患者采血压力，探讨抗凝标本让步标本血量范围。
方法 （1）血常规管：选择我院接受健康体检的志愿者，其中成人 44 例，婴幼儿 10 例。使用含 EDTA 二甲盐的真空采血管抽取全血，成人组以 1mL，1.5mL，2.5mL 为实验组，标准组为同个志

愿者 2mL 的血量，婴幼儿组以 1mL 为实验组，标准组为同个婴幼儿 2mL 的血量。在相同条件下，将上述标本在贝克曼库尔特血球分析仪进行全血细胞计数检测，比较不同采血量全血细胞计数结果的差异。（2）凝血功能检测管：选取成人 22 例，使用含 0.5mL 3.2%柠檬酸钠真空管抽取全血，以 1.5mL，2.5mL 为实验组，标准组为同个志愿者 2mL 采血量。在相同条件下，利用沃芬全自动凝血分析仪进行凝血四项检测，比较不同采血量凝血四项结果的差异。

结果（1）全血细胞计数方面，成人与婴幼儿实验组与标准组的全血细胞计数结果差异无统计学意义（p>0.05）,其相对偏差符合率在临床可接受范围内。（2）凝血方面，实验组与标准组的部分活化凝血酶原时间（APTT）存在统计学差异（p<0.05），凝血酶时间（TT）、纤维蛋白原（FIb）、凝血酶原时间（PT）结果无统计学差异。APTT、Fib、TT 相对偏差符合率分别为 20%、50%、80%。

讨论（1）成人全血细胞分析可接受样本量为 1-2.5mL。（2）婴幼儿采血相对困难，对低容量采血量有较高需求，本研究表明，3 婴幼儿全血细胞分析可接受样本量为 1-2mL，但值得注意的是，在实验过程中，婴幼儿低容量血量易造成白细胞难以分类，因此临床上仍推荐在可执行的情况下，选择 2mL 采血量。（3）凝血项目受血量影响较大，不可接受让步，应严格按照 2mL±10%采血。

PU-2436

运用 FOCUS-PDCA 改善门诊采血等候时间

李华丽
西安医学院第一附属医院

目的 通过科学的管理方法，分析门诊采血等候时间过长的原因，提出不断持续改进的措施，改善门诊采血等候时间，保障患者满意度。

方法 按照 FOCUS-PDCA 程序，对门诊患者采血等候时间过长存在的问题进行分析、制定改进措施，完善管理制度，不断规范采血流程，对采血等候时间持续进行对比，实现持续改进。

结果 通过 FOCUS-PDCA 的应用，采血平均等候时间从 2020 年 1 月份的 37 分钟降低至 2020 年 9 月份的 13.9 分钟；改善了门诊患者采血等候时间，提高了工作人员的工作效率，增加了患者的满意度，确保标本能够安全、及时、准确的服务于临床工作。

结论 FOCUS-PDCA 对于改善门诊采血等候时间起到良好效果，对实现医疗质量、患者满意度和安全持续改进有着重要的作用，值得推广。

PU-2437

探讨如何解决大规模新型冠状病毒核酸筛查中待检人群的资料信息问题

魏琦、都伟杰、李志强、袁征、毛源
合肥金域医学检验实验室有限公司

目的 为了解决大规模新冠病毒核酸筛查时待检人员的资料信息登记问题，提高采样环节的工作效率，并且减少居民排队等待检测的感染风险。

方法 2021 年 5 月安徽省六安市新冠疫情第一轮筛查期间，在当地相关部门的带领下，我司采用传统纸质登记待检人员的信息。从第二轮筛查开始，我司采样了集团开发的新冠信息采集小程序，该小程序深入街道、社区、学校，采用无纸化信息登入，一键扫码获取个人身份信息，在保障个人信息安全的同时，确保信息登记准确无误，方便后续工作的流程顺畅。

结果 第一轮大筛查（持续 2 天），我司配合相关部门完成 10 万居民采样工作；第二轮筛查（持续 2 天）, 我司配合相关部门完成 18 万居民采样工作，第三轮完成 25 万居民采样工作。

结论 新冠信息采集小程序极大提高样本前处理时信息录入的效率，成功应对大规模社区采样和核酸筛查，为助力政府保质保量推动疫情防控工作开展贡献科技应用的力量。

PU-2438

新型冠状病毒肺炎疫情期间方舱实验室的应急建设与管理

魏琦、都伟杰、李志强、毛源
合肥金域医学检验实验室有限公司

目的 为应对 2021 年 5 月六安市突发新型冠状病毒肺炎疫情，尽快配合相关部门完成主城区及重点区域全员核酸检测工作，本实验室迅速启动方舱实验室建设。
方法 从总部调集两辆方舱实验室和一辆移动检测车，成立方舱实验室应急团队，团队包括应急管理组和检测组，并配置相应的仪器设备。管理组对接当地疾控，了解相关政策，并为检测组提供后勤保障；检测组根据方舱实验室的结构与分区、压力参数、新风系统、机器人运行环境、污水排放等编写 SOP、开展方法学性能验证（包括试剂的符合率、检出限、交叉反应、精密度和抗干扰能力进行验证及评价），并接受当地临检中心的验收考核。
结果 经过各种资源调配，两个方舱实验室顺利通过验收，形成标准、规范的新型冠状病毒核酸检测实验室，具有每日 10000 管标本的检测能力。
结论 实践证明，方舱实验室具有快速、标准、有效、适用等特点，是出现大规模人群核酸筛查应急状态下的一种应对措施。同时，快速建立新型冠状病毒核酸检测实验室及扩大核酸检测能力成为当今群防群控不容忽视的问题。

PU-2439

真菌（1-3）-β-D 葡聚糖光度法在诊断 AIDS 合并真菌感染中应用价值分析

许宝妹、黄山、吕松琴、段洪芬、李晓非
昆明市第三人民医院

目的 探讨真菌（1-3）-β-D 葡聚糖光度法在诊断 AIDS 合并真菌感染中的应用价值
方法 收集 2020 年 1 月至 2020 年 12 月在云南省昆明市第三人民医院感染 1 科住院的 ＨＩＶ 患者 172 例，男性 126 例，女性 46 例，分别进行常规真菌培养鉴定和真菌（1-3）-β-D 葡聚糖光度法检测。
结果 172 例 AIDS 患者中有 30 例患者为合并真菌感染，真菌培养和真菌（1-3）-β-D 葡聚糖光度法的阳性率分别为 16％和 60％，以临床诊断为金标准，真菌（1-3）-β-D 葡聚糖光度法的特异性、敏感性、阳性及阴性预测率都高于传统真菌培养鉴定，差异无统计学意义。
结论 真菌（1-3）-β-D 葡聚糖光度法具备操作简便、快速等优点，阳性率、特异性敏感性、阳性及阴性预测率都高于传统真菌培养鉴定，连续监测更有助于提高艾滋病合并真菌感染诊断效率，可以用于早期诊断艾滋病合并真菌感染。

PU-2440

PDCA 循环在大规模人群新冠病毒核酸筛查中的应用

魏琦、都伟杰、李志强、毛源
合肥金域医学检验实验室有限公司

目的 应用 PDCA 循环提升实验室新型冠状病毒核酸检测能力，应对大规模人群新型冠状病毒核酸筛查。
方法 近期安徽六安新冠疫情期间，为应对检测需求和保证发单时间及质量，实验室应用 PDCA 循环的四个阶段，Plan(P)：制订计划；Do (D)：落实整改；Check (C)：监督评估；Action (A)：使流程标准化并优化排班制度，将常规检测流程优化为流水线作业方式。前处理组持续进行接收分发和排序，并及时调配其他岗位人员补充前处理组；检测组负责提取，为在确保质量前提下提升效率，组内确认主操作人员、试剂配置人员和辅助人员，大批量操作用 96 孔板代替八连管，使用排枪加样后封膜传给报告组上机；报告组负责扩增与结果解读，使用自行开发的“自动审核系统”辅助报告。
结果 经过 PDCA 循环后，实验室新冠核酸检测能力从 1 万/天，到 2.5 万，最终提升到 4 万/天。
结论 应用 PDCA 循环大大提升了检测能力，高效、有序的完成大筛查样本检测。

PU-2441

大规模人群新冠病毒核酸筛查检测质量现场考核结果分析

魏琦、都伟杰、李志强、毛源
合肥金域医学检验实验室有限公司

目的 为保证检测结果,了解各实验室检测能力以及检测试剂的质量状况，此次大规模筛查期间六安市临检中心对本实验室进行了 3 次技术考核。
方法 考核只针对样品检测，包括核酸提取、扩增体系、人员操作、室内质控等因素，即检验中的质量管理。分别收到 3 批考核品，每批各 5 支，包括阴性、弱阳性和阳性样本。本实验室严格按照《新型冠状病毒感染的肺炎实验室检测技术指南（第八版）》和《国家卫生健康委办公厅关于印发新型冠状病毒实验室生物安全指南（第二版）的通知》相关文件进行生物安全防护和实验操作，并严格按照试剂说明书进行 RNA 提取和扩增，记录 CT 值、上报结果。
结果 本实验室在规定时间内上报结果，临检中心反馈检测结果总符合率 100%，其中阳性样品符合率、阴性样品符合率均为 100%。三次考核，共涉及 2 个厂家试剂，各试剂检出率均为 100%。
结论 本实验室在六安市大规模人群新型冠状病毒核酸筛查中，检测能力和试剂质量均符合要求。

PU-2442

肺部细菌感染患者低分子肝素抗感染效果初探

杨悦林[1]、尹宁娜[2]、钱净[1]
1. 昆明市第一人民医院
2. 昆明学院医学检验技术系

目的 应用感染标志物对 LMWH 在肺部细菌感染患者抗感染治疗前后浓度水平的变化，探讨 LMWH 在抗感染机制方面的临床效果。
方法 1.收集 2020 年 1 月至 12 月肺部细菌感染患者资料，其中常规抗感染合并 LMWH 治疗（治疗方案 1）患者 100 例作为研究组、常规抗感染但未用 LMWH 治疗患者（治疗方案 2）100 例作为对照组，统计上述两组人群在治疗前后感染标志物（PCT、IL-6、CRP-U、WBC、MPV、D-D）结果

并行 t 检验；2.依据细菌涂片结果，将研究组和对照组进一步分组为 G+感染研究组和对照组与 G-感染究组和对照组，对不同分组中治疗前后感染标志物结果行 t 检验。
结果 1.研究组和对照组治疗前感染指标浓度水平比较无统计学差异（P>0.05），研究组和对照组治疗后 CRP-U 和 D-D 具有统计学差异（P<0.05），其余感染标志物无统计学差异（P>0.05）；2.研究组和对照组 G+感染者感染标志物治疗前后浓度水平变化除 D-D 外均无统计学差异（P>0.05）。3.研究组和对照组 G-感染者感染标志物治疗前后浓度水平变化除 D-D 外均无统计学差异（P>0.05）。
结论 本研究中 LMWH 在肺部细菌感染患者中的抗感染效果与预期不符，LMWH 在抗感染机制中的作用有待进一步研究。

PU-2443

临床检验危急值的统计分析及重要性

廖铭心
襄阳市第一人民医院

目的 了解 2021 年 1~5 月襄阳市第一人民医院西院区医院检验科危急值的报告率以及危急值在各个科室的分布情况，并根据统计分析结果合理制定危急值范围，做好临床沟通协调，提高全员医护人员对危急值的重视，及时尽力的挽救患者的生命。
方法 收集并对襄阳市第一人民医院西院区 2021 年 1~5 月期间报告的检验项目危急值及其在各科室的分布情况进行统计分析。
结果（1）统计襄阳市第一人民医院西院区 2021 年 1~5 月期间报告的检验项目危急值总数，2 月危急值报送总数明显低于其他月份，除 2 月的其余月份危急值总数变化无显著性差异。（2）2021 年 1 月危急值回复超时现象高于其余 4 个月，最高达到 7 例。（3）通过统计 2021 年 1~5 月期间报告的检验项目危急值发现，中班（12:00~14:30）期间以及夜班（17:00~次日 8:00）期间，临床科室危急值接收及回复超时情况严重，超时未回复案例明显高于正常上班时段。（4）统计 2021 年 1~5 月报告的检验项目危急值在各科室的分布情况发现，每月占据危急值报送量前四位的科室均为肿瘤科、ICU、呼吸内科和心内科。
结论 （1）各项目危急值报告率及其在各科室的分布情况均有差异，危急值报告率高的项目和科室尤其要引起重视。（2）2 月危急值报送量的减少，推测是由于春节原因，春节前大量病患出院准备过节，假期入院量也显著降低。（3）目前临床工作中贯彻落实危急值报告制度的情况不容乐观，新进低年资护理人员对临床检验危急值重要性的认知度仍需提高，医院管理者应组织医护人员共同学习,统一认识;护理管理部门应从多方面着手改善条件,以保证危急值报告制度的实施和改进。（4）定期对临床检验危急值进行分析评估、不断总结、持续改进,使检验危急值报告工作规范化、制度化,这样有助于挽救患者的生命,提高检验科的服务意识和临床医生的诊疗水平。

PU-2444

2019 年云南地区 HIV 感染者/AIDS 患者合并梅毒感染现状分析

徐丽萍、黄山、吕松琴、聂磊、李晓非
昆明市第三人民医院

目的 调查分析 2019 年云南地区 HIV 感染者/AIDS 患者合并梅毒感染现状，为云南省艾滋病防治提供一定数据基础。
方法 收集 2019 年 1 月-12 月昆明市第三人医院收治的 1052 例 HIV 感染者/AIDS 患者血清样本，进行梅毒抗体和 CD4+绝对计数实验室检测。

结果 1052 例 HIV 感染者/AIDS 患者中，梅毒感染率为 8.84％(93/1052)，感染患者中男性占比为 83.87%(78/93)远远高于女性 16.13%(15/93)，CD4+绝对计数小于 100 个/ml 占比 50.50%（47/93）远高于 100-500 个/ml 28.00%（26/93）和>500 个/ml21.51%（20/93），差异有统计学意义（P<0.001）。
结论 2019 年云南省 HIV 感染者/AIDS 患者合并感染梅毒占比不低，50%的合并感染患者 CD4+绝对计数大多数低于 100 个/ml。

PU-2445

红细胞与血小板参数在儿童骨髓增生异常综合征中的相关研究

贾茜、邵雪君
苏州大学附属儿童医院

目的 探讨儿童骨髓增生异常综合征患者外周血红细胞参数、血小板参数的水平变化及临床意义。
方法 采取回顾性研究方法，选取 2016 年 1 月至 2020 年 12 月收治的 60 例骨髓增生异常综合征(MDS)患儿的临床资料。同时选取同期于本院体检的健康对照 60 例。通过日本 Symex XN 全自动模式血液分析检测所有研究对象入院时红细胞参数、血小板参数，包括血红蛋白（Hb）、平均红细胞体积（MCV）、平均红细胞血红蛋白含量（MCH）、平均血红蛋白浓度（MCHC）、红细胞分布宽度（RDW）、血小板计数（PLT），血小板平均体积（MPV）、血小板分布宽度（PDW）、血小板比容（PCT）。利用非参数检验分析比较各组间检测指标的差异。
结果 60 例患儿男 40 例、女 20 例，平均年龄（7.53±0.42）岁。健康对照组男 31 例，女 19 例，平均年龄（5.57±0.12）岁。MDS 组与健康组红细胞参数水平比较，Hb（91.23±2.89g/L vs 125.6±0.79g/L）、MCV（95.44±0.98fl vs 81.59±0.35fl）和 RDW（15.21±0.31 vs 12.26±0.06）显著升高，差异有统计学意义（见表 1）。MDS 组与健康组红细胞参数水平比较，MCH（31.80±0.37pg vs 27.73±0.14 pg）、MCHC（333.6±1.50 g/L vs 339.1±0.99 g/L）有明显下降，差异有统计学意义（见表 1）。 MDS 组与 ITP 组血小板参数水平比较，PLT、PCT 低于健康组，MPV、PDW 高于健康组，差异均有统计学意义（P＜0.05）（见表 1）。
结论 常规检测项目血常规在 MDS 的诊断中发挥越来越重要作用，本研究提示联合血小板参数、红细胞参数对 MDS 诊断有一定指导意义。

PU-2446

乳腺癌和甲状腺癌合并患病率的 Meta 分析

鲜黎
成都市第三人民医院

目的 对乳腺癌和甲状腺癌合并患病率进行荟萃分析，为两者间进一步机制的研究提供线索，为临床的诊断治疗及随访提供依据。
研究方法 通过电子数据库（Pubmed, Embase,考克兰数据库（Cochrane Library）,中国知网(CNKI),万方数据库,维普数据库）全文检索了相关文献，用 R 3.5.2 软件和 STATA12.0 软件对检索的 70 余篇英文文献进行综合定量分析。
结果 乳腺癌合并甲状腺癌的患病率为 0.12%(95%CI：0.10-0.15)，在各研究因素中,绝经前（<50）与绝经后（≥50）（0.09% VS 0.04%）；放疗与未放疗（0.12% VS 0.17%）；2010-2019 年乳腺癌合并甲状腺癌的患病率为 0.27%，其次分别为 1990-1999 年（0.15%），2000-2009 年和 1971-1989 年（均为 0.08%）。甲状腺癌合并乳腺癌的患病率为 1.52%(95%CI：1.28-1.84)，在各研究因素中，女性与男性（1.90% VS 0.00%）；甲状腺癌病理分型中，乳头状癌、滤泡状癌、髓样癌及其它（1.85% VS 2.25% VS 1.65% VS 1.76%）；RAI 与未 RAI 治疗（1.37% VS 1.67%）；

131I 和未 131I 治疗（1.08% VS 2.59%）。在甲状腺癌合并乳腺癌的亚组分析中，未接受 131I 治疗尚不能认为与合并患病率有关，差异无统计学意义（P>0.1），余因素尚且认为与患病率有关，差异有统计学意义（P<0.1）。

结论 乳腺癌合并甲状腺癌的患病率为 0.12%，甲状腺癌合并乳腺癌患病率为 1.56%，且后者患病率远超过前者，这不能仅用基因来解释，还可能与激素、治疗方式、病理过程等因素有关。此外甲状腺滤泡状癌合并乳腺癌风险较其它甲状腺癌病理类型高。临床医生应该对有乳腺癌或甲状腺癌病史的患者提高警惕，尤其是绝经前女性。

PU-2447

143 例 HIV 感染待确定样本 快速检测替代策略试验结果分析

吕松琴、黄山、李光敏、许宝妹、黄岗、徐丽萍、张娟、李晓非
昆明市第三人民医院

目的 探讨 HIV 抗体确证试验快速检测替代策略的适用性及可行性。

方法 收集 2019 年 5 月 1 日至 2019 年 12 月 30 日昆明市第三人民医院检验科艾滋病确证实验室 143 例 HIV 感染待确定样本。采用快速检测替代策略（至少 2 种进口快速试剂和任意 2 种国产试剂）进行 HIV 抗体确证试验，满足 4 种快速检测试剂强阳性，报告“HIV-1 抗体阳性”；若出现其中 1 种快速检测试剂弱阳性或者阴性，用免疫印迹法(WB)进行抗体补充试验。同时检测 143 例样本血清 HIV 抗体 S/CO 值，抗凝血 CD4+T 淋巴细胞绝对计数及血浆 HIV 病毒载量。

结果 143 例 HIV 感染待确定样本中 107 例样本快速检测替代策略结果阳性（替代阳性组）；36 例出现 1 种或以上快速检测试剂弱阳性及阴性，其中的 30 例试验结果为 3 种快速检测试剂阳性 1 种弱阳性，占比高达 90.91%（30/33），用 WB 进行抗体补充试验，33 例结果阳性（WB 阳性组），3 例结果为不确定，快速检测替代策略不确定而 WB 阳性的 33 例选用的 4 种快速检测试剂阳性率麦美华（90.91）和硒标（87.88）远远高于 SD（57.58）和万孚（60.61），差异有统计学意义（ =9.587， =8.250，P<0.01）。替代阳性组与 WB 阳性组的 S/CO 值、HIV 病毒载量和 CD4+T 淋巴细胞绝对计数，差异均无统计学意义（Z=0.238，Z=0.403，Z=0.518，P<0.001）。

结论 我们的研究显示最终确诊的阳性样本中约有 1/5 在快速检测替代策略中检测结果不确定而二次采用 WB 试验才确诊，而这 1/5 的样本快速检测替代策略 3 种阳性 1 种弱阳性的不确定结果占比很高，主要由于不同的快速检测试剂敏感性之间差异大，造成这样二次试验，这种情况发生浪费了大量的人力、物力也极大的拖延了检测时长，我们建议采用快速检测替代策略时，在快速检测试剂的选择上应根据自身实践及文献研究综合选择一些敏感性、特异性及性价比更佳的试剂。

PU-2448

NLR、MPV 在终末期肾病患者冠状动脉疾病的程度预测价值的研究

张加勤、洪国斋
厦门大学附属第一医院

目的 目前关于这些传统血液学参数与终末期肾病患者冠状动脉粥样硬化的存在和严重程度之间关系的研究尚不多见。因此，在本研究旨在探讨 NLR、MPV 和 RDW 与 CKD 患者是否合并冠状动脉粥样硬化的存在及其严重程度的关系，并建立统计学模型，为临床上应用提供实验依据。

方法 本研究回顾性分析 249 例 CKD 患者，其中 157 例（63.1%）患者为女性，研究人群平均年龄为 53.4±12.1 岁，糖尿病 80 例(32.1%)，高血压 113 例(45。4%)，高脂血症 56 例(22,5%)，CAD 家族史 58 例(23.3%)，和 249 例健康对照者外周血血细胞计数、分类及部分生化指标。根据冠脉造影计算 Gensini 分数，计算方法为“严重程度评分×节段位置乘因子”，并按患者 Gensini 评分四分

位间距分为 Q1、Q2、Q3、Q4 组。应用 SPSS 22.0 软件包进行统计学分析，计量资料进行正态和方差齐性检验后，用`χ± s 表示，两组间比较采用 t 检验，三组间比较采用单因素方差分析（One-Way ANOVA），多组样本两两比较采用最小显著差（the least significant difference，LSD） t 检验，计数资料比较采用 χ2 检验，相关性分析采用单因素及多因素回归分析，P< 0.05 为差异有统计学意义。

结果 各组间钙磷乘积(CaxP)、CRP 水平、中性粒细胞、NLR、MPV 值差异有统计学意义（P<0.05）。Q4 组 CaxP 乘积值显著高于 Q1 组(P<0.05)。与 Q4 组相比，Q1 组 CRP 水平显著降低(P<0.05)。与 Q3 和 Q4 组相比，Q1 组的中性粒细胞水平也显著降低(P<0.05)。Q4 组 NLR 显著高于 Q1 组和 Q2 组(P<0.05)。Q1 组患者 MPV 最低，且 MPV 明显低于 Q4 组(P<0.05)。Gensini 评分与年龄、透析时间、NLR、和 c 反应蛋白 CRP 水平显著相关，与左心室射血分数负相关。多因素回归分析显示年龄、透析时间、NLR、MPV 是 CKD 患者冠心病程度相关的独立因素。

结论 NLR 和 MPV 与 CKD 患者 CAD 程度密切相关，可作为动脉粥样硬化的标志物，联合利用这些简单、常见的指标来评估 CKD 患者 CAD 患病风险，识别出长期预后较好的低风险人群及预后较差的高风险人群，并进行早期干预，可能使高危人群受益。由于实验对象数量有限，并且可能存在选择偏移，需要进行更大、更广泛的随机对照试验来阐明这些血液学参数对 ESRD 患者 CAD 程度的影响。

PU-2449

糖化白蛋白与糖尿病肾病血液透析患者预后关系的研究

张加勤、洪国斧
厦门大学附属第一医院

目的 定期检测患者血液中糖化血红蛋白的百分比(HbA1c)被认为监测糖尿病患者血糖控制的标准方法。有研究证实，HbA1c 不仅是平均时间葡萄糖的生物标志物，而与血液透析糖尿病患者的死亡率呈正相关。然而部分学者质疑 HbA1c 在预测血液透析糖尿病患者死亡率的价值。因为肾病和贫血之间存在关联，肾衰竭患者往往贫血，依赖促红细胞生成素治疗，导致红细胞寿命不可预测的变化；红细胞动力学的这些变化反过来又会导致不依赖于葡萄糖的糖化血红蛋白的比例变化。糖化血清白蛋白(GA)不受肾性贫血或促红细胞生成素治疗的影响，去除了平均血糖和糖化血红蛋白值与肾脏疾病的混杂效，因此可能会对肾脏疾病患者和其他影响红细胞寿命的疾病患者提供更准确的血糖控制评估，但关于 GA 与长期糖尿病肾病血液透析患者预后关系的研究尚不多见，为此，本研究在本研究旨在分析 GA 与长期糖尿病肾病血液透析患者死亡率之间关系，探讨 GA 作为长期糖尿病肾病血液透析患者预后指标的可行性。

方法 本研究共纳入 80 例行长期血液透析的糖尿病肾病患者，收集患者 GA、糖化血红蛋白和全因死亡率资料，根据患者 GA 基线四分位间距分组，应用 SPSS 22.0 软件包进行统计学分析，计量资料进行正态和方差齐性检验后，用`χ± s 表示，组间比较采用 t 检验，并用 Cox 比例风险模型分析长期血液透析的糖尿病肾病患者预后的危险因素。

结果 高基线 GA 患者(Q4)的 4 年死亡率比 Q1 组患者高 40.2% (HR 1.45；95% CI, 1.09 -1.89，P< 0.05)。第一年中对 GA 的重复测量也表明，Q4 组患者的 4 年死亡率较其他三组高，约为 38.3% (HR 1.32；95% CI，1.03-1.76，P< 0.05)。而运用 HbA1c 含量四分位间距进行分组比较各组之间的死亡率时，结果就不那么稳定了，HbA1c 含量 Q3 组患者死亡率明显 Q1(HR 1.37；95% CI，1.05-1.70，P< 0.05)，但在 Q2 或 Q4 风险没有显著增加。

结论 本研究结果证实 GA 作为血液透析糖尿病患者血糖控制的指标优于 HbA1c，是血液透析糖尿病患者预后的危险因素。对血液透析糖尿病患者定期监测并进行有效的血糖干预有利于降低患者心血管疾病和死亡的风险。

PU-2450

心包积液检出红斑狼疮细胞的病例报告

沙晓雯
西安医学院第一附属医院

患者，女，47 岁，因活动后胸闷 4 月余入我院心内科。之前，在当地医院查彩超有大量心包积液，住院予心包穿刺抽得淡红色血性液体 400ml，查脱落细胞、抗酸杆菌阴性，予以抗感染、抗结核治疗无效。即往史：否认高血压、糖尿病，无乙肝、结核的传染病史，无药物、食物过敏史。查体：心尖搏动位于第五肋间左锁骨中线外侧处，心前区无隆起，心界向两侧扩大，移动性浊音阳性，心率 90 次/分，律齐、心音弱，心尖区可闻及收缩期 1 级吹风样杂音，其他系统未见异常。影像学检查： 心脏彩超示心包上部略强回声团块，拌大量心包积液（心包穿刺前后共抽出血性心包液 1720ml），考虑恶性肿瘤心包转移；胸片见纵隔向两侧增宽、侧位见前纵隔内肿块影，结和病史特征可除外胸骨后甲状腺可能，因此高度怀疑“心包肿瘤或胸腺肿瘤”；胸部 MRI 提示心包恶性肿瘤、心包大量积液、左侧胸腔少量积液。实验室检查：血、尿、肝肾功能、结核抗体、电解质、肿瘤标志物等均未见明显异常。心包积液检验未见肿瘤细胞，查见 LE 细胞（但未报告给临床，因标本只申请找肿瘤细胞）。该患者疑诊为心包积液（肿瘤性）。先后请妇科、普外科、胸外科、放疗科、肿瘤科会诊，均未能明确诊断。经放疗科会诊后认为可行 1 疗程治疗，后因考虑家庭经济因素，患者及家属要求出院在门诊继续放疗治疗（以后病情不详）。此患者后经回顾病史和查阅大量相关文献，发现此病例可能存在误诊，其可能是 SLE 。

PU-2451

新冠病毒 COVID-19 疫情对我院住院未成年患者副流感病毒流行特征的影响

毕昊、石祖亮、吴春晨、夏剑波
湖北省妇幼保健院

目的 了解新冠病毒 COVID-19 疫情对我院 0-17 岁住院患者 3 种副流感病毒 (PIV1、PIV2、PIV3) 的流行特征的影响。
方法 收集 2018.1.1 至 2020.12.31 我院 0-17 岁住院患者中的 PIV1、PIV2、PIV3 的直接免疫荧光检测数据。以 2020.1.23 武汉宣布封城、2020.4.8 宣布解封作为时间节点，比较疫情前、中、后 PIV1、PIV2 、PIV3 的阳性率变化，并按年龄、性别、时间进行分组分析。
结果 在共 41169 的 0-17 岁住院患者中检出 PIV1 阳性 1155 位，阳性率为 2.81 %；PIV2 阳性 789 位，阳性率为 1.92% ；PIV3 阳性 907 位，阳性率为 4.62 %。2018 至 2020 年的 PIV1 阳性率分别为 2.6 % 、2.28 %、4.5 %； PIV2 阳性率分别为 1.84 %、2.42 %、0.94%； PIV3 阳性率为 4.74 %、 5.55 %、2.18%；如按月份分组发现 PIV1 与 PIV2 在封城后至 5 月处于 0 感染，6 月出现个小反弹峰，从 9 月至 11 月反弹出现大峰，11 月后开始下降； PIV3 在封城后一直到 8 月份处于 0 感染，从 9 月至 11 月反弹出现大峰，11 月后开始下降。按性别分组，各年份中的男女均未见明显差异。PIV1 在 2018 年与 2019 年阳性率，均为 0-2 岁>3-11y 岁>12-17 岁，但在 2020 年为 3-11y 岁>0-2 岁岁>12-17 岁；PIV2 与 PIV3 在各年份均为 0-2 岁>3-11y 岁>12-17 岁。
结论 COVID-19 疫情爆发后武汉采取的封城措施对 PIV 的流行特征产生了明显影响，除 PIV1 的感染率在 2020 年增高，其余 PIV 在 2020 年出现下降；在封城期 3 种 PIV 均为 0 感染率，但值得注意的是，3 种 PIV 在解除封城后均出现明显反弹，尤以 PIV1 反弹最为剧烈。这种流行特征的变化值得医护人员高度关注。

PU-2452

医疗机构内 POCT 血糖仪结果一致性评价体系的探讨

刘琴、张弢
复旦大学附属华山医院

目的 随着 POCT 在各个临床科室的广泛应用，相关质量问题随之凸显，尤其是医疗机构内部 POCT 检测结果一致性问题，目前尚无较好解决办法。如何保证 POCT 仪器检测结果在医院内部的可参考性，建立一致性评价体系并进行相关实践，从整体水平提高 POCT 检测质量至关重要。
方法 参考检验科多套检测系统比对的做法并结合 POCT 仪器的特点，保证一个医院内部同时使用的多台 POCT 仪器之间结果一致性，首先应建立医疗机构内 POCT 结果一致性评价体系。为确保医院内部不同实验室间 POCT 仪器之间（以使用率最高的血糖仪为代表）的一致性，华山医院采用包含经灭活、清洗和固定处理后红细胞组份的质控液，进行多地点多品牌血糖 POCT 监测系统一致性评价。在实际使用中根据评价需要，配置不同葡萄糖浓度和不同 HCT 浓度的质控液用于一致性评价和医院内仪器使用风险控制程序。
结果 目前可实现质控液有效期（10 天）内血细胞稳定（完整性>85%）、葡萄糖含量稳定（<2%衰减，减少使用时二次赋值）。配置正常 HCT 范围（如 42%）质控液，可同时适用于不同检测方法（脱氢酶法或氧化酶法）和有无 HCT 校正的 POCT 血糖监测一致性评价。在实际产品一致性比对应用中发现以往的一致性评价方法中的靶机出现偏倚值情况。
结论 以血糖仪为代表的使用分割样本或实验室自行配置的互通性较好的质控物进行医疗机构内结果的一致性评价，并根据不同项目规定相应的允许偏倚，可以得到满意结果。这样的经验可以推广至全国医疗机构应用，同时建议在 POCT 其他领域进行尝试。

PU-2453

探讨血小板数量增多对缺铁性贫血患者的临床意义

王娟
昆明医科大学第一附属医院

目的 探讨血小板增多对缺铁性贫血患者的临床意义。
方法 本研究收集了 128 例行骨髓细胞学检查明确诊断为缺铁性贫血患者的血常规、铁蛋白、及治疗后血常规等相关指标，以治疗前血小板 300X109/L 为界，把患者分为血小板增高组（n=70）和非增高组(n=58)，比较组间治疗前后血红蛋白及网织红细胞变化等指标；比较不同贫血程度间的血小板差异；比较血小板增高组和非增高组的红细胞、血小板相关参数；并做血小板或巨核细胞数量与其他相关指标间的相关分析。
结果 在所有贫血患者中，血小板增多的占 55%。血小板增高组的平均红细胞体积(MCV)和平均血红蛋白量(MCH)低于血小板非增高组(p＜0.05)，血小板增高组的血小板平均体积(MPV)、血小板分布宽度(PDW)、大血小板比例(P-LCR)和血小板压积(PCT)值高于血小板非增高组(p＜0.05)。血小板数量与 MCV、MCH 呈负相关(r=-0.296、-0.254，P 均＜0.05)，与 PCT、MPV、PDW、P-LCR 呈正相关(r=0.712、0.031、0.23、0.295，P 均＜0.05)，巨核细胞的数量与网织红细胞的数量呈正相关（r=0.176，P＜0.05）。
结论 缺铁性贫血患者中血小板越高的患者骨髓红系和巨核系增生反应越活跃，血小板增高是骨髓高反应的指标。

PU-2454

实验室危险性废物正确处理办法

李文瑛
西安金域医学检验所有限公司

近年来生态环保局逐渐重视对于实验室的环保监管力度，加大治理实验室废液污染环境的力度，根据多个地区及实验室交流经验，各级实验室对于实验室危险性废物的认知大部分停留在感染性弃物、损伤性废物、化学品废物等五大废弃物的阶段，对于逐年来不断被新认识的危险性废物及处置办法尚有不明确，故提出实验室危险性废物正确处理办法作为交流建议。

PU-2455

机会性致病真菌解脂耶氏酵母研究进展

郁谨菡
中国医学科学院北京协和医院

解脂耶氏酵母（Yarrowia lipolytica）是非常规酵母中最具代表性的一种二型性酵母，属于子囊菌门、半子囊菌纲、酵母亚门耶氏属。曾其无性状态分类为念珠菌属，命名为解脂念珠菌（Candida lipolytica）。目前认为酵母亚门芽生酵母（Budding Saccharomycotina yeasts）即为念珠菌属，广义来讲也可称之解脂念珠菌。该菌因具有独特的理化性质、代谢特点且被美国食品药品监督管理局（FDA）列为公认安全（generally regarded as safe，GRAS）微生物，在现代生物医学和生物技术领域有着广泛的应用前景，现已普遍应用于污染物或污水处理，生产生物脂质及柠檬酸。然而，其在自然环境中广泛存在，自然栖息地未知，常发现于海洋等高盐环境，也可从冷藏肉制品，乳制品，发酵食品，土壤和煤油污染环境中分离。研究表明，它属于人类正常菌群，可定殖于皮肤、呼吸道、消化道、阴道，糖尿病患者尤甚。中国医院侵袭性真菌监测网（CHIF-NET）对侵袭性念珠菌病的监测结果显示，2009 年 8 月 1 日至 2014 年 7 月 31 日，65 家三级医院 8829 株念珠菌中解脂耶氏酵母占比 0.4%，而法国 2002 年至 2014 年临床罕见念珠菌血症中占比 0.17%。近年来不断有散发病例和医院感染的报道，尤其是免疫缺陷或危重患者导管相关性化脓性血栓静脉炎和真菌血症。本文旨在强调作为工业明星菌种的解脂耶氏酵母是一种新兴罕见的机会性病原体，讨论其流行病学、致病性以及其体外抗真菌药物敏感性。

PU-2456

皮肤骨膜增厚症伴低钾血症 1 例

胡家伦
复旦大学附属华山医院

肥大性骨关节病是由于骨周围软组织增厚，广泛性骨膜新骨形成而导致的综合征，以杵状指和长骨骨膜增生为特征，分为原发性和继发性两类。原发性肥厚性骨关节病（PHO），又称厚皮骨膜增生症，占肥大性骨关节病的 5%，是一种累积骨骼皮肤的遗传性疾病。PHO 属于自限性疾病，一般治疗后预后较好，且多数患者于成年后进入无症状的稳定期。但是 PHO 易引发一系列如胃肠道疾病、贫血、低蛋白血症等并发症。现讨论 PHO 伴低钾血症 1 例。

PU-2457

健康妊娠妇女血清甲胎蛋白水平的变化及其参考区间的建立

项忠元、靳新桐
中南大学湘雅二医院

目的 检测健康妊娠妇女孕期血清甲胎蛋白水平，探讨其变化并建立不同孕期各自的参考区间。
方法 分别选取 2021 年 03 月至 2021 年 06 月期间在湘雅二医院进行产检的健康妊娠妇女早孕期 44 例，中孕期 49 例，晚孕期 50 例。并筛选 49 例育龄期健康非妊娠女性作为健康对照。采用 Roche Cobas E801 电化学发光仪检测其血清甲胎蛋白水平。对检测结果进行分析，比较健康非妊娠妇女及健康妊娠妇女各孕期之间甲胎蛋白水平的差异，并建立不同孕期血清甲胎蛋白相应的参考区间。
结果 比较健康非孕对照，早孕，中孕，晚孕各组血清甲胎蛋白水平，差异均有统计学意义（P<0.05）。本研究建立的早孕期妊娠妇女血清 AFP 水平参考区间为 1.71~54.26ng/ml，中孕期妊娠妇女血清 AFP 水平参考区间为 21.93~227.50ng/ml，晚孕期妊娠妇女血清 AFP 水平参考区间为 58.49~512.18ng/ml。
结论 妊娠妇女较健康非妊娠妇女血清甲胎蛋白水平显著升高，且大体上随着孕期增长而上升，本研究成功建立了健康妊娠妇女孕期血清甲胎蛋白的参考区间，为临床决策提供依据。

PU-2458

肿瘤睾丸相关抗原 LDH-C4 在鼻咽癌中的表达及其功能研究

罗晓莉、陈燕
福建省肿瘤医院

目的 研究乳酸脱氢酶 C4（LDH-C4）蛋白在鼻咽癌癌组织中的表达情况以及在临床诊疗过程中的价值。明确 LDHC 基因过表达在 CNE2 鼻咽癌细胞的生物学作用，并初步探讨相关分子机制。
方法 通过免疫组化染色方法检测高通量鼻咽癌组织芯片中 LDH-C4 蛋白的表达量，根据染色的结果进行评分，分析鼻咽癌患者的临床和病理分期、转移、复发及预后等临床病理特征和 LDH-C4 蛋白表达的高低的相关性。通过慢病毒载体将外源性 LDHC 基因导入 CNE2 鼻咽癌细胞，并采用稀释法结合绿荧光表达情况筛选出单克隆化且 LDH-C4 表达阳性的细胞系。通过 CCK-8 比色、平板克隆形成、划痕修复实验、Transwell 小室等实验，研究 LDH-C4 表达上调后，CNE2 鼻咽癌细胞在体外增殖能力、迁移和侵袭能力的改变；通过 Western blot 检测 AKT/mTOR 信号转导通路相关蛋白的表达改变。
结果 129 例高通量鼻咽癌组织标本结果显示：LDH-C4 主要表达于鼻咽癌细胞的细胞质中，阳性率为 88.4%（114/129）；Spearman 相关性分析结果表明，鼻咽癌的临床分期、颈部淋巴结转移均与 LDH-C4 的表达水平呈正相关（P＜0.05）；Kaplan-Meier 生存分析表明，LDH-C4 低水平患者预后明显优于高水平患者（P＜0.05）。CCK-8 比色实验、克隆形成、划痕实验、基质胶 Transwell 小室等一系列实验，证明 LDH-C4 过表达可增强 CNE2 鼻咽癌细胞的生长增殖、克隆形成以及侵袭和迁移能力；Western blot 结果证实，LDH-C4 在 CNE2 细胞中过表达可上调 AKT、mTOR 等蛋白的表达。
结论 LDH-C4 蛋白在鼻咽癌癌组织中的表达量明显增高，并与患者的临床分期、颈部淋巴结转移呈现正相关关系；LDH-C4 可作为鼻咽癌预后监测的一项重要指标，其高表达提示患者临床预后不良。上调 LDH-C4 可明显增强 CNE2 细胞体外增殖、侵袭及迁移能力，可能通过激活 AKT/mTOR 信号通路起作用。

PU-2459

乳腺癌合并甲状腺癌患者的临床病理特征分析

彭伟、陈燕
福建省肿瘤医院

目的 通过分析乳腺癌合并甲状腺癌的临床病理特征，探讨甲状腺癌、甲状腺激素功能及甲状腺相关抗原抗体在乳腺癌发生发展的作用。
方法 回顾性分析福建省肿瘤医院 2001 年 1 月-2017 年 12 月期间收治的乳腺癌合并甲状腺癌患者 76 例（合并癌组），并随机收集同期收治的单纯乳腺癌患者（对照组）116 例，同时收集患者治疗前甲状腺激素（T3、T4、FT3、FT4、TSH）、甲状腺自身抗原和抗体 (TG 、TPOAb、TGAb)、临床病理（TNM 分期、临床分期、淋巴转移、原发结节大小）和乳腺癌免疫组化指标（ER、PR、HER-2、Ki-67）等；通过 SPSS 25.0 软件统计分析合并癌组和对照组各临床病理和免疫组化指标，进一步探讨甲状腺癌在乳腺癌发生发展中的作用。
结果 合并癌组的淋巴受累率高于对照组（60.9% VS 37.7%），具有统计学差异（$p<0.05$）；甲状腺的功能状态：合并癌组与对照组 T3（1.74 VS 1.68）和 TSH（2.19 VS 10.27）具有统计学差异（$p<0.05$）；甲状腺相关抗原抗体：合并癌组与对照组 TPOAb（3.693 VS 12.3)和 TG（10.71 VS 2.77）的表达水平具有统计学差异（$p<0.05$）；其它病理特征：合并癌组与对照组在 ER、PR、HER-2、Ki-67 和 TNM 分期等免疫组化和病理特征上不具有统计学意义（$p>0.05$）。
结论 乳腺癌合并甲状腺癌组的淋巴受累率明显高于对照组（60.9% VS 37.7%）；同时发现乳腺癌合并甲状腺癌组 T3 和 TG 表达水平高于对照组，TSH 和 TPOAb 表达水平低于对照组，提示甲状腺癌在乳腺癌的发生发展中起作用，其机制可能与 T3 和 TG 的升高和 TSH 和 TPOAb 降低有关。

PU-2460

乳酸脱氢酶 C4 在乳腺癌中的表达及其对乳腺癌细胞生物学功能的影响

崔兆磊、陈燕
福建省肿瘤医院/福建医科大学附属肿瘤医院

目的 研究乳酸脱氢酶 C4（LDH-C4）在乳腺癌组织中的表达，探讨 LDH-C4 对乳腺癌预后判断的价值；探讨 LDH-C4 表达上调对 MCF-7 乳腺癌细胞中的生物学影响及分子机制。
方法 通过免疫组织化学分析 158 例乳腺癌石蜡组织中 LDH-C4 蛋白在的表达情况。分析乳腺癌不同临床病理参数与 LDH-C4 蛋白表达的相关性。对随访资料进行 Cox 回归模型，研究 LDH-C4 蛋白在乳腺癌预后判断的临床价值。通过慢病毒载体将外源 LDHC 基因导入 MCF-7 乳腺癌细胞中，通过稀释法结合绿荧光蛋白表达筛选 LDH-C4 阳性表达的单克隆细胞系。通过平板克隆、CCK-8 细胞增殖、细胞划痕、Transwell 小室等细胞生物学实验，研究 LDH-C4 表达上调对 MCF-7 细胞生物学行为的影响；Western blot 法检测 PI3K/AKT/mTOR 信号通路相关分子，探讨 LDHC 基因上调对乳腺癌 MCF-7 细胞生物学影响的可能机制。
结果 158 例乳腺癌石蜡组织切片免疫组化染色，LDH-C4 蛋白染色集中在细胞质中，呈淡棕色到深棕色，阳性率为 91.8%（145/158），其中低表达（-/+）和高表达（++/+++）分别为 41.8%（66/158）、58.2%（92/158）。经卡方检验，乳腺癌临床分期晚、腋窝淋巴结转移率高，患病年龄低者 LDH-C4 呈高表达（$P<0.05$）；Kaplan-Meier 法进行生存分析并经 Log-rank 检验结果显示，乳腺癌 LDH-C4 高表达者预后差（$P=0.035$）；Cox 回归分析显示临床分期（$P=0.000$）和 LDH-C4 表达水平（$P=0.002$）是乳腺癌预后的独立因素。2. 通过慢病毒感染成功筛选 LDH-C4 过表达的单克隆化的乳腺癌 MCF-7 细胞系；细胞学实验结果显示，LDH-C4 蛋白过表达可增强乳腺癌

MCF-7 侵袭和迁移能力，而对细胞生长增殖无显著影响；免疫印迹法初步显示，过表达 LDH-C4 蛋白可上调乳腺癌 MCF-7 细胞中 AKT 和 mTOR 蛋白的表达。
结论 LDH-C4 在乳腺癌组织中具有很高的表达阳性率，其表达与临床分期、腋窝淋巴结转移相关；高 LDH-C4 蛋白水平预示乳腺癌不良预后。过表达 LDH-C4 可增强 MCF-7 细胞增殖、侵袭和迁移能力，其机制可能与 AKT/mTOR 细胞信号通路的激活有关。

PU-2461

乳酸脱氢酶 C4 在乳腺癌中的表达及临床意义

崔兆磊、陈燕
福建省肿瘤医院/福建医科大学附属肿瘤医院

目的 检测 LDH-C4 在乳腺癌中的表达，明确其表达阳性率，分析 LDH-C4 表达与乳腺癌临床病理特征和预后的关系。
方法 基于高通量乳腺癌组织芯片 HBre-Duc140Su02，通过免疫组化技术检测 LDH-C4 蛋白在乳腺癌细胞中的表达水平。基于 HBreD145Su02 高通量组织芯片已建立的临床资料和随访数据库，分析 LDH-C4 表达与肿瘤组织分化程度、淋巴结转移、肿瘤大小、临床分期等临床病理特征的关系，应用 Kaplan–Meier 法绘制生存曲线，估计生存率，分析 LDH-C4 表达与乳腺癌预后的关系。采用 COX 比例风险模型进行多因素风险分析。
结果 LDH-C4 在乳腺癌细胞中的表达率为 91.5%，其阳性表达与患者年龄、肿瘤大小、临床分期、病理分级、淋巴结是否转移均无关（P 均>0.05），LDH-C4 阳性患者的十年生存率显著低于 LDH-C4 阴性表达患者（P<0.05）。
结论 LDH-C4 表达与乳腺癌预后相关，可作为乳腺癌预后判断的一项重要指标。

PU-2462

乳酸脱氢酶 C4 在骨肉瘤中的表达与生物学功能研究

叶倩、陈燕
福建肿瘤医院

目的 通过分析乳酸脱氢酶 C4（LDH-C4）在骨肉瘤（OS）组织中的表达情况，探讨其表达水平与骨肉瘤患者临床病理资料之间的相关性，明确 LDH-C4 表达上调后对骨肉瘤细胞 MG63 生物学行为能力的影响及相关分子机制。
方法 采用免疫组织化学染色方法对高通量骨肉瘤组织芯片进行检测，分析骨肉瘤组织中 LDH-C4 蛋白的表达水平与骨肉瘤患者临床病理特征的相关性。构建 LDHC 慢病毒过表达载体并感染骨肉瘤细胞 MG63，采用不同感染复数（MOI）和嘌呤霉素浓度筛选稳定感染的 MG63 细胞系。采用 RT-PCR 方法检测各组骨肉瘤细胞蛋白和 LDHC mRNA 表达情况。通过 CCK-8 实验、平板克隆形成实验、划痕修复实验以及 Transwell 细胞迁移、侵袭实验，检测上调 LDH-C4 后对骨肉瘤细胞 MG63 增殖和迁移侵袭等能力的影响。通过比色法检测乳酸和丙酮酸表达水平,葡萄糖氧化酶法检测葡萄糖消耗量。通过 Western blot，分析 LDH-C4 过表达对 AKT/mTOR 信号转导通路相关蛋白表达的影响。
结果 LDH-C4 蛋白主要表达于骨肉瘤细胞的细胞质中，软骨肉瘤表达在细胞核中，低表达/阴性表达占 54.29%（38/70），相关性分析结果显示，在骨肉瘤患者中临床分期和肿块直径与 LDH-C4 的表达水平呈负相关关系（P<0.05）。过表达 LDH-C4 在 CCK-8 实验、平板克隆实验、细胞划痕实验和 Transwell 小室迁移侵袭实验显示感染组 MG63 细胞的增殖能力、克隆能力、迁移能力和侵袭能力可被明显抑制。3.能量代谢实验结果显示感染组骨肉瘤细胞 MG63 葡萄糖摄取率降低，乳酸

生成减少，丙酮酸生成增多。Western blot 实验发现过表达 LDH-C4 后，下调了感染组 PI3K、AKT、mTOR 蛋白表达，HIF-1a 蛋白无明显变化。
结论 在骨肉瘤组织中 LDH-C4 为中低表达状态，并与骨肉瘤患者临床分期及瘤体直径相关。上调 LDH-C4 可明显降低 MG63 骨肉瘤细胞体外的生长增殖、克隆形成以及侵袭和迁移能力。LDHC 过表达抑制细胞正常氧化耗能，通过抑制糖酵解和负向调控 PI3K/AKT/mTOR 信号通路发挥其生物学功能。

PU-2463

乳酸脱氢酶 C4 在肝癌中的表达及其生物学功能研究

崔兆磊、陈燕
福建省肿瘤医院/福建医科大学附属肿瘤医院

目的 通过分析乳酸脱氢酶 C4(LDH-C4)在(HCC)中的表达及其与 HCC 患者的临床病理特征及其预后的关系,明确 LDH-C4 过表达对 HCC 细胞 Bel-7402 的细胞生物学行为能力的影响，并探讨相关分子机制。
方法 基于高通量肝癌组织芯片，采用免疫组化染色技术检测 HCC 癌组织中 LDH-C4 蛋白的表达水平，分析 LDH-C4 表达情况与肝癌患者临床病理特征的关系。荧光显微镜观察 GV492-LDHC 病毒感染后的 Bel-7402HCC 细胞中 EGFP 表达情况，筛选 LDH-C4 表达呈阳性的细胞系。通过 RT-qPCR 鉴定 LDH-C4 mRNA 过表达的效果。通过 CCK-8 实验、划痕修复实验及 Transwell 小室等实验分别检测 LDH-C4 对 HCC 细胞 Bel-7402 在体外的增殖、迁移及侵袭能力的影响。基于建立的 LDH-C4 稳定过表达的 Bel-7402 细胞系基础上，对各组细胞中乳酸、丙酮酸等细胞能量代谢产物含量进行检测，同时检测各组肿瘤细胞中葡萄糖消耗水平，探究 LDH-C4 过表达对 Bel-7402HCC 细胞能量代谢的影响；通过 Western blot 实验检测 AKT/mTOR 信号通路中相关蛋白表达水平受 LDH-C4 过表达的影响。
结果 HCC 中的 LDH-C4 呈现高表达状态，主要表达于 HCC 细胞的细胞质中，且 LDH-C4 的表达水平与 HCC 患者的 T 分期、临床分期及瘤体大小明显相关（$P<0.05$）；生存分析结果提示：LDH-C4 高表达患者的预后较低表达者更差（$P<0.05$）。CCK-8 实验、划痕修复实验及 Transwell 小室实验检测结果提示：LDH-C4 过表达可提升 Bel-7402HCC 细胞在体外的迁移侵袭能力，但对生长增殖无明显影响。3.能量代谢实验结果显示：Bel-7402 细胞中 LDH-C4 过表达可提高乳酸产生含量，降低丙酮酸含量，提高细胞对葡萄糖的利用；Western blot 结果提示：过表达 LDH-C4 可上调 AKT/mTOR 信号通路中 AKT 蛋白及 mTOR 蛋白的表达。
结论 HCC 组织中 LDH-C4 呈现较高表达状态，与 HCC 患者的肿瘤大小、T 分期以及临床分期呈现明显正相关；LDH-C4 可作为 HCC 患者预后监测的一项重要参考指标。Bel-7402HCC 细胞中 LDH-C4 过表达可促进该细胞在体外的迁移和侵袭能力,促进 Bel-7402HCC 细胞的能量代谢水平，可能与 AKT/mTOR 信号通路的激活有关。

PU-2464

乳酸脱氢酶 C4 在肺腺癌中的表达及意义

彭伟、陈燕
福建省肿瘤医院

目的 探讨 LDH-C4（lactate dehydrogenase C4）在肺腺癌中的表达及其与患者预后的关系。
方法 基于高通量肺腺癌组织芯片 HLugA180Su05，通过免疫组化技术检测 92 例肺腺癌患者癌组织及对应癌旁组织中 LDH-C4 蛋白的表达水平，分析 LDH-C4 蛋白在肺腺癌中的表达量及其与临床病理特征和预后的关系。

结果 LDH-C4 在癌组织中阳性表达率为 96.7%（89/92），明显高于癌旁组织 22.6%（19/84）（P<0.001），癌组织中 LDH-C4 阳性表达与患者年龄、性别、肿瘤大小、淋巴结转移、临床分期、表皮生长因子受体基因（EGFR）突变无关（均 P>0.05）。LDH-C4 高表达组患者中位生存时间（OS）为（35 个月），显著低于低表达组（62 个月）（P<0.05）；LDH-C4 高表达组患者 5 年生存率为（24.0%）显著低于低表达组（53.3%），进一步 COX 多因素回归分析显示 LDH-C4 高表达是肺腺癌患者总 OS 的独立因素，LDH-C4 高表达是低表达患者死亡风险的 3.619 倍。
结论 LDH-C4 在肺腺癌中的表达水平升高，LDH-C4 高表达肺腺患者的预后负相关，可成为肺腺患者潜在的治疗靶点。

PU-2465

HPV 病毒检测联合细胞学（TCT）对宫颈癌筛查的作用及价值

张雪娇
吉林金域检验医学检验所有限公司

目的 HPV 病毒检测联合细胞学（TCT）对宫颈癌筛查的重要性及价值
方法 选择 2018 年至 2020 年送检于我所在的检测中心检查的患者 300 例为研究对象，分别于 HPV 病毒检测、细胞学（TCT）检测及组织病理活检，将患者检测的 HPV 结果与细胞学（TCT）及组织活检结果进行对比分析，同时结合患者的临床资料进行分析。
结果 300 例患者中组织病理活检阳性患者 117 例，其中 HPV 阳性占 133 例，细胞学（TCT）阳性检出 119 例，两者联合检出阳性病例 106 例，阳性检出率为 90.56%。HPV 联合细胞学（TCT）检查的灵敏度最高。宫颈癌是第一个被明确病因的癌症，即 HPV 感染。尽管 HPV 感染普遍存在，宫颈癌确相对少见。几乎所有的宫颈癌患者都有 HPV 感染，但是通常大多数 HPV 感染并不引起任何疾病，多数人感染 HPV 却从不知道自己已经感染过，HPV 感染在女性可导致宫颈、外阴、阴道和肛门部位的癌变。HPV 感染是否一定并发宫颈细胞学异常，并不是，多数 HPV 感染并没有细胞学异常，大约 30%的 HPV 感染会产生相应的细胞病理学改变，通常非典型的变化，多数 HPV 感染在两年内消失。因超薄液基（TCT）可以保存患者被刷取下来的细胞学形态，且创伤小，经过细胞制片技术的处理，在显微镜下可以直观的观察到细胞的病变情况，再结合 HPV 的检测结果，如二者均为阳性，其组织活检结果多数为阳性。HPV 联合细胞学（TCT）不仅能检测癌细胞，更重要的意义在于能提前发现临床上毫不怀疑和毫无症状患者隐藏性的癌症。对针对早期防治及治疗宫颈癌有很大的帮助。所以二者联合筛查意义更大一些。
结论 HPV 病毒检测联合细胞学（TCT）对宫颈癌筛查具有重要价值及意义。

PU-2466

基于全外显子组测序探讨一例遗传代谢病患者的分子发病机制

马少杰
西安金域医学检验所

目的 对一个疑似遗传代谢病的新生儿进行基因突变检测，进行分子诊断，明确其发病机制。
方法 通过血串联质谱、尿有机酸分析等技术，1 新生儿高度怀疑遗传代谢病，于是采集先证者及其父母共 3 人的外周血，均进行全外显子组测序（whole exome sequencing，WES），对单核苷酸变异（（single nucleotide variation，SNV）及拷贝数变异（copy number variation，CNV）进行分析评估与致病性分类，对患儿进行辅助诊断。
结果 先证者存在可能致病的 CNV，定位于 chrXp11.4 区域发生约 30Kb 片段重复，其中涉及 OTC 基因 1-2 号外显子。而在其父母均未发现相同变异，推测其为新发变异，但也不能完全排除其母亲为嵌合体的可能性。同时对该结果进行半定量 PCR 验证，确认了该变异的存在。

结论 该遗传性代谢病的患儿存在可能致病性的拷贝数变异（CNV）,涉及 OTC 基因 1-2 号外显子的重复，且为新发突变。该结果能很好的解释患儿的症状及其发病机制。同时需要进一步思考的是，先证者不存在与表型相关的 SNVs，若选择做仅有高通量二代测序技术的遗传代谢病相关的 panel，因其没有覆盖到 CNVs，可能存在假阴性的结果。而 WES 虽然以前也常规聚焦于 SNVs，但随着生信分析的进步与优化，目前 WES 也可以对 CNV 进行相应的检测。所以 WES 覆盖面更广，能检出的变异类型更多，检出阳性率更高，在临床特别是新生儿期，怀疑遗传代谢病时，WES 能更好的助力于临床的早期诊断、早期干预和精准医疗。

PU-2467

Lactate Dehydrogenase C4 is associated with breast cancer prognosis and affects cancer cell proliferation and invasion

Zhaolei Cui 、Yan Chen
Fujian Cancer Hospital

Objective Human lactate dehydrogenase C4 (LDH-C4) is a known cancer/testis antigen (CTA). Nevertheless, its clinical effects and molecular role remains unclear in breast cancer (BC).
Methods Expression of LDH-C4 in BC tissue, paired adjacent normal tissue, and cell lines were quantified by qRT-PCR, western blotting and immunohistochemistry. Additionally, we assessed the clinical and prognostic significance of LDH-C4 in BC by Kaplan-Meier method. Cell proliferation, migration and invasion, and cell apoptosis were measured by means of a cell counting kit-8, clone forming, Transwell assay, and TUMMEL, respectively. Invio an
Results Expression levels of LDH-C4 were markedly upregualted in BC cells and tumor tissues but not expressed in normal BC tissue. Furthermore, survival showed that high LDH-C4 expression conferred reduced survival rates ($P < 0.05$). Functional analyses revealed that LDH-C4 overexpression and down-regulation attenuated cell proliferation, invasion, and migration as well as energy metabolism in BC cells. LDH-C4 could affect mTOR activity.
Conclusions Expression of LDH-C4 in BC may serve as a potential indicator for poor prognosis. LDH-C4 displays tumor suppressive behavior, warranting future investigations into its therapeutic potential in the treatment of BC.

PU-2468

ARA55 基因在 CNE2 鼻咽癌细胞中的功能研究

崔兆磊、陈燕
福建省肿瘤医院/福建医科大学附属肿瘤医院

目的 研究 ARA55 过表达对 CNE2 鼻咽癌细胞生物学特性的影响，明确 ARA55 在 TGFβ1 介导的 CNE2 细胞上皮间质转化及侵袭、迁移中的作用。
方法 构建 pCMV-ARA55-EGFP 真核表达载体，经 ZLip2000 转染至 CNE2 鼻咽癌细胞，荧光显微镜和免疫印迹检测 ARA55-EGFP 融合蛋白的表达；通过 CCK-8 比色、划痕修复实验、Transwell 小室、Annexin V-PE/7-AAD 双荧光染色、DNA 梯状电泳等实验，探讨 ARA55 过表达对 CNE2 鼻咽癌细胞生物学特性的影响。一定浓度的 TGFβ1 诱导 CNE2 细胞株中 ARA55 的表达，免疫印迹检测 ARA55 蛋白及 EMT 相关标志物 N-cadherin、Claudin-1 等的表达变化；采用 ARA55 的 siRNA 质粒，经 X-treme GENE siRNA 转染至 CNE2 细胞株；通过 CCK-8 比色、划痕修复、Transwell 侵袭迁移等实验，研究 TGFβ1 介导的 ARA55 表达上调及沉默以 ARA55 表达对 CNE2 鼻咽癌细胞 EMT 及侵袭迁移的影响。

结果 DNA 测序及双酶切分析显示 pCMV-ARA55-EGFP 重组载体构建成功。pCMV-ARA55-EGFP 组细胞生长增殖、侵袭迁移能力明显低于 pCMV-C-EGFP 空载体组和/或空白对照组（P＜0.05 或 0.01）；Annexin V-PE/7-AAD 双荧光染色及 DNA 梯状电泳结果可见，pCMV-ARA55-EGFP 组细胞产生凋亡，且凋亡率明显高于 pCMV-C-EGFP 空载体组（P＜0.05）；免疫印迹显示 pCMV-ARA55-EGFP 组细胞 Bcl-2 表达下调，Cytochrome C 表达上调，同时伴有 Caspase-9 和 Caspase-3 的激活。TGFβ1 诱导后，免疫印迹显示 ARA55 在 CNE2 细胞中的表达上调；ARA55 诱导组细胞发生间质样改变，N-cadherin 的表达上升，Claudin-1 表达下降，同时细胞的生长增殖及侵袭迁移能力明显高于对照组（P＜0.05 或 0.01）；诱导表达的 ARA55 通过 siRNA 下调后，siRNA-ARA55 组细胞生长增殖及侵袭迁移能力下降（P＜0.05 或 0.01）。
结论 成功构建 pCMV-ARA55-EGFP 重组载体； ARA55 过表达可抑制 CNE2 鼻咽癌细胞生长增殖，诱导凋亡；3. ARA55 参与了 TGFβ1 介导的 CNE2 细胞 EMT 及侵袭迁移过程。

PU-2469

Diagnostic potential for circular RNAs in gastric carcinoma: A meta-analysis

Yingfeng Lin、Zhaolei Cui、Yan Chen
Fujian Cancer Hospital

Background Circular RNAs (circRNAs) are potential, novel biomarkers for the early diagnosis of gastric carcinoma. Herein, a meta-analysis was conducted to assess the diagnostic potential for circRNAs in gastric carcinoma.
Methods Online databases were searched for eligible studies. Study quality was judged using the Quality Assessment for Studies of Diagnostic Accuracy (QUADAS) checklist-II tool. STATA 12.0 and Meta-Disc 1.4 software were used for statistical analysis.
Results Twelve studies consisting of 1278 patients and 1250 paired controls were considered for meta-analysis. The pooled sensitivity and specificity of circRNAs for gastric carcinoma was compared to normal controls and found to be 0.68 (95%CI: 0.66 - 0.71) and 0.70 (95%CI: 0.68 - 0.73), respectively. A corresponding area under the receiver operating characteristic curve of 0.78 was identified. Moreover, stratified analysis demonstrated an improved diagnostic value for circRNAs when tissue and plasma specimens were combined.
Conclusions This meta-analysis demonstrates that circRNAs are promising biomarkers for gastric carcinoma.

PU-2470

Diagnostic and prognostic value of the cancer-testis antigen LDH-C4 in breast cancer

Zhaolei Cui 、Yan Chen
Fujian Cancer Hospital

Objective Lactate dehydrogenase C4 (LDH-C4) is a cancer/testis antigen (CTA) that is expressed abnormally in certain malignant tumors. However, the expression and clinical significance of LDH-C4 in breast cancer (BC) have not been determined.
Methods Quantitative reverse transcription-polymerase chain reaction (RT-PCR) was adopted to investigate the expression of LDHC mRNA in the serum or serum-derived exosomes of patients with BC. The expression of LDH-C4 protein in BC tissues was also evaluated by using high-throughput tissue microarray analysis and immunohistochemistry.
Results The results showed that LDHC mRNA was highly expressed in the serum and serum-derived exosomes of BC patients. The area under the curve (AUC) of serum and exosome LDHC

in distinguishing BC from healthy individuals was estimiated to be 0.9587 and 0.9464, respectively. The LDHC level in the serum-derived exosomes of patients with BC was significantly associated with tumor size and positively correlated with the expression of HER2 and Ki-67 (all with P<0.05). Serum and exosome LDHC levels in BC patients were negatively correlated with medical treatment and positively correlated with recurrence. Survival analysis showed that LDH-C4 expression was negatively associated with BC prognosis.
Conclusion Serum and serum-derived exosome LDHC may be an effective indicator for diagnosis and therapeutic efficacy, as well as a predictor for the recurrence of BC. LDH-C4 may be a biomarker to determine the prognosis of BC.

PU-2471

从计量及结构角度浅谈次氯酸钠消毒剂对生物安全柜的损伤

李文瑛
西安金域医学检验所有限公司

新冠期间，大部分实验室使用次氯酸钠消毒剂对安全柜进行消毒，更甚部分实验室使用稀释盐酸对生物安全柜进行消毒试图消除核酸片段，根据设备管理经验，保证安全柜使用寿命，保护实验室安全，故从计量及结构角度浅谈次氯酸钠消毒剂对生物安全柜的损伤。

PU-2472

宫腔镜联合子宫内膜病理检查在子宫内膜病变中的诊断价值

姚晖
昆明市中医医院

目的 分析宫腔镜检查基础上联合子宫内膜病理检查诊断子宫内膜病变的价值。
方法 以 2018 年 1 月-10 约为研究时限，纳入 45 例疑似子宫内膜病变患者，先以宫腔镜检查，然后予以子宫内膜病理检查，并以手术证实结果为准，将宫腔镜检查结果与宫腔镜检查联合子宫内膜病理检查结果进行对照分析，探究在宫腔镜检查基础上联合子宫内膜病理检查的价值。
结果 经手术证实 45 例患者均有子宫内膜病变，其中 26 例为子宫内膜增生，11 例为子宫内膜息肉，8 例为子宫内膜癌。以手术证实结果为依据，宫腔镜联合病理检查的诊断符合率、灵敏度（100.00%、100.00%）明显高于宫腔镜检查（86.67%、86.67%），约登指数（2.22%）明显低于宫腔镜检查（13.33%），对比差异鲜明（P＜0.05）。
结论 宫腔镜联合子宫内膜病理检查诊断子宫内膜病变有助于提升诊断符合率、灵敏度，价值可靠。

PU-2473

SARI 蛋白在乳腺癌中的表达及其临床意义

林莺莺、崔兆磊、陈燕
福建省肿瘤医院

目的 探讨 SARI 蛋白在乳腺癌中的表达及其临床意义。
方法 采用免疫组化技术检测 SARI 蛋白在乳腺癌及其癌旁组织中的表达，探讨 SARI 蛋白表达水平与乳腺癌的临床病理特征及预后的关系。
结果 基于高通量的乳腺癌组织芯片免疫组化分析显示，在 87 例乳腺癌石蜡标本中，93.1%（81/87）的组织中 SARI 蛋白低呈现低表达或不表达，其中 80 例（98.8％）SARI 无表达，1 例（1.2%）SARI 蛋白低表达，6 例(6.9%)BATF2 高表达。SARI 蛋白在乳腺癌组织及旁组织表达差

异无相关性（P=0.950）。SARI 的表达水平与乳腺癌的临床病理分级密切相关（P=0.000），患者年龄是影响乳腺癌预后的独立因素（P=0.027）。
结论 SARI 蛋白在乳腺癌中存在低表达，可能发挥肿瘤抑癌因子的作用，其临床意义有待于进一步被证实。

PU-2474

SARI 过表达对 CNE2 鼻咽癌细胞生物学活性的影响及其机制研究

林莺莺、陈燕
福建省肿瘤医院

目的 构建 SARI 基因过表达真核表达载体并完成鉴定。研究 SARI 基因过表达对 CNE2 鼻咽癌细胞的生物学特性的影响并初步探讨相关分子机制。
方法 钓取并克隆 SARI 基因的全长 cDNA 序列，纯化后用 Bgl II 和 Xba I 进行双酶切消化，经 T4 DNA 连接酶作用，连接至 pDsRed2-C-RFP 真核表达载体，连接产物经转化、挑取克隆、扩增培养后，提取小量质粒，进行 DNA 测序鉴定，并用 Bgl II 和 Xba I 内切酶消化酶消化连接产物，琼脂糖凝胶电泳鉴定。重组质粒转染 SARI 阴性表达的 CNE2 细胞，荧光显微镜观察 SARI-RFP 融合蛋白的表达。Western blot 检测转染后 SARI-RFP 融合蛋白的表达。pDsRed2-SARI-RFP 真核表达载体转染至 CNE2 细胞，通过 CCK-8 比色绘制生长曲线、Transwell 小室侵袭实验、划痕修复实验、Caspase-3 活性检测、DNA 片段电泳检测等实验，探讨 SARI 过表达对 CNE2 鼻咽癌细胞生长增殖、凋亡等生物学特性的影响。Western blot 检测内源性线粒体凋亡途径相关蛋白的表达变化，探讨 SARI 过表达对 CNE2 细胞增殖、凋亡影响的分子机制。
结果 DNA 测序结果表明，SARI 全长 cDNA 序列已正确连接至 pDsRed2-C-RFP 载体。双酶切鉴定结果显示，pDsRed2-SARI-RFP 真核表达载体的构建成功。重组质粒转染至 CNE2 细胞后可表达 SARI-RFP 融合蛋白。CCK-8 比色、Transwell 小室侵袭、划痕修复实验结果显示 SARI 过表达组细胞生长增殖、侵袭迁移能力显著低于空载体对照组和空白对照组（P＜0.05）；Caspase-3 活性及 DNA 梯状电泳结果显示，SARI 过表达诱导 CNE2 细胞产生凋亡，明显高于空载体对照组和空白对照组（P＜0.05）。Western blot 检测显示 SARI 过表达组 CNE2 细胞较空载体对照组和空白对照组 Bcl-2 表达下调，Bax、Cytochrome C 表达上调，同时伴有凋亡途径相关蛋白 Caspase-3 和 Caspase-9 剪接激活以及 PARP 的表达上调。
结论 成功构建 pDsRed2-SARI-RFP 真核表达载体； SARI 过表达可明显抑制鼻咽癌 CNE2 细胞增殖和侵袭迁移能力，诱导细胞凋亡； SARI 可能通过激活线粒体内源性凋亡途径诱导 CNE2 鼻咽癌细胞凋亡，发挥抑癌作用。

PU-2475

妊娠期生殖道感染对妊娠结局影响的分析

项忠元、曹骆
中南大学湘雅二医院

目的 探究妊娠期妇女生殖道感染对妊娠结局的影响，并分析其影响因素。
方法 选取 2018 年 1 月至 2020 年 12 月中南大学湘雅二医院产科收治的 227 例无妊娠并发症生殖道感染产妇进行分析。根据是否接受了治疗，将生殖道感染产妇分为接受治疗组 85 例和未接受治疗组 142 例。另选取无妊娠合并症、无生殖道感染产妇 200 例。分析产妇的生殖道感染类型及构成比情况，比较生殖道感染组和无生殖道感染组、接受治疗组和未接受治疗组妊娠结局是否存在差异。

结果 本课题中生殖道感染种类及构成比：念珠菌属、支原体、大肠埃希菌、粪肠球菌、克雷伯氏菌属、无乳链球菌及其他病原微生物，构成比分别为 34.80%、27.75%、15.86%、7.93%、5.29%、4.41%和 3.96%。生殖道感染组发生不良妊娠结局的概率为 23.79%，无生殖道感染组为 7.00％，感染组显著高于无感染组，差异有统计学意义（P<0.05）。生殖道感染未接受治疗组发生不良妊娠结局的概率为 33.10%，显著高于发生率为 8.23%的接受治疗组，差异有统计学意义（P<0.05）。
结论 妊娠期生殖道感染以念珠菌和支原体较多见，妊娠期生殖道病原微生物感染会增加不良妊娠结局发生的风险，对此临床上应该努力做到积极防治、早发现、早治疗，以更好地保障母婴安全。

PU-2476

坏死性筋膜炎 16 例实验检查及临床分析

陈世东
厦门大学附属第一医院

目的 探讨实验室检查，包括血常规、生化检验、凝血四项、降钙素原（PCT）及 C 反应蛋白（CRP）等辅助坏死性筋膜炎(NF)临床诊断。
方法 回顾性分析作者单位 2018 年 1 月至 2020 年 12 月诊治的 16 例坏死性筋膜炎病患的临床资料，包括患病年龄、性别、坏死部位、住院时间、手术次数及实验室检查结果等，同时利用实验室指标危险预测系统对 16 例 NF 患者的危险等级进行评估。
结果 患者男女比例 4：1，多为中老年患者，其中 50-70 岁患者占 62.5%；研究显示发病患者男性比女性多，以中老年为主，50-70 岁患者占比 62.5%。62.5%发病部位位于肢体，37.5%位于肛周及会阴；平均住院时间 35.9 天，主要就诊科室为普外科，烧伤整形外科，重症医学科。伴有基础疾病占 75%，糖尿病占 58.3%；93.75%患者 C 反应蛋白升高，62.50%患者白细胞升高，100%患者低蛋白血症，50%患者血糖升高，约 70%患者出现贫血，约 10%患者电解质紊乱；实验室指标危险预测，75%患者低危，6.25%患者中危，18.75%患者高危；16 例患者中 9 例细菌鉴定及血培养结果为大肠埃希菌感染所致，6 例为混合细菌感染，1 例为溶血性链球菌感染。
结论 坏死性筋膜炎(NF) 进展迅速且容易误诊导致严重后果，患者性别、合并症、微生物等方面具有一定特征，C 反应蛋白升高，白细胞升高，低蛋白血症，血糖升高贫血，电解质紊乱等辅助 NF 的诊断。坏死性筋膜炎主要临床特征为多发生于老年人、糖尿病等有基础疾病的男性患者，主要生于肢体，大部分患者低蛋白血症，C 反应蛋白升高，白细胞升高，单一细菌感染多见，早期及时清创治疗效果良好。

PU-2477

Endogenous SARI induced cell apoptosis in nasopharyngeal carcinoma by targeting the intrinsic apoptotic pathway

Yingying Lin、Zhaolei Cui、Yan Chen
Fujian Cancer Hospital & Fujian Medical University Cancer Hospital

The SARI (suppressor of AP-1, regulated by IFN) gene, also named as BATF2, is associated with the risk of several kinds of cancers, and loss of SARI expression is frequently detected in aggressive and metastatic cancer. Nevertheless, the functional of SARI in nasopharyngeal carcinoma (NPC) remains exclusive. In this study, we discovered that knock-down of SARI expression suppressed cell growth and colony formation, inhibited invasion, promoted apoptosis, and induced G0/G1 and G2/M arrest in human CNE2 nasopharyngeal carcinoma cells. Of note, SARI restoration could trigger the mitochondrial pathway in CNE2 cells. Our data provide

evidence that SARI exerts a role as a tumor suppressor gene in leukemia, possibly by inhibiting proliferation and promoting apoptosis via the mitochondrial pathway.

PU-2478

自噬及其相关标志物在肿瘤中的研究进展

吴嘉慧、吴琼、罗惠丹、易斌
中南大学湘雅医院

自噬为一种生物机制，是细胞将不必要的或者损坏的蛋白质和细胞器等运送至溶酶体进行降解，以维持细胞的自我稳定。在肿瘤研究过程中，自噬被认为有促瘤和抑瘤的双重作用，大量的研究分析自噬功能在肿瘤的增殖、转移和耐药等过程中的作用。同时自噬相关标志物的应用也成为了肿瘤研究中的重点。如自噬相关蛋白微管相关蛋白 1 轻链 3（Microtubule-associated protein 1 light chain 3 ,LC3B）是自噬小体形成的自噬标志物，p62 (Sequestosome－1,SQSTM1)是选择性自噬底物，两者在肿瘤中常表达上调。除此两种标志物外，还有许多的自噬相关标志物如 Beclin-1、ATG5、LAMP 等在肿瘤细胞增殖、转移等活动中发挥了重要的作用。本综述主要就自噬相关标志物在肿瘤中的表达及应用进行讨论。

PU-2479

新型微流控芯片的设计与外泌体捕获效率的研究

陈雨晴、杜鲁涛
山东大学第二医院

目的 外泌体（Exosomes）是一种脂质膜包裹的纳米颗粒（30-150nm），携带和传递着重要的生物信号，与细胞通讯、免疫反应调节、肿瘤发生与转移等生物过程息息相关。传统提取方法过程易造成外泌体的流失。本研究旨在通过微流控提高外泌体捕获效率、克服样品试剂消耗量大等问题。
方法 将分析纯氯化钠放入球磨机，经研磨后加入 PDMS 混匀涂抹至对称型 PDMS 基片特定位置，制备微流控芯片，通过扫描电子显微镜进行表征。采用 NTA、酶标仪等检测外泌体的捕获效率。
结果 成功制备 PDMS 微流控芯片，扫描电镜显示芯片内通道具有密集的不规则立体结构。进行外泌体捕获效率实验，用 PKH67 试剂盒进行外泌体染色，将 CD9 抗体通入芯片后孵育 2 h，随后用 PBS 进行冲洗，再将染色后的外泌体通入芯片，用微量注射泵每隔 20 分钟取出口液体进行显微镜、酶标仪及 NTA 信号检测。结果显示，由荧光图像可观察到芯片表面富集了大量荧光标记的外泌体；计算进出口浓度差与初始浓度比值，芯片捕获效率可以维持在 80%左右。
结论 将微流控技术与免疫亲和法相结合，极大减少了制作成本和制作时间，并且可批量制备、更加小型化，适用于临床大规模分离富集外泌体。

PU-2480

血清淀粉样蛋白 A 与类风湿关节炎疾病活动度的关系研究

聂婷
宁夏医科大学总医院

类风湿关节炎（RA）是一种病因未明，以进行性、侵袭性关节炎为主要临床表现的慢性炎症性疾病，该疾病治疗目标主要是降低疾病活动度或者是缓解临床症状，因此，评估患者疾病活动度，对治疗、预后、疗效评估均具有十分重要的意义。血清淀粉样蛋白（SAA）是一种急性时相反应蛋

白，是一类多基因编码的多形态蛋白家族，SAA 与高密度脂蛋白具有较高亲和力，其与后者结合后发挥生物学作用。
目的 探讨血清淀粉样蛋白 A（SAA）与类风湿关节炎（RA）疾病活动度的关系以及临床意义。
方法 收集 31 例类风湿关节炎患者，16 例系统性红斑狼疮患者，10 例结缔组织疾病患者以及正常健康体检人群 30 例的临床相关信息和实验室检测数据。采用胶乳增强免疫比浊法测定血清中 SAA 的浓度，免疫散射比浊法测定血清中超敏 CRP 的浓度，魏氏法测定红细胞沉降率。
结果 31 例类风湿关节炎患者 SAA 水平均高于系统性红斑狼疮组、结缔组织疾病组及正常体检健康人群对照组，差异具有统计学意义。另血清 SAA 与超敏 CRP 和红细胞沉降率水平呈正相关关系。
结论 血清淀粉样蛋白 A 可用作评估类风湿关节炎活动度的有效参考指标。

PU-2481

偶发分枝杆菌感染引起脾肿大 1 例

丁耀东、蒋晓飞、胡越凯、张弢
复旦大学附属华山医院

非结核分枝杆菌（noutuberculous mycobacterium,NTM）在土壤、水、尘土等自然环境中广泛存在，可导致肺部、淋巴结炎、皮肤和软组织等感染[1]。偶发分枝杆菌属于非结核分枝杆菌分类中的 IV 组，即快速生长分枝杆菌，接种在培养基上 3~5 天内有肉眼可见的菌落，多数在 1 周内即生长旺盛[2]。在一般情况下，此类细菌可从尘埃、土壤、水或正常人的唾液、痰中分离出来，其致病力弱，为条件致病菌，只有当局部或全身抵抗力降低时，存在于机体内外的分枝杆菌才可繁殖致病[3,4]。下面我们以探讨偶发分枝杆菌感染引起脾肿大的临床病例 1 例，来加强该类疾病认识和及时为临床提供信息以助于临床及时诊断和治疗。

PU-2482

血红蛋白、胆红素、乳糜、羟苯磺酸钙对三种干湿生化检测系统的影响研究

欧元祝、龚敬凯、虞啸炫
上海市临床检验中心

目的 本研究系统的比较和评价了内源性干扰物质血红蛋白、胆红素、乳糜微粒及外源性干扰物质羟苯磺酸钙在三个干湿生化分析系统对临床化学项目检测的干扰影响。
方法 根据 EP7-A2 指南建议采用高、低两个浓度水平的血清或血浆基础样本，与干扰物质配制成不同浓度梯度的血红蛋白、胆红素 F、乳糜及羟苯磺酸钙干扰样本，模拟轻、中、重度干扰。分别在奥森多 Vitros 5600 检测系统、罗氏 c501 检测系统及日立-迈克系统进行分析，计算与基础对照样本检测结果的相对偏倚（%）或绝对偏倚值（umol/L）。
结果 在血红蛋白的干扰试验中，在 Ortho/Vitros 5600 检测系统 13 个分析项目中 5 个项目受到明显干扰影响，在罗氏 c501 检测系统 13 个分析项目中 6 个项目受到了干扰，在 Maker-Hitachi 分析系统 11 个项目中 6 个项目受到明显干扰。在胆红素的干扰试验中，11 个分析项目中罗氏 c501 检测系统有 4 个项目受到了胆红素的干扰影响，在 Ortho/Vitros 检测系统仅一个项目受到干扰影响，在迈克-日立检测系统 9 个分析项目有 1 个项目受到干扰影响。在乳糜的干扰试验中，12 个分析项目中罗氏 c501 检测系统 3 个项目受到了乳糜的干扰影响，在 Ortho/Vitros5600 检测系统仅 1 个受到干扰影响，在迈克-日立检测系统 10 个项目中 2 个项目受到干扰影响。羟苯磺酸钙在三个检测系统对 CREA 项目均有明显干扰影响，但 Ortho/Vitros 5600 检测系统的干扰影响要小于其他两个系统。
结论 在常规化学分析项目的检测中，干化学检测系统整体抗干扰能力强于两个湿化学检测系统。

PU-2483

我院近三年检出细菌的临床分布及耐药性分析

丁耀东
复旦大学附属华山医院

目的 了解我院检出细菌的分布特点及对临床常用抗菌药物耐药率的差异及变化，为临床合理用药、院内感染控制提供依据。
方法 收集我院 2018—2020 年临床分离的 17957 株细菌，对其标本来源分布和耐药性进行分析。
结果 我院这 3 年共分离出细菌 17957 株，标本类型主要来源于呼吸道分泌物（41.7%）和尿液（28.5%）；全院及其中住院病人分离菌株中排名前五细菌分别为肺炎克雷伯杆菌、大肠埃希菌、铜绿假单胞菌、鲍曼不动杆菌、金黄色葡糖球菌，门诊病人大肠为首，屎肠球菌排名第三；葡萄球菌属对抗菌药物的耐药率分析中耐碳青霉希类葡糖球菌对大环内酯、氨基糖苷类抗生素耐药率较高，红霉素近两年有下降趋势，左氧氟沙星耐药性在升高，非耐碳青霉希类葡糖球菌，除青霉素 G、红霉素外几乎对其他药物均敏感；屎肠球菌左氧氟沙星和氨苄西林耐药率极高，呋喃妥因和高浓度庆大霉素中等程度耐药；粪肠球菌左氧氟沙星和高浓度庆大霉素中等程度耐药，余抗菌药物均较敏感；大肠埃希菌对一二代头孢菌素、喹诺酮类药物耐药率较高，三代头孢及庆大霉素次之，耐碳青霉烯类大肠埃希菌近三年有上升趋势；肺炎克雷伯杆菌对头孢类、喹诺酮类、磺胺类和呋喃妥因药物耐药率为 50%偏上，并近一半耐碳青霉烯酶，且近三年微呈上升趋势，对阿米卡星也有 30%以上的耐药性；嗜麦芽窄食单胞菌对头孢他啶、哌拉西林/他唑巴坦耐药率极高，其中对头孢他啶耐药率呈上升趋势，洋葱伯克霍尔德菌对头孢他啶、哌拉西林/他唑巴坦、美罗培南、左氧氟沙星及复方新诺明药物敏感性较强，耐药细菌少见。
结论 加强耐药监测，微生物室严格按 CLSI 药敏分级报告，依据药敏结果合理使用抗菌药物，做好消毒隔离工作，预防和减少院内肺炎克雷伯菌、鲍曼不动杆菌等多重耐药细菌的产生和传播。

PU-2484

多发性骨髓瘤患者 IgA 检测假性降低 1 例

刘琴
复旦大学附属华山医院

多发性骨髓瘤（MM）是源于浆细胞的恶性克隆性疾病，可浸润骨髓、骨质和髓外组织产生溶骨病变，并可合成和分泌大量单克隆免疫球蛋白或其轻链，常见的症状包括骨髓瘤相关器官功能损伤的表现，即“CRAB”症状（血钙增高，肾功能损害，贫血，骨病），以及淀粉样变性等靶器官损害等相关表现。骨骼疼痛、骨折、反复感染、贫血、肾功能异常等临床表现。多发性骨髓瘤的诊断与监测相关检查主要有免疫球蛋白定量、血或尿轻链定量、血和(或)尿免疫固定电泳、骨髓穿刺涂片、扁骨摄片等。其中免疫球蛋白定量检测操作简单、能直接反应疾病的情况。在多发性骨髓瘤诊断与监测中应用最为广泛，但在检测中发现有多发性骨髓瘤的病例 IgA 结果重复性差，多次检测结果波动大，与病情不符，对其原因进行研究分析。

PU-2485

急性暴发性蜡样芽孢杆菌败血症死亡 1 例

刘琴
复旦大学附属华山医院

蜡样芽孢杆菌是革兰阳性杆菌，其分布广泛，常见于土壤、灰尘和污水中，在植物性食品和许多生熟食品中也常见。是引起食物中毒的一种病原体。进食含有蜡样芽孢杆菌或其产生的肠毒素可导致急性胃肠不适症状，主要表现为恶心、呕吐、腹痛、腹泻等。症状一般较轻，常为自限性疾病。以前有研究报道蜡样芽孢杆菌在婴儿、静脉注射吸毒者、恶性肿瘤患者和免疫缺陷患者是重要致病因子，引起暴发性败血症。我们在此描述一名患有急性白血病的患者突然死亡，死亡原因分析为蜡样芽孢杆菌暴发性败血症引起的脑出血。

PU-2486

肝炎相关再生障碍性贫血（HAAA）1 例

刘琴
复旦大学附属华山医院

肝炎相关再生障碍性贫血(Hepatitis associated aplastic anaemia，HAAA)由 Lorenz 和 Quaiser 于 1955 年首次报道[1]，多为发生于非甲非乙非丙型肝炎后 6 个月内的再生障碍性贫血(AA)。通常 HAAA 好发于急性肝炎恢复期，与肝炎严重程度无显著相关。肝炎可为急性、甚至爆发性，亦可为慢性或自限性。其临床特征和 T 细胞免疫系统的严重失衡以及对免疫抑制剂的良好反应都提示 HAAA 由免疫机制介导。另外，端粒酶的变异和遗传易感性也是 HAAA 发生的原因。该病多发于青少年男性，较之特发性 AA(IAA)，HAAA 通常病程更短、疾病进展更快、伴发严重感染及出血更为多见。预后较差，早期感染死亡率高，行异基因造血干细胞移植(allo-HSCT)和／或免疫抑制治疗(IST)前，其平均存活期仅为 2-5 个月。

PU-2487

POCT 便携式血糖仪质量管理及效果评价

安婧、颜鸣、汪佳婕、尹利民、潘永圣
昆明市第一人民医院甘美医院

目的 构建即时检验 POCT 便携式血糖仪质量管理规范，运行及评价全面质量管理的应用。
方法 针对 POCT 便携式血糖仪建立一个明确的组织构架，为落实质量管理掌握仪器与试剂管理、人员管理、质量管理和信息化管理四个方面的现状，针对现状在规章制度的要求下结合实际情况推进改善质量管理模式。
结果 POCT 医护人员培训考核人次从 304 人次普及到 854 人次，合格率从 80.59%改善至 96.72%，持证上岗达到 100%；生化比对参与率 100%,初次比对不合格率从 33.3%下降至 1.67%。
结论 持续探索合适的管理模式，落实全面质量控制提升了医务人员专业能力，保障了 POCT 便携式血氧仪检测结果的精密度和准确性，更高效的服务于患者。

PU-2488

影响羊水细胞培养成功率的原因分析及改良方法

朱瑞琪
襄阳市第一人民医院

目的 分析影响羊水细胞培养成功率的相关因素并建立一种能稳定提高羊水细胞培养成功率的制备方法。
方法 收集 2018 年 1 月—2021 年 3 月于我院就诊的具有产前诊断指征的孕妇羊水病例，对孕妇年龄、孕周、外周血中性粒细胞计数与羊水培养成功率进行 logistic 回归分析，对异常标本进行新旧方法平行处理，比较两种方法核分裂相，评估妊娠结局。
结果 孕妇年龄是羊水培养相关因素，在培养 342 例羊水中，不合格标本 13 例，成功收获 339 例，成功率 99.1%，新方法对不合格标本处理后可分析核分裂相数远较传统方法差异有统计学意义（P＜0.05）。
结论 正确处理不同状态的羊水标本，及时调整和控制影响羊水细胞生长的各个环节，准确判断收获时机，建立适合本实验室的规范操作、有序培养，可提高羊水细胞培养的成功率。

PU-2489

健康骨髓供者骨髓细胞分类计数调查及应用

武焕玲[1]、张冠军[1,2]、李远[1]、张健[1]、张树霞[3]、张之芬[1]
1. 山东第一医科大学附属省立医院
2. 山东省东明县人民医院
3. 章丘市人民医院

目的 调查健康骨髓供者骨髓细胞分类计数的范围，探讨此骨髓细胞分类计数的方法和结果用于骨髓细胞分类正常参考范围确定的价值。
方法 选取我院 82 名健康成人造血干细胞供者作为研究对象，对其骨髓细胞进行分类计数并作统计学分析，探讨其计数范围与目前使用的骨髓细胞分类计数的参考范围的不同。
结果 本研究中骨髓细胞分类计数结果用 ±1.96SD 表示，原粒细胞、早幼粒细胞、中性中幼粒细胞、中性晚幼粒细胞、中性杆状核粒细胞、中性分叶核粒细胞、原红细胞、早幼红细胞、中幼红细胞、晚幼红细胞、淋巴细胞、单核细胞、巨核细胞的计数范围分别是 0.32±0.39、1.20±0.87、9.90±3.93、9.67±3.23、14.98±4.68、16.03±6.86、0.29±0.22、1.25±1.09、10.71±4.73、11.65±4.87、19.48±6.53、2.07±1.91、68±19，与目前我们国内和部分医疗机构使用的骨髓细胞分类参考范围结果有一定差异。
结论 标准化的健康骨髓供者骨髓细胞分类计数的方法，可以运用到骨髓细胞分类计数的正常参考范围确定过程中; 由于健康骨髓供者群体的年龄、性别和移植位点选择的局限性，此群体的分类结果可以作为骨髓细胞分类的正常参考范围的调查应用，多中心合作、加大样本量是否能够代表健康成人骨髓细胞分类的正常参考范围还需进一步验证。

PU-2490

突发新冠疫情下移动方舱实验室的快速部署和应用探索

栾艺、丁睿、古文深、邓雅文、张小凡、房绮梅、段朝晖*
中山大学孙逸仙纪念医院 检验科

在此番广佛乃至广东地区新冠肺炎疫情反扑的特殊时期下，各级政府与医疗机构迅速响应，快速部署，从“控制感染源，切断传播途径，追踪易感人群”入手，重点区域重点人群实时追踪，部分区域全员开展核酸检测，贯彻落实“应检尽检”、“愿检尽检”原则，全面拉开防疫战线。

目的 面对数几千万人口的大规模新冠病毒核酸筛查工作，各级医疗机构和三方实验室的核酸检测能力扩容问题凸显，结合我院工作实际，总结移动方舱实验室快速部署的经验与不足，进一步探索其应用规范，推而广之，以期更好地应对各类突发性事件中紧急医疗卫生工作。

方法 结合我院在佛山岭南明珠体院馆快速部署方舱实验室的工作实例，从选址、周围环境布局、物资准备、人员及组织架构、实验室运行管理、生物安全、心理疏导等各方面总结经验及不足，汇总分析。

结果 方舱实验室具有建设周期短，搭建灵活，移动作业等独特优势，在做好人员安全、环境安全、检测安全的基础上，能够遵照国务院印发的《医疗机构新型冠状病毒核酸检测工作手册（试行 第二版）》要求完成检测。

结论 部署移动方舱是新冠肺炎核酸检测能力迅速扩容的重要途径，在大规模新冠病毒核酸筛查工作中使用方舱实验室可以实现 “就地采样、就地检测”，极大地提高核酸检测效率。

PU-2491

凝血流水线助力止凝血检测工作及使用经验分享

安倍莹、翟宏
吉林大学第一医院

目的及方法 本实验室全自动凝血流水线系统由西门子 Aptio 流水线系统、离心机、纯水供应系统和 Sysmex CS-5100 全自动凝血分析仪“一拖五”模式组成，软件系统包括 ADM（Atellica Data Manager）、DMS（Data Manager System)及 vVC 流水线数据管理软件、实验室信息系统（LIS）和 Sysmex Laboman 软件系统。根据本实验室样本量较大等实际工作情况，不断优化流水线设置、改进和增加 LIS 功能，使得该流水线在保证原有基础功能外，设定符合本实验室标本特点的异常标本区、增加 TAT 监控、设定自动审核功能等功能，节约了人力，提高了工作效率和检测质量，明显缩短了 TAT，为今后实现智能化实验室奠定坚实的基础。

结果（1）LIS 界面功能按钮的增加：本实验室将 Aptio 中的一些功能，如“delivery”安装到 LIS 界面中，在 LIS 界面中实现调标本功能，同时在 LIS 界面中设定对话框来锁定该标本归档位置等功能，避免操作老师在多个操作系统中切换。

（2）凝血复检规则的建立：在流水线软件中设定本实验室凝血常规复检规则，触犯规则的标本一部分可通过流水线实现自动复测功能，而另有一些标本则通过流水线将其归档在特殊区域，以方便检验人员的快速锁定标本进行后续的复检。

（3）自动审核规则的建立：本实验室通过在 LIS 系统及 laboman 软件中分别设定自动审核规则，大大缩短了 TAT 时间，实现流水线自动化及智能化。

（4）TAT 时间监控：在 LIS 软件中通过颜色提示对急诊和普诊标本 TAT 进行监控及优化程序。

结论 通过一年多凝血流水线的使用，不断探索及优化流水线设置、开发 LIS 功能、设定自动审核规则及复检规则，从而保证了本实验室每日检测在 1800-2000 人份，并且大部分都是急诊标本（门急诊凝血常规占 86.31%）的高强度工作量下，凝血常规 TAT 中位数平均在 25.6min，而在未安装流水线时 TAT 中位数平均在 50min，大大地缩短了门急诊 TAT 时间，同时保证了报告审核的质量。全自动凝血流水线的使用极大地加速了智能化血栓与止血实验室建设的进程。

PU-2492

血液学指标在福建地区β地中海贫血筛查中的价值

谢屿平
福建医科大学附属协和医院

目的 通过分析福建省各个地区之间 β-地中海贫血主要存在的基因突变的类型与构成比，再比较其对应的常规血液学指标，从而探讨出血常规指标之中的两项平均红细胞指数血红蛋白量（MCH）、平均红细胞体积（MCV），两项红细胞参数红细胞计数（RBC）、血红蛋白量（Hb）对该特定地区筛查β地中海贫血的价值。
方法 检测 β 地中海贫血使用聚合酶链式扩增法，并使用反向点杂交的方法检测其基因点突变位点（PCR-RDB），对 β 地贫相关的基因类型做进一步的具体分型确定，并分析确诊的 β 地贫患者相应的血常规指标，利用 ROC 曲线获得本地区可供临床筛查β地贫的最佳截断值。
结果 本次实验共收集β地中海贫血患者 629 例，共发现 14 种不同的突变基因类型（复合型基因突变未计），其中以 283 例 IVS 型点突变最多见（44.9%）。与健康对照组相比较，同性别不同分型的 β 地贫血液学指标中 MCV 和 MCH 的均值都具有极显著的统计学意义；与此同时患者组和对照组的 Hb 之间的均值存在的差异也具有良好的统计学意义，但因男女性别的不同，所获得的截断值差异较大。根据本次研究结果，当选取 MCV<81.2 fl、MCH<27.2pg、Hb $_{男性}$<132.5 g/L， Hb $_{女性}$<116.5 g/L 时诊断疾病具有较高的敏感性与特异性，故可用作本地区临床筛查β地中海贫血。
结论 由于各个区域流行病学存在的差异性以及各个医院的检测设备和检测环境在客观条件上的区别，不同地区临床实验室应建立适宜本地的 β 地中海贫血初筛截断值。今后本次研究所处实验室可以选择 MCV<81.2fl、MCH<27.2pg、Hb $_{男性}$<132.5g/L、Hb $_{女性}$<116.5g/L 作为临床上筛查福建地区β地中海贫血的初筛截断值。

PU-2493

四例新冠核酸检测乌龙事件回顾性分析

陈相
南通市第一人民医院

目的 通过回顾南通市四例新冠核酸假阳性事件，找出导致假阳性的原因，规范核酸阳性上报流程，杜绝此事件的再次发生。
方法 收集南通市四例新冠核酸假阳性资料，包括患者就医原因，流行病学史，实验室核酸检测的仪器、试剂、耗材、方法学等；新冠核酸检测流程以及复检流程，当出现新冠核酸检测阳性时上报流程等。
结果 4 家单位新冠核酸初检阳性，复检结果未出来之前上报单位领导，单位领导感觉责任重大，随即上报了市疫情防控指挥部，指挥部随即启动了应急机制，之后复检结果都为阴性。四起乌龙事件引起市领导的高度重视，去年 7 月至今年 5 月连续发生了四起，都是因为复检结果没出来就上报假阳性结果，这不但扰乱了医院正常就诊次序，增加了就诊患者的心理负担，还给社会带来一些负面影响，医院的公信度在哪里？医院检测结果的准确性让人担忧。调查发现，2 家单位上报初检结果之前未对患者做流行病学调查，2 家单位做了流行病学调查，都是门诊患者，1 个从河北返通，没有任何不适，自愿检测，另一患者有两次出省轨迹，有低热等症状。4 家单位的仪器设备，检测试剂和耗材都符合要求，其中有 1 家只有初检试剂没有复检试剂；4 家都未定期对核酸提取仪磁棒用酒精进行消毒，未进行环评检测，未做弱阳性室内质控。
结论 4 家单位都存在核酸检测流程问题，操作欠规范，未遵守复检规则，未定期对提取仪、扩增仪进行消毒，工作责任心不够，领导胆小怕事，这些综合因素导致了新冠核酸检测乌龙事件的发生。

PU-2494

肌钙蛋白 I 与氨基末端 B 型钠尿肽前体联合检测在急性心肌梗死诊断中的临床价值

李岚岚、叶涛、侯小洪
重庆市人民医院

目的 探讨血清肌钙蛋白 I(cTNI)与氨基末端 B 型钠尿肽前体（NT-proBNP）联合检测在急性心肌梗死诊断中的临床价值。
方法 选取 2018 年 5 月至 2019 年 11 月收治的 62 例急性心肌梗死确诊患者作为试验组，另选取同期 69 例非急性心肌梗死患者作为对照组，分别使用化学发光法和免疫荧光法检测两组受试者血清中的 cTNI 与 NT-proBNP 水平，并进行比较。
结果 试验组 cTNI 和 NT-proBNP 水平显著高于对照组，且差异有统计学意义（P<0.05）；cTNI 和 NT-proBNP 联合检测的诊断敏感性为 90.32%，特异度为 93.47%， ROC 曲线下面积（AUC）为 0.84，均高于各个指标单项检测（P<0.05）。
结论 肌钙蛋白 I 与氨基末端 B 型钠尿肽前体联合检测用于急性心肌梗死的诊断有更好的诊断性能，敏感度和特异度都较检测单项指标更为理想。

PU-2495

一例 8q24.13q24.23 微重复患儿的临床及遗传学分析

邱惠国
厦门大学附属第一医院

目的 明确 1 例 8q24.138q24.23 微重复胎儿的遗传学病因及其来源，并对该胎儿做产前诊断。
方法 采集夫妻双方外周血及胎儿羊水细胞行染色体 G 显带分析；孕妇外周血行无创产前筛查；胎儿羊水细胞行染色体微阵列分析。
结果 父亲染色体核型正常，母亲和胎儿染色体核型 46，XX，dup(8)（8q24.13q24.23）；孕妇无创产前筛查：8 号染色体长臂 8q24.13～8q24.23 存在 13.10Mb 的重复。(chr8:g.126215101～139315100dup)。染色体微阵列分析：arr[GRCh37]8q24.13q24.23(126646442_137947833)x3。
结论 8q24.13q24.23 微重复为偏良性的 CNV，建议孕妇继续妊娠。

PU-2496

细胞因子检测在临床诊疗中的应用

孙昭辉、冯一民、王芳
山东大学第二医院

目的 细胞因子（cytokine, CK）是由免疫系统细胞以及其他类型细胞主动分泌的一类小分子量的可溶性蛋白质，参与细胞生长分化、免疫功能调节、参与炎症发生等。本文拟通过检测细胞因子水平，探讨细胞因子在相关疾病发生、发展过程中的作用。
方法 收集本院诊断为银屑病、尿毒症、肺癌的住院患者标本 120 例，其中，肺炎患者 30 例，银屑病患者 20 例，尿毒症患者 37 例，肺部肿瘤患者 33 例，采用流式细胞仪测定肺炎、银屑病、尿毒症、肺癌等患者血浆中细胞因子（IL-2、IL4、IL6、IL10、IL17A、TNF-α、IFN-γ）水平。
结 果 肺 炎 IL-2(2.86±2.88)pg/ml ， IL-4(2.85±1.78)pg/ml ， IL-6(77.18±97.90)pg/ml ， IL-10(4.16±4.24)pg/ml ， TNF-α(5.59±6.77)pg/ml ， IFN-γ （ 8.64±15.88 ） pg/ml ， IL-17A（25.00±28.87）pg/ml，银屑病 IL-2(1.95±0.72)pg/ml，IL-4(2.33±1.09)pg/ml，IL-6（8.37±7.93）

pg/ml， IL-10(3.36±0.89)pg/ml， TNF-α(2.49±0.89)pg/ml， IFN-γ（2.61±0.60）pg/ml， IL-17A（7.61±0.98）pg/ml，尿毒症 IL-2(2.67±2.43)pg/ml，IL-4(2.31±0.95)pg/ml，IL-6（41.80±107.22）pg/ml， IL-10(6.82±4.22)pg/ml， TNF-α(2.44±1.27)pg/ml， IFN-γ（3.08±1.87）pg/ml， IL-17A（5.26±4.91）pg/ml， 胸部肿瘤 IL-2(1.68±0.35)pg/ml， IL-4(2.08±0.69)pg/ml， IL-6（134.51±167.31）pg/ml，IL-10(6.38±3.19)pg/ml，TNF-α(2.04±1.11)pg/ml，IFN-γ（2.37±1.01）pg/ml，IL-17A（5.35±5.06）pg/ml，经统计学分析，上述四种疾病患者的 IL-6、IL-10 与健康人群比较，具有统计学意义分别为 P＜0.01，P＜0.05，银屑病患者、尿毒症患者 TNF-α 有统计学意义（P＜0.05），IL-2、IL-4、IL-17A、IFN-γ 没有统计学意义（P＞0.05）。

结论 细胞因子检测可作为患者炎症感染程度的判别指标，亦可作为肿瘤患者肿瘤微环境炎性变化指标。

PU-2497

疫情防控措施对临床检验标本 TAT 的影响分析

孙昭辉、孟静
山东大学第二医院

目的 临床检验标本的转运时间（turn-around time,TAT）是实验室的重要质量质量指标之一，它的及时性是影响临床决策的重要因素。通过分析比较医院采取新冠疫情防控措施前后，检验样本检测流程及样本周转时间等变化，探讨疫情防控形势对 TAT 的影响及对策。

方法 收集 2020 年 1 至 5 月及 2021 年 1 至 5 月急诊、门诊、住院部检验项目检验前、检验中周转时间的运行数据，对医嘱申请检验项目、标本采集确认、标本接收、标本处理、报告审核签发等五个时间节点开展回顾性研究。（1）比较疫情防控前后，检验样本转运方式及其流程的变化。（2）统计分析疫情前后检验样本周转时间变化及分布情况。（3）分别对疫情前后检验样本检测过程进行生物安全风险评估，分析疫情对检验生物安全控制的影响。

结果（1）适当延长标本检验前处理时间，降低标本气溶胶发生的风险。（2）两个时间段不同患者标本的 TAT 时间变化不一。急诊患者血常规 TAT 90 分位数由分别由疫情前的 29 min 及 21min 延长到 39 min 及 34 min；住院患者钾离子检验前与检验中 TAT 90 分位数变化率为 3.55%和 10.19%，无显著统计学意义。（3）检验前标本处理时间延长降低了检验样本检测过程中发生生物安全事件的风险，尤其是降低了接触样品气溶胶的风险。

结论 实验室标本处理流程的严格规范适当延长了标本 TAT，降低了发生生物安全事件的风险。

PU-2498

阴道分泌物全自动检测仪性能验证

罗中兰
中国人民解放军陆军特色医学中心

目的 验证珠海丽拓 V800 全自动细菌性阴道病检测仪的性能，以满足临床工作的需求。

方法 参照仪器说明书和相关行业标准对仪器的重复性，携带污染，干化学检出限，干化学检测项目的阴性和阳性符合率，全自动仪器镜检跟传统方法的符合性进行验证。

结果 细菌性阴道病全自动检测仪，霉菌，滴虫，清洁度，线索细胞，及干化学指标重复性满足要求，携带污染：经验证，阳性和阴性标本不会影响下一个空白标本；干化学检出限:β-N-乙酰氨基葡萄糖苷酶（NAG），阳性检出限为 6.0U/L，弱阳在（5.5~6.0）U/L；唾液酸苷酶（SNA），阳性检出限为 7.0U/L，弱阳在（6.5~7.0）U/L； 白细胞酯酶（LE），阳性检出限为 9.0U/L，弱阳在（8.5~9.0）U/L； 过氧化氢（H2O2），阳性检出限为 1.8μmol/L，弱阳在（1.8~3.0）μmol/L.全自动仪器镜检识别率跟传统方法符合性比较：滴虫总符合率：96%，全自动仪器法假阳性率 25%；

霉菌符合率 94%，假阳性率 12.2%；清洁度符合率 100%，全自动仪器法假阳性率 0%；线索细胞符合率 94%，假阳性率 13，6%。
结论 珠海丽拓 V800 阴道分泌物五联检仪器霉菌、滴虫，线索细胞结果假阳性率高，不能取代显微镜镜检；而干化学项目过氧化氢、白细胞酯酶、唾液酸苷酶评价良好，仪器无交叉污染，重复性满足要求，携带污染率满足要求，跟传统镜检结果结合综合报告，可以满足基层医院临床使用要求，更好的服务临床。

PU-2499

三种不同新冠病毒抗体试剂检测结果分析

孙昭辉
山东大学第二医院

2019 年发生的新型冠状病毒（2019 Novel Corona virus，2019-nCoV）)爆发已经一年多来，已在全球多个国家和地区流行,由于疫情突发。在党中央的坚强领导下，全民同心勠力取得了阶段性胜利，国内疫情得到有效防控。但周边疫情形势依然十分严峻。为更好快速检测人群的抗体反应，国内厂家研发多种抗体检测试剂，新冠病毒抗体检测试剂经研发注册后投入临床使用，但缺少足够的有效性和安全性等性能验证，这可能导致出现与临床诊断不符的假阴性结果或假阳性结果，为临床诊断和疫情防控带来困惑或干扰。由于新冠肺炎(Corona Virus Disease 2019，COVID-19)治疗主要通过中西医结合治疗，尚无特效治疗药物。早发现、早诊断、早治疗是当前主要防控措施。本文通过对比两种不同厂家的发光检测抗体试剂盒和一种胶体金法快速检测试剂盒，探讨不同方法的优缺点，为优化 SARS-CoV-2 感染诊断提供参考。
目的 通过对三种国产新型冠状病毒（Corona Virus Disease 2019，COVID-19）肺炎抗体 IgG/IgM 的应用，比较国产发光试剂盒和胶体金快速检测试剂盒的有效性，探讨新冠肺炎抗体检测在体检人群中的应用价值。
方法 收集应检尽检、住院患者必检和体检人群 300 例血清标本，鼻咽拭子核酸检测全部为阴性。采用两种化学发光抗体检测试剂同时检测 IgG、IgM，结果判读：S/Co 值大于 1.0 为阳性。对抗体检测阳性标本采用胶体金快速检测试剂复检。
结果 300 例标本检测出 3 例阳性标本，其中试剂 A 分别检测出 IgG、IgM 阳性各 1 例，试剂检测出 IgM 阳性 1 例。同时采用胶体金法复检 3 例标本均为阴性。
结论；由于免疫检测方法中不确定干扰因素影响检测结果的判读，抗体检测不宜直接作为诊疗的筛查指标。

PU-2500

质谱在临床微生物检验领域的应用

苏迎迎
东南大学附属中大医院

目的介绍质谱技术的检测原理及其在临床微生物检验中的相关应用。质谱仪基是通过激光轰击待测样本与基质与形成的晶体，使基质与样本间发生电荷转移产生分子电离，离子在电场作用下加速飞过飞行管道，根据飞行时间与离子的质荷比成正比，可计算可测出质荷比，再通过软件处理得到病原菌特征性的图谱。质谱在微生物检验中的应用目前主要包括微生物鉴定、细菌药敏分析、细菌耐药性检测、细菌分型和同源性分析等。质谱技术不仅可以对纯培养的细菌、真菌、霉菌快速鉴定，还可以直接检测尿液、阳性血培养标本等临床样本的病原微生物，在微生物鉴定方面突破了传统微生物鉴定对细菌种类、标本类型、检测时效等局限性；质谱技术通过检测比对微生物的保守蛋白峰实现细菌种内分型和同源性分析；通过检测抗生素修饰或水解状况鉴定细菌产酶情况等。综上

所述，质谱的发展和应用极大改变了传统临床微生物检测方法，弥补了原有细菌鉴定仪器的不足，进一步提高细菌鉴定的准确性和灵敏度。质谱具有菌种对照库大，检测速度快通量高等优点，提高了微生物鉴定和感染性疾病的诊断水平。此外，质谱在临床应用的过程中也是一个菌种数据库的不断更新扩大的过程，在一定程度上推动了微生物检验的发展。

PU-2501

肾脏结石成分与尿液理化性质和尿液蛋白之间的相关性分析

杨志鹏
山东大学第二医院

目的 了解本地肾脏结石的主要成分及所占比例，探讨结石成分与尿液理化性质和蛋白构成之间的关系。
方法 纳入 20---19 年 3 月—2020 年 11 月期间在我院住院治疗的 355 例肾脏结石患者和 30 例同期非泌尿系统疾病住院患者 30 例（对照组），对结石成分分析，根据结石主要成分划分为草酸盐组、磷酸盐组、尿酸组和感染组，并对患者 24h 尿液理化性质和蛋白构成进行检测分析。
结果 355 例结石样本，以混合性结石为主共 222 例，占 62.5%，这其中又以草酸盐结石为主 169 例，占 76.1%，单纯性结石 133 例，占 37.5%，其中以草酸盐结石为主 75 例，占 56.4%；与对照组比较，草酸盐组尿液 pH（5.33±0.32）明显降低，尿钙和尿酸（7.68±0.35、3.48±0.23 mmol/24h）水平明显升高，尿镁（3.02±0.29 mmol/24h）明显降低（P<0.05）；磷酸盐组尿液 pH（6.98±0.77）升高，尿镁（10.55±0.63 mmol/24h）水平降低，尿钙（7.96±0.569 mmol/24h）水平升高（P<0.05），伴有高尿钙症的结石患者高达 69.6%；尿酸组尿液 pH 水平低至（4.97±0.48），且 80.3%的患者伴有尿液过度酸化，尿酸含量（4.14±0.37 mmol/24h）明显升高（P<0.05），伴有高尿酸尿症的患者占 50.8%；感染组尿液 pH（6.86±0.68）升高（P<0.05）；此外，草酸组尿半胱氨酸蛋白酶抑制剂 C（0.653±0.148 mg/L）、尿 α1 微球蛋白（1.53±0.56 mg/dl）和尿 β2 微球蛋白（0.585±0.088 mg/L）水平明显升高（P<0.05）。
结论 我们的研究结果表明，肾脏结石成分和相应尿液代谢变化之间具有相关性，这可以为肾脏结石的治疗和预防提供科学依据，同时也有助于我们对肾脏结石形成机制的探索。

PU-2502

实验室生物安全管理探讨

詹莉芳、学万华
德州市人民医院

近年来，流行性传染病处于高发阶段，各类细菌和病毒发展流行。临床实验室作为高危场所，工作人员每天接收大量的生物标本，极易发生污染，使实验室内存在安全隐患。杜绝医源性感染，需要加强临床实验室生物安全管理，增强人员的安全防护意识，是目前所有临床实验室亟需解决的问题。

PU-2503

重庆农村地区成年人钩虫感染调查与现状分析

刘孝波
陆军军医大学第二附属医院（新桥医院）

目的 探讨重庆农村地区成年人钩虫感染情况，为制定防治策略提供科学依据。
方法 回顾性选取陆军军医大学第二附属医院来自重庆农村的健康体检者（体检组）和来自农村的就诊患者（临床组，其中分为有无症状组和有症状组），按年龄分为青年组和中老年组。分别对各组测定的粪便钩虫卵检查结果进行统计分析。
结果（1）各组性别差异无统计学意义（P >0.05），中老年组钩虫卵检出率明显高于青年组，差异有统计学意义（P <0.05）。（2）体检组与临床组钩虫卵检出率差异无统计学意义（P >0.05）。（3）无症状组和有症状组钩虫卵差异有统计学意义（P <0.05）。（4）钩虫感染地区分布差异无统计学意义（P >0.05）。
结论 重庆农村地区钩虫感染以中老年患者为主，患者不以钩虫感染的主要症状而入院。当出现明显症状时，阳性率明显升高。各区县农村地区广泛存在，无明显聚集性分布。为科学防治钩虫病，定期体检和入院诊疗时检查粪便寄生虫是必不可少的。

PU-2504

Construction of a drugcarrier loaded with siRNA GLI1 on K562 cells

张嫄
郑州大学第一附属医院

Leukemia stem cells (LSCs) are considered responsible for leukemia initiation, relapse and resistance to chemotherapy. In order to completely eradicate leukemia cells, therapies should in principle necessarily target LSCs. The hedgehog pathway regulates GLI1 abnormal activation, leading to drug resistance of leukemia stem cells. Target nano-carriers can target specific cells with specific cell marker, with high drug loading capacity, low drug side effects. MSNs nano-drugcarrier was constructed and modified with anti CD34. In the K562 stem cells, the internalization of FITC labeled MSNs@Antibody was observed by confocal laser scanning microscopy. The inhibition effect of MSNs@siRNAGLI1@Antibody on GLI1 was tested by qPCR and western blot assay. The siRNAGLI1 were loaded on MSNs nano-drugcarriers, and the results showed that after treated by MSNs@siRNAGLI1@Antibody for 48h, the mRNA and protein expression level of GLI1 was significantly inhibited. We successfully constructed the MSNs nano-drugcarrier loaded with siRNAGLI1, which could be used for further study.

PU-2505

结核耐药分析

霍慧霞
石河子大学医学院第一附属医院

异烟肼是结核病化疗的基石，目前仍是治疗结核病的主要药物，乙硫异烟胺（ethionamide，Eto）/丙硫异烟胺 （ethionamide，Pto）是异烟肼的类似物，属于二线抗结核药物，是耐多药结核病化疗方案的重要组成药物。异烟肼和 Eto/Pto 均 抑制分枝菌酸的合成，两药存在部分交叉耐药机

制，了解其抗结核作用机制尤其是分子学耐药机制，有助于正确选择抗结核药 物，并将促靶标的抗分枝杆菌药物的开发。本文重点讨论结核分枝杆菌对异烟肼和 Eto/Pto 耐药机制的研究进展。

PU-2506

探讨如何进一步完善 PCR 移动检测车的设计与工作流程

周媛、许建成、王晓明、安倍莹、柴剑男、孙璐璐、宋佳星
吉林大学第一医院

目的 通过比较在 PCR 实验室与移动检测车上开展新冠病毒核酸检测实验工作的流程与体会，探讨如何进一步完善 PCR 移动检测车的设计与工作流程。
方法 2021 年初，吉林省通化市爆发了新冠病毒肺炎疫情，吉林省启用了移动检测车协助通化当地开展大规模新冠病毒核酸筛查工作，这是国内首次使用移动检测车参与新冠病毒核酸筛查工作，因此负责此次任务的新冠病毒核酸检测队伍积累了丰富的实践经验和教训，通过总结这些体会，与在普通 PCR 实验室中新冠病毒核酸检测工作相比较，提出对移动检测车的设计与如何开展工作等方面的进一步改良措施。
结果 新冠病毒核酸检测工作在移动检测车上进行与在 PCR 实验室中进行相比较，虽然检测工作的内容相同，但由于场地、设施及外界环境的不同，在车体设计与工作流程方面都需要更多的完善。移动车的整体空间布局需要安装更多的固定装置，如可以存放并防止样本倾斜散落的支架或储藏柜、每一个岗位的工作人员都能触手可及的感应消毒设施等。为使移动车上三个工作区之间及与外界之间的联系更加方便，除固定对讲系统以外还应配有移动对讲机。由于检测车上三个工作区域内的防护等级并不一致，应有各自的空调控温系统。受移动车检测车空间所限，建议三至四辆移动车就应配备一辆专门负责高压消毒医用垃圾的消毒车。在工作流程方面，建议在检测车附近设立更衣区，如可搭设临时帐篷。三个工作区域的工作人员在交接班前应及时报告本区工作情况，以给接班人员预留足够的时间补充试剂与耗材。在寒冷的冬天，尤其是北方，应注意保证试剂的储存条件，如常温储存的试剂应避免结冻，在工作人员脱下防护服后从检测车撤出时也应有足够的保暖措施，
结论 PCR 移动检测车因其机动灵活高效的特点在大规模新冠病毒核酸检测工作中可以起到至关重要的作用，它可以在筛查地附近就地建立起一个 24 小时不停运转的 PCR 实验室，但它在车体设计上和工作流程方面尚待进一步完善。

PU-2507

三种第三方质控品用于 SysmexSC5100 装载 Sysmex Siemens 凝血试剂

林子琪、董轲
中国人民解放军空军军医大学第二附属医院

目的 为检出一般实验室使用的试剂配套质控品可能存在无法检测出批间差或因校准品批号改变而带来的变化，而配套质控品本身也可能存在一定偏倚而无法准确评估试剂情况。探讨稳定性好，范围覆盖广的凝血第三方质控品。
方法 用三种第三方质控在 SysmexSC5100 仪器装载 Sysmex Siemens 凝血试剂，使用伯乐 1，2，3 水平；郎道 1，3 水平；积水 1，2 水平在同一仪器——Sysmex CS5100 上连续 20d 测定，分别得到 20 个质控项目 PT ，INR，APTT，FIB，TT 结果分别计算出 20d 三种质控品在不同项目中的平均数（X），标准差（S）,变异系数（CV）。
结果 PT 中伯乐，朗道，积水各水平平均 CV（%）分别 2.48，2.17，1.615。INR 中伯乐，朗道各水平平均 CV（%）分别为 3.813，1.632。APTT 中伯乐，朗道，积水各水平平均 CV（%）分别

2.3，2.62，4.64。FIB 中伯乐，朗道，积水各水平平均 CV（%）分别 3.09，2.285，4.68。TT 中伯乐，朗道，积水各水平平均 CV（%）分别 3.33，1.695，1.95。
结论 不同厂家的各个平水平均符合中国人民共和国卫生行业标准《临床血液学检验城轨项目分析质量要求 WS/T406—2012》。实验室应根据具体情况选择质控水平，合适的覆盖范围。

PU-2508

应用新鲜血比对方案完善血液分析仪日常室内质量控制

郑翠玲、王力、程焱、崔巍
中国医学科学院肿瘤医院

目的 建立新鲜血比对方案，以保证临床标本的检测结果具有可比性和一致性，并完善血液分析仪日常室内质量控制（IQC）。
方法 在每日用配套质控品完成 IQC 后，抽取检测结果在参考范围内且血量约为 2ml 的新鲜血标本。选择性能良好的血液分析仪作为靶机，其余仪器作为比对仪器。新鲜血标本在靶机中测定的结果作为靶值，比对仪器的测定结果作为测定值。将靶值和测定值进行比较，计算白细胞计数（WBC）、红细胞计数（RBC）、血红蛋白（Hb）、红细胞比容（Hct）、血小板计数（PLT）项目的相对偏差。仪器间相对偏差标准为 1988 年美国临床实验室改进法案(CLIA'88)允许误差的 1/2，而血液分析仪运行过程中的相对偏差标准为允许误差的 1/3。根据偏差标准对相对偏差进行评价。
结果 比对仪器与参比仪器间的比对数据的相对偏差符合 1/2CLIA'88 偏差范围的要求，表明仪器间检测结果的准确性，并具有可比性。全细胞分析仪运行过程的比对数据的相对偏差符合 1/3CLIA'88 偏差范围的要求，表明仪器运行稳定。
结论 新鲜血比对方案既能保证血细胞分析仪间检测结果的可比性及仪器运行过程中的稳定性，又能对血液分析仪进行方便、经济、有效的日常室内质量控制。

PU-2509

有无添加稳定剂对胃泌素 17 血清标本测定的影响

蒋建、冯晓敏、李卫滨、张胜行
中国人民解放军联勤保障部队第九〇〇医院

目的 探讨胃泌素-17 血清标本在有无稳定剂保存的条件下对 ELISA 法测定其结果的影响，以及确定本实验室 G-17 标本的适宜保存方案。
方法 随机选取 20 例就诊于联勤保障部队第九〇〇医院患者的 G-17 样本，经离心后分离血清，进行 ELISA 法检测，测定结果作为原始值；设置添加稳定剂组和不添加稳定剂组，将血清分装后保存于 4～8℃冰箱中，于第二天、第三天、第四天进行胃泌素-17 浓度的测定。通过计算实验数据的降解率、符合率指标分析血清胃泌素-17 检测结果与有无添加稳定剂、保存天数的关系。
结果 随着保存天数的增加，无添加稳定剂组血清样本中 G-17 浓度第二天平均降解率为 32.24%，第三天平均降解率为 44.46%，第四天平均降解率为 59.28%。按降解率还原后与第一天的符合率分别为 106.77%、116.99%、139.23%；添加稳定剂组血清样本中 G-17 浓度第二天平均降解率为 26.47%，第三天平均降解率为 35.69%，第四天平均降解率为 45.64%。按降解率还原后与第一天的符合率分别为 105.89%、114.24%、125.84%。
结论 添加稳定剂能够使胃泌素-17 的降解速率减慢，本实验室的 G-17 血清样本应在当天完成检测。

PU-2510

精益管理理论在检验科文件表格管理中的应用

刘春梅、刘义庆
山东第一医科大学附属省立医院

近年来，精益管理越来越普遍被应用于医疗行业。我院从引入精益管理的方式后，对科室的文件管理按照精益管理模式进行了改造，提高了工作效率。

方法 1.建立操作流程 具体的操作流程为：年初制定好相应的质量与技术记录表格，分电子版类及手工填写类，后者包括每天、每周、每月和不定时填写类。每月初上传电子版并打印所需的纸质版表格，分配到各实验区域，同时对工作人员进行相应的培训，工作中对文件表格及工作人员填写情况进行观察；定期对填写完毕的记录表格进行回收交主任审核并分类归档。2.5s 管理 ⑴整理（sort）：改善前，记录表格放置混乱易丢失。通过增加文件夹和文件盒来增加文件存放空间，并准备专门的档案柜，分门别类的存放文件，改善环境。⑵整顿（simplify）：①根据工作中实际情况编制表格，使工作流程及工作记录完整化。②配备一名文件管理员，负责对本室文件进行管理，对本室工作人员填写表格文件进行相应的培训并监督。③各表格都予以相应的分类编号。④科室实施不定期检查，及时发现不符合项。⑶清扫（sweep）：①对于与工作情况违背或者不适用的表格予以停止使用并撤离现场，②工作人员要维护好记录表格的整洁卫生，防止血渍或污水污染。⑷标准化（standardize）：工作中已经形成的表格填写、整理、放置、维护等方法组员要严格履行，文件管理员对于执行情况要不断检查，及时发现问题并进行整改，使管理制度规范化、标准化。⑸自律（self discipline）：工作人员要严格要求自己，养成良好的习惯，严格执行操作流程，并积极进行自查，出现问题要主动改正。

实施精益管理后，我室的文件填写缺陷率和保存缺陷率明显下降。这表示实施精益管理后，有了完整的管理体系和操作流程，工作人员都接受了完整的学习、培训，这有助于提高本室的表格文件的完成率和完好性，满意度也有了相应的提高。精益管理理论在文件表格管理过程中有很好的应用价值。

PU-2511

常规检验与生化检验在临床糖尿病诊断中的检出率比较分析

徐健
四川省人民医院东院

目的 比较分析常规检验与生化检验在临床糖尿病诊断中的检出率及应用价值。
方法 随机选择 2020 年 1 月~2021 年 6 月研究时间段内于本院就诊 2 型糖尿病患者 40 例（男 20 例，女 20 例，年龄区间 35~80 岁，均为原发 2 型糖尿病确诊者）及同期入院健康体检者 40 例（男 20 例，女 20 例，年龄 35~82 岁，无糖尿病史及血糖代谢功能异常）行临床对比研究。两组基线资料对比结果无差异性（P＞0.05），研究结果可比。研究纳入者均接受常规检验、生化检验。常规检验取受检者次日入院时晨间空腹中段尿行尿糖阳性检验，生化检验取受检者晨间空腹外周中心静脉血行血糖、糖耐量检验。统计检验结果及临床检出率差异。
结果（1）检验结果差异分析：2 型糖尿病患者尿常规检验所得尿糖阳性检出率（97.50%）、血生化检验所得 PBG（8.16±0.57）mmol/L、2hFBG（13.25±2.05）mmol/L 及糖耐量（12.26±5.31）mmol/L 均高于健康体检者，差异有统计学意义，P＜0.05。（2）临床检出率对比：经分析 2 型糖尿病患者检验结果后可知血生化检验所得糖尿病阳性检出率（100.00%）、诊断敏感度（100.00%）及诊断符合率（100.00%）均高于尿常规检验，差异有统计学意义，P＜0.05。

结论 尿常规在糖尿病临床检查中仅有显著筛查指向价值，对于糖尿病的准确诊断则需以血生化检验中所得完善检验结果为依据，实现准确诊断。

PU-2512

淋巴细胞亚群在儿童原发性肾病综合征中的变化及应用价值探讨

黄靖彤、褚帅
南方医科大学南方医院

目的 分析儿童原发性肾病综合征（primary nephrotic syndrome，PNS）发生发展过程中淋巴细胞亚群的变化并探讨其在治疗和预防感染中的临床应用价值。
方法 选取南方医科大学南方医院 2019 年 9 月至 2021 年 4 月收治的 PNS 患儿 89 例，其中根据疗效分组可分为活动组 40 例，部分缓解组 30 例、完全缓解组 19 例，另外 PNS 无感染组与合并感染组分别有 56 例及 33 例。19 例健康儿童纳入健康对照组。各组的淋巴细胞亚群水平使用流式细胞仪进行检测。比较健康儿童与 PNS 患儿的各淋巴细胞亚群数量和比值的差异及其与治疗疗效的关系，并与疾病相关生化指标做相关性分析，同时分析 PNS 合并感染患儿的淋巴细胞亚群水平。
结果 1.与健康对照组相比，活动组和完全缓解组的 T 细胞百分数、活动组和部分缓解组的 CD8+ T 细胞百分数和效应/记忆 CD4+ T 细胞的百分数和绝对计数均升高，活动组的 CD4+/CD8+比值和初始 CD4+ T 细胞/记忆 CD4+ T 细胞比值下降，PNS 三组的淋巴细胞总数、T 细胞与 CD8+ T 细胞的绝对计数、Tc 细胞的百分数和绝对计数以及 Tc/Ts 比值均升高而 NK 细胞的百分数和绝对计数均降低；完全缓解组患儿的初始 CD4+ T 细胞百分数与活动组患儿相比较显著增加，而与活动组和部分缓解组患儿相比较，效应/记忆 CD4+ T 细胞百分数和绝对计数显著降低，初始 CD4+ T 细胞/记忆 CD4+ T 细胞比值回升，其余淋巴细胞亚群各组间无显著性差异； 2.效应/记忆 CD4+ T 细胞百分数和绝对计数与 ALB 水平均呈负相关以及其百分数与 CHOL 水平呈正相关，而淋巴细胞总数、CD4+ T 细胞及 Treg 细胞绝对计数与 Scr 水平之间均具有负相关性，其他淋巴细胞亚群与疾病相关生化指标间均未发现显著相关性； 3.与无感染组相比，合并感染组患儿的 T 细胞和初始 CD4+ T 细胞的百分数、CD4+ T 细胞的百分数和绝对计数以及 Treg 细胞绝对计数均减少及其 CD4+/CD8+比值也明显下降，而且我们发现 CD4+ T 细胞绝对计数＜850 个/μL 是儿童 PNS 合并感染的危险因素。
结论 NK 细胞、Tc 细胞和效应/记忆 CD4+ T 细胞数量或功能的异常可能与儿童 PNS 的发病具有密切关系。淋巴细胞亚群水平能在一定程度上反映儿童 PNS 的治疗疗效和肾功能状态，其中初始 CD4+ T 细胞和效应/记忆 CD4+ T 细胞的数量和比值可能是判断儿童 PNS 病情进展与缓解的潜在指标。CD4+ T 细胞、初始 CD4+ T 细胞和 Treg 细胞数量的减少与感染的发生有关，CD4+ T 细胞绝对计数＜850 个/μL 是儿童 PNS 合并感染的危险因素。

PU-2513

Anti- psoriatic effect and underlying mechanisms of Periplogenin

Wenjing Zhang
The First Affiliated Hospital of Zhengzhou University

Propose Psoriasis is a multifactorial skin disease and it brings a lot of inconvenient in patients' life. Considering the side effects and drug resistance of the current therapy, it is urgent to discover more effective and safer anti-psoriatic drugs. We undertook experiments in an attempt to elucidate the vivo and vitro effects of Periplogenin in Psoriasis.
Methods By using a cultured human HaCaT keratinocytes as an in vitro psoriasis-relevant model, we screened over 250 traditional Chinese medicine compounds for their cell viability-inhibitory action. We undertook further experiments in an attempt to elucidate the vivo effect studies of

pepriplogenin on the psoriasis-like murine models of 12-O-tetradecanoylphorbol 13-acetate (TPA)–induced hyperplasia and imiquimod (IMQ)-induced skin inflammation.
Results Periplogenin was found to be highly significant in inhibiting the viability of HaCaT cells. periplogenin induced necroptotic cell death rather than apoptosis or autophagy. Moreover, periplogenin ameliorated skin lesions and inflammation in the murine models of TPA-induced epidermal hyperplasia and IMQ-induced skin inflammation.
Conclusion In conclusion, periplogenin exhibited selective cytoxicity against HaCaT cells in vitro and played the anti-psoriatic effect as a topical agent on psoriasis animal models in vivo.

PU-2514

间接免疫荧光法检测抗核抗体室内质控品的制备和性能验证

高雪丹、苏真珍、黄卓春、胡静、王丽、杨滨
四川大学华西医院

目的 建立抗核抗体（ANA）室内质控品自制和性能验证规范化程序，以有效监测实验室间接免疫荧光法检测 ANA 的质量，保证其检测一致性和准确性。
方法 收集 ANA 高滴度强荧光（滴度 1:3200~1:10000）单一荧光核型（均质型）临床血清样本，将其与混合阴性 ANA 血清按 1:30 比例混合制备成 1:100~1:320 滴度的弱阳性质控品，收集阴性血清作为阴性质控品。将质控品灭活后采用间接免疫荧光法检测并以人工判读和荧光判读仪判读（荧光强度值）同时进行均匀性和稳定性验证，并用自制质控品进行仪器重复性和一致性性能验证。
结果 自制弱阳性和阴性 ANA 质控均有较好的均匀性和稳定性，其荧光强度值变异系数基本在 10%以内，以自制质控品验证仪器也具有较好的重复性和一致性。
结论 采用荧光强度值可基本实现定量监测 ANA 质控品的检测结果，且本实验室自制 ANA 质控品有良好的性能，可满足临床需求并可为其他实验室制备和验证质控品提供参考。

PU-2515

Hp 感染、低氧诱导因子-1α 蛋白表达与胃癌发生及进展的关系分析

黄红娟
郴州市第一人民医院

目的 分析 Hp 感染、低氧诱导因子-1α 蛋白表达与胃癌发生及进展的关系。
方法 以 2020 年 1 月-2020 年 12 月 50 例确诊胃癌患者为胃癌组，另外选取确诊慢性胃炎患者 40 例为胃炎组，均检测 Hp 感染率、低氧诱导因子-1α 蛋白表达。
结果 胃癌组 HP 感染阳性率为 64.00%，明显低于胃炎组 HP 感染阳性率 87.50%（P＜0.05）。胃癌组低氧诱导因子-1α 蛋白表达阴性率、弱阳性率低于胃炎组，阳性率、强阳性率均高于胃炎组（P＜0.05）。胃癌组中早期患者低氧诱导因子-1α 蛋白表达阳性率低于中晚期患者（P＜0.05）；低分化患者低氧诱导因子-1α 蛋白表达阳性率明显高于中分化与高分化患者，且中分化高于高分化患者（P＜0.05）。诱导 HP 感染 MGC-803 细胞 12 小时开始低氧诱导因子-1α 蛋白表达显著增加，相较 12 小时前的结果有统计学差异（P＜0.05）。
结论 低氧诱导因子-1α 蛋白在胃癌中呈高表达，且胃癌分期越高的患者低氧诱导因子-1α 蛋白表达水平越高，胃癌分化越差的患者低氧诱导因子-1α 蛋白表达水平越高，且 Hp 感染时形成的低氧环境能对低氧诱导因子-1α 蛋白的表达形成诱导，两者具有明显相关性。

PU-2516

18-60 岁成年男性痛风患者血清生化指标分析

练明建[1,2]、兰小英[1,2]
1. 厦门大学附属第一医院检验科
2. 厦门市基因检测重点实验室

目的 近年来，痛风的发病率升高，严重地影响患者的生活。除了疼痛带来的影响，还发现痛风患者常伴随其他疾病。本研究分析 18-60 岁成年男性痛风患者的血清生化指标的特点，为痛风患者的诊治提供依据。
方法 收集 2020 年 1 月至 2021 年 4 月就诊于厦门大学附属第一医院 18-60 岁的 473 例男性痛风患者及同期就诊的 400 健康体检者的一般资料以及血清生化检查结果，分析血尿酸与各生化指标的相关性，比较两组指标的差异。比较痛风患者肾功能正常组和损害组以及<40 岁组和 40-60 岁组各指标的差异。
结果 对于所有研究对象，尿酸（UA）与谷氨酸氨基转移酶（ALT）、天门冬氨酸氨基转移酶（AST）、血糖（GLU）、肌酐（CREA）、总胆固醇（TC）、甘油三酯（TG）和低密度脂蛋白胆固醇（LDL）呈正相关（P<0.05），而与高密度脂蛋白胆固醇（HDL）和肾小球滤过率（eGFR）呈负相关（P<0.05）。痛风组的 ALT、AST、GLU、CREA、UA 、TC 、TG 和 LDL-C 均高于健康对照组，而 HDL-C 和 eGFR 低于健康对照组。比较高 TC、高 TG、低 HDL-C、高 LDL-C、高脂血症以及低 eGFR 的比例，痛风组均高于健康对照组，差异有统计学意义。痛风患者中肾功能异常组的 CREA 和 TC 高于正常组，且高 TC 的比例高于正常组。<40 岁组的 ALT、UA 和低 HDL-C 的比例高于 40-60 岁组，而病程和低 eGFR 的比例低于 40-60 岁组。
结论 痛风患者更易引起肝功能损伤、高脂血症、高血糖、肾功能损伤，肾功能的损伤可能与 TC 水平相关，年轻的患者可能更易导致肝功能受损，随着年龄的增加更易发生肾脏损伤。

PU-2517

180 例小儿甲流病毒、腺病毒感染的血常规、血清淀粉样蛋白 A 及 C 反应蛋白水平分析

杨晓平
中国人民解放军联勤保障部队第 970 医院

目的 分析 180 例于我院就诊的感染甲型 H1N1 流感病毒的患儿和感染腺病毒 7 型的患儿的血常规、血清淀粉样蛋白 A（SAA）以及 C 反应蛋白（CRP）的水平，为临床诊断以及早期治疗提供帮助。
方法 收集 2018 年 1 月至 2019 年 12 月在本院确诊感染甲型 H1N1 流感患儿 93 名，腺病毒感染患儿 87 名，并以健康查体的 80 名幼儿为正常组，统计分析三组人群的白细胞总数、中性粒细胞百分比、淋巴细胞百分比、单核细胞百分比、血小板计数、全血 CRP 和 SAA 的水平。百分率的比较采用 X^2检验；三组间水平除 SAA、CRP 数据外均符合正态分布，采用 LSD-t 检验； SAA、CRP 数据均为偏态分布，以中位数[m(P25，P75)]表示，三组间采用非参数分析的 Kruskal-Wallis H 检验，两组间采用 Mann-Whitney U 检验。
结果 甲流病毒和腺病毒患儿的白细胞和血小板多为正常；Mo%可升高，也可正常或者降低；腺病毒患儿的 Neu%多为正常，两组数据 Neu%存在显著差异；甲流病毒患儿的 Ly%多为降低，且两组间数据存在较大差异；两类患儿的 CRP 和 SAA 多为升高。皆具有统计学意义；甲流病毒组和腺病毒组两组间中性粒细胞、淋巴细胞、PLT 和 SAA 也具有显著差异。甲流组的中性粒细胞高于正常值且高于正常范围，腺病毒组中性粒高于正常值但在正常范围内；甲流组淋巴细胞低于正常值且低于正常范围，腺病毒组同样低于正常值但在正常范围内；两组间单核细胞高于正常值但在正常范围内，且两组间数据无统计学意义；两组间 PLT 低于正常值，但在正常范围内，但两组间有统计学

意义，甲流病毒组的 PLT 数值要更低；两组间 CRP 显著高于正常值，但两者之间无统计学意义；两组间 SAA 数值同样显著高于正常值，但是甲流病毒组的 SAA 更高于腺病毒组。
结论 甲流病毒、腺病毒组的 CRP、SAA、PLT、淋巴细胞百分比与正常幼儿组数据的比较存在着统计学的差异，可以引作为诊断甲流、腺病毒的初筛指标；而 SAA 和淋巴细胞百分比对初步鉴别感染甲流或腺病毒有价值。

PU-2518

15 年耳部感染性疾病分离病原菌及药物敏感性分析

刘春红、吉建、陈惠雯、曹文俊
复旦大学附属眼耳鼻喉科医院

目的 探索耳部分离病原菌的类型、药物敏感特征。
方法 收集复旦大学附属眼耳鼻喉科医院 2005 年 1 月～2019 年 12 月经临床诊断为耳部感染性疾病患者中耳及外耳分泌物标本中分离出的病原菌，分析病原菌菌谱及药敏变化，利用 SPSS 卡方检验分析进行统计学分析。
结果 共分离出病原菌 2097 株，其中 39.0 %(818) 为革兰阳性菌， 革兰阴性菌为 24.7 %(519)，36.2 %(760)是真菌。其中金黄色葡萄球菌和铜绿假单胞菌为最常见病原体。革兰阳性菌对万古霉素的敏感率为 100%。对其他药物的敏感率:复方新诺明(84.5 %)，氯霉素 (79.2 %)，左氧氟沙星(57.0%)及环丙沙星(47.5%)。革兰阴性菌对美罗培南敏感率 96.1 %，其他药物敏感性为阿米卡星 91.9 %，头孢他啶 87.3 %，妥布霉素 59.1 %，环丙沙星 46.5 %。2005-2019 年耳部分离的病原菌对左氧氟沙星、头孢他啶和哌拉西林的药物敏感率变化具有统计学意义。
结论 金黄色葡萄球菌和铜绿假单胞菌是耳部分离的常见致病菌。革兰阳性菌对复方新诺明，氯霉素敏感率高。革兰阴性菌对头孢他啶和阿米卡星的敏感性高。2005-2019 年耳部分离的病原菌对头孢他啶和哌拉西林的敏感性有升高趋势，而对左氧氟沙星敏感性有降低趋势。

PU-2519

IL-27 在炎症性疾病中的诊断作用研究进展

刘双
重庆市人民医院

白细胞介素-27（Interleukin-27，IL-27）由 EBI-3 和 p28 组成，是 IL-12 家族的新成员，主要来源于抗原提呈细胞(antigen presenting cell,APC)的分泌。之前有研究表明 IL-27 在促进 Thl 型免疫反应中起重要作用，而随后的研究也证明 IL-27 对一些 T 细胞亚群以及诱导型调节性 T 细胞具有广泛抑制作用，除此之外也可影响中性粒细胞、巨噬细胞的免疫功能。由此可见 IL-27 是一种在感染和免疫方面有着多效性的细胞因子。流感诱导产生的 IL-27 可通过损害宿主抵抗细菌感染的固有免疫力，从而促进了流感后肺炎球菌性肺炎的发展。脓毒症诱导产生的 IL-27 也可增加宿主肺部对铜绿假单胞菌感染的易感性。但是，在肠道免疫中，IL-27 可以抵抗艰难梭菌的感染。尽管 IL-27R$^{-/-}$缺陷型小鼠在念珠菌引起的血流感染中表现出对近平滑念珠菌的清除率提高，但它们并未表现出对白色念珠菌的清除率提高。因此，这些结果突出了 IL-27 在炎症性疾病的复杂作用。就 IL-27 的临床检验诊断意义而言，已有研究表明其可以在一定程度上为脓毒症的早期诊断及判断预后提供检验价值，不仅如此，IL-27 作为诊断指标与 ADA 的联合可提高结核性胸腔积液的准确性，在虫媒病毒疾病基孔肯雅病毒病(CHIKVD)中，研究人员通过分析血清细胞因子的水平及其与 CHIKVD 患者临床表现的相关性，提示其可能作为该疾病的长期标志物。因此更详细地了解 IL-27 的生物学特性并揭示不同疾病环境下 IL-27 的免疫作用，将对其日后应用于各种炎症性疾病的诊断提供新的思路。

PU-2520

厦门市某三甲医院横纹肌溶解症的临床和实验室特点

练明建[1,2]、王前明[1,2]
1. 厦门大学附属第一医院检验科
2. 厦门市基因检测重点实验室

目的 横纹肌溶解症是一种相对少见的疾病，目前尚无相关的治疗指南。本研究旨在收集分析近四年收治的横纹肌溶解症患者的临床资料从而为其诊治提供更多的依据。
方法 收集和分析 2018 年 1 月至 2020 年 12 月就诊于厦门大学附属第一医院的横纹肌溶解症患者的临床资料，包括性别、年龄、症状、病因、实验室检查结果等。横纹肌溶解症的诊断应满足肌酸激酶（CK）峰值>1000U/L 且有相应的症状或相关的病因。
结果 近四年，共诊治 98 例横纹肌溶解症患者，中位年龄为 29 岁（范围：8-88 岁），66（67.35%）为男性，2017 年-2020 年分别包含 15、24、31 和 28 例，夏秋季病例多于冬春季。剧烈运动和食用小龙虾是最常见的两个病因，分别包括 59 例（60.20%）和 9 例（9.18%）。不同病因患者的性别构成比存在差异。最常见的症状为肌肉酸疼。绝大部分患者的 CK、肌酸激酶同工酶 MB 亚型、乳酸脱氢酶肌红蛋白、丙氨酸氨基转移酶、天门冬氨酸氨基转移酶都升高。低钾血症是最常见的电解质紊乱。尿素、肌酐和尿酸升高的比例分别占 15.31% （15/98）、17.35%（17/98）和 46.94%（46/98）。白细胞、纤维蛋白原、D 二聚体和纤维蛋白降解产物升高的比例分别占 42.22%（38/90）、 22.97% （17/74）, 53.03%（35/66）和 26.67%（8/30）。85 例患者进行尿液分析，尿酮体、尿潜血和尿蛋白阳性分别占 25.88% （22/85）, 71.76% （61/85）和 63.53%（54/85）。整体的预后良好，未出现死亡病例。
结论 夏秋季节应该避免剧烈运动和慎食小龙虾。横纹肌溶解症患者的许多实验室检查指标异常，应予以重视。

PU-2521

大数据时代检验医学的变革之路

欧阳维富
广东省人民医院(广东省医学科学院）

20 世纪中叶以来，信息技术革命广泛而深刻地改变人们的生产和生活方式；当今，大数据正在以磅礴气势驱动新一轮科技革命和社会变革。作为检验医学工作者，我们需研究大数据对医学发展的影响；并研判大数据时代背景下，检验医学在未来医疗卫生价值链中的角色和定位，进而探索检验医学的高质量发展的方向和路径。

过去，得益于信息技术的发展，检验医学实验室可以对检测样本的采集、运输、检测到审核进行实时监控和记录，实现检测样本全流程的跟踪管理。当今，随着检测技术的发展，质谱分析技术、二代测序技术等高新技术正逐步进入检验医学实验室，蛋白质组、微生物组、宏基因组等组学正辅助临床医学实现精准医疗；芯片技术、微流控技术、多参数流式细胞技术正开拓检验医学的新领域；基于卷积神经网络的图像识别系统正为细胞形态学检查与鉴定提供多维信息；随着检验技术代际更迭周期的缩短，各类检验数据呈现几何级的增长。如何挖掘这些检验数据，提炼出更具价值的医学信息，辅助临床决策，这是检验医学发展过程中亟待解决的问题。

大数据时代，一种新的认识和改造世界的方法，用数据化思维和云计算的处理方式探索海量数据之间的联系和变化趋势。人工神经网络模型和数据挖掘等信息技术可实现对检验数据的集成、储存、挖掘和预测，揭示检验数据与健康状况间的逻辑关系。检验分析前，可以依据电子病历记录和患者的症状描述等信息，进行大数据挖掘和预测，优化多指标联合诊断方案，为临床医生推荐合理、有效且经济的检验项目，最大限度地提升诊断效能，最大限度地节约医疗卫生资源。检验分析后，基于大数据的临床决策支持系统的应用，实现检验数据与临床数据有效的整合，对多维数据进行系

统分析，有助于我们更加深入地认识疾病本质，为临床决策提供检验数据、解释性报告、诊断建议及诊断概率、进一步检查意见等诊断信息，实现检验医学报告模式从数据型检验报告到数字化诊断报告的转化。以基因组、蛋白质组、微生物组及常规生物学数据为基础建立的疾病预警系统，对检验数据深度挖掘、建立疾病预测模型，提升对疾病发生发展的风险预测能力，实现对疾病的早期诊断和预后判断。

大数据时代，一切皆可量化，一切皆可分析，检验数据的深度挖掘和二次利用蕴含着提升检验医学学科建设的良好机遇和空间。检验医学工作者应顺应大数据时代潮流，把握时代机遇，推进检验医学的变革，构建大数据驱动的检验医学新发展格局。

PU-2522

1 例全身网状色素异常症患者的分子诊断

余秀蓉、王志红
联勤保障部队第九〇〇医院

目的 对一例临床表现为全身网状色素异常，伴有复发性中耳炎和支气管扩张症的男性患者进行分子诊断。
方法 取患者腹部皮肤切除标本行 HE、刚果红染色及免疫组化检测。分别采集患者及其父母（表型正常）的 EDTA 抗凝外周血各 2 ml，通过家系三人全外显子组测序（Trio-WES）寻找可疑的致病变异，并用 Sanger 测序验证可疑致病变异，并进行致病性分析。
结果 腹部皮肤切除标本 HE 染色：淀粉样变；刚果红：+++；免疫组化：Kappa +，Lambda +。Trio-WES 及 Sanger 测序检出先证者 POLA1 基因 c.1375-354(IVS13)A>G 半合子变异，父亲为野生型，母亲携带杂合变异。该变异已有文献报道，功能研究表明该变异有害。生物学致病性分析：根据 ACMG 遗传变异分类标准与指南，该变异符合 PS3+PM2，判断为可疑致病性变异。此外，该变异先证者为半合子，符合 X 染色体隐性遗传（XR）疾病发病机制，先证者及其家系成员符合表型及基因型的共分离。POLA1 基因变异导致的 X-连锁网状色素异常症主要表现为：反复肺炎，角化过度，腹股沟疝，角膜瘢痕形成，视力丧失，畏光，少汗，结肠炎，胃肠道复发性感染，广泛性网状褐色色素沉着，角膜基质混浊，淀粉样变性等。以上结果提示先证者 POLA1 基因变异与先证者的临床表型相关。
结论 综合分析患者的临床表型、皮肤病理以及 Trio-WES 检测结果，该男性患者为 POLA1 基因 c.1375-354A>G 半合子变异导致的 X-连锁网状色素异常症。

PU-2523

资阳市老年人血脂异常情况统计分析

李军、郑鑫
四川金域医学检验中心有限公司

目的 通过对资阳市公卫体检老年人血脂结果统计分析，了解四川省资阳市不同性别老年人血脂异常发生的概率。
方法 统计 2021 年 3 月至 2021 年 4 月本检测中心检测的年龄在 60 岁以上的资阳市公卫体检人员的血脂结果，参照 2007 年我国《中国成人血脂异常防治建议》：血清甘油三酯（TG）≧1.70mmol/L、胆固醇（TC）≧5.18mmol/L、低密度脂蛋白（LDL）≧3.37mmol/L，高密度脂蛋白（HDL）≤1.04mmol/L,以上有任一血脂指标异常即为血脂异常。
结果 统计人数共计 62465 例，其中男性 28779 例，女性 33686 例。男性 TC 异常 14847 例（51.59%）、TG 异常 5892 例（20.47%）、HDL 异常 2529 例（8.79%）、LDL 异常 9184 例

（31.91%）；女性 TC 异常 23294 例（69.15%）、TG 异常 10467 例（31.07%）、HDL 异常 1585 例（4.71 例）、LDL 异常 14720 例（43.70%）。检测结果显示女性 TC、TG、LDL 异常明显高于男性，男性 HDL 异常明显高于女性，TC、LDL 异常发生率随着年龄的增加而降低。
结论 随着人们物质生活水平的提高，血脂异常在老年人群中普遍存在，已成为影响老年人身体健康的重要因素之一。血脂异常与高血糖、高血压一样，对脏器有缓慢不利的影响，又因为血脂异常不会引起明显的临床症状，常常容易被人们忽视。血脂异常作为引起心脑血管病的重要诱因，需要引起人们的足够认识。关爱老年人的身体健康，应该加大对血脂异常知识的宣传和教育，以此加强老年人自我保健意识。

PU-2524

SMN1 基因的 c.683T>A 及 c.844C>T 突变可触发无义介导的 mRNA 降解

张梦雅
联勤保障部队第九〇〇医院

目的 通过设计 SMN1 小基因，构建野生型及三种无义突变型表达质粒，在转录水平分析其 mRNA 表达量的变化，探究 NMD 在 SMA 中的作用机制。
方法 首先，在 NCBI 上查找 SMN1 基因组序列，选择 HGMD 数据库中记载的位于 SMN1 基因第 1、5、7 外显子的无义突变点（分别对应 c.43C>T、c.683T>A 、c.844C>T），设计包含三种拟突变点的 SMN1 小基因。其次，将其与表达载体 pcDNA3.1(-)/myc-His A 连接，构建野生型表达质粒 PcMV-Mini-SMN-WT；利用突变试剂盒及突变引物得到三种无义突变型表达质粒（E1，E5，E7）。最后，将四种质粒转染 HeLa 细胞，通过 qRT-PCR 分析质粒正常转录本的表达水平；并通过翻译抑制剂放线菌酮的处理，观察药物处理前后 mRNA 表达量的变化，从而明确 NMD 在 SMA 中的作用。
结果 实验数据显示野生型表达质粒发生正确剪接；qRT-PCR 结果显示其中两种突变型质粒（E5，E7）的正常转录本表达水平与野生型相比明显下降；而 E1 突变体与野生型质粒的 mRNA 表达量无明显差异。此外，在放线菌酮处理后，E5 和 E7 突变型质粒的 mRNA 表达量明显升高。而野生型及 E1 质粒的 mRNA 表达量无明显变化。
结论 本研究通过构建 SMN1 小基因体外模型及 NMD 体外实验发现无义突变 c.683T>A 及 c.844C>T 发生了 NMD，而无义突变 c.43C>T 未触发 NMD，提示其发生了 NMD 逃逸。这为 NMD 在 SMA 发病机制中的作用提供了线索。

PU-2525

免疫球蛋白与 hsCRP 在膝骨关节炎中的相关性分析

甘苓伶
绵阳市中心医院

目的 探讨免疫球蛋白与超敏 C 反应蛋白（high-sensitivity C reactive protein， hsCRP）在膝骨关节炎（knee osteoarthritis, KOA）中的相关性。
方法 回归性收集绵阳市中心医院 2019 年 1 月-2021 年 3 月诊断为 KOA 的患者 112 例（KOA 组）及健康体检者 89 例（HC 组），比较两组的 hsCRP、免疫球蛋白(immunoglobulin, Ig)和补体(complement, C)水平有无差异。分别根据 hsCRP 和 Kellgren-Lawrence (K-L)分级将 KOA 患者分为不同的组，并比较上述免疫指标的差异。分析 hsCRP、K-L 分级与免疫指标之间的相关关系。
结果 与对照组相比，KOA 患者血清中 hsCRP 和 IgE 升高，而 IgG 和 IgM 降低（P<0.05）。hsCRP>3g/L 的 KOA 患者 IgA 和 C4 水平较 hsCRP≤3g/L 的高（*P*<0.05）。在不同的 K-L 分级中，

显示Ⅰ和Ⅲ组间 IgA 和Ⅰ，Ⅳ组间 IgE 有统计学差异（*P*<0.05）。相关性分析显示，hsCRP 与 C3、C4 呈正相关（*r* 分别为 0.275，0.255，*P* 均<0.001），K-L 分级与 IgA 和 IgE 呈正相关(*r* 分别为 0.270，0.240，*P* 均<0.05)。

结论 免疫球蛋白的表达失衡与膝骨关节炎的炎症过程相关，可能对进一步认识骨关节炎的发病机制和临床抗炎治疗有一定的应用价值。

PU-2526

男男性行为者 HIV 辅助伴侣告知与伴侣检测：一项随机对照研究

胡清海、徐俊杰、姜拥军
中国医科大学附属第一医院

背景 辅助伴侣告知（PN）是提高异性性传播途径 HIV 感染者伴侣检测 HIV 的有效方法，但其在男男性行为人群（MSM）中的实施效果研究较少。

方法 我们在辽宁省沈阳市开展了一项随机对照试验，目的是在新诊断 HIV 阳性的 MSM 中比较被动 PN 与辅助 PN 推动伴侣 HIV 检测的效果。在采用传统伴侣告知策略的被动 PN 组（对照组）中，我们鼓励研究对象（索引病例）向其伴侣披露自身 HIV 感染状况，并推动其伴侣接受 HIV 检测。在辅助 PN 组（干预组）中，我们向索引病例提供 HIV 自检包（HIVST），由他们传递给伴侣进行 HIV 检测；或者在索引病例知情同意后，由 MSM 社区服务组织（CBO）的工作人员以匿名帮助联系并推动其伴侣接受 HIV 检测（含金钱激励）。研究的主要结局事件为在随机分组并实施干预后的四个月内索引病例推动伴侣接受 HIV 检测的比例是否有差异。该研究已在 chictr.org.cn（ChiCTR1800017813）预注册。

结果 2017 年 8 月至 2019 年 1 月，共招募了 187 名新诊断 HIV 阳性的 MSM。索引病例被随机分配到被动 PN 组（90 人）或辅助 PN 组（97 人）。在干预后四个月的随访中，被动 PN 组的每个索引病例的伴侣人数，披露/推荐伴侣检测人数，伴侣检测人数和 HIV 阳性人数分别为 3.2、0.7、0.2、0.03 个，而辅助 PN 组分别为 4.0、1.0、0.5 和 0.11 个。辅助 PN 组中有 35%的索引病例推动其伴侣进行了 HIV 检测，而被动 PN 组仅为 17% (P = 0·004)。辅助 PN 组被告知的伴侣中有 49%接受了 HIV 检测，而被动 PN 组仅为 28% (P = 0·007)。

结论 HIV 自我检测和 CBO 外展服务相结合的辅助伴侣告知策略可以显著增加 HIV 阳性 MSM 伴侣的 HIV 检测率。

PU-2527

免疫球蛋白与超敏 C 反应蛋白在膝骨关节炎中的相关性分析

甘苓伶
电子科技大学附属医学院绵阳市中心医院

目的 探讨免疫球蛋白与超敏 C 反应蛋白（high-sensitivity C reactive protein， hsCRP）在膝骨关节炎（knee osteoarthritis, KOA）中的相关性。

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C4 呈正相关（*r* 分别为 0.275，0.255，*P* 均<0.001），K-L 分级与 IgA 和 IgE 呈正相关(*r* 分别为 0.270，0.240，*P* 均<0.05)。
结论 免疫球蛋白的表达失衡与膝骨关节炎的炎症过程相关，可能对进一步认识骨关节炎的发病机制和临床抗炎治疗有一定的应用价值。

PU-2528

2 例粪类圆线虫感染病例的分析讨论

郭江梅
江西省人民医院

目的 通过粪类圆线虫感染病例诊治过程分析，提高对粪类圆线虫病的综合认识，为有效防治提供依据。
方法 针对 2 例粪类圆线虫感染病例，1 例为肾移植术后 7 个月，正在接受免疫抑制剂治疗；另 1 例是 2 月之前曾使用激素时长 7 个月的患者。查阅两患者既往史、用药史、临床症状、实验室检测等资料，分析感染粪类圆线虫的高危因素，探讨感染后的控制及治疗措施。
结果 免疫力低下、长期使用激素、免疫抑制剂及基础疾病较多的患者是感染粪类圆线虫的高风险人群。对于肾移植术后感染粪类圆线虫的患者，会面临驱虫用药时间较长，而免疫抑制剂也不能停用的两难境地。文中两例，阿苯达唑日用量不同，已停用激素的患者，阿苯达唑 400mg/d,药用时长 13 天；肾移植术后患者阿苯达唑 200mg/d，药用时长超过 60 天，期间抗排异药物未变。治疗上都获得了理想效果。
结论 粪类圆线虫在不同人群中感染率不同，感染后致病作用差异大，医务人员要区别对待，并予以重视。阿苯达唑驱虫药，日用量可视病情而异，早期、足程治疗可避免引发播散性超度感染的严重后果。

PU-2529

临床实验室标准化管理体系

陈淑婧
武城县人民医院

随着“以患者为中心，以提高医疗服务质量为核心”的医院管理活动在全国深入展开，为临床实验室的进一步发展提供了机会。根据《医疗机构临床实验室管理方法》的要求，结合我国临床实际工作，对医学实验室进行科学化、规范化、标准化管理。

PU-2530

抗 Jo-1 抗体与疾病诊断相关性的回顾性分析

杨懿祺、李欣
南方医科大学南方医院

目的 探究抗 Jo-1 抗体联合患者临床症状在疾病诊断上的意义，为该指标的临床应用提供参考和依据。
方法 将 2019-2020 年南方医院临床资料完整的 122 例抗 Jo-1 抗体阳性患者作为阳性组（观察组），以 244 例抗 Jo-1 抗体阴性、抗核抗体（antinuclear antibody, ANA）阳性患者作为阴性组（对照组）。收集两组患者的一般资料，疾病诊断，临床症状，对两组资料进行统计学分析。

结果 观察组患者男女比例为 1:1.39，平均年龄为 50（39，58.25）岁，两组患者性别、年龄组成差异均无统计学意义（P>0.05）。在临床症状方面，阳性组肌痛发生率（18.85%）高于阴性组（4.51%）（P<0.05）。在疾病诊断上，阳性组患者多发性肌炎/皮肌炎（polymyositis/dermatomyositis, PM/DM）发生率（29.51%）高于阴性组（2.87%）（P<0.05），且阳性组患者发生 PM/DM 的风险约为阴性组患者的 14 倍；糖尿病发生率阳性组（19.67%）高于阴性组（10.66%）且差异有统计学意义（P<0.05），两组糖尿病分类比例相近，均以 2 型糖尿病居多；间质性肺部病变（interstitial lung disease, ILD）以阳性组发生率较高，但两组比较无统计学差异（P=0.055）；恶性肿瘤以阴性组患者发生率略高，但差异无统计学意义（P=0.203）。
结论 抗 Jo-1 抗体阳性患者以中老年女性为主，临床症状以肌痛发生率高，疾病诊断以 PM/DM 及糖尿病，尤其是 2 型糖尿病，发生率高，提示抗 Jo-1 抗体联合临床症状对疾病诊断有重要意义。

PU-2531

肠道菌群与甲状腺相关疾病的研究进展和思考

李营
德州市人民医院

肠道菌群是人体内最大的共生菌群，与人体构成一个动态平衡的微生态系统，在促进人体健康发育方面有着重要作用。当生态失衡时，便可能诱发内分泌及免疫相关疾病、炎症、肿瘤等，这已在糖尿病、炎症性肠病、结直肠癌、肝癌、乳腺癌的研究中得到证实。甲状腺作为机体重要的内分泌腺, 其分泌的甲状腺激素在新陈代谢、生长发育等方面起关键作用。越来越多的证据表明,肠道菌群在肠-甲状腺轴功能反应中起了十分重要的作用,由此衍生出肠道菌群-肠-甲状腺轴这一新的概念。肠道菌群可以通过肠-甲状腺轴影响免疫系统，进而对甲状腺功能产生影响。健康的肠道菌群不仅对免疫系统活性有益，而且对甲状腺功能也有益。甲状腺和肠道疾病普遍并存，桥本氏甲状腺炎（HT）和 Graves 病是最常见的自身免疫性甲状腺疾病（autoimmune thyroid diseases ,AITD）。研究发现 AITD 和甲状腺癌都存在肠道菌群失调，发现致癌性和炎症性菌株数量增加。机制可能涉及到以下几个方面：（1）肠道菌群通过促进炎症反应和降低免疫耐受来改变免疫应答，破坏肠膜，导致肠通透性增加，导致局部炎症。（2）肠道菌群在营养物质、药物和激素的代谢中发挥至关重要的作用，包括外源性和内源性碘甲状腺原氨酸和涉及甲状腺体内平衡的微量营养元素，包括碘、硒、锌和铁。（3）肠道菌群紊乱可能导致甲状腺素吸收不良。动物研究表明益生菌对甲状腺疾病有益，可作为甲状腺疾病的辅助疗法，但仍需要人体研究来进一步阐明肠道-甲状腺轴的重要性和干预的可能性。考虑到上述肠道菌群和微量营养元素对甲状腺功能和药物的潜在影响，提示可以根据患者的肠道细菌组成做出更具体更精准的多元素预防策略，诊断方法，评估方案和治疗方案。未来有必要进行充分的人类研究来评估肠道微生物群对甲状腺功能和疾病的影响。

PU-2532

DSA 在肾移植术方面的研究与进展

赵云平
昆明市第一人民医院甘美医院

目前在临床中，肾移植是治疗肾衰竭最有效的治疗方法之一。 而即便在开展进行肾移植术后，移植物在受者体内依然面临着诸多挑战。抗体介导的排斥反应（AMR）的发生就是导致移植肾失去功能的主要原因，而 AMR 主要是由受者体内存在的 DSA 介导的，研究发现，患者体内的供者特异性抗体无论是预存 DSA 还是新生 DSA 都对移植物的存活产生着极其不利的影响。DSA 的检测及后期动态监测对肾移植术后受者体内移植物的存活及正常功能都有着极其重要的意义。因此针对 DSA 的来源、检测 DSA 的方法和技术的进步就变得非常重要。

PU-2533

区域检验中心的建设和前景

王晓
武城县人民医院

建设区域检验中心为了配合医共体的建设，实现本区域内的检验资源共享,增加经济收入,提升检验人员自身业务水平,为患者就诊的检验质量提供保障,使患者在基层医院也可以享受到更专业更高水平的检验技术,以“一切为了病人”为宗旨，区域检验中心的前景不可限量。

PU-2534

甲型肝炎病毒 2C 蛋白的解旋活性研究

程振云
郑州大学第一附属医院

将甲型肝炎病毒（HAV）编码的 2C 蛋白与同属小 RNA 病毒目的其它几种病毒的氨基酸序列进行同源比对后，发现该蛋白的氨基酸序列中含有三个比较保守的氨基酸基序，根据同源比对的结果设计了 2C 基因的特异性扩增引物，并在引物中引入适当的酶切位点（XbaI 和 KpnI），通过 RT-PCR 方法扩增获得 HAV 非结构蛋白 2C 的基因片段，回收该目的片段并与 T 载体进行连接后，转化到 DH5α 的感受态细胞中，挑选阳性克隆并提取其质粒，将测序正确的质粒和 pFastBacTMHTA-MBP 载体进行双酶切并回收目的片段，连接后转化到 DH10BacTMEcoli 感受态细胞中获得重组穿梭载体，经转染和感染昆虫细胞 Sf9 后，获得重组蛋白 MBP-2C，通过 SDS-PAGE 和 western-blot 分析，检测到 2C 蛋白成功表达，并确定了 2C 蛋白的解旋功能。

PU-2535

临床医学检验质量控制影响因素的探讨

马春苗
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 分析和探讨临床医学检验质量控制的影响因素，以便采取针对性控制与管理措施，提升检验质量。
方法 选取在本院进行临床医学检验的患者 300 例作为研究对象，所有患者均严格按照临床规范要求，进行检验准备、样本采集及处理和分析，当结果与预期不符、样本丢失或污染、结果差异较大等，均视为检验失误。采用 SPSS20.0 统计学软件对数据进行处理，以 P＜0.05 为差异有统计学意义，分析患者出现检验质量问题原因及质量影响因素。
结果 经过对比分析发现，在 300 例患者 812 例次检验中，失误为 36 例，占比 4.43%，且在准备阶段失误或误差概率最高，其中以患者未进行良好检验前准备为主要影响因素，与其他阶段相比，差异有统计学意义（P＜0.05）。
结论 临床检验工作开展进行时，需要充分考虑到影响因素及质量控制关键点所在，根据以上分析结果来看，尤其在检验准备阶段，受患者综合影响及采集等影响，导致最终检验质量出现问题影响因素相对较多。而患者对检验配合程度及重视程度不够，则会影响到相关检验结果准确性。针对这一特点，就临床实际工作情况来看，需要加强与完善准备阶段、采集阶段及检验阶段三个阶段的质量管控措施，做好健康宣教，提前检查标本采集器皿、部位等，相关专业人员做好专业学习及控制工作。临床医学检验过程中，不同阶段所存在影响质量因素具备着一定差异，要明确常见质量危险因素，采取针对性控制与管理措施，提升检验质量。

PU-2536

肝移植患者术后 ALT、AST 和 TBIL 的变化分析

顾怡[1]、周景艺[1]、沈薇[2]
1. 上海交通大学医学院附属仁济医院
2. 上海交通大学医学院附属仁济医院

目的 通过分析肝移植术后 ALT、AST 和 TBIL 变化规律，协助临床医生综合判断手术效果。
方法 观察分析 96 例 2020 年我院肝移植患者术前及术后 1 天，2 天，4 天和 7 天的丙氨酸氨基转移酶（ALT），天门冬氨酸氨基转移酶（AST），总胆红素（TBIL）的变化规律。
结果 96 例患者根据原发病，分为重肝组（N=24 例）和肝硬化组（N=72 例），术前及术后 1 天，2 天，4 天和 7 天 ALT 的均值分别为 78U/L 和 27.5U/L，289 U/L 和 482.5U/L，270.5 U/L 和 351.5U/L，158 U/L 和 190U/L，102.5 U/L 和 98U/L，AST 的均值分别为 106.5U/L 和 43U/L，422 U/L 和 947U/L，197 U/L 和 283U/L，55U/L 和 66.5，42.5U/L39U/L，TBIL 的均值分别为 485.7μmol/L 和 37.1μmol/L，260.5μmol/L 和 78μmol/L，138.6μmol/L 和 50.6μmol/L，93.5μmol/L 和 32.25μmol/L，62.6μmol/L 和 26.45μmol/L。
结论 重肝组 ALT 和 AST 术后先增高，再逐步恢复正常，ALT 的增幅明显小于肝硬化组，说明重肝组的缺血再灌注损伤较小，术后 AST 比 ALT 升的快，降得也快，变化更敏感。重肝组术前总胆红素明显高于肝硬化组，术后总胆红素逐步下降，肝硬化组术后略升高，然后逐步下降。

PU-2537

检验科预防医患纠纷的策略分析

邢银婷、白晶玲
哈尔滨医科大学附属第一医院

目的 本文旨在分析并提出检验科预防医疗纠纷的策略。
方法 通过临床实践工作，总结近期医患纠纷恶性事件，分析检验科工作人员在面对医疗纠纷中应采取哪些策略，能有效预防及处理面临的医疗纠纷，避免伤医事件的发生，同时维护患者的利益不受侵犯。
结果 提高检验科工作人员的检验知识及临床思维，综合素质、对患者的利益维护的责任感，建立检验监管保障体系，逐步推广医院检验的信息化、透明化操作，可以作为各级医院检验科预防医患纠纷的策略。
结论 上诉措施已证明有助于建立融洽的医患关系，降低医疗纠纷发生率，值得推广应用。

PU-2538

尿液检验、生化检验在糖尿病诊断中的对比

徐燕、黄婷、汤伟明、鲍微、俞小飞
溧阳市人民医院

目的 对比分析尿液检验与生化检验对糖尿病的诊断价值。
方法 以我院收治的糖尿病患者 50 例为研究对象，即生化组，研究时段选取范围 2019 年 1 月～2019 年 10 月，随机选取同期体检者 50 例为对照组，两组都进行生化检验及尿液检验，以患者检验有效率、检验满意度、血糖指标、血脂指标为观察指标，并统计对比观察结果。
结果 生化组进行血糖检测的有效率为 100%、检验满意度为 98.00%，显著高于生化组进行的尿糖检测（P＜0.05）。生化组空腹血糖（FPG）、糖化血红蛋白（HbA1c）分别为（7.86±1.32）

mmol/L、（8.91±1.26）%，均显著高于对照组（P＜0.05）。生化组总胆固醇（CHOL）、甘油三酯（TG）、低密度脂蛋白胆固醇（LDL-C）、高密度脂蛋白胆固醇（HDL-C）分别为（6.41±0.52）mmol/L、（2.89±0.36）mmol/L、（3.92±0.31）mmol/L、（1.09±0.20）mmol/L，与对照组比较具有显著差异（P＜0.05）。

结论 在糖尿病诊断中，生化检验有效性显著高于尿液检验，两者结合起来更有利于临床诊断与治疗。

PU-2539

疫情背景下接收多单位送检新型冠状病毒核酸标本管理方式探讨

陈曦妍、罗立权
乐山市市中区人民医院

目的 确保外单位送检新型冠状病毒核酸标本分析前质量，高效准确完成实验室内标本处理流程，即时反馈报告并上传国家平台。

方法 外单位与实验室利用信息化平台进行数据交换，包括被检人信息录入、标本核收、报告出具、信息上报等流程，同时构建网络沟通平台，实时交流传递信息；实验室制定可操作性强的标准操作程序（SOP）文件及工作手册；外包物流系统至第三方，专业转运标本。

结果 新冠病毒核酸标本保质保时送达实验室，实验室按既定流程快速处理标本。每日平均检测500（237，684）份核酸标本情况下，外单位标本到达实验室后出具报告平均时间为 3 小时 16 分钟（2 小时 1 分钟，5 小时 16 分钟）。

结论 网络实时互通与信息化平台在多单位合作中不可或缺，多部门规范一致的操作流程为实验室分析前、中质量控制保驾护航，此疫情背景下分子实验室接收多单位送检标本模式亦为日后区域医学检验中心管理方式提供参考。

PU-2540

甲状腺细针穿刺脱落细胞学检查在临床中的应用价值

韩静颖
山东第一医科大学附属省立医院

目的 探讨甲状腺细针穿刺细胞学在临床中的应用价值。

方法 2017 年至 2018 年 5 月选择在本院诊治的 51 例甲状腺结节患者作为研究对象，所有患者都给予甲状腺细针穿刺，并同时送检脱落细胞学检查及病理分析。经过脱落细胞学检查下分析后，与病理结果比对。

结果 在 52 例患者中，甲状腺细针穿刺脱落细胞学检查中阳性 21 例，阴性 26 例,+/-4 例。病理诊断阳性 23 例阴性 28 例，符合率达 82%。

结论 甲状腺细针穿刺脱落细胞学检查是一项准确可靠、简单、经济的术前诊断方法，有很好的临床应用价值。

PU-2541

免疫学检验联合检测在诊断类风湿关节炎诊断中的应用效果观察

李诗达
荣县人民医院

目的 探讨免疫学检验联合检测在诊断类风湿关节炎诊断中的应用效果。
方法 选取我院 2020 年 1 月-2021 年 1 月收治的 30 例类风湿关节炎作为本次研究对象，并将其设置为观察组；同一时期入院检查的 30 例健康体检患者作为本次对照组，两组分别进行免疫学检验联合检测，对比两组诊断效果。
结果 观察组的 RF 与抗 CCP 指标检测阳性率较对照组高，且患者的免疫球蛋白 G 水平高于对照组，（$p<0.05$）。
结论 免疫学检验联合检测诊断类风湿关节炎有极好的效果，能够提升患者的阳性检出率，值得推广。

PU-2542

检验科噪音污染现状及应对策略

邢银婷、白晶玲
哈尔滨医科大学附属第一医院

目的 本实验通过检测检验科声音分贝值，对比国家环境保护局提出的医院噪音标准，判断检验科噪音污染严重程度，并探讨解决措施。
方法 选择 SMART SENSOR AS824 数字分贝检测仪检测检验科共计 8 台大型检验分析仪及相应审核报告处作为主要研究对象，选择办公室及窗边较安静 2 处进行对照。
结果 所有分析仪及相应结果审核发放处均出现严重的噪音污染，仪器旁平均分贝值为 72.13dBA，超出医院噪音标准的 44.25%；结果发放处平均分贝值为 68.29dBA，超出医院噪音标准的 36.57%。
结论 检验科噪音污染的原因清晰，因噪音污染对医务人员健康损害较大，应在声源、传播媒介及接受者等 3 个方面采取措施，来降低噪音污染导致的职业损害。

PU-2543

D -二聚体 纤维蛋白原与 C 反应蛋白水平检测对早期诊断尘肺的价值分析

李明[1]、王雯茜[2]、张新静[1]
1. 新乡市职业病防治研究所，职业病科
2. 新乡市中心医院

目的 探讨 D-二聚体（DD）、纤维蛋白原（Fib）与 C 反应蛋白（CRP）水平检测对早期诊断尘肺的价值。
方法 选取 2018 年 8 月至 2020 年 8 月我院收治的 70 例尘肺患者作为研究组，按是否合并肺心病分为 2 个亚组，即研究 1 组（14 例，合并肺心病）、研究 2 组（56 例，单纯尘肺）。另外选取同期 40 名健康体检者作为对照组，检测 2 组患者血浆 DD、Fib 及 CRP 水平，并对比研究组不同分期患者血浆 DD、Fib 及 CRP 水平。
结果 研究组患者血浆 DD、Fib 及 CRP 水平均高于对照组，差异有统计学意义（$P<0.05$）。研究 1 组患者血浆 DD、Fib 及 CRP 水平均高于研究组、研究 2 组，差异有统计学意义（$P<0.05$）。研究组不同分期患者血浆 DD、Fib 及 CRP 水平相比，差异无统计学意义（$P>0.05$）。

结论 尘肺患者血浆 DD、Fib 与 CRP 水平均高于健康人群，检查其水平对早期诊断尘肺具有重要意义。

PU-2544

四川省资阳市雁江区老年人 ALT 检测结果分析

郑鑫、李军
四川金域检验医学检验有限公司

目的 通过对四川省资阳市雁江区老年人群的丙氨酸氨基转移酶结果分析，了解四川省资阳市雁江区 60-90 岁老年人群肝功能情况以及 ALT 上升的比例关系。
方法 回顾性分析 2021 年 3 月至 2021 年 5 月的 61308 例四川省资阳市雁江区老年人丙氨酸氨基转移酶结果检测，并按不同性别、年龄对检测结果进行统计、比较、分析。
结果 2021 年 3 月-5 月共有 61308 名 60-90 岁资阳市雁江区老年人参与健康体检 ALT 项目检测，60-70 岁男性 ALT 升高共 686 例，比例为 5.56%；女性共 1215 例，比例为 7.76%。71-80 岁男性 ALT 升高共 455 例，比例为 3.54%；女性共 736 例，比例为 5.31%。81-90 岁男性 ALT 升高共 63 例，比例为 2.05%；女性共 118 例，比例为 3.35%。数据显示，女性老年人 ALT 异常率明显高于男性老年人年龄段，并且在 60-90 岁中男性和女性都随着年龄段的增长，ALT 升高比例在降低。
结论 丙氨酸氨基转移酶（ALT），ALT 主要存在于肝、肾、心肌、骨骼肌、胰腺、脾、肺、红细胞等组织细胞中，同时也存在于正常体液如：血浆、胆汁、脑脊液及唾液中，但不存在于尿液中，除非有肾脏损害发生。当富含 ALT 的上述组织细胞受损时，ALT 从细胞中释放增加，进入血液后导致 ALT 活性上升。当除了病理性因素导致的 ALT 上升，也有许多非病理性因素导致的 ALT 上升，比如生活压力、体重指数、疲劳、服用药物等等。通过对 ALT 上升率进行分析发现，60-90 岁随年龄段的段的增加 ALT 升高比例在降低，可能老年人随着年龄的增加，儿女的长大随即肩负起的家庭重任，生活压力越来越小有关。而女性老年人 ALT 异常率明显高于男性老年人年龄段，可能在 60 岁以后，女性体质比男性体质易胖，由于老年人女性基础代谢率会下降，平均每 10 年下降 5%，特别是绝经以后的妇女。中老年以后如果摄取食物的能量和往常一样，就会因为基础代谢率的下降而变胖。所以我们在日常生活中应该合理的控制饮食，注意休息，多关注自己及家人的身体健康。当然当 ALT 检测升高时，应增加检测项目，查出具体 ATL 异常的原因。

PU-2545

检验科危急值报告现状分析

张倩
德州市人民医院

目的 危急值 （Critical Values）是指某项或某类检验异常结果，而当这种检验异常结果出现时，表明患者可能正处于有生命危险的边缘状态，临床医生需要及时得到检验信息，迅速给予患者有效的干预措施或治疗，就可能挽救患者生命，否则就有可能出现严重后果，失去最佳抢救机会。“危急值”报告制度的制定与实施，能有效增强医技工作人员的主动性和责任心，提高医技工作人员的理论水平，增强医技人员主动参与临床诊断的服务意识，促进临床、医技科室之间的有效沟通与合作。检验科及时准确的检查、检验报告可为临床医生的诊断和治疗提供可靠依据，能更好地为患者提供安全、有效、及时的诊疗服务。
方法 利用瑞美实验室信息系统（LIS）统计检验科 2020 年 1 月至 2020 年 12 月发生的 10602 例危急值，对危急值项目的上报率、及时率、科室分布、时间分布、标本类型等进行分析，并提出持续改进意见。

结果 医院 2020 年危急值上报率为 98.86% ，及时率为 95.51%，危急值排名前五位的项目分别是：B 型钠尿肽（BNP）、高敏心肌肌钙蛋白 I（hs-cTnI）、尿素（UREA）、血清总二氧化碳（TCO2）和钾（K）。发生危急值最多的科室是心内科、ICU、肾内科、急诊科和呼吸内科。一天中危急值发生高峰时段为 9:00 至 15:00，低峰时段为凌晨 1:00 至 7:00。一周中分布规律为周一至周五较多，周六、周日相对较少。从标本类型分：住院危急值最多，门诊危急值最少，生化危急值最多，其次为血液分析。
结论 危急值的管理需要检验科、 临床科室、 医务部、护理部等多部门沟通合作，过程复杂、涉及人员较多，应加强重视对危急值的管理，并将其作为医疗质量考核的一个重要的内容。实验室需要定期对危急值报告制度进行评估和分析，不断完善危急值项目和范围，解决危急值报告的影响因素，保证快速、高效的将危急值结果报告。作为临床患者的桥梁，检验科定期回顾分析危急值报告数据，修订危急值报告制度，为患者提供更好的服务。

PU-2546

缺氧与类风湿关节炎

李山山
哈尔滨医科大学第一附属医院

类风湿性关节炎（RA）是一种自身免疫性疾病，其特征在于炎症性滑膜增生，关节僵硬，进行性骨侵蚀和软骨破坏。RA 会导致血管密度的改变，新血管形成增加，进而形成慢性炎症和骨骼破坏。涉及多种细胞，其中成纤维样滑膜细胞（FLSs）被认为是导致疾病发生发展的主要细胞，其他免疫细胞大量涌入（如 T 淋巴细胞和巨噬细胞/单核细胞），起到维持炎症的作用。近年来发现缺氧与其密切相关，在此过程中，缺氧是炎症介质的主要调节剂。本文重点探讨了对缺氧和 RA 关系的最新进展。

PU-2547

资阳市地区临床检验危急值管理现状调查

魏铃程
资阳市第一人民医院

目的 调查资阳市范围内各级医院共 166 家医疗机构临床检验危急值管理制度的制订、实施、质量控制和效果评估，并基于实际存在的问题，结合文献资料和专家意见提出建议。
方法 采用网络问卷调查和电话问卷的方式向资阳市各级医院实验室发出问卷，使用专用统计软件对数据进行分析。
结果 有 158 家实验室提交信息，以公立医院、二级和三级综合医院为主。所有的实验室均制订了危急值报告制度，98.10%的实验室有危急值项目清单。有 57.14%的实验室是与临床共同制订了危急值项目；有 35.71%是借鉴其他医院，7.14%是实验室内部制订。仅有 15.58%的实验室针对不同科室设置了个性化的危急值。除血气外，有 74.68%的实验室将血清钾、血糖、白细胞计数、血红蛋白、血小板计数、凝血酶原时间、活化部分凝血活酶时间设为危急值项目。72.73%的实验室规定危急值报告时限在 30 min 内，但 7.79%的实验室对危急值报告时限没有要求。
结论 资阳市医疗机构危急值报告制度在危急值制度的实施过程、危急项目和界限的制订中还存在较大问题，各级医疗机构实验室需根据自身情况，并采纳临床医生的意见综合考虑并结合 2020 年 1 月《急诊检验能力建设和规范中国专家共识》中急诊检验危急值管理，制订出合适的危急值管理体系。

PU-2548

区域血细胞分析（CBC 项目）结果互认体系的构建及应用

王华国
资阳市第一人民医院

目的 为了落实国家卫健委构建三级质量体系的要求以及区域血细胞检验结果互认的需要，进行区域内的血细胞 CBC 项目的互认体系的构建及应用,最终达到区域内检验结果的同质化及一致性。
方法 根据卫生行业标准 WS/T406-2012 及 CLIA'88 能力比对检验的分析质量要求文件的要求，以市检验质控中心为平台，通过培训及进行二级及以上医疗机构实验室结果比对，在比对的实验室满足质量要求后，进而县、区各质控工作站向更多辖区内的医疗机构实验室进行结果互认的辐射。
结果 市质控中心实验室血液细胞分析质量符合要求，与上级临检中心比 CBC 项目达到＜1/4TEa、＜1/5 TEa 及＜1/3 TEa，持续与区域内实验室进行结果比对 CBC 项目达到＜1/3TEa。进行检验结果互认体系的构建及应用后，资阳市 40 余家医疗机构实验室 CBC 项目均符合行业标准要求。
结论 虽然各医院间的检测系统不同，质量标准也有所差异，但通过建立检验结果互认的体系，进行结果互认体系的运用，将区域内实验室检验结果控制在了允许范围内，为实现血细胞分析检验结果互认打下了良好的基础。

PU-2549

根本原因分析法在临床实验室室间质评管理中的应用

冯倩、邓德耀、周林华、薛云松
云南大学附属医院

目的 探讨应用根本原因分析法的管理方式查找室间质评不合格原因，提升检验质量的效果。
方法 云南省第二人民医院检验科运用根本原因分析法的理论和方法，建立质量改进小组，按照根本原因分析法的步骤，对室间质评不合格项目开展调查，分析导致出现不合格的根本原因，并逐条进行针对性改善，制定核查指标，对比改进前后室间质评合格情况。
结果 开展改进小组活动后，国家卫健委临床检验中心全国干化学室间质量评价的成绩由改进前的 35%，上升到改进效果追踪的 1 年中历次成绩分别为 97%、100%、98%，目标达成率为 100%。并且科室人员采用科学的手段进行质量管理的能力有所提高，解决问题的能力提高了 11%、沟通协调能力提高了 27%、自信心提高了 35%、团队凝聚力提高了 11%、工具运用能力提高了 55%、创新能力提高了 15%。
结论 采用根本原因分析法管理方式能够实际有效的解决室间质评不合格的问题，提高工作人员们运用管理工具解决检验科实际问题的能力。

PU-2550

双向 LIS 系统优化尿常规标本检验周转时间的探讨

李阳
郑州大学第一附属医院

目的 统计门诊化验室在使用双向 LIS 信息系统处理尿常规标本检测前后对尿常规标本检验周转时间的影响。
方法 利用医院的 LIS 系统统计门诊化验室使用双向 LIS 系统检测标本前后的的尿常规检验周转时间，计算 TAT 时间合格率。

结果 门诊检验尿常规检验周转时间目标值是 30min，使用双向 LIS 传输之前两个月的合格率分别为：84.53%和 83.31%。使用双向 LIS 传输之后的两个月的合格率分别为：91.23%和 94.69%
结论 双向 LIS 系统传输可有效提高尿常规检测的检验周转时间，增加尿常规检测的准确性。

PU-2551

297 例肺结核患者结核菌耐药性分析

汤新乐[1]、安嘉俊[2]
1. 新疆医科大学第六附属医院
2. 新疆医科大学第八附属医院

目的 对 297 例肺结核患者行结核耐药性检测并分析。
方法 搜集 2021.3-2021.6 月新疆医科大学第八附属医院根据《wS2882017 肺结核诊断》确诊的 297 例患者的痰培养标本及患者信息，利用结核分枝杆菌利福平耐药突变检测试剂盒、结核分枝杆菌异烟肼耐药突变检测试剂盒、结核分枝杆菌氟喹诺酮耐药突变检测试剂盒、结核分枝杆菌乙胺丁醇耐药突变检测试剂盒，分别对利福平（RFP）、异烟肼（INH）、氟喹诺酮类、乙胺丁醇（EMB）进行耐药性检测。
结果 总耐药率为 32.32%，耐多药率为 11.45%，多耐药率为 1.01%，任一耐药率分别是 INH（22.90%）、RFP（12.79%）、EMB（8.08%）、氟喹诺酮（5.39%），EMB、INH、RFP 均出现单耐药。
结论 297 株结核分枝杆菌总耐药率和耐多药率与全国第五次结核病流行病学抽样调查报告相比，总耐药率低而耐多药率高；一线抗结核药物均出现单耐药，除 EMB 外，单耐药率＞5%；多耐药率为 1.01%。耐药情况仍不容忽视，需持续进行耐药性监测和提升临床医师使用抗结核药物的正确意识。

PU-2552

血清免疫球蛋白、补体和同型半胱氨酸在儿童肾病综合征诊断中的潜在价值分析

王晔
江西省儿童医院

目的 探究血清免疫球蛋白、补体和同型半胱氨酸在儿童肾病综合征中的含量与同时期体检的相同年龄段的正常儿童的异同，建立区分标准，分析其检测价值及临床意义，并推测导致其差异存在的可能机制。
方法 收集江西省儿童医院自 2019 年 12 月至 2020 年 1 月确诊为肾病综合征的患儿 25 例作为观察组，收集同时期体检的相同年龄段的正常儿童 30 例作为对照组，检测其血清免疫球蛋白、补体和同型半胱氨酸的水平，使用 SPSS 软件分析单个研究指标诊断肾病综合征患儿的最佳截断值，分析上述部分指标联合检测区分肾病综合征患儿与正常儿童的潜在价值。
结果 与对照组健康儿童相比，原发性肾病综合征患儿血清中的 IgG 和补体 C3 水平下降，差异有统计学意义（P<0.05）；IgA、IgM、IgE 水平和同型半胱氨酸水平显著升高（P<0.01）。肾病综合征患者的补体 C4 水平与对照组健康儿童相比有所下降, 但差异没有统计学意义（P>0.05）。区分肾病综合征患儿与健康儿童相关研究指标的最佳截断值为：HCY 为 10.5g/L；IgA 为 1.06 g/L；IgM 为 1.02 g/L；IgE 为 103.15 IU/mL；IgG 为 6.72 g/L。
结论 原发性肾病综合征患儿的血清 IgG、IgA、IgM、IgE、补体 C3 和同型半胱氨酸水平与正常儿童相比存在差异，尤其是 IgA、IgM、IgE 水平和同型半胱氨酸水平显著升高，对肾病综合征早期诊断或疗效评估有一定的价值。

PU-2553

婴儿肝炎综合征患儿谷胱甘肽还原酶检测的临床意义

李卫明
江西省儿童医院

目的 探讨谷胱甘肽还原酶检测在婴儿肝炎综合征中的临床意义
方法 本实验收集自 2018 年 7 月至 2019 年 1 月就诊于江西省儿童医院并确诊的 HIS 患者共 70 例，以及正常体检者 30 例。记录患者年龄、性别、诊断、肝功能指标等。统计学处理采用 SPSS22.0 统计软件，如果数据符合正态分布，则用 表示计量数据，两组间比较采用 t 检验，符合正态分布的计量数据采用 Mann-Whitney U 秩和检验。正态分布的计量资料之间的相关性分析采用 Pearson[xb21cn1]，非正态分布的资料相关性分析采用 Spearman 相关分析。临界值用 ROC 曲线分析，P＜0.05 为有差异，认为具有统计学意义。
结果 本实验共纳入 HIS 患者 70 例，其中女性患者 35 例，男性患者 35 例，HIS 患者血清 GR 平均水平为 95.54（53.5，248.2）U/ml，正常组血清 GR 平均水平为 60.03（42.3，77.9）U/ml，HIS 患者血清 GR 平均水平显著高于正常者，组间对比存在明显差异（Z=-6.491，P=0.000）。采用 ROC 曲线分析确诊 HIS 的最佳 GR 血清浓度的临界值，结果显示确诊 HIS 的血清 GR 的最佳临界值为 72.55U/L，敏感度与特异性分别为 77.1%、93.3%，曲线下面积（AU）为 0.911。早期血清 GR 水平与 ALT、AST 水平呈负相关。
结论 血清 GR 是诊断 HIS 的重要血清学标志物，可以用于对 HIS 的早期发现。

PU-2554

海南省东方、陵水区域的育龄夫妇葡萄糖-6-磷酸脱氢酶缺乏症的检出率的筛查调查

王炜钰、陈积辉、徐春丽、陈美才
海南金域医学检验中心有限公司

目的 筛查两地葡萄糖-6-磷酸脱氢酶缺乏症患者并了解他们的患病情况，以此对他们的生活和临床用药进行一定的干预。
方法 对于这 12110 名育龄夫妇，采用葡萄糖-6-磷酸脱氢酶（G6PD）和 6-磷酸葡萄糖酸脱氢酶（6PGD）测定他们红细胞中葡萄糖-6-磷酸脱氢酶的含量。
结果 在 12110 名育龄夫妇中，检测到患有葡萄糖-6-磷酸脱氢酶缺乏症的人一共有 798 例，发病率为 6.59％。在东方市检查的 3485 例中，检出葡萄糖-6-磷酸脱氢酶缺乏症的男性和女性患者数差不多，分别为 96 例和 94 例，男性和女性的发病率分别为 5.53％和 5.42％。陵水县受检人数为 8626 人。共检出 350 名男性患者，发病率为 4.05％；共检出女性患者 258 人，发病率为 3.00％。
结论 海南省是属于葡萄糖-6-磷酸脱氢酶（G6PD）缺乏症检出率较高的地区之一，东方市和陵水地区的发病率远远高于海南省的平均发病率（3.17％）[1]。应加强对孕期夫妇的宣传教育，以促进他们了解更详细的有关于葡萄糖-6-磷酸脱氢酶缺乏症的知识，让他们对自己日常生活中的饮食进行调节，另一方面也可以使临床医生给予关注以避免严重的溶血性贫血、高胆红素血症[2]等疾病的发生。

PU-2555

Targeting the IDO-BCL2A1-cytochrome c pathway promotes apoptosis in oral squamous cell carcinoma

Qiaoping Zheng[2]、Guifang Gan[2]、Xianfu Gao[1]、Qingqiong Luo[2]、Fuxiang Chen[2]
1. Shanghai Profleader Biotech Co., Ltd
2. Ninth People's Hospital, Shanghai Jiao Tong University School of Medicine

Purpose Indolamine 2,3-dioxygenase (IDO) is the rate limiting enzyme of tryptophan degradation and plays an important role in the progress of several cancers.This research aimed to explore the role of IDO in the growth of oral squamous cell carcinoma (OSCC) cells.
Methods IDO expression in OSCC tissues was analyzed by Oncomine database and immunohistochemistry.Kaplan-Meier Plotter survival analysis was used toidentify the correlation between IDO expression and OSCC prognosis. Tryptophan (TRP) and kynurenine (KYN) content in serum samples of OSCC patients and healthy controls were determined by ultra performance liquid chromatography tandem mass spectrometry. Cell counting kit-8assay, cell proliferation assays and flow cytometerywere used to assess the effect of IDO inhibition on OSCC growth using shRNA or IDO inhibitor in vitro. Mechanistically, an apoptosis-related genes PCR array was used to explore the underlying mechanism involved in IDO-regulated apoptosis in OSCC cells. An OSCC xenograft mouse model was established to verify the predicted function of IDO inhibition and related mechanism in vivo.
Results IDO expression in OSCC tissues was upregulated. The KYN/TRP ratio in serum samples of OSCC patients was higher than that of healthy controls, indicating that IDO activity was much higher in OSCC.IDO expression was negatively correlated with OSCC prognosis. Lentivirus-mediated IDO knockdown and IDO inhibitor significantly reduced viability and promoted apoptosis of OSCC cellsin vitro andin vivowith no effect on the proliferation of OSCC cells. IDO inhibition down-regulated BCL2A1 expression and increased release of cytochrome c (Cyto C), which ultimately promoted apoptosis of OSCC cells.
Conclusion Theoverexpression of IDO promotes the growth of OSCC cells directly in vitroand in vivo. The underlying mechanism may relate to the regulation of the BCL2A1-Cyto C signal axis. IDO may be a therapeutic target for the treatment of OSCC.

PU-2556

血清标志物联合应用诊断乳腺癌的研究进展

杜纯怡
呼和浩特金域医学检验所有限公司

乳腺癌(BC)是乳腺上皮细胞在多种致癌因子的作用下，发生增殖失控的现象。它是一种类似于高血压、心脑血管病的慢性病，可在肺、肝、骨、脑等器官发生转移，并破坏其正常组织，受环境、饮食、压力等因素影响，是致女性死亡主要疾病之一。该疾病发病率仍趋于上升，目前临床对于该病的治疗手段较多，包括中药、化疗、靶向治疗、手术等[1]。随着对肿瘤疾病的深入研究，人体正常细胞在癌变的过程中部分脂类、糖蛋白会发生改变，相关抗原表达升高，处于疾病状态时该抗原会出现在血液中，且其水平随着病情进展而上升，因此临床可将脱落至体液中的抗原作为血清肿瘤标志物，通过检测标志物水平诊断疾病[2]。肿瘤标志物是一种反映肿瘤存在的化学类物质，早期诊断、早期治疗是提高生存率的关键。乳腺癌的发生与多基因损伤有关，仅通过单一指标检测的灵敏度较低，无法有效判断疾病情况，易造成漏检，因而联合检测与乳腺癌有相关性的肿瘤标志物来提高诊断效率，故本研究旨在分析这些血清指标联合检测用于乳腺癌诊断中的价值，为今后乳腺癌的诊断提供参考。

PU-2557

血清同型半胱氨酸、维生素 B12、叶酸与急性心肌梗死的相关性研究发展

杜纯怡
呼和浩特金域医学检验所有限公司

急性心肌梗死（acute myocardial infarction,AMI）是冠心病最为严重的类型。近年来，随着生活习惯的改变，急性心肌梗死的发病率逐年升高并有年轻化的趋势。普遍情况认为，老年人是 AMI 的主要发病人群，但是随着近年来经济的发展、人们生活方式的改变、社会压力的增加，近期的研究报道显示[1]AMI 的发病有越来越年轻化的趋势，再加上青年人群对 AMI 无较高的认识和警惕，容易忽视早期症状，这可能与青年人群 AMI 患病率、发病率升高密切相关。AMI 作为冠心病的急危重症，具有相当高的死亡率和致残率，不仅严重威胁人类健康和生命，而且给社会该来沉重的经济负担。血清同型半胱氨酸（homocysteine,Hcy）以及维生素 B12，叶酸等与心脑血管疾病有着密切的联系，甚至在动脉粥样硬化的发病机制中，高 Hcy 血症是一种独立危险因素[2]。故本文结合近几年来国内外相关研究，对 Hcy、维生素 B12、叶酸与急性心肌梗死的相关性作一综述。

PU-2558

探究高盐饮食促进酒精性脂肪肝疾病发展的机制

程绍民、高秀莲、许桂荣、王倩、李新、张真
禹城市人民医院

酒精是引起酒精性脂肪肝（AFLD）的明确原因，且 AFLD 的发展进程受到多种因素的影响，尤其是饮食因素。近期有研究表明，高盐饮食与脂肪细胞增大和肝损伤密切相关，本研究探究高盐饮食对 AFLD 的影响。以 8 周龄 C57BL/6J 雄性小鼠为研究对象，分别进行正常饮食（ND）、高盐饮食（HSD，4% NaCl）、酒精摄入（CE）和高盐饮食+酒精摄入（HSDE）四种处理方式干预。1 个月后，对小鼠的血清生化指标、肝脏损伤程度进行测定。

结果显示，与 ND 组相比，HSD 组、CE 组和 HSDE 组小鼠血清中天冬氨酸转氨酶（AST）、丙氨酸转氨酶（ALT）和碱性磷酸酶（ALP）的活性显著升高以及肝脏组织中的甘油三酯（TG）和丙二醛（MDA）含量显著升高，尤其是 HSDE 组显著高于 CE 组和 HSD 组，表明三组实验组小鼠肝脏均产生脂肪变，且 HSDE 组肝脏损伤程度显著高于另外两组。因此，高盐饮食可促进 AFLD 的发展进程。

PU-2559

日常样品检测结果对仪器和试剂质量监控的评估

钟政荣
上海交通大学医学院附属第九人民医院

目的 通过分析术前八项日常样品的阳性检测率能否实现对仪器和试剂的质量监控。
方法 收集 2018 年 8 月至 2019 年 1 月共 6 个月在 HISCL 5000 化学发光仪上术前八项（包括 HBsAg、HBsAb、HBcAb、HBeAg、HBeAb、HCVAb、HIVAg+Ab、TPAb）检测结果，按照月份和试剂批号进行分组，分别计算各组各指标的（初筛）阳性率以及变异系数，分析不同月份和不同批号之间结果的一致性。
结果 HBsAg、HBsAb、HBcAb、HBeAg、HBeAb、HCVAb、HIVAg+Ab、TPAb 所有月份平均阳性率（%）分别为 8.81±1.01、44.94±3.69、46.24±2.29、1.68±0.48、23.82±3.12、1.33±0.44、

0.34±0.31、2.65±0.29，变异系数（CV，%）分别为 11.44、8.20、4.95、28.47、13.10、33.40、91.59、10.48；术前八项所有批号的平均阳性率（%）分别为 8.46±0.50、43.09±5.08、47.29±2.00、1.95±0.76、25.08±2.68、1.32±0.48、0.48±0.22、2.54±0.25，CV（%）分别为 5.90、11.78、4.23、39.01、10.7、36.68、46.39、10.04；CV 小于 15%的项目有 HBsAg、HBsAb、HBcAb、HBeAb、TPAb。

结论 对于阳性率高的项目，日常样品每月和每批试剂的阳性检测率可以动态监测对仪器和试剂的质量控制。

PU-2560

胃泌素 17 和胃蛋白酶原在胃癌以及萎缩性胃炎的诊断价值

石媛媛
黑龙江金域医学检验实验室有限公司

目的 胃泌素 17 和血清胃蛋白酶原Ⅰ/ⅠⅠ在胃癌以及萎缩性胃炎中的诊断价值，

方法 本文采取的数据是来自北京平谷区中医医院胃镜室２０１９年１月到２０１９年１２月胃镜患者检查２３２例，其中１６５例为良性病例，８５例为萎缩性胃炎患者，８０例为非萎缩性胃炎患者，其中女性患者７６例，男性患者占８９例，还有６７例确诊为胃癌，空腹抽取患者血清进行胃泌素１７ PGI、PGII 的检测，并将胃蛋白酶两项的值计算出来，对上面的指标与萎缩性胃炎和胃癌中的诊断价值进行评估和对比，

结果 关于 PGI 水平胃癌组下降最明显，PGII 萎缩性胃炎组，胃癌组，和非萎缩性胃炎组有明显的降低，G17 水平萎缩性胃炎以及非萎缩性胃炎组无明显变化，但是胃癌组显著升高

结论 PGI，PGII ，两者比值，G17 在胃病良性与恶性的诊断中可以起到非常有意义的价值和一定的鉴别能力，G17 指标在胃窦胃体胃癌初步诊断具有一定意义 ，PGI，PGII 在胃癌诊断有诊断价值，临床意义：PGI/PGII 是胃蛋白酶原的比值，如果胃蛋白酶原比值下降，可能是由慢性萎缩性胃炎引起，慢性萎缩性胃炎会导致胃黏膜和腺体萎缩，需要进行胃镜检查，可以看到维体是否有病变，根据检查后的结果进行治疗。胃黏膜萎缩患者会有异常胃酸分泌，可能出现消化不良的症状，患者可以适当吃酸味食物，可促进胃消化。如果胃蛋白酶原的比值大，一般作为疾病检查的参考。如果患者比例增加明显，可能是由胃蛋白酶原 I 分泌增多引起，但是主要是由患者的胃黏膜损伤，损伤的严重程度，消化性溃疡等多方面引起，需要进一步胃镜检查，因为胃镜检查能准确检查出患者胃黏膜哪个部位具体病变，此外还需要做幽门螺杆菌检查，两者一起检查，结果会更准确些。

PU-2561

基于载脂蛋白谱的急性胰腺炎重症预警模型研究

童学东、江天、邓昆
重庆医科大学附属第三医院

目的 急性胰腺炎的早期诊断和分级有利于临床及时诊断、预测和治疗相关并发症，现有急性胰腺炎诊断指标如淀粉酶（AMY）、脂肪酶（LPS）敏感性和特异性较差。高密度脂蛋白胆固醇(HDL-C)、低密度脂蛋白胆固醇(LDL-C)、载脂蛋白如 apoA1、apoB 等在急性重症胰腺炎的发病过程中具有重要作用。本研究将通过载脂蛋白谱建立诊断模型用于急性胰腺炎的早期诊断。

方法 纳入 2020 年 10 月至 2021 年 3 月我院 62 例经临床明确诊断为急性胰腺炎的患者，同时纳入因其它原因急腹症（如胃炎、阑尾炎、肠炎等）入院的病例 127 例作为对照。分别检测各组 AMY、LPS、甘油三酯(TG)、HDL-C、LDL-C、ApoA-1、ApoB 等指标，通过 logistic 回归计算诊断预测概率，绘制 ROC 曲线并计算 AUC。

结果 与其它原因急腹症患者比较，急性胰腺炎患者早期 ApoA-1 从 1-2 天显著下降（P<0.001），HDL-C 在 3 天以后显著降低（P<0.001），LDL-C 与 ApoB 在 3 天后显著升高（P<0.001）。HDL-C、LDL-C、ApoA-1、ApoB 联合诊断胰腺炎 AUC 0.87。
结论 HDL-C、LDL-C、ApoA-1、ApoB 联合可用于急性胰腺炎早期诊断。

PU-2562

1 例肺炎克雷伯菌重症感染引起骨髓抑制的案例分析

闫荔
山西省心血管疾病医院

目的 通过对一例肺炎克雷伯菌重症感染引起骨髓抑制从而导致三系减低的病例进行临床病理特征及主要原因的分析，从而使临床医生能够快速做出判断，并及时准确的为患者提供正确有效的治疗，提高患者的生存率。
方法 对我院一例肺炎克雷伯菌重症感染引起白细胞，血小板急剧降低的病例进行回顾性分析，此患者白细胞 2020.11.26 做痰培养检测出肺炎克雷伯菌，白细胞于 11 月 26 日一天内从 11.35×10^9/L 降至 2.94 $\times10^9$/L，并与 28 日逐渐回升；血小板于 27 日开始降低并于三天内从 170 $\times10^9$/L 逐步降至 38×10^9/L，血红蛋白于 12 月 1 日开始降低, 从 120 g/L 降至 98 g/L。研究该患者的临床病理特征并对其主要原因进行分析。
结果 该患者三系减低符合骨髓抑制 2 级，并且白细胞、血小板、血红蛋白依次下降，下降的先后时间顺序符合血细胞的生存时间。其病理机制可能与白细胞附壁，非免疫性血小板破坏以及促红细胞生成素（EPO）水平降低等原因有关。
结论 肺炎克雷伯菌重症感染可以引起骨髓抑制并导致三系减低，甚至会达到危急生命值，因此该病例可以为临床医生提高意识，遇到重症感染引起的骨髓抑制可以迅速判断，并采取针对性的治疗措施，改善患者的病情，降低患者的死亡率，提高患者的生命安全。

PU-2563

糖尿病的危害及常见患病因素

张文龙
黑龙江金域医学检验实验室有限公司

据国际糖尿病联盟数据，全球约 4.25 亿成人患糖尿病，中国占 1.14 亿，这意味着全世界有 1/4 的糖尿病患者都在中国，糖尿病人数占全球第一。糖尿病已成为日趋严峻的全球问题。中国 18 岁及以上的成人糖尿病患病率已高达 11.6%，糖尿病前期的患病率更是达到了惊人的 50.1%。

常见患病因素: 1.遗传和体质因素:流行病学研究发现：糖尿病发病具有种族和家族遗传易感性。若双亲都是糖尿病患者，其子二代中约有 5%会患糖尿病;若双亲中只有一个患糖尿病，则子一代得糖尿病的机会更少，且常常是隔代相传。
2.饮食与肥胖因素:糖尿病患者尤其是 2 型糖尿病患者，与长期高糖、高脂肪饮食，体力活动少，身体肥胖有关。人若肥胖，脂肪在细胞积聚，降低了组织细胞对胰岛素的敏感性，使血糖升高。
3.病毒感染和自身免疫因素:包括肠道病毒、柯萨奇 B4 病毒、流行性腮腺炎、脑炎、心肌炎等都会破坏人的胰岛细胞，使人体免疫失控，引起胰岛 B 细胞功能减低，导致糖尿病。
4.情绪与精神神经因素:现代医学认为：精神紧张，情绪激动，心理压力大以及突然遭受心灵创伤等，会引起一系列胰岛素对抗激素的分泌，使血糖升高。
5.酒色因素与化学药物:饮酒是发生糖尿病的危险因素。色欲过度则会伤人肾精。滥服温燥壮阳药，以致机体紊乱，燥热内生，阴津亏损，引起消渴。酒、色对防治糖尿病都十分不利。另外，长期服

用糖皮质激素类、利尿药、降压药、苯妥英钠、兴奋药等化学药物，引起葡萄糖的不耐受性，也会导致糖尿病。
6.胰岛疾病 胰腺炎、胰腺瘤、胰腺全切除或半切除引起胰岛素相对不足而导致糖尿病。
7.妊娠 妇女妊娠时，由于生理变化，身体对胰岛素需要量增加，产生相对性胰岛素不足，可造成糖尿病。
结论 建议糖尿病患者及时去医院就诊。注意饮食，少吃含糖量高的食品和饮料。多运动，多吃水果。

PU-2564

大肠埃希菌的临床分布及耐药性分析

柴小飞[1]、乔飞飞[2]
1. 陕西省府谷县人民医院
2. 陕西省府谷县中医医院

目的 了解大肠埃希菌的临床分布特点以及抗生素耐药情况，为临床合理使用抗生素提供正确依据。
方法 回顾性分析 2020.01.01-2020.12.31 共检出 181 株大肠埃希菌进行抗生素耐药性分析。
结果 2020.01.01-2020. 12.31 共检出 181 株大肠埃希菌，其中女性感染 132 株（72.93%）明显高于男性感染 49 株（27.07%）。感染部位以尿路感染为主 123 株(67.96%)，其次血液 25 株（13.81%），脓液 22 株（12.15%）等。科室主要分布在肾内科 70 株（38.67%），其次普外科 34 株（18.79%），内分泌科 31 株（17.13%）等。阿莫西林/克拉维酸、氨苄西林、氨苄西林/舒巴坦、氨曲南、环丙沙星、莫西沙星、哌拉西林、头孢吡肟、头孢噻肟、头孢他啶、左氧氟沙星 11 种抗生素的耐药率产 ESBLs 菌明显高于非产 ESBLs 菌有显著性差异（P<0.05）。阿米卡星、复方新诺明、哌拉西林/他唑巴坦、庆大霉素、四环素 5 种抗生素耐药率产 ESBLs 菌和非产 ESBLs 菌无显著性差异（P>0.05）。产 ESBLs 菌和非产 ESBLs 菌均未发现对多粘菌素 B、美洛培南、亚胺培南 3 种抗生素耐药。
结论 大肠埃希菌中产 ESBLs 菌 75 例（41.44%）检出率高，且为多重耐药。碳青霉烯类抗生素和多粘菌素 B 是目前治疗产 ESBLs 菌感染的有效抗生素，在临床实践中，应充分参考细菌培养及药敏试验结果，结合患者实际情况进行抗生素的选择，从而降低产 ESBLs 菌，提高临床治疗具有重要意义。

PU-2565

尿镜检法在尿液检测中的重要性

多佳
黑龙江金域医学检验实验室有限公司

目的 探讨尿镜检法在尿液检测中的重要性
方法 选取我合作单位验科于 2019 年 11 月-2019 年 12 月间收治的 400 份合格尿液标本,均采用尿液镜和干化学尿液分析仪进行分别检验,并对于检测结果进行对比。
结果 在所选的 400 例尿液标本中,将红、白细胞两项用两种不同的方法进行比较,结果对比显示,白细胞:干化学法阳性人数为 50 例,阳性率为 12.5%,镜检法阳性人数为 70 例,阳性率为 17.5%。红细胞:干化学法阳性人数为 71 例,阳性率为 17.75%,镜检法阳性人数为 53 例,阳性率为 13.25%。结论 两种方法检测尿液结果有一定的差异,由于许多其他因素的干扰,故应将两种方法结合起来,以提高检出率。 尿液镜和干化学尿液分析仪检测结果有着一定的差别,主要表现在干化学尿液分析仪检测结果会产生个别假阳性、假阴性,引发检测缺陷,诊断准确率不高。

结论 尿液分析是医学检验方法的一种,在临床上许多疾病都需要尿液分析的结果来提供诊断和治疗的依据,尤其是对于泌尿系统疾病更是有着决定性的作用。随着尿液分析仪的逐渐普及,在带来便利的同时也使得许多工作人员产生了惰性,忽略了对于尿沉渣进行镜检的过程,容易导致尿液出现假性诊断。尿镜检能够有效的发现红细胞、白细胞以及病理结晶等具有较高诊断价值的成分,所以尿沉渣的镜检是检查工作中必不可缺的部分。在尿常规检查中,尿液镜检是一个重要的环节, 而尿液镜配合检测则能有效避免误诊或漏诊问题，值得临床推广应用。

PU-2566

慢性粒单核细胞白血病累及淋巴结 1 例实验室检查结果分析并文献复习

敬敏、黄林林
四川金域医学检验中心有限公司

目的 探讨慢性粒单核细胞白血病（CMML）累及淋巴结的实验室检查结果特征分析、鉴别诊断及预后。
方法 本次研究对象是广西医科大学第一附属医院血液内科一名 67 岁男性患者，初诊为 CMML，治疗后病情未见好转，并出现肝、脾肿大，颌下、锁骨上、双侧腋窝及腹股沟多发淋巴结肿大，直径最大约 1cm，手术切除左侧腋窝淋巴结送病理检查，通过临床表现、病理形态、免疫组化及分子检测等进行诊断及鉴别诊断，并结合文献复习总结临床病理特征。
结果 淋巴结结构破坏，中等大小母细胞样细胞呈片状浸润，免疫组化染色示上述细胞 MPO、CD15 均为阳性，Ki-67 约 80%阳性，CD20、PAX-5、CD3、CD5、CD30、CD163 均为阴性，CD34、TdT 少数弱阳性。髓系血液疾病 67 种基因突变分析：查见 ASXL1、CSF3R、TET-2、U2AF1 基因突变阳性。FISH 检测：BCR/ABL 融合基因阴性。
结论 骨髓增生异常/骨髓增殖性肿瘤（MDS/MPN）是重叠有骨髓增生异常综合征（MDS）和骨髓增殖性肿瘤（MPN）的临床及实验室表现的一类髓系肿瘤，具有较强的异质性，慢性粒单核细胞白血病（CMML）是其中最常见的一种亚型，好发年龄以老年人为主，且常有伴随疾病，是最具侵袭性的慢性白血病之一，确诊需依赖外周血分类计数、细胞形态学、流式细胞术、免疫组织化学、髓系血液疾病基因检测并结合临床表现。CMML 需与急性白血病、急性粒-单核细胞白血病、慢性粒细胞白血病伴单核细胞增多以及 MDS/MPN 中其他类型的血液肿瘤鉴别。此类疾病肝大和脾大都可存在，但淋巴结肿大少见，一旦出现淋巴结肿大，提示有急性转化的可能。慢性粒单核细胞白血病（CMML）的生存时间在各文献报道中相差甚大，短者仅 1 个月，长者可 100 个月，但中位生存时间多为 20-40 个月，约 15%-30%的患者可进展为急性白血病。

PU-2567

贵州地区血清肿瘤标志物甲胎蛋白、癌胚抗原和 CA19-9 参考区间的初步建立

陈国敏、刘婷、龙贵萍、彭朝燕、付正乾、苏蒙
贵州金域医学检验中心有限公司

目的 建立贵州地区健康成人血清 AFP(安图)、CEA(安图)和 CA199(迈瑞)的参考区间。
方法 对 2020 年 5 月至 2021 年 4 月送检本机构的贵州地区健康体检人群，共 10618 例，年龄 20-69 岁，其中使用安图全自动化学发光仪 A2000plus 进行 AFP 检测 10618 例，CEA 检测 10531 例，使用深圳迈瑞全自动化学发光仪 CL-6000i 进行 CA19-9 检测 10366 例的结果进行不同性别、不同年龄组间系统性地回顾性分析研究。

结果 AFP 有 10618 例，数据呈正态分布，男女组都表现出随着年龄的增长 AFP 含量随之略微增高，其中男性组 5991 例各年龄组（20-69 岁）检测 AFP 结果之间无统计学意义（P> 0.05 ），女性组 20-39 岁组（2356 例）和 40-69 岁组（2356 例）检测 AFP 结果之间有统计学意义（P< 0.05 ）；CEA 有 10531 例，数据呈正态分布，男女组都表现出随着年龄的增长 CEA 含量随之增高，CEA 含量与年龄呈显著相关性，39 岁前后变化明显，其中男、女组各 20-39 岁(男性组：2154 例，女性组：2359 例)，40-69 岁(男性组：3751 例，女性组：2266 例)检测 CEA 结果之间有统计学意义（P< 0.05 ）；CA19-9 有 10366 例，数据呈正态分布，男性组表现出随着年龄的增长 CA19-9 的含量随之增高，CA19-9 含量与年龄呈显著相关性，男性组 49 岁前后变化明显，男组各年龄组 20-39 岁（2135 例），40-69 岁（3698 例）检测 CA19-9 结果之间有统计学意义（P< 0.05 ），而女性组随着年龄的增长，血清中 CA19-9 的含量变化不明显，女性组(4533 例)各年龄组检测 CA19-9 结果之间无统计学意义（P>0.05 ），采用单侧 95%位数表示为 AFP(安图)、CEA(安图)和 CA199(迈瑞)在贵州地区参考区间。
结论 各地区健康人群血清中 AFP、CEA 和 CA19-9 含量会因为年龄、性别、检测方法和检测设备的不同，而有所变化，应建立适合本地实验室的参考区间。

PU-2568

乌鲁木齐市 4408 名体检人群幽门螺杆菌感染与血脂异常的相关性分析

刘涛、邹媛、杨晓萍、王淑霞、陈兆云、张峰波
新疆医科大学第一附属医院

目的 分析乌鲁木齐某三家医院 4408 名健康体检人群幽门螺杆(Helicobacter pylori,Hp)感染状况，并探讨与血脂异常的相关性。
方法 采用 13C-尿素呼气试验法检测幽门螺杆菌的感染状况，同时收集研究对象的人口学资料和血脂四项指标结果，比较 HP 阳性组和 HP 阴性组血脂异常的差异及在不同分层分析中血脂异常率的差异，并行二分类 logistic 回归分析，探讨 HP 感染与血脂异常的关系。
结果 乌鲁木齐市 4408 名健康体检人群 HP 的感染率为 35.62%，在年龄分组中发现 HP 感染率随年龄逐渐增加而增高，在性别分组中，男性组 HP 感染率大于女性，差异有统计学意义（P<0.05）。分层分析发现，男女性别组中 HP 感染组血脂异常率均高于 HP 未感染组，差异有统计学意义（P<0.05）；而在年龄分层中，51 岁至 60 岁组别中，血脂异常率在 HP 感染和 HP 未感染组有统计学差异（P<0.05）；在体质指数分组中，超重组和肥胖人群中 HP 感染组的血脂异常率均显著高于 HP 未感染组，且具有统计学差异（P<0.05）。进行 logistic 回归分析模型显示，HDL-C 可能是 Hp 感染的保护因素，而总胆固醇异常是 HP 感染的危险因素。
结论 HP 感染与年龄和性别有关，并且可能影响血脂异常的发生率。

PU-2569

自动化技术在 25-羟基维生素 D 质谱法检测前处理环节的应用

赵蓓蓓[1,2]、余木俊[1]、董衡[1,2]、李卓阳[1,2]、林清娜[1]、佘旭辉[1,2]
1. 广州金域医学检验中心有限公司
2. 广州医科大学金域检验学院

目的 色谱质谱技术具有高灵敏度、高特异性、可同时检测多种化合物，方法开发灵活等优势，但由于其技术高度复杂，对人员专业能力要求高，多数操作需要手工处理，前处理操作步骤繁琐,自动化程度低，限制了该技术在临床实验室中的应用与推广。本研究以液相色谱串联质谱法（LC-

MS/MS）检测 25-羟基维生素 D2 和 25-羟基维生素 D3 为例，通过在前处理环节引入自动化技术，减少操作步骤，提升检测通量，降低其临床应用的难度和挑战。

方法 ①通过引入自动化扫码取样设备，优化吸液参数，替代人工加样环节；②在标本预处理环节，以自动化移液设备为基础，搭建包括蛋白沉淀、液液萃取和复溶震荡的处理程序；③收集签署知情同意书的 50 例临床样本，分别采用自动化法和手工法进行前处理操作；④经过两种方法前处理后的临床样本进行 LC-MS/MS 检测，采用 Passing & Bablok regression 对测定结果进行统计分析。

结果 ①自动化法取样设备可将取样效率从 150 例/小时提升到 300 例/小时，且自动化取样误差在±1.5%以内；②在标本预处理环节，自动化移液可将操作步骤从 15 项减少到 7 项，人均检测效率从 130 例/天提升到 400 例/天；③对于 25-羟基维生素 D2，50 例临床标本浓度分布范围为 3.4ng/mL 到 54.2ng/mL，Passing & Bablok regression 检验的线性回归方程为 y =-0.0490654+1.074883x，Cusum 检验证实线性无显著性偏差(P=0.89)。对于 25-羟基维生素 D3，50 例临床标本浓度分布范围为 9.0ng/mL 到 47.3ng/mL，Passing & Bablok regression 检验的线性回归方程为 y =-0.466120+1.027322x，Cusum 检验证实线性无显著性偏差(P=0.89)。

结论 本研究通过对取样和预处理环节引入自动化技术，简化 25-羟基维生素 D 质谱法检测前处理操作步骤、降低操作误差、整体检测效率提升至少 65%。自动化法与手工法的结果相关性高，结果差异无统计学意义。

PU-2570

小而密低密度脂蛋白胆固醇在中国人群冠心病中的预测价值

张娜
山西医科大学第二医院

The ability of small dense low-density lipoprotein (sdLDL) alone to sufficiently predict CHD risk in the Chinese population was evaluated.

Methods Patients with CHD (139) and healthy controls (58) were included in this study. Serum sdLDL was measured using the peroxidase method. Other lipid parameters were also determined.

Results The sdLDL level in the CHD group was significantly higher than that in the control group ($p < 0.001$). Logistic regression analysis revealed that sdLDL was an independent risk factor for CHD. Based on the receiver operating characteristic curves, the area under the curve (AUC) of sdLDL alone for CHD was0.722.The AUC of triglycerides (TG), high-density lipoprotein (HDL),and sdLDL combined was 0.763, which was larger than that of the independent ones or combinations of any two; however, the value was not significant.

Conclusions sdLDL alone can predict CHD risk efficiently similar to the combination of TG, HDL, and sdLDL. This finding suggests that sdLDL can be considered as an ideal parameter for the preliminary diagnosis of CHD in Chinese people.

PU-2571

血清 IGF1 在黑色素瘤靶向治疗耐药监测的临床应用价值

罗娅
陆军军医大学第二附属医院检验科

目的 探讨肿瘤耐药标志物 IGF1 在监测黑色素瘤靶向治疗耐药的临床应用价值。

方法 采用细胞共培养等方式在细胞水平和动物模型中研究肿瘤源性 IGF1 对肿瘤相关成纤维细胞（CAFs）功能的影响，探讨 IGF1 介导的肿瘤细胞与 CAFs 交互作用导致耐药的分子机制；收集 20 例黑色素瘤肿瘤病人以及 20 例正常健康人的血清，分析血清 IGF1 在临床治疗监测的意义。

结果 CAFs 表面表达 IGF1R，IGF1 可能以旁分泌方式作用于 CAFs，并介导 CAFs 膜表面 IFN-γR 下调，进而影响 CAFs 功能，促进肿瘤耐药。血清 IGF1 水平与肿瘤病人分期成正相关，与病人治疗效果有一定的相关性。
结论 肿瘤细胞分泌的 IGF1 以旁分泌的方式影响 CAFs 进而促进肿瘤耐药；血清 IGF1 水平可作为肿瘤病人分期和治疗效果的提示指标，IGF1 在监测肿瘤耐药具有一定的指导意义。

PU-2572

血液检验红细胞参数在贫血鉴别诊断的检验价值

高霏
复旦大学附属中山医院青浦分院（上海市青浦区中心医院）

目的 剖析血液检验红细胞参数在贫血鉴别诊断的检验价值。
方法 实验的研究时段为：2020 年 1 月至 2020 年 7 月，研究对象为：此时段本院接治的 42 例贫血患者（实验组），该时段本院进行体检的 42 例健康人群（对照组）。所有研究对象均进行血液检验，比较分析两组的各项红细胞参数。
结果 在 42 例贫血患者中包含 31 例中巨幼细胞性贫血，其余 11 例为缺铁性贫血。血液检验结果显示，有 28 例巨幼细胞性贫血，14 例缺铁性贫血，3 例误诊，误诊率为 7.14%，诊断准确率为 92.86%。比较两组的红细胞各项数据，对照组和实验组之间有显著差异，且 P＜0.05。
结论 针对贫血患者，应用血液检验红细胞参数可以帮助患者尽快确诊，并了解贫血患者的血液浓度变化，对贫血类型进行有效鉴别，为临床治疗提供依据，值得推广和应用。

PU-2573

联合检测 M 蛋白对多发性骨髓瘤的诊断价值

王晗、向莉莉
天津金域医学检验实验室有限公司

目的 M 蛋白与多发性骨髓瘤的发病机制有着密切的关系，本研究旨在探讨三种方法联合检测 M 蛋白对多发性骨髓瘤的诊断价值，提高多发性骨髓瘤的检出率，降低其误诊、漏诊的几率。
方法 本论文的研究数据来源于多发性骨髓瘤患者筛查 M 蛋白的 50 份标本，其中预后样本 17 例，初诊样本 33 例。采用血清蛋白电泳，以证实 M 蛋白的存在，然后进行血清免疫固定电泳和血清游离轻链，做进一步的定量分析和分型鉴定。比较三种单项检测及三项联合检测 M 蛋白对多发性骨髓瘤的诊断价值。
结果 血清蛋白电泳图谱中发现 M 蛋白条带 21 例，检出率为 63.6%；血清免疫固定电泳发现异常克隆条带 29 例，检出率 87.9%,血清游离轻链检出阳性 29 例,检出率为 90.9%；联合总检出 50 例，检出率为 100%。结果三种方法联合检测 M 蛋白的检出率高于单项检测的检出率，有显著统计学差异(P<0.01)。
结论 血清蛋白电泳、血清免疫固定电泳、血清游离轻链联合检测 M 蛋白对多发性骨髓瘤的诊断有意义,检出率高，可为临床早期干预治疗提供准确依据,从而及早干预，最终有助于改善患者预后。

PU-2574

COPD 患者呼吸道分离的黏液罗氏菌相关研究

陈钰静
南方医科大学珠江医院

目的 分析 COPD 患者的病原谱，了解黏液罗氏菌的流行率、耐药情况及临床相关因素分析。
方法 从广州呼吸疾病研究所收集 2018 年 1 月至 2019 年 4 月共 132 例 COPD 病患标本，其中分离出黏液罗氏菌的有 19 例（实验组）；并在南方医科大学附属第一医院、广州呼吸疾病研究所招募的 33 例合格志愿者中随机抽取 21 例（对照组）。用安图生物的质谱分析仪 Autof MS1000 对细菌进行鉴定，用法国 bioMerieux VITEK 2 全自动微生物鉴定及药敏分析系统对黏液罗氏菌进行药敏分析，分析吸烟、激素、合并感染对黏液罗氏菌的检出率的影响。
结果 COPD 患者呼吸道标本中分离出的病原菌以革兰阴性菌为主，前三名依次是肺炎克雷伯菌、铜绿假单胞菌、嗜麦芽窄食单胞菌。132 例 COPD 患者中，罗氏菌属检出率为 21.97%，黏液罗氏菌最高，占 14.39%，其次是龋齿罗氏菌、气罗氏菌。影响黏液罗氏菌检出率的相关因素有使用激素、吸烟具有统计学意义（P<0.05），是否合并其他病原菌感染不具有统计学意义（P>0.05）。COPD 患者呼吸道标本分离出的黏液罗氏菌对左氧氟沙星、莫西沙星、环丙沙星耐药率较高，对替考拉宁、万古霉素、利福平、复方新诺明、头孢唑啉、头孢曲松、头孢吡肟、厄它培南、丁胺卡那霉素、亚胺培南、氨苄西林、氯霉素、四环素大多敏感。
结论 对于免疫力低下的 COPD 患者，罗氏菌属于一种重要的机会致病菌属，特别是黏液罗氏菌，随着越来越多的耐药细菌出现，建议临床要常与微生物室保持紧密联系，密切监视 COPD 患者的正常菌群的组成变化，关注有无产生耐药细菌。根据药敏结果合理选用抗生素，以减少机会性感染的发生。

PU-2575

重庆市健康体检人群体内维生素 D 含量研究

李丽、舒黎
重庆市人民医院

目的 了解重庆市人群体内维生素 D 营养状态，为重庆市人群合理补充维生素 D 提供科学依据。
方法 采集 2018 年 1 月至 2019 年 10 月来该院进行健康体检的人群空腹静脉血，用电化学发光法检测其血清中 25-羟基维生素 D（25(OH)D）水平，对结果分别按性别、检测时间进行分组分析。
结果 调查了 2018 年 1 月至 2019 年 10 月重庆市 4653 名健康体检人群血清中 25(OH)D 水平。其血清中 25(OH)D 水平充足（30 ng/mL≤25(OH)D<100 ng/mL）者 316 例，占比 6.79%；水平不足（20 ng/mL≤血清 25(OH)D<30 ng/mL）者 1178 例，占比 25.32%；水平缺乏（10 ng/mL≤血清 25(OH)D<20 ng/mL）者 2451 例，占比 52.68%；严重缺乏（25(OH)D<10 ng/mL）者 708 例，占比 15.22%。男性 196 例，血清 25(OH)D 平均水平为 20.32±10.12 ng/mL；女性 4457 例，血清 25(OH)D 平均水平为 17.26±7.44 ng/mL，差异有统计学意义（P<0.05）。男性人群中维生素 D 充足者占比 18.88%，女性充足者占比 6.26%，明显低于男性（P<0.05）；男性缺乏者占比 36.73%，明显低于女性的 53.38%（P<0.05）；男性不足者 30.61%，女性不足者 25.08%，男性严重缺乏者 13.78%，女性 15.28%，差异无统计学意义（P>0.05）。春季（3-5 月）人群血清 25(OH)D 水平为 17.87±7.45 ng/mL，夏季（6-8 月）水平为 20.64±8.00 ng/mL，秋季（9-11 月）水平为 16.46±7.04 ng/mL，冬季（12-2 月）水平为 14.52±6.42 ng/mL，冬季明显低于夏季（P<0.05）。
结论 重庆市健康人群维生素 D 含量总体偏低，其中女性尤其明显，冬季平均水平明显低于夏季，在冬季应加强维生素 D 的补充，女性应更加重视。

PU-2576

我院 2017 年-2020 年铜绿假单胞菌的临床分布和耐药性分析

朱海兵
湖南株洲市三三一医院

目的 分析 2017 年-2020 年株洲市三三一医院铜绿假单胞菌的临床分布和耐药性，为临床合理使用抗菌药物和院内感染控制提供依据。
方法 对本院临床标本分离的 1036 株铜绿假单胞菌的临床分布特点和药敏结果进行回顾性分析。
结果 铜绿假单胞菌感染主要集中在呼吸内科、ICU、老年消化内科，分别占 25.4%、34.6%、15.7%。铜绿假单胞菌菌株主要来源于痰液标本，占 75.9%；其次为尿液标本，占 6.3%。铜绿假单胞菌多黏霉素 B 耐药率最低，其次是阿米卡星；耐药性最高的是亚胺培南。头孢哌酮/舒巴坦、头孢他啶、左氧氟沙星三种抗菌药物的耐药率四年有所下降，其中头孢他啶和左氧氟沙星耐药率下降明显（P<0.05），差别具有统计学意义。
结论 铜绿假单胞菌感染以上呼吸道为主，同时可引起多部位感染，其耐药性现状严重，应加强对铜绿假单胞菌感染的管理，规范临床用药，同时加强铜绿假单胞菌耐药性监测，减少耐药的发生。

PU-2577

线粒体 DNA 单倍型遗传背景下长寿机制的初步研究

马琳
郑州大学第一附属医院

前期研究结果表明，在中国人群中线粒体 D4a 与 B4a、N9 分别是长寿人群高频、低频单倍型。我们构建细胞核相同线粒体 DNA 单倍型不同的融合细胞模型，开展相关的线粒体功能实验，以初步探究线粒体 DNA 单倍型遗传背景下长寿的相关机制。

PU-2578

2020 年吉林地区超薄液基细胞妇科（TCT）标本结果分析

刘新宇
吉林金域医学检验所有限公司

目的 宫颈癌的发病率在女性生殖系统肿瘤中仅次于乳腺癌，居第二位。本文分析吉林地区超薄液基细胞妇科病变类型及其占比，为科普两癌筛查提供参考依据。
方法 选取 2020 年 1 月至 2020 年 12 月送检我公司的 184551 例超薄液基细胞妇科样本，使用杭州海世嘉国产耗材采样，应用杭州海世嘉震荡仪震荡，震荡时间 10min、离心机转速 800 转，离心时间 3min，使用徕卡染封一体机染色（染色试剂为广州微米提供成品液）、封片，副高及以上职称医生阅片，排除不满意及细胞量少标本共 408 例后，选取合格样本 184143 例，对以上标本进行 HSIL、LSIL、ASC-H、ASCUS 及 AGUS 阳性病例数量及占比分析。
结果 184143 例标本中，鳞状上皮内高度病变（HSIL）共 231 例，占比 0.125%；非典型鳞状细胞，不除外高度病变（ASC-H）共 607 例，占比 0.330%；鳞状上皮内低度病变（LSIL）(CIN1)共 1721 例，占比 0.935%；非典型鳞状细胞(ASCUS)共 5257 例，占比 2.855%；非典型腺细胞（AGUS）共 128 例，占比 0.070%；HSIL、LSIL、ASC-H、ASCUS 及 AGUS 阳性病例共 7944 例，占比 4.314%。
结论 实验表明，2020 年吉林地区超薄液基细胞妇科标本中，HSIL、LSIL、ASC-H、ASCUS 及 AGUS 占总标本的 4.314%，略低于省内整体阳性率，考虑为第三方医检实验室样本来源较复杂，

以体检为主，故阳性率低于省内整体数值。目前，宫颈癌作为最常见的妇科恶性肿瘤之一，其检出率逐年上升，要引起社会各界的重视。而超薄液基细胞妇科（TCT）技术是一项可以大大提高宫颈上皮病变细胞检出率的良好技术，尤其是对恶性病变的早期发现，可达到早期诊断和早期治疗的目的。

PU-2579

促红细胞生成素、血清铁蛋白、叶酸、维生素 B12 检测在贫血中的应用研究

付杰
陆军军医大学第二附属医院检验科

目的 探讨血清铁蛋白（serum ferritin，SF）、促红细胞生成素(Erythropoietin，EPO)、叶酸（folic acid，FOL）、维生素 B12(Vitamin B12，VB12)检测在贫血诊治中的应用。
方法 回顾 2020 年 1-12 月我院就诊贫血患者 522 例为实验组，随机非贫血患者 51 例为对照组，并根据血红蛋白浓度，将观察组分为轻度贫血组，中度贫血组，重度贫血组，极重度贫血组，分析实验组与对照组，各实验组亚组患者 SF、EPO、FOL、VB12 含量差异，评估联合检测对贫血的诊：断率。
结果 ①实验组 EPO 明显高于对照组，差异有统计学意义（P<0.05），实验组 SF、FOL、VB12 与对照组差异无统计学意义（P>0.05）②各实验亚组，随贫血程度增加，EPO 含量增加，差异有统计学意义（P<0.05），实验亚组 SF、FOL、VB12 间差异无统计学意义（P>0.05）
结论 在贫血诊断中和贫血程度分型中，EPO 发挥重要作用，SF、FOL、VB12 作用不强。

PU-2580

常用临床实验室检验项目在 SLE 患者活动性评估中的应用评价

蒋兴宇
陆军军医大学第二附属医院检验科

目的 讨论系统性红斑狼疮实验室检查项目的应用价值，并筛选出有价值的检测项目。
方法 收集 2021 年 1 月至 2021 年 3 月期间于陆军军医大学第二附属医院就诊的 SLE 患者病历资料共计 104 人次。通过纳入和排除标准筛选后共纳入研究对象 49 人次；收集研究对象的血常规检测（23 项）、尿干化学检测（8 项）、抗核抗体核型与滴度（Antinuclear antibody,ANA）、抗可溶性抗原抗体（Extractable nuclear antigens，ENAs）检测（15 项）、免疫球蛋白 Igs（4 项）、补体 C3 和 C4 以及常用于评价各器官损伤的常用生化项目共计 82 项指标。
结果 对 82 项指标进行特征筛选（特征的单一唯一值、特征间共线性以及特征的重要性），最后选取了 12 项指标，分别为 ANA 核型, ALT, ALP, ALB, CREA, HBDH, RBC, LYM#, MCHC, MPV, IGA, IGG 进行后续的建模评价。挑选出上述 12 项指标的统计学检验结果，项目 ANA 核型，ALP，MCHC，MPV 差异无统计学意义；RBC，ALB，CREA，HBDH，LYM#，IGA，IGG，ALT，差异有统计学意义。
结论 通过绘制 ROC 曲线，发现除了 DT，剩下的建模方法 LR，SVC，RF，XGB 得到的 AUC>0.8，认为 ANA 核型, ALT, ALP, ALB, CREA, HBDH, RBC, LYM#, MCHC, MPV, IGA, IGG 这 12 项检验项目具有较好的应用价值。

PU-2581

血清 IgG4 及 IgG4/IgG 用于 IgG4 相关疾病诊断的价值研究

王海、王春玲、李丽
东南大学附属中大医院

目的 在 IgG4 检测阳性患者中，探讨并比较血清 IgG4 水平和 IgG4/IgG 比值对于 IgG4 相关疾病（IgG4-RD）的诊断价值。
方法 回顾性分析 2017 年 1 月~2021 年 1 月东南大学附属中大医院 549 例血清 IgG4 检测阳性（IgG4>2.01g/L）患者的临床数据，采用独立样本 t 检验法比较 IgG4-RD 组和非 IgG4-RD 组的血清 IgG4 和 IgG4/IgG 水平差异，并绘制 IgG4 和 IgG4/IgG 比值用于诊断 IgG4-RD 的 ROC 曲线。
结果 549 例血清 IgG4 检测阳性患者的平均年龄为 62.1 岁（9~93 岁），其中 17 例（3.1%）确诊为 IgG4-RD，15 例为男性（15/351），2 例为女性（2/198），男性发生率显著高于女性（4.2% vs 1.0%，P<0.05）；且 IgG4-RD 组患者年龄显著高于非 IgG4-RD 组（68.4±10.3 vs 61.9±17.9，P<0.05）。IgG4-RD 组血清 IgG4 浓度(10.09±8.17 g/L vs 3.71±3.42 g/L, P<0.05)和 IgG4/IgG（0.47±0.24 vs 0.23±0.17, P<0.05）均显著高于非 IgG4-RD 组。血清 IgG4 浓度和 IgG4/IgG 用于区分 IgG4-RD 和非 IgG4-RD 患者的最佳截断值分别为 4.035g/L 和 0.30；IgG4 取最优截断值时，敏感性为 0.727，特异性为 0.818，曲线下面积为 0.802；IgG4/IgG 取最优截断值时，敏感性为 0.818，特异性为 0.862，曲线下面积为 0.843。
结论 男性 IgG4-RD 发病率高于女性，且 IgG4-RD 患者年龄高于非 IgG4-RD。血清高 IgG4 水平和 IgG4/IgG 比值对于临床 IgG4 检测阳性患者中 IgG4-RD 的诊断具有一定价值。

PU-2582

采用室内质量控制和室间质量评价评定甲功内分泌指标的测量不确定度

赵婕、王苗
天津金域医学检验实验室有限公司

目的 利用室内质量控制和室间质量评价综合评定的方法，简单快捷地进行甲功内分泌指标的测量不确定度的评估，以提高检测结果质量，帮助实验室和临床更好地理解、认识和解释检测结果，并恰当地应用于临床诊断和医疗。
方法 依据中国合格评定国家认可委员会（CNAS）技术报告《医学实验室-测量不确定度的评定与表达》,采用"自上而下（top-down）"方法,收集 2020 年室内质量控制（IQC）数据以及 2019-2020 年参加卫生部临床检验中心室间质评（EQA）数据,计算甲状腺激素（T4）、游离甲状腺激素（FT4）、三碘甲腺原氨酸 （T3）、游离三碘甲腺原氨酸 （FT3）、促甲状腺激素（TSH）共 5 个检验项目的相对合成标准不确定度和扩展不确定度,并与卫生部临床检验中心 EQA 计划中的允许总误差（TEa）及生物学变异推导出的 TEa 进行比较,以观察甲功内分泌指标的检测质量。
结果 本实验室 5 项甲功内分泌项目的相对扩展不确定度分别是 T4（7.823％/9.350％）、FT4（11.901％/10.772％）、T3（10.871％/9.555％）、FT3（8.073％/7.089％）TSH（9.662％/10.018％），5 项检验指标均符合卫生部临床检验中心室间质量评价和基于生物学变异最佳的 TEa 质量规范要求。
结论 采用室内质量控制和室间质量评价综合评定的方法评估测量不确定度，操作简易方便,可作为定期评定测量不确定度的方法，具有良好的临床应用前景。

PU-2583

TCT 检测联合 HPV E6/E7 在宫颈癌筛查中的应用价值

杨琳
山东第一医科大学附属省立医院

目的 分析液基薄层细胞（TCT）联合 HPV E6/E7 在宫颈癌筛查中的临床应用。宫颈癌是一种妇科恶性肿瘤，其发病与高危型人乳头瘤病毒（HPV）持续感染密切相关，大部分患者伴有高危型 HPV 感染。目前，临床上普遍使用宫颈癌的筛查方法有 HPV 的检测、液基薄层细胞学检查（TCT）及阴道镜组织活检等。阴道镜组织活检目前是诊断宫颈癌前病变最有效的手段，但是此方法有一定伤害。HPV 和 TCT 检测作为筛查宫颈癌前病变的联合手段，具有一定的阳性提高诊断率。
方法 选取 2018 年 12 月至 2019 年 12 月在山东省立医院妇科门诊行宫颈癌联合筛查的女性 1223 例,其中接受 TCT 及高危 HPV 分型者纳入对照组(n=784),接受 TCT 及 E6/E7 mRNA 检测者纳入观察组(n=439),以组织病理学为基础, Bethesda 分类、不同病理分型中 HPV 和 E6/E7 mRNA 阳性率及患者满意度,分析 HPV DNA 及 HPV E6/E7 mRNA 分别合 TCT 的筛查价值。
结果 观察组 HPV E6/E7 mRNA 初筛阳性率为 30.01%,较低于对照组高危 HPV 初筛阳性率 35.16%。Bethesda 分类中,NILM 及鳞状上皮内低度病变(LSIL)、鳞状上皮内高度病变(HSIL)病患的 HPV DNA 阳性率高于 E6/E7 mRNA 阳性率);根据病理分级的增加,E6/E7 mRNA 阳性率、HPV DNA 的阳性率拷贝数上升,而 DNA 拷贝数比较差异无统计学意义,(CIN)1 级、 CIN2 级、CIN3 级患者中 HPV DNA、HPV E6/E7 mRNA 阳性率比较差异无统计学意义; TCT 及 E6/E7 mRNA 筛查评估高级别宫颈上皮内瘤变 (CIN 分 级 2 ~ 3 级)及宫颈癌的特异度、灵敏度、准确度高于 TCT 及 HPV DNA 联合筛查。
结论 与 TCT 联合 HPV DNA 筛查相比,TCT 联合 HPV E6/E7 mRNA 筛查应用在宫颈癌筛查中,特异度、灵敏度更高。

PU-2584

2665 例急性上呼吸道感染患儿的病原学及临床特征

丁细霞
南方医科大学珠江医院

目的 分析急性上呼吸道感染儿童患者的病原学及临床特征。
方法 以南方医科大学珠江医院 2009 年 11 月-2015 年 9 月收治的 2665 例急性上呼吸道感染儿童为研究对象，采用 qRT-PCR 方法检测临床上常见的 8 种（流感病毒，呼吸道合胞病毒，副流感病毒，腺病毒，人类博卡病毒、人类冠状病毒、人类偏肺病毒、鼻病毒）呼吸道病毒。
结果 共检测患儿标本 2665 份，其中阳性标本 1566 份，总阳性率为 58.8％。四个季节中 8 种呼吸道病毒检出率存在明显差异（P＜0.0001），并以春季最高，夏冬季次之，秋季最低。儿童呼吸道病毒感染率随着年龄增加而逐渐降低（P＜0.0001），并以 0-1 岁婴幼儿病毒检出率最高 64.5%。男童呼吸道病毒感染率明显高于女童（P < 0.05），住院患儿呼吸道病毒检出率明显高于门诊患儿（P＜0.0001）。混合感染标本 260 份，占阳性标本数的 16.6%，主要集中于 0-3 岁儿童患者标本中，并因季节而异，秋冬季节较少，而春夏季节较为普遍。咳嗽为呼吸道病毒感染的主要临床症状，咳痰和流涕次之，各种临床症状在 8 种呼吸道病毒感染患儿中存在差异（P＜0.0001）。
结论 本调查增加了我们对急性上呼吸道感染患儿中 8 种常见呼吸道病毒的病原学及临床特征的了解，为指导临床治疗及防控提供相关数据。

PU-2585

铜绿假单胞菌的临床分布及耐药趋势分析

丁健生
郑州大学第一附属医院

目的 了解铜绿假单胞菌的分布特点及耐药性情况，为临床合理使用抗菌药物及防治铜绿假单胞菌感染提供参考依据。
方法 收集郑州大学第一附属医院 2020 年 5 月至 2021 年 3 月期间临床标本分离的铜绿假单胞菌，利用全自动微生物鉴定仪对其进行菌种鉴定及抗菌药物敏感性试验，采用 WHONET 软件和 SPSS 统计软件进行数据分析。
结果 共分离出铜绿假单胞菌 579 株，其中标本类型主要为深部痰液标本、尿液和血液，三者占比分别为 69.97%、18.73%和 9.14%，来源科室分布则主要为呼吸与重症科、ICU 及神经内科。药敏试验结果显示，铜绿假单胞菌对 β-内酰胺类抗生素的耐药率均较高，而对头孢三代/四代类、喹诺酮类、氨基糖苷类、碳青霉烯类等抗生素耐药率较低，对哌拉西林/他唑巴坦、庆大霉素及阿米卡星等抗生素较为敏感。
结论 铜绿假单胞菌是该院感染的主要致病菌之一，主要存在于侵入性操作较多、应用抗菌药物广泛且住院周期较长的临床科室，患者来源以呼吸道感染为主，应积极防控院内感染，同时加强细菌耐药监测，提高抗菌药物的临床管理水平，避免耐药菌在医院流行和播散。

PU-2586

WNT 信号通路在白血病干细胞治疗中的作用

李惠
德州市人民医院

急性髓细胞白血病是由造血干细胞和骨髓祖细胞的致癌转化诱导的严重的血液恶性肿瘤。它导致骨髓衰竭和相关的并发症，包括感染，贫血或出血。尽管大多数患者在最初的化学治疗后达到缓解，但复发频繁。研究表明癌症干细胞在肿瘤的复发，转移，耐药性和人类癌症胡其他恶性表型中起重要作用，在许多癌症类型中，难以完全消除癌症干细胞并且通常导致癌症的复发。研究发现急性髓细胞白血病中也存在白血病干细胞。已经证明靶向白血病的常规化学治疗药物难以完全根除白血病干细胞，因此找到靶向治疗白血病干细胞的治疗靶点对急性髓细胞白血病的愈后将其着重要作用。据报道，活化的 Wnt/bwta-catenin 信号传导对人类急性白血病干细胞的自我更新能力和耐药性起着重要作用，导致患者生存率低下，Dickkopf(DKK)蛋白家族可通过竞争性结合 WNT 共同受体 LRP5/6 来抑制 Wnt/bwta-catenin 信号传导。有人提出 DKK1 可能通过诱导 LRP6 内化或通过跨膜 Kermen(Krm)蛋白降解来抑制 WNT 信号传导。已经证明 IL-3a(CD123) 是人类急性髓性白血病干细胞的独特标志物。本研究旨在探讨 Wnt/bwta-catenin 信号通路和 IL-3a 链受体在人类急性髓细胞白血病中的相互作用，从而为急性髓性白血病的治疗寻找新的靶点。

PU-2587

分析前因素导致 DD 二聚体异常升高一例

张桦挺
复旦大学附属华山医院

D-二聚体（D-Dimer）是交朕纤维蛋白（Fb）在纤溶酶的作用下水解产生的特异性降解产物，其水平的升高反映高凝状态和继发纤溶亢进，D-二聚体的含量变化可以作为体内高凝状态和纤溶亢

进的标志性物质 1。D-二聚体检测以简便、快捷、经济、安全、无创伤性为特点，其高度的敏感性和阴性预示能力，在深静脉血栓和肺栓塞的排除，DIC 的诊断及溶栓治疗监测等方面具有良好的应用价值。本文将从 DD 二聚体检测不一致的临床病例入手，回顾 DD 二聚体检测的干扰因素以及排查方法，注重临床与实验室检查相结合以避免错误诊断与治疗。

PU-2588

甲状腺激素假性升高一例

张桦挺
复旦大学附属华山医院

甲状腺疾病是内分泌科的常见病。实验室检测在甲状腺疾病的功能诊断中发挥了重要参考作用。本文将从一个甲状腺功能检测不一致的临床病例入手，回顾甲状腺激素检测的干扰因素以及排查方法，注重临床与实验室检查相结合以避免错误诊断与治疗。

PU-2589

吉林地区丙型病毒性肝炎结果统计

邵阿敏
吉林金域医学检验所有限公司

目的 由于丙型病毒性肝炎呈全球性流行，不同性别、年龄、种族人群均对丙型肝炎病毒易感。加上我国丙肝检测和监测体系不够完善，公众对丙肝认识较低等现状，因此丙肝筛查非常重要。通过分析吉林地区近 5 年丙肝检测情况，为流行病学调查提供参考依据。
方法 选取送检我公司的丙型肝炎病毒抗体 IgG 样本，检测方法为 ELISA 法。分析 2017 年 1 月 1 日到 2021 年 6 月 1 日的检测结果，统计其阳性率及变化趋势。
结果 2017 年共收取标本 1999 例，阳性结果为 57 例，阳性率为 2.85%，2018 年共收取标本 6453 例，阳性结果为 127 例，阳性率为 1.97%，2019 年共收取标本 6694 例，阳性结果为 199 例，阳性率为 2.97%，2020 年共收取标本 4771 例，阳性结果为 213 例，阳性率为 4.46%，2021 年共收取标本 2476 例，阳性结果为 101 例，阳性率为 4.08%.统计结果显示吉林地区丙肝阳性率较高，过去五年有增高的趋势。
结论 目前丙型肝炎病毒还没有有效的疫苗，缺乏足够有效的预防措施，主要是阻断传播途径和传染源，避免与他人共用刮胡刀，避免去无正规资格的机构进行纹身、洗牙等。当出现乏力、食欲减退、腹胀、肝区痛等可疑症状时，一定要及时就医检查诊断并治疗。丙型病毒性肝炎一部分患者经过急性期积极治疗后就可痊愈；还有一大部分患者会转为慢性丙型肝炎，经过近 20 年的发展部分患者会发生肝硬化，甚至转化为肝癌而致命。丙型病毒性肝炎患者大多因肝硬化或肝癌而死亡。因此尽可能将丙型肝炎检测纳入健康体检范畴。

PU-2590

重庆地区血小板聚集率检测对复发性流产患者的诊断价值

殷勤
陆军特色医学中心（大坪医院） 检验科

目的 分析血小板聚集率检测在复发性流产（RSA）患者中的应用价值.
方法 1）收集 2017 年 1 月至 2021 年 5 月源于陆军军医大学第三附属医院的患者样本，选取 96 例 RSA 患者作为试验组，同时选取 81 例非孕期且无流产史的健康女性作为健康对照组，对两组血小

板聚集率进行比较。均采用静脉全血检测，EDTA-K2 抗凝。2）运用光学比浊法对样本进行血小板聚集率检测。3）应用 t 检验进行病例组与健康对照组组间差异分析，运用单因素方差非参数分析进行病例组不同诱导剂间差异分析。
结果 病例组不同诱导剂亚组之间：ADP-COLL 比较结果没有显著差异（P=0.413）。ADP-EPI 比较结果没有显著差异（P=0.398）。ADP-AA 比较结果具有显著差异（P=0.01）。COLL-EPI 比较结果没有显著差异（P=0.979）。COLL-AA 比较结果具有显著差异(P=0.015)。EPI-AA 比较结果具有显著差异(P=0.017)。病例组与健康对照组之间均有显著性差异。
结论 RSA 患者血小板聚集率明显增高。对 RSA 患者进行血小板聚集率检测具有重要的临床诊断价值。

PU-2591

MCV 对不同水平原始细胞比例初诊成人骨髓异常增生综合征患者的预后影响

李凤龙
东南大学附属中大医院

目的 分析平均红细胞体积（MCV）对不同水平原始细胞比例骨髓异常增生综合征（MDS）患者预后的影响。
方法 收集 2012 年 6 月-2016 年 5 月于我院血液科初诊治疗的原发 MDS 患者 242 例，按照 MCV 水 平分为 HMCV 组（≥100fl）和 LMCV 组（<100fl），按照不同水平原始细胞比 例将入组患者分为 H 亚组（≥5%）和 L 亚组（<5%），比较不同 MCV 水平患者 总生存期差异；单因素及多因素分析 MCV 对所有患者及 L 亚组患者总生存期影 响；比较 L 亚组不同水平 MCV 患者临床指标差异。
结果 HMCV 组 OS 较 LMCV 组显著延长（P<0.05）；单因素分析结果显示，HGB、MCV、原始细胞比例、 染色体核型及基因突变数目与入组患者 OS 密切相关（均 P<0.05）；多因素分析 结果显示，原始细胞比例、染色体核型及基因突变数目与入组患者 OS 独立相关 （均 P<0.05），MCV 与入组患者 OS 非独立相关（P>0.05）。L 亚组中，HMCV2 组 OS 较 LMCV2 组显著延长（P<0.05）；单因素分析结果显示，年龄、HGB、 MCV、染色体核型、等位基因突变数量与 L 亚组患者 OS 密切相关（均 P<0.05）； 多因素分析结果显示，HGB、MCV 及基因突变数目均与 L 亚组患者 OS 独立相 关（均 P<0.05）。L 亚组临床指标中，LMCV2 组患者染色体核型差、IPSS-R 高 危及等位基因突变数量高的比例较 HMCV2 组患者显著升高，差异均有统计学意义（均 P<0.05）。2 组患者各单等位基因突变频率均未见明显统计学差异（均 P>0.05）。
结论 低水平 MCV 为低水平原始细胞比例 MDS 患者的独立不良预后影响因素，可能与染色体核型、IPSS-R 预后及基因突变数目密切相关。

PU-2592

生化检验全程质量控制管理的应用研究

熊飞良
宁乡人民医院

目的 研究全程生化检验中应用质量控制管理的效果。
方法 研究时段 2017.6-2019.5，研究对象是我院接收的 200 例生化检验患者，采纳生化检验先后顺序分观察组（质量控制管理）与对照组（常规控制管理）各 100 例，比较两组管理效果。
结果 与对照组比较，观察组生化检验准确率高，重现性及时效性高，误差值低；观察组医师满意率（95.00%）高于对照组 70.00%，P＜0.05。
结论 质量控制管理应用在全程生化检验能规范生化检验操作，提高检验工作质量。

PU-2593

利用 Syncthing 软件实现检验信息系统数据局域网远程自动备份

何增品
昆明医科大学第一附属医院

目的 随着科学技术的发展医学检验科的工作已经全面迈入了自动化、电子化、无纸化时代，随之产生的大量数据有效保存工作，就成为我们工作的重点。
方法 通过利用 syncthing 软件实现单机版检验报告系统数据的远程自动数据同步备份方案，来做好检验科信息系统安全工作，能有效保护检验数据。
结果 远程备份系统的搭建，能使数据实现同步备份。
结论 当电脑发生故障或意外，发生数据丢失，恢复工作就显得尤为重要，此时数据备份工作就是决定数据恢复成败的关键因素，所以远程自动备份方案的建设刻不容缓。

PU-2594

BMP9 对共培养体系中人乳腺癌 MDA-MB-231 细胞迁移和侵袭的影响及其机制探讨

王林
西安市第一医院

目的 采用体外细胞共培养技术模拟骨微环境，探讨人骨形态发生蛋白 9 (bone morphogenetic protein 9，BMP9) 对人乳腺癌 MDA-MB-231 细胞迁移和侵袭的影响，并探讨其机制。
方法 实验分为对照组和 BMP9 处理组，骨髓基质细胞 HS-5 与 MDA-MB-231 细胞在 Transwell 共培养体系中分别加入 PBS 和重组 BMP9 蛋白(100ng/ml)，培养 2 天后，细胞划痕实验检测 MDA-MB-231 细胞迁移能力的改变；TranswellTM 细胞侵袭实验检测 MDA-MB-231 细胞侵袭能力的改变；Western blot 法及明胶酶谱法分别检测 MDA-MB-231 细胞基质金属蛋白酶（MMP-9、MMP-2）蛋白表达及相对活性的改变； Western blot 法检测 HS-5 和 MDA-MB-231 两种细胞中基质细胞衍生因子-1(SDF-1)及 MDA-MB-231 细胞中趋化因子受体 CXCR4 和细胞信号通路 P-Akt 表达的变化。
结果 在共培养体系中加入 BMP9 后，划痕实验结果显示实验组和对照组 MDA-MB-231 细胞的平均愈合率分别为 84.28%±2.54%、44.49%±4.86%，TranswellTM 实验结果显示穿模 MDA-MB-231 细胞数分别为 481±22、121±11，表明 BMP9 对共培养体系中 MDA-MB-231 细胞的迁移和侵袭有明显的抑制作用（P<0.05）；MDA-MB-231 细胞 MMP9、MMP2 的蛋白表达实验组分别为 0.10±0.01、0.11±0.03，较对照组 0.79±0.03、0.82±0.05 显著下调（P<0.05），相对活性实验组分别为 0.14±0.03、0.12±0.02，较对照组 0.90±0.07、1.04±0.14 也均显著下降（P<0.05）；MDA- MB-231 细胞中 CXCR4 受体及其配体 SDF-1 的蛋白表达实验组分别为 0.08±0.01、0.06±0.02，和对照组 0.07±0.01、0.05±0.01 差异无统计学意义（P>0.05）；p-Akt 蛋白表达实验组（0.09±0.01）较对照组（0.48±0.07）显著降低（P<0.05）；HS-5 细胞中 SDF-1 的蛋白表达实验组（0.14±0.01）较对照组（0.42±0.06）显著降低（P<0.05）。
结论 在模拟骨微环境的共培养体系中，BMP9 可能通过 SDF1/CXCR4-PI3K/Akt 信号通路抑制人乳腺癌 MDA-MB-231 细胞的迁移和侵袭。

PU-2595

一例 18 号染色体嵌合异常的细胞遗传学分析

耿丹、杜荷香、吕喆、栗二娇、任孝慧
太原金域临床检验所有限公司

目的 通过对一例发育迟缓，高度近视的患者进行染色体核型分析，明确发病原因，并探究临床表现与染色体变异的相关性，同时评估染色体核型分析技术在临床中的应用价值。
方法 采集 10 岁女患者的肝素钠抗凝全血，进行外周血染色体 G 显带核型分析。
结果 患者传统染色体核型分析结果为：46,XX,del(18)(p11.2)[50]/46,XX,i(18)(q10)[10]。此核型符合嵌合体核型，其中一种核型为 18 号染色体短臂部分缺失，即 18 号染色体部分单体；另一种核型为等长臂 18 号染色体，即 18 号染色体部分三体；二者嵌合比例为 50/10。
结论 该患者发育迟缓、高度近视可能是由 18 号染色体部分单体与 18 号染色体部分三体两种核型共同作用所致，但患者未表现出严重的出生缺陷，这可能与嵌合体核型及嵌合比例有关。染色体核型分析利用 G 显带技术清晰地显示了染色体的具体形态，是目前较成熟的遗传学诊断技术之一，在出生缺陷领域颇具临床意义。

PU-2596

17 例主次侧交叉配血不合患者输血疗效分析

王钰箐、王学锋、蔡晓红
上海交通大学医学院附属瑞金医院

目的 回顾比较主次侧交叉配血不合患者，输注 ABO 同型去白细胞悬浮红细胞或洗涤红细胞后的输血效果。
方法 检测患者输血前后血红蛋白及总胆红素，应用 IBM SPSS Statistics 22.0 软件进行统计分析。
结果 17 例主次侧交叉配血不合患者合计输血次数 34 次，输注 ABO 同型的去白细胞悬浮红细胞或洗涤红细胞均使 Hb 水平明显升高（P=0.000<0.001），输血疗效无显著性差异（P=0.484>0.05），均未使 TBIL 水平上升（P=0.472>0.05）。
结论 对于有明确输血需求的主次侧交叉配血不合患者，应及时给予红细胞输注，且优先考虑去白细胞悬浮红细胞，最大限度避免输血延迟。

PU-2597

培训和考核对提高检验标本合格率的影响

陈景章、游柠彰
益阳市第一中医医院

目的 通过全面检验标本正确采集及运送的培训和考核，提高检验标本合格率。
方法 通过护理部、质控科、医务部、检验科相互合作，重点培训临床医师、护士、运送标本护工，内容包括病人检验前准备、标本正确采集、标本运送等重点工作。编制详细检验标本采集、运送工作考核制度，细化考核内容，每月及时考核通报。根据改进情况，重点人群再培训指导。
结果 通过三个月的持续培训、考核和改进，标本不合格率由 2.03%下降到 0.95%，其中标本类型错误、标本容器错误、标本量不足的问题得到了明显提升。
结论 严格的培训和考核可明显提高检验标本合格率。

PU-2598

乙醇-琼脂法在细胞蜡块制作中的应用

刘秀生、程梦月、高俊美
合肥金域医学检验实验室有限公司

目的 避免细胞丢失，提高肿瘤细胞检出率。
方法 收集合肥金域医学实验室有限公司病理中心 2019-2020 年体外培养细胞标本 20 例。细胞经固定、脱水后，加入琼脂，使琼脂溶液充分包裹细胞，凝集成块后进行包埋、脱水、切片、染色等实验步骤。
结果 琼脂对标本处理无任何影响，可将细胞集中，可以连续切片，制成的细胞蜡块可长期保存。制作的细胞蜡块 HE 染色清晰透亮，红蓝对比明显；免疫组化染色定位准确，细胞集中，染色清晰无背景。
结论 此方法对于送检极少量体外培养细胞处理很有优势，细胞量基本不会丢失，可以大大提高阳性率，制成细胞蜡块可长期保存。为后续免疫组化染色、分子检测提供充分的材料。满足病理诊断和科研实验室的需求。

PU-2599

检验科优质服务流程应用效果评价

王潘
资阳市中医院

目的 评价在检验科应用优质服务流程的效果。
方法 选取 66 例自 2019 年 2 月-2019 年 5 月来检验科进行检测的患者，将其划分为常规组(33 例)和优质组(33 例)。常规组实施常规检验流程，优质组实施优质服务流程。比较两种流程标本检验等待的时间。
结果 优质组标本检验等待的时间要少于常规组，差异有统计学意义($P<0.05$)。
结论 在检验科实施优质服务流程能缩短患者样本检验等待的时间，值得推广。

PU-2600

通过下发室内质控品对四川省妇幼医院实验室血常规室内质控体系进行的调查与评价

张鸽
四川大学华西第二医院

目的 通过下发血常规室内质控品的方式对四川省妇幼医院检验科血常规室内质控的运行情况进行调查以及评价。
方法 四川省妇幼检验质量控制中心作为组织方，随机抽选 40 家四川省妇幼系统医院检验科，下发血常规室内质控品，要求参与调查检验科使用下发质控品进行至少 20 天的室内质控并反馈每日室内质控结果，失控处理以及定期的质控评价等数据，通过对回报数据进行评价，分析四川地区妇幼系统的室内质控体系建立情况。
结果 40 家参与调查单位均能够自行累积室内质控靶值，40%的单位使用了只能显示一个浓度质控数据的质控图；15%的单位质控允许限设置不合理，超出行业标准的允许范围；10%的单位未对单个项目进行质控月分析；20%的单位有室内质控失控处理不当。

结论 四川省妇幼检验系统的血常规室内质控体系建设水平亟需改善，需从质控允许范围制定，失控处理原则，质控定期评估要求等方面加强理论培训，并对实验室的质控软件进行优化。

PU-2601

医学检验质量控制分析

王潘
资阳市雁江区中医医院

由于时代取得了飞速的进步，从而推动了现阶段医学的持续发展，而医学检验技术也因此更加先进，在对疾病进行诊治与预后环节，都应该凭借医学检验结果进行参考，可以说，医学检验在医学临床工作实施中扮演着至关重要的角色，其结果也给患者的疾病诊断发挥着关键的影响，为了进一步确保医学检验的质量，进行相应的质量控制十分关键。本文主要分析了医学检验质量的控制对策，以期提供一定的参考作用。

PU-2602

NLR 与 PLR 联合检测与冠脉病变严重程度相关性研究

崔文浩
广东省人民医院

目的 分析 NLR 与 PLR 联合检测与冠脉病变严重程度的相关性。
方法 采用回顾性的研究方法，以 Gensini 积分 30 分为界划分低分组和高分组，另收集同期健康者 153 例的 NLR 和 PLR 值作为健康对照。
结果 健康组、低分组、高分组的 NLR 检测水平分别为 1.50(0.67)、2.24(0.86)、2.07(1.55)，三组两两之间差异具有统计学意义，PLR 水平在三组两两之间的差异不具有统计学意义。
结论 NLR 对冠脉病变严重程度具有一定的预测价值，PLR 对于 Gensini 评分积分＞30 分的冠心病患者有一定的预测价值。NLR 与 PLR 联合检测对于冠脉病变严重程度无明显预测价值。

PU-2603

浅析提高临床医学基础检验技术的措施

王潘
资阳市雁江区中医医院

目的 由于现代化医疗水平的持续优化，所规定的临床医学基础检验技术标准也在不断提升，需要更加精准、快速的在医疗工作中进行检验，给患者提供更高的治疗水平。
方法 临床医学检验技术重点包括了充分合理的收集与测试临床标本，并根据及时准确的检测报告，给临床疾病的诊断、治疗和预防提供一定的依据。
结果 所以在我国专门开放了临床医学检验的课程，目的是为了培养出更多具备医学检验技术的人才。
结论 目前临床医学检验技术中的不足，并对提高检验技术的措施展开了一定的分析，以推动临床医学检验技术的完善优化。

PU-2604

Prevalence and Genotype Distribution of High-risk HPV Infection among Women in Beijing, China

Xiaoyan Zhu、yaxuan wang、zhi lv、jianrong su
Beijing Friendship Hospital, Capital Medical University

Cervical cancer is highly associated with high-risk human papillomavirus (HPV) infection and genotype distribution of high-risk HPV(HR-HPV) infection varies greatly in different regions. Clinical specimens were collected from 46365 patients at Beijing Friendship Hospital, Capital Medical University from January 2017 to December 2020. HPV DNA genotype testing was performed using Real-time PCR. The infection rates based on disease group were compared using the chi-square test. The linear-by-linear association test and gamma value were used to assess the changes in HPV prevalence over calendar year and age group. A total of 10514 women were infected with HR-HPV, with an overall positive rate of 22.7%. The most prevalence HR-HPV types were HPV 52, 58, 16, 51 and 66 and HPV 59 had a higher prevalence except for HPV16, 58 and 52 in cervical cancer group. Single infection of HR-HPV was dominant among different diseases groups. The infection rate of HR-HPV decreased first and then increased from below 20 years old to over 60 years old. There were significant differences in the HR-HPV infection rates among the age and disease groups. Our findings demonstrate that the genotype distribution of HR-HPV varied with age and diseases. The HR-HPV genotypes prevalence were found to be directly useful for local governments to promote HPV targeted vaccination in the study region.

PU-2605

临床医学检验中影响血液细胞检测质量的有关因素及其控制方法探讨

王潘
资阳市雁江区中医医院

目的 探讨临床医学检验中血细胞检测质量的相关因素及控制方法。
方法 2018 年 1 月至 2019 年 12 月，选取我院 150 例血型和血细胞检测条件相同的患者为研究对象。通过设置不同的检测条件，分析了影响血细胞检测质量的因素。
结果 稀释倍数为 1 的血细胞检测结果稀释比为 1 时，可提高 10000 倍： 两者差异有统计学意义（P<0.05）。不同室温保存时间的血液检测结果有显著性差异（P<0.05）。低温环境下不同保存时间血液检测结果差异有显著性（P<0.05）。同时，室温与低温血液检测结果有显著性差异（P<0.05）。
结论 在血细胞检测过程中，血液稀释率、血样放置时间和温度会影响检测结果。在今后的临床医学检测工作中，要严格控制血细胞检测的各个环节，尽量避免不利因素对检测结果的影响，保证检测结果的准确性。

PU-2606

男性不育症患者外周血染色体核型分析的临床应用分析

田维娟
云南大学附属医院

目的 分析男性不育症患者精液分析与外周血染色体核型的关系。
方法 收集云南大学附属医院从 2019 年 1 月至 2021 年 3 月到生殖医学科就诊男性共 194 例，用外周血染色体 G 显带操作方法进行外周血染色体核型分析；同时留取精液进行精液常规检验。
结果 194 例男性患者中，正常精液组有 83 例，异常染色体有 3 例，异常检出率为 3.61%，有 2 例为染色体多态性;有 95 例弱精症患者，染色体异常共 8 例，异常率为 8.42%，有 1 例为染色体多态性;有 16 例为弱精症患者，染色体异常有 3 例，异常率为 18.75%。以上三组染色体异常差异具有统计学意义(P＜0.05)。194 例男性患者中发现染色体异常有 11 例，异常检出率为 7.2%。其中有 2 例患者为染色体数目异常患者，其检出率为 1.03%；有 9 例患者为染色体结构异常，其检出率为 4.64%。而且发现 46,XXY 是最常见的染色体数目异常，即克氏综合征且为非嵌合型；染色体倒位和相互易位是最常见的结构异常，本组数据中还出现了罗伯逊易位，而且还检出 3 例染色体多态性，检出率为 1.55%。
结论 男性不育症患者中染色体异常率较高，染色体异常是导致男性不育症的重要遗传因素之一，导致男性不育的临床表现分别表现为弱精症、无精子症等。对于患有男性不育症的患者进行外周血染色体检查，有助于发现病因和辅助诊断。

PU-2607

长沙地区女性抗缪勒氏管激素水平与年龄的相关性分析

袁璐
中南大学湘雅三医院

目的 通过分析长沙地区 AMH 水平在不同年龄阶段女性体内的变化，探究 AMH 水平检测对临床评估卵巢储备功能的应用价值，从而帮助女性进行有效备孕。
方法 回顾性分析 2019 年 4 月～2021 年 4 月湖南省长沙市中南大学湘雅三医院参与健康体检的 1985 例女性的血清检查结果。按照年龄将被检者分为 7 组，A 组：20～25 岁，共 88 例；B 组：26～30 岁，共 316 例；C 组：31～35 岁，共 385 例；D 组：36～40 岁，共 411 例；E 组：41～45 岁，共 420 例；F 组：46～50 岁，共 285 例；G 组：＞50 岁，共 80 例。采用磁微粒吖啶酯化学发光法检测被检者血清 AMH 的含量，分析其与年龄的相关性。
结果 （1）B 组血清 AMH 水平稍微高于 A 组，但差异不具有统计学意义(p＞0.05)；B 组与 C 组、C 组与 D 组、D 组与 E 组、E 组与 F 组、F 组与 G 组进行组间两两比较，发现血清 AMH 水平依次下降，且各组间差异均具有统计学意义(p＜0.05)。（2）30 岁左右血清 AMH 含量相对最高，随后，AMH 水平随年龄增长逐渐下降。
结论 30 岁左右是女性怀孕的最佳年龄阶段；随后，女性卵巢储备功能下降，提示怀孕几率减小。随着年龄的增长，30 岁以后，女性血清 AMH 水平逐渐下降，临床中可以恰当的进行 AMH 检测为判断生育能力提供临床指导作用,以帮助女性进行有效备孕。

PU-2608

探讨如何应对新冠病毒大规模筛查结果快速分区上报

卞林翠
合肥金域医学检验实验室有限公司

面对六安突发疫情，大规模筛查迫在眉睫，大量样本集中送达合肥金域医学检验实验室有限公司。随同样本一同到达的还有被采样人员信息，不同区域相关采样信息表中，包含不同市区、不同社区、不同小区，但不同区域的筛查结果需分别上报至相应区政府。在大筛查样本涌入实验室后需快速进行灭活、提取、检测、结果分析、上报。为提高灭活及检测速度，样本在整理灭活过程中，不同区域相互混合，但在结果上报中区域被打乱，不能分区快速上报检测结果；且资料分析小组在采样信息表资料录入、区域划分中任务量较大，可能需要涉及与前端采样人员或物流人员确认样本来源区域，造成人力及沟通成本的提高。因此需标本到达实验室前做好采样信息表中每个区域所填信息完整并做好特有标记，在大量样本信息混合中有特有标识，可进行区域筛选；在小程序采样信息录入中也应对不同区域有特有标识。检测分析结果出来后，资料分析小组即可根据录入的特有采样信息标识，将不同样本人员筛选分配至相应区域，完成结果上报中区域的划分。节省后期分区域时间，可更高效将实验结果上报至各区政府。

PU-2609

不同年龄和性别的消化道出血病人血栓弹力图参数比较与临床意义

欧淳
南华大学附属南华医院

目的 分析不同性别和年龄对消化道出血病人血栓弹力图各项参数的差异及临床指导意义。
方法 选取 2020 年 1 月至 2020 年 11 月南华大学附属南华医院收治的 165 例消化道出血患者作为研究对象，检测其凝血功能与血栓弹力图（TEG）的 5 项主要指标：R 值（反映凝血因子活性）、K 值（反映纤维蛋白原功能）、MA 值（反映血小板功能）、CI 值（反映凝血综合指数）、α 角（反映血块形成速度）。分别按照年龄和性别进行分组，分析性别和年龄对 TEG 各参数的影响。
结果 165 名消化道出血病人 TEG 的 R 值、K 值、MA 值、CI 值和 α 角在不同的性别组中均无统计学差异（$P>0.05$）。不同年龄组中，MA 值、CI 值和 α 角差异均具有统计学意义（$P<0.05$）。在男性组中，低龄组与高龄组比较仅 CI 值的差异有具有统计学意义（$P<0.05$）。在女性组中，低龄组与高龄组比较 K 值、MA 值、CI 值和 α 角的差异均具有统计学意义（$P<0.05$）。低龄组中，男性 MA 值与女性比较仅有 MA 差异具有统计学意义（$P<0.05$）。高龄组中，男性与女性的 R 值、K 值、MA 值、CI 值和 α 角均无统计学意义（$P>0.05$）。
结论 消化道出血病人中，性别对 TEG 参数影响不明显，年龄对 TEG 参数有一定的影响。各实验室应根据实际情况建立合适的 TEG 参考区间。

PU-2610

临床生化质控自动化的设计与应用

汤涛
陆军军医大学第二附属医院

目的 开发一套适用于临床生化多项目的室内质控自动化系统，实现临床生化类项目的室内质控自动化，并对该系统进行临床应用价值评估。

方法 参考 WS/T 641-2018《临床检验定量测定室内质量控制》室内质量控制指南，依靠 Beckman Coulter 公司的 Power Processor 自动化流水线的中间体软件 Data Manager 2（DM2）为工具整合实验室 LIS 系统，针对 69 项临床生化检验定量项目编写规则给出指令将质控品从储存冰箱获取、轨道等待复温、进入仪器检测、失控重测等，并对临床生化血液定量室内质控项目进行验证，比较了室内质控自动化与手工项目平均值、变异系数、离散程度、西格玛值、失控检出率、样本上线平均时间、报告平均 Tturnaround Time（TAT）等参数关键指标。
结果 2020 年 1 月到 6 月使用室内质控自动化系统期间，自动化室内质控与传统手工质控图极其相似。其中自动化质控与手工质控平均值比较差别无明显统计学意义（P>0.05）；变异系数比较差别无明显统计学意义（P>0.05）；离散程度比较差别无明显统计学意义（P>0.05）；失控检出率比较差别无明显统计学意义（P>0.05）；西格玛值差别无明显统计学意义（P>0.05）。检测时间方面，第一批样本上线平均时间提前了 38min（P<0.05），门诊样本平均 TAT 下降了 28min（P<0.05）；住院样本平均 TAT 下降了 26min（P<0.05）；急诊样本平均 TAT 下降了 24min（P<0.05）。
结论 本研究开发了一套适用于多个定量项目的临床生化室内质控自动化系统，能够满足日常临床工作需求，可以极大缓解第一批样本上线时间，降低 TAT 和提高检验质量，能高度做到人机协调融合模式，其应用价值具有一定的推广性。

PU-2611

一个新的 ABO*A 等位基因导致的 AwB 亚型及其分子机制研究

周璐[1]、雷航[2]、洪叶[1]、金爽[1]、董永勤[2]、王学锋[2]、蔡晓红[2]
1. 上海交通大学医学院附属瑞金医院舟山分院
2. 上海交通大学医学院附属瑞金医院

目的 以一个血型 AwB 亚型家系为研究对象，进行血清学鉴定及分子机制研究。
方法 ABO 血清学定型使用标准血清学实验方法；对 ABO 基因 7 个外显子及其侧翼序列做 PCR 扩增、基因克隆和测序分析；采用 Chimera 软件进行 N-乙酰半乳糖胺基转移酶（GTA）突变体构建,PyMOL 软件作图并进行分析。
结果 家系的血清学鉴定结果先证者为 A_wB 亚型，家系其他 2 名成员为 B 型。DNA 克隆和测序分析显示先证者为 *A/B* 基因型，其他成员为 *B/O* 基因型。先证者的 A 等位基因上 *A1.02* 基础上发生 c.838C>T 错义突变，导致 GTA 发生 p.L280F 氨基酸置换。通过对 GTA 空间结构的分析，认为 p.L280F 未导致 GTA 蛋白整体结构的改变，但改变了 GTA280 位氨基酸与周围氨基酸残基的氢键网络，导致局部构象的改变。
结论 p.L280F 突变可能通过改变邻近氨基酸间的作用力导致 A 酶活性减弱，在与 B 等位基因共表达时形成 A_wB 亚型。

PU-2612

中老年慢性肾脏病凝血纤溶指标水平变化与临床指标相关性研究

张玲、刘华伟、龚蓉
成都市第三人民医院

目的 观察分析中老年慢性肾脏病患者凝血纤溶指标变化，探讨 D 二聚体、抗凝血酶 III 与临床指标的的相关性。
方法 收集我院 2020 年 1 月～2020 年 11 月我院住院的中老年 CKD 患者。根据有无肾病综合征表现分为肾病综合征（NS））组 79 例，非肾病综合征组 89 例，同期健康体检者 30 例作为对照组。

比较健康对照、NS 组与非 NS 组凝血纤溶指标变化，用相关分析、回归分析及 ROC 曲线分析中老年慢性肾病凝血纤溶指标与相关实验室指标及血栓事件的关系。

结果 ①NS 组与非 NS 组 ATII 水平均低于健康对照组(P<0.05),D-D、FIB 水平均高于健康对照组(P<0.05），NS 组与非 NS 组 D-D、AT-III 统计学显示有显著差异(P<0.05）。②相关分析显示 D-D 水平与血清 ALB 负相关，与尿蛋白、尿蛋白/ALB 比值正相关，AT-III 水平与血清 ALB、CHOL、HDL-C、LDL-C 正相关。③回归分析显示血清 ALB 是 AT-III 与 D-D 水平的独立影响因素。④对血栓事件的诊断 D-D 检测价值优于血浆 ALB，血浆白蛋白优于 AT-III。

结论 中老年慢性肾脏病患者存在凝血功能异常，血清 ALB 是 D-D 及 ATII 水平的独立影响因素，D-D、血清 ALB、ATII 水平对中老年 CKD 血凝状态和血栓事件具诊断价值。

PU-2613

Possibility of EDTA anti-coagulated plasma instead of serum for insulin detection in hemolytic specimens

娄鉴芳
江苏省人民医院（南京医科大学第一附属医院）

The aim of this study was to determine the interference of hemolysis on insulin (INS) determination in serum and EDTA anti-coagulated plasma by electrochemiluminescence immunoassay (ECLIA) method and the possibility of using plasma for INS determination. Serum/EDTA anti-coagulated plasma with/without hemolysis were detected by ECLIA for INS determination and the results were then compared.1. INS levels between non-hemolytic serum and EDTA anti-coagulated plasma showed no significant difference (P> 0.05). 2. INS levels in light hemolysis (A group) showed no significant difference after 0.5, 1h compared with non-hemolytic serum (P> 0.05) but decreased significantly after 2, 4h (P<0.05). INS levels in moderate to severe hemolysis (B/C/D group)showed significant decrease after 0.5h. 3.Plasma INS levels of A (mild hemolysis), B (mild hemolysis), C (moderate hemolysis) group showed no significant difference with time compared with non-hemolytic plasma except only that of D (severe hemolysis) group showed a significant decrease(P<0.05).

PU-2614

提高 POCT 血气分析检验质量的管理实践研究

潘婕
南京大学医学院附属鼓楼医院

目的 应用质量管理方法提高 POCT 血气分析检验质量并评估其实施效果。

方法 纳入 3 个使用雅培 i-STAT1 手持式血气分析仪病区，建立针对性的 POCT 血气分析质量管理方案。将 POCT 血气分析质量管理前、管理后 6 个月、管理后 12 个月共 3 组室间比对进行分析，比较 3 个组的项目得分、项目平均偏倚（%）及检测合格率（%），并对管理后的室内质控变异系数进行分析评价。

结果 A 病区 PO2、PCO2、Na＋和 Ca2＋管理后 6 个月、管理后 12 个月较管理前项目得分提高。pH 和 K＋3 个组项目得分均为 100。pH、PCO2、Na＋、Ca2＋管理后 6 个月较管理前平均偏倚减小（P<0.05）。pH、PO2、PCO2、Na＋、K＋和 Ca2＋管理后 12 个月较管理后 6 个月平均偏倚减小（P<0.05）。A 病区管理后 6 个月、管理后 12 个月室间比对检测合格率均为 100%，较管理前（50%）均有增高。B 病区 pH、PO2、PCO2、Na 和 Ca2＋管理后 6 个月、管理后 12 个月较管理前项目得分提高。K＋3 个组项目得分均为 100。PO2、PCO2、Na＋、K＋和 Ca2＋管理后

6 个月较管理前平均偏倚减小（P<0.05）；pH、PO2、PCO2、Na＋、K＋和 Ca2＋管理后 12 个月较管理后 6 个月平均偏倚减小（P<0.05）。B 病区管理后 6 个月、管理后 12 个月室间比对检测合格率分别为 83%和 100%，较管理前（67%）增高。C 病区 pH、PO2、PCO2 和 K＋管理后 6 个月较管理前项目得分提高；pH、PO2、PCO2、Na＋和 K＋管理后 12 个月较管理前项目得分亦提高。Ca2＋3 组室间比对项目得分均为 100。pH、PO2、PCO2、K+和 Ca2+管理后 6 个月较管理前平均偏倚减小（P<0.05）。PCO2、Na＋和 K＋管理后 12 个月较管理后 6 个月平均偏倚减小（P<0.05），但 pH、PO2 和 Ca2+管理后 12 个月较管理后 6 个月平均偏倚增大（P<0.05）。C 病区管理后 6 个月、管理后 12 个月室间比对检测合格率均为 100%，较管理前（33%）提高。除 PO2 外，3 个病区在 POCT 统一质量管理后血气分析各项目的室内质控变异系数均在允许不精密度范围内。

结论 建立并施行针对性的 POCT 血气分析质量管理，可提升 POCT 血气分析的检验质量。

PU-2615

miRNA 在类风湿关节炎中的表达及意义

周韶松
南方医科大学珠江医院

小 RNA（miRNA）是小分子非编码 RNA，负调控基因表达后的转录水平。目前，有 939 成熟的人类小 RNA 序列 Sanger 小 RNA 的注册表更新。预计人类基因组可能有大约 1500 的小 RNA 在控制我们三分之一基因的表达。在细胞中通过控制合成目标蛋白的，这些调控 RNA 分子，参与多种生理网络和主要职能，他们的管制已经牵连严重的人类疾病的发病机制，如癌症和感染。

PU-2616

HDAC 抑制剂通过下调内质网蛋白 RCN1 逆转肺癌耐药及增加药物敏感性的作用机制研究

张璐
山东大学第二医院

肺癌是全世界高发病率、高死亡率的恶性肿瘤，放化疗、免疫治疗是转移性肺癌的主要治疗手段，和其它肿瘤一样，治疗失败的重要原因之一是耐药性的产生。由于化疗依然是肺癌的一线治疗手段，对其耐药的机制也较为深入，目前克服肺癌化疗耐药的策略主要有：１）研究耐药机制，发现新的逆转药物，例如，药泵蛋白 P-gp 高表达是多西他赛（docetaxel, Doc）的耐药机制之一，而卡巴他赛（Cabazitaxel）P-gp 的亲和力低，可作为治疗方案用于对 Doc 耐药患者；2）选择新的治疗方案，例如，一线化疗失败后采用免疫治疗，这也是新型的逆转方法；３），选择无交叉耐药的联合化疗方案，例如，在以铂类药物为主的一线化疗失败后，可采用多西他赛进行治疗，而且二者进行交叉治疗的肺癌患者生存期得到延长等。

本研究论文发现内质网蛋白 reticulocalbin-1 (RCN1)在肺癌中高表达，而且 RCN1 在多种肿瘤耐药细胞中的表达显著升高、与肿瘤细胞耐药性密切相关。因此我们重点探讨 RCN1 在肺癌耐药中的作用，并通过筛选降低 RCN1 的药物，发现 HDAC 抑制剂能显著降低 RCN1 的表达、且能增加耐药细胞对化疗药物、特别对多柔比星的敏感性，降低其毒性的作用，并对 HDAC 抑制剂能显著降低 RCN1 表达的机制进行初步探讨。RCN1 作为内质网蛋白，其生理病理功能研究不多，主要集中于肿瘤中的表达，本论文通过研究 RCN1 与肿瘤多药耐药中的关联以及对化疗药物的影响，为耐药肺癌患者的临床用药提供新的依据。

PU-2617

基于机器学习算法建立的 IgA 肾病与非 IgA 肾病鉴别诊断模型

杨晗、刘记宏、张慧、刘子杰
昆明医科大学第一附属医院

目的 基于患者的流行病学资料和临床实验室常规检测结果，用机器学习算法建立 IgA 肾病与非 IgA 肾病鉴别诊断模型。
方法 本研究共纳入经肾穿刺活检确诊的患者 260 例，其中 IgA 肾病 130 例，非 IgA 肾病 130 例。收集患者的流行病学资料和临床实验室常规检测结果。将 260 例数据分为训练集(70%，182 例)和测试集(30%，78 例)。分别使用决策树、随机森林、支持向量机(SVM)、极限梯度提升算法（XGBOOST）建立鉴别诊断模型。并使用混淆矩阵，ROC 曲线评估模型效能。
结果 与决策树、随机森林和支持向量机相比，XGBOOST 模型性能最佳，其准确率为 83.33%，ROC 曲线下面积为 0.83，诊断为 IgA 肾病的敏感度、特异度分别为 89%、79%。
结论 采用 XGBOOST 方法建立的 IgA 肾病与非 IgA 肾病鉴别诊断模型具有较好的临床性能。

PU-2618

A novel long non-coding RNA RNF144A-AS1 promotes bladder cancer metastasis through mediating epithelial-mesenchymal transition

Yifan Wang
The Second Hospital, Cheeloo College of Medicine, Shandong University

Long non-coding RNAs (lncRNAs) play critical roles in tumor initiation and progression. However, little is known about the functional role of lncRNAs in the tumor metastasis Here, through lncRNA-expression and functional mining computational framework of primary bladder cancer (BC) tumor and adjacent non-tumor tissues from The Cancer Genome Atlas database, we discovered a highly expressed lncRNA RNF144A-AAS1, which involved in extracellular matrix organization. Gain-of-function assays demonstrated that RNF144A-AAS1 promotes BC cells migration and invasion in vitro. Mechanistically, Knocking down RNF144A-AS1 significantly inhibited the epithelial-mesenchymal transition (EMT) by inducing the expression of epithelial markers (E-cadherin and ZO-1) and suppressing the expression of mesenchymal markers (N-cadherin and Vimentin). In conclusion, this study highlighted that positive role of RNF144A-AS1 in BC metastasis via the activation of multiple EMT regulators, suggesting its great potential to serve as effective therapeutic target for patients with BC.

PU-2619

流式细胞术法检测白介素-6、白介素-10 在脓毒症患者中的诊断价值

吴春香
四川省人民医院东院

目的 脓毒症是由感染引起的不平衡炎症反应综合征，细胞因子参与脓毒症的免疫反应。流式细胞术法检测血浆各细胞因子在脓毒症诊断效力的优劣比较还不明确，本文旨在比较流式细胞术法检测血浆细胞因子在诊断脓毒症的效力，并探讨 IL-6、IL-10 在成人脓毒症患者早期诊断中的应用价值。

方法 分析 2020 年 1 月至 2021 年 1 月期间四川省人民医院收治的成人脓毒症患者 122 例为实验组，以同期年龄、性别相匹配的 99 例健康体检者作为对照组。收集入组人群的相关资料：患者临床资料，流式细胞术法检测血浆 IL-2、IL-4、IL-6、IL-10、TNF-α、IFN-γ 的水平，患者 PCT 及 CRP 等水平，并记录患者 APACHEII、SOFA 评分。对各指标执行受试者工作曲线（ROC）及相关性分析，评估并比较各细胞因子对脓毒症早期诊断的应用价值。
结果 脓毒症患者血浆 IL-6、IL-10、TNF-α、IFN-γ、IL-2 等水平显著高于对照组(P<0.05)，而血浆 IL-4 在脓毒症患者与正常组之间无统计学差异（P=0.320，P=0.168）。执行 ROC 曲线各指标的 ROC 曲线下面积(AUC)分别为：IL-2 为 0.58[P=0.03，95% confidence interval(CI)，0.51-0.66]，IL-4 为 0.53（P=0.45, 95% CI,0.45-0.61），IL-6 为 0.97 (P<0.0001, 95% CI, 0.95-0.99)，IL-10 为 0.94 (P<0.0001, 95% CI, 0.90-0.97)，TNF-α 为 0.64(P=0.0003,95% CI，0.57-0.71)和 IFN-γ 为 0.66(<0.0001,95% CI，0.59-0.73)。IL-6 和 IL-10 对脓毒症的诊断价值尤为突出，TNF-a 与 IFN-γ 诊断价值相当，次于 IL-6 和 IL-10,而 IL-2 与 IL-4 在脓毒症早期诊断中的价值不明显。Spearman 相关性分析结果显示,脓毒症患者血清 IL-6 和 IL-10 呈正相关，r=0.57（P<0.0001, 95% CI ，0.43-0.68）。
结论 流式细胞术检测各细胞因子在预测脓毒症方面效力各不相同，IL-6、IL-10 对脓毒症患者的早期诊断价值尤为突出，可为临床脓毒症早期诊治提供依据。

PU-2620

妊娠中期血清 β-HCG 和血脂预测妊娠高血压综合症发生的价值研究

司马小可[1]、牛和平[2]、司马晓朋[1]
1. 郑州金域临床检验中心有限公司
2. 新密市妇幼保健院

目的 探讨妊娠中期血清 β-HCG 和血脂预测妊娠高血压综合症发生的价值。
方法 本研究对送往我中心的 120 名妊娠患者进行了前瞻性研究。 所有患者在妊娠中期（14-20 周）接受血清 β-HCG 和血脂的筛查，并随访至分娩。 本研究将血压正常组（I 组）和妊娠高血压组（Ⅱ组）的血清 β-HCG 和血脂进行了比较。
结果 发生 PIH 的女性（组 II）的 TG，总胆固醇，VLDL 和 LDL 值显著高于血压正常组（I 组）的患者，p 值<0.05，具有统计学意义。 组 II 的 HDL 和 β-HCG 值不高于组 I，p 值>0.05，差异无统计学意义。
结论 妊娠血质检测对于中期妊娠的孕妇是一项很好的非侵入性的检查，可用于临床前期妊娠高血压的预测。 而孕妇血清 β-HCG 与妊娠高血压无明显相关性。

PU-2621

对 372 例性染色体异常患者的统计学分析

司马小可、张美玲、张磊、张丽敏、李红敏
郑州金域临床检验中心有限公司

目的 探讨河南地区性染色体异常患者的临床表现及类型，并对其进行统计学分析。
方法 对 2018 来我中心做外周血染色体核型分析的 13235 例患者采用外周血进行染色体培养，常规 G 显带徕卡自动扫片仪扫片并进行核型分析。
结果 在 13235 例外周血染色体核型分析标本中，共检出性染色体异常患者 372 例，检出率为 2.81%， 其中女性 123 例，占 33.06%；男性 249 例，占 66.94%。在 372 例性染色体异常核型中

Y 多态性 130 例，占 34.94%；Klinefelter 综合征 95 例，占 25.54%；Tuner 综合征 88 例，占 23.66%；性反转 27 例，占 7.25%，其中女性性反转 15 例，占 4.03%；男性性反转 12 例，占 3.22%；超雌综合征 11 例，占 2.96%；超雄综合征 7 例，占 1.88%； 48,XXYY 综合征 1 例，占 0.27%；两性畸形 1 例，占 0.27%；其他异常 12 例，占 3.23%。
结论 性染色体异常最常见的是 Y 染色体多态性，其次依次为 Klinefelter 综合征、Tuner 综合征、性反转、超雌综合征、超雄综合征等，是导致第二性征发育不良、不孕不育、流产的重要原因，对具有明显临床表现的患者，要进行外周血染色体检查，有助于临床诊断和治疗。

PU-2622

结核患者 T-SPOT 结果与结核患者疾病进展的相关性研究

杨舒婷
新疆维吾尔自治区人民医院

目的 探究结核患者 T-SPOT 结果与肺结核患者疾病进展的相关性。
方法 收集 2020 年 6 月至 2021 年 6 月在新疆某三甲医院就诊并诊断为结核病的患者共 60 人，年龄中位数 59.5 岁。其中男性 30 人，女性 30 人。共收集继发性肺结核 14 例；继发性肺结核（浸润型）8 例；陈旧性肺结核 24 例；结核瘤 1 例；腰椎结核 2 例；肾结核 1 例；结核性胸膜炎 2 例；原发性肺结核 4 例；浸润型肺结核 4 例。对患者病史、T-SPOT、血沉、痰涂片、结核杆菌基因检测以及肺部 CT 结果进行分析。为方便研究，将患者肺部 CT 结果赋值处理。肺部出现斑片影、实变影、树芽征、结节、空洞、条索、肺门淋巴结肿大均赋值为 1。一方面，按照 T-SPOT 数值将病例分为两组（T-SPOT 结果≥16 以及 T-SPOT 结果≤4），分别计算两组中痰涂片阳性率、结核杆菌基因检测阳性率。另一方面，计算 T-SPOT 结果与血沉、肺部 CT 结果的相关性。
结果 痰涂片阳性率在 T-SPOT 结果≥16 以及≤4 的分组中分别是 9.09%，0%；结核杆菌基因检测阳性率在 T-SPOT 结果≥16 以及≤4 的分组中分别是 31.8%，40%。结核患者 T-SPOT 检测结果同血沉结果、赋值后的 CT 结果做相关性分析显示二者并无相关性。
结论 现有研究表明 TB 患者外周血中 Th2 细胞比例显著升高，Th1 细胞比例变化不明。INF-γ 主要由 Th1 细胞分泌，是一种高效的抗病毒生物活性物质，又是一种具有广泛免疫调节作用的淋巴因子。有研究表明肺结核病灶中 INF-γ 表达显著高于正常组。T-SPOT 是 γ 干扰素释放试验的一种，因此 T-SPOT 的检测值可能与结核患者病情相关。本研究结果提示结核杆菌基因检测阳性率在 T-SPOT 数值高组中阳性率低，结核患者 T-SPOT 检测结果同血沉结果、赋值后的 CT 结果做相关性分析显示二者并无相关性。考虑是由于纳入病例数较少，后期研究可以扩大纳入病例数量，同时检测外周血 INF-γ 水平与 T-SPOT 结果对照研究。

PU-2623

双区法质控图在化学发光测定 HBsAg 室内质控的效能分析

陈新瑞
中南大学湘雅二医院

目的 评价双区法质控图(由 Levey-Jennings 定量控制图和 cutoff 定性控制图绘制成一张质控图的图表)，对化学发光测定 HBsAg 室内质控的控制效能。
方法 运用 SPSS26 统计软件的质控图功能，回顾分析 2020 年 3 月至 2021 年 4 月我院采用微粒子化学发光测定 HBsAg 的室内质控数据 ，比较在双区法质控图与单值-移动极值图的控制效能。
结果 HBsAg 低、中二种水平的室内质控物中，低值阴性水平的质控物，其数据表现为以 0 为趋势的偏态对数分布，在双区定性质控图上，不出现失控状态，不能反映低值阴性水平的质控状态；在单值-移动极值图上能较好的反映低值阴性水平的质控状态。而中值水平质控物，其数据基本呈正

态分布，双区法中的 Levey-Jennings 控制图和单值-移动极值图都能较好的反映中值水平的质控状态。
结论 定量定性双区法在化学发光测定 HBsAg 室内质控中，对低值阴性水平质控物控制效能低下，应采用单值-移动极值图才能较好的反映低值阴性水平的质控状态。

PU-2624

天津地区 1670 例湿疹、荨麻疹患儿过敏原特异性 IgE 定量测定结果分析

娜仁、沈永明
天津市儿童医院

目的 分析天津地区湿疹、荨麻疹患儿的过敏原特异性免疫球蛋白 E（sIgE）定量检测结果，为临床诊疗提供参考。
方法 采用酶联免疫捕获法，对 2019 年 8 月到 2020 年 3 月就诊于天津市儿童医院的 1023 例湿疹及 647 例荨麻疹患儿进行吸入及食物过敏原 sIgE 检测，并对检测结果进行统计分析。
结果 1670 例患儿中，共 1254 例检出过敏原 sIgE 阳性，检出率为 75.09%；1185 例检出食物过敏原 sIgE 阳性，检出率 70.96%；739 例检出吸入过敏原 sIgE 阳性，检出率 44.25%。食物过敏原 sIgE 检出前三位依次为鸡蛋白 蛋黄（943 例，56.47%）、牛奶（533 例，31.92%）、小麦面粉（336 例，20.12%），吸入过敏原 sIgE 检出前三位依次为屋尘（561 例，33.59%）、交链孢霉（182 例，10.90%）、粉尘螨（127 例，7.60%）。男女过敏原 sIgE 检出率无明显差异，鸡蛋白蛋黄、屋尘、牛奶、小麦面粉在 1-3 岁组检出率最高，而交链孢霉与粉尘螨分别在 4-6 岁组与>6 岁组检出率最高。荨麻疹患儿屋尘 sIgE 检出率高于湿疹患儿，其余几种过敏原 sIgE 检出率在湿疹及荨麻疹患儿中无明显差异。
结论 本研究能够在一定程度上反映湿疹、荨麻疹患儿的过敏原 sIgE 流行特征，有助于疾病的防治和诊断。

PU-2625

应用 CPG-寡脱氧核苷酸 DSP30 和白介素 2 提高慢性淋巴细胞白血病的细胞遗传学异常检出率

李建伟[1]、毛翠[2]
1. 天津金域医学检验实验室有限公司
2. 广州金域医学检验中心有限公司

目的 验证 CpG-寡脱氧核苷酸(CpG-olig0deoxynucleotide,CpG-ODN)免疫刺激是否能提高慢性淋巴细胞白血病(chronic lymphocytic leukemia,CLL)的细胞遗传学异常检出率。
方法对 150 例 CLL 患者的骨髓液标本，并行进行培养: 24 小时未刺激，CPG-寡脱氧核苷酸联合 IL-2 刺激培养 72 h，常规收获细胞制备染色体并进行 G 显带分析。
结果 在 CLL 中，24 小时未刺激组和 CpG-寡脱氧核苷酸联合 IL-2 组染色体分析成功率(可分析分裂象≥20 个)分别为 82.67％ 和 96.67％ ，异常核型检出率分别为 57.63％和 0％。异常核型检出率显著高于未加刺激剂组(x2=103.562，P =0)。
结论 应用 CPG-寡脱氧核苷酸 DSP30 和白介素 2 能有效提高慢性淋巴细胞白血病的细胞遗传学异常检出率。

PU-2626

Analysis of lipid distribution characteristics in a health examination population in Chengdu (2009–2017)

Shanshan Liang、Guixing Li
四川大学华西医院实验医学科

Background The prevalence of cardiovascular disease is rapidly increasing in the recent years. Dyslipidemia associated atherosclerosis and other complications are posing a serious threat to human health. The present study aimed to analyze the blood lipids distribution characteristics within a large size of health examination population of Sichuan province, China.
Method This was a retrospective study conducted in 888,143 subjects (495,599 males and 392,544 females) aged more than 18 years old from the Health Examination Center at West China Hospital, Sichuan University during 2009 to 2017. The blood lipids levels were compared in different age groups and different years.
Result The blood lipids levels were significantly increased in recent years. The percentage of cases with high lipids levels was significantly higher in males than that in females since 2009 to 2017. Moreover, the blood lipids levels and the percentage of dyslipidemia in aged 51-60 individuals were significantly higher than those in other population every year.
Conclusion The health examination population showed increased percentage of blood lipids levels, and so regular physical examination and lipids control are highly important in aged population.

PU-2627

昆明地区妇女 HPV 感染的流行病学特征

黄松苓、赵滢
昆明医科大学第一附属医院

目的 探讨昆明地区妇女宫颈人乳头状瘤病毒（human papillomavirus，HPV）感染的分子流行病学特征及其近三年变化趋势。
方法 收集昆明医科大学第一附属医院 2016 年 1 月—2019 年 1 月在妇科门诊和住院的进行 HPV 分型检测的患者 36304 例，统计分析感染分型特征。
结果 HPV 感染率为 7.98%，其中高危型 HPV 感染占 93.81%。HPV 感染以单一感染（67.30%）为主，HPV52、58、16 型最常见，而在多重感染中，70.32%为二重感染，以 52 型合并其他高危型（58、16、53 型）感染最常见。不同年龄组的 HPV 感染率差异有统计学意义（P＜0.001），其中 21~30 岁年龄组 HPV 感染者占比（9.92%）最高，其次为 31~40 岁年龄组（9.64%）和 41~50 年龄组（9.29%）。2016~2018 年 HPV 感染率由 2.57%上升至 14.67%。
结论 与国内已报道地区相比昆明地区 HPV 感染率较低，但是近三年增长较快。感染年龄分布集中于中年，基因分型分布有明显的地区特异性。研究结果对研制适合昆明地区妇女的特异性 HPV 疫苗，以及宫颈癌的筛查与防治具有参考价值。

PU-2628

烟台某医院 2018-2020 年血培养病原菌分布及耐药性分析

尹潇[1]、徐勤辉[2]
1. 联勤保障部队第 970 医院
2. 滨州医学院

目的 了解该院血培养阳性住院患者检出菌的分布以及耐药性分析,为临床抗生素的使用提供科学的指导，同时也能一定程度上增加该地区患者对抗生素的选择。
方法 收集该院 2018-2020 年血培养数据，对血培养阳性标本做阳性率、主要检出菌占比、阳性标本的患者科室分布情况及耐药性等分析。
结果 2018-2020 年间全院共采集了 8077 分血培养标本，其中有 441 分标本检测出病原菌，阳性率为 5.46%。在这些病原菌中，革兰氏阴性菌有 248 株，占总检出数的 56.23%;革兰氏阳性菌 180 株，占比 40.82%;真菌 13 株，占总检出数的 2.95%。阳性标本主要来自肝胆外科 85 份(占比 19.27%)、重症医学科(ICU)38 份(占比 8.62%)、肾内科 35 份(占比 7.94%)、胃肠外科 31 份（占比 7.03%）、神经内科 28 份（占比 6.35%）。大肠埃希菌数量在总检出菌中占比最大，为 22.0%，其次为肺炎克雷伯菌肺炎亚种、金黄色葡萄球菌，分别占比 16.1%、6.8%。在耐药性方面，革兰氏阳性菌中，葡萄球菌对替加环素和万古霉素耐药全部敏感；链球菌对左氧氟沙星，万古霉素全敏感。革兰氏阴性菌中，97 株大肠埃希菌对检测的抗生素中氨苄西林的耐药率最高，为 77.11%，其次为复方新诺明和氨苄西林/舒巴坦，耐药率分别为 54.32%和 50%。肺炎克雷伯菌肺炎亚种对检测的抗菌药物耐药率均较低，均小于 30%。14 株阴沟肠杆复合菌同肺炎克雷伯菌肺炎亚种类似，对所测抗菌药物耐药率均较低，均不超过 30%。产 ESBLs 的大肠埃希菌和肺炎克雷伯菌肺炎亚种的检出率分别为 29.9%（29/97）和 15.5%。
结论 2018-2020 年该院血流感染以 G-为主，临床应及时对疑似血流感染患者进行血培养检测，并加强对血流感染致病菌耐药性监测，对合理使用抗生素有重大意义。

PU-2629

简易操作卡在医学实验室的作用

韩亚荣、齐利明
西安金域医学检验所

目的 通过简易操作卡在医学实验室中新员工入职后实验操作中的作用，来分析简易操作卡在提高实验操作效率中的作用。
方法 实验室制作仪器及项目的简易操作卡，作为作业指导书的附录，简易操作卡采用实际工作中仪器及项目的全流程图片，可以清晰的看到实验操作中的每一步骤，包括试剂的复温，试剂瓶的颜色，加样的步骤，加样量，孵育的时间，温度，洗板次数及方法，读取吸光度，结果判读与处理；仪器的开关机，使用维护保养，报警处理等，在关键步骤图片旁备注注意事项，让实验室新员工进入实验室后，对照简易操作卡可以快速掌握项目及仪器的全操作流程，且此简易操作卡严格按照作业指导书以图片的形式呈现，可以确保所有员工操作的一致性，减少人员之间的差异。
结果 实验室新员工对照简易操作卡，可以独立完成项目及仪器的全流程操作，减少了由于不同人员带教导致的操作差异性。
结论 简易操作卡在医学实验室新员工入职后实验操作中有很强的指导性，可以快速提高实验工作效率，可广泛应用于医学实验室作为作业指导书的附录使用，更直观的展现全操作流程，为医学实验室带教提供了更直观有效的方式。

PU-2630

耐碳青霉烯类肺炎克雷伯菌临床分布特征及耐药分析

张伟[1,2]、王娜[1]、陈新飞[2]、王瑶[2]
1. 河北北方学院附属第一医院
2. 中国医学科学院北京协和医院

目的 分析河北省耐碳青霉烯类肺炎克雷伯菌（Carbapenem Resistant Klebsiella Pneumoniae，CRKP）临床分布特征及耐药情况；
方法 收集河北省 2017～2019 年 CRKP6328 株，采用全自动药物敏感性分析仪器 MIC 法及纸片扩散法（K-B）对其进行药物敏感性试验，用 WHONET5.6 软件对实验数据进行统计分析；
结果 河北省 2017-2019 CRKP 的检出率逐年上升，分别为 13.4%、14.5%、14.6%，其中男女比例约为 2:1，老年人 53.6%，成年人 39%，未成年人 4.8%，新生儿 2.5%；CRKP 对碳青霉烯类抗菌药物耐药率呈上升趋势耐药率呈上升趋势，耐药率普遍>90%；对氨基糖苷类药物耐药率逐年下降，降至 50%左右；主要分离自痰液，占 70.9%。CRKP 对碳青霉烯类及其他 β－内酰胺类抗菌药物对喹诺酮类药物耐药率基本保持在 80%左右；对各类抗生素的 MIC50/MIC90 值均大于相对应的耐药折点；
结论 2017-2019 年河北省 CRKP 对多种抗菌药物的耐药率均较高，对 β－内酰胺类抗生素的耐药率呈逐年升高的趋势。

PU-2631

2017—2019 年河北省 CR-ECO 病原菌分布特征研究

张伟[1,2]、詹明华[1]、陈新飞[2]、徐英春[2]
1. 河北北方学院附属第一医院
2. 中国医学科学院北京协和医院

目的 探究 2017-2019 年河北省碳青霉烯类耐药大肠埃希菌病原菌(CR-ECO)分布的情况
方法 分析 2017—2019 年河北省 CR-ECO 耐药情况，收集河北省 CR-ECO 1439 株，采用全自动药物敏感性分析仪器 MIC 法及 K-B 纸片扩散法对其进行药物敏感性试验，用 WHONET5.6 软件对数据进行统计分析。
结果 2017—2019 年河北省共分离大肠杆菌 54377 株，其中 CR-ECO1439 株（2.65%）；从尿液中分离出的占比最多，且近 3 年检出率呈现缓慢上升趋势；河北省内 CR-ECO 的检出率存在地域性差异，石家庄位居首位。河北省 2017—2019 年 CRECO 感染患者男女比例为 1.5:1，老年人和成年人分别占约 59.6%和 30.8%，新生儿和未成年人分别占 4.7%和 4.9%。2017—2019 年，对于 CR-ECO，亚胺培南，美罗培南耐药率逐年上升、多粘菌素基本不变，其他抗菌药物的耐药率呈逐年上升趋势。
结论 2017—2019 年河北省 CRECO 分离率保持稳定，但耐药率呈上升趋势。

PU-2632

2018-2020 年河南省 275 家医院布鲁菌血清学检测结果分析

史彩琴
郑州金域临床检验中心有限公司

布鲁菌病是由布鲁氏菌属的细菌侵入机体，引起变态反应性的疾病， 我国布鲁菌病发病率呈逐年上升趋势，本研究通过对河南省 275 家医院送检的 20360 例布鲁菌试管凝集试验（SAT）检

测结果的分析，以 WS269-2019《布鲁氏菌病诊断》为方法依据，通过对样本阳性率、年龄组、性别、季节分布的分析，并与全国及其他地区的数据进行比较，为布鲁菌病的防治提供参考依据。

PU-2633

中药洗液治疗宫颈锥切术后高危型人乳头瘤病毒持续感染的临床疗效研究

荆哲
吉林大学第一医院

目的 评价宫颈高级别鳞状上皮内病变（ high-grade squamous intraepithelial lesion ，HSIL）锥切术后(冷刀／LEEP 锥切)高危型人乳头瘤病毒(high-risk human papillomavirus，HR-HPV)持续感染，派特灵治疗的临床疗效。
方法 选取 2019 年 3 月-2020 年 3 月锥切术后 4-6 个月复查 HR-HPV 阳性符合纳入标准的 101 例患者，采用随机对照方法，48 例患者做为观察组，53 例患者为对照组。观察组 48 例患者采用派特灵治疗，对照组 53 例患者不采用任何药物治疗。观察组于用药结束后第 3-4 个月进行 HR-HPV 检测，对照组也按相同时间间隔检测，分析两组患者 HR-HPV 感染的转阴情况。
结果 观察组 48 例患者中，脱落 3 例，HR-HPV 感染的转阴率为 77.8％(35／45)；对照组 53 例患者中，2 例脱落，HR-HPV 转阴率为 25.5％(13／51)。两组患者转阴率比较，差异具有统计学意义(P<0．05)。治疗过程中，1 例患者出现经间期少量阴道流血；1 例分泌物增多；3 例下腹部胀痛；以上症状均未影响患正常生活，停药后上述症状消失。
结论 中成药洗液对宫颈 HSIL 锥切术后 HR-HPV 持续感染的治疗有效。

PU-2634

非小细胞肺癌中的 LncRNA

张栩晟
昆明医科大学第一附属医院

肺癌是一种高发病、高死亡和差预后的疾病，其中非小细胞肺癌占了肺癌的 85%。长链非编码 RNA(Long non-coding RNAs,LncRNAs)是长度超过 200 个核苷酸的非编码 RNA 分子，在基因表达和信号通路中发挥着重要作用。最近，lncRNA 被发现与癌症有关，在癌症中，lncRNA 的表达被异常调节，导致异常的功能。

LncRNA 的功能主要体现在其亚细胞定位上，核 LncRNA 主要在转录过程中发挥作用，而胞质 LncRNA 则往往在转录后发挥作用，并影响信号级联。LncRNA 可以通过与不同的 RNA 靶标相互作用，在基因表达中发挥作用。LncRNA 还可以通过促进蛋白复合物的组装，破坏蛋白质的相互作用，影响其细胞定位来调控蛋白功能。

对于 NSCLC 中的 LncRNA，除了调节 NSCLC 增殖，还参与抑制细胞凋亡。LncRNA 还可以通过调控通路激活和关键信号成分来调控控制生长、增殖、凋亡和转移的致癌信号通路。

由于 NSCLC 中的 LncRNAs 出现了失调，就提示了我们 LncRNA 在 NSCLC 的治疗中存在着潜力。首先是与传统活检相比，基于 LncRNA 的生物标志物可能更好地为患者所接受，并且微创；其次是随着 NSCLC 对化疗和靶向治疗的耐药性增加，需要探索新的方法，而许多 LncRNAs 与增强的化疗耐药性有关，因此，它们的靶向性也可能恢复癌细胞对化疗药物的敏感性；最后，LncRNA 虽然优点众多，但与蛋白质不同，LncRNAs 的三维结构在很大程度上仍然未知，缺乏保守结构域可能会阻碍小分子抑制剂的设计。缺乏对 NSCLC 中许多 NSCLC 相关基因的机制和调控网络的全面了解也可能限制了 LncRNA 的使用和特异性靶向。

PU-2635

苏州地区不同类型过敏原对哮喘患儿肺功能的影响分析

高媛媛、李阳、沈佳
苏州市苏州大学附属儿童医院

目的 探讨苏州地区不同类型过敏原对哮喘患儿肺功能的影响，以及哮喘患儿的过敏原阳性率、免疫球蛋白水平、肺炎支原体感染情况。

方法 随机选取 2018 年 02 月至 2021 年 02 月在苏州大学附属儿童医院确诊的 144 例哮喘患儿作为研究对象。根据过敏原检测结果分为多重致敏组、单一致敏组和无致敏组，观察三组患儿的过敏原阳性率和分布情况、肺功能指标：FEV_1、FVC、FEV_1/FVC、PEF、$MMEF_{75/25}$ 水平，以及总 IgE 水平和肺炎支原体感染情况。

结果 苏州地区多重致敏组的哮喘患儿占 59.0%（85/144），单一致敏组和无致敏组的哮喘患儿分别占 22.2%（32/144）和 18.8%（27/144）。哮喘患儿的吸入性过敏原主要为尘螨组合（屋尘螨/粉尘螨）47.2%（68/144），其他包括屋尘 22.9%（33/144）、霉菌组合（点青霉/分枝孢霉/烟曲霉/交链孢霉）9.0%（13/144）等；食入性过敏原主要为鸡蛋白 35.4%（51/144）和牛奶 18.8%（27/144），其他包括牛肉 11.1%（16/144）、蟹 11.1%（16/144）、黄豆 10.4%（15/144）等。男性哮喘患儿在多重致敏组中占 69.4%（59/85）、单一致敏组中占 81.3%（26/32）、无致敏组中占 60.3%（16/27）；多重致敏组 FEV_1、FVC 以及 $MMEF_{75/25}$ 水平均低于无致敏组，有统计学差异（P_{FEV1}=0.0134；P_{FVC}=0.0285；$P_{MMEF75/25}$=0.0423），而 FEV_1/FVC 水平无统计学意义（$P_{FEV1/FVC}$=0.2018）；单一致敏组与无致敏组之间的肺功能比较，无明显统计学差异（P_{FEV1}=0.1680；P_{FVC}=0.3811；$P_{FEV1/FVC}$=0.6683；$P_{MMEF75/25}$=0.1285）；三组哮喘患儿之间 PEF 值相比，无明显统计学差异（$P_{多重致敏组/单一致敏组}$=0.8982；$P_{多重致敏组/无致敏组}$=0.0586；$P_{单一致敏组/无致敏组}$=0.0582）。多重致敏组总 IgE 水平明显高于单一致敏组和无致敏组，差异具有统计学意义（$P_{多重致敏组/单一致敏组}$=0.0064；$P_{多重致敏组/无致敏组}$=0.0028）。多重致敏组患儿肺炎支原体 IgG 抗体的检测结果较单一致敏组高，有统计学差异（P=0.0457）。

结论 过敏相关性哮喘在苏州地区发病率较高，且多数为多重致敏的哮喘患儿，其通气功能改变主要为小气道阻塞性通气功能障碍，免疫功能改变主要为变态过敏性反应，多重致敏的哮喘患儿多存在肺炎支原体感染史。

PU-2636

青岛地区 652 例尖锐湿疣患者流行病学分析和人乳头瘤病毒基因型检测

李海艳[1]、于海洋[2]
1. 青岛市海慈医疗集团
2. 青岛市市立医院

目的 对青岛地区 652 例尖锐湿疣患者进行人乳头瘤病毒基因型检测和流行病学分析，为有效防治该病提供可靠的科学依据。

方法 采用调查表的方式对确诊患者进行一般情况、生活方式及性行为等情况调查，根据调查结果将患者分为两组：A 组为性接触所致 CA 患者，B 组为疑似非性接触患者。同时采用基因分型试剂盒检测 21 种 HPV 基因型。

结果 652 例尖锐湿疣患者中 A 组占 81.7%，B 组占 18.3%，A 组、B 组年龄构成比有差异，B 组发病人群以以非性活跃人群为主，病程偏长。B 组女性较多（$\chi2$=10.57，P＜0.05）。B 组合并系统疾病和肛周疾病的发病率明显高于 A 组（$\chi2$=39.34，P＜0.05；$\chi2$=35.85，P＜0.05）。两组 HPV

分型均以 6 和 11 型等低危型为主，高危型主要为 16 和 31 型。CA 患者 HPV 感染以单一型别为主，且单一高危型仅存在 A 组，B 组单一型均为低危型，差异具有统计学意义。
结论 非性接触也是感染尖锐湿疣的一种重要途径，非性接触患者发病可能与机体免疫力下降及局部皮肤屏障功能破坏有关，为减少 CA 的发病率和复发率应该积极治疗合并疾病。HPV 亚型以 6 型和 11 型等低危型为主。对性接触导致尖锐湿疣患者应重点随访，积极治疗，降低远期肿瘤发生率。

PU-2637

基于 LC-MS 的慢性胰腺炎血清代谢组学研究

吴玲、谭超超、卢婉莹、黄湘平
湖南省人民医院

目的 本研究运用高效液相色谱-质谱联用技术对正常人血清与慢性胰腺炎患者血清进行组分对比分析，筛选出两者之间有显著差异的血清小分子代谢物及其相关代谢通路，筛选有助于慢性胰腺炎诊断的血清生物标记物，从代谢组学的层面上为慢性胰腺炎的诊疗提供新思路。
方法 收集湖南省人民医院 2020 年 9 月—2021 年 1 月经确诊的慢性胰腺炎患者血清样本 32 例及正常人血清 31 例。采用高效液相色谱-四级杆飞行时间串联质谱联用技术（HPLC-Q-TOF-MS/MS）对所收样本进行代谢物分析。用 Metaboscape 3.0 软件对获得的原始数据进行峰提取、降噪、标准化等预处理。在 MetaboAnalysis 5.0 平台上对数据进一步进行主成分析（PCA）、偏最小二乘法判别分析（PLS-DA）和正交偏最小二乘法判别分析（OPLS-DA）等分析，以 t 检验（$p<0.05$）、差异性倍数（FC＞1.5）和变量权重值（VIP＞1）的标准筛选慢性胰腺炎和正常人间的差异性代谢物。最后进行代谢物通路分析，寻找与慢性胰腺炎相关的代谢通路。
结果 本研究基于 LC-MS 技术平台成功构建 PCA、PLS-DA、OPLS-DA 等模型，结果说明正常人和慢性胰腺炎患者存在血清代谢组学上的显著差异，并成功筛选出 56 种差异性代谢物（FC＞1.5、$p<0.05$ 且 VIP＞1.0）。与正常人相比，在慢性胰腺炎患者中，血清中 3-磷酸甘油、苹果酸、3-羟基马尿酸、雌酮、氢尿酸、磷酸胆碱、葡萄糖醛酸乙酯、卵磷脂、半乳糖醇、鞘氨醇、羟戊烯醇等 30 种代谢物呈增多趋势；5-脱氧腺嘌呤核苷、褪黑素、黄尿酸、雌二醇、胱氨酸、6-甲基巯基嘌呤、1-水杨酸葡糖苷酸、L-组氨酸、脱氧皮质酮等 26 种代谢物呈减少趋势。并根据差异代谢物筛选出了 5 条代谢通路，包括苯丙氨酸、酪氨酸和色氨酸的生物合成、甘油磷脂代谢、鞘脂代谢、类固醇激素生物合成、组氨酸代谢通路。
结论 本次研究发现了慢性胰腺炎患者与正常人血清代谢物轮廓存在明显的差异，说明可以通过 LC-MS 技术识别血清代谢差异进行慢性胰腺炎和正常人之间的区分；本次实验成功筛选出 56 种差异代谢物和 5 条异常代谢通路。

PU-2638

检验实验室管理

闫妁
山东大学第二医院

检验科室虽然只是一个辅助科室，但它发挥的作用是巨大的，由于目前临床诊断大部分需要检验指标来辅助，以及明确治疗效果，所以加强检验实验室管理是非常重要的。

检验分为免疫室、细胞室、体液门诊等，由于试剂管理、标本保存等需要的条件不同，这就需要我们把检验科室更加细化，对不同要求进行不同管理，这样才可以更加精准检验样本。就拿我们医院的体液门诊来说，门诊主要对尿液、粪便进行检验，我们有非常先进的机器，先对样本进行质控，调整参数，随后可以很快速的对样本进行一轮检验，随后检验师们进行结果审核，对异常的样本行显微镜下观察；由于技术引进，减少我们检验师工作量，极大提高工作效率，但是我认为每个

地区的人由于各种因素影响正常参考范围会发生变化，所以当技术引入后，需要对该地区的正常人进行统计，判断出每一项指标的正常参考范围，将各种影响因素考虑进去，才可以更加精确反应人体的身体状况，便于临床医生的明确诊断。检验异常粪便，需要涂片、显微镜下检查，镜检过程中不能有风，否则会减慢工作效率，尤其夏天，气候炎热，实验室较封闭，使工作环境及其难受，我觉得是否可以改进显微镜，在防止玻片位置可以增加一些材料，来防止外来空气影响，使检验实验室可以既不影响检验结果，又优化检验环境。

PU-2639

不同核酸检测方法在 SARS-CoV-2 核酸检测中的比较

张世慧
山东大学第二医院

新型冠状病毒 2（SARS-CoV-2）肺炎的爆发给全球带来了严峻挑战，目前核酸检测仍然是检测病毒感染的金标准，快速检测出病毒的感染者有利于病情的诊断以及指导后续的治疗，提高预后，同时有利于疫情的防控，因此迫切需要快速且敏感性和特异性都较高的检测方法。目前采用实时荧光逆转录聚合酶链反应（RT-PCR）是临床常用的检测方法，但此方法需要专业的技术人员，且试剂和设备的获取不足减缓了疾病检测速度，CRISPR-Cas（Clustered regularly interspaced short palindromic repeats，CRISPR）系统是一种高效、实用的基因编辑工具，被广泛应用于基因组编辑和调控机制研究，目前发现的 Cas 系列核酸酶工具为开发用于各种目的的不同类型核酸检测，具有广阔的应用前景。CRISPR-Cas 系统的高灵敏度和高特异性，使其在病原体检测、单核苷酸多态性（SNP）分析以及基因突变检测等发挥了极其重要的作用；另外，CRISPR-Cas 系统在核酸检测领域的精确、高效性，间接推动了基础生物学和应用生物学研究的进展。本研究拟比较 RT-PCR 和基于 CRISPR/Cas 系统的核酸检测技术对新型冠状病毒 2（SARS-CoV-2）核酸检测结果的符合率、重复性及检出限,优选出提取效率高、耗时短、成本低的核酸检测方法。方法采用同一种核酸提取方法的商品化核酸提取试剂,分别对阴性样本、阳性样本及不同浓度的 SARSCoV-2 RNA 标准品进行 RNA 提取，然后分别以实时荧光逆转录聚合酶链反应（RT-PCR）及检测,以 Ct 值评价不同核酸检测方法的性能。结果 2 种核酸提取试剂的阴性和阳性样本结果符合率均为 100%。结论基于 CRISPR 的检测平台是准确检测和治疗 SARS-CoV-2 的新方法。

PU-2640

造成血液样本异常状态的常见原因分析

陶明雨
黑龙江金域医学检验实验室有限公司

目的 血液样本是目前临床检验中最普遍的样本之一，临床检验中涉及到血液样本的检测项目也是非常之多的。通过对血液样本的检验能够为患者病情的监测、药物的选择以及预后的评估提供可靠的依据。但在临床检验中往往会有很多样本在检验人员进行检测时发现样本处于异常状态，比如：溶血、脂血、黄疸等。造成血液样本异常状态的影响因素有很多，现对造成血液样本异常状态的常见原因进性分析探讨。
方法 选取某医院 2020 年的异常状态的血液样本进行研究分析，找出造成其异常状态的原因并分析。
结果 一.造成血液样本异常状态的常见原因
1.脂血：首先是被采血患者自身患有高脂血类疾病，这种情况是人为无法不避免，遇到这种情况时，医务人员首先应事先询问患者是否有过类似病史。其次可能是由于患者在采血前一天食用大量高血脂的食物，如肥肉、动物内脏，油炸食物等都会造成脂血样本。

2.溶血：首先也是考虑患者自身患有此类疾病导致样本溶血，其次就是考虑患者是否服用某些药物导致溶血。或者是采血后样本被用力晃动碰撞，储存温度过低等都会导致样本溶血。
3.黄疸：黄疸样本一般在婴儿的血液样本中发现居多，主要分为生理性和病理性两种，生理性是由于胆红素含量过高，未能及时排除，一般可自行缓解；病理性则是由于婴儿发生肝炎或者是感染性疾病，胆道堵塞，新生儿溶血等疾病。以上两种情况均会导致患者血液样本出现异常状态。
结论 由此可见造成血液样本异常状态的因素复杂多样，这就需要医务人员在工作时格外认真细心，及时沟通询问患者病史，正确进行采血，规避人为原因导致的血液样本异常状态，避免影响临床医生的做出正确判断，耽误病人的治疗和用药。

PU-2641

乙型肝炎病毒两对半方法的临床应用及分析

李坤
黑龙江金域医学检验实验室有限公司

目的 探讨该分析方法在临床乙肝病毒患者确证过程中的实用性，并对数据进行分析，提高临床防治的有效性。
方法 收集受乙肝病毒性肝炎（下称乙肝）检测的体检者的体检数据 300 例，采用用的是酶联免疫吸附试验(ELISA)来检测乙肝两对半五项的数据，然后将数据收集进行统计，来查看乙肝各项数据的阳性率。
结果 收集的这 300 份体检者数据中，经过统计大三阳的阳性率为 4%（12/300），小三阳的阳性率为 7.7%（23/300），双项的阳性率为 2%（6/300），试验中存在误差，影响实验结果的因素可能有实验样本的采集和样本是否符合正常标准，血样如果出现溶血、脂血、黄疸的情况下会对实验结果产生影响，试剂如果存放不规范也会造成结果不稳定，人为操作也会对结果的准确性产生影响，尽量避免这些因素让结果更加可靠。
结论 乙肝病毒在我国是一种具有较高感染率的病毒，对我国人民造成了巨大的困扰，是一种严重危害国民健康的传染病，酶联免疫吸附实验(ELISA)拥有简便、快捷、特异性高的特点，成为了现在乙肝检测的主要方法，但是酶联免疫吸附法的测定影响因素很多，容易出现假阳性和假阴性的情况，所以进行实验操作时要严格规范操作，尽量避免误差提高结果的准确性。
目前，临床上常用的检测乙肝病毒型肝炎感染的方法是两对半检测法，其能够将患者是否感染乙肝，以及其具体感染情况来进行一个初步判断，并且能够将大、小三阳区分出来。与此同时，其还能够将体内抗原以及抗体的携带模式反映出来，将机体在不同条件时的免疫情况检测出来，为临床防治提供有效的证据支持。

PU-2642

浅谈临床医学检验的质量控制

王芃开
黑龙江金域医学检验实验室有限公司

目的 分析临床医学检验质量控制的主要措施，从而为医生的治疗提供准确的数据依据。从实验前，实验中，试验后等诸多环节的质量控制进行分析，进一步加强医学检验重要环节的质量控制，对保证检验结果的起到了非常重要的作用。
方法 针对实验前、实验中、试验后等环节可能对检验结果造成影响的因素进行分析
结果 1、实验前的质量控制：
（1）患者样本的要求：对于要求空腹抽血进行检测的项目，坚持空腹抽血；对体位有要求的检测项目，要坚持正确的体位进行采集；输液前后进行标本采集时，要根据检查项目选择标本采集时间；

采集标本时，患者应该处于静止运动的状态，而不是刚刚运动完成之后进行标本采集；避免脂血、溶血、黄疸等异常状态样本；同时，加强标本送测时间的管理同样非常重要。
（2）实验设备的质量控制：应使用经具有相应资质校准机构校准合格的实验设备。
2、加强检验过程中的质量控制：
（1）应有一套完整的工作制度，检验人员应有明确的岗位和职责分工。
（2）要做好实验室的质量控制，确保检测结果的准确性和及时性。
（3）对于检测技术人员要加强理论和操作技巧培训，并且制定相应的操作规范和标准。
3、试验后的质量控制：
应对检测后的样本进行一个妥善的保存，以便有需要时对样本进行复检和及时的清理；对于一些危重患者以及对时间有要求的项目，也应注意结果报告的及时性。
结论 总之，加强临床医学检验的重要环节的质量控制，对于提升检验数据的精确性，及时性和可靠性都具有极为重要的作用。

PU-2643

病理会诊切片常见问题及其处理

王庆泽
黑龙江金域医学检验实验室有限公司

病理会诊的病例在各大医院呈明显上升趋势，病理会诊切片质量的优劣直接影响病理医师进行病理诊断的及时性和准确性。随着《医疗事故处理条例》的实施,医疗风险不断增大,医疗纠纷逐年增多,病理会诊切片在医疗纠纷中的作用引起了病理医师更多的关注,也得到人们的重视。在实际工作中,经常遇到会诊切片出现各种问题：会诊切片上常会出现组织部分掉片、皱褶、破碎,细胞核与细胞质染色对比不清晰、透明度不好等现象。造成切片质量差的原因很多,主要有标本的前期处理不当如标本固定不及时,脱水浸蜡不充分;切片刀不锋利,导致切片时自行卷起或皱起;染色试剂使用时间过长影响等因素。

尽管各单位采取交押金等办理借片手续,但仍然存在患者或家属持片不归的现象;同时,借用方在保存或使用时不当,造成切片破损。患者或其家属没有意识到切片及时归档的重要性,有时因路途遥远放弃归还;也有因保管不当,致切片破损或切片丢失,无法归档;抑或患者为了方便以后的会诊诊断治疗需要而留用切片。

处理方法

为了确保外借切片的质量,在平时工作时,技术人员应严格遵守病理临床技术操作规范,注意带教工作,对年轻的技术人员进行规范化培训,多学习,多实践,互相切磋切片的心得。每天进行抽查切片,发现不合格切片及时重切。对一些特殊组织如淋巴结、皮肤、骨髓等请有经验的老师传授心得体会和注意事项。

当患者及其家属借病理切片去外单位会诊时,病理科工作人员有责任告知借片者了解切片的重要性,让他们从思想上重视会诊切片等资料,知晓病理切片对患者以后的疾病诊断、治疗很有帮助,使其在应用时注意保护切片,妥善保管,防止切片破损并及时归还。对于外借路途遥远者,适当提高借片押金,以督促其及时还片,以防切片逾期不归。

PU-2644

乙肝五项与乙型肝炎病毒核酸检测的比对分析

张雪娇
黑龙江金域医学检验实验室有限公司

目的 乙型肝炎（简称乙肝）是目前最为常见的传染病之一，据调查统计全球约有 4 亿人感染乙肝病毒，约为艾滋病毒感染人数的 8 倍，据 2006 年乙肝流行病学调查统计中国乙型肝炎病毒携带率为 7.18%，可以推算出中国的慢性乙型肝炎病毒感染者约为 9300 万，由此可以看出中国在乙肝防治上形势非常严峻。
方法 乙肝五项常见的检测方法为酶联免疫，乙型肝炎病毒核酸检测方法为实时荧光定量 PCR 法。
结果 乙肝五项仅能反映机体内的抗原、抗体携带模式，检测在一定条件下机体的免疫情况，同时可为乙肝病毒感染提供间接证据，是用来排查机体是否存在乙肝病毒的感染，对于乙肝传染性强弱不能作出准确的判断，也不能作为判断乙肝病毒是否存在复制。乙型肝炎病毒核酸定量检测是用来检查乙肝患者体内的病毒含量，能够精确的判断出乙肝病毒在体内的复制、传染强弱情况，是证实乙肝病毒存在的直接证据，是临床诊断的有力依据。HBV-DNA 检测通过扩增乙肝病毒核酸使对体内低水平乙肝病毒敏感，此方法是判断病毒复制的常用手段。
结论 乙肝五项和乙型肝炎病毒核酸检测联合检测可对疑似乙肝患者进行较好的临床诊断，既能判断该患者是否感染乙肝病毒又能判断该患者处于乙肝病程发展的某个时期，为临床提供一定的诊断依据

PU-2645

叶酸检测的必要性

解春岩
黑龙江金域医学检验实验室有限公司

目的 叶酸参与氨基酸和核苷酸代谢，参与细胞生长和组织修复，是胚胎发育过程中不可缺少的营养素。叶酸不足会导致新生儿出现神经管畸形，唐氏综合征，唇腭裂或先心病，同时还可能使孕妇妊娠高血压，先兆子痫和婴儿早产及习惯性流产等。若叶酸过量，则会掩盖维生素 B12 缺乏，而导致的其引起的神经损害进行性发展；会干扰锌的代谢，使胎儿发育迟缓，还能增加儿童期哮喘风险。
方法 叶酸代谢能力基因检测首先采用从人外周血细胞中提取的基因组 DNA，而后准备 PCR 扩增液，将待检测的 DNA 样本进行配制，完成后开始在 PCR 扩增，结束后再用检测卡进行检测试验，最后进行结果判读。
结果 以阳性对照液为模板进行 PCR 反应，对 PCR 产物进行检测，检测线有条带出现，作为阳性对照；以阴性对照液为模板进行 PCR 反应，对 PCR 产物进行检测，检测线无条带出现，为阴性对照。MTHFR 1298AA 表示正常野生型;MTHFR 1298CC 即为纯合突;MTHFR 1298AC 即为杂合突变；若质控线无条带或质控线与检测线均无条带，即为无效检测。
结论 叶酸代谢能力基因检测可检测与叶酸代谢相关的基因是否发生异常，及早发现个体对叶酸德吸收利用水平，从而筛查出容易引起叶酸缺乏的高危人群，实现个性化增补叶酸
从而增加叶酸补充依从性，降低新生儿出生缺陷风险。为了达到个体健康化，叶酸代谢能力的检测对特定人群是非常有必要性的，当受检者清楚和明确自己的叶酸利用水平后，最终才能真正实现科学增补叶酸。

PU-2646

新型冠状病毒核酸筛查工作的快速开展

谢滨姣、祖爽、卢润章、张俊涛
黑龙江金域医学检验实验室有限公司

目的 全球各地疫情反复出现，金域医学近两年一直抗战在抗疫的最前线，各地检验实验室均在政府进行新冠核酸筛查工作中承担着重要的工作任务。为了对疫区人口进行快速的感染情况摸底调查，如何检测快速、结果准确的开展新型冠状病毒核酸筛查工作变得尤为重要。
方法 要快速完成全面核酸筛查工作，实验室产能必须及时快速跟上。在金域医学集团一盘棋的调度下，通过场地利用、流程梳理、人员调配、资源匹配、后勤保障等多方面举措，快速提升产能。为了提高标本收集的效率，同时满足实验室 96 孔板检测的排板特点，设计了新型的 96 孔采样管摆放架，每个摆放架出场时即配有唯一序列号供识别。外部配有 3 层包装系统，使其符合防水、防破损、防外泄、耐高温、耐高压的要求。第一孔不摆标本，每架采集 90 管标本，样本采集时可随机空余 5 个孔位，用于实验室的阴阳性质控品（三阴、一阳、一弱阳）的摆放。
结果 通过匹配中心实验室、移动方舱实验室，以及整合地方医院实验室三种方式，集团内部调拨设备、人员等方式，快速将产能提升至日检 5 万管标本，帮助政府尽快完成全员筛查任务，落实疫情防控工作。
样本管摆放架的应用大大提高了标本采集后交接的工作效率，节省了大量清点标本、拆卸标本包装的时间，省去了标本接收上架的步骤，只需一个序列号即可对整架标本进行识别及溯源，为快速开展全民核酸筛查工作提供了便利的工作方法。
结论 通过集团一盘棋的一体化管理，可以实现快速建立高产能的检测能力；通过创新设计，大大提高了标本收集、接收、检测的工作效率，基本实现了一体化操作流程。

PU-2647

新型冠状病毒核酸检测实验室防污染措施

徐梦尧
黑龙江金域医学检验实验室有限公司

目的 核酸检测在疫情防控中起到非常重要的作用，实验室污染会导致结果假阳性，降低实验室污染，保证结果的准确性至关重要。
方法 1.实验前：新冠核酸检测实验前应对试剂准备区、样本制备区、扩增和扩增产物分析区用 2000mg/L 含氯消毒剂对实验台面、地面、生物安全柜柜内、超净工作台柜内进行彻底的擦拭，含氯消毒剂应现用现配，配置使用时间不得超过 24 小时。2.实验中：实验中应严格遵循 pcr 实验室操作要求，加样时技术员手臂不应拿出生物安全柜以外，若需离开生物安全柜，需要用酒精喷洒消毒手臂在拿出。如有样本或质控品泄漏情况发生，应立即用吸水纸覆盖并喷洒 5500mg/L 含氯消毒剂。3.实验后：实验结束后应对实验台面地面用 2000mg/L 含氯消毒剂进行彻底擦拭，移液器等设备也应用 75%酒精进行擦拭，生物安全柜内废弃物应放入医疗垃圾袋中，表面喷洒 75%酒精后转运至高压间高压灭菌。实验室消杀结束人员离开前应开启移动紫外车及固定紫外灯照射 2 小时。如遇实验室严重污染时，还可使用核酸清除剂进行彻底清除。
结果 通过上述方法进行后，对新冠核酸检测环境进行检测，对生物安全柜（台面、按键、防护窗、表面等）、核酸提取仪（表面、按键等）、扩增仪（仪器表面、电脑表面、鼠标按键、键盘、仪器内侧等）、移液器、实验台面、地面等进行采样检测，核酸检测结果均为阴性。
结论 新冠 pcr 实验室核酸污染是导致结果假阳性的重要原因之一。

PU-2648

大肠癌早期筛查方法比对分析

马丽娜
黑龙江金域医学检验实验室有限公司

目的 大肠癌是源于大肠腺上皮的恶性肿瘤，又称结直肠癌。可发生在各段大肠，70％发生于左侧，尤以乙状结肠和直肠最多。目前病因尚不清楚，流行病学调查发现，大肠癌的发病主要与人们的生活方式、环境和饮食结构、某些化学致癌物质等因素有关。全球发病率有明显地域分布差异，北美、西欧、澳大利亚和日本发病率较高，非洲及大部分亚洲地区发病率较低。在中国，50%以上的肠癌患者是直肠癌，国内经济发达的城市，大肠癌发病率均有明显上升。对于 40 岁以上中老年人，进行定期体检非常有必要，一旦体检中发现便隐血试验阳性都需要在医生的指导下进一步检查，但是仅仅依靠患者自己在日常生活中发现或者体检中的隐血试验阳性，很难在早期就能发现大肠癌。
方法 目前肠癌的检测方法众多，本文主要通过对目前肠癌检测及早期筛查的方法，肠镜、粪便隐血、粪便中大肠癌相关基因标志物的检测、血样中大肠癌相关基因标志物的检测等方法进行详细的对比分析，给出不同群体不同时期大肠癌检测的推荐方式。
结果 粪便中大肠癌相关基因标志物的检测不仅能够早发现大肠癌，而且对患者来说无痛苦，但是目前该方法尚部非常成熟，灵敏度和准确度都不是非常理想，必要时仍需借助肠镜的检查。
结论 肠镜目前仍然是大肠癌检测的金标准，但是由于其检测的特殊性，导致很多人望而却步，甚至很多人肠镜发现时为时已晚；粪便隐血试验没有痛苦但是灵敏度低，影响大肠癌的检出率；DNA 的异常甲基化可为非侵袭性检测结大肠癌提供一种新的策略，通过对无症状人群进行筛查或对有大肠癌家族史或确诊有癌前病变的患者进行监测是发现早期癌的重要途径。

PU-2649

糖尿病视网膜病变 AI 筛查

谢滨姣、赵冬梅、董蔓莉、卢润章
黑龙江金域医学检验实验室有限公司

目的 近年来，人工智能在各领域内发展迅速，目前也在逐步深入医疗诊断器械产品中，为多种疾病的诊断、慢性病的监测与管理提供了更为高效的技术手段。如用于对癌症、心脑血管、骨折、眼科等疾病的监测、诊断与检验。
我国约有 1 亿多糖尿病患者，其中 2 千万以上患有糖尿病视网膜病变（俗称糖网），患病率高于 20%，这种疾病是由慢性高血糖引起，损害视网膜中的血管，最终导致视力失真或丧失，已成为工作年龄人群排名第一位的致盲性眼病。
方法 II 型糖尿病患者每年进行 1 次眼底筛查，可使失明风险降低 94.4%，因为在早期阶段，患者通常没有症状，但是在此阶段损害是可以逆转的，因此定期筛查对糖尿病患者而言非常重要。通过有效的筛查途径早期发现，可以有效控制血糖和血压对糖尿病视网膜病变进行早期干预。目前由于我国眼科医生人数少、缺乏便捷的诊断设备等原因，全国的医疗机构对于眼底疾病的筛查还未能普及，导致门诊糖尿病患者眼底筛查率不足 10%；目前全国很多偏远地区或社区医院、体检中心等相对来说没有较强的医生资源，能掌握眼底阅片的医生更是数量甚少。人工智能应用与糖网筛查可以很大程度上改观目前状态。
结果 人工智能糖网筛查方法为给出已收集患者数据的状态分类（糖网 0 期~VI 期）数据。通过多分类混淆矩阵测算评估本人工智能算法的灵敏度、特异性、准确率参数，从而确定本算法的性能及对糖网筛查的适用性。在确认人工智能性能后，采取人工智能与常用的临床检查对比的方式进行临床性能验证，结果证明，通过散瞳检查、FFA、OCT 结合的检查结果与 AI 筛查结果基本一直，可确认此人工智能可有效辨别糖尿病患者的视网膜病变程度。

其应用过程为，服务器通过自适应算法，对眼底照相机获得的眼底彩色图像进行识别，判断视网膜病变及其程度，并由软件自动给出结果，轻度及以上糖网、未检测出糖网、因图片质量不符无法判断结果。其适用的人群为已确诊糖尿病患者。
结论 此糖网筛查 AI 仅为医疗诊断领域的一个基础应用。当下，在医学诊断数据不断积累、AI 技术不断发展过程中，人工智能对疾病的诊断应用会不断增多，为人类健康提供更有力的支撑。

PU-2650

如何降低核酸检测过程中扩增试剂的损耗的探讨

吴丽
黑龙江金域医学检验实验室有限公司

目的 新型冠状病毒核酸检测大筛查期间，样本量剧增。检验人员在扩增试剂的配置是用排枪分装到八连管中使用。最后做试剂盘点及试剂损耗计算时，发现扩增试剂损耗严重，已达到 13.72%。本文旨在根据本实验室的实际情况，提高试剂使用情况，降低试剂损耗.
方法 为了提高试剂使用情况，降低试剂损耗，采取以下几点措施：1.不再使用排枪分装试剂，改用单枪分装；2.分装完的试剂瓶，再用掌上离心机瞬离后还会有残留在瓶壁的液体到底部；3.试剂不再倒在加样槽中，也减少了试剂残留在加样槽中；4.强化人员培训，减少不必要的复查；5.强化维护的工作，与工程师有良好的沟通和配合，保证日常维护工作的规范操作，减少设备故障的发生。
结果 本实验室运用此方法后，大大提高试剂的利用率。
结论 试剂的分装，良好的设备运行状态，加强检验人员的培训，提高操作者的责任心和实验技能，都是提高试剂利用率，降低损耗的环节。掌握如何降低试剂分装过程中产生的损耗，能分辨设备的运行状态，提高了试剂利用率，降低了试剂的损耗，为公司的降本增效做出了贡献。

PU-2651

溶血对神经元特异性烯醇化酶（NSE）检测结果的影响

于跃
黑龙江金域医学检验实验室有限公司

神经元特异性烯醇化酶(NSE)为糖酵解关键酶,在临床上应用非常广泛,可作为神经元损伤的标志物,也可作为肿瘤标志物用于神经母细胞瘤、小细胞肺癌、垂体腺瘤等疾病的诊断。由于血小板和红细胞中存在其同工酶，因而标本溶血，红细胞中可释放大量的神经元特异性烯醇化酶（NSE），因此溶血可导致结果偏高，严重影响检测结果的真实性和可靠性。本文重点验证不同溶血标本对神经元特异性烯醇化酶（NSE）检测的影响程度，从而给临床医生很好的判断和依据
目的 探讨溶血程度对血清检测神经元特异性烯醇化酶（NSE）的影响程度。
方法 采用罗氏 cobas 6000 e601 全自动电化学发光免疫分析仪，检测正常人血清标本及不同溶血程度的血清标本的神经元特异性烯醇化酶（NSE）含量，溶血（+-++++）的溶血各选择 5 个标本进行检测，其工作原理是电化学发光免疫分析的方法。
结果 当血清标本无异常，结果正常，标本出现溶血，就会使神经元特异性烯醇化酶（NSE）结果偏高出现假阳性情况，且溶血程度越高，神经元特异性烯醇化酶（NSE）结果越高。
结论 溶血对血清检测神经元特异性烯醇化酶（NSE）存在严重影响，神经元特异性烯醇化酶（NSE）含量随溶血程度的增加而增加，临床检测神经元特异性烯醇化酶（NSE）要杜绝溶血标本。

PU-2652

Role of mesenchymal stem cell in metastasis of ErbB2-positive bladder cancer

Zhuolin Li[1,2]、Ruxue Jia[1,2]、Yating Wu[1,2]、Xiaoming Huang[1,2]、Huimin Niu[1,2]、Jin Chen[1,2]、Shenghang Zhang[1,2]、Shuiliang Wang[1,2]
1. 厦门大学附属东方医院福建省适配体技术重点实验室
2. 联勤保障部队第九〇〇医院检验科

Objective Tumor progression towards metastasis is often depicted as a multistage process. Each stage of metastasis is closely related to the genetic and epigenetic changes of tumor cells and the regulation of many factors in the microenvironment. In recent years, studies have shown that mesenchymal stem cells (MSC), as an important cell component of tumor microenvironment, are closely related to tumor metastasis. Our study focused on the role of MSC in the metastasis of ErbB2-positive bladder cancer.
Methods ErbB3 overexpression ErbB2-positive bladder cancer cell line was constructed by lentiviral transfection; Transwell migration and invasion assay was used to detect the effect of MSC on the metastasis and invasive growth of ErbB2 positive bladder cancer and its ErbB3 overexpression subline; Western blot assay was used to detect the expression and activation of related proteins after co-culture with MSC; In the animal experiment, the xenograft tumor model of bladder cancer was established by injecting the above two cell lines through the tail vein of nude mice, and the ability of MSC to form metastatic tumor of ErbB2 positive bladder cancer cells in vivo was explored by injecting mesenchymal stem cells.
Results At the cellular level, MSC could promote the metastasis of ErbB2-positive bladder cancer cells and ErbB3 overexpression ErbB2-positive bladder cancer cells, and the promotion effect was more significant in ErbB3 overexpression cell lines. In addition, Western blot analysis showed that the expression of MMP2 and MMP9 was up-regulated after co-culture with MSC. The results of animal experiment were consistent with that of cell experiment, that is, MSC could promote the formation of metastatic tumor in ErbB2-positive bladder cancer cells in vivo, and this effect was more significant in the model of ErbB3 overexpression.
Conclusion Our data suggest that MSC can promote the metastasis of ErbB2- positive bladder cancer cells, and this effect may be achieved by activating ErbB2/ ErbB3 and its downstream signaling pathway.

PU-2653

溶血标本不同时间对同型半胱氨酸（HCY）的影响

赵日晖
黑龙江金域医学检验实验室有限公司

目的 观察溶血标本不同时间对同型半胱氨酸（HCY）的影响。近年来研究资料表明，同型半胱氨酸（HCY）是心脑血管疾病的独立危险因素，因此，准确测定 HCY 非常重要。溶血是检测项目结果影响较大的一个因素，但是不同时间溶血对 HCY 的是否有影响还缺少报道，本实验进行探讨，现报道如下。
方法 5 例溶血标本，使用罗氏 cobas 8000 c702 全自动生化分析仪用酶循环法分别检测新鲜标本、放置 1 小时的样本、放置 2 小时的样本、放置 4 小时的样本、放置 8 小时的样本，查看同型半胱氨酸不同时间对结果的影响程度，将五例标本结果进行比较。
结果 测试了五例标本，同型半胱氨酸（HCY）的浓度依次降低，结果相差较大。
结论 本研究结果表明，溶血标本不同时间会对同型半胱氨酸（HCY）检测结果有显著影响，标本检验结果的可靠性和真实性直接关系到临床诊断的准确性，在工作中一旦发现溶血 HCY 标本，应主动与临床联系，结合临床首先排除体内溶血的可能，若不是体内溶血，建议重新采集标本。随着

全自动生化分析仪的普及使用，检查血清标本外观是否溶血已成为试验过程中的重要一环节，正确处理溶血，才能得出准确的结果，更好地把握检验工作质量并为临床提供优质服务。

PU-2654

霍乱弧菌不再是漏网之鱼

邹雪
新化县人民医院

目的 我们如何才能在微生物日常工作中不漏掉罕见的细菌呢。下面以霍乱弧菌为例。霍乱是我国法定管理的甲类烈性肠道传染病，但是随着现代污水和饮用水的处理，在我国，这些年很少有霍乱的流行。所以微生物检验人员特别是基层工作人员在日常工作中很难去发现这个古老的生物。霍乱弧菌分为 200 多个血清群，其中只有 O1 和 O139 可以引起霍乱（但其他血清群也可能导致严重腹泻），由于它的传染特性，我们依然不能对霍乱放松警惕，需要对 O1 和 O139 病人和病原携带者及时隔离和治疗，所以使得在日常实验室工作中对它们的不漏检至关重要。
方法 1.微生物工作是离不开临床的。
2.微生物实验室工作。如何在实验室工作中去发现它，显得至关重要。
3.血清学分型：如果发生凝集（应做盐水对照），是 O1 或 O139 群，须立即报告给主治医生，因为霍乱会引起严重脱水。还应该报 CDC，并将分离株和病人原始标本送到 CDC 进行确认和毒素检测。
结果 实验室鉴定要点有悬滴动力试验和制动试验，菌落形态，格兰染色，tcbs，碱性蛋白胨水，血清学分型。条件允许还可以借助质谱仪或者全自动生化仪。最终的确认还是需要 CDC 做进一步检测。
结论 所有的实验室鉴定等都离不开临床，所有脱离临床的检验工作都是耍流氓。大便细菌生态环境比较复杂，我们微生物工作中最重要的是从复杂多样化生长的平板上发现致病的细菌。就需要我们在日常工作中多积累临床经验多与临床沟通互相促进。

PU-2655

人类 SDC2 甲基化检测结果与年龄相关性分析

张雪娇
黑龙江金域医学检验实验室有限公司

目的 目前结直肠癌是较为常见的肿瘤之一，每年发病率和致死率有上升趋势且年轻化。本文根据黑龙江金域 2021 年 3 月份 229 例人类 SDC2 基因甲基化检测结果，探讨其检测结果与年龄的相关性。
方法 SDC2 基因相对于正常组织，在大肠癌和腺瘤组织中呈现高水平的甲基化现象，并且 SDC2 基因在大肠癌和腺癌组织中的表达也显著高于正常组织，SDC2 基因在大肠癌不同分期中也呈现高度的甲基化。通过对 229 例筛查人员粪便样本中 SDC2 基因甲基化检测，发现在特异性为 90.9% 时，大肠癌的检测灵敏性为 90.0%。这一结果证明其作为大肠癌早期标志物具有较高的临床应用价值。
结果 本次筛查共计 229 例，平均年龄为 51.07 岁，阳性总数为 15 例，阳性患者平均年龄为 52 岁，阳性率为 6.55%。以下用 N 表示年龄，N≤40 岁共计送检 47 例，其中阳性 0 例，阳性率为 0；40＜N≤50 共计送检 56 例，其中阳性 4 例，阳性率为 7.14%；50＜N≤60 共计送检 86 例，其中阳性 7 例，阳性率为 8.14%；60＜N≤70 共计送检 27 例，其中阳性 2 例，阳性率为 7.41%；N＞70 共计送检 11 例，其中阳性 2 例，阳性率为 18.18%。

结论 大肠癌的发生与年龄关系密切，40 岁以上阳性率明显增高，进一步证实了该年龄段以上人群早期粪便 SDC2 基因甲基化筛查的必要性，明确了 SDC2 基因检测对大肠癌早期筛查和早期预防的重要作用，该研究为大肠癌的早期筛查提供一定的佐证和支持，未来将持续进行粪便 SDC2 基因甲基化对于大肠癌早期筛查的临床应用与研究，不断辅助临床提高患者生活质量和延长患者生存期。

PU-2656

略论金域医学东北大区核酸实验室如何加快新冠检测速度

马晓影
黑龙江金域医学检验实验室有限公司

目的 研究在新冠疫情筛查时金域医学东北大区作为第三方检测机构如何在保证质量和安全的情况下加快检测速度。
方法 疫情稳定时金域医学检测机构各子公司参与核酸检测的主干人员进行汇总经验，经由子公司实验室负责人员通过线上会议的形式进行经验的交流与总结。
结果 新冠疫情筛查期间各子公司人员及时相应，对于支援人员及时带教熟悉工作环境，当班结束后及时汇总反馈问题发现不足实时进行改正，使临时组建的团队发挥最大的产能。检测设备方面各子公司提前联系支援设备的厂家型号及数量，提前安排出设备存放的位置，使分析工作有条不紊。对于试剂配置方面专人专用，与检测人员沟通所需要检测试剂的数量，做到在标本数量多时也不造成试剂的浪费。创新方面筛查期间在加样过程中产生创新点，检测人员发明了裂解液精准定位加样辅助器，已进行专利的申报。在新冠筛查期间沈阳子公司历时 16 天完成 504292 标本检测数，吉林子公司历时 30 天完成 673885 标本检测数，黑龙江子公司历时 45 天完成 835678 标本检测数。
结论 在疫情爆发标本量剧增的情况下，通过各子公司抗疫筛查的经验总结交流与分享能够更加优化新冠筛查期间的检测流程，提高检测速度。

PU-2657

结直肠癌肿瘤标志物研究进展

张世慧
山东大学第二医院

结直肠癌是常见的消化道肿瘤之一，在目前世界范围内的致死性肿瘤中排名第四，每年约有 90 万人死于结直肠癌，且结直肠癌易发生肝转移，远期生存率差，因此早期诊断结直肠癌具有重要意义。目前临床常应用糖类抗原（ＣＡ）１９9 和癌胚抗原（CEA）检测结直肠癌，但特异度较低，因此，迫切需要找到灵敏度高的最佳标志物。液体活检技术是近年来肿瘤诊断领域的一大突破性技术，通过捕获和分析外泌体、核酸、蛋白质及细胞等肿瘤衍生物质来解读癌细胞生物学进程，主要包括对体液中外泌体、血液的循环肿瘤细胞（CTCs）和循环肿瘤 DNA（ctDNA）的检测。该项技术在结直肠癌中的研究进展有利于发现结直肠癌的潜在标志物，有利于结直肠癌的早期诊断，对于患者的早期临床治疗及预后评估也具有重要意义。目前对外泌体的研究仍处于初始阶段，存在诸多不足，如针对外泌体的分离及保存等尚存在诸多争议，需进一步改进，但随着蛋白质组学、高通量测序等技 术的飞速发展及应用，外泌体终将成为 CRC 研究领域的新曙光，进而实现巨大的临床及科研价值。CTCs 检测对复发、转移性 ＣＲＣ 具有更重要的意义，与传统诊断手段相比，在 ＣＲＣ 的早期诊断中还需更多的临床数据支持， 目前大部分 CTCs 研究局限在转移性癌中，对于早期癌特别是非转移性 ＣＲＣ 中的 CTCs 研究相对较少。除临床试验之外，没有临床 有效性或临床效用的证据表明 ctDNA 测定可用于 癌症筛查。ctDNA 在结直肠癌诊断的应用仍需 要进一步研究。

目前液体活检仍面临巨大困难，首先，应该寻找灵敏性和特异性更高的检测 方式；其次应规范检测流程，包括样本取材方式，运输及保存方式以及检测方式。最后还需要更多大样本、多中心、

大规模前瞻性临床研究证实液体活检对临床诊疗的作用。相信在不久的将来，液体活检能够广泛应用于临床，为患者提供更加及时、精准的个体化治疗方案。

PU-2658

检验分学科诊疗

闫妁
山东大学第二医院

随着社会不断发展、人民生活水平不断提高，各种棘手疾病也随之而来，这对医生来说是一个极大的挑战，对我们检验人员来说也发出了一个急需进步的信号。目前疑难杂症呈现的问题：1.临床症状并不典型，2、存在多学科疾病，3、各科室间缺乏交流等，下面我就临床科室与检验科室间交流展开阐述。

临床疾病纵横交错，病人初步就诊医院，一般就现阶段最明显症状就诊于相应科室，为明确诊断住院治疗，住院第一步就是完善“相关”辅助检查，所谓“相关”就是与本科室疾病相关检查，以便佐证诊断，这时候我们辅助科室就发挥巨大的作用；由于人体是一个整体，多种疾病可能会引起相同的指标异常，这个检验指标用来引导医生诊断，由于检验人员对病人病史及体征缺乏了解，与临床医生缺乏交流，仅通过检验技术检出结果，并不能完全反映病人的病情，所以我认为应该实行检验分学科诊疗。 我认为可以将检验部门可以分级诊疗，向临床医生靠拢，每个临床科室可以有相应的检验人员，了解病人情况，与临床医生充分交流，针对不同病人情况，采取不同技术行相关检验指标，当然还应设有体检部门，专门针对健康查体人群；我们可以用实验验证一下，以血液科室病人作为研究对象；选出能力、知识、经验等相一致检验人员，将他们分别于不同临床科室对应，然后对他们进行对血液内科理论学习及针对相关疾病检验方法；同时选出同一批病人，就诊于同一个医生，判断那种方式可以更快、更准确明确诊断。我实验的主要目的是检验分学科诊疗，可以提高疾病诊断速度及准确性，使检验部门起到更好的引导作用。

PU-2659

两种化学发光仪对于铁蛋白（FER）检测结果的比较

林迪
黑龙江金域医学检验实验室有限公司

目的 近年来随着检验行业的迅猛发展，化学发光分析法作为一种灵敏度高，检测时间短，检测范围宽，分析方法简便快速，安全性好及使用期长的痕量分析方法，不断深入到临床检验、药物、食检、环境、生命和材料科学等各个领域。化学发光具有荧光的特异性，同时不需要激发光，避免了荧光分析中激发光杂散光的影响从而提高了灵敏度，并且避免了放射分析造成的环境污染和健康危害，是一种非常优秀的定量分析方法。由于化学发光分析的发光体系日益增多，本文介绍了使用雅培品牌的免疫分析仪和迈瑞品牌的免疫分析仪分别检测铁蛋白（FER），探讨不同免疫分析系统以及不同化学发光方法对于结果的可比性和准确性。
方法 使用雅培 i2000SR 全自动发光免疫分析仪和迈瑞 CL-6000i 全自动化学发光免疫分析仪分别检测铁蛋白（FER），雅培和迈瑞两个品牌的检测方法采用的均是双抗体夹心法，雅培采用两步法，迈瑞采用一步法。雅培为样本中的铁蛋白与铁蛋白抗体包被的微粒子结合，冲洗后，加入吖啶酯标记的铁蛋白抗体结合物形成反应混合物。迈瑞为样本与包被着抗 FEER 抗体的超顺磁性磁珠以及抗 FEER 抗体-碱性磷酸酶标记物添加到反应管中，经过孵育反应完成后，磁场吸附磁珠，洗去未结合的物质。
结果 进行了样本比对，同一标本不同检测系统 95%在相似的参考区间里阴阳性符合。

结论 对比的两个品牌的两个方法的具有高度的一致性同时稳定性良好。解决了我们在工作中关于不同的检测平台对于结果一致性解读的困扰。也成为我们对临床服务强有力的后盾。

PU-2660

基于 GEO 数据库的在线 SCLC 差异表达基因分析

谢雨彤
黑龙江金域医学检验实验室有限公司

目的 挖掘与小细胞肺癌（small cell lung cancer, SCLC）发生发展显著相关的基因，探索 SCLC 的发病机制，为 SCLC 临床鉴别诊断、评估潜在的靶向治疗选择及寻找新的治疗策略提供理论基础。
方法 本研究选取 2013 年发表在 Scientific Reports 上的论文（Gene repression with H3K27me3 modification in human small cell lung cancer）的中的 65 例样本，包括实验组的 23 例 SCLC 样本和对照组的 42 例正常组织样本。通过挖掘其 GEO 数据库中 SCLC 癌组织及正常组织的微阵列基因表达(Microarray gene expression)的原始数据（GEO Series GSE43346），利用 NetworkAnalyst 平台进行差异表达基因筛选（|log-foldchange|>2，Adjusted P<0.01）。并使用 Functional Annotation Tool 平台对选取出的前 250 个显著上调和下调基因进行 GO 分析、KEGG 信号通路分析和蛋白质互相作用网络分析。
结果 质检结果的箱体图（Box plot）和主成分分析（PCA plot）结果皆显示 65 个样本中存在基因表达差异，limma 统计法对实验组和对照组的比较总共筛选出与 SCLC 显著相关的基因 5000 个，这与 GEO2R 分析结果相符。在前 250 个表达差异显著的基因中，上调基因 46 个，下调基因 204 个。GO 富集分析得出 51 个条目（FDR<0.01），显示这些基因的分子功能主要集中在蛋白质结合和细胞核功能。KEGG 通路分析得出这些基因涉及 12 个通路（P<0.01），主要富集在 DNA 修复，姊妹染色单体粘着、细胞分裂等信号通路上。蛋白质互作网络分析结果提示处于网络中心节点的蛋白有：淀粉样 β 前体蛋白（APP）、瘤蛋白 p53（TP53）、X 射线修复交叉互补蛋白 6（XRCC6）、赖氨酸去甲基化酶（KDM1A）、增殖细胞核抗原（PCNA）和 DNA 修复相关蛋白（BRCA1）等。
结论 通过生物信息学对 SCLC 相关基因的分析，发现 SCLC 的发生发展可能与 APP 、TP53 、XRCC6 、KDM1A、PCNA 和 BRCA1 等基因结构和表达异常有关。

PU-2661

全自动血培养仪阳性报警时间（TTP）对分离细菌多重耐药性的预测价值探讨

曹啟新
内蒙古自治区内蒙古人民医院

目的 监测血培养分离菌的临床分布及探讨阳性报警时间（TTP）对细菌多重耐药性的预测价值。
方法 对内蒙古自治区人民医院 2017-2020 年期间 534 株血培养分离菌进行回顾性分析，采用 SPSS 22.0 软件对细菌 TTP 值进行统计比较，受试者工作曲线（ROC）分析 TTP 值对细菌多重耐药性的预测价值。
结果 534 株血培养阳性菌株中，以肠杆菌科（49.5%），葡萄球菌属（29.2%）和肠球菌属（5.2%）为主。主要病区分布为 ICU（25.1%），普外科病房（15.4%）和肾内科病房（7.3%）及其他病房（52.2%）。根据药敏结果将细菌分为多重耐药组与非多重耐药组，将二者之间的 TTP 值进行统计比较，发现除肺炎克雷伯菌外细菌多重耐药组的 TTP 值均高于非多重耐药组，且差异有统计学意义(P<0.05)；ROC 曲线分析 TTP 值预测大肠埃希菌、耐甲氧西林的金黄色葡萄球菌（MRSA）、耐甲氧西林凝固酶阴性葡萄球菌（MRCNS）、肠球菌属、链球菌属、鲍曼不动杆菌和阴沟肠杆菌

多重耐药的最佳截断值为 TTP≧0.69d，TTP≧1.0d，TTP≧1.07d, TTP≧075d，TTP≧0.69d, TTP≧0.69d 和 TTP≧0.59d，曲线下面积分别为 0.87，0.71，0.64, 0.76, 0.84, 0.75 和 0.86，准确度均为中度。

结论 血流感染患者病原菌及其分布复杂，细菌多重耐药性不断增强，实验室可以通过监测血培养分离菌的分布为临床治疗提供相关依据，以及通过 TTP 值的大小对细菌多重耐药性提示预警，指导临床早期合理用药。

PU-2662

火焰原子吸收和 ICP-MS 测定全血中 5 种元素的比较

赵式樱
黑龙江金域医学检验实验室有限公司

目的 微量元素与人的健息息相关，它们的摄入过量或缺乏都会不同程度地引起人体生理的异常或发生疾病，准确、快速、方便地测定人体内微量元素的含量成为急需解决的问题。火焰原子吸收法（FAAS 法）是从光源辐射出具有待测元素特征谱线的光，通过试样蒸气时被蒸气中待测元素基态原子所吸收，由辐射特征谱线光被减弱的程度来测定试样中待测元素的含量。具有灵敏度高、抗干扰能力强、精密度高、选择性好、仪器简单、操作方便的特点。随着技术的发展，电感耦合等离子体质谱法（ICP-MS 法）越来越普及，可分性痕量及超痕量元素，具有快速且多元素同时测定、精密度高、准确性好、检出限低等优点，可以达到快速检测人体内多种元素含量的要求。本文对 FAAS 法和 ICP-MS 法测定全血中铜、锌、钙、镁、铁含量进行了对比，找到更高效的分析方法。

方法 本文同时建立了 FAAS 法和 ICP-MS 法检测全血中 12 种元素的方法。从检出限、准确度和精密度三个方面对两种检测技术进行了对比。

结果 经验证，ICP-MS 法测定全血中 5 中元素的线性范围 R>0.9950，偏倚在 0.16%-7.81%之间、精密度在 0.80-2.10%之间，定量限为微克级。FAAS 法测定全血中 5 中元素的线性范围 R>0.9950，偏倚在 0.11%-12.43%之间、精密度在 0.88-4.30%之间，定量限为微克级。

结论 ICP-MS 法和 FAAS 法在测定全血中铜、锌、钙、镁、铁的含量对比中，ICP-MS 法和 FAAS 法的定量限均为毫克级，但 ICP-MS 法的定量限较低。准确度和精密度 ICP-MS 法均优于 FAAS 法。对比结果表明对于全血中铜、锌、钙、镁、铁的测定 ICP-MS 法更具优势。

PU-2663

不同类型采血管对叶酸项目影响

祝晓捷
黑龙江金域医学检验实验室有限公司

目的 为缩短分析前样品处理的时间，提高检验速度，越来越多的临床实验室选择采用肝素锂凝管或分离胶促凝管来分离血样。由于市场的需要近年来我国的采血管厂家也开始大量的生产分离胶采血管，并被大量实验室采用，一些类型的采血管在制造过程中添加了一些物质并且试管中的一些物质有潜在的吸收被分析物或者释放可能影响化学物质分析的干扰物，直接影响检测结果。因此采血管可能成为实验室分析前误差的主要来源。由于各种类型采血管日益增多并被应用，本文评估不同类型的采血管用化学发光免疫分析技术测定叶酸结果之间的差异。

方法 采集同一志愿者肘正中静脉血分别至普通采血管、血清分离胶管、肝素锂血浆分离管、玻璃采集管 4 种采血管中，分离血清后使用雅培 i2000SR 化学发光法测定叶酸指标。叶酸项目采用两步法免疫检测，经过两部预处理后样本中的叶酸结合到 FBP 包被的微粒子上。冲洗后加入吖啶酯标记的蝶酸结合物，并结合到 FBP 包被的微粒子的空位点上。随后向反应混合物中加入预激发液

和激发液测量产生的化学发光反应以相对发光单位表示。样本中的叶酸含量与雅培光学系统检测到的发光单位成反比。以普通采血管作为对照评估他们之间的差异。
结果 血清分离胶管、肝素锂血浆分离管、玻璃采集管与普通采血管进行评估，被评估的采血管与对照管的差异小于 10%。
结论 应用真空采血管前，必须要对其不同类型进行综合评估，择取对叶酸检验结果影响较小的真空采血管，可提高实验结果精准性。

PU-2664

巨噬细胞 M1/M2 转化在急性肺损伤病理生理中的研究进展

黄湘平、谭超超
湖南省人民医院

急性肺损伤是由多种因素引起的危急重症，病情恶化会导致患者死亡。巨噬细胞参与了急性肺损伤的不同病理阶段，包括渗出期、恢复期、纤维化期，其中 M1 巨噬细胞主导促炎作用，M2 巨噬细胞主导抑炎反应和组织修复的作用。在急性肺损伤的发病过程中，巨噬细胞通过向 M1/M2 转化参与了肺组织的损伤与恢复。本文将对急性肺损伤 ALI 不同时期 M1/M2 的转化方向及机制进行归纳总结，为急性肺损伤的探索研究提供思路

PU-2665

利用现代管理工具助力提高医学实验室质量管理水平

周博、吉阳涛、赵敏
中国医科大学附属第一医院

目的 在新冠疫情背景下，我国医学实验室进入到了大发展的阶段。有相当数量的实验室已经在此前通过了国际质量管理体系 ISO15189（CNAS CL-02）认可或美国病理家学会（CAP）认证，但管理水平的提高需要时间和经验的积累，各级医院的管理水平仍然参差不齐，未通过认证认可的实验室管理水平更加难以保证。本文旨在探讨如何利用现代企业的管理工具，快速帮助实验室精简管理流程，提高管理水平。
方法 充分分析提炼 ISO15189 认可指南中的核心内容，编制管理体系基准调查表，全面覆盖实验室管理体系各个要素，评价实验室现行管理状况，并分析指出存在缺陷。根据认可自查表提炼各要素必需的管理流程及记录，制定个性化检查表，使有缺陷的工作一目了然。利用 RACI 项目责任管理工具，记录管理各项工作进展，责任到人，并专人审核，且保证相关人员全部知悉项目进展。利用 6S 管理工具优化实验室管理流程，减少八大浪费，提高生产效率和安全性。
结果 将各种管理工具合理应用在实验室中，可有效提高实验室对于质量管理的认知，为实验室提供简单、有效的管理思路，并保证不遗漏任何重要要求。节约了实验室的学习时间和试错成本，提供了清晰的管理路线，清楚的管理职责。
结论 在实验室高速发展变化的今天，质量管理的核心职责不能改变，医学实验室一切应以病人为中心，为患者和医护服务，以保证结果的质量为己任。在这种背景下，适当引进科学的现代管理工具，将极大的帮助实验室提高整体管理水平。

PU-2666

sST2 联合 hs-CRP、RDW-CV、hs-TnT 和 NT-proBNP 检测 在慢心力衰竭中的临床价值探讨

黄蔚[1]、彭瀚霆[2]
1. 广东省人民医院
2. 中山大学南方学院

目的 探索 sST2 联合 hs-CRP、RDW-CV、hs-TnT 和 NT-proBNP 在慢性心力衰竭的临床诊断价值以及其预后价值。
方法 选择 2019 年 9 月到 2020 年 12 月在广州市广东省人民医院心内科收治的心力衰竭患者 82 例（其中 22 例为心血管不良事件发生组 N 组，60 例为无心血管不良事件发生组 P 组）作为实验组，对照组为非心衰患者 64 例。分别检测 sST2、hs-CRP、hs-TnT 和 NT-proBNP、RDW-CV，同时，通过门诊随访调查患者预后并进行相关性分析以及预测价值评价。
结果 实验组 sST2、NT-proBNP、hs-TnT、RDW-CV 水平显著高于对照组，差异均具有统计学意义（P＜0.05）；Spearman 直线相关分析显示，实验组 sST2 水平与 NT-proBNP（r=0.268，P=0.015）、hs-TnT（r=0.385，P=0.000）、hs-CRP（r=0.391，P=0.000）、RDW-CV（r=0.275,P=0.013）呈正相关；发生心血管不良事件患者与无心血管不良事件患者比较，除 NT-proBNP 显著升高（P<0.01）外,sST2、hs-cTnT、hs-CRP、RDW-CV 差异均无统计学上意义（P＞0.05）；另外，NT-proBNP 为心力衰竭心血管不良事件发生情况的独立预测因子，OR 值为 1.000；同时,NT-proBNP 在 ROC 曲线下的面积为 0.310（95%CI：0.170-0.450，P＜0.05），联合 sST2 和 NT-proBNP 为 0.690（95%CI：0.601-0.778，P＜0.05）。
结论 1、sST2 水平在心衰患者中呈上升趋势，且与 hs-CRP、RDW-CV、hs-TnT 和 NT-proBNP 联合检测具有正相关性，sST2 可以作为心力衰竭的病程进展的一个监测指标和预后判断的相关指标；2、NT-proBNP 虽然是心衰患者再次发生心血管事件风险的独立预测因子，对慢性心衰的预后评估起主要作用，但是 sST2 的敏感度比 NT-proBNP 要高，因此 sST2 联合 NT-proBNP 检测可以提高慢性心衰预后评估的敏感度和特异性。

PU-2667

新型冠状病毒肺炎疫情下医共体 PCR 实验室生物安全管理探讨

张示渊[2]、刘晓聪[1]
1. 新疆维吾尔自治区石河子市人民医院
2. 新疆维吾尔自治区石河子市人民医院

目的 总结新型冠状病毒肺炎疫情下石河子市总院医共体下 PCR 实验室的防控教训和经验，并探讨如何做好检验科的生物安全防护，对其六家新冠 PCR 实验室的建立和运行做一全面的梳理，以供大家探讨和借鉴。
方法 新型冠状病毒肺炎疫情已成为全球公共卫生的重大威胁，核酸检测是检测病毒最重要的手段之一。2020 年石河子总院在团场医共体内新建 5 所 PCR 实验室，用于应对新型冠状病毒的检测工作，在疫情当前保证一线操作人员的身体健康与环境安全，实验室生物安全管理工作成为了重中之重。针对团场基层医院自身认识不足，缺乏风险管理意识、流程优化不足、制度落实不到位等情况，生物安全存在诸多影响实验室安全规范运行的现实问题或隐患，因此需要采取行之有效的管理手段避免标本送检、检测、废弃物处理等环节中可能出现的医院感染，总院根据国家发布的医务人员防护指南等相应要求制定了一系列措施，制定了核酸检测的详细流程；梳理了各环节的风险点以及各环节参与人员的责权范围，将标准统一下达医共体团场 5 家实验室，并要求严格落实各项规章制度并加强监督执行；同时，为了解团场五家团场实验室软硬件条件现状、改进方向等情况，不定期下团场指导、梳理，不断优化生物安全流程，以问题为导向实行了扁平化管理，与此同时还加强了对

所有员工进行健康监测，如有异常及时上报。采用 PDCA 管理对石河子市总医院六家 PCR 实验室生物安全管理进行监控与分析。

结果 石河子市总医院医共体成员 6 家 PCR 实验室严格遵守国家制定的管理规定，做好每日生物安全工作，防控工作也得到了安全有序的开展；通过工作团队的不懈努力，为石河子市总院所有 PCR 实验室感染管控和避免人员感染等方面取得了阶段性成果，从未发生医务人员感染事件，也为下一步有关工作探索出进一步的努力方向。

结论 检验科实验室生物安全防护措施对防止医务人员感染有良好的预防和控制效果,可以为新冠病毒肺炎期间做好 PCR 室的生物安全防护以及病毒检测的有序开展提供参考作用。

PU-2668

Efficacy of anti-inflammatory and lipid-lowering activities of Costunolide and Dehydrocostuslactone in vitro

Wanyi Li[1,2]、Honglin Li[1]、Xi Chen[1]、Tao Hu[1]、Huaqiang ZHU[1]
1. Departmant of Clinical Laboratory, Mianyang Central Hospital, School of Medicine, University of Electronic Science and Technology of China
2. 广东医科大学

Purpose Costunolide(CE) and dehydrocostus lactone(DCE) are two natural sesquiterpene lactones, which have been extensively investigated for a wide range of biological activities. Multiple lines of preclinical studies have reported these compounds possesse antioxidative, anti-inflammatory and anticancer properties. In this study, we investigated the effects of anti-inflammatory and lipid-lowering activities of costunolide and dehydrocostus lactone, which have been isolated from Saussurea lappa using activity-guided isolation on phorbolmyristateacetate(PMA) treated THP-1 macrophages. And we will facilitate the development of CE and DCE with therapeutic applications in atherosclerosis-related cardiovascular diseases.

Methods Macrophage foam cells were prepared by loading THP-1macrophages with acetylated low-density lipoprotein(ac-LDL)and apolipoprotein A-1(apoA-1) ,and inflammatory cells were prepared by loading macrophages with lipopolysaccharide(LPS). Cell viability were respectively assessed by CCK-8 assay under different concentrations of DCE and CE. To analyse the anti-inflammatory activity of CE and DCE, the experiment was setted up the blank group, control group , CE group and DCE group. Griess method was employed to detect Nitric Oxide(NO) on inflammatory cells , which were based on the chemical diazotization reaction that was originally described by Griess in 1879, which uses sulfanilamide and N-1-napthylethylenediamine dihydrochloride (NED) under acidic (phosphoric acid) conditions.The THP-1 inflammatory cell culture supernatant was collected, and the productions of tumor necrosis factor-α(TNF-α) were measured by enzyme-linked immunosorbent assay(ELISA). To analyse the lipid-lowering activity of CE and DCE, the experiment was setted up the LDL group, apoA-1 group , CE group and DCE group. The liquid scintillation counting was used to detect the cholesterol efflorescence rate in macrophage foam cells. The expression of ABCA1 protein in macrophage foam cells was detected by Western Blot.

Result We established the Macrophage-derived foam cell and inflammatory cell model of THP-1 cell line. CCK8 assays indicated that treatment with below 20 μmol/L CE and DCE had no toxic reaction on THP-1 macrophage induced by PMA.

The concentration of NO released by inflammatory cells treated with 20 μmol/L DCE and 20 μmol/L CE was (0.124±0.002) μmol/L and (0.290±0.003) μmol/L, respectively, which were lower than LPS group (6.144±0.005) μmol/L,and the difference was statistically significant($P<0.001$). The concentration of TNF-α released by inflammatory cells treated with 20 μmol/L DCE and 20 μmol/L CE was (0.192±0.001) pg/mL and (0.225±0.001) pg/mL, respectively, which were lower than LPS group (0.425±0.021), and the difference was statistically significant ($P<0.001$).

The cholesterol efflorescence rates in macrophage foam cells treated with 20 μmol/L DCE and 20 μmol/L CE were (15.393±0.763) % and (12.285±0.219) %, respectively, which were higher than apoA-1 group (12.227±0.290) %, the difference was statistically significant only in DCE group (P <0.001). The analysis of Western Blot results show that compared with apoA-1 group, the expression of ABCA1 protein in macrophage foam cells treated with 20 μmol/L DCE and 20 μmol/L CE was up-regulated by 2.52 times and 0.17 times, and the difference was statistically significant only in DCE group (P <0.001).
Conclusion In this experiment,we investigated that both CE and DCE may have superior anti-inflammatory activity in vitro, and DCE has better anti-inflammatory activity than CE. Only DCE has superior lipid-loweringactivity in vitro, no better lipid-lowering activity of CE has been found yet.

PU-2669

职业道德建设是军队医院检验科全面建设的前提和基础

陈黔、贾雄飞、王 珂
中国人民解放军联勤保障部队第九二〇医院

目的 探讨职业道德建设在军队医院检验科全面建设中的现实地位、作用和意义，以及职业道德建设的具体制度、方法和措施。
方法 运用军队卫生事业管理学的相关原理和方法。
结果和结论 职业道德建设是“改革强军、军民融合”大环境下确保检验安全、保证检验质量的基础和前提，是军队医院检验科全面建设的关键和保证。只有建立、健全和完善一整套职业道德建设的制度和机制，才能保证检验人员的政治站位和综合素质，以及工作安全的整体确保、检验质量的全面提高。军队医院检验人员的职业道德建设是一项长期、艰巨而复杂的系统工程，军队医院检验科领导必须依据军队改革、市场经济的客观变化和形势要求，及时调整教育内容、保证教育常抓不懈。

PU-2670

基于 Web 的临床试验 EDC 系统的设计与构建

许克[1]、朱放[2]
1. 上海交通大学医学院附属瑞金医院
2. 上海交通大学医学院附属儿童医学中心

目的 本文的目标是开发一款网页端的临床试验电子采集系统,该系统在 EDC 理论框架的基础上,依托 Web 实现,具备 eCRF 设计、录入数据、SDV、数据质疑、核查留痕、用户权限管理和数据导出等 EDC 系统常用功能,且符合具体法律法规和相关行业标准。
方法 本文通过对目前国内外的几大 EDC 网站的功能及业务流程的了解分析,并结合《临床试验数据管理工作技术指南》等相关法律法规和 CDISC 标准等行业标准,从可行性、功能、角色和非功能四个方面进行需求分析,然后对系统的整体架构、功能模块、数据库结构和工作流程进行详细设计和清晰的图表说明。之后对系统各板块的具体功能进行代码分析与实现。最后进行系统的测试。系统开发采用 Thinkphp 框架,将系统的整体结构架构分为两层:即视图层和控制层。视图层主要负责前端 UI 界面内容的展示,实现与用户的交互;控制层负责数据的处理,并控制用户界面数据显示。此外,Layui 框架作为系统的前端 UI 框架,可实现模块化的开发形式,简化了开发的过程。该系统采用 Mysql 数据库,来存储临床试验数据,保证数据的安全。
结果 该系统包含 9 个模块:管理员管理、权限管理、eCRF 设计、病例采集、稽查痕迹、数据 SDV、数据清理、数据导出、系统设置等常用模块，通过了用户界面、功能、浏览器兼容、性能、安全性试等五个方面的测试。

结论 该系统是一款基本完整的,交互友好的轻量级 EDC 系统,相较于其他 EDC 网站,具有低成本、易配置、开发周期短等优势,在后期功能扩展与维护方面也有很大优势。

PU-2671

独立医学实验室医学伦理的工作建设思考

孙维娜、杨勇、张宏磊、赵雪粉、朱佳丹
甘肃金域医学检验所有限公司

本文主要通过目前在医学检验实验室建设伦理委员会的工作制度中出现的情况如：制度建设的实用性和全员培训中的效果评估，探讨甘肃金域医学检验所在《金域医学伦理委员会章程》和《金域伦理评估管理程序》基准之上，建立的《甘肃金域伦理评估管理程序》文件。管理程序中定义伦理审查和伦理评估的内容，这两项工作由伦理委员会在伦理原则的基础上，依据伦理评估流程发挥职能进行评估。正文中第一部分按照目前医学检验业务内容将审查范围分为：常规临床检验样本、科研检验样本、特殊检验项目的生物信息三部分中涉及的医学伦理问题进行分析；第二部分介绍甘肃金域医学检验所伦理委员会的审查体系建立；第三部分思考内部对于医学伦理学认识的匮乏和外界对于医学检验和医学伦理学关联认识的片面性。对医学检验实验室伦理委员会建设的重要性和必要性，伦理委员会的工作建设内容，伦理委员会制度的颁布和落实，结合内部、外部对于医学检验中涉及医学伦理学的认识等方面，思考独立医学实验室的医学伦理审查情况。

PU-2672

综述 CTRP9 在动脉粥样硬化性疾病中的作用

赵海燕、关秀茹、王超
哈尔滨医科大学附属第一医院

补体 C1q 肿瘤坏死因子相关蛋白 9(C1q/TNF－related protein9，CTRP9)，是 CTRP 超家族成员之一，主要由脂肪组织分泌，是与脂联素高度同源的脂肪因子[1]。大量研究表明，CTRP9 具有稳定动脉粥样硬化斑块和保护心脏的作用[2]， 而且 CTRP9 表达水平的降低已被证明可作为冠心病的独立危险因素[3]。由此可见 CTRP9 或可在未来缓解冠状动脉粥样硬化性疾病中发挥巨大潜力。本文就近几年对 CTRP9 及其与心脑血管疾病之间关系的研究做一归纳综述，以用作后期研究的背景支持。

PU-2673

急性脑梗死早期白细胞计数与中性粒细胞计数检测的临床意义

刘瑜佳
西安医学院第一附属医院

目的 探讨在 acute cerebral infarction)患者早期血常规白细胞计数与中性粒细胞检测的临床意义。
方法 回顾性收集西安交通大学第一附属医院 2017 年 1～12 月 129 例急性脑梗死患者的一般资料及入院 24 小时内血常规检查结果以及同期在该院体检的 105 例健康体检者血常规检查结果。收集并整理性别、年龄、白细胞、淋巴细胞、单核细胞、中性粒细胞以及中性粒细胞与淋巴细胞比值等数据。所得数据采用统计学软件 SPSS17.0 进行分析。
结果 急性脑梗死组 WBC、L、M、N、NLR 均不同程度高于健康对照组，差异有统计学意义（P<0.05)；急性脑梗死组性别间比较，无统计学差异（P>0.05）；急性脑梗死组按不同年龄段分

组比较，N、NLR 随年龄增长而增高，差异具有统计学意义（P<0.05），WBC、L、M 的变化无统计学差异（P>0.05)。
结论 急性脑梗死患者血常规检测中 WBC、L、M、N、NLR 在早期均有不同程度的升高，且随着年龄的增长，N 和 NLR 的变化也愈加明显，可预估急性脑梗死发病，为诊断提供参考依据。

PU-2674

六西格玛质量管理在全血细胞分析室内质量控制中的应用

刘慧敏、刘春燕、张艳、葛若卿、陈硕、刘爽、邓朝晖
新疆生产建设兵团医院

目的 采用六西格玛(6σ)理论对迈瑞 BC-6800 全自动血细胞分析系统检测项目进行性能评价，选择合适的质控方案，指导质量改进。
方法 收集 2017 年度本院全血细胞计数 8 个检测项目(WBC、RBC、Hb、Hct、PLT、MCV、MCH、MCHC)的室内质量控制及室间质量评价数据。依据中华人民共和国卫生行业标准 W S/T 406-2012 制定的允许总误差(TEa)标准，计算各项目的 σ 值、绘制标准化 6σ 方法性能决定图、计算项目的质量目标指数(QGI)，评价项目检验性能及设计质量控制方案，并采用质量改进措施后的质控方案回顾性分析 2017 年室内质控数据。
结果 8 个检测项目中，3 个(HCT、MCHC 和 MCV)项目的 σ 值>6σ，3 个(MCH、RBC 和 HB)项目的 σ 值在 5σ～6σ，1 个(WBC)项目的 σ 值在 4σ～5σ。1 个(PLT)项目的 σ 值在<4σ。σ 值<6σ 的 5 个项目中，WBC、RBC 和 HB 项目需要优先改进精密度，PLT 和 MCH 项目需要优先改进准确度。WBC 和 MCH 需采用 13.5s(N=3，R=2)质量控制规则；HCT、MCHC 和 MCV 需采用 15s(N=3，R=2)质量控制规则；RBC 和 HB 需采用 14s(N=3，R=2)质量控制规则；PLT 需采用 13s 和(2 of 3)2s(N=3，R=2)质量控制规则。回顾性分析 2017 年室内质控数据，失控率由 0.56%降至 0.04%，警告率由 0.70%降至 0%。
结论 6σ 质量管理方法可以有效地应用于血细胞分析仪的质量管理，降低假失控率，并指导实验室质量的持续改进。

PU-2675

Predominant Frequency of HLA-B*2704 in patients with Ankylosing Spondylitis in Southeastern China

Jiaojiao Lu、Jing Yang、Wenxu Dong、Baojia Tang、Luoyuan Cao、Xianguo Fu
Ningde Hospital Affiliated to Ningde Normal University

Objectives This study was to investigate the polymorphism and distribution of alleles of HLA-B*27 in patients with ankylosing spondylitis in Han population of southeastern China.
Methods A total of 89 peripheral blood samples from southeastern Chinese Han patients with AS that diagnosed according to Modified New York criteria were subtyped using the high-resolution PCR-SSP.Exon 2-3 of HLA-B*27 gene was amplified and sequenced to further confirm the HLA-B*27 subtype.
Results The frequency of HLA-B*27 was 99.87% in AS patients.Three subtypes, B*2704, B*2705 and B*2706,were identified.The frequencies for these three alleles were B*2704 in 84/88(95.46%),HLA-B*2705 in 3/88(3.41%) and HLA-B*2706 in 1/88 (1.13%) of the B*27 positive patients,respectively.
Conclusions Our study shows that B*2704 has an overwhelming frequency in southeastern Chinese Han AS patients.A combined analysis including previous studies of B*27-subtype distributions in Chinese Han populations showed that HLA-B*2704 and B*2705 were the predominant subtypes in Chinese Han AS patients.The frequency of HLA-B*2704 subtypes are

increasing from north to south,while B*2705 has a decreasing North-South gradient.The results show that B*2704 may originate from the southern Han and then migrate and spread to the northern areas,and B*2705 show the opposite result. One AS patient was identified as the B*2706 subtype which was previously widely recognized as a protective subtype.It suggests that other than genetic background,many pathogenic factors could be associated with AS.

PU-2676

检验 TAT 调查分析与改进措施

山德生、柏魏、徐文波、赵冠程
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 通过对检验 TAT 的调查分析，了解影响 TAT 的关键因素，制定整改措施并实施改进，力求满足评审要求，满足临床诊疗需求。
方法 建立检验 TAT 监控表，嵌入 LIS 系统，调试成功后，调阅 2020 年 7 月监控表单删除无效数据后对采样与实验室验收时间、验收与检测时间、检测与报告时间及报告与临床打印时间等进行时间分析，进行分析。
结果 2020 年 7 月检测样本 120461 份，全部采样－报告时间 11 小时 01 分。
结论 TAT 未达到要求。

PU-2677

Forskolin Enhances Antitumor Effect of Oncolytic Measles Virus by Promoting Rab27a Dependent Vesicular Transport System

Mao Xia
Drum Tower Hospital, Medical School of Nanjing University

Measles vaccine strain viruses (MV-Edm) are an ideal platform for developing safe and effective oncolytic vectors. However, despite promising pre-clinical data, understanding of determinants of efficacy and, thus, the interplay between oncolytic virus and particular agents remain limited. We investigated the potency of Forskolin enhancing the antitumor effect of oncolytic measles virus by promoting Rab27a dependent vesicular transport system. Cells were infected with MV-Edm and the vesicles were observed by TEM. The oncolytic effects of MV-Edm/Forskolin were investigated in vitro. Herein we demonstrated that the MV-Edm infection and spread in tumor, which are indispensable processes for the viral oncolysis, depending on vesicular transport system of tumor cells. On the contrary, the tumor cells displayed a responsive mechanism to restrain the MV-Edm spread by down-regulating the expression of Rab27a, which is a key member of the vesicle transport system. Over-expression of Rab27a promoted the oncolytic efficacy of MV-Edm towards A549 tumor cells. Finally, we found a Rab27a agonist Forskolin that is capable of promoting the oncolytic effect of MV-Edm in vitro. Our study revealed the important role of vesicle transporter Rab27a in the whole MV-Edm mediated oncolysis pathway. We also provide a combined strategy for Forskolin and MV-Edm that may exert a synergistic anti-tumor effect for clinical treatment of patients with tumors.

PU-2678

XN-9000 全自动血细胞分析流水线室内质控品使用体会

朱江贤、沈华仙、张兴锋、杨美兰
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

由日本 sysmex 公司生产的 XN-9000 全自动血细胞分析流水线是目前最先进的血细胞分析仪器之一。该流水线采用流式细胞荧光染色激光技术和电阻抗原理对血液中的细胞进行检测分析，它具有自动化程度高、支持双向通讯、结果准确、精密度好、操作简单、检测速度快、可大批量进样、检测参数全、可根据复检规则自动进行复检和推片染色读片等优势。在日常工作中，为了监测 XN-9000 流水线工作状态是否正常，每天开机后需要用质控品做室内质量控制，室内质控在控说明仪器工作状态正常，才可以开始检测患者样本。我们采用 XN-9000 流水线配套的质控品 XN-check Level 1、Level 2、Level 3 三个水平做室内质控，在长期做室内质量控制的过程中，我们发现要用质控品做好室内质量控制应注意一些细节问题。

PU-2679

Vitros4600 干化学分析仪的维护保养及常见故障处理

张兴锋
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

Vitros4600 干化学分析仪在各大医院中被广泛应用，但是如何进行维护保养及常见故障的处理，是许多仪器操作人员最为关心的问题。实施有效保养、排除常见故障，是保证仪器正常运行的重要条件。文中笔者根据仪器特性，进行维护保养；分析故障原因，采取不同的处理方法并总结工作经验。有效的保养和故障处理措施是延长仪器使用寿命和正常使用的重要保证。

PU-2680

带状疱疹神经痛合并晚期胰腺癌癌痛一例临床分析

陈剑、张大莲、周利、徐文波、毛星星、朱莹、冯磊
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

带状疱疹(herpes zoster, HZ)是由水痘-带状疱疹病毒引起的一种急性感染性皮肤病，带状疱疹病毒具有亲神经性，受侵犯的神经和皮肤产生强烈的炎症，并伴有剧烈的疼痛，年龄越大，神经疼痛越剧烈。而胰腺癌是一种预后极差的恶性肿瘤，近年来该病在我国的发病率呈不断上升的趋势。胰腺癌疼痛是导致胰腺癌患者生活质量降低和影响寿命的主要原因之一，超过 50%的患者伴有疼痛。晚期患者的疼痛 VAS 评分甚至可以达到 10 分。回顾分析一例带状疱疹的剧烈疼痛与晚期胰腺癌疼痛混合难以区分。

PU-2681

Increased endogenous PKG I activity attenuates EGF-induced proliferation and migration of epithelial ovarian cancer via the MAPK/ERK pathway

Ying Li[1]、ting lan[2]、ping ma[1]、yue wang[2]、lan luo[2]
1. Affiliated Hospital of Xuzhou Medical University
2. 徐州医科大学

Rationale The overexpression of epidermal growth factor receptor (EGFR) is linked to poor epithelial ovarian cancer (EOC) outcomes. The type I cGMP-dependent protein kinase (PKG I) is recognized as a tumor suppressor, but its role in EGFR regulated EOC progression remains unclear.
Methods We first assessed the expressions of EGFR and PKG I in EOC tissues and cell lines (SKOV3 and A2780). We then evaluated the in vivo and in vitro effects of activated PKG I in EGF-induced EOC cell proliferation, migration, and invasion. And the underlying mechanisms were elucidated using molecular and biochemical Methods
Results The expressions of EGFR and PKG I were elevated, but the activated PKG I was decreased in EOC tissues and cells. The supplement of 8-Br-cGMP, a specific PKG I activator, attenuated the EGF-induced EOC cell proliferation, migration, and invasion in vitro. Such effects were abolished by Rp-8-Br-cGMPS (antagonist of 8-Br-cGMP). In an EOC xenograft nude mouse model, activated PKG I also attenuated EOC progression in vivo. Activated PKG I interacted with EGFR, leading its threonine 693 site phosphorylation, and decreased tyrosine phosphorylation of EGFR, resulting in disrupted EGFR-SOS1-Grb2 combination. Subsequently, the downstream signal pathway proteins, including the cytoplasmic phosphorylation of c-Raf, MEK1/2, and ERK1/2 were declined, impeding the phosphorylated ERK1/2's nucleus translocation. Also, the reduction of phosphorylated tyrosine EGFR and ERK1/2 induced by the activated PKG I were also abolished by its inhibitor Rp-8-Br-cGMPS.
Conclusions Our results suggest that the activation of PKG I attenuates EGF-induced EOC progression, and the 8-Br-cGMP-PKG I-EGFR/MEK/ERK axis is a potential target for EOC therapy.

PU-2682

PDCD4 Deficiency Aggravated Colitis and Colitis-associated Colorectal Cancer Via Promoting IL-6/STAT3 Pathway in Mice.

Liyang Wang
Qilu Hospital of Shandong University

OBJECTIVE Although programmed cell death (PDCD) 4 is generally considered to be a tumor suppressor, the consequence of Pdcd4 deficiency in tumorigenesis is not well established. The role of PDCD4 in colitis-associated colorectal carcinoma (CRC) remains unknown.
METHODS Experimental colitis and CRC were induced by dextran sodium sulfate and dextran sodium sulfate with azoxymethane, respectively, in wild type and Pdcd4 knockout (Pdcd4-/-) mice and were evaluated by clinical examination and histopathology. Levels of cytokines were detected by enzyme-linked immunosorbent assay. Changes in signaling pathways were examined by Western blot and immunofluorescent staining. Cell proliferation was determined by BrdU incorporation and Cell Counting Kit-8 staining.
RESULTS Pdcd4 deficiency not only aggravated the dextran sodium sulfate-induced acute colitis but also promoted the development of colitis-induced CRC. Mechanically, Pdcd4 deficiency

accelerated epithelial cell proliferation during tumorigenesis, markedly up-regulated the expression of proinflammatory cytokines, such as interleukin (IL)-6, and enhanced the activation of signal transducer and activator of transcription (STAT3), a IL-6 downstream effector. Using purified cells, we found that Pdcd4 deficiency increased IL-6 expression in vitro and the susceptibility to IL-6/STAT3 pathway-mediated cell proliferation significantly. Furthermore, blockade of IL-6/STAT3 pathway through sgp130Fc reversed the promoting effect of Pdcd4 deficiency on colonic epithelial cell proliferation in vivo.
CONCLUSION The Pdcd4 deficiency accelerates colitis and colitis-associated CRC presumably through up-regulating IL-6/STAT3 pathway, suggesting that PDCD4 plays a protective role in inflammation-associated carcinoma and might be a potential target for the treatment of CRC.

PU-2683

LC-MS/MS 方法研究白术茯苓汤中多种有效成分在大鼠体内的药动学

季彬
中国医科大学附属第一医院

目的 白术茯苓汤由白术，茯苓两位中药组成，在临床上主要用于心脑血管疾病的治疗。虽然白术茯苓汤在临床上已经应用多年，但是其药效物质基础尚不明确，复方中药中多成分药代动力学可通过揭示中药成分能否被机体有效利用来帮助发现可成为药效物质基础的中药成分。为此，本研究开展了同时测定白术茯苓汤中白术内酯 I，白术内酯 II，白术内酯 III，土莫酸，去氢土莫酸，猪苓酸 C 的 UPLC-MS/MS 方法。
方法 以五味子醇甲为内标，血浆样品采用乙酸乙酯进行液-液萃取处理制备。使用 C18（2.1mm×100mm，1.9μm）柱进行梯度洗脱，进行反相色谱，用于血浆样品分离。在 MRM 模式中使用正离子测定分析物和内标。 日间和日间精度和准确度的结果均在可接受的范围内。 矩阵效应很小。该方法中所有分析物的回收率为 80.7％至 96.7％。 稳定性测定表明，所有分析物在所有加工和储存条件下都是稳定的。该方法成功应用于研究白术茯苓汤口服后多种化合物在大鼠血浆中的药代动力学。

PU-2684

Changes of blood pressure in patients with acute ischemic stroke

Liping Jing、xuewei zhuang
Shandong Provincial Third Hospital

Objective To study the blood pressure of ischemic stroke patients during 72 h of admission, and to explore the influencing factors, so as to provide clinical evidences for the management of blood pressure during the acute phase of stroke and to guide the treatment and prognosis prediction of the disease.
Methods The blood pressure of the ischemic stroke patients was measured at admission and was monitored for 72 h following admission, and the influencing factors were studied. The correlations of the neurological deficits and the level of consciousness with the blood pressure were observed.
Results (1) About 86.2% of ischemic stroke patients had hypertension in the acute phase.
(2) The history of hypertension, age, high-salt diet, level of consciousness, and severity of neurological deficits were important influencing factors for elevated blood pressure in stroke patients ($P<0.05$).

(3) The blood pressure of most acute ischemic stroke patients decreased spontaneously to a stable level within 72 h of admission (not given antihypertensive drug treatment). The systolic blood pressure (SBP) decreased rapidly during the first 12 h of admission, while diastolic blood pressure (DBP) decreased rapidly within 24 h of admission, suggesting that the blood pressure mostly fluctuates within 12 h after the onset of the disease (P<0.05).
(4) In TOAST classification, the incidence of large-artery atherosclerosis was the highest, followed by stroke of undetermined etiology and stroke of other determined etiology.
Conclusion The blood pressure spontaneously decreased with time. Age, the history of hypertension, the level of consciousness, the severity of neurological deficits, and high-salt diet were important influencing factors for elevated blood pressure in ischemic stroke patients.

PU-2685

rhEGF 对受损的人子宫内膜间质细胞的修复作用

杨菁、金文芳、陈良玉、曹罗元、林婷婷、富显果、陈惠华
宁德师范学院附属宁德市医院

目的 研究 rhEGF 对受损的人子宫内膜间质细胞（ESCs）的作用，为子宫内膜损伤的临床治疗提供新思路。

方法 选择手术切除的子宫内膜，用 1%Ⅰ型胶原酶消化过滤后，分离纯化 ESCs，用免疫荧光法鉴定细胞。采用不同浓度米非司酮损伤 ESCs，以正常细胞为对照组；设置不同损伤时间，用 MTS 法检测细胞活性，确定最佳的损伤浓度和时间。用不同浓度的 rhEGF 与受损的 ESCs 共培养 24h，检测细胞活性，明确 rhEGF 对受损的 ESCs 是否有修复作用。通过划痕实验，观察 24h 细胞迁移情况，计算愈合比，验证 rhEGF 对受损的 ESCs 迁移能力的影响。

结果 ESCs 分离 24h 即可贴壁，刚开始呈三角形，单个分布，随后生长成为呈现有成纤维细胞形态的梭形细胞，通过鉴定间质细胞的纯度可达 95% 以上。米非司酮对 ESCs 的损伤呈时间-剂量效应，作用时间超过 48h ，ESCs 活性急剧下降（P<0.05），选择 48h 作为最适损伤时间。米非司酮浓度超过 60μmol/L 时，ESCs 活性显著下降（P<0.05），选择 60μmol/L 作为损伤最适浓度。rhEGF 与受损的 ESCs 共培养 24h，高剂量 rhEGF 能够显著提高损伤 ESCs 活性（P<0.05）。划痕实验中，细胞迁移速度随 rhEGF 剂量增大而提高，100 ng/mL rhEGF 以上的剂量组愈合比具有统计学意义（P<0.05）。

结论 rhEGF 与米非司酮损伤的 ESCs 共培养后，细胞活性和迁移能力能够显著提高，rhEGF 对其具有明显的修复作用。

PU-2686

Pdcd4 对巨噬细胞自噬及其相关动脉粥样硬化的影响

王璨旸
山东大学齐鲁医院

目的 巨噬细胞泡沫化对于动脉粥样硬化的发生发展具有重要的作用。脂自噬是自噬的一种重要形式，能够将细胞内的脂质通过自噬降解，从而调节动脉粥样硬化。前期研究证实抑癌基因 Pdcd4 对于自噬和动脉粥样硬化均有一定的调节作用，本研究旨在研究 Pdcd4 在巨噬细胞脂自噬及其相关动脉粥样硬化中的作用。

方法 使用氧化低密度脂蛋白刺激野生型小鼠及 Pdcd4-/-小鼠腹腔巨噬细胞，通过 Western-blot、免疫荧光染色、油红“O”染色等多种方式检测巨噬细胞自噬及泡沫化程度，通过 Real-time PCR 检测脂质流出相关基因的表达。并利用高脂饮食在 Apoe-/-小鼠和 Apoe-/-Pdcd4-/-（DKO）小鼠中建立动脉粥样硬化模型，通过免疫荧光染色、免疫组化染色及油红“O”染色检测小鼠动脉粥样硬化斑

块局部自噬相关指标、免疫细胞浸润及动脉粥样硬化斑块面积。并通过骨髓移植模型确定免疫细胞在这一过程中的作用。

结果 小鼠巨噬细胞中 Pdcd4 基因的缺失能够明显促进自噬，并能够显著改善氧化低密度脂蛋白导致的自噬流受阻情况。Pdcd4 基因缺失能够显著促进脂质流出相关基因的表达。小鼠腹腔巨噬细胞中 Pdcd4 基因的缺失能够通过促进自噬从而显著抑制巨噬细胞泡沫化。同时，在小鼠动脉粥样硬化斑块局部，Pdcd4 基因缺失能够显著促进巨噬细胞自噬，减小动脉粥样硬化斑块的面积，减轻脂质堆积，降低免疫细胞浸润的程度。骨髓移植模型的结果进一步证实，Pdcd4 对脂自噬及动脉粥样硬化的调控作用是通过影响巨噬细胞的功能实现的。

结论 Pdcd4 基因的缺失能够通过促进巨噬细胞脂自噬加速胆固醇流出从而抑制动脉粥样硬化的发生发展。

PU-2687

无创呼吸机治疗阻塞性睡眠呼吸暂停低通气综合症疗效观察

陈剑、周利、张毅、冯磊
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨无创呼吸机用于治疗阻塞性睡眠呼吸暂停低通气综合症的临床应用价值。

方法 选取 2016-2020 年玉溪市人民医院收治的阻塞性睡眠呼吸暂停低通气综合症 102 例，按是否进行呼吸机无创通气治疗分为实验组（n=28）和对照组（n=74）。实验组持续长时间（超过 3 个月）坚持使用无创呼吸机通气治疗，对照组仅进行健康知识教育，多加强运动，减肥，积极防治并发症。比较二组患者 3 个月后的 PSG 结果、OSAHS 的病情分度和治疗有效率，观察无创呼吸机的治疗效果。

结果 实验组 PSG 较治疗前有明显改善（P<0.05），治疗后，对照组疾病分度改善 9 例，不变 65 例，实验组疾病分度改善 26 例，不变 2 例。实验组治疗有效率为 96.4%，远远高于对照组的 16.2%，差异有统计学意义（P<0.05）。

结论 无创呼吸机用于长期治疗阻塞性睡眠呼吸暂停低通气综合症疗效显著，非常值得临床推广运用。

PU-2688

第三方检验机构与医院合作存在问题的分析与对策

袁方方
西安金域医学检验所有限公司

目的 通过分析第三方检验机构各部门与医院合作中所出现的问题,加强机构与医院的合作，开展更多适合临床诊断的项目。

方法 利用我公司各部门近年来与医院沟通工作中发现的问题进行分析。

结果 通过与合作医院各部门的沟通，对现存在的问题进行整理。①物流部门收取标本及运送的及时性不够;②实验室某些项目检验报告的时效过长;③对特殊检验项目的报告解读不清楚。

结论 加强检验机构各部门与医院的沟通，提高各部门员工的知识技能水平及责任心，缩短项目的报告时间，安排专职人员对特殊项目的报告进行解读，有助于更好地达成公司与医院的双赢合作，切实帮助临床医生进行诊断，推广更多有助于临床治疗的项目，推动检验行业的发展。

PU-2689

JAK/STAT 信号通路在狼疮肾炎中的研究进展

林婷、林青
福建中医药大学附属人民医院

狼疮肾炎(LN)是系统性红斑狼疮(SLE)最常见和最严重的并发症，约 20%-60%的 SLE 患者可发展为 LN，约 10%-20%的 LN 患者在十年内死亡。Janus 激酶/信号转导和转录激活因子(JAK/STAT)信号通路参与多种细胞因子信号转导的过程，在调节免疫应答与炎症反应中发挥重要作用。近年研究显示 JAK/STAT 信号通路或与 LN 的发生发展有关。本文回顾 JAK/STAT 信号通路的结构与转导过程，阐述其在 LN 发生发展中的作用以及通过阻断 JAK/STAT 信号通路治疗 LN 的研究进展，以期对 LN 发病机制研究及治疗有所帮助。

PU-2690

ELISA 法检测试剂混用确认程序的建立

符俊超、方伟
广东省人民医院

目的 ISO15189 技术要求的 5.3.2.3 条款，明确指出在工作中 ELISA 法检测试剂混用的情况有无对检验质量的影响，建立的确认程序。
方法 根据不同项目（13 个）各留 60 例样本，分阴性 20 份，弱阳性 20 份，阳性 20 份。检测从第 1 天开始测不混用试剂，到第 3 天混用、第 5 天混用、第 7 天混用、第 10 天混用、第 14 天混用。分别和第 1 天不混用试剂做比较，对比分析结果。
结果 根据每个项目到第几天和第一天的符合率不是 100%而确定混用试剂的天数（有效期）。
结论 ELISA 法检测试剂混用要进行混用方法的确认才可以应用于临床样本的检测，避免试剂混用造成的质量变化对检验结果的影响。

PU-2691

肉桂酰雷公藤内酯醇通过抑制核因子 κB（NF-κB）通路下调小鼠肾小球系膜细胞 IP-10 表达并抑制其增殖

林婷
福建中医药大学附属人民医院

目的 探讨肉桂酰雷公藤内酯醇（T32）对 γ 干扰素诱导蛋白-10（IP-10）在小鼠肾小球系膜细胞（SV40MES13）表达及促增殖作用的影响，为 T32 应用于临床治疗狼疮肾炎奠定理论基础、提供实验依据。
方法 利用 CCK-8 法检测 T32 和 IP-10 对 SV40MES13 细胞生存率的影响，通过实时荧光定量 PCR 法及酶联免疫吸附试验（ELISA）检测 SV40MES13 细胞及培养上清液中 IP-10 mRNA 相对表达量和 IP-10 蛋白分泌量，应用蛋白质印迹法（Western blot）检测 SV40MES13 细胞 NF-κB 信号通路相关蛋白 NF-κBp65、IκBα 及其磷酸化蛋白 p-NF-κBp65、p-IκBα 的表达情况。
结果 （1） γ 干扰素（IFN-γ）刺激可促进 SV40MES13 细胞 IP-10 mRNA 和蛋白表达增加（P 均＜0.01），NF-κBp65、IκBα 蛋白的磷酸化水平与空白组相比明显增加（PNF-κBp65＜0.05、PIκBα＜0.01）。（2）NF-κB 信号通路经特异性抑制剂 PDTC 阻断后，SV40MES13 细胞 IP-10 mRNA 和蛋白表达与 IFN-γ 刺激组相比明显降低（P 均＜0.05），NF-κBp65、IκBα 蛋白磷酸化水平下降（PNF-κBp65＜0.05、PIκBα＜0.01)。（3）经不同浓度（2 ng/mL～20 ng/mL）T32 干预

后，SV40MES13 细胞 IP-10 mRNA 和蛋白表达与 IFN-γ 刺激组相比明显降低（P＜0.05 或 P＜0.01），NF-κBp65、IκBα 蛋白磷酸化水平分别下降 44.03%和 48.68%（P 均＜0.05）。（4）不同浓度（1 ng/mL~500 ng/mL）IP-10 与 SV40MES13 细胞共同孵育 24 h 后细胞生存率提高，IP-10 浓度为 10 ng/mL 时细胞生存率为 119.83%（P＜0.01），随后进入平台期；经 4 ng/mL～20 ng/mL T32 干预后，细胞生存率与 10 ng/mL IP-10 刺激组相比明显降低（P 均＜0.01）。
结论 肉桂酰雷公藤内酯醇不仅能通过阻断 NF-κB 信号通路下调 IFN-γ 诱导的 SV40MES13 细胞表达 IP-10，还能抑制 IP-10 促增殖作用。

PU-2692

Periostin contributes to adventitial remodeling of arteriosclerosis by activating adventitial fibroblasts

Tan Tan、Xiaomei Lei、Yingfen Wang、Wei Zhang、fen Li、Qiaotu Liu
CHENZHOU hospitol

Objective In order to study the effect of adventitial remodeling of arteriosclerosis by periostin.
Methods We examined the effect of periostin by Immunofluorescence cell staining and collagen gel contraction assay.
Results Our data indicated that periostin is highly expressed in adventitia of atherosclerotic arteries. And TGF-β1 induced the expression of periostin in fibroblasts of adventitia. While periostin can promote activation and enhance the contractility of adventitial fibroblasts. Periostin also induces adventitial fibroblasts to produce collagen I and TGF-β1 and activate FAK and Src phosphorylation. These results suggest that periostin contributes to adventitial remodeling of arteriosclerosis by activating adventitial fibroblasts.
Conclusion These results suggest that periostin contributes to adventitial remodeling of arteriosclerosis by activating adventitial fibroblasts.

PU-2693

耐碳青霉烯铜绿假单胞菌临床感染特征及危险因素研究

李从雅、童学东
重庆医科大学附属第三医院

目的 系统评估 2019-2020 重庆某三甲医院耐碳青霉烯铜绿假单胞菌(CRPA)的临床感染特点以及危险因素，为临床诊断、治疗、监测 CRPA 提供参考依据。
方法 回顾性分析 2019-2020 分离的 337 例铜绿假单胞菌感染患者病历资料及药敏结果，根据分离菌株对碳青霉烯类抗生素的药敏值，分为碳青霉烯耐药铜绿假单胞菌组（CRPA）和碳青霉烯敏感铜绿假单胞菌组（CSPA）。通过病例对照研究的方法分析 CRPA 的临床感染特点以及相关危险因素。
结果 本院 2019-2020 共分离铜绿假单胞菌 337 株，其中 CRPA 共计 51 株（15.1%）；CRPA 标本来源以呼吸道为主（56.9%），其次为分泌物（13.7%）和尿液（9.8%）；科室分布以神经疾病中心为主（21.6%），其次为重症监护室（17.6%）、呼吸疾病中心（17.6%）和肝胆胰外科（17.6%）；对阿米卡星耐药率最低（15.4%），其次为庆大霉素（21.6%）；CRPA 除对碳青霉烯类抗生素耐药，对临床其他类别抗生素的耐药率也显著高于 CSPA；多因素 logistic 回归分析表明转院、留置引流管、分离病原菌前使用碳青霉烯类药物是 CRPA 感染的主要危险因素。
结论 本研究表明定期分析院内 CRPA 的临床感染特征以及药敏情况可指导临床合理使用抗生素，同时针对病原菌感染发生的主要危险因素进行提前干预以有效控制感染散播。

PU-2694

新冠病毒核酸检测阳性质控品污染原因分析及解决办法

龚文娟、陈宝荣、孙慧颖、郑燕华
北京金域医学检验实验室有限公司

新冠核酸检测为新冠疫情的防控起到了重要作用。在新冠核酸检测过程中，实验室防污染是个备受重视的质量问题，是保证新冠核酸检测质量的重要因素。核酸扩增实验室的污染源有多种，其中因阳性质控品造成的污染是个不可忽视的问题。本文针对新冠病毒核酸检测过程中可能存在的质控品污染从污染途径、发生原因、去污染措施、效果监测等方面进行详细的分析和讨论，从质控品污染角度为相关实验室提供一些实验室防污染的措施及应对办法。

PU-2695

Samotolisib attenuates acute liver injury through inhibiting caspase-11-mediated pyroptosis via regulating E3 ubiquitin ligase Nedd4

Yangyang Zhao
成都医学院第一附属医院

Objective Acute liver injury (ALI) occurs at any stage of sepsis and is an independent risk factor for sepsis-induced death. Sepsis is characterised by life-threatening organ dysfunction caused by a dysregulated host response to infection. It is a common cause of death in intensive care units. Inflammation is the main feature of sepsis, and the liver, as a lymphatic organ, plays an important role in inflammation. Clinical and experimental data suggest that liver dysfunction is an early sign of sepsis, and early hepatic dysfunction in patients with sepsis is a specific and independent risk factor for poor outcomes. Attenuating liver injury and restoring the balance of pro- and anti-inflammatory responses in the liver will lower sepsis morbidity and mortality rates by regulating systemic immune responses and protecting organs from injury . However, there is no specific therapy for sepsis-induced liver injury. Recent studies have shown that cytosolic Lipopolysaccharide (LPS)-mediated pyroptosis is the main driver of endotoxic shock. LPS promotes caspase-4/5/11 activation, leading to pyroptosis, a major sepsis driver. Caspases-11/4/5 play an essential role in defending against intracellular bacterial infection upstream of the canonical NLRP3 inflammasome. However, currently, few known drugs can control caspase-11 activation. Inhibition of caspase-11 may be a new way to prevent sepsis caused by gram-negative bacteria. This study aimed to identify novel drugs that can control hepatocyte caspase-4/5/11 activation during sepsis.
Method In vitro experiments were performed using LPS-induced caspase-11 activation and pyroptosis in RAW 264.7 cells lacking ASC expression, and the model of ALI was established using LPS-treated mice. In the current study, we screened 441 small molecule compounds with known targets in RAW264.7 cells. Six compounds with inhibitory effects were identified following the primary and secondary screenings, of which ST had the best effect on py-roptosis suppression. Subsequently, in vivo experiments confirmed that ST showed significant liver protection against LPS-induced acute liver damage. We employed lactic acid dehydrogenase (LDH) release and CCK-8 assay, Flow cytometry, quantitative reverse transcriptase-polymerase chain reaction (qRT-PCR), western blotting, immunofluorescence(IF) and immunohistochemical(IHC) staining, Glycogen Periodic Acid Schiff (PAS) and Hematoxylin and Eosin (H&E) Staining to evaluate the effect of Samotolisib (ST).
Result In the current study We identified ST, a promising new dual inhibitor of phosphoinositide 3-kinase (PI3K) and mammalian target of rapamycin (mTOR), screened a library of 441 Pyroptosis Compounds with known targets.ST dose-dependently inhibited Caspase-11 activation

and generation of N-terminal fragment of gasdermin D (GSDMD-NT) leading to reduced pyroptosis in RAW 264.7 cells. In the LPS-induced acute liver injury mouse model showed that ST preconditioning improved survival ,attenuated LPS-induced the serum ALT and AST activity, inhibit the incidences of severe liver inflammation. Additionally, the liver histological evaluation revealed that ST protects against LPS-induced liver damage. Importantly, our data show that ST treatment could activate the E3 ubiquitin ligase Nedd4 in liver. Nedd4 directly interacts with caspase-11 and mediates ubiquitination and subsequent degradation of caspase-11, and its inhibitory action on caspase-11 activation was largely abrogated by PI3K activator IGF-1. We demonstrated that ST ameliorated LPS-induced hepatotoxicity by inhibiting pyroptosis the Caspase-11/ GSDMD-NT signaling pathway via regulating the PI3K/AKT/mTOR/Nedd4 signaling pathway.
Conclusion The above results demonstrate that ST may play a key role in prevention of liver injury in sepsis patients.

PU-2696

黄绿青霉素对神经细胞 PC-12 损伤作用的研究

杨菁、曹罗元、董文婿、富显果
宁德师范学院附属宁德市医院

目的 研究黄绿青霉素（Citreoviridin，CIT）诱导神经细胞 PC-12 的损伤作用。
方法 CIT 处理组分为三组，终浓度分别为 2.5 μmol/L、5 μmol/L、10 μmol/L，设 DMSO 为空白对照组。药物处理细胞 24 h 后，观察细胞形态的变化，CCK-8 法测细胞活性，流式细胞仪测 ROS 荧光值；取细胞培养液测 LDH 释放率、NO 含量及 MDA；细胞裂解液检测 GSH 含量及 SOD 活力。
结果 PC-12 与 CIT 共培养后，细胞成团，出现空斑。与对照组比较，CIT 组的细胞活力显著降低（$P<0.01$），LDH 释放率显著升高（$P<0.01$）；NO 含量明显下降（$P<0.05$），呈剂量效应关系；氧化应激相关指标 MDA 含量显著升高（$P<0.01$）；ROS 含量在低、中、高剂量组中均显著升高（$P<0.01$，$P<0.05$）；GSH 含量呈下降趋势，10 μmol/L 组效果显著（$P<0.05$）；SOD 活力显著升高（$P<0.01$）。
结论 黄绿青霉素对神经细胞 PC-12 有明显的损伤作用，可能与氧化应激机制有关。

PU-2697

第三方实验室安全指标考核的建立

冯媛媛、吴晓玲
西安金域医学检验所

目的 建立一套适合实验室个人安全考核指标体系
方法 安全考核是安全管理的表现形式，主要为安全理论考核，场景模拟考核，以及日常操作中观察个人的安全意识。 考核培训方法 A-阅读相关文件；B-由合格人员进行示范或演示；C-在合格的带教人员监督下执行操作；D-其他：包括自学、讨论、上课等。
培训效果评估： 优秀(90 分-100 分)；满意(80 分-89 分)；基本合格(60 分-79 分)；不合格(60 分以下)。
评估方法 A-设备操作；B-安全知识考核；C-日常观察；D-评估解决问题的能力，对口头提出的相关的问题的反应； E-回顾关键要素的记录。
结果 安全考核作为实验室管理的有效方法，对于提高实验室整体水平，提升实验室人员安全意识具有重要意义。
结论 通过对员工安全各项指标的考评，提升了员工的安全意识，特别是新入职员工，预防和减少安全事故的发生，从而为实验室人员的安全提供保障。

PU-2698

外周血中性粒细胞与淋巴细胞比值结合 C-反应蛋白在不同程度急性胰腺炎诊断中的应用价值

刘偲媛
荣县人民医院

目的 急性胰腺炎（AP）是一种临床常见的急腹症，致死率极高。而外周血中性粒细胞和淋巴细胞数值是反应系统性炎症反应的定量指标之一。本文拟探讨血常规中性粒细胞/淋巴细胞比值（NLR）及 C-反应蛋白（CRP）在不同程度急性胰腺炎中的情况，评估二者与病情严重程度的相关性。
方法 选取 2020 年 6 月-2021 年 3 月间本院收治的 100 例急性胰腺炎患者作为研究对象,设置为实验组。同时选取同期本院健康体检者 50 例作为对照组。其中将实验组分为重度急性胰腺炎（SAP）65 例（SAP 组），轻度急性胰腺炎（MAP）35 例（MAP 组），收集所有研究对象入院 24h 内 NLR 和 CRP 的数值，并通过绘制受试者工作特征曲线（ROC），评估各指标和胰腺炎病情严重的相关性。
结果 实验组 NLR、CRP 明显高于对照组（P<0.05），SAP 组与 MAP 组比较，NLR，CRP 更高，差异具有统计学意义（P<0.05）。通过绘制 ROC 曲线可知，NLR、CRP 对 SAP 和 MAP 鉴别的曲线下面积（AUC）分别为 0.689、0.603，此两项联合鉴别诊断的 AUC 为 0.723。
结论 急性胰腺炎患者发病时 NLR、CRP 会明显升高，同时与病情严重程度相关，均是帮助诊断 AP 的理想实验指标。而二者联合检测在预测 AP 方面诊断价值更高。同时 NLR 和 CRP 均随急性胰腺炎患者病情严重程度的升高而上升，能较好预测 SAP。

PU-2699

不同标本处理时间和标本放置时间对特异性神经元烯醇化酶测定结果的影响

高琦、张凤、于淼、丁洁
山东第一医科大学附属省立医院

目的 探讨不同标本处理时间和标本放置时间对特异性神经元烯醇化酶测定结果的影响。
方法 征集健康志愿者 30 人，空腹，用 BD SST 惰性分离胶促凝真空采血管采集静脉血样本 3ml，室温分别放置 15min，30min，1h 和 2h 后离心，离心后用罗氏 cobas 8000 e801 电化学发光免疫法对特异性神经元烯醇化酶进行测定，结果显示标本于室温放置 15min 检测结果与放置 1h 的检测结果差异显著（15min V.S. 1h: 10.65 ± 0.31 v.s. 12.12 ± 0.38，P<0.005），放置 2h 后进行离心的检测结果较放置 15min 后进行离心的结果明显升高（15min V.S. 2h: 10.65 ± 0.31 v.s. 14.29 ± 0.69，P<0.001）。室温放置 15min 后检测结果与放置 30min 后的检测结果无明显差异。故我们选择室温放置 30min 后进行离心的标本，分别于离心后立即、放置 1h、2h、4h 进行 NSE 检测，结果发现离心后的标本于室温放置不同时间，检测结果无明显的差异。
结论 标本不同处理时间对 NSE 检测结果有明显的影响，这就要求我们采集标本凝固后尽早离心分析血清，进行测定，分离血清对 NSE 检测结果影响不大，这对指导临床标本采集送检规范性及提高检测结果的准确性有非常重要的临床意义。

PU-2700

Tspan5 通过促进肝癌转移影响患者预后

谢谦
广东省人民医院（广东省医学科学院）

目的 1.阐述 Tspan5 的表达与肝癌病理分型、患者预后的关系。
2.明确 Tspan5 与肝癌细胞转移的关系。
方法 1.利用肝癌临床芯片样本和生物信息学数据库，分析 Tspan5 在肝癌组织和癌旁正常组织中的表达情况，以及 Tspan5 表达和肝癌患者临床病理特征、预后的关系。
2.用慢病毒感染肝癌细胞，构建高表达和干扰 Tspan5 的重组肝癌细胞株，并用 qRT-PCR 和 Western Blotting 进行鉴定。
3.用划痕实验和 Transwell 实验检测 Tspan5 在体外对肝癌细胞迁移的影响；用裸鼠尾静脉转移模型检测 Tspan5 在体内对肝癌细胞转移的影响。
结果 1.利用肝癌临床芯片样本和生物信息学数据库，发现 Tspan5 在肝癌组织和癌旁正常组织中的表达有差异，并且 Tspan5 的表达随肝癌患者病程进展而升高，与患者预后负相关。
2.慢病毒感染肝癌细胞后，用 qRT-PCR 和 Western Blotting 进行鉴定，显示高表达和干扰 Tspan5 的重组细胞株构建成功。
3.划痕实验和 Transwell 实验结果显示 Tspan5 在体外可提高肝癌细胞的迁移能力；裸鼠尾静脉转移模型结果显示 Tspan5 在体内可促进肝癌细胞的转移过程。
结论 综上所述，我们研究发现 Tspan5 在肝癌组织和癌旁正常组织中的表达有差异，并且 Tspan5 表达随肝癌患者病程进展而升高，与其预后负相关。Tspan5 在体外可提高肝癌细胞的迁移能力；在体内可促进肝癌细胞的转移过程。因此，我们初步认为，Tspan5 可以通过影响肝癌细胞的转移过程，从而进一步影响肝癌患者的进展和预后。

PU-2701

不同程度的溶血标本对叶酸项目的影响

白凯嘉
黑龙江金域医学检验实验室有限公司

目的 叶酸（Folic Acid）也称为维生素 B9，是一种水溶性维生素，属于维生素 B。叶酸是人体在利用糖分和氨基酸时的必要物质，是机体细胞生长和繁殖所必需的物质，与维生素 B12 共同促进红细胞的生成和成熟，是制造红血球不可缺少的物质。叶酸也作为干酪乳杆菌（Lactobacillus casei）及其它微生物的促进增殖因子而起作用。叶酸是胎儿生长发育不可缺少的营养素。孕妇缺乏叶酸有可能导致胎儿出生时出现低体重、唇腭裂、心脏缺陷等，叶酸可用于治疗由叶酸缺乏症引起的贫血，也是孕妇的营养补充品。在新生儿的神经管缺损病例中，有超过一半认为是因为怀孕初期叶酸不足所造成。有超过 50 个国家利用加入叶酸的营养强化食品来减少神经管缺损的比例。所以叶酸的检测结果在临床应用中就显得异常重要，本文旨在探讨溶血标本不同时间对化学发光微粒子免疫检测法测定叶酸结果的影响。
方法 采集同一志愿者肘正中静脉血用普通采血管分离血清后使用雅培 i2000SR 化学发光法测定叶酸指标分别以离心后立即检测，12:00，16:00,20：00,00:00 分别检测叶酸的含量，并对结果进行比较和分析。
结果 对于叶酸检测的分析前，分析中的质量对结果有一定程度的影响，溶血标本随着时间推移对化学发光微粒子免疫检测法测定叶酸结果有干扰。
结论 随着时间的推移，叶酸测定结果有不同程度升高。溶血标本随着时间推移与叶酸结果呈正相关。一个合格的标本可提高实验结果精准性和对于临床叶酸的监测也起着至关重要的作用。

PU-2702

双氢青蒿素作为肿瘤治疗增敏剂的研究进展

李青容
川北医学院

目的 恶性肿瘤是威胁人类健康的主要疾病之一。尽管几十年来人类一直在与癌症作斗争，但目前治疗大多数肿瘤的疗效仍不理想。双氢青蒿素（Dihydroartemisinin，DHA）是我国自主研发的抗疟疾一线药物青蒿素的衍生物，同时还具有显著的抗癌活性，但其对正常细胞无明显毒性。本文通过对双氢青蒿素增敏抗癌药物及分子机制进行系统深入的研究，为双氢青蒿素作为抗癌增敏剂应用于临床提供依据。
方法 以双氢青蒿素（DHA）作为研究对象，通过查阅 2000-2020 年间发表的 77 篇关于双氢青蒿素抗肿瘤治疗的文献，系统的分析了 DHA 抗肿瘤治疗的机制及作为抗癌药物的增敏剂的具体作用及分子机制，为 DHA 作为抗癌增敏剂应用于临床提供指导依据。
结果 1、DHA 可通过诱导细胞周期、细胞凋亡、抑制肿瘤血管的生成、抑制肿瘤侵袭转移、与其他抗肿瘤药物联合杀伤肿瘤细胞。
2、DHA 抗肿瘤和抗疟疾的主要作用机制是通过分子内部“过氧化桥”与细胞内亚铁离子相互作用后产生过量的 ROS，从而产生细胞毒作用。
3、DHA 可增强肿瘤放化疗及分子靶向治疗疗效。在化疗药物方面，DHA 和吉西他滨(gemcitabine, GEM)联合应用时，细胞凋亡率较二者单独应用时明显增加；且在卵巢癌异种移植瘤模型中，DHA 与 GEM 联合治疗组中，肿瘤在第 14 天时完全消失。DHA 联合吉非替尼以时间依赖的方式显著抑制肺腺癌细胞 A549 的增殖和迁移，并阻滞细胞周期于 G0/G1 期。此外，DHA 联合放疗可显著降低人肺癌细胞 S 期细胞比例，增加 G0/G1 期细胞比例，并诱导细胞凋亡增加；同时，DHA 对肺癌 GLC-82 移植瘤裸鼠具有较高的抑瘤作用和放射增敏作用。
结论 双氢青蒿素可具有抗肿瘤作用，且可作为抗肿瘤治疗的增敏剂。

PU-2703

HIV 自检试剂发放促进 MSM 安全性行为的逐步阶梯随机对照研究

楚振兴[1]、陆天意[2]、徐俊杰[1]
1. 中国医科大学附属第一医院
2. 浙江大学医学院附属邵逸夫医院

背景 COVID-19 流行让男男性接触者(MSM)参加基于场所的艾滋病自愿咨询检测(VCT)受阻，线上的 VCT 模式与线下 VCT 相比，具有更好的定位高危性行为 MSM 和促进 HIV 检测的能力，然而线上 VCT 对 MSM 性行为影响缺乏评估。
目的 明确线上咨询与 HIV 自检试剂发放干预对 HIV 阴性 MSM 的安全性行为影响作用。
方法 2018 年 8 月至 2019 年 12 月，通过微信公众号在全国招募 MSM 参与逐步阶梯随机对照(Randomized Controlled Trial,RCT)研究，入组标准为≥18 周岁且近六个月与男性发生过肛交或口交的 HIV 阴性 MSM。工作人员将合格的调查对象随机分配到(A，B，C，D)四个研究组，采用逐步阶梯 RCT 的方法开展为期一年的前瞻性在线干预和调查，研究人员在研究对象分别入组后 0、3、6、9 个月，依次为 A-D 组 MSM 开展干预。干预措施包括：在线 HIV 检测前后咨询和邮寄 HIVST 试剂（2-4 份/3 个月）。线上收集近三个月相关信息。NCCAI 的定义为不知性伴感染状况或感染状况不一致且发生无套肛交。血清学配对的定义：已知自己的 HIV 感染状况后，仅与自己 HIV 感染状况一致的人发生性行为。采用广义估计方程（GEE）评价干预对研究结局的影响作用（多因素模型矫正年龄和文化程度）。

结果 2018 年 8 月-2019 年 12 月，560 名符合条件的 MSM 被纳入 RCT 研究，每组研究对象均为 140 人。研究对象年龄为 26.1±5.6 岁，83.2%(466/560)具有大专及以上学历，至少参加一次前瞻性随访的研究对象有 465 名(83.0%)。在研究期间申请 HIVST 试剂者 74.4%(346/465)，累计邮寄 HIVST 试剂 1556 人份。GEE 模型分析显示干预阶段显著高于对照阶段的行为有安全套使用 (68.6% VS. 62.9%，P=0.012)，血清学配对 (55.0% VS. 45.2%，P= 0.001)， HIV 检测率（84.5% VS. 37.1%；P＜0.001），HIVST 使用率（81.4% VS. 22.9%；P＜0.001）；干预后显著降低的行为有 NCCAI (21.7% VS. 16.7%， P=0.013) ，多性伴（34.4% VS. 26.1%； P=0.001）和群交（11.0%VS. 7.7%；P=0.025）。

结论 在线 HIV 咨询和 HIV 发放检测，可有效促进 MSM 安全性行为和 HIV 检测。在新冠疫情仍然影响出行的背景下，社区组织和疾控中心可以通过在线的检测咨询改变 HIV 关键人群的高危性行为和 HIV 检测现状，从而控制 MSM 群体的 HIV 疫情感染扩散。

PU-2704

Inhibitory of Berberine Hydrochloride Against Candida albicans and the Role of the HOG-MAPK Pathway

li yan
Chengdu University of Traditional Chinese Medicine

Purpose Berberine hydrochloride (BH), an active component of Coptis chinensis and other plant taxa, has broad antimicrobial activity and may be useful for the treatment of Candida infections. In this study, the mechanisms underlying the inhibitory effect of BH against Candida albicans was evaluated, with a focus on the high-osmolarity glycerol mitogen-activated protein kinase (HOG-MAPK) pathway, which regulates multiple physiological functions.

Methods The minimum inhibitory concentration (MIC) of berberine hydrochloride and fluconazole in inhibiting the growth of Candida albicans was determined by using the microdilution method. determine The intervention concentration of berberine hydrochloride in this study were used as 4MIC, MIC, 1/4MIC while the intervention concentration of fluconazole was 4MIC.The intracellular glycerol content of Candida albicans was measured by Trinder method, the level of reactive oxygen species (ROS) was determined by DCFH-DA fluorescence probe, the content of ATP was determined by chemiluminescence, and the levels of chitin and β-1,3-glucan of cell wall in Candida albicans cells were measured by fluorescent dye method. The intracellular ROS level, hypha formation and bud tube formation rate of Candida albicans were observed by inverted fluorescence microscope, and the exposure of cell wall chitin was observed by laser confocal microscope (CLSM). Real-time fluorescence quantitative PCR (RT-qPCR) was used to detect the expression of key genes of HOG-MAPK central signaling pathway after the intervention of berberine hydrochloride, and the expression level of HOG1 protein in Candida albicans was detected by Western Blot.

Results BH had good antifungal activity against ATCC10231 with a MIC of 64 μg /ml. In further analyses, BH at 4 × MIC, MIC, and ¼ × MIC were evaluated, using fluconazole (4 × MIC), currently one of the most effective drugs available for Candida albicans infection, as a positive drug control 1 μg/mL. BH (256μg/mL and 64 μg/mL) significantly increased intracellular glycerol and ROS levels in Candida albicans, inhibited germ tube and hyphal formation, and increased chitin and β-1,3-glucan exposure on the cell wall. The inhibitory effect of BH was positively correlated with its concentration, and the inhibitory effect of 256μg/mL BH was greater than that of 4 μg/mL fluconazole. As determined by RT-PCR, 256μg/mL and 64 μg/mLBH altered the HOG-MAPK pathway in Candida albicans. In particular, the upregulation of the core genes SLN1, SSK2, HOG1, and PBS2 may affect the expression of key downstream factors related to glycerol synthesis and osmotic pressure (GPD1), ROS accumulation (ATP11 and SOD2), germ tube and hyphal formation (HWP1), and cell wall integrity (CHS3 and GSC1). Compared with levels in the control group, HOG1 protein levels in the 256 μg/ ml BH group were significantly higher (P <

0.05); HOG1 was slightly upregulated in the 64 μg/ ml and 16 μg/ ml BH groups but the differences were not statistically significant (P > 0.05).
Conclusion BH has multiple antimicrobial pathways and targets, making the development of drug resistance more difficult. Although we evaluated core genes in the HOG-MAPK central signaling pathway and downstream effector genes, interactions between these genes need to be studied further. This study provides a reference for the application of BH to inhibit Candida albicans, and contributes to the development of new antifungal agents and the clinical treatment of Candida albicans infection.

PU-2705

遗传代谢病血片采样流程异常对结果的影响分析

廖倩、余羊羊
重庆金域医学检验所有限公司

遗传代谢病（Inherited Metabolic Disorders，IMD）是因维持机体正常代谢所必需的某些酶、受体、载体及膜泵等生物合成发生缺陷而导致的疾病。IMD 病种繁多，已发现超过 5000 种，而唐氏患儿发生率为 1/750。采用串联质谱检测干血滤纸片中的氨基酸和酰基肉碱谱，对 IMD 进行筛查和诊断。王晶晶等人调查了 IMD 血片不合格的情况，其检测结果会导致假阳性和假阴性发生，引起疾病误诊、漏诊。血片采集是新生儿遗传代谢病筛查技术流程中的首个重要环节，标本合格与否直接影响实验室检测结果和临床诊断。

PU-2706

Enhanced histone H3 acetylation of the PDL1 promoter via the COP1/c-Jun/HDAC3 axis is required for PD-L1 expression in drug-resistant cancer cells

Haifang Wang
Nanfang Hospital, Southern Medical University

Background Drug resistance is a major obstacle to treating cancers because it desensitizes cancer cells to chemotherapy. Recently, attention has been focused on changes in the tumor immune landscape after the acquisition of drug resistance. Programmed death-ligand-1 (PD-L1) is an immune suppressor that inhibits T cell-based immunity. Evidence has shown that acquired chemoresistance is associated with increased PD-L1 expression in cancer cells. However, the underlying mechanism is still largely unknown.
Methods PD-L1 expression in three drug-resistant A549/CDDP, MCF7/ADR and HepG2/ADR cell lines was detected by qRT-PCR, western blotting and flow cytometry, and a T cell proliferation assay was performed to test its functional significance. Then, the potential roles of JNK/c-Jun, histone H3 acetylation, histone deacetylase 3 (HDAC3) and the E3 ligase COP1 in the PD-L1 increase were explored through ChIP assays and gain- and loss-of-function gene studies. Furthermore, murine xenograft tumor models were used to verify the role of JNK/c-Jun and HDAC3 in PD-L1 expression in A549/CDDP cells in vivo. Finally, the correlations of PD-L1, c-Jun and HDAC3 expression in clinical cisplatin-sensitive and cisplatin-resistant non-small cell lung cancer (NSCLC) tissues were analyzed by immunohistochemistry and Pearson’s correlation coefficient.
Results PD-L1 expression was significantly increased in A549/CDDP, MCF7/ADR and HepG2/ADR cells and was attributed mainly to enhanced JNK/c-Jun signaling activation. Mechanistically, decreased COP1 increased c-Jun accumulation, which subsequently inhibited HDAC3 expression and thereby enhanced histone H3 acetylation of the PD-L1 promoter.

Furthermore, PD-L1 expression could be inhibited by JNK/c-Jun inhibition or HDAC3 overexpression in vivo, which could largely reverse inhibited CD3+ T cell proliferation in vitro. PD-L1 expression was significantly increased in the cisplatin-resistant clinical NSCLC samples and positively correlated with c-Jun expression but negatively correlated with HDAC3 expression.
Conclusions Enhanced histone H3 acetylation of the PD-L1 promoter via the COP1/c-Jun/HDAC3 axis was crucial for the PD-L1 increase in drug-resistant cancer cells. Our study reveals a novel regulatory network for the PD-L1 increase in drug-resistant cancer cells and that combined PD-L1-targeting strategies could improve T cell-based immunity in drug-resistant cancers.

PU-2707

HAX-1 overexpression in multiple myeloma is associated with poor survival

Xiaoli Feng
Clinical laboratory center of the second hospital of Shandong university

HAX-1 has been shown to be involved in multiple cellular processes, including apoptosis, calcium homeostasis and cell migration，Multiple myeloma (MM) is a late B cell/ plasma cell malignancy characterized by the accumulation of monoclonal plasma cells in the bone marrow, increased monoclonal immunoglobulin in serum and lytic bone destruction。 To elucidate the potential role of HAX-1 in MM，the current study suggests that high expression of HAX-1, a protein implicated in cell survival and cell migration, is associated with poor survival in MM patients, and we provide evidence that HAX-1 regulates MM cell migration, thus making HAX-1 a potentially important target for therapeutic intervention.

PU-2708

血清球蛋白和 β2 微球蛋白与 2 型糖尿病合并冠心病的关系

李海霞、魏静、李萍、贾彩霞、严辰媛、马菲菲、魏书瑶、冯珊珊、哈小琴
中国人民解放军联勤保障部队第九四〇医院

目的 探讨 2 型糖尿病合并冠心病（T2DM 合并 CHD）患者的血清球蛋白（G）以及 β2 微球蛋白（β2-MG）的变化，并分析其与 T2DM 合并 CHD 的关系。
方法 回顾性收集兰州市某三甲医院 2019 年 1 月-2020 年 6 月在心血管内科和内分泌科住院的 2 型糖尿病（T2DM）患者 416 例，将其是否合并冠心病（CHD）分为 T2DM 组和 T2DM 合并 CHD 组，分析两组患者血清学指标的变化，采用 Logistic 回归分析血清 G 和 β2-MG 与 T2DM 合并 CHD 的关系，以 P<0.05 为差异具有统计学意义。
结果 T2DM 组患者 212 例，其中男 157 例、女 55 例；T2DM 合并 CHD 组患者 204 例，男 153 例、女 51 例，经统计检验发现，两组患者性别分布差异无统计学意义（P>0.05）。与 T2DM 患者比较，T2DM 合并 CHD 患者的白蛋白（ALB）、白球蛋白比值（A/G）、超氧化物歧化酶（SOD）、前白蛋白（PA）和糖化血清蛋白（GSP）水平降低，球蛋白 G 和 β2-MG 水平升高，差异具有统计学意义。将 T2DM 患者是否合并 CHD 为因变量进行二元 Logistic 回归显示，年龄（OR=1.116，95%CI：1.085~1.148，P<0.001）、糖尿病家族史（OR=4.165，95%CI：1.935~8.965，P<0.001）、G（OR=1.086，95%CI：1.022~1.153，P=0.008）和 β2-MG（OR=2.199，95%CI：1.464~3.304，P<0.001）是 T2DM 合并 CHD 的危险因素，P（OR=0.067，95%CI：0.016~0.277，P<0.001）是 T2DM 合并 CHD 的保护因素。
结论 年龄、糖尿病家族史、G 和 β2-MG 是 T2DM 合并 CHD 的危险因素，可能对 T2DM 合并 CHD 的诊断具有一定参考价值。

PU-2709

上海地区病毒性肝炎血清学标志物室间质量评价

赵晓君、陆银华、朱宇清
上海市临床检验中心

目的 通过开展室间质量评价（简称室间质评），对上海地区医疗机构实验室病毒性肝炎血清学标志物检测质量进行评价，为检验结果互认提供依据。
方法 收集 2018-2020 年上海地区医疗机构实验室 HAV-IgM、HBsAg、HBsAb、HBeAg、HBeAb、HBcAb、抗 HCV、HBcAb-IgM、HEV-IgM、HEV-IgG 项目室间质评回报数据，按照试剂厂家进行分组，以组内普遍值作为靶值进行评价。
结果 HAV-IgM 项目，2018 年度两次室间质评合格率为 98.25%和 100%，2019 年度均为 100%，2020 年度分别为 99.22%及 98.45%；HBsAg 项目 2018 年度合格率为 98.71%和 97.88%，2019 年度均为 98.25%，2020 年度分别为 97.27%及 99.12%；HBsAb 项目 2018 年度合格率均为 100%，2019 年度分别为 100%和 99.54%，2020 年度分别为 99.59%及 99.60%；HBeAg 项目三年合格率均为 100%；HBeAb 项目 2018 和 2019 年度合格率均为 100%，2020 年度分别为 100%及 99.60%；HBcAb 项目 2018 年度合格率分别为 99.10%和 98.68%，2019 年度为 99.54%和 100%，2020 年度均为 100%；抗 HCV 项目 2018 年度为 98.96%和 99.48%，2019 年度分别为 99.48%和 100%，2020 年度均为 100%；HBcAb-IgM 项目 2018 年度合格率分别为 100%和 98.21%，2019 年度均为 100%，2020 年度分别为 98.70%及 100%；HEV-IgM 项目 2018、2019 年合格率均为 100%，2020 年度分别为 99.07%及 100%；HEV-IgG 项目 2018-2020 年度均为 100%。
结论 上海地区病毒性肝炎血清学标志物室间质评结果良好，为病毒性肝炎检验项目结果互认提供依据。

PU-2710

Sestrin2 和血栓四项在角叉菜胶诱导的 2 型糖尿病血栓大鼠中的表达

李萍、贾彩霞、严辰媛、马菲菲、魏静、李海霞、魏书瑶、何斯、李香影、冯珊珊、刚乔建、哈小琴
中国人民解放军联勤保障部队第九四〇医院

目的 分析 2 型糖尿病血栓模型大鼠体内 Sestrin2 蛋白和血栓四项指标的水平及之间的相关性，为 2 型糖尿病及血栓的研究提供参考。
方法 采用高脂高糖联合链脲佐菌素的方法建立 2 型糖尿病大鼠模型，采用角叉菜胶诱导形成血栓；用双抗体夹心法酶联免疫试验测定血液中 Sestrin2 蛋白和血栓四项（TM、TAT、PIC、t-PAIC）的水平；用方差分析比较各组间研究指标的差异性，用线性相关分析指标间的相关性。
结果 四组间在 WBC、NEU、MON、PLT、MPV、PDW 和 SESN2、TM、TAT、t-PAIC 之间的差异具有统计学意义（$P<0.05$）。SESN2 与其他指标间的相关性分析发现，NC 组内 SESN2 与 MCV 呈负相关（$r=-0.692$，$P<0.05$），T2DM 组内 SESN2 与 MPV 成负相关（$r=-0.659$，$P<0.05$），T 组内 SESN2 未见与其他指标间有相关性（$P>0.05$），T2DM+T 组内 SESN2 与 WBC 和 TAT 呈正相关（$r=0.618/0.623$，$P<0.05$），总体来看，SESN2 与 FPG、GSP、MPV 和 PDW 呈负相关，与 TM 呈正相关（$P<0.05$）。
结论 Sestrin2 和血栓四项参与了 2 型糖尿病血栓的形成，且指标间密切相关，有望进步探讨其在 2 型糖尿病血栓形成中的机制。

PU-2711

2 型糖尿病各血管并发症患者凝血六项指标水平的临床意义

李萍、魏静、李海霞、贾彩霞、严辰媛、马菲菲、魏书瑶、冯珊珊、何斯、李香影、刚乔建、哈小琴
中国人民解放军联勤保障部队第九四〇医院

目的 探讨凝血六项（APTT、PT、TT、FIB、FDP 和 D-Dimer）指标在 2 型糖尿病各血管并发症中的水平及与其他临床检测指标的相关性，为临床 2 型糖尿病血管并发症的防治提供参考。
方法 回顾性分析 2 型糖尿病无血管并发症组（A 组，n=153），2 型糖尿病微血管并发症组（B 组，n=156），2 型糖尿病大血管并发症组（C 组，n=161）和 2 型糖尿病微+大血管并发症组（D 组，n=160）的基本信息，凝血 6 项及相关临床实验室指标在组间的差异性及关联性并寻找疾病影响因素。
结果 以 A 组做为参考，logistics 回归分析发现 B 组的影响因素是病程、HCY、APTT、MCV 和 PT；C 组中年龄、HCT、TG、APTT、MCV 和 D-Dimer 是其影响因素；D 组年龄、病程、合并高血压、HbA1c、APTT 和 PT 是其影响因素。各组共同的危险因素是 APTT。相关性分析中发现，APTT 与 FPG、HbA1c、TG、TC、HDL-C 和 LDL-C 负相关，与其他指标间未显示有统计学相关；PT 与 FINS、WBC、NEU、MON 和 HCY 正相关，与 HbA1c、RBC、HGB、HCT、MCV、PLT、TG、TC、HDL-C、LDL-C 和 SOD 负相关；TT 与 NEU 负相关，与 RBC、HGB、HCT、TG、TC 和 SOD 正相关；FIB 与 FPG、FINS、HOMA-IR、HbA1c、WBC、NEU、MON 和 PLT 正相关，与 RBC、HGB、HCT、MPV 和 SOD 负相关；FDP 与 NEU、MON 和 HCY 正相关，与 RBC、HGB、HCT、MCV、PDW、TG 和 SOD 负相关；D-Dimer 与 WBC、NEU、MON 和 HCY 正相关，与 RBC、HGB、HCT、MCV、TG 和 SOD 负相关。
结论 T2DM 各血管并发症者存在不同程度的凝血异常，这种异常与血糖、血细胞、血脂等因素密切相关，及时监测凝血等指标有助于早期防治和延缓 T2DM 并发症的进展。

PU-2712

信息时代下的实验室质量管理

何秋蓉、唐宇帆
四川大学华西公共卫生学院/华西第四医院

目的 实验室质量管理涉及“人、机、料、法、环”。很多三甲医院实验室或检测中心引进实验室质量管理系统，但不适用于一般级别医院，并且经济成本和维护成本高。在信息时代下，充分运用现有实验室信息系统（LIS），开发实用的质量管理模块十分必要。
方法 基于质量管理的 5 个环节，LIS 系统采用 C/S 架构，全面支撑各类功能扩展，逐步建立多个质量管理模块。实验室内部增设人员管理、设备管理、耗材管理权限等。人事管理员维护人员档案类别，每人依据类别上传个人信息，含：学历、继续教育、培训及考核、科研、教学等，定期自主更新，人事管理员审核；建立设备管理路径，设备管理员设计设备使用及维护模板，各专业组上传设备基本信息，含：安装报告、校准及验证记录、标准操作程序、培训记录、使用记录及维护记录、仪器比对、设备不良事件报告等；通过对接院内物资管理系统，设备科作为一级库，检验科作为二级库，科室各专业组作为三级库，实现检验科试剂分级管理，运用试剂条形码识别系统完成试剂使用全流程的信息化，扫码实现出入库省去人工录入操作，并且在原有试剂管理的模式下增加了请购审批功能、试剂批号更换提醒、入库效期提醒、临期试剂报警等。利用仪器质控管理模块支撑 SOP 文档管理、科室内部通知管理、交接班管理、实验室日志管理等，在 LIS 中增加多维度管理模块。
结果 通过对 LIS 的开发，实现实验室质量管理信息化及高效化。从人、机、料三个维度完善实验室人员、设备及耗材各类相关记录，通过 LIS 存档，实现无纸化。工作人员充分利用工作碎片化时

间在实验室工作区即可完成文档整理，提高工作效率，在培训与学习随机随需的基础上实现了 LIS 统一管理。
结论 实验室质量管理必须借助信息化手段，充分调用 LIS 功能，帮助管理者提升检验质量，为实验室认可做准备。下一步从 LIS 中提取各节点信息进行质量指标统计，实现“法、环”的高效管理，实现全面全流程信息化实验室质量管理模式。

PU-2713

产前诊断发现孕妇自身 22q11.2 缺失综合征一例

谢梅花、龚燕飞、李博洁
岳阳市一人民医院

目的 对 1 例无创产前检测提示 22q11.21 存在 2.4 Mb 缺失的胎儿进行产前诊断，确定缺失来源，为其家系提供遗传咨询。
方法 行羊水穿刺术后，通过常规染色体核型分析和基因组拷贝数变异测序技术（CNV-Seq）对胎儿进行产前诊断，应用 CNV-Seq 对母亲外周血进行比对分析。以明确无创提示的高风险的来源。
结果 无创补充报告提示 22q11.2 缺失综合征高风险；胎儿羊水染色体核型：46,XN,21Ph+，胎儿羊水全基因组拷贝数变异测序（CNV-Seq）结果 Seq(1-22)x2,(X,N)x1；孕妇外周血全基因组拷贝数变异测序（CNV-Seq）结果 seq[hg19]22q11.21(18,954,452- 21,449,606)x1，即母亲 22q11.21 区域存在片段大小约 2.4Mb 的拷贝数缺失，为致病性 CNV。考虑之前无创结果 22q11.2 缺失综合征高风险是因为母亲本身为该疾病的患者。
结论 无创提示 22q11.2 缺失综合征高风险为母亲本身为该疾病的患者，胎儿未遗传。

PU-2714

多发性骨髓瘤患者外周血 Tregs/Th17 细胞在多治疗方案中的变化研究

刘博
中国医科大学附属第一医院

目的 探究不同分期多发性骨髓瘤患者体内调节性 T 细胞 Tregs、辅助性 T 细胞 17、Tregs/Th17 细胞水平及其在不同治疗方案中 Tregs 细胞变化，探讨其与病程分期和化疗药物的相关性。
方法 采用流式细胞术检测体检健康者和多发性骨髓瘤患者 Tregs、Th17、Tregs/Th17 细胞水平，应用 SPSS 26.0 统计学分析软件，Student’s test 比较分析均值差异，进行对比分析。
结果 通过检测多发性骨髓瘤患者与体检健康者体内的 Tregs 细胞与 Th17 细胞，可以发现与体检健康者相比，多发性骨髓瘤患者体内的 Tregs 细胞明显升高（P＞0.05）且 DS I 期和 DS III 期 Treg 细胞绝对值均明显升高 ，而 DS II 期组 Treg 细胞绝对值未见明显变化；而且观察组 DS 分期三组间 Treg 细胞百分含量无明显差异。多发性骨髓瘤患者与体检健康者的 Th17 细胞无明显差异；与健康者相比，多发性骨髓瘤患者的 Tregs 细胞与 Th17 细胞的比值显著升高（P＞0.05）。经过三种化疗方案治疗的多发性骨髓瘤患者，Tregs 细胞百分含量均明显增加，VAD 化疗方案和其他化疗方案分组中多发性骨髓瘤患者 Treg 细胞绝对值明显增加，而 BD 化疗方案组中多发性骨髓瘤患者 Treg 细胞绝对值未有明显改变。
结论 1.多发性骨髓瘤患者外周血的 Tregs 细胞显著升高、Th17 细胞与健康者无明显差异、多发性骨髓瘤患者体内的 Tregs/Th17 细胞比值升高。2.多发性骨髓瘤患者外周血的 Tregs 细胞与病程、治疗用药有关。

PU-2715

MicroRNA-29a affects the drug sensitivity and transcriptome of breast cancer cells

Qian Zhou
Nanfang Hospital, Southern Medical University

MiR-29a is related to DNA methylation and drug sensitivity in cancers. This study aims to explore the effect of miR-29a on the sensitivity of DNA methyltransferase (DNMT) inhibitors and anti-estrogen drugs in breast cancer cells. The miR-29a-overexpressing and -knockdown cell lines were constructed to detect the proliferation and the sensitivity of breast cancer cells to DNMT inhibitors (decitabine) and anti-estrogens (fulvestrant, tamoxifen). High-throughput sequencing was performed to explore the underlying mechanism of miR-29a on affecting drug sensitivity in breast cancer. Bioinformatics analyses were also conducted on the differentially expressed mRNAs and lncRNAs, including methylation analysis, transcription factor analysis, PPI network, GO and KEGG analyses. Finally, we found that miR-29a was hyper-methylated and down-regulated in breast tumor tissues and it inhibited the proliferation of breast cancer cells. Additionally, miR-29a decreased the sensitivity of MCF-7 cell line to decitabine and increased the sensitivity of MCF-7 to fulvestrant and tamoxifen. In miR-29a overexpressing MCF-7 cell line compared with negative control, there were 165 differentially expressed mRNAs and 613 differentially expressed lncRNAs. Differentially expressed mRNAs (FZD5, JUN, CHAC1, C15orf41, SLITRK5, FBXL17, etc.) were primarily related to transcription factors like ESR1, CTCF, ESR2, etc. and involved in biological adhesion, chemo-attractant activity, AMPK signaling pathway and PPAR signaling pathway, etc. In conclusion, miR-29a functions as a tumor suppressor miRNA and could silenced by the methylation of miR-29a CpG island thus causing breast carcinogenesis. The decreasing effect of miR-29a on the sensitivity of breast cancer cells to DNMT inhibitors may because the dysregulation and methylation of miR-29a and its target genes affected the binding between DNMT and DNMT inhibitors. Also, miR-29a increased the sensitivity of breast cancer cells to antiestrogens through affecting the binding between by negatively regulating the expression of JUN, or changing the ERα activity or expression.

PU-2716

从腺病毒流行性分析角度浅谈呼吸道病原传播途径控制的重要意义

李玲锦、代冰、唐春燕、张青、唐笑
长沙金域医学检验实验室有限公司

目的 据研究资料表明，腺病毒是我国重点防控的呼吸道病原体之一。多年监测数据表明，仅靠流调分析与数据统计结果报告，对腺病毒防控的作用效果有限。2021 年，呼吸道病毒相关项目，特别是腺病毒的阳性率明显降低。因此，对比 2019 年与 2021 年的送检长沙金域医学检验实验室的监测数据分析，找出控制呼吸道疾病感染与传播因素，为呼吸道疾病防控做出贡献。
研究对象与方法 研究对象来源于 2019 年，2021 年湖南省 14 个地级市送检长沙金域医学检验实验室的 10 周岁以下人群的临床样本，检测方式是直接免疫荧光法检测鼻咽拭子中的抗原。
结果 2019 年腺病毒在湖南省全年整体阳性率为 4.58%，主要感染流行月份是 4-7 月，最高感染月在 6 月，达 10.20%，与之前 2016 年湖南省腺病毒主要流行季节在春季有差异，与相关报道湖南省腺病毒夏季感染率在不断上升报道一致。腺病毒感染有男女差异，P<0.05。2021 年 1-4 月，整体腺病毒阳性率为 1.00%，相较于 2019 年同期阳性率下降 71%，4 月同期降幅达 93.50%，与 2019 年同期阳性率对比有显著的统计学差异，P<0.05，2021 年 1 月至 2021 年 4 月腺病毒感染无

明显线性相关上升趋势，4 月整体阳性率出现统计周期内最低值，4 月腺病毒感染阳性率为为 0.33%。

结论 每年流行性监测是预防和控制腺病毒爆发的主要手段，多年的监控，并无降低腺病毒在孩童中的的感染率。在 2020 年新冠疫情爆发下，我们从呼吸道腺病毒的流行统计数据得出，在政府的领导下，全民共同参与呼吸道病毒防控，自觉做到清洁消毒工作是最有效的控制手段。

PU-2717

G 蛋白偶联雌激素受体与孤独症谱系障碍的相关性分析

赵艳玲、肖鸽飞
珠海市妇幼保健院

目的 通过研究 G 蛋白偶联雌激素受体（GPER）与孤独症谱系障碍（ASD）儿童相关性，寻找新的能够早期筛查该病的血清标志物。

方法 选取 2017-2018 年珠海市妇幼保健院就诊的 ASD 患儿 79 例，年龄、性别相匹配的正常对照组儿童 88 例，诊断标准参照美国《精神障碍诊断与统计手册第 5 版》（DSM-5），GPER 浓度测定采用酶联免疫法，并对 GPER 基因编码区进行 Sanger 测序，比较病例组与正常对照组间的 GPER 浓度差异和基因多态性的影响。

结果 在控制性别因素后，正常对照组儿童的年龄与 GPER 水平经偏相关分析呈正相关（r=0.259，P＜0.05）。GPER 结果经独立样本 t 检验分析，ASD 组的 GPER 水平显著低于对照组，结果分别为（3.62±4.28）ng/L 和（6.42±7.37）ng/L（t=-3.342，P＜0.05），差异有统计学意义。伴或不伴精神发育迟滞的 ASD 患儿血清 GPER 水平分别为（2.69±3.14）ng/L 和（4.06±5.44）ng/L，差异未见统计学意义（t=1.411，P＞0.05）。GPER 基因编码区的 c.-9T＞C 和 c.789G＞A 两个多态位点同组等位基因型的 GPER 水平经单因素方差分析及两两比较 t 检验分析，结果的差异均未见统计学意义（P＞0.05）。

结论 GPER 在神经系统功能中发挥重要作用，GPER 基因编码区虽然未找到与 ASD 有关的多态性位点，但该基因表达的 GPER 蛋白水平与 ASD 呈显著相关，提示此因子有可能成为 ASD 早期筛查的潜在血清标志物。

PU-2718

蛋白酶体抑制剂 PS-341 增强化疗药物紫杉醇和依托泊苷对人骨肉瘤 U2-OS 细胞的抑制作用

冯少婷
天津医科大学肿瘤医院

目的探讨蛋白酶体抑制剂硼替佐米(ps-341)单独或联合化疗药物紫杉醇(Ptx)和依托泊苷(Vp 16)对人骨肉瘤 u2-os 细胞生长及生物学机制的抑制作用。培养的 U2-OS 细胞分别用不同浓度的 PS-341、4μmol/L PTX、20ug/ml VP16 及其联合作用。MTT 法检测细胞增殖率，流式细胞仪分析细胞周期分布，AnnexinV-FITC/PI 双染法检测细胞凋亡率，Western blot 检测细胞核 NF-κB、Bcl2、Bax、CyclinB1 和 CDK1 的蛋白表达。PS-341 单独对 U2-OS 细胞有生长抑制和诱导凋亡作用，且呈剂量依赖性。蛋白酶体抑制剂联合化疗药物(PTX 和 VP16)可促进化疗药物对 U2-OS 细胞的抑制作用，G2/M 期阻滞显示。核内 NF-κB 蛋白表达明显降低，凋亡基因 bax 表达上调，bcl-2 表达下调，细胞周期蛋白 cyclinB1 和细胞周期蛋白依赖性激酶 1 表达降低。蛋白酶体抑制剂 PS-34 1 可进一步促进化疗药物 PTx 和 VP16 降低 NF-κB、CyclinB1、CDK1 和 Bcl2 的表达，上调 Bax 的表达，从而增强化疗药物 PTx 和 VP16 对人骨肉瘤 U2-OS 细胞的抑制作用。

PU-2719

胶质瘤微环境中 CCL2 通过诱导上皮间质样变降低肿瘤替莫唑胺的敏感性

张琳
山东大学齐鲁医院

背景 胶质瘤是脑内最常见的原发性恶性肿瘤，虽然以手术为主的综合治疗在胶质瘤的治疗方面取得了一些进展，但胶质母细胞瘤患者的中位生存时间仍然仅有 14.6 个月。目前认为，胶质母细胞瘤对化学药物的抗性是导致肿瘤复发和患者生存期短的主要因素之一。寻找逆转胶质母细胞瘤抗药性或者提高化疗敏感性的新方案对于改善患者的预后具有重要的临床意义。已知肿瘤微环境与肿瘤的恶性生物学行为密切相关。
目的 探讨胶质瘤微环境中 CCL2 对肿瘤药物耐药的影响以及相关的作用机制。
方法 利用网络基因芯片数据库，分析 CCL2 在胶质瘤中的表达情况。采用 Westren Blot、侵袭、迁移以及免疫荧光，检测胶质瘤的上皮间质样变。利用流式细胞仪检测肿瘤细胞的药物敏感性。利用荷瘤小鼠体内检测 CCL2 对肿瘤细胞药物敏感性的影响。
结果 在本课题中，我们通过分析胶质瘤网络基因芯片数据库，发现 CCL2 在肿瘤微环境中高表达且与肿瘤病理级别呈正相关，与患者的预后成负相关。体外研究发现，重组人源 CCL2（rhCCL2）可诱导胶质瘤细胞上皮-间质转化（EMT）及相关蛋白表达。我们进一步在胶质瘤组织中证实了 CCL2 与 Twist1 的表达具有相关性。同时，rhCCL2 可以明显降低胶质瘤细胞对替莫唑胺（TMZ）的敏感性，而敲除 Twist1 可以消除 rhCCL2 介导的药物敏感性降低。此外，体内实验表明，抗 CCL2 抗体与 TMZ 联合治疗可以延长 U87 荷瘤裸鼠的生存时间。
结论 总之，我们的研究结果表明，CCL2 在胶质瘤微环境中可以通过 Twist1 降低肿瘤细胞对 TMZ 的敏感性，靶向肿瘤微环境中的 CCL2 可能是一个改善胶质母细胞瘤患者预后的新策略。

PU-2720

2020 年晋东南某医院细菌耐药性监测分析

白杨、纪爱芳、弓艳娥、李晖
长治医学院附属和平医院

目的 了解 2020 年晋东南某医院临床分离菌株的分布及耐药情况。
方法 收集该院 2020 年 1 月 1 日至 12 月 31 日临床分离的非重复菌株，采用纸片扩散法或自动化仪器法进行药敏试验，依据 2020 年 CLSI 药敏试验执行标准判断药敏结果，采用 WHONET 5.6 进行统计分析。
结果 2 992 株非重复菌株中革兰阳性菌占 34.4%(1 029 株)，革兰阴性菌占 65.6%(1 963 株)。MRSA 和 MRCNS 在各自菌种中的检出率分别为 29.3%(77/263)和 75.9%(195/257)。葡萄球菌和肠球菌中未发现万古霉素和利奈唑胺耐药的菌株。大肠埃希菌、肺炎克雷伯菌、阴沟肠杆菌、产酸克雷伯菌以及奇异变形杆菌的菌株数依次位列肠杆菌科前 5 位。碳青霉烯类抗生素耐药的肠杆菌科细菌比例为 1.3%(18/1 379)。鲍曼不动杆菌和铜绿假单胞菌对亚胺培南的耐药率分别为 77.3 %(150/194)和 7.5 %(19/252)。流感嗜血杆菌 β 内酰胺酶阳性率为 38.2%。
结论 2020 年我院细菌耐药情况整体低于全国上年水平，但仍不容乐观，应继续做好细菌耐药性监测工作，了解本院细菌的耐药性变迁，为医院感染控制及抗生素合理应用提供科学依据。

PU-2721

耐碳青霉烯类鲍曼不动杆菌耐药机制研究

李代碧、伏改芬
昆明市第一人民医院

鲍曼不动杆菌(Acinetobacter baumannii，AB)，是引起医院感染最常见的条件致病 菌之一，耐药性及其耐药机制的研究已经成为全球关注的热点问题之一。其广泛地存在于自 然界和人体表面。近几年，临床分离率呈上升趋势，居非发酵菌的第二位，仅次于铜绿假单 胞菌，耐药率性也日趋严峻，出现了多重耐药的鲍曼不动杆菌，而且已在全球范围内出现播 散现象，有些地区甚至造成了爆发性流行。碳青霉烯类药物是治疗鲍曼不动杆菌重症感染的 首选药物，近几年，随着碳青霉烯类药物的广泛的使用，出现了碳青霉烯类耐药的鲍曼不动 杆菌（Resistance to carbon and resistant strains of Bauman acinetobacter CRAB）。 其产生耐药主要包括碳青霉烯酶的产生、青霉素结合位点、外膜通透性改变和外排泵增强等 因素有关，一旦耐药菌感染病死率极高，因此对于耐碳青霉烯类鲍曼不动杆菌（CRAB）感染 的预防及控制尤为重要。本文就主要的碳青霉烯酶和耐药机制加以概述。

PU-2722

Comprehensive analysis of 65 brucellosis cases between 2010-2019 in Guangdong province to promote clinical and public awareness

Honglin Gao
Guangdong provincial hospital

Background Human brucellosis is a kind of prevalent zoonotic diseases and becoming a major public health issue. Clinical features of patients with brucellosis are intricate and diverse. The aim of this single-center, retrospective study was to promote awareness of brucellosis by anatomizing epidemiology, clinical characteristics and laboratory findings.
Method Clinical data of brucellosis cases was collected retrospectively through electronic medical records in Guangdong Provincial People's Hospital between January 1, 2010 and December 1, 2019. Demographic, clinical features, laboratory findings and treatment protocols were analyzed in this research.
Finding We totally gathered 65 brucellosis cases, from the specimens of whom brucella were isolated. 60 valid cases (36 males, 24 females) were obtained for missing electronic records of 4 emergency cases and 1 inpatient case. The median age of brucellosis cases was 51.5 (41.75-60). Half (n=30) had no underlying diseases. Risk factors related to infection were close contact with animals (20%), ingestion of animal products (11.7%) and intimate contact with brucellosis (5%). There was a high peak from March to August. Fever (80%) was the most common clinical manifestation, following with chilly/ague (43.3%), weight loss (38.3%), fatigue (35%), cough (25%), headache/dizziness (23.3%) and sweating (20%). Different kinds of musculoskeletal pains were always accompanying brucellosis cases, among which arthralgia (41.7%) and lumbar ache (30%) came top. Higher level of ESR (81.6%), CRP (80%) and lower level of ALB (70%), HGB (65%) were the most typical laboratory findings. Two-drug therapy combining DOX and RIF was the most common medication methods, the proportion of which was 50% (n=30).
Interpretation Clinical diagnosis of brucellosis needs a high degree of suspicion and valid inspection including effective laboratory examination and elaborate inquiry of exposure risk factors for the variety and non-specificity of clinical presentation.

PU-2723

cobas E801 全自动免疫分析仪检测甲胎蛋白的性能验证

吴华仙
南方医科大学珠江医院

目的 验证罗氏 E801 全自动免疫分析仪电化学发光法检测血清甲胎蛋白的性能验证。
方法 参考美国临床和实验室标准化协会（NCCLS）系列文件和相关的国内行业标准等要求对 AFP 的精密度、正确度、分析测量范围和参考区间进行验证及评价。
结果 甲胎蛋白在浓度为 11.4μg/L 的批内和批间精密度分别为 0.75%和 0.97%，在浓度为 135μg/L 的批内和批间精密度分别为 0.6%和 0.1%，均小于标准要求；正确度验证达到行标文件要求，线性范围在 1.17-1132μg/L，a 值为 0.993 在 0.97-1.03 内，R2=0.9998;生物参考区间复合要求。
结论 罗氏 E801 全自动免疫分析仪电化学发光法检测 AFP 分析性能符合标准，适用于临床。

PU-2724

基于双位点催化发夹自组装技术对肿瘤细胞检测的方法学研究

江秀娟
南方医科大学南方医院

循环肿瘤细胞从实体肿瘤组织中脱落下来并进入患者循环系统，其随着血液循环播散到远处组织形成转移灶，从而加速癌症患者的死亡。目前已经有相当多的文献报道，稀有肿瘤细胞的检测在肿瘤的早期诊断以及预后评估方面具有重要的意义。与已知的传统的肿瘤诊断方法相比，对肿瘤细胞进行检测的方法具有无创、简便、可重复取样检测、方便动态监测等优势。所以说，建立一种迅速、精确、简易的肿瘤细胞检测方法是具有巨大的发展潜力的。然而，由于临床血液标本中肿瘤细胞的浓度相对较低，因此检测血液中极低丰度的循环肿瘤细胞具有很大的挑战性。

我们提出了基于双位点催化发夹组装技术的循环肿瘤细胞检测方法，这一方法能选择性识别靶肿瘤细胞并产生相应信号，最佳反应条件下，其在 10~1000 个细胞/毫升检测范围内具有良好的线性，线性方程为：y=0.831+0.215log10C，通过统计分析，检测限为 4 个细胞/毫升。除此之外，该细胞传感器能优秀地区分靶肿瘤细胞与非靶细胞（包括靶蛋白表达量不同的乳腺癌细胞、正常细胞和白细胞）。而且，这一方法在对不同浓度的靶肿瘤细胞进行检测时，无论是在缓冲液中，还是在复杂基质中，得到的检测结果相差无几。最后通过对健康者以及乳腺癌患者的全血标本进行检测，最终的结果是该传感器可以实现乳腺癌患者和健康者之间的区分（AUC：0.955，灵敏度达到 85%，特异度达到 100%）。

总的来说，我们建立了一种基于双位点催化发夹自组装技术的肿瘤细胞传感平台，整个平台无需酶参与，操作简便，并且可以通过改变不同适体即可检测不同来源的循环肿瘤细胞。该平台也在临床标本中得到初步验证。该检测方法的通用性和简便性将会使其能更广泛地应用于临床诊断、即时检验及生物医学研究。

PU-2725

免疫功能监测在脓毒症患者治疗中的临床意义

朱杰、王娇
大连医科大学附属第二医院

目的 (1)探究脓毒症患者外周血淋巴细胞亚群及各细胞因子水平与预后水平是否相关。(2）追踪患者病情发展过程中淋巴细胞亚群及各细胞因子水平变化情况。

方法 (1)选择 2019 年 1 月-2020 年 12 月大连医科大学附属第二医院收治的 38 名脓毒症患者和 20 例健康人作为研究对象，分别设为患病组与健康组，用流式细胞仪检测淋巴细胞亚群（T 淋巴细胞计数、B 淋巴细胞计数、辅助 T 细胞计数、细胞毒 T 细胞计数、NK 细胞计数）及细胞因子水平（TNF-α、IL-6、IL-10），进行病例对照研究。(2)将脓毒症患者根据预后情况分为缓解组、姑息组、死亡组。检测脓毒症患者各组淋巴细胞亚群及细胞因子水平。两两比较判断以上淋巴细胞亚群及细胞因子水平。(3)选择收集的病例中有多次监测的患者，将其分为好转组与恶化组。选取入院第一次和最后一次检验结果进行比较分析，监测研究对象相关指标，记录其波动情况并探索临床意义。
结果 (1)在患病组与健康组的对照中，发现 T 淋巴细胞计数、辅助 T 细胞计数、细胞毒 T 细胞计数、NK 细胞计数、IL-6 具有统计学意义，。 B 淋巴细胞计数、TNF-α、IL-10 无统计学意义。(2)不同预后组两两比较：在缓解与死亡的 T 检验中 IL-6 具有统计学意义。在缓解与姑息的 T 检验中各指标含量无统计学意义。在姑息与死亡的独立样本 T 检验中 CD4/CD8、NK 细胞计数具有统计学意义。(3)追踪病程：好转组和恶化组细胞毒 T 细胞计数、NK 细胞计数改具有统计学意义。
结论 (1)患病组 T 淋巴细胞计数、辅助 T 细胞计数、细胞毒 T 细胞计数、NK 细胞计数均小于对照组，提示患者免疫功能受损，患病组 IL-6 水平远高于健康组，提示患者可能存在炎症因子风暴风险。(2)可根据 IL-6 水平判断患者预后。(3)脓毒症患者 NK 细胞计数计数、细胞毒 T 细胞计数计数波动水平可作为监测病人病情及判断预后情况的一个重要指标。

PU-2726

绞股蓝总苷抑制角蛋白 17 改善银屑病样皮肤损伤

李丹丹
复旦大学附属华山医院

目的 探讨绞股蓝总苷（gypenosides，GP）对咪喹莫特（Imiquimod，IMQ）诱导的小鼠银屑病样皮肤损伤的改善作用及其作用机制。
方法 将 20 只 BALB/C 小鼠编号后随机等分为 4 组：对照组、GP 组、模型（IMQ）组、GP 治疗（IMQ+GP）组，每组 5 只。所有小鼠背部剃毛后，空白组小鼠涂抹 62.5 mg 凡士林（Vaseline），模型组小鼠涂抹 62.5 mg 的 5%咪喹莫特乳膏，绞股蓝治疗组涂抹 62.5 mg 的 5%咪喹莫特乳膏同时使用 40mg/kg 绞股蓝总苷灌胃。连续 6 d。第 6 天处死所有小鼠。每日记录小鼠背部皮损严重程度指数（Psoriasis area and severity index, PASI），取背部皮肤进行 HE 染色。取脾脏及皮肤获取单细胞悬液，进行流式细胞检测。实时荧光定量（qRT-PCR）检测组织角蛋白 17（K17）、IL-17A、IL-19 及 IL-23 mRNA 表达；Western blotting 检测 K17、STAT3、P-STAT3 蛋白表达。
结果 在第 6 天处死时，IMQ 组银屑病样皮损典型，PASI 评分最高，为（10.50±0.56）。与模型组比较，GP 治疗组小鼠红斑面积明显减少，表皮鳞屑减少，皮肤厚度显著降低；HE 染色结果表明，GP 治疗组背部组织表皮厚度明显减轻，炎细胞浸润减少；与对照组比较，模型组 K17、IL-17A、IL-19 及 IL-23 mRNA 水平、K17 蛋白表达明显升高，GP 治疗后 K17、IL-17A、IL-19 mRNA 水平、K17 蛋白表达显著降低。
结论 绞股蓝总苷通过抑制 K17 及炎症分子表达，改善 IMQ 诱导的银屑病样皮肤损伤。

PU-2727

基于咖啡环效应的尿液中微量白蛋白和白细胞的同步定量检测新方法

关淑娟
南方医科大学南方医院

慢性肾脏病已成为全球重大的公共卫生健康问题之一，早期诊断可最大限度 地减少慢性肾脏疾病所造成的损害及负担。然而，目前仍缺乏简单有效的慢性肾 脏病筛查方法。本研究介绍了一种可在 20 分钟内对尿液中的微量白蛋白和白细 胞实现同步敏感定量的检测新方法。本研究开发了一种具有聚集诱导发光特性的 智能探针，其可以同时标记尿液中的微量白蛋白和白细胞。在咖啡环效应作用下， 液滴中的白蛋白在蒸发过程中聚集于液滴接触线边缘并形成环状结构，而白细胞则均匀分布在接触面中央。通过分析环状结构的荧光强度和接触面中央荧光散点 的数目可以确定液滴中白蛋白和白细胞的浓度，检出下限分别达 9.375 mg/L 和 2/μL。该方法无需精密的仪器设备和复杂的技术操作，可为慢性肾脏病的日常预 防、筛查和动态监测提供一种简单、低成本、有效的工具。

PU-2728

柔性电化学传感器检测汗液中的葡萄糖和乳酸

余梦珂
湖北省中西医结合医院（湖北省职业病医院）

目的 在柔性基板上镀上金膜，分别滴涂葡萄糖氧化酶和乳酸氧化酶溶液，使用金纳米松针（AuNNs）作为信号放大策略来检测汗液中的葡萄糖和乳酸。
方法 首先使用光刻在聚萘二甲酸乙二醇酯（PEN）基底上对金电极进行构图。然后使用电子束蒸发器沉积 Ti（5 nm）/ Au（60 nm）层。然后使用光刻法对 Ag 电极进行构图，然后使用电子束蒸发器沉积 200 nm 的 Ag 层。另外，为了制造 Ag / AgCl 参比电极，通过计时电位法将涂有 Ag 的电极浸入 3M KCl 溶液中进行氯化。为了将准备好的传感器与电化学工作站相连，使用导电银胶将每个电极的底端与铜线连接，然后将绝缘的指甲油（环氧树脂）涂在接头部分上。然后通过将电极浸入 3 mg ml-1 HAuCl4 溶液中 20 分钟进行电化学沉积获得金纳米松针。然后，将上述制备好的电极浸入 0.1Mβ-巯基乙胺溶液中 24 小时，用去离子水冲洗并用氮气干燥后，再将 5μL 的 BSA / PEGDE /葡萄糖氧化酶溶液的液滴滴涂到 AuNNs / Au 电极上来获得葡萄糖传感器。将 5μL 的 BSA / PEGDE /乳酸氧化酶溶液的液滴滴涂到 AuNNs / Au 电极上来获得乳酸传感器。然后将传感器在 55℃的烘箱中干燥 2 小时，然后在 4℃的冰箱中保存过夜。
结果 制备的电极可以在标准葡萄糖溶液和标准乳酸溶液中产生很好的信号响应，并且不会被汗液中的其他物质所干扰。对实际汗液样本也进行了测试，和分光光度法测试的结果具有很好的相关性。
结论 我们制备的柔性电化学传感器可以很好地检测汗液中的葡萄糖和乳酸，并且由于 PEN 的良好柔性和可弯曲性，将来有望进一步设计成为可穿戴式传感器来无创实时地监测人体健康。

PU-2729

维生素 D 检测技术及临床应用

蒋洁
重庆金域医学检验所有限公司

1、维生素 D：维生素 D 是类固醇衍生物，主要包括维生素 D2（麦角钙化醇）和维生素 D3（胆钙化醇）。维生素 D3 可由 7-脱氢胆固醇在人体皮肤和脂肪组织中经阳光照射后合成，亦可通过从食物中摄取，主要存在于奶类、乳制品类、深海鱼类以及动物肝脏中。维生素 D2 不能由人体自身合成，只能从外界摄取，多含于植物性食物中，由植物的麦角固醇经阳光照射合成。维生素 D 的主要生理作用是调节钙的代谢，从而维持骨骼健康。此外，维生素 D 可通过噬菌作用而增强免疫力，在抗肿瘤活性和免疫功能调节方面发挥着重要作用。最新的研究指出，除骨质疏松、龋齿、儿童佝偻病等“经典”维生素 D 缺乏病外，多种慢性病（如动脉硬化、高血压、冠心病、糖尿病、乳腺癌、结肠癌、前列腺癌，慢性感染性疾病、自身免疫病等）的发生均与维生素 D 缺乏有关。

PU-2730

miR-33 对线粒体、糖脂代谢关键基因的调控作用

景伟[1]、袁二凤[2]
1. 郑州大学第一附属医院
2. 郑州大学第三附属医院

miRNA 是一段长度约为 18～25 个核苷酸的核内单链非编码微小 RNA，可与靶 mRNA 的 3’UTR 区特异性结合在转录后水平直接降解靶 mRNA 或抑制蛋白质翻译从而抑制靶基因表达。miRNA-33a/b 是定位于 SREBP 基因内含子的 miRNA，其可通过抑制线粒体功能相关基因 PPARGC1、PDK4 等的表达以实现对细胞内线粒体呼吸供能状态的调控。此外，miRNA-33a/b 还可以靶向作用于糖脂代谢关键基因 G6PC、PCK1、ABCA1、CPT1A、CROT 等在体内糖脂代谢的调控中发挥重要作用。异常的 miRNA-33a/b 表达水平可能与代谢类疾病发生有重要关系。

PU-2731

检验学科机动组的运营小结

童梦佳、谢莹莹
重庆金域医学检验所有限公司

机动组的发展不仅关系到个人发展平台的一个上升，更关系到公司持续变革的决心。根据目前机动组运营的方式，从培养更多实验室优秀人才入手，以发展的理念高度把握和完善公司高质量运行的体制，同时提升整个公司的整体机动水平，优化工作效率。

PU-2732

COVID-19 with bronchogram – a potential indication of prolonged treatment

xu jing
The Second Hospital of Shandong University

Novel coronavirus disease-19(COVID-19) has widely spread all over the world and seriously threatened people's health. This disease is currently diagnosed by clinical features, chest computed tomography (CT) scan, and nucleic acid test of severe acute respiratory syndrome coronavirus (SARS-CoV-2). Recently, some studies have suggested parenchymal consolidation and air bronchogram in severe cases. However, the effective treatment for COVID-19 patients with bronchogram has not been discussed. Herein, we report a case of 47-year-old woman who suffered from COVID-19 with bronchogram. These findings revealed that the body temperature and clinical laboratory test all returned to normal after this patient received a prolonged treatment. Furthermore, chest CT showed the bronchogram and consolidation resolved and nucleic acid retest of SARSCoV-2 was also negative. These results provide an important reference for treatment option of COVID-19 with bronchogram.

PU-2733

标本送检时间对支原体培养结果的影响和解决方法

何文燕、陈春竹
重庆金域医学检验所有限公司

目的 分析泌尿生殖道分泌物在检测支原体培养项目送检时间和采样要求对培养结果产生的影响及其原因，为临床送检解脲脲原体和人型支原体培养时采样要求提供数据支持并保证项目开展的质量。
方法 收集重庆金域医学检验所有限公司 2020 年全年支原体培养数据和 2021 年 3 月份及 4 月份泌尿生殖道分泌物支原体培养数据，计算 2020 年全年生长解脲脲原体阳性率、生长人型支原体阳性率及同时生长解脲脲原体和人型支原体阳性率；同时统计科室近期即 2021 年 3 月份相应数据以及 2020 年 3 月份相应数据。分析 将 2021 年 3 月科室接收到的支原体项目的培养结果与 2020 年全年培养结果以及 2020 年 3 月培养结果进行比较分析。
结果 2021 年 3 月科室检测支原体培养阳性率降低。
结论 支原体培养在其他条件不变的情况下，支原体培养结果阳性率与送检时间有关。

PU-2734

浅谈第三方独立医学实验室仪器维护保养的重要性

柳文章、江再菊、张小莲
杭州迪安医学检验中心有限公司

目的 现在人们生活质量水平越来越高，做的体检越来越多，导致医院及第三方实验室日检量激增，这就需要实验室引进和添加先进的仪器以满足检测需要。为了减少仪器出现的各种故障，检验人员需及时发现问题并妥善解决，按照仪器性能的相关要求，及时维护保养仪器，使仪器设备处于良好的状态，便于随时使用，充分发挥最佳效益。
方法 从仪器开始投入使用前，先必须熟读使用说明书，按要求检查自有保护装置，控制环境温度、湿度、连续工作时间、电源电压等，注意防潮、防尘、防腐。要精通设备的各项性能及操作规范，

建立设备管理档案，妥善保管设备的技术资料及使用说明书。定期对实验室仪器设备进行通电检查，注意用电安全，发现有异常时，要立即关机，防止因短路损坏仪器，延长仪器的使用寿命。定期对实验室仪器设备进行维护保养，及时排除仪器故障，如罗氏 c701、罗氏 c513 等仪器可根据实际损耗一个月或两个月更换比色杯和卤钨灯，做好维护保养记录，设备每次实验结束后还需进行每日的日常保养，大保养至少每年一次。每台仪器还得在校准有效期前让厂家工程师对其进行校准，避免由于机械磨损、灰尘、性能和实验频次等引起的各种实验误差，导致实验结果不准确。实验室设备管理员也应提高自身的维护、保养水平，平时多和厂家工程师沟通，不懂就问，积极参加实验室仪器维保等培训活动。

结果 通过定期对仪器进行维护与保养，能降低仪器的故障率，提高工作效率，能大大延长仪器的使用寿命。

结论 第三方实验室由于其本身的性质就决定着必须每天出具大量的实验报告，而只有实验仪器正常高效的运行，才能确保其实验结果及时、准确的被病人拿到手中。在日常工作中，严格按照仪器性能的相关要求，定期做好仪器的保养维护工作并做好记录，仪器设备才具有良好的运行状态，才能保质保量的完成工作。

PU-2735

尿微量白蛋白定量检测联合尿蛋白电泳在早期肾损伤中的作用

岳嘉波、丁少君、周紫燕
杭州迪安医学检验中心有限公司

目的 本实验主要研究尿微量白蛋白定量检测联合尿蛋白电泳在预判早期肾损伤中的作用。

方法 通过罗氏 c8000 全自动生化仪检测尿微量白蛋白的含量，采用法国希比亚半自动电泳仪对患者非浓缩尿液中的尿蛋白成分进行分析，与前者检测结果联合推断得出相关结论。

结果 两项联合检测可以弥补检测其中一项的所带来的不足。

结论 尿微量白蛋白定量检测与尿蛋白电泳联合检测对肾脏早期损伤的判断意义十分重要，是检测早期肾损伤的敏感指标，并能对损伤部位和损伤程度进行判断。

PU-2736

外泌体在胶质瘤微环境中的研究进展与应用

刘小柳
深圳市第五人民医院深圳市罗湖人民医院

外泌体(Extracellular Vesicles，EVs)是由活细胞主动向胞外分泌的囊泡样小体，直径 30-150nm。EVs 作为众多信号分子的运载体，它可调控受体细胞的信号通路及基因表达，在介导肿瘤干细胞及其微环境中其他细胞间通讯和物质交流中扮演重要角色。胶质瘤肿瘤干细胞在神经胶质瘤的发生发展，包括恶性增值、迁移、侵袭和肿瘤血管生成等均可发挥其作用，是导致肿瘤治疗失败和复发的重要原因。因此探究外泌体在肿瘤干细胞微环境中的作用，有助于研究者将进一步深入了解胶质瘤发生和发展过程。本文对 EVs 在胶质瘤微环境中的作用进行综述，为胶质瘤的靶向及综合治疗提供临床参考。

PU-2737

体检人群中一例 CA242 检测结果假阳性案例报道

江再菊、韩文、杨丽红、董咏翠、冉金波
杭州迪安医学检验中心有限公司

目的 探讨 CA242 检测结果假阳性的影响因素和解决方法。
方法 本文报道了 1 例 64 岁的女性体检个体，在 2020 年企退体检中发现 CA242 结果 62.56U/mL（参考区间：≤15.00U/mL），遂去当地三甲医院进行进一步检查，重新抽血检测 CA242，结果为阴性，于是怀疑我方检测结果不准。接到这一临床反馈，我方立即就此事成立了专门的调查小组，找出原始标本核对信息无误，发布结果与原始结果一致，当天质控在控，再次复查 CA242 结果与当初报告吻合。我们又对这个标本用生理盐水 1:1 稀释后再次进行检测，计算回收率为 96.5%，排除非特异性干扰。同时检测消化系统相关肿瘤指标 CA199、CA50，结果均为阴性。为了进一步排查试验操作上的问题，我们将该患者样本寄去试剂供应商实验室进行检测，其检测结果测值为 63.3U/mL，和我们报告结果吻合。在此同时，我们又将标本外送某三甲医院使用不同厂家试剂检测，检测结果为 1.4KU/L（阴性）。为了弄清楚结果不一致的原因，我们又与我方试剂供应商讨论并对此样本进行了不同阻断剂分析试验，加入不同阻断剂测值均没有明显变化。
结果 1.通过加入不同阻断剂及样本回收率试验，说明我方检测的阳性结果，不是常见的内源性物质干扰引起。2.因 CA242 作为糖链抗原结构复杂，存在多个抗体结合位点，分析测值结果的差异可能是由于不同厂家使用抗体原料的结合位点不同导致。3.厂家将通过改进试剂原料成分配比等办法实施改进，用以规避这一风险。
结论 CA242 假阳性案例少见，介于目前肿标检测方法存在假阳性以及厂家众多等情况，所以在遇到一些可疑的阳性结果时，应通过与临床的沟通，必要时可通过与使用不同试剂的实验室进行结果比较，这样可以更好的为客户提供服务，保证临床检验结果的准确性和可靠性。

PU-2738

ISO 15189 与临床实验室管理要素定期评审

任亚萍
中南大学湘雅二医院检验科

国际标准化组织(International Standard for Organization， ISO) 15189: 2012 是目前国际最权威、全球通行的医学实验室认可规范，涵盖管理体系、质量体系、流程控制、服务评价、持续改进等。ISO15189: 2012 管理要素中要求为了确保质量管理体系的持续改进需要进行定期评审。我院检验科是集医疗、教学、科研、社会服务于一体的湖南省规模最大的综合性临床医学实验室,于 2015 年以优异成绩顺利通过了中国合格评定国家认可委员会(CNAS)认可。本文结合 ISO 15189: 2012、本检验科在实验室认可过程中的经验以及实验室管理的相关文献，主要从文件评审、服务协议的评审、外部服务机构和供应商的评审、申请、程序和样品要求适宜性的定期评审、用户反馈的评审、质量指标的评审、管理评审等方面着手，每个评审按照评审前准备、评审实施、评审后续、体会和建议等进行介绍。总结在准备认可的过程中的体会并提出一点改进建议，希望对临床实验室的定期评审提供帮助。

PU-2739

一例血管内 NK/T 细胞淋巴瘤临床病理、分子学特征并文献复习

董清蓉、杨友谊、敬敏、王彩容、唐梅、陈虹、黄林林
四川金域医学检验中心有限公司

目的 探讨发生于血管内 NK/T 细胞淋巴瘤的临床病理、免疫组化及分子学特征。
方法 本次研究对象是一名 66 岁的男性患者，右侧鼻腔新生物，手术切取鼻腔新生物送病理检查，通过临床表现、组织形态、免疫组化及分子检测等进行诊断及鉴别诊断，并结合文献复习总结临床病理特点。
结果 粘膜上皮下血管扩张，血管腔内充满中等偏大的异型细胞，胞质中等，淡染，个别细胞胞浆嗜酸性，核呈卵圆形及不规则形，染色质粗，核仁明显，可见病理性核分裂，局灶血管腔内见纤维素样坏死，血管腔外未见异型细胞。免疫组化染色示异型细胞 CD3、CD56、GrB 阳性，Ki67 高增殖活性，约 90％阳性表达，CD5 丢失，阴性，CD20、PAX-5、BCL-6、CD10、MUM-1、MPO、CD34、CD31、S-100、PCK 均为阴性。EBV 原位杂交（EBER）检测：异型细胞弥漫阳性。患者转上级医院治疗，复查外周血及骨髓检查，排除了侵袭性 NK 细胞白血病。综合上述改变，病理诊断为：血管内 NK/T 细胞淋巴瘤。
结论 血管内 NK/T 细胞淋巴瘤是一种高度侵袭性的罕见淋巴瘤，临床表现多样，缺乏特异性，多发于亚洲人群。其病理特点是肿瘤细胞选择性在血管内浸润生长，免疫组化表达 NK/T 细胞表型，结合文献复习， EBV 原位杂交：EBER 肿瘤细胞均阳性，TCR 基因重排发现均为胚系，提示 NK 细胞来源。该肿瘤需与侵袭性 NK 细胞白血病、血管内大 B 细胞淋巴瘤、血管肉瘤、转移性癌、粘膜恶性黑色素瘤等进行鉴别，避免误诊，在肿瘤未广泛累及多器官之前进行早期治疗，能有效改善患者预后。该肿瘤进展快、预后差，治疗以 CHOP 及改良 CHOP 方案为主的化疗，文献中显示有 2 例接受干细胞移植治疗，但是疗效不满意，肿瘤的预后相关因素及治疗方案尚待更多病例积累观察。

PU-2740

TLR-9 介导吗啡诱导的巨噬细胞凋亡及药物依赖

冯一民
山东大学第二医院

目的 探讨 TLR-9 在吗啡诱导的巨噬细胞凋亡及吗啡依赖中的作用及机制，为吗啡的戒断治疗及免疫抑制的改善提供潜在的靶点。
方法 1.体外及体内分析吗啡对 TLR-9 表达的影响：分别用吗啡处理小鼠巨噬细胞系 RAW264.7 及分离获得的腹腔巨噬细胞及吗啡腹腔注射 BALB/C 小鼠后，实时定量 PCR 检测相关细胞及组织中 TLR-9 的表达水平。2，体内及体外分析 miR-146a 在吗啡诱导细胞凋亡中的作用：体外利用 TLR-9 的模拟物及抑制剂处理细胞，TUNEL 分析及流式细胞术检测 TLR-9 对吗啡诱导的巨噬细胞凋亡的影响。体内实验用 TLR-9 敲基因小鼠进行吗啡腹腔注射，检测对细胞凋亡的影响。3.小鼠模型分析 miR-146a 在吗啡的药物依赖中的作用：分别在野生型及 TLR-9 敲基因小鼠中，通过剂量递增法腹腔注射建立小鼠吗啡成瘾模型，采用吗啡受体抑制剂纳洛酮催瘾造小鼠吗啡成瘾戒断模型，观察戒断模型小鼠的跳高、西狗样甩动、体重减轻指数、爪子震颤及腹泻等症状。
结果 1.体内及体外实验均表明，吗啡能够时间及剂量依赖性地上调 TLR-9 的表达水平。2.TLR-9 激活下游信号通路介导吗啡诱导的巨噬细胞凋亡。3.小鼠吗啡成瘾-戒断模型中，TLR-9 介导吗啡诱导的药物依赖。
结论 TLR-9 通过下游信号通路介导吗啡诱导的细胞凋亡及药物依赖，为进一步解释吗啡滥用所导致的免疫系统破坏及神经系统药物依赖及成瘾提供了理论依据。

PU-2741

日立 7600 生化分析仪常见故障分析

楚亚东
联勤保障部队第九〇三医院

在临床生化分析仪的使用过程中，需要不断的积累经验，要根据不同的仪器，试剂和医院特点等对仪器进行调整维护，使仪器能够更好地满足临床诊断的需要，更好地服务于临床， 提高医院的诊疗水平。通过长期使用这台日立 7600 生化分析仪，我们体会到要对仪器进行规范化的维护保养，每日，每周，每月，每年都应按照仪器说明书认真执行相关的维护保养，其中每日保养是仪器运行的基础，仪器每日开关机时应认真执行杯子清洗，针清洁，管路冲洗，杯空白，光学检查等常规维护保养程序，只有科学合理的对全自动生化分析仪进行管理，才能发挥仪器的最大效能，服务临床，服务社会。

PU-2742

64 岁类风湿关节炎女患者合并钩虫感染 1 例

樊春红、康蕊、张凤、王辉*
北京大学人民医院

患者：黎 XX，女，64 岁，汉族，四川，农民，已婚。2019-2021 年平均每 6 个月住院 1 次，因严重贫血输血 4 次。2 年内在 3 家三甲医院就诊。2021.5.11 因“多关节肿痛 3 年余，发现三系减少 1 年半余，下肢水肿半年。”收入北大人民医院风湿科。入院检查：白细胞计数 6.20×10^9/L，血红蛋白含量 59→65→88→93g/L↓，血小板计数 232×10^9/L。γ 谷氨酰转肽酶 84U/L↑，总蛋白 56.9g/L↓，白蛋白：31.4g/L↓。球蛋白 19.2%↑，补体 3：0.714g/L↓，补体 4：0.125g/L↓，RF 1040.0IU/mL↑，抗 CCP 抗体 207.02U/mL↑，ANA 1:80 均质型, 免疫球蛋白 E：1395 IU/mL↑。其他检查均在参考区间 。进行肺灌洗液涂片，骨髓涂片、活检，血管彩超，支气管镜等一系列检查。该病例考虑合并 felty 综合征，有贫血的症状，按类风湿关节炎治疗，2021.5.24 胃镜检查时发现十二指肠异物，为肉红色或粉红色约 1CM，样本送检验科鉴定结果十二指肠钩虫成虫，是临床确诊的直接依据。给予患者阿苯哒唑（肠虫清）400mg QD *3 天治疗，第二天出院。

结论 该患者类风湿关节炎合并钩虫感染，两种疾病都有进行性血红蛋白降低是延误诊断原因之一。在临床上寄生虫感染比较少见，便查虫卵易漏检，成虫很少人认识，也是造成延误诊断的原因。寄生虫感染患者除看嗜酸细胞外，还要关注 IgE，其升高提示寄生虫感染或过敏，检测寄生虫感染除便查虫卵还可以用酶免法，免疫印迹、胶体金、PCR 等方法检测。寄生虫感染一般病程长，反复发作，久治不愈，疑难杂症时医务工作者一定要加以重视，提高对寄生虫病的认识，加强临床与检验科沟通，开拓自己的诊疗思路，做好鉴别诊断。

PU-2743

Dynamic changes of throat swabs RNA and serum antibodies for SARS-CoV-2 and their diagnostic performances in patients with COVID-19

Xueping Qiu、Yang Xiang、Yirong Li、Fang Zheng
Zhongnan Hospital of Wuhan University

Dynamic changes of RNA and antibodies in SARS-CoV-2 infected patients remain largely unknown, and influence factors for antibody production have not been fully clarified. In this study,

consecutive throat swabs specimens (n=1875) from 187 patients were collected to analyse the dynamic changes of RNA. Moreover, 162 serial serum samples from 31 patients were tested for seroconversion of IgM and IgG. Meanwhile, IgM and IgG were also detected in 409 COVID-19 patients and 389 controls. Additionally, the logistic regression analysis was executed to identify the possible influence factors for antibody production. The median positive conversion time for RNA was day 7 (IQR, 3-11), and the positive rate was the highest in day 1-5 (74.59 %) and then gradually decreased. The median time of seroconversion for IgM and IgG were both day 12 (IQR, 10-15). The sensitivity and specificity for IgM (or IgG) was 87.04 % and 96.92 %, respectively. Multivariate logistic regression indicated that reduced lymphocytes and short positive conversion time for SARS-CoV-2 RNA were independent factors for negative results of IgM and IgG tests. In conclusion, RNA and antibodies should be combined for COVID-19 diagnosis, and delayed seroconversion could be influenced by the decreased lymphocytes and short positive conversion time for RNA.

PU-2744

杭州地区 CA724 医学参考范围的确立

王磊
联勤保障部队第 903 医院

目的 通过对 2015 至 2021 年之间杭州地区健康体检人群的 CA724 结果的回顾性分析建立一个适合本地区的 CA724 参考范围。
方法 用化学发光方法检测健康体检人群血清，对不同性别及不同年龄段的 CA724 结果的比较，分析 CA724 结果在不同性别及不同年龄段之间的差异。
结果 杭州地区健康体检人群的 CA724 结果在男女之间存在显著性差异，且随着年龄的增高，CA724 的结果存在升高的趋势。
结论 现有的参考范围不适合杭州地区，应按不同性别及不同年龄设定合适的参考范围。

PU-2745

糖尿病的分型及药物治疗机理

郑悦
雅安市人民医院

糖尿病是一种慢性进行性疾病，主要表现为高血糖或糖尿，持续高血糖会导致许多并发症的产生，如视网膜、肾脏、神经系统病变及血管并发症。I 型 DM 的研究方向是开发给药方便，II 型 DM 应以改善胰岛素抵抗 IR 和保护胰岛 β 细胞功能为主，除胰岛素外临床常用药物有双胍类、磺酰脲类、列耐类、噻唑烷二酮类等。近年来，随着对糖尿病基础理论的深入和分子生物学的进展，人们对糖尿病的发病机制有了新的认识，并研发了众多糖尿病新型药物，为糖尿病的治疗提供了更多的选择。

PU-2746

应用医疗失效模式与效应分析提高尿液常规检查的质量

李欢
昆明医科大学第一附属医院

目的 通过运用医疗失效模式与效应(Healthcare Failure Mode and Effect Analysis, HFMEA) 分析现代管理工具对尿液常规检查流程中影响检验质量的高风险因素，针对性的进行整改，从而提高尿液常规检查的质量。
方法 成立 HFMEA 小组，对尿液常规检查全流程进行分析找出高风险因素，得出各个因素的 RPN 风险值，针对风险系数最高的前 5 个潜在高风险因素制定针对性的整改措施并实施。实施六个月后，再次统计流程中潜在风险最高的 5 个高风险因素来评估措施的有效性。并且对整改前后的检验报告的准确率和及时率进行比较以评价实施效果。
结果 运用 HFMEA 方法分析并实施六个月后，尿液常规检查潜在高风险因素的 RPN 得分下降，检验报告的准确率和及时率显著上升（P<0.01）。
结论 运用 HFMEA 对尿液常规检查流程中的各个环节进行防范性的风险管理，可有效的提高尿液常规检查的质量，提升医疗服务质量。

PU-2747

Sysmex CA-7000 全自动血凝分析系统检测项目 PT、APTT、FIB 性能验证实验分析

王玉霞
新疆生产建设兵团第四师医院

目的 Sysmex CA-7000 全自动血凝分析系统检测血浆凝血酶原时间（PT）、活化部分凝血活酶时间（APTT）、纤维蛋白原（FIB）等项目的性能验证。
方法 依据实验室及临床标准，观察、验证 Sysmex CA-7000 全自动血凝分析系统检测 PT、APTT、FIB 等项目的批内精密度、批间精密度、正确性以及厂家说明书中提供的相关参考区间的有效性。
结果 Sysmex CA-7000 全自动血凝分析系统检测 PT、APTT、FIB 等项目的批内精密度均低于 1/4CLIA’88Tea，批间精密度均低于 1/3CLIA’88Tea，正确性均符合 1/2CLIA’88Tea，参考区间均与厂家提供的参考区间相符。
结论 Sysmex CA-7000 全自动血凝分析系统检测 PT、APTT、FIB 等项目在批内精密度、批间精密度、正确性及参考区间等方面均符合质控要求及厂家提供的分析性能。关键词：血凝分析系统、性能验证、质量管理

PU-2748

Apelin-13 在小鼠脊髓上水平痛觉调控中的作用研究

许宁
山东大学第二医院

目的 探究 apelin-13 在脊髓上水平痛觉调控的作用及其机制。
方法 1. 选取热甩尾实验作为实验模型，研究侧脑室注射不同剂量 apelin-13 对痛觉的影响。
2．侧脑室注射 APJ 受体抑制剂 apelin13(F13A)，观察对 apelin-13 引起的镇痛作用的影响。
3．侧脑室注射不同亚型阿片受体抑制剂，观察对 apelin-13 引起的镇痛作用的影响。
4、侧脑室同时注射 apelin-13 及吗啡，观察 apelin-13 对吗啡引起的镇痛作用的影响。

结果 1. 侧脑室注射 apelin-13 产生剂量及时间依赖的镇痛效应。
2. APJ 受体抑制剂 apelin13(F13A)阻断 apelin-13 引起的镇痛效应，表明 APJ 受体介导 apelin-13 引起的镇痛作用。
3. 纳洛酮，β-FNA 及 naloxonazione 完全阻断 apelin-13 的镇痛作用；而 NTI 及 nor-BNI 对 apelin-13 的镇痛作用没有影响，表明 u 阿片受体介导 apelin-13 引起的镇痛作用。
4. 侧脑室注射 apelin-13 能增强吗啡引起的镇痛作用，并且这一作用能被纳洛酮逆转。
结论 1.神经肽 apelin-13 在脊髓上痛觉调控中发挥镇痛作用。
2. Apelin-13 的镇痛作用是通过激活 APJ 受体及内源性阿片系统介导的。

PU-2749

Wnt 分子在小鼠抑郁行为中作用研究

许宁
山东大学第二医院

目的 探究 Wnt 分子在束缚应激引起的抑郁样行为中作用及其机制。
方法 1. 选取慢性束缚应激(CRS) 作为实验模型，研究小鼠海马脑区 Wnt 分子在抑郁行为中作用。
2．通过 Real-time PCR 及 Western blot 分别检测 CRS 后小鼠海马脑区不同 Wnt 分子 mRNA 及蛋白的表达变化特征。
3．通过慢病毒特异性敲除海马脑区 Wnt2 或 Wnt3，观察 Wnt/β-catenin 信号通路，神经再生及抑郁样行为的改变。
4、通过慢病毒过表达 Wnt2 或 Wnt3，观察对 CRS 引起的抑郁样行为的影响。
5、注射抗抑郁药盐酸氟西汀，观察对 Wnt2 或 Wnt3 分子的影响；特异性敲除 Wnt2 或 Wnt3 后注射盐酸氟西汀，观察抑郁样行为的变化。
结果 1. CRS 训练引起小鼠腹侧海马而非背侧海马脑区 Wnt2 及 Wnt3 特异性表达减少。
2. 基础状态下，慢病毒特异性干扰腹侧海马脑区 Wnt2 或 Wnt3 引起 Wnt/β-catenin 信号通路及神经再生的损伤，并导致抑郁样行为的产生。
3. 慢病毒过表达 Wnt2 或 Wnt3 能纠正 CRS 引起的抑郁样行为。
4. Wnt2 和 Wnt3 能引起 CREB 的激活；Wnt3 与 Wnt3 之间存在 CREB 依赖的正反馈。
5. 注射盐酸氟西汀能引起 Wnt2 与 Wnt3 表达的升高；敲除 Wnt2 或 Wnt3 阻断盐酸氟西汀的抗抑郁作用。
结论 腹侧海马脑区 Wnt2 和 Wnt3 在 CRS 引起的抑郁样行为中发挥抗抑郁作用。

PU-2750

小鼠脑内 Wnt 分子对记忆调控的研究

许宁
山东大学第二医院

目的 探究小鼠海马脑区 Wnt 分子在恐惧记忆中的作用及其机制。
方法 1. 选取场景性恐惧记忆(CFC) 作为实验模型，研究小鼠海马脑区 Wnt 在学习记忆中作用。
2．通过 Real-time PCR 及 Western blot 分别检测 CFC 训练后不同时间点 Wnt mRNA 及蛋白的表达变化特征。
3．通过 Western blot 检测 Wnt/β-catenin 与 Wnt/Ca2+通路的激活情况。
4. 通过脑内埋管技术实现特异性向海马脑区注射干预药物，观察小鼠行为的改变情况。
5.通过 Lentivirus 载体系统构建，过表达持续激活型 β-catenin，并观察其在记忆形成中的作用。
结果 1. CFC 训练引起小鼠背侧海马脑区 Wnt3a 特异性表达增加。

2. CFC 训练引起 Wnt3a 依赖的 Wnt/β-catenin 及 Wnt/Ca2+通路的激活。
3. 训练前向海马脑区注射 Wnt3a 抗体损伤 CFC 记忆的获得。
4. 训练后向海马脑区立即注射 Wnt3a 抗体损伤 CFC 记忆的整合。
5. Wnt/Ca2+及 Wnt/β-catenin 信号通路分别参与 CFC 记忆的获得及整合。
6. 海马脑区注射重组 Wnt3a 增强 CFC 记忆的形成。
7. β-catenin 作为 Wnt3a 的下游分子增强 CFC 记忆的整合。
结论 1. CFC 学习记忆训练能诱导小鼠海马脑区中 Wnt3a 特异性表达增加。
2. CFC 训练能引起 Wnt3a 下游信号通路 Wnt/Ca2+及 Wnt/β-catenin 信号通路的激活。
3. Wnt3a 是 CFC 记忆形成的必要且充分条件。
4. Wnt/Ca2+及 Wnt/β-catenin 信号通路分别参与 CFC 记忆的获得及整合过程。
5. 在海马脑区内过表达激活型 β-catenin 能特异性纠正 Wnt3a 抗体引起的 CFC 记忆整合的缺陷，而对 CFC 记忆的获得没有影响。

PU-2751

抗-M 引起 ABO 血型正反定型不符一例

张正康
东南大学附属中大医院

患者入院后采用微注凝胶法检测患者 ABO、Rh(D)血型发现正反定型不符，采用微注凝胶法检测患者不规则抗体发现抗体筛查阳性，随后进行不规则抗体的鉴定。
血型卡显示的结果正定型为 B+，反定型为 O+
不规则抗体筛查显示的结果 2 号孔为阳性，阳性程度 4+
不规则抗体的鉴定：患者血清与 M 抗原阳性的 1、3、4、5、7、8、9、10 号谱细胞的盐水试验和抗球蛋白试验均凝集，与 M 抗原阴性的 2 号、6 号谱细胞的盐水试验和抗球蛋白试验均阴性。反应格局说明该患者血清中存在盐水反应性抗-M 抗体。
经 DTT 处理后：抗筛阴性 正反定型相符，均为 B+

该患者正定型检测结果为 B 型，红细胞上含有 B 抗原；反定型检测结果为 O 型，患者血清与 A、B、O 细胞均为阳性反应，结合不规则抗体筛查结果为阳性，提示血清中有不规则抗体的存在，通过不规则抗体检测试剂（人血红细胞）抗原谱的对比，以及与相应的不规则抗体鉴定细胞的阳性反应，可以确定该患者血清中含有抗 M 抗体。在人类血清中，抗 M 抗体通常以 IgM 形式存在。而抗 A 抗 B 抗 D 以 IgG 形式存在。将患者血清用 DTT 处理后，可以有效灭活 IgM 型抗体的活性，而不影响 IgG 型抗体的活性，所以经过 DTT 处理后的血清，反定型检测结果为 B+，抗筛结果为阴性。能够明确地判断出患者血清中含有 IgM 性质抗 M 抗体，配血时有目的的寻找无 M 抗原的血液与其进行配合。

抗-M 抗体是 MN 血型系统中常见的抗体，是一种不规则抗体，可以引起血型定型困难以及交叉配血不合。通过试验证明血型的正反定型检测以及不规则抗体的筛查试验是十分必要的，能够及时发现问题以及确保安全输血，可以有效避免和减少输血不良反应的发生。

PU-2752

多发性骨髓瘤引起 ABO 血型正反定型不符一例

张正康
东南大学附属中大医院

男性，64 岁，因“确诊多发性骨髓瘤 1 年余，再治疗”入院，查血常规：血红蛋白:72g/L↓;查 M 蛋白分析:检出 λ 型 IgG 单克隆免疫球蛋白抗体。体液免疫特定蛋白检测：免疫球蛋白

G:49.6g/L↑;LAM 轻链:16.8g/L↑;血清 β2 微球蛋白 8.81g/L↑；24h 尿蛋白:1.271g/24h↑;肾脏穿刺病理考虑淀粉样变性；骨髓穿刺示：骨髓中浆细胞占 30%；FISH：13q-（22%）、+1q21（39%）。患者血样经微注凝胶卡式法检测结果为正定型为 A+，反定型为 AB+。同一份样本经抗体增强法检测结果与 3 个单人份的 B 细胞反应结果分别为 1+，2+，2+；与 3 个单人份的 O 细胞反应结果均为阴性。

该患者正定型检测结果为 A 型，红细胞上含有 A 抗原；反定型检测结果为 AB 型，多发性骨髓瘤患者由于蛋白异常导致抗体减弱是非常常见的。通过抗体增强完以后发现与 3 个 B 细胞均发生较弱阳性反应，与 3 个 O 细胞均发生阴性反应，可以确定该患者为 A 型伴抗 B 减弱。多发性骨髓瘤患者血型鉴定异常的原因主要是抗体减弱，其次是抗体缺失、白球比倒置、抗原减弱。不同原因导致的血型异常需要结合患者病史和实验室检查结果，采用不同的实验方法，必要时采用分子生物学技术辅助鉴定血型，确保输血安全。

PU-2753

新型血清生物标志物对急性心肌梗死早期诊断的意义

于颖
哈尔滨医科大学附属第一医院

The blood transcriptome reflects the status of the disease, and characteristic molecular markers provide a new direction for gene expression before acute coronary events. Our goal is to identify molecular markers of acute coronary syndrome (ACS) based on blood transcriptome, and to identify new serum biomarkers of early myocardial infarction. Many noncoding RNAs are differentially expressed in patients with acute coronary syndrome (ACS), but the expression of miR-30a-5p in ACS patients has not been studied accurately. The goal for our current study is to investigate whether the miR-30a-5p with clinical indicators would have the potential to predict the occurrence of ACS.

PU-2754

基于岗位能力评估开展住院医师分层递进培训实践探索

羊建、田甜、岳菲、陈吉惠、任平、陈卉
雅安市人民医院

为探索提高住院医师规范化培训质量的方法，在一个基层国家住院医师规范化培训基地医院，按照住院医师规范化培训大纲要求，开展基于住院医师岗位能力评估进行临床工作权限授权的分层递进培训实践探索，希望为住院医师分层递进培训标准制定积累经验。

PU-2755

抗 TNF-a 抗体通过抑制下丘脑中 Erk 的活化削弱蛛网膜下腔出血诱导的神经元凋亡

马玲[1]、张旭华[1]、毛海婷[2]
1. 山东大学第二医院
2. 山东大学

目的 蛛网膜下腔出血能够诱导多个脑区出血神经元凋亡，比如：皮层和海马。极少有关于蛛网膜下腔出血后下丘脑中凋亡的研究。虽然已有大量关于蛛网膜下腔出血后抗凋亡的研究，比如 TNF-a

抗体，然而其分子机制目前仍不明确。因此，我们的目的是探讨蛛网膜下腔出血能否诱导下丘脑神经元凋亡及其作用机制。
材料方法 大鼠蛛网膜下腔出血造模前 30min 前，左侧侧脑室微量注射 TNF-a 抗体或 Erk 抑制剂 U0126。RT-PCR、WB 和免疫组化用于检测 caspase-3,bax,bcl-2,p-Erk 和 Erk。最终，矿场实验用于检测大鼠焦虑样行为。
结果 蛛网膜下腔出血后下丘脑中 caspase-3、bax 和 bcl-2 表达升高，提示蛛网膜下腔出血诱导该脑区发生凋亡。有趣的是，我们发现微量注射抗 TNF-a 抗体能选择性的阻断 bax 的升高，提示抗 TNF-a 抗体能够抑制蛛网膜下腔出血导致的下丘脑中的凋亡。另外，我们发现 Erk 的活化对于蛛网膜下腔出血后的凋亡是必须的，且抗 TNF-a 抗体能够通过抑制 Erk 磷酸化抑制神经元凋亡。最后，我们的研究表明，抗 TNF-a 抗体能够改善焦虑样行为。
结论 我们的研究表明抗 TNF-a 抗体能够通过抑制 Erk 磷酸化阻断蛛网膜下腔出血后诱导的下丘脑神经元凋亡。

PU-2756

CTA 记忆消退诱导岛叶中 BDNF 分泌并抑制神经元凋亡

马玲、张旭华、毛海婷
山东大学第二医院

目的 记忆消退与多种精神疾病密切相关。BDNF 合成和分泌通过激活 TrkB 参与多种记忆的过程。然而，不同脑区 BDNF 分泌和合成早记忆消退中的作用目前仍不明确。本项研究的目的是探讨岛叶中 BDNF 分泌和合成在 CTA 记忆消退中的作用。
材料方法 大鼠经过 CTA 消退训练。CTA 消退测试完毕后立即在大鼠岛叶微量注射 BDNF 抗体或等体积溶剂。RT-PCR 和原位杂交用于检测 BDNF、NGF 和 NT4mRNA 的变化。BDNF Elians 用于检测 BDNF 蛋白的变化。另外，免疫沉淀和 WB 用于检测磷酸化 TrkB 和 TrkB。WB 用于检测 c-Fos,总 Erk、磷酸化 Erk 和 caspase-3。
结果 我们发现阻断岛叶中 BDNF 信号通路能够抑制 CTA 消退，表明岛叶中 BDNF 信号通路参与 CTA 消退。岛叶中 c-fos 表达增加提示 CTA 消退能够激活神经元。另外，CTA 消退能够诱导岛叶中 BDNF 基因和蛋白表达水平升高。同时，我们还发现在 BDNF 表达增加前，磷酸化 TrkB 升高，提示 CTA 消退能够诱导岛叶中活性依赖的 BDNF 分泌增加。最后，我们发现 CTA 消退后导致岛叶中 caspase-3 表达降低。
结论 CTA 消退诱导岛叶中 BDNF 分泌及合成，并抑制神经元凋亡。

PU-2757

应用 PDCA 管理方法降低动脉血气标本不合格率

孟静
山东大学第二医院

目的 加强临床沟通，降低动脉血气标本采集不合格率。
方法 利用 PDCA 全面质量管理工具，以实验室信息系统统计的质量指标为依据，分析比较 PDCA 实施前后住院患者动脉血气标本采集合格率的变化。
结果 运用 PDCA 管理工具进行人机料法环各方面的改进后，住院患者动脉血气标本采集不合格率显著下降，由原来的 12.0%降低至 2.1%，差异有统计学意义（P<0.05）。建立了《动脉血标本采集流程》规范并通知到临床，进一步完善了检验医学中心《标本采集临床检验手册》。
结论 应用 PDCA 的管理理念和方法可持续改善检验服务临床的质量，提高临床满意度，更好地保障患者安全。

PU-2758

联合检测血清自身抗体和 IL-17 在类风湿关节炎中的临床意义

贾颖
泰安市中心医院

目的 类风湿关节炎是一种慢性系统性自身免疫炎症性疾病，主要引起软骨和骨组织的不可逆性破坏，造成患者运动功能丧失和生活质量下降。RA 患者血清中存在多种与其发病机制相关的自身抗原和抗体，其中，类风湿因子、抗环瓜氨酸肽抗体和葡萄糖-6-磷酸异构酶已应用于临床检测，但文献报道其诊断 RA 的敏感性或特异性不尽一致。近期研究发现，由 CD4+ T 细胞产生的前炎症因子白细胞介素-17 与 RA 的病情密切相关。本研究通过检测 RF、抗 CCP 抗体、GPI 和 IL-17 在 RA 患者中的表达情况，研究 RF、抗 CCP 抗体、GPI 联合检测以及 IL-17 的辅助检测对类风湿关节炎的诊断价值和临床意义。
方法 收集 40 例类风湿关节炎患者（RA 组），40 例其他自身免疫性疾病患者（非 RA 组）以及 20 例健康体检者（正常对照组）血清，采用速率散射比浊法检测血清 RF，采用酶联免疫吸附法（ELISA）检测血清抗 CCP 抗体、GPI 和 IL-17，并进行相关统计分析。
结果 RF、抗 CCP 抗体和 GPI 在 RA 组血清中的阳性率明显高于非 RA 组和正常对照组($P<0.01$)；RF 诊断 RA 的敏感性高于抗 CCP 抗体和 GPI，而抗 CCP 抗体和 GPI 对 RA 的特异性显著高于 RF；RF、抗 CCP 抗体和 GPI 两两联合检测或三者联合检测其敏感性和特异性均明显增高；RA 组血清 IL-17 水平高于非 RA 组($P>0.05$)和正常对照组($P<0.05$)，且与 RF 呈正相关($P<0.05$)，与抗 CCP 抗体和 GPI 无明显的相关性($P>0.05$)。
结论 RF、抗 CCP 抗体、GPI 和 IL-17 的联合检测可显著提高 RA 的临床诊断和病情治疗监测。

PU-2759

标本智能分拣系统的设计与应用分析

徐宏忍、赵云平、蒲丹、潘永圣
昆明市第一人民医院

目的 介绍标本智能分拣系统替代传统人工分拣在标本转运和降低分拣错误率方面的优势。
方法 通过标本智能分拣系统的应用与人工分拣方式做比较。
结果 标本转运方面：缩短了标本转运时间，分拣错误率方面：降低了标本分拣错误率，科室人力资源方面：提高了工作人员的效率，TAT 方面：缩短了 TAT，患者满意度方面：提高了患者满意度。
结论 标本智能分拣系统优化了实验室工作流程，提高了科室人员工作效率，降低了分拣错误率，优化了 TAT，提高了患者满意度。

PU-2760

县级医院检验科检验结果质量控制能力要求

公衍文
山东大学第二医院

目的 探讨建立适合县级医院检验科检验结果质量控制能力的基本要求和推荐要求。
方法 ISO15189 虽已等同转化为国家标准 GB/T 22576-2018,部分三级医院和二级医院已经通过 ISO15189 医学实验室质量和能力认可，但鉴于我国地域广阔发展很不均衡，多数县级医院并未启动实验室认可工作，我们参照 GB/T 22576-2018 并结合《临床实验室管理办法》、二级综合医院

评审标准（2015 版）、《县医院医疗服务能力基本标准和推荐标准》等，尝试制定适合县级医院检验科检验结果质量控制能力的基本要求和推荐要求。

结果 实验室应在规定条件下进行检验，并采取必要的质量保证措施，包括室内质控、能力验证和/或室间质评, 实验室间比对等方式以保证每一项检验结果的准确性，达到质量控制目标。实验室不应编造结果。包括开展室内质控 基本要求 10 项、推荐要求 9 项；参加室间质评或能力验证计划 基本要求 5 项、推荐要求 5 项；检验结果的可比性 推荐要求 2 项； POCT 项目的质量控制基本要求 2 项、推荐要求 4 项；委托检验的质量保证 基本要求 6 项、推荐要求 3 项；以及检验结果互认的基本要求等。

结论 根据县级医院检验科发展的基本情况，提出适合其能力建设，包括检验结果质量控制能力建设的基本要求和推荐要求，有助于明确其能力建设的重点和发展方向，促进检验质量提高。

PU-2761

67 例噬血细胞淋巴组织细胞增生症患者回顾性临床分析

李林燕
昆明医科大学第一附属医院

目的 回顾性分析 67 例 HLH 患者的临床特点、实验室检查特征、转归及治疗方法。为。。。。。

方法 选取昆明医科大学第一附属医院 2017 年 1 月到 2020 年 12 月住院治疗的 67 例 HLH 患者，回顾性分析 67 例患者的临床特点、实验室检查特征、转归及治疗方法。

结果 67 例 HLH 患者均有发热，超过 40℃总的有 22 例（占 32.83%），持续时间中位数 14 天；肝、脾大 37 例（55.22%），血细胞两系减少 48 例（占 71.64%），其中全血减少 23 例(占 47.91%)；高甘油三脂血症或低纤维蛋原血症 25 例（占 37.31%）；骨髓检查发生嗜血现象 57 例（占 85.1%）；血清铁蛋白均高于 500ug/L,其中高于 10000ug/L 者 13 例（占 19.4%）；NK 细胞活性降低 16/23（占 69.57）；可溶性 IL-2 受体（scd25）升高 9/11（占 81.82%）。研究该 67 例 HLH 患者的实验室的 ESR、NSE、ACE、CRP、PCT 的均值或中位数均高于参考范围，其中 ESR、CRP、PCT 的中位数或均值明显高于参考范围；Ca 的中位数低于参考范围 。住院期间死亡 3 例，可能死于多器官功能衰竭、全身炎症反应综合征及严重脓毒血症。EBV 病毒感染相关 HLH 与其他相关 HLH 的临床特征比较，两组在 FIB（P=0.027）、CRP(P=0.009)的差异有统计学意义（P 值<0.05）,EBV 感染相关 HLH 更易发生低纤维蛋白原血症；而其他相关 HLH 更易发生感染。

结论 患者出现不明原因的发热，肝脾肿大并伴有实验室检查血细胞两系或两系以上的血细胞减少、低蛋白血症或高甘油三酯血症，血清铁蛋白升高时，应高度重视 HLH，需做相关检查明确诊断，以达到早诊断、早治疗、降低死亡率。

PU-2762

Calponin 3 Promotes Human Vascular Smooth Muscle Cells Migration and Proliferation via Upregulating β-catenin Expression

Changmeng Wu
Laboratory Medicine Center, Nanfang Hospital, Southern Medical University, Guangzhou, Guangdong 510515, China.

AIMS Atherosclerosis is a highly progressive and complex pathophysiological process occurring in large and medium arteries walls that has a poor prognosis. Accumulating evidence indicates that calponin 3 (CNN3) may perform critical roles in the development and progression of stomach cancer, colorectal cancer and epilepsy etc., but the underlying molecular mechanisms remain

largely unknown. The purpose of the present study was to explore the role of CNN3 in atherosclerosis, as well as the underlying mechanism.
METHODS AND RESULTS In this project, immunohistochemistry staining showed that CNN3 was predominantly expressed in atherosclerotic plaque compared with normal arterial intima tissue. In addition, the level of CNN3 in serum of patients with coronary artery heart disease (CHD) were detected by enzyme linked immunosorbent assay (ELISA), these results shown that a significant rise in serum level of CNN3 in CHD patients compared with healthy people, and the correlation analysis between the level of CNN3 and the degree of coronary stenosis in patients with CHD was conducted. Functionally, a transwell, wound healing assay, 5-ethynyl-2′-deoxyuridine incorporation assay (EdU), and a cell counting kit-8 assay (CCK8) were performed to determine cell migration and proliferation in VSMCs, respectively. Overexpression of CNN3 significantly upregulated migration-related molecules expression of MMP3, MMP7 and MMP10, and promoted proliferation-related molecules expression of CDK4 and CDK6, downregulated P21, P16 and P53 at the level of protein, assessed by western blot analyses, respectively. Mechanistically, immunofluorescent staining and western blotting of cytoplasmic and nuclear extracts found that in VSMCs overexpression CNN3, β-catenin expression increased in the cytoplasmic and nuclear, which may possibly be associated with CNN3 targeting β-catenin. Furthermore, knockdown of β-catenin expression substantially attenuates CNN3-induced increasing of CDK4, CDK6, MMP3, MMP7 and MMP10 expression, and inhibition of P16, P21 and P53 expression.
CONCLUSIONS Our results revealed that CNN3 was dramatically upregulated in atherosclerotic plaque compared with normal arterial intima tissue, and highly expressed in serum of patients with CHD. CNN3 is thought to play pro-atherosclerosis roles in activation of β-catenin signaling molecules related to the migration and proliferation of VSMCs. Thus, therapeutic interventions targeting the CNN3/β-catenin signaling pathway may provide a new approach for anti-atherosclerosis treatment.

PU-2763

医院内疑似丙型肝炎病毒感染患者管理之检验科的贡献

公衍文
山东大学第二医院

目的 发挥抗-HCV 抗体筛选试验价值，提高丙型肝炎病毒感染患者检出率。
方法 丙型肝炎病毒（HCV）在国内的感染率约为 0.7%，早期发现、早期治疗可有效避免发展为肝硬化甚至肝癌。如何让更多的疑似丙肝病毒感染患者（抗-HCV 阳性）得到确诊是医院内疑似丙型肝炎病毒感染患者管理的重要环节。为此，我们统计了 2021 年 3、4 月住院和门诊患者抗-HCV 抗体检测情况，以及抗体阳性人群丙肝病毒 RNA 检测情况。以期了解临床和患者对 HCV 相关检测的了解情况，提出提高 HCV 感染患者确诊率的管理措施。
结果 2021.3-4 月检测抗 HCV-Ab 的患者达 6922 人，抗 HCV-Ab 阳性者 93 人（1.34%），但进一步做丙肝病毒 RNA 检测的只有 57 人（占 61.29%）。为此，实验室在报告单上增加备注：抗-HCV S/CO 介于 1-5 之间的，备注“需持续关注，必要时做丙肝病毒 RNA 检测并请肝病科会诊”；S/CO>5 的，备注“建议做丙肝病毒 RNA 检测并请肝病科会诊”；丙肝病毒 RNA 检测阳性的非肝病科患者，备注“建议请肝病科会诊”。
结论 非感染科或肝病科医生对 HCV 感染筛查和确诊试验了解不够，对 HCV 感染患者早期发现、早期治疗的价值和方法认识不足，有必要完善管理流程，提高其检出率和治愈率。

PU-2764

检验科不合格标本的原因分析和改进措施有效性探讨

孙昌瑞
四川省医学科学院·四川省人民医院

目的 分析四川省人民医院检验科标本不合格的原因，探讨针对这些导致标本不合格的原因进行的改进措施的有效性，为标本采集质量的持续提高提供策略支持，保障分析前质量控制。
方法 统计四川省人民医院检验科 2018 年 9 月-2020 年 12 月住院患者不合格标本数量并进行原因分析；2021 年 1 月-2021 年 6 月针对不同原因及重点高发科室采取干预措施，通过统计不合格标本发生率来分析干预措施的有效性，制订有效的改进措施。
结果 四川省人民医院住院患者标本不合格的原因主要为临床工作人员标本采集操作不规范、临床新员工（特别是参加住院医师规范化培训的学员）未经过有效采血培训、部分临床工作人员责任心不强及未有效告知患者标本采集注意事项，不合格原因主要有抗凝标本凝集、标本溶血、标本量不足、采集容器错误、送检时机不对等；不合格标本高发科室主要为 ICU、EICU、心内科、儿科、新生儿科；采取干预措施后，不合格标本总体发生率都有下降趋势，重点干预科室不合格标本发生率大部分有下降趋势。
结论 检验科应建立有效的与临床医护人员的沟通途径，保证及时、密切与临床医护人员、标本运输人员进行沟通，实施质量改进方案，对关键环节进行有针对性的持续改进，从而使标本采集、标本运输的质量得到有效指导和监督，使检验科不合格标本出现的概率降低，使分析前的质量得到有效控制。检验科应建立完善的检验前质量管理体系，管理体系应包含分析前质量指标、评价方法及标准、实施方案等，发现可以改进的环节及时采取有效的干预措施，降低不合格标本的发生率，从而提高检验质量。

PU-2765

原发性肝癌患者血清 25-羟基维生素 D 及总胆汁酸水平调查

肖玲[1]、徐玉兵[1]、张蜀豫[2]、程雅婷[3]、黎春宝[1]
1. 上海金域医学检验所有限公司
2. 东方肝胆外科医院肝外四科
3. 广州金域医学检验中心有限公司

目的 调查原发性肝癌患者血清 25-羟基维生素 D(25OHD)水平、总胆汁酸(TBA)水平。
方法 选取东方肝胆外科医院就诊的 204 例肝细胞癌患者（HCC 组）和 167 例胆管细胞癌患者（ICC 组）共 371 例为研究对象组，371 例健康体检者为对照组，采用高效液相色谱-串联质谱法检测血清 25OHD 水平， 采用酶循环法检测血清 TBA 水平，对肝癌患者与健康体检人群的维生素 D 营养状况和胆汁酸代谢状况进行比较分析。
结果 HCC 组和 ICC 组血清 25OHD 水平均低于对照组， 差异有统计学意义（P<0.05），HCC 组和 ICC 组血清 25OHD 水平比较，差异无统计学意义（P >0.05）； 从维生素 D 营养状况来看，HCC 组严重缺乏率最高, 达 19.12%，ICC 组 15.57%，均显著高于对照组 4.04%，组间差异有统计学意义（$\chi2$=51.223, P<0.05）；HCC 组和 ICC 组血清 TBA 水平均高于对照组，差异有统计学意义（P<0.05），HCC 组和 ICC 组血清 TBA 水平比较，差异有统计学意义（P<0.05）；HCC 组和 ICC 组血清 TBA 异常率显著高于对照组，组间差异有统计学意义（$\chi2$=14.190, P<0.05）。
结论 肝癌患者血清维生素 D 严重缺乏率显著高于健康体检人群，血清 TBA 异常率显著高于健康体检人群。

PU-2766

妊娠期高血压疾病病因学的研究进展

宁晓姝、杨晓东、杨华
三峡大学附属仁和医院

妊娠期高血压疾病(HDCP)是妊娠与血压升高并存的一组疾病，发生率为 5%~12%，包括妊娠期高血压、子痫前期、子痫、以及慢性高血压并发子痫前期。 迄今为止其病因不明，因该病在胎盘娩出后常很快缓解或可治愈，有学者称之为“胎盘病”， 但很多学者认为是由母体，胎盘，胎儿等众多因素引起。 找出相关的病因和高危因素， 加强产前筛查，及时预防和对症处理，可减少并发症的发生。以下对近年对妊娠高血压疾病的病因的探讨和研究进行总结和综述。

PU-2767

采用行业标准 WS/T224-2018 评价四种类型真空采血管

张艳
新疆生产建设兵团医院

目的 评价本院四种类型采血管的性能指标，确保采血管质量的可靠。
方法 参照中华人民共和国卫生行业标准 WS/T224-2018 对我院使用的 EDTA-K2 抗凝采血管（批号 20180401）、3.2%柠檬酸钠抗凝采血管（批号 20180821）、3.8%柠檬酸钠抗凝采血管（批号 1811327）、分离胶真空采血管（批号 1806336）的外观、抽吸量、管体强度、纤维蛋白挂壁、溶血、抗凝管凝血、无菌测试及结果可比性进行评价。
结果 四种类型采血管外观均为透明、无异物、无变形或破损、标识清楚、管盖无脱落，分离胶采血管内的分离胶胶体呈 凝胶状。EDTA-K2 抗凝采血管、3.2%柠檬酸钠抗凝采血管和 3.8%柠檬酸钠抗凝采血管的抽吸量与公称液体容量的相对偏差分别为-2.5%、-2.0%和 8.7%，均符合要求。四种类型采血管充装水离心后，外壁均未破裂且无液体渗漏，管体强度符合要求；采血离心后均未发生溶血现象。分离胶真空采血管采血离心后无纤维蛋白挂壁情况。三种类型抗凝采血管采血混匀后，显微镜下均未出现凝块。将含有供试液的四种类型采血管放置生化培养箱 48h 后，均无细菌生长。分离胶真空采血管不同项目比对结果的相对偏倚符合分析质量指标的要求。
结论 四种类型采血管的性能良好，可以满足临床血液标本采集、转运、分析及储存的要求。

PU-2768

急诊留观病房老年患者血培养病原菌分布及耐药性和影响因素分析

徐宁
云南省第一人民医院

目的 分析患者感染的多重耐药菌的来源，并对培养阳性和阴性患者进行临床和实验室特征比较，并同时分析特殊用药史及存在基础疾病是否是血流感染的独立危险因素。并对细菌耐药性进行分析，为急诊科有效控制老年患者血流感染的预防和经验治疗提供实验室依据。
方法 回顾性分析 2020 年 1 月—2020 年 12 月云南省第一人民医院急诊科年龄≥65 岁急诊科患者血培养数据及其临床资料，应用 WHONET 5.6 软件对数据进行统计。
结果 不重复患者的 2890 份血标本检出病原菌 456 株，其中革兰阴性菌 58.99％、革兰阳性菌 38.82％、真菌分别占 2.19％。居前五位的病原菌依次为大肠埃希菌、肺炎克雷伯菌、表皮葡萄球菌、鲍曼不动杆菌、金黄色葡萄球菌。革兰阴性菌患者 28 天病死率(46．4％VS．22．8％，

1=0．018)和住院病死率(53．6％VS．26．6％，P=0．009)均高于革兰阳性菌患者。大肠埃希菌、肺炎克雷伯菌对亚胺培南的耐药率分别为 0、11.32％，对阿米卡星的耐药率 ＜5％；鲍曼不动杆菌对亚胺培南的耐药率达 82.93％，对大多数抗生素高度耐药。耐甲氧西林金黄色葡萄球菌（MRSA）检出率为 43.78％，耐甲氧西林凝固酶阴性葡萄球菌（MRCNS）检出率高于 MRSA，屎肠球菌对万古霉素和利奈唑胺的耐药率分别为 14.29％和 4.76％。

结论 老年患者血培养病原菌以革兰阴性菌为主，耐碳青霉烯肺炎克雷伯菌增长较快，未发现耐替加环素和多粘菌素菌株。未发现对万古霉素和利奈唑胺耐药的葡萄球菌属细菌；鲍曼不动杆菌耐药率最高，临床应给予足够的重视，采取针对性的预防与控制措施，根据药敏结果合理使用抗生素，减少抗生素压力。

PU-2769

六西格玛理论对血凝项目分析质量的应用

马瑜婷
西安医学院第一附属医院

目的 应用六西格理论对血凝检测项目的质量水平进行评价，加强实验室质量评价的科学管理。

方法 收集 2019 年实验室室内质控的变异系数（CV）作为不精密度，采用 2019 年国家卫生部临床检验中心室间质量评价回馈数据中的偏移（Bias ）;美国临床实验室改进修正案（the Clinical Laboratory Improvement Amendment of 1988， CLIA’88）制定的允许总误差（TEa）为标准。根据公式 σ=(TEa- |Bias|)/CV，QGI=Bais/（1.5×CV）计算测凝血酶原时间 （PT),部分凝血酶原时间（APTT),凝血酶时间（TT),纤维蛋白原（FIB), 纤维蛋白原降解 产物（FDP)与 D-二聚体（DD)的 σ 值和质量目标指数(QGI)。为实验室的检测能力的改进提供方案。

结果 APTT 的 σ 值大于 6，达到世界一流水平；PT 为优秀；DD 为良好；FIB 和 FDP 为临界；而 TT 欠佳。根据质量目标指数结果显示：FIB 与 PT 优先需要改进的方向为精密度；FDP 为正确度；TT 和 DD 两个方向均需改进。

结论 六西格玛理论有利于临床实验室血凝项目质量控制的评价，提高了实验室质量评价的科学管理。

PU-2770

单人份心肌高敏肌钙蛋白 I 性能评价

黄睿
新疆维吾尔自治区人民医院

目的 对心肌肌钙蛋白 I 进行试剂性能验证评价。

方法 参考 CNAS-CL02 ：《医学实验室质量和能力认可准则》（ISO 15189:2012）对医学实验室检测系统性能评价的相关要求对医学实验室检测系统性能评价的相关要求,对 Perkinelmer(以下简称 PKD)公司生产的 cTnI 试剂，进行精密度，第 99 百分位，正准度（方法学比对），检测范围，以及同源血相关性进行验证与评价。

结果 PKD 生产的 cTnI 试剂的精密度，正确度，检测范围，第 99 百分位的建立，以及同源性相关性均符合说明书申明要求。两个浓度的商品质控物的重复性和中间精密度分别是 1.51%和 2.71%、1.65%和 2.41%；第 99 百分位 cTnI 值男性为 0.027ng/ml,女性为 0.024ng/ml，健康人群为 0.0256ng/ml，与说明书申明的 0.03ng/ml 比较接近；通过 Beckman DXI800 试剂的方法学比对，两种试剂盒检测相关性分析 r=0.9559，一致性检验阴性符合率 99.17%，阳性符合率 97%，总符合率 98.66%；EDTA 血浆结果与肝素锂血浆相关性 r=0.999， EDTA 血浆结果与 EDTA 全血相关性 r=0.998 。

结论 PKD 公司生产的 cTnI 的主要分析性能验证结果与厂商说明书提供的分析性能一致，适合床旁辅助诊断以及连续性跟踪并对早期诊断具有重大的意义。

PU-2771

微生物检验不合格样本原因及质量改进对策回顾性分析

苏迎迎
东南大学附属中大医院

目的 分析微生物检验中存在的不合格样本原因并探讨改进对策。
方法 使用 LIS 系统统计 2020 年 1 月至 2020 年 12 月微生物实验室核收的不合格样本的资料，统计不合格样本数量并对不合格原因进行分析。
结果 据统计 2020 年 1 月至 2020 年 12 月微生物实验室共核收不合格样本 756 例。不合格原因主要有医嘱原因和标本原因。医嘱原因包括医嘱取消（21%）和医嘱错误（30%）等，标本原因包括患者未遵循检验规定采样导致标本污染(17%)、采样容器错误（8%），此外收到未完成采样的空管（2%）。
讨论 本文中医嘱原因是影响微生物检验样本及时检验的一大原因，其次患者未遵循检验规定、采样容器不合格和标本采集部位、时间错误等均是微生物检验不合格标本存在的主要因素。微生物标本的检验合格率可直接影响患者的诊断及治疗方案，检验样本质量改进至关重要。因此加强临床检验人员检验能力的培养，降低检验过程失误概率，以提高临床检验准确性。加强临床检验人员对临床样本质量监督，定期统计并反馈临床；加强临床与检验科的交流，使临床及时准确了解检验项目相关信息。规范样本留取运送及检验相关步骤，逐步降低样本不合格率。

PU-2772

新冠疫苗犹豫及影响因素和应对策略

王娜、张利霞
内蒙古科技大学包头医学院第一附属医院

目的 疫苗接种是预防传染病最经济有效的措施，但是近年来世界范围内拒绝或延迟接种现象凸显，世界卫生组织已将疫苗犹豫列为“2019 年全球卫生面临的十项威胁之一”。新冠疫苗犹豫可能成为全世界尽快彻底控制疫情的最大绊脚石之一，必须引起高度关注，鉴于此，本文将疫苗犹豫的现状、影响因素及应对策略进行综述。
方法 1.通过文献查阅了解国内外新冠疫苗的犹豫现状及原因。2.通过参与疫苗犹豫调查问卷的分析总结，了解新冠疫苗的犹豫现状及原因，探讨解决策略。
结果 1.、新冠疫苗犹豫现状 Jeffrey V.Lazarus 教授报道的对 19 个国家 13426 名受访者中关于中国新冠疫苗接种意愿是 88.6%[31]， Yu lan Lin 等[32]在线调查]我国全国范围内的新冠肺炎疫苗接种意愿 83.5%，说明通过接种新冠疫苗来预防新冠病毒的感染是民众迫切希望的，然而仍有部分人存在犹豫现象。文献表明，目前不同的国家对新冠疫苗的接种意愿是由差别的，Kimberly 教授研究的美国新冠疫苗接种意愿 57.6%[33]。2、引起新冠疫苗犹豫的因素有：疫苗的安全性和有效性，对感染风险的轻视，以及疫苗接种的便利性和可及性等。3.解决策略：加强媒体沟通，宣传接种的必要性；调动医务人员积极性，提升接种服务质量；加强监管和监测能力，保证民众对疫苗的科学认知。
结论 疫苗犹豫是一个在特定背景下的复杂问题，会因为疫苗种类、时间、地点的不同而出现变化。全球免疫行动的成功必须有赖于实现和保持高的疫苗接种率。因此，“疫苗犹豫”问题应该作为国家免疫规划的优先事项得到关注和应对。

PU-2773

急性缺血性脑卒中患者血清同型半胱氨酸及血脂水平的分析

薛云松
云南大学附属医院

目的 通过观察急性缺血性脑卒中患者血清 HCY 及血脂水平的变化，探讨急性缺血性脑卒中与血清同型半胱氨酸及血脂水平之间的关系。
方法 根据急性缺血性脑卒中诊断标准，选取我院 2020 年 9 月至 2021 年 2 月收治的急性缺血性脑卒中患者 85 例为对象，将其归入治疗组，再随机选择同一时期在我院进行健康体检的 20 例正常人群作为对照组，用雅培 C16000 全自动生化分析仪和配套试剂对两组人群进行 HCY 和血脂水平的检测，包括血清总胆固醇(TC)、甘油三酯(TG)、高密度脂蛋白胆固醇(HDL-C)、低密度脂蛋白胆固醇(LDL-C)以及 HCY，所有受试者测定前均未服用影响同型半胱氨酸水平的药物。清晨空腹采集肘静脉血，2h 内分离血清待测。TG 的测定采用甘油磷酸氧化酶法，TC 的测定采用胆固醇氧化酶法，HDL-C 和 LDL-C 采用直接法测定，hcy 采用循环酶法法进行检测，并对检测结果采用 SPSS 19.0 软件对数据进行统计分析，数据资料以均数±标准差(ˉx±s)表示，组间的比较采用成组设计的两样本 t 检验，若 P＜0.05，表示对比差异显著，有统计学意义，p＞0.05 表示差异不显著，无统计学意义。
结果 治疗组患者的血清 HCY，血清 LDL 以及血清 TG 都明显高于对照组，血清 HDL 明显低于对照组，差异有统计学意义,P＜0.05。血清 TC 之间无明显差异。
结论 血脂和 HCY 水平升高与脑卒中有明显的关系，有效控制血脂和血清 HCY 水平，对降低脑卒中发生率具有显著的作用。对于缺血性脑卒中的预防，高脂血症病人应积极采取药物治疗，以及定期监测 HCY 水平。积极的体格锻炼，合理膳食等都可以干预并降低其发生率。

PU-2774

4 项生化指标测量不确定度评估及允许范围的初步研究

李伟、吴文礼、李燕
新疆生产建设兵团第四师医院

目的 探讨血清钠（Na）、钾（K）、甘油三酯（TG）、总胆固醇（TC）这 4 项生化指标的测量不确定度及其允许范围。
方法 参照中国合格评定国家认可委员会(CNAS) 技术报告《医学实验室－测量不确定度的评定与表达》和 Nordtest 准则，收集新疆生产建设兵团第四师医院检验科临床生化室 4 项生化指标 2020 年 11 月～2020 年 12 月的室内质量控制（Internal Quality Control，IQC）数据和国家卫计委临床检验中心 2019 年～2020 年连续 6 次的室间质量评价（External Quality Assessment，EQA）回报结果，计算实验室内测量复现性和偏倚，作为分量引入测量不确定的计算；基于检测项目 95%CI 导出的允许不精密度和偏倚，计算 4 项指标测量不确定度及其允许范围；并使用质量指标等级模式进行评估。
结果 Na、K、TC 和 TG 这 4 项生化指标的测量不确定度分别为 3.32%、4.97%、7.65%、9.28%，允许不确定度分别为 2.72%、6.08%、7.66%、9.84%。其中 K、TC 和 TG 的测量不确定度达到质量指标等级模式 2 的要求，Na 的测量不确定度达到等级模式 3 的要求，Na、K 的允许不确定度达到质量指标等级模式 3 的要求，TC、TG 的允许不确定度达到质量指标等级模式 2 的要求。
结论 4 项指标中，TC 和 TG 测量不确定度和允许范围均达到质量指标等级模式 2 的要求，Na 的测量不确定度和允许范围均未达到质量指标等级模式 2 的要求，K 的测量不确定度达到质量指标等级模式 2 的要求，而允许范围未达到质量指标等级模式 2 的要求。目前实验室 Na 的方法学和操作技术未达到较为严格的质量标准，应与临床医师沟通，了解临床对 Na 的决策需求，由临床和实验室共同研究确定合理的检测允许不确定度范围。

PU-2775

基于标准化的六西格玛理论性能验证图规范实验室尿液定量化学检验项目性能

杨璐、蒋叶
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨采取基于标准化的六西格玛理论性能验证图规范实验室尿液定量化学检验项目性能的可行性。
方法（1）允许总误差的计算：参照卫生部室间质评的评价标准作为所有尿液定量化学项目的允许总误差。（2）不精密度数值描述：收集 2016 年 1-12 月江苏省人民医院生化专业组尿液定量分析所有月度 CV 值，取其平均值完成计算。（3）偏倚数值描述：收集 2016 年参加卫生部尿液定量化学室间质评的 5 个偏倚的绝对值的平均值进行计算。按照公式 σ ＝ （TEa-丨Bias丨）/ CV，计算每个检测项目的 σ 水平。
结果 尿钠、尿氯、尿糖、尿尿素、尿肌酐、尿尿酸、尿蛋白、尿钙检测水平评价为世界一流，尿镁评价为优秀，尿磷、尿钾、尿淀粉酶评价为欠佳。
结论 实验室可以采用基于标准化的六西格玛理论性能验证图来规范尿液定量化学检验项目性能，提高尿液定量化学检验项目的准确性。

PU-2776

新型冠状病毒核酸检测经验与思考

刘婕
山东大学第二医院

目的 总结公立医院日常及大规模新型冠状病毒核酸检测的经验，探究新型冠状病毒核酸检测的优化与发展。
方法 结合日常及大规模新型冠状病毒核酸检测工作，解读政策法规，复习相关文献，针对在新型冠状病毒核酸检测过程中遇到的问题，对新型冠状病毒检测要点方面进行分析，对其优化与发展进行探讨。
结果 在常态化疫情防控的形势下，生物安全及质量控制为新型冠状病毒核酸检测工作的重中之重，且作为新型冠状病毒核酸检测基地，需做好大规模新型冠状病毒核酸检测的预案及各方面的储备。
结论 总结新型冠状病毒核酸检测经验，思考优化工作流程，保障新型冠状病毒核酸日常检测的安全性、准确性，提升了公立医院应对突发公共卫生事件的能力。

PU-2777

探讨凝血检查对非小细胞肺癌疗效监测的价值

左娅薇
天津医科大学肿瘤医院

目的 探讨血浆中 ATIII、FDP 和 D-二聚体对非小细胞肺癌诊断和对手术疗效、病程进展、化疗前后效果观察和预后判断的临床应用价值。
方法 回顾性分析 108 例非小细胞肺癌患者手术前后和化疗前后血浆中 ATIII、FDP 和 D-二聚体的变化水平，并与 30 例肺良性肿瘤患者和 30 例健康体检者进行比较。
结果 非小细胞肺癌患者手术前血浆中 FDP 和 D-二聚体含量明显高于肺良性肿瘤患者（P<0.05）和健康对照组（P<0.05），ATIII 水平低于肺良性肿瘤患者（P<0.05）和健康对照组（P<0.05），

术后 FDP 和 D-二聚体水平明显下降，但仍高于肺良性肿瘤患者（P<0.05）和健康对照组（P<0.05），ATIII 水平有所上升，仍低于肺良性肿瘤患者（P<0.05）和健康对照组（P<0.05），肺良性肿瘤患者和健康对照组血浆中 ATIII、FDP 和 D-二聚体水平差异没有统计学意义（P>0.05），患者化疗前后血浆中 ATIII、FDP 和 D-二聚体的水平差异有统计学意义（P<0.05）。
结论 本研究证明了血浆中 ATIII、FDP 和 D-二聚体联合检测在非小细胞肺癌诊断和手术治疗中的意义及其对手术疗效、病程进展、化疗前后具有较高的临床应用价值，其变化对肺癌的转移及疾病的预后有重要意义。

PU-2778

探讨 PDCA 循环对检验报告及时率的效果

宋煜中
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 PDCA 循环法是程序化、标准化的一种工作方式，是一种全面有效的质量管理方法，由美国戴明博士提出的 PDCA 循环法，广泛应用于质量管理。通过对各类检验项目报告时间的统计分析，了解检验的工作现状，分析其报告不及时的原因，为检验的优化提供依据。
方法 利用 LIS 功能将运用 PDCA 循环前后的各类检验项目的原始数据导出，统计在规定的时限内完成的检验报告数（及时率），并比较分析记录检验报告超时的原因。
结果 运用 PDCA 循环对检验报告超时原因进行分析并持续改进，检验报告及时率从 92.85%提高至 97.65%。
结论 在检验过程中运用 PDCA 循环可有效提高工作效率，改善检验人员的技能操作能力和仪器保养能力，最终达到提高检验报告及时率的目的。

PU-2779

PLD1 蛋白在胰腺癌中的临床应用

赵然
天津医科大学肿瘤医院

目的 探讨磷脂酶 D1 在胰腺癌中的表达，结合相关病例进行分析明确磷脂酶 D1 蛋白分子的表达水平与胰腺癌临床病理特征之间的相互关系，为胰腺癌的诊断、患者的治疗及预后提供新的思路。
方法 采用生物信息学的方法分析 PLD1 在胰腺癌组织及癌旁组织中的表达水平，并分析 PLD1 表达水平与胰腺癌患者的生存率之间的关系；回顾性分析 68 例接受手术治疗的胰腺癌患者的临床病理资料，采用免疫组化染色法分析 PLD1 的表达情况与胰腺肿瘤的发展进程之间的关系，应用 c2 检验分析 PLD1 表达水平与胰腺肿瘤患者临床病理特征之间的关系；肿瘤标志物糖类抗原 CA199、CA242 以及癌胚抗原 CEA 采用电化学发光方法进行检测，利用仪器 CobasE801 电化学发光仪进行分析，并使用相应配套的检测试剂盒，严格依照使用说明书进行检测，检测前严格确保仪器质控数据良好。
结果 生物信息学分析结果显示 PLD1 在胰腺癌组织中存在高表达，并且与患者总生存率和无病生存率相关；免疫组化结果表明正常的组织中 PLD1 不表达，在癌前病变组织中有少许的 PLD1 表达，在胰腺癌组织细胞 PLD1 呈现强阳性表达；PLD1 在胰腺癌组织中的高表达与肿瘤的分化程度、血清标志物 CA199、CA242 相关（P<0.05），而与年龄、性别、肿瘤大小、肿瘤的复发转移、血清标志物 CEA 无关（P>0.05）。
结论 PLD1 参与了胰腺癌的发生发展进程，未来可作为胰腺癌新型分子标志物参与疾病诊断及预后判断。

PU-2780

慢性肾脏病患者的甲状腺功能和血脂水平分析

张伟
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨慢性肾脏疾病（CKD）患者的甲状腺功能和血脂状况。
方法 收集 2017 年 1 月至 2017 年 10 月南京医科大学第一附属医院肾脏科 CKD 患者 412 例，分别检测血清尿素（Urea），肌酐（Cr），总胆固醇（TC），甘油三酯（TG），高密度脂蛋白胆固醇（HDL-C），低密度脂蛋白胆固醇（LDL-C），三碘甲状腺原氨酸（FT3），游离甲状腺素（FT4）和促甲状腺素（TSH），计算估算肾小球滤过率（eGFR）。比较 CKD 各期患者的甲状腺功能和血脂水平，对甲状腺功能和血脂血清学指标与肾功能指标 Cr 和 eGFR 进行相关性分析，并对 CKD 各期患者的甲状腺功能和血脂疾病状态进行比较。
结果 CKD 各期间 Urea、Cr、TC、LDL-C、HDL-C、FT4 和 TSH 差异有统计学意义（P＜0.05），FT3 差异无统计学意义（P＞0.05）。FT4、HDL-C 与 Cr 呈负相关，与 eGFR 呈正相关；TSH、TC、LDL-C 与 Cr 呈正相关，与 eGFR 呈负相关。CKD 患者中高胆固醇血症，高甘油三酯血症，低 HDL-C 血症，高 LDL-C 血症发生率分别为 18.93%，21.12%，58.25%，12.14%。有 20.88% 的 CKD 患者存在甲状腺功能紊乱，最常见的是亚临床甲状腺功能减退（14.08%），其次是临床甲状腺功能减退（3.64%）和亚临床甲状腺功能亢进（3.16%）。
结论 甲状腺功能紊乱和血脂异常是 CKD 患者常见的症状，动态监测 CKD 患者的甲状腺功能和血脂的血清学水平可为早期诊断并治疗甲状腺和血脂疾病提供理论依据。

PU-2781

2020 年吉林省 0-6 岁儿童微量元素铁检测结果分析

刘琳
吉林金域医学检验所有限公司

目的 检测吉林省 0-6 岁儿童全血中微量元素铁的含量，了解吉林省 0-6 岁儿童微量元素铁的含量情况，为预防缺铁而导致缺铁性贫血，合理的提供相应的营养指导。
方法 选取 2020 年在吉林金域医学检验所有限公司检测的例全血铁微量元素数据，按照年龄一共分为 3 组:分别为 0-2 岁、2-4 岁及 4-6 岁。采用电感耦合等离子体质谱法来进行微量元素铁的检测，分析各组铁元素的检测结果，并讨论铁元素对儿童生长发育的影响，数据采用 SPSS22.0 统计学软件分析。
结果 1.0-2 岁有 1348 例，2-4 岁有 1550 例，4-6 岁有 395 例，分析不同年龄儿童铁元素缺乏水平，结果发现不同年龄的儿童的铁元素的平均值之间差异有统计学意义(P＜0. 05)。2.不同年龄儿童铁元素缺乏率分别为 0-2 岁 7.93%，2-4 岁 5.10%，4-6 岁 3.30%。
结论 在吉林省 0-6 岁儿童全血铁元素检测中，随着年龄的增长，缺铁情况逐渐降低。缺铁性贫血是最常见的营养性疾病，所以它的预防十分重要，主要是做好卫生宣教工作，使家长认识到，缺铁性贫血对孩子的危害性，以及做好预防工作的重要性。所以我们应该在婴儿时期就要按部就班的添加辅食，要尽早的添加含铁食物，比如红肉类的食物和肝脏，这样补充铁剂的效果是最好的。我们还提倡母乳喂养，并做好喂养指导，还可以在孩子的食品当中加入适量的铁剂加以强化，搭配合理的膳食，合理的补充微量元素，早发现早预防！

PU-2782

2021 年长春地区孕妇维生素 D 检测结果分析

曲丹
吉林金域医学检验所有限公司

目的 检测长春地区孕妇体内 25-羟基维生素 D 含量，为本地区孕妇维生素 D 缺乏情况研究提供理论支持。
方法 选取 2021 年在我公司检测的表现健康的孕妇 2365 例，根据孕期阶段分为三组：孕早期，孕中期，孕晚期，采用蛋白沉淀及液液萃取等方法对样本进行前处理，运用高效液相色谱串联质谱仪，经过三重四极杆对其进行筛选，根据相应子离子在检测器产生的信号强度及所绘制的标准曲线来定量待测物的浓度。
结果 1、在不同孕期阶段孕妇维生素 D 检测中孕早期组 845 人，孕中期组 1257 人，孕晚期组 263 人，分析不同阶段孕妇维生素 D 水平，结果发现不同阶段孕妇维生素 D 的平均值之间差异有统计学意义 (P＜0. 05)；2、不同阶段维生素 D 缺乏率分别为：孕早期 68.17%，孕中期 92.02%，孕晚期 82.10%，分析不同阶段维生素 D 的缺乏率，对比参考标准值，发现不同阶段孕妇维生素 D 的缺乏率差异有统计学意义(P＜0. 05)；3、分析不同阶段孕妇维生素 D 缺乏率差异无统计学意义（P＞0.05）。
结论 在长春地区孕妇维生素 D 检测中，随着孕期的增长，缺维生素 D 的情况有所差异但差异不大。维生素 D 可调节钙的代谢，从而维持骨骼健康。若孕妇存在维生素 D 缺乏情况，则可能造成钙的缺失，也可能影响胎儿健康，危害极大，家长和社会各方面应当对孕妇予以，进行合理膳食，科学补充，监测及维持孕妇体内的维生素 D 处于正常水平，保证其健康生育。

PU-2783

新疆伊犁地区 13437 例孕妇产前传染病 4 项检测结果分析

潘贞贞、吴文礼
新疆生产建设兵团第四师医院

目的 分析新疆伊犁地区不同民族孕妇乙肝、丙肝、梅毒及艾滋病 4 种血源性传染病的感染状况，为有效控制传染病的传播提供科学依据。
方法 以近 5 年在我院门诊进行围产期检查的汉族和维吾尔族孕妇为研究对象，分别检测乙肝五项、丙型肝炎抗体（抗-HCV）、梅毒螺旋体抗体（TP-AB）和人类免疫缺陷病毒抗体（抗-HIV），均采用酶联免疫吸附试验（ELISA）。
结果 共检测 13437 名孕妇，年龄在 16~47 岁之间，本地区汉族和维
吾尔族孕妇 4 种传染病标志物阳性检出率为 6.97%（936/13437）。
乙肝表面抗原（HBsAg）总阳性率为 6.44%（865/13437），其中汉族 HBsAg 阳性率为 6.63%（836/12608），维吾尔族 HBsAg 阳性率为 3.63%（29/829）(χ2=12.673, P=0.000)；抗-HCV 总阳性率为 0.16%（21/13437），其中汉族抗-HCV 阳性率为 0.15%（19/12608），维吾尔族抗-HCV 阳性率为 0.24%（2/829）(χ2=0.034, P=0.853)；TP-AB 总阳性率为 0.34%（46/13437），其中汉族 TP-AB 阳性率为 0.24%（30/12608），维吾尔族 TP-AB 阳性率为 1.93%（16/829）(χ2=65.280, P=0.000)；抗-HIV 总阳性率为 0.03%（4/13437），其中汉族抗-HIV 阳性率为 0%（0/12608），维吾尔族抗-HIV 阳性率为 0.48%（4/829）(P=0.000)。
结论 孕妇传染病检测有利于传染病的早发现、早预防、早治疗，减少院内感染，有利于优生优育提高人口素质。

PU-2784

对新生儿 25-OHD 检测值的分析

孙悦
吉林金域医学检验所有限公司

目的 维生素 D 是一种类固醇衍生物，主要生理作用是调节钙的代谢，维持骨骼健康；还可以通过噬菌作用而增强免疫力，在抗肿瘤活性和免疫功能调节方面发挥着重要作用。25OHD 是维生素 D 在体内的稳定存在形式，其含量能客观的反映人体内维生素 D 的水平近年来，人们对维生素 D 的检测开始重视起来，所以了解新生儿 VD 含量的现状是很有必要的。
方法 在吉林金域医学检验所有限公司 2021 年 3 月 1 日到 2021 年 3 月 31 日维生素 D，共 9480 例样本中，选取年龄≤1 岁样本，共 379 例，经蛋白沉淀、液液萃取、氮吹、复溶等步骤，采用液相色谱串联质谱仪对新生儿维生素 D 的含量进行检测，运用 SPSS 进行数据分析。
结果 根据中华儿科杂志 25-OHD 参考区间，按照 D2+D3 的总 D 值进行分组，分如下 5 组：总 D 值＜5.0，共 4 例，占 1.1%；5.0＜总 D 值＜15.0，共 23 例，占 6.1%；15.0＜总 D 值＜20.1，共 20 例，占 5.3%；总 D 值＞20.1，332 例，占 87.6%。
结论 本公司样本的新生儿维生素 D 含量普遍正常，占筛查样本的 87.6%，维生素 D 不足和缺乏的占筛查样本的 12.4%。新生儿维生素 D 的含量主要于儿童佝偻病相关，人们对维生素 D 检测意识的上升，是预防儿童佝偻病的有效手段，关注新生儿维生素 D，加强人们检测意识，仍不可以掉以轻心。

PU-2785

柳州地区儿童哮喘血清过敏原 IgE 检测结果分析

罗宇程
柳州市妇幼保健院

目的 分析柳州地区儿童哮喘的常见过敏原，为儿童哮喘的诊治提供参考。
方法 选取本院 2020 年 5 月至 2021 年 4 月收治的 230 名哮喘患儿作为研究对象，参照 2016 年版《儿童支气管哮喘诊断与防治指南》，患儿前七天停用美喘清、强的松、扑尔敏等抗过敏药物及全身糖皮质激素，统计并分析其检测结果。实验结果采用江苏浩欧博公司试剂免疫捕获法测定。实验检测患儿血清中总 IgE、食物性过敏原特异性 IgE、呼吸性过敏原特异性 IgE 结果。以血清中总 IgE 判断患儿哮喘严重程度，将哮喘患儿分为轻度组、重度组，其中以总 IgE < 200 为轻度组，以≥200 为重度组，对其中两组中的食物性过敏原特异性 IgE、呼吸性过敏原特异性 IgE 阳性结果进行统计。
结果 从整体来看，在特异性 IgE 中，呼吸性过敏原以屋尘螨、粉尘螨、屋尘所占比例较大，食物性过敏原以鸡蛋、牛奶所占比例较大。以总 IgE 将患儿分为轻度组与重度组，在轻度组中，呼吸性过敏原 IgE 以屋尘为主，屋尘螨、粉尘螨、柳树也占有一定比例；食物性过敏原 IgE 以鸡蛋为主，牛奶、牛肉也占有一定比例；在重度组中，呼吸性过敏原 IgE 以屋尘螨、粉尘螨为主，屋尘、柳树、交链孢霉也占有一定比例，食物性过敏原 IgE 以鸡蛋、牛奶为主，牛肉、鳕鱼、虾、蟹等也占有一定比例。女性哮喘患儿过敏原阳性率与男性无显著差异。
结论 在哮喘患儿的诊疗过程中，血清过敏原检测可帮助临床医生准确、全面、有方向地了解患儿哮喘过敏原的具体因素，及时采取有效的治疗措施，加快哮喘患儿的康复进程。

PU-2786

The frequency window effect of sinusoidal electromagnetic fields in promoting osteogenic differentiation and bone formation involves extension of osteoblastic primary cilia and activation of protein kinase A

jian zhou、zhuo li
Department of Laboratory Medicine, The First Affiliated Hospital of Xi'an Medical University

Electromagnetic fields (EMFs) have emerged as a versatile means for osteoporosis treatment and prevention. However, its optimal application parameters are still elusive. Here we optimized the frequency parameter firstly by cell culture screening and then by animal experiment validation. Osteoblasts isolated from newborn rats (ROBs) were exposed 90 min/day to 1.8 mT SEMFs at different frequencies (ranging from 10 to 100 Hz, interval of 10 Hz). SEMFs of 1.8 mT inhibited ROB proliferation at 30, 40, 50, 60 Hz, but increased proliferation at 10, 70, 80 Hz. SEMFs of 10, 50 and 70 Hz promoted ROB osteogenic differentiation and mineralization as shown by alkaline phosphatase (ALP) activity, calcium content and osteogenesis-related molecule expression analyses, with 50 Hz showing greater effects than 10 and 70 Hz. Treatment of young rats with 1.8 mT SEMFs at 10, 50 or 100 Hz for 2 months significantly increased whole body bone mineral density (BMD) and femur micro-architecture, with the 50 Hz group showing the greatest effect. Furthermore, 1.8 mT SEMFs extended primary cilia lengths of ROBs and increased protein kinase A (PKA) activation also in a frequency-dependent manner, again with 50 Hz SEMFs showing the greatest effect. Pretreatment of ROBs with the PKA inhibitor KT5720 abolished the effects of SEMFs to increase primary cilia length and promote osteogenic differentiation/mineralization. These results indicate that 1.8 mT SEMFs have a frequency window effect in promoting osteogenic differentiation/mineralization in ROBs and bone formation in growing rats, which involve osteoblast primary cilia length extension and PKA activation.

PU-2787

用溴化乙锭改良人外周血染色体制备方法

吴斌
海南金域医学检验中心有限公司

目的 人类高分辨技术由于能显示出大量结构精细的带纹，在医学中可以发现之前不能发现的染色体微小畸变，有助于阐明染色体细微结构的异常与疾病之间的关系。但由于制备方法较为繁琐，我们参考以往制备高分辨染色体技术进行改良，使外周血染色体条带水平达到 500 以上，易于批量制备工作。

方法 随机选取送检本单位的无血液病实验对象 10 例，用肝素抗凝管抽取空腹外周静脉血 3 mL。每例标本接种 4 瓶培养基，每瓶培养基接种 0.6 ml 外周血。混匀置 37 ℃培养箱培养 72 小时。其中两瓶收获前 0.5 h 加入 1mg/ml EB 0.1ml 作为 EB 组，另外两瓶不加 EB 作为对照组。收获前 10 min 加入 20 ug/ml 秋水仙胺 0.1ml。将培养基以 2100r/min 离心 5 分钟，弃上清液。加入 37℃预热的 0.075M/L KCL 8ml，充分混匀，37℃水浴 30 分钟。加入 2ml 固定液轻轻混匀，以 2100r/min 离心 7 分钟，弃上清液。加入固定液 8ml，轻轻混匀，以 2100r/min 离心 7 分钟，弃上清液。重复上述步骤，再固定两次。视管底细胞量加入 1~2ml 适量固定液，轻轻混匀制成细胞悬液。使用 4℃冰水浸泡的玻片，距离 10~15cm 高度滴片 2 张，放入染色体分散仪（温度：25℃,湿度：50%）进行风干。90℃烤箱烘烤 1 h。胰酶消化显带，吉姆萨染色后用自来水冲洗、晾干。

结果 EB 组可获得约 550 左右条带，带纹清晰，相比于对照组长度有明显差异。
结论 本研究采用 EB 阻止凝缩法，参考高分辨染色体制备技术进行改良，制备的染色体条带水平在 500 以上，分裂指数和分散程度良好，且操作流程更加简便，有较好的应用和推广价值。

PU-2788

甘肃 32161 例微量元素钙不同年龄段及不同地区结果分析

王小凤
甘肃金域医学检验所有限公司

目的 微量元素钙是机体生长发育，生命活动及繁衍等必不可少的元素，是构成骨骼和牙齿的必须成份；维持心脏的正常波动，神经、肌肉的正常兴奋性以及细胞内外水分和渗透压的平衡，调节体液容量，参与血液的凝固过程；生物膜的组成成份，维持细胞胶质的完整性。所以微量元素钙的检测具有重要的临床意义。
方法 微量元素钙的检测通过火焰原子吸收光谱法对 32161 例甘肃各地区医院的临床患者及体检样本。
结果 通过对 32161 例样本进行检测分析，分析发现男女性别之间无显著差异性 P>0.05（X2=0.000,P=0.833），即不具有统计学意义；按照不同年龄段进行分析，分析可得，不同年龄段之间具有显著差异性 P<0.001（X2=2902.949,P=0.000），即具有统计学意义，按年龄段分析发现，婴幼儿在 6 月-12 月异常率最高，成年后随着年龄的不断增长，异常率逐渐增加；按照不同地区进行分析，各地区之间全血微量元素钙检测结果具有显著差异性 P<0.001（X2=350.652,P=0.000），即具有统计学意义，异常率最高的地区为陇南，异常率为 77.23%，异常率最低的地区为临夏，异常率为 56.54%。

PU-2789

福建省某三甲医院检验科 2006-2019 年投诉原因分析与改进思考

马跃飞、刘灿、王炳龙、林锦骠、欧启水、杨滨
福建医科大学附属第一医院

目的 分析投诉产生的原因，探讨改进措施及成效，为进一步改善服务、提高医疗质量和满意度提供思路。
方法 回顾性分析。收集某医院检验科自 2006 年到 2019 年间受理的 47 起来自服务对象的投诉，分析投诉的性质、特点、产生原因和趋势。针对投诉内容，该科室不断改进和优化服务质量和检验流程，包括建立完善的质量管理体系，提高执行力；升级硬件设备、完善信息系统软件功能；加强专业素养人文素养的培训；以问题为导向，加强与临床沟通等，并通过了 ISO15189 实验室认可。
结果 47 份投诉中，26 份为有效投诉。有效投诉贯穿于分析前、中、后各阶段；以急诊临检组和门诊组受理的居多，分别有 10 起和 8 起。归因于“制度和流程”的有效投诉最多，有 23 起，与“技术水平”和“服务质量”相关的分别有 11 起和 8 起。制度不完善、执行不力是“制度和流程”类投诉的主要原因。与服务相关的投诉主要为检验与临床沟通不到位。技术类投诉主要由检验错误和报告延时所致。以中间时间点（2012 年）为界作前后对比发现，与制度流程和服务质量相关的投诉量均有增加；与技术层面相关的投诉量明显下降。优化信息系统、升级硬件、完善制度明确岗位职责和有力推行定期能力验证计划等措施能明显降低投诉量。从可查阅的数据看，投诉发生率总体趋势（线性）下降，服务对象满意度总体趋势（线性）上升。

结论 投诉是质量和管理薄弱环节的综合暴露。夯实质量体系、优化软硬件功能和提高专业能力和服务水平的举措对降低投诉发生率、提高满意度具有重要作用。

PU-2790

抗人缪勒氏管激素（AMH）在女性卵巢健康领域的临床应用

后江红
甘肃金域医学检验所有限公司

卵巢健康对于女性来说非常重要，这是每个女性都必须要关注的问题，当卵巢健康出现问题时，身体各方面都会有异常，也是女性身体年轻的一种表现，因此卵巢健康是女性身体是否健康的一个晴雨表。而抗人缪勒试管激素（AMH）在评估女性生育能力、辅助不孕病因诊断、提早预测卵巢相关疾病是非常重要的指标之一。

PU-2791

中药鸡骨香中抗肿瘤活性成分检测分析

林兆民、高冬芳、张璐、王鹏、林御星、陈元
山东大学第二医院

以抗肿瘤活性为指导，从民间中药鸡骨香的干燥根中找寻具有肿瘤细胞增殖抑制作用的萜类化合物，并对其活性机制进行研究。以 MTT 法测试肿瘤细胞增殖抑制作用，以此活性结果为指导，分离过程中只选择活性部位，直至分到纯化合物。柱层析法分离并纯化化合物，包括正相硅胶，葡聚糖凝胶，反相硅胶，制备高效液相等柱层析，通过各种波谱方法确定化合物结构：核磁共振，高分辨质谱，紫外光谱，红外光谱等。从中药鸡骨香提取物中分离得到了 15 个萜类化合物，鉴定了其结构。进一步的抗肿瘤活性筛选结果显示部分化合物呈现出很好的活性。中药鸡骨香中含有具有抗肿瘤活性的萜类化合物，值得进一步进行研究，为药物研发打下基础。

PU-2792

2018~2020 年岳阳市儿童临床常见多重耐药菌感染及耐药性分析

李童、杨昊
岳阳市妇幼保健院

目的 了解某院儿童感染多重耐药菌的分布特点及趋势，指导临床合理使用抗生素及预防和控制多重耐药菌。
方法 收集 2018 年 1 月-2020 年 12 月我院住院患儿 (包括新生儿科和儿科) 多重耐药菌检测结果及细菌药敏试验结果，对其分布特点和耐药性进行分析。
结果 三年来本院送检的 19033 例标本中共分离到病原菌 2199 株，其中多重耐药菌 282 例，占 12.82% (282/2199)。2018 年、2019 年和 2020 年多重耐药菌感染率分别是 13.30%、12.67%和 12.47%。三年来本院主要病原菌排名前三位的是大肠埃希菌、金黄色葡萄球菌和肺炎克雷伯。痰液为送检率最高的标本，也是检出多重耐药菌最主要标本；其次为咽拭子、尿液和血液。革兰阴性多重耐药菌对氨苄西林、替卡西林、哌拉西林、头孢噻吩、头孢唑啉、头孢呋辛、头孢克肟和头孢噻肟 8 种药物的耐药率均大于 80%，对亚胺培南、美洛培南和阿米卡星的耐药率均低于 10%。革兰阳性多重耐药菌对青霉素和苯唑西林的耐药率达 100%，对红霉素、庆大霉素、克林霉素和泰利

霉素耐药率大于 50%，对替考拉宁、喹奴普汀/达福普汀、米诺环素耐药率较低小于 5%，对呋喃妥因和万古霉素均为 100%敏感。
结论 2018 -2020 年本院儿童临床常见多重耐药菌以革兰阴性菌为主，大肠埃希菌呈上升趋势，金黄色葡萄球菌呈下降趋势。本院多重耐药菌感染的主要来源是呼吸道感染、泌尿系统感染和血流感染。三年来本院检出革兰阴性多重耐药菌对氨苄西林和替卡西林的耐药率较高，而对亚胺培南、美洛培南和阿米卡星的较为敏感。革兰阳性多重耐药菌对青霉素和苯唑西林的耐药率较高，对呋喃妥因和万古霉素均较为敏感。因此在临床多重耐药菌抗感染治疗的过程中，临床医生应根据患儿临床症状和以上分析的结果选择较为敏感的抗菌药物进行治疗，然后根据细菌培养和药敏结果及时进行药物调整，避免耐药菌株和泛耐药菌株的产生和传播。

PU-2793

结直肠癌患者血浆中细胞因子的诊断价值研究

蒋琰[1]、刘嘉妮[2]
1. 湖南省人民医院
2. 湖南师范大学

目的 探讨六种细胞因子（IL-4、IL-6、IL-10、IL-17、TNF-α、IFN-γ）在结直肠癌患者外周血的表达水平变化及其与结直肠癌的 TNM 临床病理参数（手术病理分期、组织分级、淋巴结转移程度）的关系，为评价结直肠癌的疾病进展情况提供可靠的参数值，以期成为参与结直肠癌临床病情评估的指标。
方法 随机选取 2020 年 10 月-2021 年 3 月湖南省人民医院收治的 30 例结直肠癌患者的肠活组织标本为结直肠癌实验组，按照 TNM 国际肿瘤分期系统将其分为 ＴⅠ、TⅡ、TⅢ、TⅣ组，患者年龄多为 50-70 岁，另外收集医院病理诊断为正常者 30 例作为正常对照组。留取此 30 例结直肠癌患者术前以及正常对照组 EDTA 抗凝全血，运用流式细胞术检测结直肠癌实验组、对照组循环血中此六种细胞因子的表达情况。
结果 IL-6、IFN-γ、TNF-α 在结直肠癌实验组外周循环血液中的表达水平高于对照组（P＜0.05）。随着病理分期的逐渐增高，IL-6 在结直肠癌中的表达水平呈逐渐上升趋势，且各个分期之间具有统计学意义（P＜0.05）。随着肿瘤分化程度的逐渐降低，IFN-γ 在外周血的表达升高（P＜0.05）。IL-6 与 IFN-γ 在结直肠癌实验组外周血中表达具有正相关性（r=0.50，P＜0.05）。
结论 结直肠癌实验组患者外周血中 IL-6、IFN-γ、TNF-α 表达水平增高。其中 IL-6 随着结直肠癌患者临床分期的升高逐渐增高，IFN-γ 随着结直肠癌分化程度的降低而逐渐升高。IL-6 与 IFN

PU-2794

Age-Specific Reference Intervals for High-Sensitive Cardiac Troponin T Among the Apparently Healthy Children

Jia Wei、Hanjun Shen
Children's Hospital of Soochow University

Background High-sensitivity troponin T (hs-cTnT) assay was widely used in the diagnosis of myocardial injury. However, the 99th percentile upper reference limits (URLs) derived from Roche’s product manual was established from multi-clinical centers in the United States and Europe for adults. Relatively few studies explored to determine the indications for the hs-cTnT application and how to interpret the values among children. Some investigators postulated that the higher level of troponin T in neonates may be caused by programmed cell death during the first 3 months of life. Therefore, it is necessary to establish the pediatric reference interval (RI) of

hs-cTnT to provide a basis for the clinical interpretation. Our study aimed to establish suitable RIs of hs-cTnT for Chinese children.
Methods A total of 1126 reference individuals presented to the Children's Hospital of Soochow University from December 2019 to March 2021were enrolled in our study. The laboratory data and medical history of children were retrospectively reviewed and exported from the laboratory information system (LIS) and electronic medical records. The hs-cTnT assay was carried out on the electrochemiluminescence (Cobas e 411, Roche Diagnostics, Germany), using a ruthenium labeled antibody. The inter-assay coefficient of variation for hs-cTnT was 4.74%. According to the Clinical and Laboratory Standards Institute C28-A3 guideline, the 99th percentile URLs with 90% confidence intervals (CIs) were calculated in different age and sex subgroups. The imprecision profile was assessed by repeatedly measuring 3 levels of serum pools. According to the CLSI guideline EP5-A2, these pools of mean, the inter-assay precision and total CVs were calculated Data of hs-cTnT were analyzed through SPSS ver 24.0 (IBM Corp, USA) and GraphPad Prism ver 8.0 (GraphPad Software, USA). $P<0.05$ was considered statistically significant. The distribution of data was obtained based on the Shapiro-Wilk test and non-Gaussian distribution data were expressed as median with interquartile range (IQR). The Wilcoxon signed-rank test was utilized to compare the levels of hs-cTnT in paired children. The hs-cTnT level between different age groups was compared by the Kruskal-Wallis one-way analysis of variance. Besides, the Spearman correlation analysis was used to evaluate the association between hs-cTnT and months of age. The Mann-Whitney U test was used to determine different sex subgroups.
Results In total, 1124 samples were drawn to analyze hs-cTnT (Median (IQR) of hs-cTnT: 6.27(4.28, 10.71) ng/L). There was no individual excluded as outliers from the reference population. Elevated hs-cTnT were observed in the infants (< 3 months) and gradually decreased with months of age ($r=-0.736$, $P<0.001$). Median values of hs-cTnT among neonates and infants younger than 3 months old were 33.60 ng/L and 24.04 ng/L respectively, which were both higher than 14 ng/L. The 99th percentile URLs of hs-cTnT were 37.31 (90%CI: 36.87-37.74) ng/L for 1-3 months old, 25.89 (90%CI: 24.46-28.26) ng/L for 4-12months old and 12.10 (90%CI: 11.25-12.95) ng/L for 1-18 years old, respectively. For children older than one year old, boys had a higher 99th percentile limit than girls (12.35 (90%CI: 11.05-12.95) ng/L VS 12.08 (90%CI: 11.02-14.50) ng/L). More than 99% of children elder than one year old had hs-cTnT below 14 ng/L in our study. However, owing to the insufficient sample size, further research about the RIs among neonates (≤28 days) was needed. The limit of blank (LoB) and limit of detection (LoD) were mentioned to be 3 ng/L and 5 ng/L in the manufacturer's specifications. The percentage of troponin concentrations measurable above the LoD in all groups exceed 50%
Conclusion Our study first established the age-specific RIs of hs-cTnT for children. The above RIs of hs-cTnT in different age groups may assist clinicians to better interpret and use hs-cTnT values in pediatric cardiomyopathies.

PU-2795

浅谈精神专科医院检验科的科学发展

蔡燕姗、薛雄燕、陈家强
佛山市第三人民医院（佛山市精神卫生中心）

结合精神专科医院的实际情况，对检验科目前的发展的影响因素做出分析，从实际工作经验中提出实用可行的建议，并对未来精神专科的发展方向和潜力作出分析。

检验科作为医院的辅助科室目前检验科所开展的项目，则多数用于躯体疾病的诊疗和预后观察，对辅助诊断精神病的检查项目开展比较少。因此，对精神专科检验科的发展，必须做好科学的计划我们从检验项目开展、质量控制、医疗服务模式创新、与临床建立沟通的桥梁几方面进行探讨。
对药物浓度监测、中枢神经递质及其代谢产物、神经内分泌激素和神经肽胺体项目的开展提出可行性的依据。对于特异性高的基因项目的检测也要开始进行我们精神专科的发展规划里。就实验室质

量体系的建设提出一些存在的难点，包括分析前和分析中的两个常见问题，并提出信息化系统的相关建议，更保证检测结果的准确性。

提出医疗服务模式的创新理念，精神专科医院逐步推行精神病人社区信息管理网格化，检验科应该强化信息化支撑，推进建设与之相匹配的智能检验服务体系。

如何建立检验科与临床沟通的桥梁 ？检验科与临床之间由于知识结构的不同，沟通交流总是存在着一些不可避免的问题。检验医师的培养对双方沟通有着积极的作用，还能促进科室的发展。检验科是医院不可或缺的一部分，除了做好日常的标本检测工作，还应该关注检验科的发展规划，我国目前大部分专医院对检验科发展还不够重视，对检验科发展的投入占比也比较少，因此，不能只依靠医院的投入，立足自身，提高整体。

PU-2796

检验科护士专利申请特点与应用

白璐、陈丽勤
陆军军医大学第一附属医院（西南医院）

目的 了解门诊检验科护士专利申请特点，为拓展护理创新思路和获得专利授权提供参考。
方法 采用回顾性统计分析法，2017 年 6 月-2020 年 12 月检验科护理组获得国家专利授权共 20 项，其中发明专利 6 项，实用新型专利 14 项。授权发明类型涉及:采血用留置针的改进；止血带装置设计；葡萄糖水调配装置；清洁消毒装置；弹力绷带缠绕装置。授权实用新型专利类型涉及:试管架功能、外观的改进；采血管收集、流转装置；采血物品的规范放置和使用仪器；便携指血采集装置；辅助沟通设备改进；垃圾分类装置。
结果 授权专利设计思路源于发现和解决临床实践中的护理问题，在自动化和智慧护理的背景下，应用机械设备等多学科知识，大胆创新，设计可能用于临床、符合逻辑的设施设备。由此，做好流程管控，节省人力物力财力和时间成本，提高患者满意度的同时提升护理效率和质量。
结论 护理专利是日常工作的梳理、总结，体现护理创新思维在护理实践中的应用，有助于护理科研的进一步挖掘。

PU-2797

长角血蜱中携带日本立克次体和新立克次体

秦祥荣
山东大学第二医院

立克次体属革兰氏阴性专性细胞内细菌，通过节肢动物媒介的叮咬感染人类和各种脊椎动物。硬蜱是斑点热组 (SFG) 立克次体的主要传播媒介。最近，发现几种新出现和重新出现的 SFG 立克次体可感染人类。日本立克次体是日本斑疹热的病原体。自 1984 年以来在日本、韩国和泰国均有报道。我们采集了山东省的蜱，通过 PCR 方法进行扩增，PCR 扩增表明立克次体感染率最低。在中国山东省采集的长角血蜱中为 0.66%。基于 rrs、gltA、ompA 和 ompB 基因的系统发育分析表明，蜱携带 R. japonica、Candidatus Rickettsia longicornii 和与 R. canadensis 相关的新立克次体物种。

PU-2798

长角血蜱携带无形体种类的检测

秦祥荣
山东大学第二医院

无形体（Anaplasma）是一种蜱传播的细胞内寄生细菌，可以感染人类和其他动物。中国的蜱携带的无形体种类目前还不是很清楚，本文目的是检测山东省胶南市蜱携带无形体的种类。从2013 年至 2015 年，我们在中国的山东省胶南县的植被中收集了 3145 只长角血蜱，包括 120 只幼虫，2460 只若虫和 565 只成虫。我们通过巢式 PCR 扩增了无形体的 16S rRNA 基因，检测了所有蜱携带的无形体种类。为了进一步区分 Anaplasma capra 与 Anaplasma centrale，我们又进一步使用 gltA 和 msp2 基因的引物进行扩增及测序。结果在若虫和成虫中检测到了三种无形体的种类，我们以最小感染率来计算蜱的病原体携带率，蜱的最小感染率如下：Anaplasma bovis 的感染率为 1.55％,Anaplasma phagocytophilum 的感染率为 0.10％, Anaplasma capra 的感染率为 0.03%。这些结果表明，胶南县的长角血蜱携带多种无形体种类，在很大程度上也说明蜱携带的无形体是公共卫生面临的重要挑战。

PU-2799

m6A 与程序性细胞死亡的相关性

刘莉
南华大学附属第一医院

In recent years, m6A methylation has increasingly caught scientists′ and researchers′ eyes, becoming a hot research topic. m6A plays multifunctional roles in bioprocesses, normal and abnormal. Aside from the earliest known apoptosis, more emerging programmed cell death(PCD) pathways get much-watched.The regulations among them tend to be plastic and feasible at the molecular level. Herein, what we want to have our minds on is a taste of high-complexity linked m6A and PCD types, e.g. pyroptosis, autophagy, and apoptosis, which is associated with the initiation and progression of cancer. There is a deserved focus—— that is, to realize that m6A functions largely dependent on its regulators and they are frequently context-reliant.

PU-2800

2020 年东北地区高苯丙氨酸血症结果分析

郝静
吉林金域医学检验所有限公司

目的 高苯丙氨酸血症为东三省常见的遗传代谢病之一，通过分析高苯丙氨酸血症结果以及复查结果了解疾病治疗情况，为临床提供参考依据。
方法 回顾本公司 2020 年 1 月至 2020 年 6 月经检测确诊为高苯丙氨酸血症患者 68 例，以及患者高苯丙氨酸血症复查结果,监测治疗情况。采用高效液相色谱质谱联用仪，检测苯丙氨酸（Phe）、苯丙氨酸与酪氨酸比值（Phe/Tyr），本实验室方法 Phe＞150，Phe/Tyr＞2.0 即可初步筛查为高苯丙氨酸血症。
结果 临床上有一过性高苯丙氨酸血症，可能由于苯丙氨酸羧化酶未成熟，导致血中苯丙氨酸浓度升高，但随着年龄的增长，血苯丙氨酸浓度可降至正常。患者一经确诊，应暂停天然饮食，低或者无苯丙氨酸饮食治疗；现主要方式为给予患者无苯丙氨酸特殊奶方治疗，根据患儿体重以及苯丙氨酸水平在，确定治疗方案。回顾结果发现，高苯丙氨酸血症患者治疗效果较好，相关指标明显降低，

若控制良好，苯丙氨酸可在正常范围内，可根据具体情况调整无苯丙氨酸奶粉用量适当加入母乳治疗。
结论 高苯丙氨酸患者开始治疗的年龄越小，预后越好，新生儿早期治疗者智力发育科接近正常人。遗传代谢病临床表现复杂多样，轻重不同，体内任何器官以及系统均可受累，一般的临床表现为智力发育落后，抽搐，昏迷，呼吸异常等表现，遗传代谢病患者若不得到及时治疗，常可致残，甚至危及生命。所以我们应该提高对遗传代谢性疾病的检测意识，做到早期诊断，及时处理、挽救生命、避免或者减少严重并发症及神经系统伤残的关键。

PU-2801

Identification of Novel Glycolysis-Related Gene Signatures Associated With Prognosis of Patients With Clear Cell Renal Cell Carcinoma Based on TCGA

Chengjiang Wu
The Second Affiliated Hospital of Soochow University

Objective The purpose of the present study was to detect novel glycolysis-related gene signatures of prognostic values for patients with clear cell renal cell carcinoma (ccRCC).
Methods Glycolysis-related gene sets were acquired from the Molecular Signatures Database (V7.0). Gene Set Enrichment Analysis (GSEA) software (4.0.3) was applied to analyze glycolysis-related gene sets. The Perl programming language (5.32.0) was used to extract glycolysis-related genes and clinical information of patients with ccRCC. The receiver operating characteristic curve (ROC) and Kaplan–Meier curve were drawn by the R programming language (3.6.3).
Results The four glycolysis-related genes (B3GAT3, CENPA, AGL, and ALDH3A2) associated with prognosis were identified using Cox proportional regression analysis. A risk score staging system was established to predict the outcomes of patients with ccRCC. The patients with ccRCC were classified into the low-risk group and high-risk group.
Conclusions We have successfully constructed a risk staging model for ccRCC. The model has a better performance in predicting the prognosis of patients, which may have positive reference value for the treatment and curative effect evaluation of ccRCC.

PU-2802

持续质量改进在采血和护理中的应用分析

杜秋明、王海燕、郭笑然
吉林大学第一医院

目的 探讨和分析持续质量改进在采血护理中的应用价值。
方法 质量持续改进于 2019 年 6 月开始。 分别于 2019 年 1-6 月和 2019 年 7-12 月随机抽取 600 名患者，对持续质量改进前后采血护理质量进行比较，对患者采血相关知识进行评分，统计改进前后不良事件发生率。
结果 实施持续质量改进后，患者对穿刺技术、健康教育、排队、样品运输等问题的满意度明显高于实施持续质量改进前。 同时患者对穿刺技术，健康教育，排队，样本运输等方面的满意度均显著高于实施持续质量改进前，差异具有统计学意义(P<0.05)。 持续质量改进后 0.0%的不良事件发生率明显低于改进前 3.0%，P 值<0.05。
结论 在医院门诊采血护理中实施持续质量改进，可有效提高采血护理水平，提高患者对采血知识的了解，降低护理不良事件发生率，具有较高的应用价值。

PU-2803

吉林地区糖尿病患者维生素 D 结果分析

廉春晖
吉林金域医学检验所有限公司

目的 通过分析对吉林地区糖尿病患者血清 25OHD 检测结果，了解糖尿病与维生素 D 缺乏相关性。
方法 采用高效液相色谱串联质谱仪，取 200ul 血清，经过液液萃取，蛋白沉淀等前处理方法后进行检测，选取 2020 年本公司检测 2 型糖尿病 1396 例，根据维生素 D 水平情况，分为 3 组，分别为维生素 D 缺乏：<20 ng/mL（935 例），维生素 D 不足：20-30 ng/mL（272 例），维生素 D 正常：30-100 ng/mL（189 例）；数据采用 SPSS22.0 统计学软件分析。
结果 2 型糖尿病患者各组维生素 D 水平情况如下：缺乏 66.9%；不足 19.5%；正常：13.6%；吉林地区 2 型糖尿病患者维生素 D 水平缺乏以及不足情况比较常见，发现各组之间缺乏率差异有统计学意义(P＜0.05)。
结论 2 型糖尿病患者血清 25 羟维生素 D 缺乏较普遍，可能与 2 型糖尿病合并其他脏器疾病有相关性，2 型糖尿病常见的并发症有糖尿病肾病，肾脏是维生素 D 作用的重要靶器官，肾小球系膜细胞、肾远曲小管、近曲小管、足细胞、集合管、髓袢等均具有维生素 D 受体。维生素 D 通过与相关受体结合具有一定的肾脏保护作用，故肾脏等相关脏器受损，可能影响血清维生素 D 合成及发挥作用，故而可能增加了疾病发生的风险。现研究表明除经典的维生素 D 缺乏疾病（佝偻病、骨质疏松等），多种慢性病例如，高血压、动脉粥样硬化以及肿瘤等均与维生素 D 缺乏有关，需要提高维生素 D 补充的意识，避免疾病的发生和发展。

PU-2804

新辅助化疗引起激素受体状态改变的研究

公娉
山东大学第二医院

乳腺癌是一种异质性疾病，内分泌治疗靶向治疗是乳腺癌治疗过程中重要有效的治疗方法。时下，乳腺癌常用病理学生物标志物，如雌激素受体、孕激素受体、HER2、Ki-67，常用来进行诊断指导乳腺癌患者术后的辅助治疗(41)。

新辅助化疗是局部肿块较大的乳腺癌患者术前常用的减瘤方案。其主要目的在于 1. 对于不适用手术的局部晚期乳腺癌患者降低其分期，使手术成为可能，使早期乳腺癌患者提高实行保乳手术的可能性。新辅助化疗之前通常进行核心针穿刺活检来明确诊断，并进行免疫组织化学检测来确定 ER、PR、HER2、Ki-67 等生物标志物的状态，有利于新辅助化疗后及术后辅助治疗的选择以及患者预后的判断。

过去的研究已经证实，新辅助化疗可以改变患者的激素受体（HR）、原癌基因人类表皮生长因子受体（HER2）、Ki-67、P53 等指标的状态。ER 表达从阳性变为阴性的患者相对于 ER 从阴性变为阳性或者没有改变的的患者从新辅助化疗中受益的要小。然而，新辅助化疗后激素受体的改变对于患者预后有什么影响还知之甚少。我们本次研究的目的是探究乳腺癌患者新辅助化疗前后生物标记物的改变，以及各类型的预后情况分析。

1．研究方法

回顾性研究分析了于 2005 年 1 月 1 日至 2016 年 11 月期间确诊为乳腺癌并于山东大学齐鲁医院接受乳腺外科手术的 5305 位女性患者的临床病理资料。接受新辅助化疗的患者共计 301 位，只接受术前穿刺未进行术前新辅助化疗的患者 71 位。本次研究的纳入标准为：住院期间接受手术治疗；术后的大体病理结果为乳腺癌，新辅助化疗组为完成 4 个周期化疗且有完整的病理信息的女性乳腺癌患者，穿刺组为术前接受穿刺但未接受新辅助化疗且有完整的病理信息的患者。排除标准：

男性乳腺癌；双侧乳腺癌；新辅助化疗后达到病理完全缓解的患者，PCR 定义为乳腺原发灶和腋窝淋巴结手术标本病理检查无浸润性肿瘤细胞残余。

PU-2805

乳腺癌治疗过程中内分泌治疗依从性的研究

公娉
山东大学第二医院

研究目的 在中国，乳腺癌的发病率逐年上升，乳腺癌是女性常见的恶性肿瘤之一，也是女性常见的死亡原因。手术治疗是其主要的治疗方式，化疗、放疗、内分泌治疗、靶向治疗等个体化综合治疗策略的不断成熟使得乳腺癌获得了理想的疗效和预后，但仍有一部分患者出现复发和转移。乳腺癌激素受体状态的测定是内分泌治疗选择的基础，所以，乳腺癌原发肿瘤的激素受体状态已经成为常规的分子病理学检查。但是，乳腺癌患者的激素受体状态缺乏大数据的统计。乳腺癌患者激素受体状态在治疗前后是否出现改变，经过治疗之后的复发转移癌巢的激素受体状态与原发肿瘤是否存在差异尚知之甚少。本研究旨在大数据统计分析山东省乳腺癌患者激素受体状态，研究乳腺癌患者雌激素受体（estrogen receptor, ER）、孕激素受体（Progesterone receptor, PR）等生物标志物在乳腺癌原发肿瘤、新辅助化疗、复发转移过程中的变化，探讨生物学特性改变的临床意义以及对预后的影响。
研究方法 回顾性分析 2005 年-2016 年于山东大学齐鲁医院收治的乳腺癌患者 5305 例，其中有完整的病理信息的患者 4786 例。回顾性分析其临床病理资料，其中术前接受穿刺的患者 71 例，接受新辅助化疗的患者 301 例，原发肿瘤及转移部位均进行病理学检查的患者 39 例。应用内分泌治疗的患者 1839 例，统计分析应用内分泌治疗的患者服药的种类及其依从性情况。计量资料比较采用 t 检验，计数资料比较采用卡方检验（Chi-square test，X2 检验），等级资料的比较采用 wilcon 秩和检验。Kaplan-Meier 法计算生存率及绘制生存曲线。以 $p<0.05$ 视为异有统计学意义。
研究结果 乳腺癌患者依从性为 62.7%
研究结论 乳腺癌患者依从性有待提高。

PU-2806

发酵支原体 MALP-2 生物学作用研究进展

梁珂莹
南华大学附属南华医院

巨噬细胞活化脂肽-2(MALP-2)是发酵支原体(Mf)上极具代表性的外膜脂肽,N 端为特殊的二酰化半胱氨酸残基结构。 MALP-2 是一把“双刃剑”,在致炎与抗炎、细胞凋亡与抗凋亡、免疫佐剂、生物协同与抑制、 血管损伤和血管修复等方面发挥重要作用。 因此,了解 MALP-2 复杂的生物学作用能为理解 Mf 的致病机制及其 临床治疗方案提供依据,同时也为 MALP-2 的临床应用提供理论基础。

PU-2807

急性肾损伤诊断及预后标志物研究进展

刘春梅[1]、李博慧[2]
1. 江苏省苏北人民医院
2. 大庆第三人民医院

目的 通过对最新文献的学习，总结近几年急性肾损伤（Acute kidney injury,AKI）诊断及预后的最新指标，为开展进一步的分子机制研究提供思路，也为临床的早期诊断和治疗提供理论依据。
方法 在中国知网数据库使用关键词“急性肾损伤”，在 PubMed 数据库使用关键词“Acute kidney injury”搜索近五年的中英文文章，通过文章题目或摘要筛选出需要精读的论文 ，进行全文阅读，精读文章共计 63 篇。总结急性肾损伤的最新诊断与预后标志物的研究思路。
结果 急性肾损伤的诊断仍然沿用 2012 年 KDIGO 的诊断标准，以血清肌酐和尿量作为诊断指标，以 AKI 分期及患者透析效果判断患者的预后。过去几年新兴起的标志物，如中性粒细胞明胶酶相关脂质体运载蛋白(NGAL),肾损伤分子-1（KIM-1）,L 型脂肪酸结合蛋白（L-FABR）都因检测技术难度大，诊断效能不理想，而未能应用到临床的诊疗工作中。最近对于急性肾损伤诊断标志物的研究大都集中于亚细胞水平，如线粒体损伤，内质网应激，代谢重编程，细胞周期阻滞等方面，这些指标可以在细胞发生损伤之前就出现变化，可以更早期识别急性肾损伤的发生。对于急性肾损伤预后指标的研究大都集中于实验室常规指标的联合分析，如中性粒细胞/淋巴细胞比值（NLR）,红细胞分布宽度（RDW）,高密度脂蛋白/中性粒细胞比值，血清白蛋白水平等，这些常规指标的新应用，在减轻患者经济负担的同时还能更大程度发挥这些指标的临床价值。
结论 目前对 AKI 诊断与预后评估的标志物研究进展缓慢，在亚细胞水平研究 AKI 的早期诊断标志物，利用实验室信息系统和住院电子病历，分析实验室常规指标在 AKI 预后中的价值将是未来科研工作者的研究方向。

PU-2808

陕西省西安地区围绝经期妇女阴道微生态状况分析

李春娟、赵小军
西安医学院第二附属医院

目的 了解本地区围绝经期妇女阴道微生态状况并探讨其失衡的原因。
方法 通过收集 2019 年 7 月-2021 年 4 月到我院妇科就诊的围绝经期患者 154 例，进行阴道微生态检测分析，并对结果进行分析。
结果 154 例就诊患者中，阴道微生态微失衡 111 例（72.0%），其中细菌性阴道炎（BV）43 例（27.9%），滴虫性阴道炎(TV)18 例（11.7%），念珠菌阴道炎(VVC)8 例（5.2%），BV 和 TV 双重感染 2 例（1.3%），BV 和 VVC 双重感染 1 例（1.6%）。阴道分泌物干化学法和革兰氏染色镜检的三种主要病原体结果无统计学差异（BV P=0.395、TV P=0.627、VVC P=0.64，P>0.05）。两个年龄组相比 BV(P=0.041)、菌群异常或抑制(P=0.008)两者有统计学意义（P<0.05）。
结论 本地区围绝期妇女阴道微生态的清洁度随着年龄的增长而下降，最常见的阴道炎为 BV、TV、VVC,还有少数为双重病原体感染,严重影响了围绝经期妇女的生活质量，所以需重视围绝经期妇女的生殖系统的卫生健康，做到早重视、早预防、早治疗。

PU-2809

721 例唐氏综合征患者外周血染色体核型分析的回顾性研究

张倩、张美玲、张丽敏、赵旷怡、潘攀
郑州金域临床检验中心有限公司

目的 探讨河南地区 2018 年至 2020 年 721 例唐氏综合征患者的年龄、性别、类型等分布情况，并对其进行统计学分析。
方法 对 2018 年至 2020 年在我中心进行外周血染色体核型分析的 42719 例标本，从中筛选出 721 例唐氏综合征患者，采用外周血淋巴细胞培养和 G 显带技术，进行染色体核型分析。
结果 在 42719 例外周血染色体核型分析标本中，共检出唐氏综合征患者 721 例，检出率为 1.69%，其中男性 419 例，占 58.11%，女性 302 例，占 41.89%；年龄段集中在 0-10 岁，共 663 例，占 91.96%；共检测 38 种核型，其中单纯性三体 675 例，占 93.62%，易位型 31 例，占 4.30%，嵌合型 15 例，占 2.08%。
结论 对 721 例唐氏综合征患者的外周血染色体进行统计学分析，发现年龄段集中在 0-10 岁，男性略高于女性，共检测 38 种核型，其中单纯性三体最为常见，易位型次之，且以 der(21;21)最多，嵌合体最少。

PU-2810

六西格玛和 5s 质量管理在临床生化实验室应用

张苹
暨南大学附属第一医院

目的 应用六西格玛质量管理方法，对我院引进的全自动生化分析系统贝克曼 AU5800 的性能验证数据进行分析，熟悉各生化项目的分析性能，设计质量控制方案，指导质量改进。利用 5s 管理理念即“整理- 整顿-清扫-清洁-素养”提高工作质量和工作效率，有效利用空间，提高科室形象。
方法 选取 26 个常规生化项目，分析贝克曼 AU5800 在 2020 年 1 月至 12 月时的性能验证数据，主要包括偏移(BIAS) 和不精密度(CV) ，根据卫生行业标准 WS /T403-2012 规定的项目允许总误差(TEA) ，计算西格玛值(σ) 并绘制标准化的西格玛性能验证图从而设计质控规则。同时计算所有项目的质量目标指数(quality goal index，QGI) ，查找 σ 值小于 6 的检验项目分析性能不佳的主要原因。
结果 26 个常规生化项目中，分析性能 σ 值≥6、5、4 和 3 者分别占 61.54% 、3.85% 、11.54% 和 7.69% ，全部检验项目的平均 σ 值为 7.105; 在未达六西格玛的 11 个检验项目中，43.75% 的项目需要优先改进精密度; 12.50% 的项目需要优先改进正确度;有 43.75% 的项目需要同时改进精密度和正确度。
结论 对于我院生化检测系统，基于性能验证数据的六西格玛质量管理可以快速了解检验项目的分析性能，指导质量控制工作。结合实验室的 5S 管理和整顿，提高了科室形象。

PU-2811

54 例性染色体嵌合体的遗传学分析

张磊、张美玲、李红敏、司马小可、张丽敏、阎安澜
郑州金域临床检验中心有限公司

目的 探讨河南地区 2018 年性染色体嵌合体患者的临床表现及嵌合类型。

方法 采用患者外周血进行细胞培养，常规外周血染色体 G 显带，徕卡自动扫片仪扫片并进行核型分析。
结果 在 13235 例外周血染色体核型分析标本中，共检出性染色体嵌合体患者 54 例，检出率为 0.40%，其中特纳综合征嵌合体 44 例，占 81.48%；克氏综合征嵌合体 5 例，占比 9.26%；超雌、超雄综合征嵌合体共 5 例，占比 9.26%；两种核型的嵌合体 51 例，占比 94.45%；三种核型的嵌合 2 例，占比 3.70%；四种核型的嵌合 1 例，占比 1.85%。
结论 性染色体嵌合体患者中最常见的是特纳综合征嵌合体核型，且以两种核型的嵌合为主；其主要临床表现为身材矮小、生殖功能障碍、发育不良、不孕不育、流产等。对具有明显临床表现的患者，要进行外周血染色体检查，有助于临床早发现、早诊断和早治疗。

PU-2812

分析比较不同类型肿瘤相关静脉血栓栓塞症的特征

刘艳红、李悦、马汝飞、胡敏、孙晓芳、郑培明、高岚
河南省人民医院检验科，郑州大学人民医院，河南大学临床医学院

目的 比较不同类型肿瘤合并静脉血栓栓塞症（VTE）的临床特征，为肿瘤合并 VTE 的防治提供参考。
方法 回顾性分析 2013 年 4 月-2019 年 4 月河南省人民医院肿瘤合并 VTE 患者的临床资料和实验室指标检测结果，分析比较不同类型肿瘤患者 VTE 的临床特点。
结果 符合入组条件的患者中，患者数量前三位的肿瘤类型分别为消化系统肿瘤、肺癌和妇科肿瘤。本研究共纳入消化系统肿瘤组 49 例，肺癌组 31 例，妇科肿瘤组 31 例。消化系统肿瘤组、妇科肿瘤组手术人数显著高于肺癌组（69.4%和 80.6%比 12.9%，p 均<0.001）。肺癌组采取溶栓治疗的患者人数显著低于妇科肿瘤组（0 比 25.8%，P=0.005）。妇科肿瘤组红细胞计数（RBC）和血红蛋白（HBG）显著低于肺癌组（P=0.005 和 0.009），消化系统肿瘤组红细胞分布宽度（RDW）显著高于肺癌组和妇科肿瘤组（P=0.015 和 0.003）。妇科肿瘤组凝血酶原时间（PT）显著低于消化系统肿瘤组和肺癌组（P<0.001 和 P=0.002），肺癌组活化部分凝血活酶时间（APTT）显著高于消化系统肿瘤组和妇科肿瘤组（P=0.01 和 0.001）。
结论 不同类型肿瘤的 VTE 危险因素不完全一样，实验室检测结果也存在差异，应针对不同类型肿瘤特点采取血栓防治措施。

PU-2813

稳抓降本增效，促进医学实验室高质量发展

张举、常中宝、冯广东、汪芬芳
南京金域医学检验所有限公司

降本增效措施作为精益管理的重要工具，在医学实验室日常运营中对提升人员工作效率，降低医疗资源浪费具有重要的发展意义。
目的 本文通过与南京金域医学检验所合作共建的 15 家医学实验室长期进行降本增效措施后的效果评估及运营改善回顾，将医学实验室精益管理的宝贵经验进行分享，希望对当下医院管理过程中医疗资源的合理使用提供参考和帮助。
方法 整理 15 家医学实验室（包括 1 家三级医院、12 家二级医院及 2 家一级医院）在人、机、料、法、环模块进行降本增效的改善措施，并做效果评估。
结果 经过降本增效改善措施的 15 家医学实验室在人均产能、效益提升和质量改善上均取得明显效果。

结论 医学实验室在重视质量安全和患者服务工作的同时，需要树立精益管理意识，并通过降本增效措施提高实验室工作效率，将医疗资源利用最大化。

PU-2814

吉林地区 0-6 岁儿童微量元素钙结果分析

张洋
吉林金域医学检验所有限公司

目的 随着生活水平的不断提高，人们对人体的健康意识不断加强，人体微量元素对健康的影响也逐步受到关注，通过检测吉林地区 0-6 岁儿童微量元素钙含量，分析吉林地区儿童微量元素钙含量情况，为儿童预防疾病，科学并且合理的膳食提供参考依据。
方法 选取 2020 年 1 月至 2020 年 12 月送检我公司的儿童微量元素钙 21772 例，按照年龄分为 3 组:0-1 岁婴儿组；1-3 岁幼儿组，3-6 岁学龄前组。采用稀释液(0.1％HNO3+0.1％曲拉通)对血样进行 1:20 稀释后直接用电感耦合等离子体质谱仪进行检测，数据采用 SPSS22.0 统计学软件分析。
结果 0-1 岁婴儿组共 6073 例，其中钙缺乏样本 40 例，钙缺乏率为 0.66%；1-3 岁幼儿组共 7341 例，其中钙缺乏样本 49 例，钙缺乏率为 0.67%；3-6 岁学龄前组共 8358 例，其中钙缺乏样本 10 例，钙缺乏率为 0.12%；分析不同年龄段儿童微量元素钙水平，结果发现 0-6 岁儿童微量元素钙整体钙缺乏率为 0.45% ，各组之间缺乏率差异有统计学意义(P＜0.05)。
结论 实验证明，2020 年吉林地区 0-6 岁儿童的微量元素钙整体缺乏率均不是很高，这可能与现阶段人们对微量元素的重视与及时补充程度有关。随着儿童年龄段的变化及喂养方式的不同，导致体内钙元素含量有所变化，钙元素缺乏需注意调整饮食或给予必要的药物补充。因此，儿童应每天适当的晒晒太阳，在饮食上多食用奶类、海带和虾皮、豆制品、动物骨头等，但在食用这些含钙丰富的食品时，应避免过多食用含磷酸盐、草酸、蛋白质丰富的食物，以免影响钙的吸收。同时，也应实时关注儿童体内微量元素情况，保证儿童健康成长。

PU-2815

硬皮病的研究

赵曼宇
呼和浩特金域医学检验所有限公司

硬皮病是一种慢性疾病，本文主要研究硬皮病的临床表现与治疗进展，通过一些常见临床表现以及部分可能引起发病的原因，具体原因尚在探索中，结合临床整理出部分现有治疗方法，但效果不一。药物可延缓该病进展，预后大多良好。

PU-2816

168 例高胆红素血症新生儿溶血病检测血清学结果分析

田甜
重庆医科大学附属第三医院检验科

目的 分析母婴 ABO 血型不合新生儿溶血病血清学检测结果。
方法 选择我院 2018 年 7 月至 2020 年 12 月收治的 168 例诊断为新生儿高胆红素血症且母婴 ABO 血型不同患儿作为此次研究对象，分别进行 ABO 血型和 Rh 血型鉴定及新生儿溶血病三项检测试验（直接抗人球蛋白试验、血清游离抗体试验、红细胞抗体释放试验）。

结果 168 例患儿中确诊为新生儿 ABO 溶血症 132 例，阳性率 78.6%，不同试验阳性率差异有统计学意义（P<0.05）；不同性别新生儿溶血病阳性率差异无统计学意义，血型 O-A 组与 O-B 组新生儿溶血病阳性率差异无统计学意义；日龄<4d 组 87.1%较日龄>4d 组 12.9%高，差异有统计学意义（P<0.05）。
结论 对于 O 型母亲产后出现新生儿黄疸、水肿、肝脾肿大等症状时应尽早进行产后新生儿溶血病三项试验检测，早发现、早治疗，才能有效降低新生儿溶血病后遗症的严重性。

PU-2817

长春地区 0-15 岁儿童全血中锌结果分析

高洪宇
吉林金域医学检验所有限公司

目的 分析吉林省长春地区 0-15 岁儿童全血中锌元素的含量，掌握长春地区儿童全血中锌元素的含量情况，为儿童预防疾病，科学并且合理的膳食提供数据支持及指导。
方法 选取 2020 年 1 月至 2020 年 12 月在送我公司检测的 29392 例儿童全血锌微量元素样本，按照年龄一共分为 3 组:分别为 0-5 岁、5-10 岁及 10-15 岁。采用电感耦合等离子体质谱法来进行微量元素锌的检测，仪器选用 ICP-MS(Agient 7900)；分析各组儿童锌元素检测结果，并讨论锌元素对儿童生长发育的影响。数据分析采用 SPSS22.0 统计学软件进行，以 P＜0.05 为差异有统计学意义。
结果 29392 例样本中，共有 7587 例缺乏锌样本，整体的锌缺乏率为 25.81% ，0-5 岁儿童一共 19545 例，其中有 7217 例缺乏锌，锌缺乏率为 36.93%；5-10 岁儿童一共 5825 例，其中有 266 例缺乏锌，锌缺乏率为 4.57%；10-15 岁儿童一共 4022 例，其中有 104 例缺乏锌，锌缺乏率为 2.59%。
结论 实验证明，2020 年在长春地区 0-15 岁儿童全血中锌元素总缺乏率为 25.81%，其中 0-5 岁的儿童锌缺乏率高达 36.93%，远高于 5-10 岁儿童的 4.57%与 10-15 岁儿童的 2.59%。因此，长春地区儿童的新缺乏率随年龄的增长呈现递减趋势，在不同性别儿童中，锌缺乏率无显著差别。锌在人体生长、发育、生殖遗传、免疫、内分泌等生理过程起重要作用。缺锌容易导致多种疾病发生，比如厌食，偏食，腻食，口腔溃疡受损，伤口不愈合，青春期痤疮，身材矮小，发育不良，免疫力低下，常患有感冒发烧，呼吸道感染疾病，智力落后。因此要加强对 0-5 岁儿童的合理膳食及对锌元素的合理补充，做到早预防、早治疗，以提高儿童的身体素质。

PU-2818

吉林通化地区老年人微量元素硒检测结果分析

李飞
吉林金域医学检验所有限公司

目的 运用电感耦合等离子体质谱法(ICP－MS)直接测定老年人血液中微量元素硒的含量，为吉林通化地区老年人的身体健康、预防疾病提供理论指导依据。
方法 选取吉林通化地区 2020 年在吉林金域进行体检的老年人（60-70 岁），检测项目为微量元素硒的样本 191 例，采集肝素抗凝全血 1-2 ml，采用 0.1%TritonX-100 和 0.1%HN03 对血样稀释 20 倍混匀后直接用等离子体质谱仪进行分析。
结果 硒方法的检出限分别为 2.3ug/L；精密度＜3.3%，加标回收率为 93.2-104.6%。在 191 例结果中，缺硒人数占比 10.5%，其中女性占比稍多一些，但无显著差异（P＞0.05）；硒摄入过量占比 1.6%。

结论 20 世纪 70 年代，我国将硒列为 15 种每日膳食营养元素之一，缺硒会严重影响人体健康，缺硒是苯丙酮尿症及各种心血管疾病的诱因，是人体克山病、大骨节病和白内障的主要原因。补硒可以有效预防多种疾病的发生，但硒摄入过量会导致人体中毒，补充要合理。据文献报到，中国缺硒现象非常普遍，有 72%的县市不同程度缺硒，本次分析结果显示通化地区老年人缺硒现象不十分明显，这可能与通化地区所处地理位置、环境及饮食习惯有关。人类所需的硒主要来源于土壤，硒在环境的迁移转化受多种因素制约和影响，因此，各地动植物中硒含量差距大，形态各不相同。适量补硒，提高人体免疫力，达到抗衰老，助长寿的目的。同时，ICP－MS 法测定微量元素硒的含量，方法操作简便、稳定、灵敏，准确度高，可用于临床大数据量分析。

PU-2819

一例新生儿不哭患儿的基因诊断

胡炜晨[1]、陈水平[2]、刘伟红[2]、代冰[1]、王雨[1]、袁悉奥[1]、龚强*[3]、黄晓亮*[2]
1. 长沙金域医学检验实验室有限公司
2. 浏阳市妇幼保健院新生儿科
3. 广州金域医学检验集团股份有限公司

目的 通过临床患者表型的收集和综合分析，结合高通量测序（NGS）、生信分析、ACMG 指南对张力减退-共济失调-发育迟缓综合症（HADDS)[mim:617330]相应基因变异进行定级，进而从遗传病因上对患者进行确诊。
方法 对患儿进行体格检查、常规辅助检查、影像学检查收集临床表型，结合临床症状完善染色体核型分析和家系全外显子组测序(WES）。WES 采用 VAHTS 试剂构建文库、IDT 探针杂交捕获、Illumina NovaSeq 6000 高通量测序。原始数据采用 fastp 软件过滤，以 hg19 为参考基因组、BWA 软件拼接序列，使用 GATK4 进行变异鉴定。检出变异使用 ANNOVAR 并结合 ClinVar、HGMD 和 OMIM 等数据库进行变异注释，SIFT、Polyphen 等生物信息学软件对变异进行致病性预测并利用人群基因变异频率数据库对变异进行频率注释。Sanger 测序对家系目标变异进行验证。根据《ACMG 遗传变异分类标准与指南》对变异进行评级。
结果 患儿表现为肌张力低、脸尖、耳位低、足内翻、轻度脑损伤、哭声小，对疼痛不敏感。与张力减退、共济失调和发育迟缓综合症较为符合。常规辅助检查、影像学检查及染色体核型分析等均无异常。测序质控结果如下：cleanBases:8.5G、Q30:91.2%、平均覆盖 119×,符合 NGS 测序要求。患儿检测到携带 *EBF3* 基因 c.578A>T(p.Lys193Met）杂合变异。父母未携带该变异，为新发变异；gNOMAD 数据库未收录；有报道该变异会导致 EBF3 表达量减少。根据现有证据，该变异被定义为“可能致病”变异。症状、变异级别、遗传模式（张力减退、共济失调和发育迟缓综合症为常染色显性遗传病）三个方面均符合，可以确诊。
结论 该患儿基因诊断的确诊，丰富了 HADDS 综合征的临床表型以及基因变异类型，为遗传基因检测、变异评级和遗传病的诊断丰富了证据。

PU-2820

50 例肺隐球菌病的临床分析

王甜甜
大连医科大学

目的 探讨肺隐球菌病的临床特征，提高对该病的认识和诊治能力。
方法 回顾性分析大连医科大学附属第一医院 2013 年至 2021 年收治肺隐球菌病患者的临床资料。包括患者的一般情况、易感因素、临床表现、影像学特征、治疗及预后。

结果 纳入研究肺隐球菌病患者 50 例中男性 25 例，女性 25 例。年龄范围在 27-82 岁,40-60 岁为高发病年龄段。48 例无明确的鸟粪、霉土等接触史,2 例有鸟类接触史。15 例伴有 1 种或多种基础疾病。20 例有免疫功能低下的相关因素。22 例有下列临床表现中的一种或多种:咳嗽、胸痛、胸闷、气短、咳痰、痰中带血、发热、乏力。入院诊断有肺部阴影、胸/肺部肿物、肺炎、肺占位、肺肿瘤、肺空洞、肺结节病、气短。影像学表现的病灶类型主要有结节/结节影、索条影/灶、团片影、团块影、粟粒影/灶、肺大泡、局限性气肿、斑片影、占位、团片影、钙化灶。病灶分布特点为：下叶多于上叶、右肺大于左肺。5 例存在阻塞性肺通气功能障碍，2 例存在混合型肺通气功能障。病理检查主要呈现肉芽肿的表现。47 例由肺组织行病理检查确诊，2 例由血清学确诊，1 例于隐球菌涂片中检查出隐球菌确诊。手术切除治疗 43 例、抗真菌药物治疗 6 例。1 例合并肺结核转院治疗。

结论 肺隐球菌病以中老年多发,在免疫功能正常和受损的人群中均可发病。基础疾病主要为高血压及恶性肿瘤，免疫力不同人群临床表现无统计学差异，肺部结节为影像学主要表现。手术切除为主要治疗手段，治疗疗效显著。

PU-2821

精神分裂症患者伴发高血压的概率及伴发的风险因素分析

陈倩
武汉大学人民医院

目的 探究精神分裂症患者伴发高血压的概率，并对其风险因素进行系统分析。

方法 纳入 2019 年 1 月至 2020 年 5 月在武汉大学人民医院确诊为精神分裂症的患者 246 例，收集所有患者的年龄、家族史、精神类药物服用史、病程等信息。检测并分析所有患者的血压、血清总胆固醇（TC）、甘油三酯（TG）、高密度脂蛋白（HDL-C）、低密度脂蛋白（LDL-C）、载脂蛋白 A1(ApoA1)、载脂蛋白 B(ApoB)、C-反应蛋白(CRP)等指标。根据患者的血压值，分为高血压组与非高血压组。

结果 在 246 例精神分裂症患者中 46 人伴发高血压，其伴发高血压概率为 23%。高血压组患者的年龄与病程均显著大于非高血压组（P＜0.01）；高血压组的受教育年限显著低于非高血压组（P＜0.05）；高血压组的 TC、TG、LDL-C、ApoB、CRP 均显著高于非高血压组（P＜0.05）。两组的性别、精神疾病家族史、精神类药物服用史、HDL-C、ApoA1 的差异无统计学意义（P＞0.05）。Logistic 回归分析显示，精神分裂症伴发高血压与患者的性别、年龄、血清 CRP 有关（P＜0.05）。

结论 精神分裂症患者伴发高血压的概率较高；同时，患者的性别、年龄、CRP 是精神分裂症患者伴发高血压的风险因素。

PU-2822

胃溃疡患者纤维结合蛋白和胆碱酯酶的变化及临床意义

陈倩
武汉大学人民医院

目的 分析胃溃疡患者纤维结合蛋白的变化并探讨其临床意义。

方法 收集武汉大学人民医院 2018 年 10 月至 2019 年 12 月收治并诊断为慢性胃炎患者 74 例作为 A 组、胃溃疡患者 59 例作为 B 组、胃癌患者 31 例作为 C 组。检测所有受试对象的白细胞（WBC）、中性粒细胞（NEUT）、淋巴细胞（LY）、单核细胞(MONO)、补体（C1q）、纤维结合蛋白（Fn）、胆碱酯酶（CHE）的水平，并比较组间差异。采用 pearson 线性相关分析各项指标与胃溃疡发生发展的相关性。

结果 B 组的 C1q、Fn、CHE 显著低于 A 组（P<0.001 或 P<0.05），WBC、NEUT、LY 和 MONO 显著高于 A 组（P<0.001 或 P<0.05）；C 组的 WBC、LY、MONO、Fn、CHE 显著低于 B 组（P<0.001 或 P<0.05），C1q 显著高于 B 组（P<0.05）。Spearman 相关性分析显示，Fn、CHE 与疾病分组呈负相关（r=-0.25、r=-0.246; p<0.01、p<0.01）。
结论 白细胞、中性粒细胞、淋巴细胞、单核细胞、补体 C1q、纤维结合蛋白、胆碱酯酶等血清指标的变化与胃溃疡的发生发展关系密切，对判断胃溃疡的愈合情况及是否有恶变倾向有一定价值。

PU-2823

组织工程技术和生物材料在肿瘤液体活检领域中的应用

毕庆庆、闫清、张磊、牟晓峰
青岛市中心医院

目的 综述组织工程技术和生物材料在肿瘤液体活检领域中的应用。
方法 组织工程作为一个新兴学科，经过三十余年的发展，已经在医学研究和应用方面取得了很多突破性的进展。肿瘤是当今时代人类面临的重大健康问题，在预防筛查、早期诊断、治疗监测、预后判断等肿瘤诊疗的各个环节中，越来越多的新兴学科开始展现出令人眼前一亮的作用。组织工程作为一门多学科交叉的新兴学科也已经在肿瘤诊疗的各个层面中崭露头角。本文综述了组织工程技术和生物材料在肿瘤液体活检领域中的应用。
结果 组织工程中常见的纳米生物材料、生物材料表面修饰和微流体等技术方法为体外捕获循环肿瘤细胞提供了新的思路。有研究者构建了一种新的基于拟生态方法和纳米技术相结合的捕获 CTC 的方法。该方法在纳米材料表面模拟了 CTC 与内皮细胞的相互作用，利用多价固定黏附和连接在纳米聚合物上的上皮细胞黏附分子（EpCAM）来捕获 CTC，效率较高。另外，基于组织工程的微流控技术也可以从腹水、胸腔积液和尿液等多种人体体液中捕获 CTC。捕获 CTC 的具体方式不同，各有优缺点。
结论 综上所述，组织工程技术在肿瘤液体活检领域中的应用研究已经十分广泛，但都存在一个共性的问题：虽然取得了很多令人兴奋的研究结果，但是研究的临床转化成功率不高。期望这些研究能最终回到临床，为临床肿瘤诊疗提供切实的帮助，造福肿瘤患者。

PU-2824

含羞云实的活性成分研究

王小玲
山东大学第二医院

目的 对含羞云实(Casealpinia mimosoides Lam.)的化学成分进行系统研究，发现其中具有抗肿瘤活性的化合物。
方法 采用 95%乙醇对植物进行提取，采用硅胶柱色谱、葡聚糖凝胶 Sephadex LH-20 柱色谱、C18 反相硅胶柱色谱，以及半制备型高效液相色谱等技术进行化合物的分离纯化，采用 NMR、MS、IR 和 CD 等波谱学技术进行化合物结构鉴定，采用 MTT 法测定化合物对肿瘤细胞增殖的抑制活性。
结果 共分离获得了 7 个化合物，其中包括 2 个新化合物，分别鉴定为 1 个高异黄酮类化合物(R)-3-(2¢,4¢-dimethoxybenzyl)-7-hydroxychroman-4-one (1)和 1 个卡萨烷型二萜 caesalpin I (2)。获得的已知化合物包括 1 个卡萨烷型二萜 neocaesalpin (3)、1 个黄酮类化合物 5,3’-diydroxy-3,7,4’-trimethoxyflavone (4)、1 个高异黄酮类化合物 bonducellin (5)，以及 2 个简单芳香化合物 1,2,4-trimethoxybenzene (6)和 vanillic acid (7)。活性实验显示化合物 1 和 5 对 PC3 和 A549 肿瘤细胞的增殖具有抑制活性。
结论 高异黄酮作为含羞云实中抗肿瘤活性化合物，值得进行深入研究。

PU-2825

C 反应蛋白在两种检测系统中的对比分析与偏倚评估

刘双、冯彩虹、李学武、丛琳、周汉王
解放军总医院海南医院

目的 通过对罗氏 cobas c702 全自动生化分析仪（简称罗氏 cobas c702）和迈瑞 BC-5180CRP 全自动血液细胞分析仪（简称迈瑞 BC-5180CRP）所测 C 反应蛋白（C-reactive protein，CRP）结果进行对比分析和偏倚评估，探讨两台仪器间是否具有可比性，如果具有可比性则新购入的迈瑞 BC-5180CRP 可投入使用。
方法 根据美国临床实验室标准研究所（CLSI）EP9-A2 作为参考文献，随机收集门诊或病房患者血清 60 例，以罗氏 cobas c702 作为目标系统，测定血清中 CRP 浓度，迈瑞 BC-5180CRP 作为待检测系统，测定血清中 CRP 浓度，将两者结果进行比较分析。
结果 两个系统在低、中、高 3 种不同浓度水平的 CRP 测定结果差异无统计学意义(P>0.05)，相关系数 r2≥0.9954，相关性较好，系统误差均在 1/2 CLIA'88 要求的可接受总误差限制范围内，因此，在低、中、高这三大浓度水平处可以接受。
结论 两个系统的测定结果具有良好的可比性，定期对仪器进行对比校正，这样可以保证测定结果的稳定性，从而满足实验室结果的一致性要求。

PU-2826

2015-2020 年腹腔感染患者引流液病原体分布及其抗菌药物敏感性分析

王雅轩、朱晓雁、马立艳、苏建荣
首都医科大学附属北京友谊医院

目的 分析腹腔感染患者引流液中的病原体分布及其耐药性。
方法 收集北京友谊医院 2015-2020 年间收治的 890 名腹腔感染患者的腹腔引流液标本，对其进行细菌的培养鉴定以及抗生素敏感性试验，分析其病原体分布情况及药物敏感性。
结果 在 890 名腹腔感染患者中，共分离出 1664 株病原菌。其中，常见病原菌的分离率分别为大肠杆菌（17.85%）、屎肠球菌（14.18%）、肺炎克雷伯菌（10.88%）、铜绿假单胞菌（7.87%）、粪肠球菌（5.59%）、阴沟肠杆菌（3.18%）、金黄色葡萄球菌（3.12%）和奇异变形杆菌（2.34%）。革兰阴性菌中的大肠杆菌、肺炎克雷伯菌、铜绿假单胞菌、阴沟肠杆菌和奇异变形杆菌对阿米卡星的敏感率均大于 80%。大肠杆菌和肺炎克雷伯菌对氨苄西林的耐药率均大于 80%，肺炎克雷伯菌对氨曲南、头孢曲松、庆大霉素和左氧氟沙星的耐药率均低于大肠杆菌。革兰阳性菌中，屎肠球菌、粪肠球菌和金黄色葡萄球菌对利奈唑胺和万古霉素的敏感率均大于 90%。屎肠球菌对氨苄西林、环丙沙星和左氧氟沙星的耐药率均大于 80%，粪肠球菌对喹努普汀/达福普汀和四环素的耐药率均大于 70%，金黄色葡萄球菌对青霉素的耐药率大于 90%。
结论 腹腔感染患者引流液中分离出的病原菌主要为大肠杆菌、屎肠球菌和肺炎克雷伯菌，临床应严密监测耐药结果，以便采取有效措施控制耐药菌的增长，并及时更换治疗方案。

PU-2827

MiR-7 在肿瘤中的分子调控机制和治疗潜力

李淼[1,2]、窦骏[2]
1. 南京鼓楼医院检验科
2. 东南大学医学院病原生物学与免疫学系

目的 综述 miR-7 在肿瘤中的多种分子调控机制及诊治潜力的研究进展。
方法 通过检索和阅读文献，对文献内容进行综合分析、归纳整理和讨论。
结果 miR-7 在正常组织中主要特异表达于脑和胰腺组织，其表达受到多种机制的调控。除在生理发育过程中发挥作用外，miR-7 还可以有效抑制肿瘤的发生发展与转移，是肿瘤治疗的重要潜在靶标。研究表明，miR-7 能通过抑制肿瘤细胞增殖和转移、促进肿瘤细胞自发 DNA 损伤、逆转肿瘤耐药、调控肿瘤干细胞的功能等，在乳腺癌、肺癌、脑肿瘤、骨肿瘤、胃癌、肝癌等多种肿瘤中发挥抑癌效应。此外，miR-7 在肿瘤的预测、诊断和预后方面也具有很大的潜力。目前，关于 miR-7 在肿瘤中的生物学行为有了广泛的研究，但基于 miR-7 的抗肿瘤治疗仍有许多问题尚待克服，如有效的体内递送。
结论 miR-7 可作为一种潜在的肿瘤抑制因子，在肿瘤的诊治和预后判断中具有临床应用前景。

PU-2828

乙型肝炎患者血清中发现 RR 抗体一例

夏欢、邱梅花
海口市人民医院

目的 探讨乙型肝炎病毒与 RR 抗体的关系。
方法 分析一例有“多囊肾、慢性肾脏病、乙型肝炎”既往史的患者血清中发现的 RR 抗体。
结果 本例在发现 RR 抗体后继而又发现乙型肝炎病毒呈低浓度复制。
结论 RR 抗体可以出现在乙型肝炎患者，可能与乙型肝炎病毒复制有关。

PU-2829

MiR-7 下调 CD44 表达抑制乳腺癌干细胞致瘤性的研究

李淼[1,2]、窦骏[1]
1. 东南大学医学院病原生物学与免疫学系
2. 南京鼓楼医院检验科

目的 探究 miR-7 降低乳腺癌干细胞（BCSCs）致瘤性的作用机制，为基于 miR-7 调控 BCSCs 治疗乳腺癌提供实验依据。
方法 免疫磁珠分选法从 MDA-MB-231 细胞中分选出 BCSCs，构建荷 BCSCs 异种移植物鼠原位瘤模型，通过蛋白芯片技术检测经 miR-7 agomir 治疗后肿瘤组织中的蛋白表达情况，筛选差异表达蛋白；q-PCR 和 WB 检测四株人乳腺癌细胞系中 miR-7 和 CD44 的表达水平；构建过表达 miR-7 的慢病毒重组体，感染人乳腺癌原代细胞（LD 细胞），筛选出稳定过表达 miR-7 的单克隆细胞株（Lenti-miR-7 细胞），采用 qPCR、WB 及 FCM 检测细胞中 miR-7 和 CD44 的表达量；构建荷 Lenti-miR-7-BCSCs 异种移植物鼠原位瘤模型，监测荷瘤鼠的一般状况及肿瘤生长，IHC 检测肿瘤组织中 CD44 的表达情况。
结果 蛋白芯片结果显示 miR-7 agomir 治疗组肿瘤中 CD44 的表达量较对照组降低了 2.4 倍；四株人乳腺癌细胞系中，CD44 在相对高表达 miR-7 的 MCF-7 细胞中低表达；对筛选出的 Lenti-miR-7 细胞的检测结果显示，通过慢病毒系统过表达 miR-7 后可有效降低 LD 细胞中 CD44 的表达水平；

相较对照组和化疗药治疗组，荷 Lenti-miR-7-BCSCs 异种移植物鼠的肿瘤生长显著受抑，肿瘤组织中 CD44 的表达下调。
结论 过表达 miR-7 可以有效抑制荷 BCSCs 异种移植物鼠的肿瘤生长，其机制可能是 miR-7 通过下调细胞中 CD44 的表达水平，从而降低了 BCSCs 在 NOD/SCID 小鼠体内的致瘤性。

PU-2830

2014-2020 年 11889 例新生儿及其产妇梅毒血清学检测结果分析

夏欢、洪云、范维丽、赵庆珠、邱梅花
海口市人民医院

目的 通过分析 2014-2020 年 11889 例新生儿及其产妇梅毒的血清学检测结果，为制定孕产期梅毒的防治策略提供依据。
方法 回顾性分析 2014-2020 年本院产科所有新生儿及其产妇的梅毒血清学检测结果。用酶联免疫吸附试验(TP—ELISA)和梅毒螺旋体明胶颗粒凝集试验(TPPA)检测梅毒密螺旋体抗体，甲苯胺红不加热血清反应素试验(TRUST)检测梅毒非密螺旋体抗体，最后采用卡方检验进行统计学分析。
结果 共计检测产妇 11843 例，新生儿 11889 例，其中双胞胎 46 例。产妇 TP 抗体共阳性 80 例，总阳性率为 6.76‰，2017 年 TP 抗体阳性率最高，呈现先增后降的趋势。产妇 TRUST 阳性共 50 例，总阳性率为 4.22‰，2017 年 TRUST 抗体阳性率最高，呈现先增后降的趋势。新生儿 TP 抗体共阳性 62 例，总阳性率为 5.21‰,2017 年 TP 抗体阳性率最高，呈现先增后降的趋势。TRUST 阳性共 20 例，总阳性率为 1.68‰，2017 年 TRUST 抗体阳性率最高，呈现先增后降的趋势。深入分析分娩梅毒阳性新生儿的产妇资料发现，<20 岁产妇分娩出 TP、TRUST 阳性新生儿占比均最高，不同年龄段占比率差异有统计学意义（$\chi2=11.838$，df=3，P=0.008；$\chi2=10.935$，df=3，P=0.012）；初中及以下文化程度的产妇分娩出 TP、TRUST 阳性新生儿占比率显著高于初中以上（$\chi2=4.209$，df=1，P=0.040；$\chi2=5.047$，df=1，P=0.025）；农村户籍的产妇占比率显著高于城镇户籍（$\chi2=4.758$，df=1，P=0.029；$\chi2=4.747$，df=1，P=0.029）。
结论 2014-2020 年产妇和新生儿梅毒 TP、TRUST 阳性率均呈现先增后降的趋势，不同年龄、文化程度、户籍的产妇分娩出梅毒阳性新生儿的比例有显著差异，未来梅毒的防治应重点向这部分人群扩大。

PU-2831

上海地区 2020 年度甘胆酸室间质量评价结果分析

金中淦、居漪、虞啸炫、欧元祝
上海市临床检验中心

目的 血清甘胆酸（Cholyglycine，CG）是胆汁酸的主要成分之一，是胆酸与甘氨酸在肝内结合而成的结合型胆汁酸，是临床检验中常见且重要的项目之一，在肝癌、胆管癌、肝内胆汁淤积症、肝硬化、胰腺癌、慢性阻塞性肺疾病等疾病的临床诊断和病情监测中具有重要的意义。本研究拟通过开展室间质量评价（EQA）了解上海地区临床实验室 CG 检测质量。
方法 2020 年 EQA 共发放 10 份样本进行甘胆酸测定，通过实验室反馈结果及仪器试剂信息对 GCA 进行统计分析。
结果 2020 年两次 EQA 结果显示，不同实验室间检测结果总体变异系数分别在 41.7%～59.8%、42.2%～78.8%，实验室间结果差异非常大；免疫比浊法结果远低于均相酶免疫法检测结果，第一次两种方法间结果偏差在-46.7%～-61.8%，第二次两种方法间的偏差在-48.7%～-73.6%，结果之

间不存在可比性。 即使都采用免疫比浊法，不同试剂检测结果的变异在 30.6%～42.5%，结果差异比较大。
结论 上海地区临床实验室检测系统和试剂品牌多样，不同方法不同试剂品牌间测量结果缺乏可比性， CG 检验结果的一致性和可比性有待进一步提高，质量控制对于保证检测结果的准确可比具有十分重要的作用，开展 CG 的量值溯源工作是努力的方向。

PU-2832

临床实验室设备管理系统功能与应用

姚恒、李敏、吕康琪、郭非凡、承宝贵、张秀明、熊丹
深圳市罗湖集团医学检验中心

目的 设备管理是保障医院正常运转的支持系统，随着医改的推进与深化,新形势与旧思维引发的冲突带来一系列设备管理上的问题，其健康发展关系到临床工作的正常开展,已成为医疗质量管理、医疗风险防范和医疗成本控制的重要一环。
方法 在实验室信息管理系统平台上，基于 Is015189 认可准则和模块化设计的智能化管理系统。
结果 该系统能在论证、采购、验收、入库、维修、保养、调拨、计量、报废等全生命周期内实施精确、高效的管理。
结论 本实验室在临床实验室设备管理信息系统中建立了设备管理模块，该模块实现了临床实验室设备管理全过程的实时记录监控、维修保养等各环节有机结合。是医疗设备管理部门，设备使用部门等部门机构的强力工具和助手。

PU-2833

血液质量对骨髓染色体核型分析的影响

翟贺、陈超
吉林金域医学

目的 探究不同质量的血液样本对骨髓染色体培养制片的影响，进一步提高骨髓染色体核型分析的效果。
方法 随机选取 2021 年 1 月至 2021 年 5 月的 60 例骨髓标本，观察血液样本状态，一般分为四种，良好，油脂，凝块，血量不足，对其进行细胞计数，取 20 微升血液放入 380 微升白细胞稀释液中，混匀，在血细胞计数板上充池，进行计数，通过细胞数量来计算在培养瓶中需接种的血量。48 小时后进行收获，进行制片，镜下观察分裂相的长短与粗细，是否有条带，可分析分裂相的数量。
结果 经观察，在 60 例骨髓标本中，有 30 例血液状态良好，14 例凝块，6 例油脂，10 例血量不足。计数时 30 例血液状态良好的细胞数均大于 50，接种比较顺利，经二氧化碳培养箱培养 48 小时后，培养后加入秋水仙素再次培养一小时，进行收获，所获得的沉淀细胞较多，显微镜下的分裂相也较多，染色体条带清晰，形态较好，便于分析。14 例带有凝块的血液计数基本小于 50，进行接种时较难将血液吸出注射到培养瓶中，导致接种血量不足，或者将小凝块注射到了培养瓶中，导致培养收获后沉淀细胞带有渣子，影响镜下分裂相的观察，分析时增加了难度，影响条带分析。6 例油脂的标本进行细胞计数时覆盖在细胞上，影响计数，导致接种血液数量不准，收获沉淀细胞不一，影响悬液浓度，导致镜下过密或过稀，可分析分裂相较少，会重滴。10 例血量不足标本导致接种血液不够，收获的沉淀细胞较少，镜下可分析分裂相较少。
结论 实验表明，标本中带有凝块，油脂以及血液的量不足均会影响到收获的沉淀细胞的量，以及镜下可分析分裂相的量以及形态条带，增加了退单率，延迟发单时间。因此，进行标本采集时，应

从是否有凝块、油脂及血液量等多方面注意标本的质量，以提升染色体培养制片质量，提高骨髓染色体核型分析的效果。

PU-2834

临床实验室业务管理决策支持系统的设计与应用

李敏、陈大洋、熊丹、姚恒、张秀明
深圳市罗湖医院集团

目的 建立全面满足行业标准的区域医学检验中心以业务流程优化重组为基础的实验室管理平台，提高实验室精细化管理和绩效管理水平。
方法 iLab 标准化智慧实验室管理平台利用数据库技术、计算机技术和网络技术，使用 SPRING+SHIRO+SNAKERFLOW 三个框架搭建而成的 B/S 型架构模式，WINDOWS/LINUX 作为操作系统，MYSQL5.7 作为数据库管理系统，JAVA+R 语言作为开发语言，并使用 REDIS 缓存提高读取效率，通过与 LIS、HIS 对接，数据挖掘和统计分析而搭建的平台。
结果 系统自动生成业务管理所需要的各种统计图、统计表、趋势图；按照标本量、项目量、业务收入等多维度，实现不同实验室、同一实验室不同专业组、同一专业组不同岗位的业务量对比、同比、环比分析及趋势分析；实时显示业务工作量数据和标本来源；实时显示委托实验室和受托实验室的检验项目、标本量和业务量；实时显示和监控关键质量指标、环境监测指标。
结论 数据管理中心满足实验室数据的利用、数据管理要求、支持实时可视化的统计分析，为医院管理和决策提供有力保障，为相关工作管理人员实施质量控制工作提供有效的工具。

PU-2835

评价三种检测系统检测糖化血红蛋白的一致性

李世红[1,2]、李永林[3]、栗秀芳[1]、钱净[1]、张水丽[1]、保梦珏[1]
1. 昆明市第一人民医院
2. 昆明医科大学附属甘美医院
3. 昆明学院

目的 对三个不同检测系统检测糖化血红蛋白（HbA1c）结果的一致性进行分析。
方法 分别使用 Sebia（毛细管电泳法，法国 Sebia Capillarys）、XPT（乳胶增强免疫比浊法，上海执诚）、贝克曼 AU5800（酶法，日本积水）三种检测系统同时检测 125 个 EDTA 抗凝血样本，用 Spearman 相关分析、Passing-Bablok 回归和 Bland-Altman 图分析三种检测系统检测 HbA1c 的一致性；以 HbA1c≥6.5%作为切点，结合临床诊断计算灵敏度、特异性、阳性预测值和阴性预测值绘制 ROC 曲线，分析 HbA1c 诊断糖尿病的最佳阈值。
结果 1.毛细管电泳法-乳胶增强免疫比浊法：Spearman 相关分析（r=0.965，p<0.001），Passing-Bablok 回归方程 y=-0.3396+1.0513x，p=0.67；毛细管电泳法-酶法：Spearman 相关分析（r=0.961，p<0.001）；Passing-Bablok 回归方程 y=0.2470+0.9630x，p=0.52；乳胶增强免疫比浊法-酶法：Spearman 相关分析（r=0.961，p<0.001），Passing-Bablok 回归方程 y=0.5491+0.9160x，p=0.12。2.ROC 曲线分析显示 Sebia 毛细管电泳法、乳胶增强免疫比浊法和酶法曲线下面积（AUC）分别为 0.98、0.97 和 0.98，最佳截断值分别为≥6.45%、≥6.35%和≥6.24%.
结论 Sebia Capillarys、XPT 和 AU5800 三个系统检测 HbA1c 的结果具有一致性，ROC 曲线分析显示最佳阈值均小于诊断标准 6.5%。

PU-2836

昆明某三甲医院中段尿培养的病原菌分布与耐药性分析

吕红玲
云南大学附属医院

目的 了解某院 5 年间中段尿培养病原菌分布及耐药情况，为抗菌药物的合理使用提供依据。
方法 回顾性分析 2015 年 1 月至 2019 年 12 月住院及门诊患者中段尿液标本中分离培养的非重复病原菌，采用 VITEK 2 Compact 全自动微生物鉴定仪进行菌种鉴定及药敏试验，使用 WHONET5.6 软件进行数据分析。
结果 按患者首次分离菌株进行统计分析，从尿液标本中分离出 4974 株病原菌，其中革兰阴性 3892 菌株，占 78.2%,革兰阳性菌 1082 株，占 21.8%。尿液标本分离细菌居前 5 位者依次为大肠埃希菌、肺炎克雷伯菌、屎肠球菌、铜绿假单胞菌、粪肠球菌。大肠埃希菌对含酶抑制剂的复方制剂的耐药率有升高趋势；肺炎克雷伯菌对大多数抗菌药物耐药率均较高；铜绿假单胞菌对所有测试抗菌药物耐药率均有升高趋势，且 2019 年耐药率较高，均≥70%；屎肠球菌和粪肠球菌对抗菌药物的耐药情况较平稳。
结论 大肠埃希菌和肠球菌是尿路感染的主要病原菌，该院尿培养病原菌中大肠埃希菌、肺炎克雷伯菌和铜绿假单胞菌的耐药率较高应重点监测。尿培养病原菌的耐药性监测，可为尿路感染抗菌药物的合理使用提供依据。

PU-2837

血清 CA72-4、SCC、IGF-1、CYFRA21-1 联合检测对食管恶性肿瘤的临床诊断价值

杨利萍[1]、李登云[2]
1. 衢州市人民医院（衢州中心医院）
2. 浙江省衢化医院

目的 探讨联合检测血清糖类抗原 72-4（CA72-4）、鳞状细胞癌（SCC）、胰岛素样生长因子 1（IGF-1）、细胞角蛋白 19 片段（CYFRA 21-1）在食道癌诊断中的意义。
方法 收集 144 例食道癌患者为恶性组，143 例健康体检者作为对照组，同时检测比较两组的血清 CA72-4、SCC、IGF-1、CYFRA21-1 水平差异，运用 logitic 回归并绘制 CA72-4、SCC、IGF-1、CYFRA21-1 以及联合检测的受试者工作曲线（ROC），并评价各指标对食道癌的诊断效能。
结果 食道癌组的血清 CA72-4、SCC、IGF-1、CYFRA21-1 水平（8.79±24.49、2.81±6.81、204.02±55.70、7.01±14.45）均高于对照组（1.75±1.46、0.86±0.42、97.01±61.12、1.93±0.85），差异均有统计学意义（P＜0.05），并且随着病情的恶性程度发展，CA72-4、SCC、IGF-1、CYFRA21-1 指标逐步升高。CA72-4、SCC、IGF-1、CYFRA21-1 诊断食道癌的 ROC 曲线下面积（AUC）分别为 0.74、0.75、0.71、0.70，灵敏度分别为 68.30%、62.50%、72.20%、56.25%，准确度分别为 64.45%、66.90%、65.85%、64.45%,均不能达到很好的诊断效果，四项指标联合检测的 AUC 提高到 0.86，灵敏度、准确度分别提高到 86.8%、78.10%，（P＜0.05），诊断效能优于单项检测。
结论 在食道癌诊断中，联合检测 CA72-4、SCC、IGF-1、CYFRA21-1 可以提高检测的准确度、灵敏度，并且各指标可作为病情评估的参考指标，联合检测可提高对恶性肿瘤的诊断效能，为临床提供更优质的实验诊断支持

PU-2838

miR-34a 靶向 CD47 对弥漫性大 B 细胞淋巴瘤生物学行为的影响

李凤龙
东南大学附属中大医院

目的 探究 miR-34a 靶向 CD47 对弥漫性大 B 细胞淋巴瘤生物学行为的影响。
方法 体外培养人弥漫性大 B 细胞淋巴瘤细胞 SU-DHL-2，随机分为对照组、miR-34a mimics 阴性对照组、miR-34a mimics 组三组，以 CCK-8 法和流式细胞术分别测定各组 SU-DHL-2 细胞活力、凋亡率；以细胞划痕和 Transwell 侵袭实验检测各组 SU-DHL-2 细胞迁移、侵袭能力；以实时荧光定量 PCR（qRT-PCR）实验检测各组 SU-DHL-2 细胞 miR-34a 和 CD47 mRNA 表达水平；以免疫印迹实验检测凋亡相关蛋白（Bcl-2、Bax）、上皮-间质转化（EMT）相关蛋白（Vimentin、E-cadherin）和 CD47 蛋白表达水平；以双荧光素酶报告基因实验检测 miR-34a 对 CD47 的靶向调节关系。
结果 相比对照组，miR-34a mimics 组 SU-DHL-2 细胞凋亡率、miR-34a 表达、E-cadherin 及 Bax 蛋白表达明显升高（P＜0.05），细胞活力、迁移细胞数、侵袭细胞数、CD47 mRNA 表达及 CD47、Vimentin、Bcl-2 蛋白表达显著降低（P＜0.05），miR-34a mimics 阴性对照组 SU-DHL-2 细胞各指标差异无统计学意义（P＞0.05）。miR-34a 可靶向下调 CD47 表达。
结论 miR-34a 能靶向下调 CD47 表达，抑制弥漫性大 B 细胞淋巴瘤细胞增殖，诱导其凋亡，降低其侵袭转移力。

PU-2839

新型冠状病毒核酸检测要点及经验

杨芳[2]、迪力拜尔·玉素甫[1]、杨萍[1]
1. 新疆兵团第三师图木舒克总医院
2. 新疆兵团第三师图木舒克总医院

新型冠状病毒从 2019 年 12 月以来在全球范围内爆发，截至 6 月初，累计确诊人数高达 1.71 亿人，现有确诊人数 1391 万人，其中 356 万人因传染该疾病治疗无效死亡，死亡率 2.08%。由于国外的输入型病例依然零星发生，所以国内防疫形势依然严峻，而核酸检测结果作为目前唯一可靠新冠肺炎确诊依据，在新冠疫情内防扩散中发挥作用显著，对核酸检测的速度、质量提出较高要求，为了进一步提高核酸检测结果的准确性，本文对核酸检测中各环节的要点加以分析总结，探讨检测中的注意事项，分析进一步加强核酸检测速率方法。

PU-2840

新型冠状病毒肺炎疫情下临床实验室生物安全防护知识教学实践与思考

刘颖
陆军特色医学中心（大坪医院）

随着现代医学的快速发展，生物安全防护工作也越来越被人们所关注和重视。积极开展生物安全防护知识教学实践是在临床实验室医院感染管理培训的重点内容。生物安全防护教育依托于医院感染学，实验室生物安全防护教育是改善全体实验室工作人员对生物安全防护知识认知及技能的重

要方式，也是提升实验室整体医院感染防控意识、提升医疗质量的重要方式。本研究就检验科生物安全防护知识的教育与实践进行了论述，并对培训方案实施情况进行了深入思考和展望，以期为新型冠状病毒感染的生物安全培训工作提供新的思路。

PU-2841

Beckman Coulter AU5800 全自动生化分析仪的性能验证

王瑶、李卓
西安医学院第一附属医院

目的 对 Beckman Coulter AU5800 全自动生化分析仪进行性能验证。
方法 参照美国临床实验室标准化协会（CLSI）和美国临床实验室改进法案 CLIA'88 的质量要求，本文针对 10 个常规检测项目：总胆红素(TBIL)、谷草转氨酶(AST)、谷丙转氨酶(ALT)、总蛋白(TP)、白蛋白(ALB)、尿素(BUN)、尿酸(UA)、总胆固醇(TC)、甘油三酯(TG)、葡萄糖(GLU)精密度、正确度、线性范围、参考区间进行性能评价。
结果 批内精密度小于 CLIA'88 标准限值要求的 1/4，合格；批间精密度小于 CLIA'88 标准限值要求的 1/3，合格；正确度不超过 CLIA'88 标准限值要求的 1/2，合格；各检测项目引用的线性范围、参考区间均符合要求。
结论 Beckman Coulter AU5800 全自动生化分析仪检测符合质量要求，可以为临床提供可靠的依据。

PU-2842

上海地区载脂蛋白 E 基因分型检测室间质量评价

鲍芸、肖艳群、权静、张芃胤
上海市临床检验中心

目的 通过开展载脂蛋白 E（*ApoE*）基因分型检测室间质量评价计划（简称室间质评），评估参评实验室检测能力及存在的问题，提高临床实验室该项目检测质量。
方法 *ApoE* 基因分型与人体的血清总胆固醇和低密度胆固醇水平密切相关，不同基因型与高血脂症、心血管疾病及阿尔兹海默症的患病风险密切相关，同时影响他汀类药物的降脂效果。人体内存在的三种 ApoE 蛋白异构体（E2、E3 和 E4）是由两个常见的单核苷酸多态性（single nucleotide polymorphism, SNP）位点 rs429358 和 rs7412 共同决定的。针对 *ApoE* 基因以上 2 个 SNP 位点检测开展室间质评计划，并要求根据 SNP 检测结果报告 *ApoE* 分型结果。2020 年室间质评计划为一年 2 次，样本盘包含 5 支样本，类型为基因组 DNA。要求参评实验室收到样本后在规定时间内检测样本并网上上报结果。依据回报结果计算各实验室成绩，汇总样本的总体符合率和基因分型判定符合率，并分析不同检测方法的符合率和检测错误类型。
结果 2 次室间质评中成绩满分的实验室分别为 93.75%（30/32）和 100%（31/31），样本检测的总体符合率分别为 99.38%（318/320）和 100%（310/310），基因分型判定总体符合率分别为 97.5%（156/160）和 100%（155/155）。回报错误结果中包括 2 例 SNP 检测错误和 4 例分型结果判定错误。
结论 各实验室检测总体准确率较高，但个别实验室检测和基因分型判断能力有待提高。检测错误和基因分型判断错误集中出现在第 1 次室间质评中。实验室上报的错误结果中包含 2 例 SNP 检测结果正确、分析结果判定错误情况，表明实验室人员遗传学分析能力有待提高。室间质评计划能帮助实验室发现检测中存在的问题，提高检测质量。

PU-2843

动物源性屎肠球菌 FH65 耐药性分析研究

吴飞
南通市第三人民医院

为了研究温州农场鸡粪中分离的屎肠球菌 FH65 菌株氯霉素耐药基因的表型和耐药基因相关序列的结构分析。对屎肠球菌 FH65 进行分子克隆，克隆出 *fexA*、*optrA*、*tet*(M)、*tet*(L)等耐药基因，并用最低抑菌浓度(MICs)以确定克隆基因活性及耐药性水平。使用测序和比较基因组学方法分析耐药基因相关序列结构。结果表明，屎肠球菌 FH65 全基因组由一条编码 2,374 个预测开放阅读框(ORF)及长度为 2.53Mb 染色体，和三个分别编码 41、48 和 222 个 ORF 的质粒 p38、p48 和 p219 组成。屎肠球菌 FH65 被鉴定为一种新的序列类型 ST5781。屎肠球菌 FH65 对卡那霉素、链霉素、四环素、氟苯尼考、阿米卡星、红霉素、庆大霉素和氯霉素均表现出耐药性。本研究首次发现屎肠球菌在染色体和质粒中同时携带 *fexA* 基因。屎肠球菌 FH65 染色体中带有 *fexA* 的序列与粪肠球菌 L12 非常相似。聚类分簇结果表明簇 2、簇 6、簇 18 和簇 25 中大细菌来自粪肠球菌，只有一种屎肠球菌菌株的序列与携带 *fexA* 的 p48 序列相似。本研究结果表明，氯霉素抗性基因 *fexA* 广泛存在于不同菌种、不同来源的细菌之间，其中主要存在于肠球菌中。转座子可能携带 fexA 基因及其他耐药基因不同菌株之间水平转移。

PU-2844

60 例流行性出血热的诊断分析

束梅燕、葛秋霞
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨流行性出血热的诊断依据。
方法 对我院近期 60 例流行性出血热住院病人临床资料进行回顾性分析。
结果 60 例患者分别入住于 5 个科室,提示该病早期临床表现多样化;有明显的五期临床表征者占 90%;血、尿常规及肾功能表征者 100%,但流行性出血热 IgM、IgG 抗体阳性率仅 18.5%;居住农村者占 97%。
结论 目前,流行性出血热仍无特异性诊断方法,其临床表现、实验室检查、流行病学史均为必要的诊断依据。

PU-2845

LncRNA HCP5：a potential biomarker for diagnosing gastric cancer

shiyi Qin [1,2,3]、lei Yang[1,2,3]、shan Kong[1,2,3]、yanhua Xu[1,2,3]、bo Liang[4]、shaoqing Ju[2]
1. 南通大学医学院
2. 南通大学附属医院检验科
3. 南通大学附属医院临床医学研究中心
4. 南通大学附属医院超声科

Background It has been reported that long non-coding RNAs (lncRNAs) can be regarded as a biomarker and had particular clinical significance for early screening and gastric cancer (GC) diagnosis. Recently, the treatment effect and prediction were still poor and low. Surgical resection was still the primary treatment at present. LncRNA can be divided into sense, antisense, intronic, bidirectional transcripts, intergenic, and enhancer RNAs. Current studies have shown that

lncRNA carried out strict regulation and abnormal expression during the development of different cancers. Simultaneously, more and more pieces of literature have confirmed that lncRNA can be used as a potential biomarker for tumor screening and prognosis monitoring. Therefore, this study aimed to investigate whether serum HCP5 could be a new diagnostic biomarker.
Methods Filtered out the HCP5 from the GEO database. The specificity of HCP5 was verified by real-time fluorescence quantitative PCR (qRT-PCR), and then the stability of HCP5 was verified by room temperature storage and repeated freeze-thaw experiments. Meanwhile, the accuracy of HCP5 was verified by agarose gel electrophoresis (AGE) and Sanger sequencing. Simultaneously, the expression level of serum HCP5 was detected by qRT-PCR in 98 patients with primary gastric cancer, 21 gastritis patients, 82 healthy donors, and multiple cancer types. Then, the methodology analysis was carried on. Moreover, receiver operating characteristic (ROC) was used to evaluate its diagnostic efficiency. Besides, the Fluorescence in Situ Hybridization (FISH) assay showed the subcellular localization of lncRNA HCP5. In addition, the survival curve showed the overall survival (OS) rate of patients.
Results qRT-PCR method had good repeatability and stability in detecting HCP5. The expression level of HCP5 in the serum of gastric cancer patients was remarkably higher than that of healthy donors, and it could distinguish gastritis patients from healthy donors. Moreover, the statistics of 20 pairs of GC tissues showed that HCP5 had a conspicuous trend of high expression. Besides, the expression of HCP5 was increased dramatically in MKN-45 and MGC-803. The FISH assay showed that HCP5 was mainly distributed in the cytoplasm of MKN-45 and BGC-823 cells. When HCP5 was compared with existing tumor markers, the diagnostic efficiency of HCP5 was the best, and the combined diagnosis of carcinoembryonic antigen (CEA), carbohydrate antigen199 (CA199), and HCP5 can significantly improve the diagnostic sensitivity. Besides, compared with the expression levels of thyroid cancer (THCA), colorectal cancer (CRC), and breast cancer (BRCA), serum HCP5 in gastric cancer was the most specific. Besides, clinicopathological parameters also showed that the high expression of serum HCP5 in GC was notably correlated with differentiation ($P<0.05$), lymph node metastasis ($P<0.05$), and nerve invasion ($P<0.05$), indicating that serum HCP5 expression was correlated with some GC clinicopathological parameters. Besides, by comparing the expression of serum HCP5 in patients with primary gastric cancer, patients undergoing surgery, and patients with postoperative recurrence, serum HCP5 rebounded in patients with tumor recurrence. Meanwhile, the expression level of HCP5 in 15 pairs of GC patients before and after an operation was also detected. The results showed that the expression level of HCP5 after gastrectomy was strikingly lower than that in patients with primary GC. What's more, the survival curve showed that the OS rate of patients with high serum HCP5 was significantly lower than that of patients with low expression of serum HCP5.
Conclusion Our study showed that the increase of serum HCP5 could significantly distinguish between patients with primary gastric cancer and healthy donors as well as gastritis and healthy donors. Besides, the combined diagnosis of HCP5, CEA, and CA199 had high diagnostic efficiency, which means serum HCP5 could be used as a potential biomarker of non-invasive fluid biopsy and had a unique value in the diagnosis, development, and prognosis of gastric cancer.

PU-2846

检验回报时间的研究进展

陶创
昆明市中医医院

报告周转时间（TAT）是衡量临床实验室的重要指标之一，不仅直接影响患者和临床对实验室的满意度，甚至可能威胁到患者的生命安全[2]。因此，确保临床医学检测的及时性是实验室的重要职责，而报告周转时间是参考和监督报告及时性的首选指标[1]。本文对 TAT 的概念,包括的内容,对临床工作的重要性及卫计委对 TAT 所提的要求进行分析，进一步提出改进措施，并且制定规范实

验室流程的相关措施，缩短报告周转时间，提高实验室服务质量及检验报告的准确性及时性，为患者及临床提高优质的服务。

PU-2847

Relationship between postoperative hemoglobin level and clinical outcomes in patients undergoing mitral valve surgery

Kexin Fan[1]、Rong Gui[2]、Hongwen Ji[3]、Xianjun Ma[4]、Yuanshuai Huang[5]、Jingyi Wu[6]、Bingyu Chen[7]、Yongjun Wang[1]
1. Second Xiangya Hospital of Central South University
2. 中南大学湘雅三医院
3. 中国医学科学院阜外医院
4. 山东大学齐鲁医院
5. 西南医科大学附属医院
6. 厦门大学附属心血管病医院
7. 浙江省人民医院

Background To investigate the association of optimal hemoglobin level and clinical outcomes after mitral valve surgery (MVR).
Methods This multicenter study included 1,518 patients undergoing MVR from 2016 through 2018. Patients were separated into six predefined groups based on initial postoperative hemoglobin (<7.5g/dL, 7.5-8.4g/dL, 8.5-9.4g/dL, 9.5-10.4g/dL, 10.5-11.4g/dL, ≥11.5g/dL). Multivariable analyses were used to adjust laboratory results and surgical features of patients to evaluate the relationships between initial hemoglobin after MVR and clinical outcomes.
Results Patients with initial postoperative hemoglobin < 7.5 g/dL had longer length of stays [mean(95% CI), 1.9(1.093~1.367)] in comparison with reference group of 9.5-10.4 g/dL. Similarly, for those with hemoglobin < 7.5 g/dL, the odds (95% CI) for secondary outcomes included myocardial infraction 11.801 (1.353~22.966) and thrombosis 5.113(1.340~9.508). However, for clinical outcomes, there was no significant difference between five groups with hemoglobin greater than 7.5 g/dL.
Conclusions In patients after MVR, initial postoperative hemoglobin values below 7.5 g/dL was associated with worse outcomes compared to other values. Given similar outcomes between hemoglobin more than 7.5 g/dL groups, targeting treatment to initial postoperative hemoglobin value at the lower may be more desirable.

PU-2848

梅毒螺旋体 Tp0971 经 MAPKs、NF-κB 和组蛋白乙酰化途径诱导巨噬细胞分泌 IL-8 及 GM-CSF

张跃军
株洲市中心医院

目的 研究梅毒螺旋体膜蛋白 Tp0971 对巨噬细胞分泌 IL-8 及 GM-CSF 的影响，并研究其作用机制。
方法 体外培养人单核细胞系 THP-1 并将其诱导分化为巨噬细胞，随后加入不同浓度的重组膜蛋白 Tp0971，ELISA 检测 IL-8 及 GM-CSF 分泌，qRT-PCR 检测 GM-CSF mRNA 表达，Western blot 检测组蛋白 H3 和 H4 的乙酰化，以及组蛋白去乙酰化酶（HDAC）1 和 HDAC2 表达，荧光发光法检测细胞内 HDAC 的活性，染色质共沉淀技术检测组蛋白与 IL-8 启动子的结合。

结果 ELISA 结果显示，10 μg/mL Tp0971 处理巨噬细胞 24 h 后可诱导巨噬细胞分泌 GM-CSF，并呈一定的时间依赖性。qPCR 结果也显示，Tp0971 也能上调 GM-CSF mRNA 表达。ERK1/2 抑制剂 U0126、p38 抑制剂 SB203580 以及 NF-κB 抑制剂 IKK-NBD 均能显著抑制 IL-8 和 GM-CSF 分泌，而 JNK 抑制剂 SP600125 对两者的分泌无明显影响。Tp0971 处理巨噬细胞 2 h 后，可显著上调乙酰化 H3 和 H4 表达水平，并能促进乙酰化 H3 和 H4 结合至 IL-8 启动子上。此外，组蛋白去乙酰化酶抑制剂 TSA 预处理细胞后，IL-8 的分泌水平显著增加。Western blot 结果也显示，Tp0971 处理后 HDAC1 和 HDAC2 表达水平明显降低，细胞核内 HDAC 的酶活性也有所降低。
结论 梅毒螺旋体膜蛋白 Tp0971 激活 ERK1/2、p38 和 NF-κB，并诱导组蛋白乙酰化从而诱导巨噬细胞分泌 IL-8 和 GM-CSF。

PU-2849

Co-delivery of Docetaxel and Resveratrol by liposomes synergistically boosts antitumor efficiency against prostate cancer

Lu Zhang
The Second Hospital of Shandong University

Combination therapy is frequently used in cancer treatments. Delivery of combined anticancer agents loaded in a nanocarrier would be a promising option for combination therapy. Here, we designed PEGylated nano-liposomes for co-delivery docetaxel (Doc) and resveratrol (Res) to evaluate antitumor efficiency of the combined drugs in prostate cancer. The average diameter of the liposomes was 99.67 nm with a spheral-like shape. Drug release studies showed that both drugs could synchronously leak from the liposomes in a sustained release behavior. Cellular uptake results demonstrated that liposomes could effectively deliver more coumarin 6 into cells than other formulations. Moreover, co-loaded liposomes with Doc/Res in a molar ratio of 1:2 exhibited significantly higher cytotoxicity than a mixed solution containing both drugs on cancer cells. Animal studies revealed that co-encapsulated Doc/Res in liposomes predominantly inhibited tumor growth in PC3 bearing Balb/c nude mice, as evidenced by a change in cell proliferation and apoptosis parameters. Importantly, little toxicities and prolonged survival time were observed in mice treated with liposome-loaded Doc/Res than control group exposed to liposome-free Doc/Res. These results provided evidence that loading of Doc/Res in a nano-liposome is an efficient delivery formulation for synergistic treating prostate cancer.

PU-2850

Quantification of m6A RNA methylation modulators pattern was a potential biomarker for prognosis and associated with tumor immune microenvironment of pancreatic adenocarcinoma

Lianzi wang、yuan hong Xu
Department of Clinical Laboratory, the First Affiliated Hospital of Anhui Medical University, No. 218 Jixi Road, Hefei, Anhui, 230032, China

Background m6A is the most prevalent and abundant form of mRNA modifications and is closely related to tumor proliferation, differentiation, and tumorigenesis. In this study, we try to conduct an effective prediction model to investigated the function of m6A RNA methylation modulators in pancreatic adenocarcinoma and estimated the potential association between m6A RNA methylation modulators and tumor microenvironment infiltration for optimization of treatment.

Methods Expression of 28 m6A RNA methylation modulators and clinical data of patients with pancreatic adenocarcinoma and normal samples were obtained from TCGA and GTEx database. Differences in the expression of 28 m6A RNA methylation modulators between tumour (n = 40) and healthy (n = 167) samples were compared by Wilcoxon test. LASSO Cox regression was used to select m6A RNA methylation modulators to analyze the relationship between expression and clinical characteristics by univariate and multivariate regression. A risk score prognosis model was conducted based on the expression of select m6A RNA methylation modulators. Bioinformatics analysis was used to explore the association between the m6Ascore and the composition of infiltrating immune cells between high and low m6Ascore group by CIBERSORT algorithm. Evaluation of m6Ascore for immunotherapy was analyzed via the IPS and three immunotherapy cohort. Besides, the biological signaling pathways of the m6A RNA methylation modulators were examined by gene set enrichment analysis (GSEA).
Results Expression of 28 m6A RNA methylation modulators were upregulated in patients with PAAD except for MTEEL3. An m6Ascore prognosis model was established, including KIAA1429, IGF2BP2, IGF2BP3, METTL3, EIF3H and LRPPRC was used to predict the prognosis of patients with PAAD, the high risk score was an independent prognostic indicator for pancreatic adenocarcinoma, and a high risk score presented a lower overall survival. In addition, m6Ascore was related with the immune cell infiltration of PAAD. Patients with a high m6Ascore had lower infiltration of Tregs and CD8+T cells but a higher resting CD4+ T infiltration. Patients with a low m6Ascore displayed a low abundance of PD-1, CTLA-4 and TIGIT, however, the IPS showed no difference between the two groups. The m6Ascore applied in three immunotherapy cohort (GSE78220, TCGA-SKCM, and IMvigor210) did not exhibit a good prediction for estimating the patients' response to immunotherapy, so it may need more researches to figure out whether the m6A modulator prognosis model would benefit the prediction of pancreatic patients' response to immunotherapy.
Conclusion Modulators involved in m6A RNA methylation were associated with the development of pancreatic cancer. An m6Ascore based on the expression of IGF2BP2, IGF2BP3, KIAA1429, METTL3, EIF3H and LRPPRC is proposed as an indicator of TME status and is instrumental in predicting the prognosis of pancreatic cancer patients.

PU-2851

增龄是我国东北地区成人糖尿病的重要危险因素，40 岁以后糖尿病高危人群应尽早开展健康干预

云科
中国医科大学附属第一医院

前言 关于我国糖尿病患病与出生年代相关性的研究报道文献有限。本研究以中国东北地区 30~80 岁体检人群为研究对象，探讨不同出生年代人群糖尿病患病率及其影响因素。
材料和方法 收集中国医科大学附属第一医院体检中心 2019 年体检人群数据，包括人口学、检验、检查等资料。计算不同时期出生体检人群糖尿病患病率。单因素和多因素 Logistic 回归模型被用来探讨不同时期出生人群糖尿病患病的影响因素。
结果 共收集 40235 名体检患者（糖尿病患者中位年龄 61 岁，非糖尿病患者中位年龄 44 岁）。分析显示糖尿病患病率：出生早于 1959 的人群（60 岁及以上年龄组）为 14.48%，1960~1969 年代出生人群（50 岁年龄组）为 7.29%，1970~1979 年代出生人群（40 岁年龄组）为 2.91%，1980~1989 年代出生人群（30 岁年龄组）为 0.57%。与 1980~1989 年代出生人群相比，1970~1979 年代出生人群（OR=5.21，95%CI: 4.09~6.69，P<0.001），1960~1969 年代出生人群（OR=13.7，95%CI: 10.9~17.3，P<0.001），出生年代早于 1959 年人群（OR=29.4，95%CI: 23.7~37.1，P<0.001）糖尿病患病风险均显著升高，且患病风险随年龄升高而显著升高（P<0.05），40 岁以后上升最为明显。其它糖尿病发生的显著影响因素包括：癌胚抗原测定、收

缩压、腰围、尿素测定、BMI、血清高密度脂蛋白胆固醇测定、血小板计数、血清甘油三酯测定（P<0.05）。
结论 增龄是我国东北地区成人糖尿病的重要危险因素，对 40 岁以后糖尿病高危人群尽早开展健康教育和基于多种风险因素的综合干预是十分必要的。

PU-2852

Primary cutaneous extranodal nasal NK/T cell lymphoma: a case report

Fan Bu、Qiang Feng
Taian City Central Hospital

Extranodal NK/T-cell lymphoma, nasal type(ENKTCL) is a rare type of non-Hodgkin's lymphoma (NHL) and is closely related to Epstein Barr virus infection. Most cases originate from the nasal cavity and above the throat, a few cases originate outside the nose, such as the skin, gastrointestinal tract, lungs, etc., and a very small number of cases show systemic dissemination at the beginning of the onset, without obvious nasal involvement. Its pathological manifestations are unique, with pleomorphic lymphocyte infiltration centered on blood vessels, tumor cell infiltration destroying blood vessels and causing necrosis. This article reports a rare case of primary ENKTCL on the left calf, manifesting as several dark purple-red subcutaneous nodules on the left anterior tibia. Pathological examination showed that the dermis and subcutaneous tissue of the affected area were diffused with small to medium-sized lymphoid cells. Infiltration, the infiltration phenomenon centered on blood vessels can be seen, EBER in situ hybridization (+), the diagnosis is ENKTCL.

PU-2853

Serum SYPL1 is a promising diagnostic biomarker for colorectal cancer

Lei Liu
Third People's Hospital of Chengdu

Background At present, the overall sensitivity and specificity of blood biomarkers are insufficient for a diagnosis of colorectal cancer (CRC).
Methods We analyzed the serum synaptophysin like 1 (sSYPL1) in controls, adenoma patients, CRC patients, pre- and postoperative CRC patients by ELISA.
Results The upregulation of SYPL1 was confirmed in CRC tissues at both mRNA and protein levels. Consistently, sSYPL1 was significantly higher in CRC patients than in either controls ($t = 14.50$, $P < 0.0001$) or adenoma patients ($t = 10.56$, $P < 0.0001$) and was associated with lymph node invasion ($\chi2 = 4.27$, $P = 0.039$). ROC curves showed that sSYPL1 performed superbly in distinguishing CRC patients from controls (AUC: 0.9481; sensitivity: 86.09%, specificity: 91.01%) and adenoma (AUC: 0.8631; sensitivity: 98.68%, specificity: 78.08%). This performance was much better than that of carcinoembryonic antigen (CEA) or carbohydrate antigen 19-9 (CA19-9). Even for patients with low CEA levels (under 5 ng/mL), SYPL1 maintained the same high performance for identification of CRC. Furthermore, sSYPL1 levels declined significantly after radical surgery ($t = 5.903$, $P < 0.0001$).
Conclusion sSYPL1 might be an outstanding marker for CRC diagnosis, especially for patients with low CEA levels.

PU-2854

淋巴细胞亚群、PCT、CRP 以及免疫球蛋白在小儿细菌性支气管肺炎中的临床应用

杨利萍[1]、李登云[2]
1. 衢州市人民医院（衢州中心医院）
2. 浙江衢化医院

目的 探讨淋巴细胞亚群（CD3+、CD4+、CD8+、CD4+/CD8+、CD19+、CD16+CD56+）、PCT、CRP 以及免疫球蛋白（IgG、IgA、IgM）在小儿细菌性支气管肺炎中的临床应用意义。
方法 收集 65 例小儿细菌性肺炎患儿作为观察组，30 例健康体检者作为对照组，同时检测 2 组研究对象的淋巴细胞亚群、PCT、CRP 以及免疫球蛋白的水平。使用 SPSS20 .0 软件，经 t 检验比较两组间血清淋巴细胞亚群、PCT、CRP 以及免疫球蛋白水平是否存在显著性差异，并绘制受试者工作曲线（ROC 曲线），评价各检测项目的诊断效能。
结果 观察组的 CD19+、PCT、CRP 水平（19.94±7.57、0.66±2.53、17.59±23.39）均高于对照组水平（15.79±2.91、0.04±0.02、1.83±1.49）P＜0.05,；观察组的 CD4+、CD4+/CD8+、CD16+CD56+、IgG、IgA 水平（36.94±9.87、1.57±0.83、9.68±7.61、5.95±2.80、0.60±0.49）低于对照组（41.71±5.66、2.11±0.64、14.79±3.92、9.53±2.28、1.30±0.26）P＜0.05。CD4+、CD4+/CD8+、CD19+、CD16+CD56+、PCT、CRP 、IgG 以及 IgA 的 ROC 曲线下面积分别为 0.64、0.67、0.63、0.80、0.94、0.92、0.837 和 0.83，灵敏度分别为 50%、60%、76%、83%、93%、89%、75%和 72%,特异度分别为 75%、72%、55%、69%、85%、84%、79%和 75%。
结论 细菌性支气管肺炎患儿的细胞及体液免疫均存在失衡紊乱，所以对细菌性支气管肺炎患儿提供免疫调节治疗有一定的临床必要性，其中 PCT 以及 CRP 有较好的诊断效能，能有效指导临床实用抗生素等诊疗活动。

PU-2855

2019-2020 年广州地区四项传染病的感染情况及分析

马建宏、刘长鈺、黄锦维
广东省人民医院（广东省医学科学院）

目的 通过调查广东省人民医院四项乙类传染病的感染率，收集和分析传染病监测信息，预测广州地区传染病的发生和流行趋势,为疾病预防控制策略的制度和医院感染防控措施提供依据。
方法 调查 2019 年 1 月 1 日至 2020 年 12 月 31 日广东省人民医院所有科室行传染病筛查的服务对象共 89735 个案例，年龄分布在 0-106 岁，其中男 44583 人，女 45151 人。
结果 2019-2020 年此四项传染病总的感染率为 13.99%，男女比例为 1.41：1。乙肝的患病人数最多，接着是梅毒、丙肝和艾滋病。从近 2 年的感染趋势来看，四项传染病的感染率均呈下降趋势；在所有感染的人群中，年龄在 20 岁以上的比例超过 98%。
结论 医院开展传染病检测是发现传染病人的重要手段，还能为传染病的流行病学调查提供信息，为提出疾病预防控制措施及保健对策提供依据。实施规范的操作，防止传染病的医源性感染和医院感染，以保障人体健康和公共卫生。

PU-2856

apoM-S1P activates hepatic stellate cells by activating STAT3 and Wnt/β-catenin signaling through S1PR3

Zhiyang Chen、Weimin Wu、Xing Lv、Min Hu
The Second Xiangya Hospital of Central South University

apolipoprotein M (apoM) is the major carrier and regulator of sphingosine-1-phosphate (S1P), a multifunctional bioactive lipid. Most recently, the apoM-S1P axis has been identified of great importance to many fundamental cellular processes through binding to and activating S1P receptors (S1PRs). Targeting S1PRs have become a novel and potent therapeutic strategy for many diseases, however, the biological function of apoM-S1P, and whether S1PRs can be a latent therapeutic target or not in liver fibrosis are remain unknown. Hepatic stellate cells (HSCs) are the core effectors for hepatic fibrosis of any aetiology, here, by using human HSCs line LX-2, we demonstrated that apoM-S1P promotes activation, proliferation, migration, as well as inhibits apoptosis of HSCs. Furthermore, after verified the S1PRs expression pattern in HSCs, we used receptors antagonists and illustrated that apoM-S1P exerts pro-fibrogenesis role via S1PR3 and downstream STAT3 and β-catenin signaling pathways. In summary, our findings clarified the role of apoM-S1P in HSCs and provide potential therapeutic targets for liver fibrosis.

PU-2857

军事飞行员甲状腺功能检测指标参考区间的建立

巩蓓
空军特色医学中心(原空军总医院)

目的 建立军事飞行员甲状腺功能检测指标-三碘甲状腺原氨酸(T3)、甲状腺素 (T4)、游离三碘甲状腺原氨酸 (FT3)、游离甲状腺素 (FT4) 、促甲状腺激素(TSH)的参考区间。
方法 选取 2019 年 10 月至 2021 年 3 月在我院就诊的军事飞行员 605 名，按年龄分为四组。根据 IFCC 相关要求制定参考区间的合理方法和可靠依据，以非参数方法确定 T3、T4、FT3、FT4、TSH 的 95%参考区间。
结果 各组按年龄段划分参考区间：A 组（20-30 岁）T3 1.09-2.07、T4 62.18-125.87nmol/L，FT3 4.21-6.06、FT4 13.79-21.88pmol/L、TSH 0.045-3.603 mIU/L；B 组（30-40 岁）T3 1.04-2.18n、T4 55.99-135.21nmol/L，FT3 3.99-6.17、FT4 12.20-22.81pmol/L，TSH 0-4.472 mIU/L；C 组（40-50 岁）T3 1.09-2.18、T4 60.94-124.04nmol/L，FT3 4.17- 5.92、FT4 13.06-20.34pmol/L，TSH 0.057-3.463 mIU/L；D 组（>50 岁）T3 1.12-2.08、T4 55.66-121.15nmol/L，FT3 4.01-5.94、FT4 11.92-20.87pmol/L，TSH 0-7.043 mIU/L。其中 B 组与 D 组 T4，A 组与 D 组的 FT3，A 组与 C 组、A 组与 D 组的 FT4，B 组与 C 组、B 组与 D 组的 FT4，A 组与 D 组、C 组与 D 组的 TSH 之间差异有统计学意义。
结论 建立了军事飞行员不同年龄阶段甲状腺功能检测指标参考区间，有助于了解高空特殊飞行环境对飞行人员甲功的影响，有助于飞行员甲状腺疾病的诊断、治疗和监测。

PU-2858

Correlation Between APOBEC3B Expression and Clinical Characterization in Lower-Grade Gliomas

Zhiyang Chen[1]、Min Hu[1]、Zhixiong Liu[2]、Quan Cheng[2]、Hao Zhang[2]
1. The Second Xiangya Hospital of Central South University
2. 中南大学湘雅医院

Background As the most aggressive tumors in the central nervous system, gliomas have poor prognosis and limited therapy Methods Immunotherapy has become promising in the treatment of gliomas. Here, we explored the expression pattern of APOBEC3B, a genomic mutation inducer, in gliomas to assess its value as an immune biomarker and immunotherapeutic target.
Methods We mined transcriptional data from two publicly available genomic datasets, TCGA and CGGA, to investigate the relevance between APOBEC3B and clinical characterizations including tumor classifications, patient prognosis and immune infiltrating features in gliomas. We especially explored the correlation between APOBEC3B and tumor mutations. Samples from Xiangya cohort were used for immunohistochemistry staining.
Results Our findings demonstrated that APOBEC3B expression level was relatively high in advanced gliomas and other cancer types, which indicated poorer prognosis. APOBEC3B also stratified patients' survival in Xiangya cohort. APOBEC3B was significantly associated with infiltrating immune and stromal cell types in tumor microenvironment. Notably, APOBEC3B was involved in tumor mutation and strongly correlated with the regulation of oncogenic genes.
Conclusion Our findings identified that APOBEC3B could be a latent molecular target in gliomas.

PU-2859

β-Catenin: oncogenic role and therapeutic target in cervical cancer

Bingqi Wang
The Second XiangYa Hospital of Central South University

Cervical cancer is a common and fatal malignancy of the female reproductive system. Human papillomavirus (HPV) is the primary causal agent for cervical cancer, but HPV infection alone is insufficient to cause the disease. Actually, most HPV infections are sub-clinical and cleared spontaneously by the host immune system; very few persist and eventually develop into cervical cancer. Therefore, other host or environmental alterations could also contribute to the malignant phenotype. One of the candidate co-factors is the β-catenin protein, a pivotal component of the Wnt/β-catenin signaling pathway. β-Catenin mainly implicates two major cellular activities: cell–cell adhesion and signal transduction. Recent studies have indicated that an imbalance in the structural and signaling properties of β-catenin leads to various cancers, such as cervical cancer. In this review, we will systematically summarize the role of β-catenin in cervical cancer and provide new insights into therapeutic strategies.

PU-2860

西格玛度量值在肿瘤标志物检测质量持续改进中的应用

高娟、王青、王云杰、马梦影、王科勇、李卓
西安医学院第一附属医院

目的 应用西格玛(σ) 度量值分析本科室常规开展的肿瘤标志物项目质量控制数据， 评价其精密度分析性能， 设计质量控制方法， 指导质量持续改进。
方法 收集 2018 至 2019 年西安医学院第一附属医院检测的 AFP、CEA、CA125、CA199、CA153、tPSA、fPSA、铁蛋白(FERR) 、β-HCG 和 β2 微球蛋白(β2-MG) 共计 10 个参加国家卫健委临床检验中心室间质评的肿瘤标志物室内质控及室间质评数据， 按照国家卫健委临床检验中心室间质评允许总误差(TEa) 标准， 采用 6σ 计算公式计算检验项目 σ 值， 评价检测项目分析性能， 设计质量控制方法， 计算检测项目的质量目标指数(QGI) ， 运用鱼骨图分析导致性能不佳的主要原因， 提出优先改进方案。
结果 2018 年数据结果显示， 在 10 个肿瘤标志物项目中， 平均 σ 值为 4．25， 其中 σ≥6 项目 2 个， 5≤σ＜6 项目 5 个， 4≤σ＜5 项目 4 个， 3≤σ＜4 项目 7 个， 2≤σ＜3 项目 2 个; 根据 QGI 值，需要优先改进精密度的项目有 7 个， 分别为: AFP、CA125、CA199、CA153、FERR、β-HCG 和 β2-MG; 需要优先改进正确度的项目有 3 个， 分别为 CEA、t-PSA 和 f-PSA。通过持续改进，2019 年 σ 值平均值为 6．58， 其中 σ≥6 项目 16 个， 5≤σ＜6 项目 3 个， 4≤σ＜5 项目 1 个。与 2018 年 σ 值相比， 世界一流水平项目比例明显增多， 差异具有统计学意义(P＜0．05) 。
结论 6σ 质量管理是实验室开展质量控制的一项有效的管理工具， 可以评价检测项目的性能， 指导质量持续改进。

PU-2861

PAGE4 在宫颈癌中的表达及其对癌细胞增殖、凋亡和转移的影响

王冰琦
中南大学湘雅二医院

目的 探究前列腺相关基因 4（PAGE4）在宫颈癌中的表达水平及作用机制。
方法 通过转录组学筛选出宫颈癌的抑癌基因 PAGE4，利用 GEPIA 数据库及 Kaplan-Meier Plotter 数据库分析 PAGE4 在宫颈癌中的表达，探究其与宫颈癌临床特征及预后的关系。采用 qRT-PCR 检测 PAGE4 在宫颈癌组织和细胞中的水平。构建并验证 PAGE4 过表达载体，随后转染宫颈癌 Hela、Siha 细胞系，运用 CCK8 实验、克隆形成实验、流式细胞术、划痕愈合实验、Transwell 迁移实验探究 PAGE4 在宫颈癌细胞增殖、凋亡和转移中的作用。
结果 转录组分析发现 PAGE4 在宫颈癌组织中表达明显下调，下调倍数约为 457 倍。GEPIA 数据库结果提示 PAGE4 在宫颈癌中存在差异表达，且与宫颈癌 FIGO 分期相关。Kaplan-Meier Plotter 数据库结果表明 PAGE4 表达水平与宫颈癌患者总生存期、无复发生存期长短无关。qRT-PCR 检测发现 PAGE4 在宫颈癌组织及宫颈癌细胞系中均呈低表达。细胞实验结果显示， 与对照组相比，过表达 PAGE4 组细胞增殖能力、细胞周期改变、细胞凋亡率无明显差异， 细胞迁移能力明显减弱。
结论 PAGE4 是宫颈癌潜在的抑癌基因，过表达 PAGE4 对宫颈癌细胞的迁移具有抑制作用。

PU-2862

微生物检验样本阳性率及病原菌分离情况分析

苏迎迎
东南大学附属中大医院

目的 了解我院临床微生物标本送检量及样本培养阳性率，分析主要病原菌及多重耐药菌检出及分布状况。
方法 使用 FORMA 3111 型二氧化碳培养箱和 BACTEC FX 全自动血培养系统进行细菌培养，使用 VITEK MS 质谱仪、 VITEK 2 全自动微生物鉴定及药敏分析仪对阳性标本进行菌株鉴定和药敏实验，使用 LIS 系统对 2021 年第一季度全院各个科室中送检标本和检出病原菌进行统计分析。
结果 经统计，2021 年第一季度全院送检样本共 21129 份，共检出病原菌 4164 株，全院样本阳性检出率平均值为 19.71%。其中革兰阳性球菌 982 株（23.5%），主要包括金黄色葡萄球菌、屎肠球菌、粪肠球菌，革兰阴性杆菌 2457 株（59%），主要包括肺炎克雷伯菌（15.2%）、大肠埃希菌（14%）、鲍曼不动杆菌（12.6%）、铜绿假单胞菌（7.8%）。此外，还检出真菌 544 株（13%）。第一季度全院共检出多重耐药菌 965 株，各耐药菌构成比分别为 MRSA（14%）、VRE（0.2%）、CRE（4%）、CRABA（51%）、MDRPA（8%）、CRK(22.5%)。
结论 微生物检验的阳性率与标本质量密切相关，。密切监测全院病原菌检出状况及多重耐药菌检出率及构成比，了解病原菌流行状况，为后续加强微生物检验及细菌耐药监测，指导抗菌药物的使用，降低医院感染的发生提供依据。

PU-2863

The roles and mechanisms of hypoxia in liver fibrosis

Jingyao Cai、Min Hu、Zhiyang Chen、Ling Zeng
The Second Xiangya Hospital of Central South University

Liver fibrosis occurs in response to any etiology of chronic liver injury. Lack of appropriate clinical intervention will lead to liver cirrhosis or hepatocellular carcinoma (HCC), seriously affecting the quality of life of patients, but the current clinical treatments of liver fibrosis have not been developed yet. Recent studies have shown that hypoxia is a key factor promoting the progression of liver fibrosis. Hypoxia can cause liver fibrosis. Liver fibrosis can, in turn, profoundly further deepen the degree of hypoxia. Therefore, exploring the role of hypoxia in liver fibrosis will help to further understand the process of liver fibrosis, and provide the theoretical basis for its diagnosis and treatment, which is of great significance to avoid further deterioration of liver diseases and protect the life and health of patients. This review highlights the recent advances in cellular and molecular mechanisms of hypoxia in developments of liver fibrosis.

PU-2864

Carbapenem-resistant Klebsiella pneumoniae Gastrointestinal carriage developed to infections：a pair of premature twins

Xiaofan Wang[1]、Min Wang[1]、Chunmei Chen[2]
1. The Second Xiangya Hospital , Central South University
2. 中山大学附属第七医院（深圳）

Background Premature infants admitted to the neonatal intensive care unit (NICU) have been identified as a significant population for acquiring and transmitting multidrug-resistant pathogens (MDR). Among them, Carbapenem-Resistant Klebsiella pneumoniae (CRKP) is of great concern due to limited therapeutic options. Until now, the relationship between its colonization and infection is much unclear. Longitudinal sampling beginning at birth is essential in identifying events prior to the presentation of any pathological conditions.
Methods A pair of premature twins with CRKP-associated colonization and infection, one of which even developed septicemia, were found in the NICU of a teaching hospital in mainland China and immediately raised our alarm. Their clinical course and laboratory examination data were analyzed retrospectively. Samples of the gut and other body sites with clinical infection symptoms were collected for strain isolation and culture. Antibiotic susceptibility tests, polymerase chain reaction (PCR), and drug resistance gene sequencing were conducted to explore the resistance of these isolated strains. The phylogenetic relationship of the isolates was studied by random amplified polymorphic DNA (RAPD) and multi-site sequence typing (MLST).
Results Five isolates from the twins were collected in this study, and four isolates were determined to be CRKP. Isolates collected from the same patient have almost identical antibiotic susceptibility. These isolates have slightly different resistance genes, and both TEM-1 and SHV were expressed in all isolates. The molecular typing experiments demonstrated that gut carriage and infection isolates own the same genotype and sequence type (ST54).
Conclusions The gut carriage and infecting isolates of the premature twins were highly homologous. Our results suggest that premature infants were infected with their colonizing strains, supporting the strong association between colonization and infection among neonates. Thus, actively surveillance on CRKP colonization in certain patients is a possible strategy to prevent infections.

PU-2865

乙型肝炎病毒核心抗原（HBcAg）通过 WNT/β-catenin 信号通路调节肝癌的侵袭和转移

荆振唐
山东大学第二医院

目的 明确乙型肝炎病毒核心抗原（HBcAg）是否通过上调 WNT/β-catenin 信号通路促进肝癌细胞的迁移和侵袭。
方法 1.将 HBcAg 基因转染 HepG2、Huh7 细胞，筛选获得稳定表达 HBcAg 蛋白的 HepG2、Huh7 细胞株；2. 采用 CCK8，克隆形成实验，划痕实验，Transwell 迁移及侵袭实验检测 HBcAg 过表达对肝癌细胞 HepG2、Huh7 迁移及侵袭的影响，并通过对裸鼠原位注射的方法研究 HBcAg 过表达对肝癌转移能力的影响；3. 利用 realtime-qPCR 和 Western blot 方法检测 HBcAg 对肝癌细胞上皮细胞-间充质转化(EMT)相关蛋白 E-cadhrin,ZO-1,Vimentin,N-cadherin 和 snail 影响；4.采用激光共聚焦技术检测 HBcAg 过表达对 β-catenin 蛋白定位的影响，运用免疫组化技术检测 30 对肝癌（同时是表达 HBcAg 的乙肝患者）及癌旁组织中 HBcAg 及 β-catenin 的表达水平；5.检测 wnt1-

GSK3β-β-catenin 轴相关蛋白 Wnt1、GSK3β、p-GSK3β(Ser9)、p-β-catenin(Ser33/37/Thr41)和 β-catenin 表达的影响。
结果 1. HBcAg 的过表达可在体内、外促进肝癌细胞的侵袭和转移；2. HBcAg 的过表达促进肝癌细胞 EMT 进程；3. HBcAg 上调 β-catenin 在肝癌细胞内的水平，β-catenin 在肝癌 EMT 以及迁移、侵袭中发挥调控作用；4. HBcAg 正向调控 wnt1,通过 wnt1-GSK3β-β-catenin 信号轴上调 β-catenin 水平，WNT/β-catenin 信号通路在 HBcAg 调控肝癌细胞 EMT、迁移和侵袭中发挥重要作用。
结论 HBcAg 能够通过正向调控 WNT/β-catenin 信号通路促进肝癌侵袭与转移。

PU-2866

SC-514 保护 LPS/D-Gal 诱导的小鼠急性肝衰竭

荆振唐
山东大学第二医院

目的 明确 SC-514 是否参与 LPS/D-Gal 对小鼠急性肝衰竭的保护作用。
方法 一定剂量的 LPS/D-Gal 联合应用，可引起 BALB/c、C57BL/6 两种不同品系小鼠产生急性肝衰竭甚至死亡。将 BALB/c、C57BL/6 分别分组，通过生化、病理和分子生物学技术研究手段，探究 SC-514 对 LPS/D-Gal 诱导小鼠急性肝衰竭的抑制作用。
结果 SC-514 的预处理，可以显著降低 LPS/D-Gal 诱导小鼠急性肝衰竭的死亡率或延长小鼠死亡时间，减轻相同时刻试验组的病理损伤，同时降低相同时刻试验组谷丙转氨酶（ALT）、谷草转氨酶（AST）的生化水平。进一步研究表明，SC-514 可抑制 LPS/D-Gal 诱导下小鼠体内肿瘤坏死因子 TNFα 的产生水平，而 TNFα 是 LPS/D-Gal 诱导急性肝炎模型中促使细胞凋亡的主要因素；并且 SC-514 作用下，试验组肝细胞凋亡率明显降低。
结论 SC-514 通过抑制 TNFα 的产生，减轻肝细胞所受细胞因子风暴的影响，降低实验小鼠急性肝衰竭的死亡率。提示对于 SC-514 的合理应用与研发可减少 LPS/D-gal 诱导的肝损伤和致死率。

PU-2867

BAY 11-7082 保护对乙酰氨基酚（APAP）诱导的小鼠急性肝衰竭

荆振唐
山东大学第二医院

目的 明确 BAY 11-7082 是否参与对乙酰氨基酚（APAP）对小鼠急性肝衰竭的保护作用。
方法 使用一定剂量 APAP，可引起 BALB/c、C57BL/6 两种不同品系小鼠产生急性肝衰竭甚至死亡。将 BALB/c、C57BL/6 分别分组，通过生化、病理和分子生物学技术研究手段，探究 BAY 11-7082 对 APAP 诱导小鼠急性肝衰竭的抑制作用。
结果 BAY 11-7082 的预处理，可以显著降低 APAP 诱导小鼠急性肝衰竭的死亡率或延长小鼠死亡时间，减轻相同时刻试验组的病理损伤，同时降低相同时刻试验组谷丙转氨酶（ALT）、谷草转氨酶（AST）的生化水平以及血氨浓度。进一步研究表明，BAY 11-7082 可抑制 APAP 诱导下小鼠体内 AHF 产生水平，而 AHF 与蛋白结合、线粒体功能障碍、氧化应激有关；并且 BAY 11-7082 作用下，试验组肝细胞凋亡率明显降低。
结论 BAY 11-7082 通过抑制 AHF，减轻肝细胞线粒体功能障碍，降低实验小鼠急性肝衰竭的死亡率。提示对于 BAY 11-7082 的合理应用与研发可减少对乙酰氨基酚诱导的肝损伤和致死率。

PU-2868

HBV DNA 聚合酶驱动糖代谢重编程 促进肝癌细胞的恶性行为

赵晓晴
山东大学第二医院

肝细胞癌（HCC）是全球第六大常见恶性肿瘤，是癌症相关死亡的第四大主要原因。慢性乙型肝炎病毒（HBV）感染是 HCC 的主要危险因素之一。最近，癌症代谢的重编程已被确定为癌症的标志。HCC 中从氧化磷酸化代谢途径向糖酵解途径的转变不仅满足了肝癌细胞快速增殖的需求，还为肿瘤的发展提供了良好的微环境。HBV DNA 聚合酶（HBV-DNA-Pol）具有逆转录酶（RT）和 DNA 聚合酶的活性，可以调节 HBV 复制，先天免疫等多种生物学功能。近期有研究发现，HBV-DNA-Pol 在肝癌细胞生长中起关键作用，但是 HBV-DNA-Pol 是否通过影响 HCC 的糖代谢来影响 HCC 的恶性行为还不是很清楚。本实验研究证实了 HBV-DNA-Pol，TRIM21 都可与 PYGL 相互作用，并且 TRIM21 可以促进 PYGL 经泛素-蛋白酶体途径降解，HBV-DNA-Pol 与 TRIM21 的强相互作用减弱了 TRIM21 对 PYGL 的泛素化修饰，从而上调了肝癌细胞中 PYGL 的蛋白水平，PYGL 的增加促进糖原分解，导致葡萄糖进入糖酵解的流量增加，最终促进 HCC 的发展。

PU-2869

E3 泛素连接酶 TRIM21 促进 HBV DNA 聚合酶的降解

赵晓晴
山东大学第二医院

三方基序 (TRIM) 蛋白家族是 E3 泛素连接酶家族。近期有研究已经表明一些 TRIM 蛋白具有抗病毒功能，尤其是在抗逆转录病毒这一方面。 然而，目前大多数研究主要集中在 TRIM21 与干扰素或其他抗病毒效应物这一方面。 而 TRIM21 对病毒编码蛋白的影响尚不清楚。在这项研究中，我们通过 FLAG 亲和纯化筛选 HBV DNA 聚合酶（Pol）的候选相互作用蛋白并通过质谱分析确定 TRIM21 作为 HBV DNA Pol 调节蛋白。我们首先使用了免疫共沉淀 (co-IP) 分析证明 TRIM21 与 HBV DNA Pol 的 TP 结构域相互作用。此外， TRIM21 使用其 RING 结构域促进 HBV DNA Pol 的泛素化和降解。 HBV DNA Pol 的 Lys260 和 Lys283 被确定为 TRIM21 介导的泛素化。最后，我们发现 TRIM21 将 HBV DNA Pol 降解为 限制 HBV DNA 复制，其 SPRY 域对这一活动至关重要。综合起来，我们的结果表明 TRIM21 主要通过促进 HBV DNA Pol 泛素化来抑制 HBV DNA 复制 ，可能为 HBV 的治疗提供新的潜在靶点。

PU-2870

Cell membrane remodeling mediates polymyxin B resistance in Klebsiella pneumoniae: an integrated proteomics and metabolomics study

Xinyi Chen、Jingjing Tian、Can Luo、Min Wang、Xianping Li、Xiaofan Wang
The Second Xiangya Hospital of Central South University

Polymyxin B (PB) is introduced into the clinic as the last-line therapy against carbapenem-resistant Klebsiella pneumoniae (CRKP). Unfortunately, increased resistance to PB in Klebsiella pneumoniae (K.pneumoniae) has threatened global health. This study employed TMT-labeled quantitative proteomics and LC-MS/MS metabolomics analysis to investigate the key biological processes associated with PB resistance in K.pneumoniae. The K.pneumoniae strains were

isolated from neonates and continuously passaged with different PB concentrations in vitro to develop PB resistance. A total of 315 differentially expressed proteins (DEPs) were identified, of which 133 were upregulated, and 182 were downregulated in the PB-resistant K. pneumoniae. GO annotation showed that DEPs were significantly enriched in transport, establishment of localization, and localization terms. KEGG enrichment analysis revealed that the DEPs were mainly involved in ATP-binding cassette (ABC) transporters and cationic antimicrobial peptide (CAMP) resistance. Proteins related to central carbon metabolism were inhibited in the PB-resistant K.pneumoniae, but proteins mediating LPS modification were activated. Transcriptional levels of CAMP resistance-related proteins were significantly different between PB-susceptible and -resistant K.pneumoniae. Metabolomics data demonstrated that 23 metabolites were significantly upregulated in PB-resistant K.pneumoniae, 18 were upregulated. The differential metabolites were mainly lipids, including glycerophospholipids, sphingolipids and fatty acids. Integrated omics showed that increased glycerophospholipids might be transported to the cell membrane through the upregulated Mla system to help bacteria grow under PB pressure. Our study suggested that membrane remodeling and inhibited central carbon metabolism are conducive to the development of PB resistance in K.pneumoniae.

PU-2871

PX Domain-Containing Kinesin KIF16B and Microtubule-Dependent Intracellular Movements

Jie Chen
The First Affiliated Hospital Of University Of South China

as a member of the kinesin-3 family, kinesin family member 16B (KIF16B) has a characteristic PhoX homology (PX) domain that binds to membranes containing phosphatidylinositol3phosphate (PI(3)P) and moves along microtubule flaments to abnormal lipid metabolism, and tumor brain metastasis. In this review, we summarize recent advances in the structural and obtained from clinical research suggest that KIF16B has a potential efect on the disease processes in intellectual disability, the plus end via a process regulated by coiled coils in the stalk region in various cell types. The physiological function of KIF16B supports the transport of intracellular cargo and the formation of endosomal tubules. Rasrelated protein (Rab) coordinates many steps of membrane transport and are involved in the regulation of KIF16B-mediated vesicle trafcking. Data physiological characteristics of KIF16B as well as diseases associated with KIF16B disorders, and speculating its role as a potential adaptor for intracellular cholesterol trafcking.

PU-2872

衡阳地区某三甲医院 2017-2019 年耐碳青霉烯菌检出情况分析

肖春兰
南华大学附属第一医院

目的 分析本院近 3 年耐碳青霉烯菌的分离情况和药物敏感性测试结果，分析近期耐碳青霉烯菌感染和耐药变迁趋势。
方法 回顾分析本院 2017 年 1 月—2019 年 12 月临床耐碳青霉烯菌的分离结果、标本来源和耐药情况，采用 Whonet5.6 和 SPSS 22.0 软件处理分析数据。
结果 2017—2019 年临床标本共检出耐碳青霉烯菌 2387 株，检出率 20.77%，其中非发酵革兰氏阴性杆菌 1774 株，肠杆菌科细菌 613 株，检出率居前三位的是脑膜脓毒性菌(100%)、产吲哚金黄杆菌(76.92%) 、鲍曼不动杆菌(73.12%)。阳性标本来源最多为痰，占比 77.50%。药物敏感性

测试结果显示耐碳青霉烯菌肠杆菌科细菌对阿米卡星、妥布霉素、庆大霉素具有较高敏感性，耐碳青霉烯非发酵革兰氏阴性杆菌对阿米卡星、哌拉西林/他唑巴坦、妥布霉素和庆大霉素具有较高敏感性，而耐碳青霉烯菌对其它抗生素均表现出高度耐药性。
结论 近期耐碳青霉烯菌检出数量呈上升趋势，并显示出广泛的抗生素耐药性，建议加强其分布和耐药性监测，以指导临床合理使用抗生素。

PU-2873

某儿童医院尿路感染病原菌分布及耐药性分析

方盼盼、王颍源、贾静、高凯杰、杨俊文、杨俊梅
郑州大学附属儿童医院

目的 了解郑州大学附属儿童医院尿路感染分离菌的分布及耐药性，为临床合理选择用药提供依据。
方法 将 2015 年 1 月至 2020 年 12 月就诊于郑州大学附属儿童医院 1236 例尿路感染患儿作为研究对象，收集其一般临床资料，采用 WHONET 5.6 软件分析其病原菌及抗菌药物耐药情况。
结果 1236 例患儿（非复杂尿路感染组 599 例和复杂尿路感染组 637 例）共检出 1309 株细菌，大肠埃希菌、屎肠球菌、粪肠球菌为主要病原菌。687 株革兰阴性菌前 2 位的是大肠埃希菌（352 株）和肺炎克雷伯菌(102 株)；562 株革兰阳性菌中前 2 位的是屎肠球菌（270 株）和粪肠球菌（215 株）；60 株真菌中最常见的是白念珠菌(34 株)。碳青霉烯类耐药的肺炎克雷伯杆菌菌株 41 株(40.20%)、大肠埃希菌 52 株(14.77%)。大肠埃希菌对阿米卡星、头孢哌酮/舒巴坦、亚胺培南、美罗培南耐药率均在 10%左右，对三、四代头孢菌素及其含酶抑制剂耐药率在 70%以上，呋喃妥因耐药率为 2.27%，未发现对替加环素耐药革兰阴性杆菌。非复杂尿路感染组与复杂尿路感染组中的革兰阴性菌对常见抗生素耐药率比较差异无统计学意义(P>0.05)。屎肠球菌对青霉素类、喹诺酮类及氨基糖甙类等抗生素的耐药性明显高于粪肠球菌，说明屎肠球菌比粪肠球菌耐药形势更为严重，且研究显示屎肠球菌和粪肠球菌非复杂尿路感染组诺氟沙星耐药率明显高于复杂尿路感染组(P<0.05)，未发现万古霉素、利奈唑胺耐药的革兰阳性菌。
结论 革兰阴性菌是尿路感染的主要病原菌，呋喃妥因可以作为轻症患儿经验性应用的推荐。耐药情况严峻，临床诊治工作应重在防控、及时送检及合理使用抗菌药物。

PU-2874

“沟通”助力“诊断”

王敏
江苏省人民医院（南京医科大学第一附属医院）

目的 患者，女，81 岁，慢性肾功能不全、肾病综合征于外院就诊。因计划肾穿刺活检，行凝血检查发现纤维蛋白原（FIB）为 1.10g/L，隔日复查 0.88g/L。遂转至我院血液科就诊，初步诊断为低纤维蛋白原血症（低纤症）。探讨该病人纤维蛋白原是否为真的降低。
方法 取患者静脉抗凝血用 CS5100 血凝仪检测，查看 Clauss 法和 PT 演算法结果有无差异
结果 本实验室两种 FIB 检测方法结果分别为：0.56 g/L（Clauss 法）及 2.20 g/L（PT 演算法)
结论 FIB 检测最常用两种方法（1）Clauss 法检测血浆中具有功能的 FIB 含量。（2）PT 演算法则根据 PT 检测过程中吸光度的变化而间接计算 FIB 的总含量。故与患者的接诊医生进行了两方面沟通：（1）患者 Clauss 法结果偏低，而 PT 演算法结果在正常范围内，故考虑为异常纤维蛋白原血症（异纤症）。（2）鉴于患者从未有出血症状，因此建议输注适量法布莱士后，可予以行肾穿刺活检。最终患者安全行肾穿刺术，并未出现大出血等不良后果。
检验对于临床诊断来说是必不可少的重要环节，检验结果是临床诊断的重要依据之一。多数临床实验室仅用 Clauss 法检测功能性 FIB，当其结果表现为降低时，有时会使临床医生将异纤症误判为

低纤症或无纤症。本例即为检验与临床沟通助力患者确诊的典型案例。本实验室两种 FIB 检测方法，有效降低了异纤症的漏诊和误诊。

PU-2875

湖南地区 34474 例葡萄糖-6-磷酸脱氢酶筛查结果回顾性分析

谭惠霞、陈偲、卢琴、闫一妮、申雨雅、何君兰、胡艳群、朱露、代冰*
长沙金域医学检验实验室有限公司

目的 对 2019 年~2020 年湖南地区 34474 例葡萄糖-6-磷酸脱氢酶（glucose -6-phosphate dehydrogenase ,G-6-PD）筛查的数据进行回顾性分析，了解现湖南地区人群 G-6-PD 缺乏情况，以加强人们进行 G-6-PD 筛查的意识，使之能够早诊断早预防，更大的降低此病的影响。
方法 运用速率法分别检测红细胞中 G-6-PD 和磷酸葡萄糖酸脱氢酶（6-PGD）活性，计算两者比值（G-6-PD/6-PGD），判断样本是否缺乏 G-6-PD。运用统计学分析性别、湖南各市区、高阳性率地区新生儿和成人之间的阳性率差异。
结果 筛查的 34474 例样本中，G-6-PD 缺乏人数为 1600 例，筛查阳性率为 4.64%，其中男性 1023 例，阳性率为 6.92%，女性 577 例，阳性率为 2.93%，男女阳性率之比为 2.4:1，男性阳性率高于女性，差异具有统计学意义（P<0.05）。湖南 14 个市区中郴州市（6.88%）和永州市（6.64%）阳性率最高，张家界市的阳性率（0.45%）远低于其他市区及总阳性率，G-6-PD 高阳性率地区新生儿和成人差异统计中，郴州市和永州市新生儿和成人的阳性率差异具有统计学意义（P<0.05），成人阳性率高于新生儿阳性率，推测是因为新生儿做的是筛查，而成人样本存在复查和监测的情况。
结论 湖南地区 G-6-PD 缺乏症阳性率较广西、广东、海南等高发地区低，但湖南地区 G-6-PD 缺乏症还是存在，我们应该重视开展 G-6-PD 缺乏症的筛查，进行早期的诊断和防治，避免接触诱因，做到最大限度地降低此疾病的影响。

PU-2876

The ratio of NT-proBNP to CysC^1.65 predicts heart failure in patients with chronic kidney disease

Sheng Wang、Xiaoyong Duan、Xiangyu Wang、Yulin Zou、Jing Luo
Sinopharm Gezhouba Central Hospital

Background Heart failure remains a considerable threat to patients with chronic kidney disease (CKD). The widespread use of the N-terminal pro B type natriuretic peptide (NT-proBNP) test has brought new insight to the prognosis of heart failure in patients with CKD. However, the levels of NT-proBNP are easily affected by renal insufficiency, which limits its use in this population. **Methods** A total of 292 consecutive patients with CKD were included in this study. The plasma levels of NT-proBNP, Cystatin C (CysC), and highly sensitive cardiac troponin T (hs-cTnT) were measured at admission. Meanwhile, the ejection fraction, left ventricular ejection fractions (LVEF), left ventricular end-diastolic dimension (LVDd), left ventricular end-systolic dimension (LVDs), left atrial volume index (LAVI), and the echocardiographic ratio of early diastolic mitral inflow velocity to early diastolic mitral annulus velocity (E/e') were detected. The age and body mass index (BMI) of all patients were recorded. Patients were divided into two groups based on their cardiac function: the heart failure group and the control group. Univariate analysis was used to examine the associations of cardiac insufficiency in CKD with age, BMI, LVEF, LVDd, LVDs, hs-cTnT, and NT-proBNP. Binary logistic regression analysis was performed to evaluate the degree of influence of all statistically significant factors on predicting cardiac dysfunction in patients with CKD. Pearson correlation analysis was used to analyze the relationship between the ratio of NT-

proBNP to $CysC^{1.65}$ (NT-proBNP/$CysC^{1.65}$) and the levels of NT-proBNP. ROC analysis was performed to analyze the sensitivity and specificity of five indicators (NT-proBNP, NT-proBNP/$CysC^{1.65}$, LVEF, E/e', and LAVI) for predicting cardiac dysfunction in CKD patients. **Results** Binary logistic regression analysis showed that NT-proBNP/$CysC^{1.65}$ was an independent risk factor for cardiac dysfunction in CKD (OR=1.002, 95% confidence interval: 1.000–1.003, P=0.000). Pearson correlation analysis showed that NT-proBNP/$CysC^{1.65}$ was not correlated with the levels of NT-proBNP (r=0.376, p=6.909) in all patients. In ROC analysis, the area under the curve (AUC) of NT-proBNP/CysC1.65 was 0.827 (95% confidence interval: 0.779-0.875), with a cut-off point of 738.125, a sensitivity of 78.47%, and a specificity of 79.73%.
Conclusion The ratio of NT-proBNP to CysC1.65 was superior to NT-proBNP alone in predicting cardiac dysfunction in patients with CKD.

PU-2877

海南省新生儿脐带血元素参考区间分析与建立

路淼
海南金域医学检验中心有限公司

目的 了解海南省新生儿脐带血常见微量元素水平，建立其正常参考值范围。
方法 收集海南省 2018 年 1 月 1 日至 2019 年 12 月 31 日送往海南省金域医学检验中心检测的 2511 名自然分娩或剖腹方式出生的新生儿（其中男性 1364 名、女性 1147 名）脐带血样本，采用电感耦合等离子体质谱法（ ICP-MS）对 Ca（钙） 、Mg（镁）、 Cu （铜）、Fe（铁） 、Zn（锌）、 Mn（锰）、 Pb（铅）元素进行检测和分析。为保证建立的参考范围的可靠性，数据处理采用 SPSS19.0 统计软件，将离群值以 D（疑似离群值与其相邻点的差值）/R（数据全距)≥1/3 为原则进行删除。采用非参数统计方法确定百分位数 p2.5 和 p97.5 作为参考限，确定 95%可信区间参考范围。
结果 Ca 元素的男性新生儿参考值是 44.80~71.70 mg/L，女性新生儿的参考值是 45.14~72.14 mg/L；Mg 新生儿可以共用参考值：29.70~49.07 mg/L； Mn 的男性新生儿参考值是 13.10~75.30μg/L， 女性新生儿的参考值是 12.30~73.80；Pb 新生儿可共用参考值：4.40~22.48μg/L；Zn 新生儿可共用参考值：1.50~3.30 mg/L；Cu 的男性新生儿参考值是 483.88~1140.79μg/L，女性新生儿的参考值是 477.19~1114.15μg/L；Fe 的男性新生儿参考值是 392.42~635.13 mg/L，女性新生儿的参考值是 393.65~624.27mg/L。
结论 初步建立了海南省新生儿脐带血常见的部分微量元素的参考区间。通过监测新生儿脐带血元素检测可为新生儿脐血中常见金属元素的水平含量评估提供参考依据；能及时发现新生儿微量元素情况，降低疾病发生和避免因元素含量异常而导致新生儿发育异常有重要的意义;可作为出生后元素补给的参考依据和日常监测依据。

PU-2878

甲状腺素的作用

李倩倩
山东大学第二医院

甲状腺素主要用于甲状腺功能亢进症和甲状腺功能减退症的鉴别诊断

血液中大于 99%的 T3.T4 和血浆蛋白结合，还有少量和前白蛋白结合。只有约占血浆中总量 0.4%的 T3 和 0.04%为游离的，结合型 T4 是血浆中含量最多的甲状腺激素，而只有游离的 T3.T4 才能进入靶细胞发挥作用。

血清游离甲状腺素（FT4）和三碘甲状腺原氨酸（FT3）,FT3.FT4 不受甲状腺激素结合球蛋白（TGB）影响。甲状腺激素的合成和分泌主要受下丘脑——垂体——甲状腺轴的调节，血液中游离 T3.T4 水平的波动，负反馈地引起下丘脑释放促甲状腺激素释放激素(TRH)和促甲状腺激素（TSH）的增加或减少。其中血液中游离 T3.T4 水平对垂体释放 TSH 的负反馈调控最重要。

主要为促进三大营养物质代谢，提高大多数组织的耗氧量，促进能量代谢，增加产热和提高基础代谢率。可与生长激素产生协同作用，促进机体生长发育，影响神经系统的发育。

甲状腺功能亢进：为多种病因导致甲状腺激素分泌过多导致的临床综合征，患者乏力.怕热.多汗.体重减轻心悸,食欲亢进.紧张.焦虑.易怒等.甲状腺功能减退:俗称甲减,多种原因引起甲状腺激素合成.分泌或生物效应不足所致的内分泌疾病.

甲状腺功能试验检查(1)FT3 和 FT4 不受甲状腺激素结合球蛋白影响,直接反馈甲状腺功能状态.(2)1.血清总甲状腺素是判断甲状腺功能最基本的筛选试验.2.TT3 是早期 Graves 病疗效观察及停药后复发的敏感指标。

PU-2879

多发性骨髓瘤患者血清 CRP 浓度与血清肌酐、血清尿酸浓度的相关性

刘子豪
石河子大学第一附属医院

目的 多发性骨髓瘤（Multiplemyeloma，MM）是浆细胞恶性增殖性疾病，疾病特征是骨髓中的浆细胞像肿瘤细胞一样无限制地增生，并且大部分病例伴有单克隆免疫球蛋白分泌，最终导致器官或组织损伤，它是严重威胁中老年人身体健康的恶性血液系统肿瘤，近年来发病率呈现出逐年上升的趋势。与健康体检者比较,多发性骨髓瘤患者的血清 CRP 水平值明显增高,且随疾病的进展而增高。肌酐(creatinine，Cre)是肌肉在人体内代谢的产物，主要由肾小球滤过排出体外，可反应肾损伤的程度。尿酸是嘌呤代谢的终产物，各种嘌呤氧化后生成的尿酸随尿排出，体液中尿酸含量变化，可以充分反映出人体内肾脏代谢机能的状况，检测血清尿酸可用于对多发性骨髓瘤患者肾功能的临床早期诊断。本研究探索 MM 患者血清 CRP 水平与血清肌酐、血清尿酸水平的关系。

方法 一般资料收集石河子大学第一附属医院 2012 年 1 月至 2021 年 5 月收治的初诊 MM 患者 34 例，年龄 46~86。通过 t 检验分析 MM 患者血清 CRP 水平是否与血清肌酐、血清尿酸水平存在联系，通过 Pearson 相关分析探索 MM 患者血清 CRP 与血清肌酐、血清尿酸水平的相关性。

结果和结论 结果显示，13 例 CRP 升高的 MM 患者血清肌酐明显高于 21 例 CRP 正常的 MM 患者,差异有统计学意义(P<0.001)。10 例 CRP 升高患者血清尿酸水平高于 24 例 CRP 正常患者血清尿酸水平,差异有统计学意义(P<0.05)。表明在 MM 患者中，血清中 CRP 水平与血清中肌酐、尿酸水平具有一定联系。通过 pearson 相关性分析得出，随着血清 CRP 水平的升高，其血清肌酐水平呈升高趋势,两者间呈正相关(r=0.643,P<0.05)；CRP 水平越高，血浆尿酸越高,两者呈正相关（r=0.659,P<0.05）。表明随 CRP 水平的升高，MM 患者的肾功能损害程度越高，预后越差。

PU-2880

Using FOCUS-PDCA to improve the management level of hazardous chemicals

Huali Li
The First Affiliated Hospital of Xi'an Medical University

Objective To standardize the management of hazardous chemicals by scientific management methods, improve the accuracy of registration of hazardous chemicals in and out of warehouse, as well as ensure the safety and accurate use of hazardous chemicals in clinical work.
Methods According to the FOCUS-PDCA procedure, the problems existing in hazardous chemicals storage and registration were analyzed, the improvement measures were formulated, the management system was improved, hazardous chemicals files were established, and the management of hazardous chemicals in and out of the warehouse was standardized and improved continuously.
Results Through the application of FOCUS-PDCA, the registration accuracy of hazardous chemicals was increased from 12.5% to 98.9%; It improves the staff's understanding and familiarity of hazardous chemicals, so as to ensure using them in clinical laboratory safely, timely and accurately.
Conclusion FOCUS-PDCA has a good effect on standardizing the entry, classification, and storage of hazardous chemicals, and plays an important role in achieving continuous improvement of medical quality and safety, which is worth promoting.

PU-2881

2015-2018 年郴州市恶性肿瘤发病状况的统计分析

周丹旎、曹红
郴州市第一人民医院

目的 分析 2016-2018 年郴州市恶性肿瘤的发生状况，为科学防治本地区恶性肿瘤提供依据。
方法 收集 2015-2018 年郴州市二级及三级医院住院患者的诊断资料，按照国家疾病分类标准编码 ICD-10 进行统计分类，分析恶性肿瘤（C00-C97）在不同年龄段和不同性别的分布情况。
结果 2015-2018 年郴州市恶性肿瘤报告人数为 63048 例，其中 2015 年 13930 例、2016 年 15087 例、2017 年 16837 例、2018 年 17194 例，四年来逐年增长；恶性肿瘤报告病例数前五位分别为支气管和肺恶性肿瘤、肝和肝内胆管恶性肿瘤、胃恶性肿瘤、乳房恶性肿瘤、直肠恶性肿瘤；在 6 个年龄段中，报告病例数较高的年龄段为 40 岁≤年龄＜65 岁和年龄≥65 岁，报告病例数分别为 35774 例、23463 例；男性恶性肿瘤报告病例为 37042 例；男性恶性肿瘤报告病例前五位为支气管和肺恶性肿瘤、肝和肝内胆管恶性肿瘤、胃恶性肿瘤、直肠恶性肿瘤、结肠恶性肿瘤；女性恶性肿瘤报告病例为 26006 例；女性恶性肿瘤报告病例前五位为乳房恶性肿瘤、支气管和肺恶性肿瘤、宫颈恶性肿瘤、胃恶性肿瘤、结肠恶性肿瘤。
结论 2015-2018 年郴州市恶性肿瘤报告病例数逐年增加；恶性肿瘤的发病人群以中老年为主；男性发病人群明显高于女性；男女的主要恶性肿瘤分布有差异，应依据本地区恶性肿瘤分布特征制定有效防控措施。

PU-2882

Targeted Metabolism Study in Normal Pregnancy Women

Rui Zhang [1]、lei zhou[1]、liu yang[1]、yueyun ma[2]、jiayun liu[1]
1. Air force medical uiversity xijing hospital
2. 空军军医大学特色医学中心

There are always unique metabolisms in pregnant women especially with the amino acid (AA) metabolism for their physical changes. Our research aims are to investigate different metabolomics in healthy pregnancies with normal women and provide possible baseline data for pregnant studies in the future. The 21 amino acids, 2 branch chain amino acid (BCAA) metabolites, and 3 catecholamine metabolites analysis in the serum of healthy second trimesters, third trimesters, and normal women were investigated by the high-performance liquid chromatography−mass spectrometry (HPLC-MS/MS). The concentration of the most analyses were decreased, and that of three amino acids were increased for maternal women compared with normal women. After orthogonal partial least squares discriminant analysis (OPLS-DA), some of the compounds with the most significant differences were selected in normal pregnancy. Then the most significant compounds were applied for the enrichment analysis and pathway analysis to find out the different metabolic pathways in pregnant women. After the above comprehensive analysis, we find that the difference in the ratio of related compounds is more valuable for metabolites in pregnant women research. Under the guidance of this conclusion, we found that the metabolomics of branched-chain amino acids in pregnant women's serum to α-ketoisovaleric acid is much faster than that of branched-chain amino acids to methyl-2-oxovaleric acid. The dominant pathway of branched amino acids to metabolism is the α-ketoisovaleric acid pathway. These normal profiles of metabolites and pathway information related to pregnancy have the potential to explore the complex mechanisms of physiological and metabolomic challenges in pregnant women and may produce the ability to have new hypotheses, which in turn can provide ideal hypotheses to begin large-scale epidemiological studies of women who subsequently develop diseases.

PU-2883

衍生化串联质谱检测 55 种酰基肉碱方法的建立及其临床应用

张瑞、周磊、杨柳、刘家云
空军军医大学西京医院

目的 建立衍生化串联质谱（MS/MS）检测人体中 55 种酰基肉碱的方法，考察该方法的影响因素及其在西部新生儿遗传代谢性病筛查中的应用和意义，为其有效防治提供科学的依据。
方法 利用衍生化 MS/MS 法分析比较了 2 869 例出生 3 d 至 1 岁婴幼儿的干血滤纸片。采足后跟血于空白采血滤纸上，完全渗透。用已知浓度的酰基肉碱同位素内标液液萃取干血滤纸片中的 55 种酰基肉碱，经过 20 min 衍生化反应后，用串联质谱仪分析标本中的 55 种酰基肉碱并计算其浓度。
结果 采用衍生化质谱法对新生儿进行遗传代谢病筛查最好不使用含有抗凝剂的血，标本于 4 ℃存放两周内进行检测，使用的内标液于 4 ℃条件下存放不超过一个月，氮气吹干 15 min 以上可得到较为理想的结果。酰基肉碱批内变异系数为 7.3%~9.9%，批间变异系数为 11.3%~13.9%。经统计学分析男、女之间酰基肉碱浓度差异无统计学意义(P>0.5)。
结论 衍生化串联质谱法进行血滤纸片中 55 种酰基肉碱分析，有较高的回收率，能够达到较高的精确性和准确性，能灵敏、特异地测定血中酰基肉碱浓度，为相关疾病的筛查诊断提供更多可能性，满足临床对遗传代谢疾病筛查及诊断的需要。

PU-2884

22 种氨基酸衍生化串联质谱高通量检测方法的建立

张瑞、杨柳、周磊、刘家云
空军军医大学西京医院

目的 考查衍生化串联质谱（MS/MS）法高通量快速检测全血中 22 种氨基酸并分析其影响因素。
方法 新生儿采足后跟血，儿童采末梢血于空白采血滤纸上，完全渗透，晾干。用已知浓度的氨基酸同位素内标液萃取干血滤纸片中的 22 种氨基酸, 衍生化 20 分钟,建立衍生化串联质谱法高通量快速检测全血中 22 种氨基酸法，采用方差分析优化其影响因素并分析了 2869 例 2014 年至 2018 年西部五省部队出生 3 天至 1 岁婴幼儿的干血滤纸片。
结果 建立衍生化串联质谱法高通量快速检测全血中 22 种氨基酸并优化了该方法的影响因素：使用不含抗凝剂的全血，标本 4℃保存不超过两周，内标液 4℃保存不超过一个月，氮气吹干时间为 15 分钟。本方法定量检出限为 0.3-10.0μM；批内变异系数为 5.3 % -7.9 %, 批间变异系数为 7.0 %-8.9 %，经统计学分析男、女之间氨基酸含量无显著性差异(P>0.5)；加标回收率为 96.1%-98.1%；偏倚<10%。
结论 衍生化串联质谱法高通量快速检测全血中 22 种氨基酸有较高的回收率,精确性和准确性,可以灵敏，特异地测定全血中 22 种氨基酸浓度，满足临床对遗传代谢疾病筛查及诊断的需要。

PU-2885

心理干预是否对儿童末梢采血的作用

王敏
山东大学第二医院

目的 探讨心理干预是否对儿童末梢采血疼痛感有明显影响。
方法 运用心理学的思想，从积极的角度针对我院随机 100 名不同年龄的儿童患者，采血时进行心理干预，再同样随机选取 100 名不同年龄的儿童患者，采血时不进行心理干预。
结果 心理干预组儿童患者恐惧率明显低于无心理干预组儿童患者。
结论 有效的心理干预能有效的减小或消除儿童患者对采血的恐惧。

PU-2886

一种简易高效的大鼠原代肝细胞分离方法

张秀莉、郭红云、张永东、王涛、梁涛、苏海翔*
甘肃省肿瘤医院、甘肃省医学科学研究院

目的 寻找一种简易高效的大鼠原代肝细胞分离方法，
方法 在 Selgen 两步胶原酶灌注法的基础上加以改进，按门静脉灌注法分离培养大鼠肝细胞,重复 10 次分离肝细胞实验，观察各项指标结果。采用胰酶、Ⅳ型胶原酶经门静脉灌注，大鼠肝脏肝门部结构、肝上及肝下腔静脉封闭保留胶原酶消化分离获取肝细胞，经 80 目和 200 目的筛网依次过滤细胞后，细胞悬液分别以 1000，500, 300rpm/min 离心各 5min 以纯化肝细胞,以台盼蓝排染法测定细胞活性，HE 染色鉴定肝细胞纯度。
结果 平均每只成年 Wistar 雄性大鼠可以获得（1.53±0.31）×108 个肝细胞，平均获得肝细胞活率可达到 94.63%，平均获得肝细胞纯度为 96.7%。
结论 本实验介绍的方法简便易行，且肝细胞产量较高，活力好，纯度高，适宜在一般条件的实验室推广和应用。

PU-2887

三级医院对口帮扶贫困县医院检验科的实践与体会

郭建林[1]、张志平[2]、侯勇[2]
1. 地区第二人民医院检验科
2. 喀什地区叶城县人民医院

为贯彻落实党中央、国务院关于打赢脱贫攻坚战的决策部署坚决打赢健康扶贫攻坚战，进一步夯实三级医院对口帮扶贫困县县级医院工作精神，从“输血式”支援向“造血式”支援转变的新模式。强化县级医院人才培养和学科建设为抓手，虽说县级医院是“二级甲等”医院，但是其人员素质，设施环境，人才梯队建设患者素质参差不齐等问题日益突出。而检验科与患者接触时间相对较短，为提升治疗服务质量，提升医患满意度，其中的任务可谓艰辛，下面是笔者在帮扶工作中的几点体会。

PU-2888

补体系统与子痫前期

薛宇廷[1]、贾珂珂[1]、杨楠[1]、邓兴宇[2]
1. 北京大学第三医院
2. 北京大学医学部

许多研究表明，补体系统(Complement system)与子痫前期(Preeclampsia, PE)存在一定的联系。补体系统的异常表达可在某种程度上参与到子痫前期的发病机制中从而诱发子痫前期，而子痫前期的病理生理过程中同样也存在补体系统的异常激活。本文从发病机制出发，结合临床患者资料，总结了补体系统在子痫前期中的变化，探讨补体系统在子痫前期的发病、辅助诊断以及预测等方面的临床价值。

PU-2889

METTL3 regulates m6A in endometrioid epithelial ovarian cancer independently of METTl14 and WTAP

Qin Li
Yantai Yuhuangding Hospital

N6-methyladenosine (m6A) RNA methylation, one of the common RNA modifications, has been determined to execute crucial functions on tumorigenesis and cancer development. The m6A “writers” including Methyltransferase like 3 (METTL3), METTL14 and Wilms tumor 1-associated protein (WTAP) contribute to the m6A modification process initiation. However, the coordination of m6A methyltransferase complex is not fully understood in endometrioid epithelial ovarian cancer (EEOC). In this study, mRNA and protein levels of METTL3, METTL14 and WTAP were detected in 33 EEOC cases using qPCR, immunohistochemistry and western blot. The overall m6A methylation was detected by dot plot. The METTL3 expression and overall m6A level were elevated in EEOC tissues, while the expressions of METTL14 and WTAP have no Accepted ArticleThis article is protected by copyright. All rights reserved. significant difference in EEOC compared to the adjacent tissues. The expression of METTL3 was an independent factor to correlate with poor malignancy and survival of EEOC patients. Moreover, METTL3 knockdown in TOV-112D and CRL-11731D cells weakened the capability of cell proliferation and migration, and promoted the cell apoptosis compared to negative control and cells with WTAP or METTL14 knockdown using CCK-8 assay, transwell assay, wound healing assay and TUNEL assay. Furthermore, METTL3 knockdown also reduced m6A enrichment of the genes associated with

ovarian cancer including EIF3C, AXL, CSF-1, FZD10 in TOV-112D and CRL-11731D cells by RIP-qPCR assay. Taken together, the high expressed METTL3 indicated poor malignancy and survival of EEOC via modulating the aberrant m6A RNA methylation. METTL3-mediated m6A modification, independent of WTAP and METTL14, was considered as a novel mechanism underlying m6A modulation and a potential therapeutic target of EEOC.

PU-2890

乳腺癌与 Wnt 信号通路的研究进展

毛杰[2]、谢小兵[1]
1. 湖南中医药大学第一附属医院医学检验与病理中心
2. 湖南中医药大学第一附属医院

Wnt 信号通路包括经典的 Wnt/β-catenin 信号通路和非经典的 Wnt 信号通路（Wnt/Ca2+信号通路、细胞极性通路），研究发现 Wnt 信号通路的异常激活与乳腺癌的发生和发展相关。乳腺癌由于高发病率和死亡率，长期以来一直是热门的临床研究课题。因此需要不断探索乳腺癌增殖、迁移、侵袭、复发的分子机制，寻找潜在的干预靶点，以期为临床提供新的治疗途径和方法。本文就 Wnt 信号通路在乳腺癌中的研究进展做一综述。

PU-2891

copeptin 的临床研究进展

毛杰[1]、卢晴晴[1]、李萍[2]、石盛洁[1]、李菁[1]、邓长娟[1]、谢小兵[2]
1. 湖南中医药大学第一附属医院
2. 湖南中医药大学第一附属医院医学检验与病理中心

近年来随着人民生活水平的提高，许多急慢性疾病的发病率逐年增高，这其中就包括心血管疾病、肾脏疾病、呼吸道疾病和脑卒中等，由此导致的各种慢性并发症造成了严重的社会及经济负担，如何早期发现该疾病并及早进行一些生物标志物的检测，从而为临床疾病的早期治疗和干预并发症的进展提供新的思路。和肽素（copeptin)作为一种敏感性较高的标志物应用于临床疾病的筛查检测，对疾病的早期、进展和预后有重要的监测作用。近年来大量研究结果表明和肽素在心脑血管疾病、肾脏疾病及脑卒中等预测方面有重要的临床价值，本文对和肽素在临床的研究进展作一综述

PU-2892

血晶案例

梁涵瑜
江苏省人民医院（南京医科大学第一附属医院）

目的 1 例穿刺液血晶案例
方法 湿片镜检可见棕黄色斜方形结晶及线型细丝状结晶
结果 血晶是血红素分解代谢的产物，橙色或褐色，通常表现为针状、菱形状或无定型
结论 血晶是红细胞外渗在一个封闭的组织隔室并且在低氧分压条件下血红蛋白代谢的结果。多见于陈旧性出血

PU-2893

Rh-D-稀有血型免疫血清学及遗传背景分析
——附新生儿溶血病报告 1 例

彭小友、阳爱丽、李胜涛、周杰英
郴州市第一人民医院

目的 对 1 例严重高胆红素血症新生儿及患儿母亲进行免疫血清学和分子生物学检测，诊断新生儿溶血病。
方法 对患儿进行直接抗球蛋白试验,放散试验及游离试验；对患儿母亲进行抗体筛查及抗体鉴定；检测患儿母亲 Rh 表现型并对其 RHCE 基因进行基因分型和外显子测序。
结果 母亲为 Rh-D-稀有血型,产生了针对高频抗原的抗体引起新生儿溶血病。该表型由ＲＨＣＥ基因外显子 5 和 6 缺失所致。
结论 发现了 1 名由ＲＨＣＥ基因 5 和 6 外显子缺失所致的 Rh-D-稀有血型个体,诊断了 1 例抗－Ｈｒ 0 抗体导致新生儿溶血病。

PU-2894

关于静脉采血的总结

郭雪焕
山东大学第二医院

目的 提高静脉采血的成功率，减轻病人痛苦，提高标本质量。
方法 认真选好血管是穿刺成功的第一步。我们在采血时应选择弹性良好、粗且直的静脉。对于不好找的血管，首先应有足够的耐心，足够的自信能力，才能摸清采血的具体位置，提高采血的成功率。消除患者的疑虑和负面因素，在众多的患者中，会有少数人心存疑虑，面对心存疑虑的患者，我们要耐心、细致的与他们交流，科学的解释他们提出的一系列问题，已彻底消除他们心中存在的焦虑问题，善于总结，加强与同事之间技术的交流，摆脱工作壁垒。
结果（1）、采血者应该加强自身的素质修为。应注重自己的仪表形象，工作期间着装要规范、干净、整洁。要以热情周到的服务在第一时间获得患者的信任。
（2）、采血者在整个采血过程中应该要求严肃认真，要严格执行采血各项标准与流程，遵守无菌操作，做到穿刺采血一次成功性，以严谨的工作作风和精湛的采血技术换取患者的绝对信任。
结论（1）、采血作为医师工作的重要部分，采血穿刺的一次成功率是衡量业务素质的最基本要素。而熟练的穿刺技术是保障穿刺成功的基本要素。只有掌握过硬的穿刺技术，才能在采血过程中保障穿刺的一次性成功。
（2）、良好的心里素质也是采血所必不可少的一部分。我们需要良好的自我控制能力，调整好自己的情绪，取得患者的信任与合作，才能有效的提高穿刺成功率。
（3）、加强沟通，做好采血前的健康教育，提供热情周到的服务，减少患者的紧张情绪，提高穿刺成功率。

PU-2895

乏氧饥饿状态下 IL-35 通过诱导乳腺肿瘤细胞自噬促进生长

陈茜
山东大学第二医院

背景 IL-35 是 IL-12 家族的新成员，在肿瘤发生发展和肿瘤免疫过程中发挥重要作用。但是，在乏氧饥饿状态下，IL-35 对乳腺肿瘤细胞的存活是否有影响目前尚未报道。
材料方法 我们利用免疫细胞化学、免疫荧光和流式细胞术检测乳腺癌细胞中 IL-35 及其受体的表达;在乏氧饥饿状态下，将乳腺癌细胞系用不同浓度的 IL-35 刺激观察乳腺癌细胞的生存及自噬情况。接着我们检测 IL-35 在乳腺肿瘤中促存活和促自噬的关系。利用 CCK8、细胞周期、凋亡试剂盒和 western blot 技术检测乳腺肿瘤的存活情况；利用自噬相关蛋白及底物检测自噬流情况。利用 MDC 方法和 western blot 检测细胞自噬情况，相关信号通路主要通过 western blot 方法检测。
结果 首先我们检测乳腺癌细胞中 IL-35 及其受体的表达。在乏氧饥饿状态下，外源性 IL-35 通过诱导自噬抑制凋亡促进肿瘤细胞存活；在阻断自噬的情况下可抑制 IL-35 的促存活作用。最后我们检测发现 IL-35 在乏氧饥饿状态下促肿瘤自噬主要通过激活 PI3K/AKT/mTOR 信号通路。
结论 本研究发现 IL-35 在乏氧饥饿状态下可通过诱导自噬促进乳腺肿瘤细胞存活，为乳腺肿瘤免疫及发生发展提供了新思路。

PU-2896

120 例肾病综合征患者的实验室检测结果分析

马汝飞、李刚
河南省人民医院

目的 分析肾病综合征（NS）患者的肾小球滤过率 (eGFR)、血脂、血清白蛋白、抗凝血酶、D-二聚体检测结果，对比其与健康对照组的结果差异，探讨实验室指标在肾病综合征患者诊疗中的应用。
方法 选择临床确诊的肾病综合征患者 120 例，并根据肾小球滤过率 (eGFR)的高低分为肾损伤轻度、中度、重度三组，轻度组患者肾小球滤过率 (eGFR)为 50-80ml/min，中度组患者肾小球滤过率 (eGFR)为 20-50ml/min，重度组患者肾小球滤过率 (eGFR)为小于 20ml/min，同时选取正常体检者（排除肾脏相关疾病）100 例作为对照组，对照组肾小球滤过率 (eGFR)为 80-120ml/min，同时检测总胆固醇（TCH）、血清甘油三酯（TG）、血清白蛋白、抗凝血酶（AT）、D-二聚体的水平，并对各组进行统计学分析。
结果 三组 NS 患者的 TCH、TG、D-二聚体水平显著高于健康对照组（P<0.05），AT、 血清白蛋白水平显著低于健康对照组（P<0.05）。NS 患者检验结果的组间差异为：重度组 TCH、TG、D-二聚体水平显著高于轻度、中度组（P<0.05），重度组 AT、 血清白蛋白水平显著低于轻度、中度组（P<0.05），中度组 TCH、D-二聚体水平显著高于轻度组（P<0.05），中度组 AT 水平显著低于轻度（P<0.05），中度组和轻度组间的 TG、血清白蛋白水平差异不显著（P<0.05）。
结论 肾病综合征（NS）患者的血脂、血清白蛋白检测水平跟肾损伤严重程度显著相关，检测指标抗凝血酶降低和 D-二聚体升高反映了肾病综合症患者高凝状态和纤溶亢进的存在，提示了患者处于易栓状态，对这些实验室指标的密切检测有利于肾病综合征的病情评估和疗效观察。

PU-2897

传染性单核细胞增多症患儿免疫状态与疗效观察分析

穆原[1]、单鸣凤[2]
1. 江苏省人民医院（南京医科大学第一附属医院）
2. 南京市儿童医院

目的 观察传染性单核细胞增多症（IM）及常见合并症患儿的细胞免疫与体液免疫指标，并分析其疗效间的关系。
方法 查阅 2019 年全年收治的 129 例 IM 患儿病历资料，将其中明确诊断的 116 例患儿淋巴细胞亚型和体液免液检测结果纳入本研究。对单纯 EBV 感染组 35 例，单纯 IM 组 24 例，IM 合并肝损伤组 19 例，IM 合并肺炎支原体（MP）感染组 38 例的淋巴细胞亚型、IgG、IgM 及疗效数据进行统计分析。
结果 IM 患儿 CD8+T 细胞显著高于健康对照组（$P < 0.05$），而 CD4+T 细胞与 CD19+B 细胞均显著低于健康对照组（$P < 0.05$），以杀伤 T 细胞增殖与辅助 T 细胞受抑为主要表现，当合并 MP 感染时这种差异更为显著（$P < 0.01$）。IM 患儿的血清 IgG 与 IgM 浓度均较健康对照组有显著升高（$P < 0.05$）。EBV 感染所致不同程度肝损伤的病例高达 16.4%（19/116），列 IM 合并症之首。单纯 IM 组在退热时间、咽峡炎好转时间及异型淋巴细胞<0.05 时间上均明显短于其它两组。
结论 IM 患儿免疫功能异常，提示临床在抗感染治疗同时，适当使用一些免疫调节剂，对缩短患儿病程、加速患儿康复、减少 EBV 感染后相关疾病的发生具有一定实践意义。

PU-2898

青年男性甲状腺功能血清学标志谱的初步分析

顾敏
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨普通人群中青年男性甲状腺功能血清学指标的异常状况，提高人们对青年男性甲状腺疾病的认识和警惕，为预防、早期发现和治疗此类疾病提供参考。
方法 回顾性分析 2019 年 8 月至 2020 年 1 月在我院进行健康体检人群 847 例，其中青年男性 412 例，青年女性 435 例，分别行甲状腺功能血清学标志谱（FT3、FT4、TSH、TPOAb 和 TGAb）检测并进行对比研究。
结果 青年男性和青年女性人群甲状腺功能血清学指标总异常检出率分别为 16.75%和 30.11%，两者存在显著差异（$p<0.001$）。青年男性和青年女性的血清 TSH、TPOAb 和 TGAb 异常检出率均高于 FT3 和 FT4，其中青年女性中所有的差异均有统计学意义，而青年男性中仅血清 TSH 异常检出率显著高于 FT3 和 FT4。
结论 青年女性甲状腺功能血清学指标总异常检出率明显高于青年男性，但青年男性甲状腺功能血清学指标总异常检出率也处于较高水平。因此我们在研究女性和中老年人群甲状腺健康状况的同时也应对青年男性甲状腺健康给予更多的关注。

PU-2899

肝移植患者中性粒细胞的特殊形态变化

王丹、张怡婷、张丽霞
江苏省人民医院（南京医科大学第一附属医院）

背景 中性粒细胞是人体循环系统中数量最多、寿命最短的白细胞。研究表明，中性粒细胞参与先天免疫、病原体杀灭和肝脏疾病。中性粒细胞的错误激活参与了包括肝衰竭在内的多种炎症性疾病的发病机制。此外，中性粒细胞的形态也发生了特殊的变化。
方法和结果 本文报告两例肝移植患者外周血涂片(peripheral blood smears, PBSs)中一组特殊的中性粒细胞，其形态与单核细胞相似，导致血液分析仪(hematology analyzer, HA)将中性粒细胞误认为单核细胞。
结论 本案例中，特殊的中性粒细胞核形态变化是非常罕见的。HA 对中性粒细胞和单核细胞的错误识别，应引起实验室的重视。

PU-2900

如何提高采血人员的综合素质

高珍琪
山东大学第二医院

目的 随着社会的发展，患者对医务人员的要求也越来越高。窗口采血工作压力倍增，对采血人员的综合素质也提出了更高的要求和挑战。
方法 •采血人员要提高服务意识。
•采血人员要有耐心和爱心。
•采血人员要提高处理突发事件的能力。
•采血人员要提高静脉穿刺技术。
•采血人员要提高无菌意识，做到一人一针一带一纸一手消。
•采血人员要穿戴整洁，保持良好的个人形象。
•采血人员要根据患者的需求，及时调整工作状态。
•采血人员要提高个人修养，业余时间多读书学习。
结果 通过提高综合素质，采血人员能更好的服务患者，赢得患者的称赞和满意。通过提高综合素质，采血人员的自我认可度提高，工作更加自律、勤恳。通过提高综合素质，采血人员能调节自我，释放压力，从而自信的投入工作。
结论 采血人员综合素质的提高有利于更好地开展工作，服务患者，减少投诉的发生，保障医院与患者的权益。

PU-2901

同型半胱氨酸检测意义及临床应用研究进展

朱佳丹、杨勇、张宏磊
甘肃金域医学检验所有限公司

近年来，临床不断深入研究了同型半胱氨酸，发现其和肾脏疾病、心血管疾病等关系均极为密切，同时比传统指标的临床应用价值高。在心血管疾病的预防与治疗中，检测血清同型半胱氨酸能够将重要依据提供给临床[1]与此同时有研究表明高同型半胱氨酸血症(hHCY)是诱发胎儿血管疾病和出生缺陷的一个独立的危险因素与周围血管阻塞疾病也息息相关。因此同型半胱氨酸检测在临床

治疗患者疾病预测具有非常重大的意义。本文主要针对同型半胱氨酸的临床检测意义和临床应用情况进行综述。

PU-2902

长沙某医院血流感染病原性真菌分布及药敏分析

徐文[1]、吴玲[2]
1. 湖南省人民医院
2. 湖南师范大学

目的 通过收集和分析真菌血流感染中的真菌分布、耐药情况及相关因素，为真菌血流感染的诊断和治疗提供重要依据。
方法 回顾性统计分析湖南省人民医院 2020 年 01 月到 2020 年 12 月的临床真菌血流感染病例 80 例。根据患者的性别、年龄、科室、基础疾病等进行统计，分析探讨湖南省人民医院近期临床真菌血流感染的病原菌种类及耐药情况和其他相关因素。
结果 近平滑念珠、白色念珠菌、热带念珠菌、光滑的念珠菌分离率分别为 38.75%、26.25%、15.00%、15.00%。其中患者主要分布科室为 ICU，普外科和肝胆科。药敏结果中，主要为对唑类药物耐药，其中热带念珠菌对氟康唑、伏立康唑的耐药率高达 41.69%。
结论 在真菌血流感染中，病原菌以近平滑念珠菌、白色念珠菌、热带念珠菌、光滑念珠菌为主。临床医师在诊断治疗过程中，应密切关注患者危险因素，警惕病原性真菌的耐药情况，及时进行科学有效的抗菌治疗。

PU-2903

槲皮素抑制神经母细胞瘤生长作用及机制研究

张宗桃
广州医科大学附属第三医院（在读研究生）

目的 探讨槲皮素抑制神经母细胞瘤生长作用及分子机制。
方法 用神经母细胞瘤细胞株种植于裸鼠皮下构建肿瘤种植瘤动物模型，每两天一次腹腔注射槲皮素，测量神经母细胞瘤异位种植瘤的体积，大小，重量；体外实验采用不同浓度的槲皮素处理神经母细胞瘤株 N2a 和 SH-SY5Y 细胞，MTT 法检测槲皮素处理前后肿瘤活性的变化，流式细胞术检测槲皮素对肿瘤细胞凋亡作用及 Western blot 检测凋亡相关分子表达；转录组测序进一步阐明槲皮素诱导神经母细胞瘤凋亡的分子机制。
结果 槲皮素处明显抑制神经母细胞瘤异位种植瘤的生长。体外结果显示槲皮素明显抑制神经母细胞瘤细胞 N2a 和 SH-SY5Y 的生长。流式细胞术结果显示槲皮素诱导神经母细胞凋亡。Western blot 结果显示槲皮素明显上调肿瘤细胞的 caspase-3 水平和活性，同时下调 bcl-2，上调 bax 水平。转录测序结果显示槲皮素明显下调细胞周期通路、嘌呤和嘧啶合成通路以及 DNA 复制通路。
结论 槲皮素明显抑制神经母细胞瘤的生长，可能通过抑制嘌呤和嘧啶合成通路以及 DNA 复制通路，进而上调 caspase-3 活性 和调控凋亡相关蛋白 bcl-2 和 bax，最终诱导神经母细胞瘤凋亡。

PU-2904

检验与临床沟通方式探讨

吴宗勇[1,2]、张晓煜[1]、张丽[1]、齐军[1]
1. 中国医学科学院肿瘤医院深圳医院
2. 中国医学科学院肿瘤医院

目的 探讨检验科与临床科室之间如何建立有效的沟通方式，以便为临床诊疗提供更好的服务。
方法 列举法。检验科与临床沟通的方式有书面沟通，包括：(1)在检验前的质量控制阶段，定期向临床发放《检验用户手册》和《标本采集及运送指南》并定期更新。(2)细菌耐药率的定期通报等。当面沟通，包括：(1)定期（每年 2 次）召开检验科与临床沟通会。(2)举办全院继续教育项目，向临床医护人员介绍检验新技术与新方法以及行业新进展。(3)深入临床进行小讲课及新项目宣传，结合科室具体情况进行专项授课并向临床介绍新项目的临床意义以及开展注意事项。（4）对护理人员进行专项培训，介绍标本采集方法及注意事项。(5)认真处理临床抱怨与投诉等。信息化沟通：利用医院信息化管理系统(His)、微信群、电话通讯及医院自动化办公系统(OA)等平台介绍检验项目应用知识，及时宣传科室动向。其他沟通方式：参加临床多学科联合治疗（MDT）会议，提升检验医学在临床治疗中的地位。与临床进行科研协作，缩短检验与临床之间的距离，增进检验人与临床医生的友谊，同时提升检验人的学术水平。检验与临床联合举办学术会议，可促进新技术新项目在临床的顺畅应用。
结果和结论 检验与临床沟通可随时随地进行，并贯穿检验流程的全过程。检验与临床沟通渠道通畅，会助力检验医学发展，从而更快、更好地为临床服务。

PU-2905

NOD2 在高血压肾病中的作用及机制研究

李荃新
山东大学第二医院

目的 高血压肾病是高血压患者常见的、严重的并发症，也是导致终末期肾病的主要原因之一。目前高血压肾病的主要治疗策略是使用降压药物控制血压，包括血管紧张素转化酶抑制剂等。但是这种治疗方法不能逆转高血压肾病的发展，并且最近流行病学资料显示，因高血压造成患者发展为慢性肾脏疾病的人数呈逐年增多的趋势。因此，寻找治疗高血压肾病新的靶点已经迫在眉睫。NOD2 作为 NOD 样受体家族中新发现的的成员，近些年来受到了广泛的关注。研究发现 NOD2 可以通过结合 MHC I 类分子启动子上的特定区域来促进其的转录，NOD2 还可以调控细胞的炎症反应、增殖以及纤维化等。此外近些年来的研究发现，NOD2 与多种急慢性肾脏损伤，如肾缺血再灌注损伤、糖尿病肾病以及肾脏纤维化有密切的关系。本课题主要探究 NOD2 在高血压肾病中的作用及调控机制，为高血压肾病的治疗提供新的靶点。
方法 本课题运用细胞、动物模型及临床标本，借助体内外转染技术，通过形态学、细胞和分子生物学、流式细胞术、激光共聚焦、和免疫共沉淀等方法明确 NOD2 在高血压肾病中的作用及机制。
结果 在药物诱导的高血压肾病小鼠肾脏组织中 NOD2 表达升高，敲除 NOD2 可以明显降低小鼠的血压和白蛋白与肌酐的比值，减轻肾脏的损伤。基因沉默肾小球内皮细胞中的 NOD2 可以显著改善细胞凋亡，增加一氧化氮合酶的活性，增加一氧化氮的合成。
结论 在高血压肾病中，NOD2 通过下调一氧化氮合酶的活性加重肾脏损伤。

PU-2906

NLRC4 在小鼠缺血再灌注损伤中作用的研究

李荃新
山东大学第二医院

目的 缺血再灌注损伤(Ischemia reperfusion injury，IRI)是指组织或器官缺血后恢复血液供应不仅不能使其功能得到恢复、损伤得到修复，反而造成其功能障碍和结构破坏进一步加重的现象。临床上肾脏缺血再灌注损伤（ Renal ischemic reperfusion injury，RIRI）比较多见，常见于失血或中毒性休克、弥散性血管内凝血、肾移植、肾部分切除、肾实质切开取石等手术过程中。RIRI 是急性肾衰竭常见的原因，也是肾脏移植术后影响移植物功能和移植物长期存活的主要因素之一。因此，深入认识 RIRI 的机制及降低其损伤程度是临床上密切关注的问题。本课题主要探究 NLRC4 在肾缺血再灌注损伤中的作用及调控机制，为肾缺血再灌注损伤的治疗提供新的靶点。
方法 本课题运用细胞、动物模型及临床标本，借助体内外转染技术，通过形态学、细胞和分子生物学、流式细胞术、激光共聚焦、和免疫共沉淀等方法明确 NLRC4 在肾缺血再灌注损伤中的作用及机制。
结果 在肾缺血再灌注小鼠肾脏组织中 NLRC4 表达升高，敲除 NLRC4 可以明显降低小鼠血清中肌酐尿素氮的水平，减轻肾脏的损伤。基因沉默肾小管细胞中的 NLRC4 可以显著改善细胞凋亡，降低肾脏中炎性因子的表达水平。
结论 在肾缺血再灌注损伤中，NLRC4 高表达通过上调炎症反应和细胞凋亡加重肾脏损伤。

PU-2907

甲功五项化学发光法检测评价甲状腺功能及意义

李巧霞、王昌敏、郝立君、刘红、黄国虹、李智伟、庞秀惠、宋雪
新疆自治区人民医院

目的 探讨甲功五项检测指标在甲状腺功能减退症预测中的临床价值。
方法 选择我院甲状腺功能减退症患者 58 例为观察组，另设健康体检者 50 例为对照组，两组均采用化学发光法检测血清三碘甲状原氨酸（T3）、血清甲状腺素（T4）、血清游离三碘甲状原氨酸（FT3）、血清游离甲状腺素测（FT4）、血清促甲状腺激素（TSH）的浓度水平，采用 ROC 曲线分析评价各项检测指标的敏感性。
结果 观察组血清 T3、T4、FT3、FT4 及 TSH 阳性率均明显高于对照组，通过 ROC 曲线、诊断试验结果显示：血清 T3、T4、FT3、FT4 及 TSH 的曲线下面积分别为 0.658、0.748、0.720、0.812、0.829， 95%可信区间分别为 0.562～0.754、0.661～0.836、0.630～0.810、0.736～0.888、0.746～0.911，联合检测的曲线下面积及 95%可信区间为：0.855（0.801～0.920），差异均有统计学意义（P＜0.001）。
结论 血清 TSH、FT3 及 FT4 的敏感性高于 T4、T3，联合检测可作为甲状腺功能减退症的早期诊断指标，对预防甲状腺功能减退症的发生、发展及疗效评价有着重要的临床价值。

PU-2908

自动进样架操作固定装置

何娟
空军军医大学西京医院

在医学检验领域中，各种全自动分析仪在临床中广泛应用。在样本检测上机之前，分析前处理均有人工操作完成。从标本接收，编号，信息录入的一系列操作后，需要对样本进行开盖后上机。在这个环节中，因自动进样架为独立单架，外形窄而长，缺乏稳定性，易受外力因素影响而倾斜翻倒，从而引起标本溢漏流洒，致使样本量减少而需要再次采样，增加了患者的负担与不便，且加大工作量与工作成本，在生物安全方面存在一定的风险。此设计增加了自动进样器上机操作前的稳定性，且在标本接收时具有明显的条理性，在外观上具备收纳整齐功能四：此设计可选用 ABS 塑料，该材质具有强度高，轻便，表面光滑易清洁处理的优点。自动进样架外形尺寸：长 20 厘米，宽 2.5 厘米。操作固定装置可设计外形尺寸为：长 20 厘米，宽 25 厘米，可纵向排列放置十个自动进样架，标本孔为 100 孔。自动进样架的右侧底部有一凹槽，因此在设计时，在固定装置的右侧底部设计了突出的卡条，两者相互吻合，妥帖的固定自动进样架，从而不会再出现自动进样架倾翻情况。

PU-2909

西南地区 306845 例男女性高危型人乳头瘤病毒感染情况分析

谭筱醴、冯敏、邓方芳、张玮佳
四川金域医学检验中心有限公司

目的 了解西南地区男女性 17 种高危型人乳头瘤病毒（HPV）感染的亚型分布及流行病学特点，为该地区人群感染 HPV 的早筛、早诊及预防提供科学依据。
方法 选择 2018 年 4 月至 2021 年 4 月送检至四川金域医学检验中心的 306845 例男女性拭子样本，采用聚合酶链式反应（PCR）-反向点杂交法检测其 HPV 基因亚型，样本主要来自于中国西南地区（四川省、贵州省、云南省、重庆市和西藏自治区）的 56 个市、自治州及地区。
结果 306845 例样本包括女性宫颈拭子样本 304451 例，男性拭子样本 2394 例，送检样本性别比例为 127.17：1，男女性样本总体 HPV 阳性率为 19.0%。304451 例女性样本中，共 55774 例检出不同型别的 HPV 病毒，阳性率为 18.9%；在所有女性 HPV 阳性样本中，阳性率最高的型别为 HPV16 亚型（占比 14.16%）和 HPV52 亚型（占比 12.38%）。2394 例男性样本中共 787 例检出不同型别的 HPV 病毒，阳性率为 32.9%；在所有男性 HPV 阳性样本中，阳性率最高的型别为 HPV52 亚型（占比 20.46%）和 HPV16 亚型（占比 11.90%）。年龄分布显示，20 岁以下、21~40 岁、41~60 岁、61 到 80 岁及 81 岁以上人群 HPV 阳性率分别为 35.4%、18.0%、19.0%、30.6%和 23.6%。地区统计分析显示，四川省、贵州省、云南省、重庆市和西藏自治区高危型 HPV 阳性率分别为 18.9%、21.6%、22.1%、20.8%和 20.3%。
结论 西南地区男性感染 HPV 阳性率高于女性，男女性感染 HPV 均以 HPV52 亚型和 HPV16 亚型为主，高发于 20 岁以下及 61~80 岁人群，各省及自治区 HPV 感染阳性率差异不大。

PU-2910

包头地区汉族人群 ESR2 基因 SNPrs1256049、SNPrs4986938 多态性与男性弱精子症的相关性研究

李得春
内蒙古科技大学包头医学院第一附属医院

目的 探讨包头地区汉族人群 ESR2 基因 rs1256049、rs4986938 多态性与男性弱精子症的相关性。
方法 采用病例对照研究方法，选取 78 例男性弱精子症为实验组，同时选取精液正常、有正常生育史的正常男性 124 例为对照组，设计统一调查问卷收集男性一般人口统计资料以及临床流行病学调查资料，通过 PCR 扩增目的片段，应用测序法检测 ESR2 基因 rs1256049、rs4986938 基因型，分析 ESR2 基因 SNPrs1256049、SNPrs4986938 多态性在各组中的分布及差异，采用 Logistic 回归法分析 ESR2 基因 SNPrs1256049、SNPrs4986938 多态性与男性弱精子症的关系。
结果 本研究中，SNPrs1256049 多态位点在实验和对照组间，等位基因频率（P=0.805）；经 Logistic 回归法分析，以 GG 为对照，GA 基因型频率（P=0.622），AA 基因型频率（P=0.424），差异没有统计学意义； SNPrs4986938 多态位点在实验和对照组间，基因型（AG 基因型 P=0.044，GG 基因型 P=0.012）和等位基因（P=0.005）频率差异有显著意义；在调整相关影响因素后，ESR2 基因 rs4986938 位点 GA+AA 基因型与男性不育风险降低显著相关(P=0.018)。
结论 包头地区汉族人群中 ESR2 基因 rs1256049 位点多态性与男性弱精子症无显著相关性；包头地区汉族人群中 ESR2 基因 rs4986938 位点多态性与男性弱精子症风险降低显著相关。

PU-2911

TCT 联合高危型 HPV 定量检测在宫颈病变中的意义

付玉华
内蒙古科技大学包头医学院第一附属医院

目的 分析液基薄层细胞学（TCT）联合高危型人乳头状瘤病毒（HPV）定量检测在宫颈病变中筛查的临床意义。
方法 在我院妇科门诊及病房收集 2019 年到 2020 年两年间 3690 例妇女同时行两种方法检查，对其中任何一项阳性者行阴道镜下活检，以病理学诊断为金标准。
结果 共 720 例进行阴道镜活检，TCT 诊断阳性 565 例（15.3%），HPV 阳性 621 例（16.8%），与病理学诊断一致率：TCT 为 45.8，HPV 为 26%。TCT 联合 HPV 检测定宫颈病变的诊断价值优于单项检测。
结论 TCT 联合 HPV 检测灵敏度很高，可提高宫颈癌的检出率。

PU-2912

针对 600 例儿童食入物过敏原 IgG 检测结果的分析

曹健
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 通过分析多例儿童特异性过敏 IgG 的检测结果，对儿童食入物过敏性疾病预防和治疗提供理论支持。
方法 采用酶联免疫吸附法对我院 2020 年 5 月-2021 年 5 月期间的 600 例儿童（保健门诊、儿科门诊和住院患儿）食入物过敏原特异性 IgG 结果，进行统计学分析。

结果 在 600 例患儿中检出总阳性率 86.66%蛋清/蛋黄阳性率最高 27.85%，牛奶次之 25.33%，一份血清标本可出现多种食入物过敏原存在。
结论 食物过敏原中蛋清/蛋黄和牛奶是最主要的儿童食入性过敏原，采取有效的预防措施，可以有效降低儿童因食入物导致过敏的疾病发生。

PU-2913

LRP10 基因相关遗传疾病的研究现状

成洋、刘靳波
西南医科大学附属医院

LRP10(低密度脂蛋白受体相关蛋白 10)基因是 LDLR 家族的一个新的亚家族成员， LRP10 基因编码跨膜蛋白 LRP10，可能在神经退行性变中具有广泛的作用。近年的研究发现 LRP10 基因可能与常染色体显性遗传帕金森病、帕金森病痴呆、路易体痴呆、阿尔兹海默病、进行性核上性麻痹等相关，但具体的致病机制还需要更多的复制研究及功能研究来阐明。

PU-2914

miR-451a 对胰腺癌细胞转移的影响及机制研究

陈佳、陈伟琴、李贞、胡晓波
上海中医药大学附属龙华医院检验科

目的 探究 miR-451a 在胰腺癌转移中的作用及分子机制，为认知胰腺癌转移相关机制提供新的视角，并发现胰腺癌治疗的潜在靶标。
方法 采用 qRT-PCR 检测胰腺癌组织和细胞中 miR-451a 的表达，采用 Transwell 小室实验和划痕实验确定 miR-451a 对胰腺癌细胞转移能力的影响，通过生物信息学软件进行预测，筛选出 miR-451a 可能的下游靶基因活化转录因子-2（activating transcription factor-2, ATF2），利用双荧光素酶报告基因实验、qRT-PCR 及 Western blot 对 miR-451a 的靶基因进行验证，采用 Transwell 小室实验和划痕实验确定 ATF2 对胰腺癌细胞侵袭和迁移能力的影响，并通过挽救实验进一步证实上述机制。
结果 miR-451a 在胰腺癌组织和细胞中均高表达；miR-451a 可显著增强胰腺癌细胞的转移能力；miR-451a 可作用于 ATF2 的 3'-UTR 并抑制其表达；ATF2 能抑制胰腺癌细胞的转移，减弱 miR-451a 对胰腺癌细胞转移的促进作用。
结论 miR-451a 在胰腺癌中高表达；miR-451a 可通过调控靶基因 ATF2 的表达，从而有效地促进胰腺癌细胞转移。

PU-2915

四个新冠病毒核酸快速检测系统初步性能验证

杨永长、蒋黎
电子科技大学附属医院·四川省人民医院

目的 验证 4 个新冠病毒核酸快速检测系统的检测限、重复性和符合率，为临床提供快速、准确的检测结果。
方法 采用样本保存液分别将中国计量研究院的标准物质稀释至 4 个检测系统（3 个 PCR 荧光法，1 个等温扩增法）的检测限，每个检测系统检测 5 次。采用样本保存液将商品化的质控品稀释至 1000 拷贝/ml，根据检测系统的通量不同，测定 5-10 次，计算各系统 ORF1ab 基因和 N 基因 Ct 值

的变异系数。采用阴性样本、模拟阳性样本（由样本保存液和阳性质控品制备不同浓度的模拟样本）初步验证 4 个检测系统的符合率。
结果 4 个检测系统在各自检测限浓度的 N 基因均能检出，部分系统的 ORF1ab 基因有未检出的情况。在 1000 拷贝/ml 浓度时测定 5-10 次，3 个检测系统 ORF1ab 基因平均 Ct 值分别为 20.9，27.8，39.3，变异系数分别为 0.53%，4.27%，2.57%。N 基因平均 Ct 值分别为 20.6，26.4，33.0，变异系数分别为 0.74%，3.26%，0.97%。1 个检测系统为等温扩增，无法计算变异系数。分析阴性样本和模拟阳性样本检测结果，4 个检测系统的阴性符合率和阳性符合率均为 100%。
结论 4 个新冠病毒核酸快速检测系统的检测限、重复性和符合率基本满足要求。临床应用中，对于高度疑似样本，建议多个系统同时检测避免假阴性。

PU-2916

携带 psm-mec 基因 MRSE 菌株 MLST 分析

杨永长
电子科技大学附属医院·四川省人民医院

目的 分析携带 psm-mec 基因 MRSE 菌株的同源性。
方法 收集临床分离表皮葡萄球菌，通过微生物学和分子生物学技术鉴定筛选携带 psm-mec 基因 MRSE。菌株 MLST 分型按照数据库公布的方法进行，扩增 arcC，arcE，gtr，muts，pyrR，tpiA 和 yqiL 管家基因，扩增产物经切胶回收后纯化测序，并将测序结果提交至 MLST 数据库中查询等位基因号和菌株 ST 型别。
结果 临床分离菌株中共有 17 株携带 psm-mec 基因 MRSE。MLST 分型结果显示，17 株携带 psm-mec 基因 MRSE 共产生了 3 个 ST 型别，其中 ST2 型菌株为 15 株，占菌株总数的 88%，另外 2 株 ST 分型无结果。
结论 临床分离携带 psm-mec 基因 MRSE 菌株以 ST2 型为主。

PU-2917

骨科术后患者血栓分子标志物的变化及其临床价值的探究

李广华
广东省人民医院

目的 分析不同危险等级骨科患者在接受手术后机体血栓分子标志物的改变，并探究其临床意义，为临床治疗提供帮助。
方法 选取 2020 年 7 月-2021 年 3 月在广东省人民医院进行治疗的 90 例患者为研究对象，并根据 Caprini 血栓风险评估将患者分为三组，分别在术前、术后 24 h 以及术后 3d 进行血栓早期分子标记物凝血酶-抗凝血酶复合物 (thrombin-antithrombin complex，TAT)、纤溶酶 -α2 纤溶酶抑制物复合物 (α2-plasmin inhibitor-plasmin complex，PIC)、血栓调节蛋白 (thrombomoduline，TM)、D—二聚体 (D-dimer，DD)以及常规凝血项目进行检测，并同期选取广东省人民医院健康查体人群 29 例纳入对照组，对不同时间点和不同组别之间进行比较。
结果 三组危险等级分组骨科患者术前 TAT、D-二聚体、PIC、TM、PT 均显著高于正常对照 (P 均 ＜ 0.001)，且不同危险分级的骨科术后患者血栓早期分子标志物 TAT、PIC、TM 和 D-二聚体均明显高于正常对照组 (P ＜ 0.05)；不同危险层次组别在各组内 TAT、PIC、TM 和 D-二聚体指标在术后 24 h 的水平，与术前相比均有不同程度的增加（P<0.05）；高危险分级患者血浆 D-二聚体浓度明显大于低危组和中危组患者，高危险分级存在着明确的血浆 D-二聚体浓度升高，并随 VTE 风险分层不同而有明显区别。

结论 血栓分子标志物的水平变化对凝血及纤溶系统功能紊乱有重要的提示作用，尤其是对于 VTE 高危险等级评估的患者的监测。TAT、PIC 等血栓标志物的术后变化趋势也进一步显示有部分患者仍存在一定的血栓风险。

PU-2918

血清 HCY 及 LP(a)的水平与冠心病的严重程度的相关性研究

王宇鹏[1]、王宏波[1]、石婷[1]、彭剑桥[1]、谭超超[1]、叶湘漓[2]
1. 湖南省人民医院
2. 湖南师范大学医学院

目的 探讨冠心病(CAHD)患者的血清 HCY 和 LP(a)水平与疾病严重程度的关系及其诊断价值。
方法 收集 CAHD 患者的 HCY 和 LP(a)的血清水平数据，将其分为稳定性心绞痛、不稳定性心绞痛及心肌梗死组，与健康人群进行比较；依据冠脉狭窄情况将 CAHD 患者分为单支以下狭窄、双支狭窄和多支狭窄组，分析三组之间的 HCY 和 LP(a)水平，探讨二者血清水平与 CAHD 严重程度之间的关系；作 ROC 曲线分析，探讨联合检测 HCY 与 LP(a)对 CAHD 的诊断价值。
结果 与健康对照组相比，不稳定性心绞痛和心肌梗死组的血清 HCY 和 LP(a)的血清水平均明显升高，且差异有统计学意义(p1 = 0.002； p2 ＜0.001；p3 =0.009；p4 =0.003)；与单支以下冠脉狭窄组相比，双支狭窄组的 HCY 水平更高(p = 0.003)，多支狭窄组的 HCY 和 LP(a)水平均升高明显(p ＜0.001；p = 0.008)；ROC 曲线分析显示，相比单独检测，联合检测 HCY 和 LP(a)有更高的诊断敏感性和特异性(AUC=0.841)。
结论 血清 HCY 和 LP(a)可能与 CAHD 的严重程度密切相关，对二者联合检测可以提高 CAHD 的预测和诊断价值。

PU-2919

广州地区 2012-2020 年肺炎链球菌分布与耐药性变迁

吕婧雯、顾兵
广东省人民医院

目的 分析 2012-2020 年广东省人民医院肺炎链球菌分离株中抗生素耐药的分布情况及耐药率与样本来源、医院病房、患者性别及年龄等独立因素的关系。
方法 收集 2012 年至 2020 年的电子临床数据登记记录进行回顾性分析，采用奥普托欣试验和 VITEK 2 Compact 全自动细菌鉴定系统与纸片扩散法进行菌株的鉴定与药敏试验，数据采用 WHONET5.6 和 SPSS23.0 软件进行统计分析，以研究广东省人民医院（GDPH）肺炎球菌分离株的耐药情况。
结果 共收集 1110 株菌株，将其中 753 株纳入分析，标本类型主要是痰液标本（73.7%）。年龄段主要集中在小于 5 岁的婴幼儿及儿童（53.9%），性别以男性居多。科室分布主要集中在重症监护室 ICU（51.4%）。肺炎链球菌对红霉素（95.5%）、克林霉素（92.2%）、四环素（91.6%）、和复方新诺明（63.8%）等高度耐药，对青霉素（43.0%）、阿莫西林（34.9%）、头孢噻肟（24.0%）、头孢吡肟（37.9%）、美罗培南（28.7%）等中度耐药，对其他抗生素较敏感，特别是厄他培南、利奈唑胺、万古霉素的使用没有出现耐药菌株的情况。9 年间多重耐药菌的总分离率为 75.3%，红霉素耐药率一直维持在较高的水平，美罗培南耐药率存在逐年增长的趋势。
结论 GDPH 肺炎球菌分离株中耐药菌株和多重耐药株流行率的增加，要求明智地使用抗生素并定期监测耐药性。

PU-2920

福州地区 3887 例羊水染色体核型分布

毛雅珍
福州市第一医院

目的 探讨 3887 例妊娠中期孕妇羊水染色体核型类型和分布，并分析不同产前诊断指征与胎儿染色体异常的关系。
方法 回顾性分析本院 2014 年 1 月至 2019 年 12 月共 3887 例有不同产前诊断指征并行羊膜腔穿刺术进行羊水染色体核型分析的病例。
结果 共检出异常染色体核型 178 例，异常检出率 4.58%，其中染色体数目异常 128 例，其中 21-三体 58 例，18-三体 24 例，13-三体 7 例，性染色体异常 16 例；染色体结构异常 50 例，其中易位 22 例，缺失 9 例，标记染色体 6 例。胎儿超声异常、产前血清学筛查高风险、高龄孕妇为主要染色体异常分布指征。
结论 目前，羊膜穿刺术结合核型分析仍是诊断胎儿染色体疾病的金标准；孕妇具有多项产前诊断指征染色体异常检出率高于单项产前诊断指征，临床咨询者要尽力劝服具有多项指征的孕妇进行产前诊断。

PU-2921

RBC、RET 系统参数在地中海贫血和缺铁性贫血的鉴别诊断应用

陈勇
福州市第一医院

目的 探讨红细胞 3 项系统参数：红细胞计数（RBC）、平均红细胞体积（MCV）、平均红细胞血红蛋白量（MCH）；网织红细胞 6 项系统参数：网织红细胞百分率（RET％）、网织红细胞绝对值（RET＃）未成熟网织红细胞比率（IRF%）、低荧光强度网织红细胞百分率（LFR％）、中荧光强度网织红细胞百分率（MFR％）、高荧光强度网织红细胞百分率（HFR％）在地中海贫血（thalassemia trait，TT）和缺铁性贫血（iron deficiency anemia，IDA）的鉴别诊断中的应用。
方法 将 100 例 TT 患者设为地贫组，100 例 IDA 患者设为缺铁贫组，100 例健康人设为对照组，用希森美康 XN9000 系列全自动血液分析仪检测红细胞参数及网织红细胞参数，用 SPSS 23.0 统计软件分析各组参数间的差异，多组间数据采用单因素方差（one-way ANOVA）分析，多组间比较采用 Tukey 校正，同时采用受试者工作特征曲线（ROC）分析各参数曲线下面积（AUC）,评价各项指标的在鉴别 TT 和 IDA 中的诊断效能。
结果 TT 组和 IDA 组 RBC、MCV、MCH、RET%、RET#、IRF%、LFR%、MFR%、HFR%与对照组比较，其差异均有统计学意义（P＜0.05）；地中海贫血组 RBC、MCV、RET%、RET#、IRF%、LFR%、MFR%、HFR%与缺铁贫组比较，其差异均有统计学意义（P＜0.05）。α 地中海贫血与 β 地中海贫血在这些参数上进行比较，差异无统计学意义（P＞0.05）。用 ROC 分析各项指标时，HFR%的曲线下面积（AUC）=0.862，在各项指标中 AUC 下面积最大，在鉴别 TT 和 IDA 中 HFR%的 cut-off 值为<2.680。
结论 在 TT 和 IDA 的鉴别诊断中 HFR%的诊断效能最大，有望作为两者鉴别诊断重要的实验室指标。

PU-2922

NSCLC 骨转移风险预测模型的建立和验证

胡春晓
安徽理工大学附属肿瘤医院

目的 构建列线图来预测非小细胞肺癌（NSCLC）患者骨转移的发生风险。
方法 回顾性分析 2016 年 1 月至 2020 年 12 月确诊的 NSCLC 患者的临床资料及血液学资料，包括是否发生骨转移、年龄、性别、病理类型、吸烟状况、PS 评分、T、N 分期、骨转移前是否有其他部位的转移、癌胚抗原（carcinoembryonic antigen,CEA）水平、甲胎蛋白（alpha fetoprotein,AFP）水平、血清钙浓度（Ca）、血清磷浓度（P）、碱性磷酸酶（alkaline phosphatase,ALP）水平，利用单因素分析筛选与 NSCLC 骨转移发生相关的潜在危险因素，并纳入多因素 Logistic 回归，筛选 NSCLC 骨转移发生的独立危险因素并建立预测模型，使用受试者工作特征曲线（receiver operating characteristic curve,ROC）、决策曲线分析法（decision curve analysis ,DCA）验证模型的准确性及临床获益度，使用使用“ RMS”软件包绘制列线图以进行模型可视化。
结果 ROC 曲线下面积（AUC）显示，在建模组的 132 例患者中，联合指标（年龄、性别、病理类型、CEA、ALP）预测的 AUC 值(AUC=0.790)要高于单一指标预测值，年龄、CEA、ALP 的特异度分别为 81.54%、78.46%、81.54%，灵敏度分别为 41.79%、47.76%、38.52%，而联合指标的特异度和灵敏度分别为 76.92%、76.12%。基于同一个模型，将验证组的 98 例 NSCLC 患者进行 ROC 分析，联合指标（年龄、性别、病理类型、CEA、ALP）预测的 AUC 值为 0.641，特异度为 45.83%，灵敏度为 86%。
结论 本研究构建的预测模型效果良好，可在早期识别容易发生骨转移的 NSCLC 患者，为临床筛选 NSCLC 骨转移的高危患者提供参考。

PU-2923

男性骨质疏松症患者肠道菌群组成及基因功能分析

吕静、于燕、曾玉红、赵和平
西安交通大学附属红会医院

目的 探讨男性骨质疏松症患者肠道菌群结构和基因功能改变与骨密度之间的关系。
方法 选取 2019 年 03 月-12 月到我院就诊的 50 岁及以上的初诊男性骨质疏松症患者 14 例、低骨量者 26 例及骨量正常者 21 例，收集粪便样本提取肠道微生物 DNA，进行 16S rRNA V3~V4 区和宏基因组扩增，使用 Illumina 平台进行高通量测序，对测序结果进行物种注释、菌群结构差异和基因功能分析，并观察其与骨密度之间的相关性。
结果 大多数肠道菌群在三组人群中是共同存在的，在门、纲、目、科、属、种各水平均存在一定的差别。相对于骨量正常组人群，Leuconostocaceae、Weissella 和 Lactobacillus gasseri 是骨质疏松症组患者肠道内丰度显著升高的关键差异菌群；而 Cardiobacteriales、unidentified Cardiobacteriales 和 Ignatzschineria 是骨量正常组人群肠道内丰度显著升高的菌群。相关性分析指出，Selenomonadales 和 Lactobacillus salivarius 相对丰度与骨密度之间具有一定的相关性（P<0.05）。肠道宏基因组功能注释分析显示，在 KEGG 1 级水平，细胞过程、环境信息加工和新陈代谢功能区域与骨密度呈正相关；在 KEGG 2 级水平，碳水化合物代谢和信号转导功能与骨密度呈正相关；在 KEGG 3 级水平，淀粉和蔗糖代谢、二组分系统注释功能与骨密度呈正相关；基因功能信号转导、蔗糖和淀粉代谢、二组分系统对于鉴别骨质疏松症患者具有较好的灵敏度和特异性。
结论 16S rRNA 和宏基因组测序分析有助于明确 50 岁及以上男性骨质疏松症患者的肠道菌群结构和基因功能的变化，为研究肠道菌群与骨代谢的关系提供理论依据。

PU-2924

宁夏医科大学总医院心脑血管病医院

张永华[2]、张成磊[1]、黄勇翔[1]
1. 宁夏医科大学总医院
2. 宁夏医科大学总医院

目的 探讨离心条件和溶血对高敏肌钙蛋白（hs-cTn）检测结果的影响。
方法 选取 2020 年 3 月至 12 月在我院就诊的患者 280 例作为研究对象，根据 hs-cTn 结果分组，不同离心条件处理后检测结果。另外配制不同溶血程度的 hs-cTn 样本，观察结果的变化。
结果 低浓度组标本经 5、10、15min 离心后，结果偏移分别是 13.51%和 15.48%，大于中浓度组（5.78 %和 10.17 %）和高浓度组（1.88 %和 4.28 %）。低浓度组中 3000 r/min、5min 与其他条件相比均有统计学意义（P=0.0484，0.0167，0.0314）；在中、高浓度组中，4000 r/min、5min 离心条件下的检测结果与其他结果均无统计学差异。在不同溶血程度的条件下，L 组结果增高幅度最大，最大偏移为 20.65%；H 组偏倚很小，不超过 1%。另外，L 组中各结果间均有明显差异（P<0.0001）；M 组中除 2g/L 外，其它各组结果与 0g/L 相比差异均有统计学意义（P=0.0057，<0.0001，<0.0001，<0.0001）；H 组中除 10g/L 外，其它各组间均无明显差异。
结论 不同离心速度、时间对结果的影响 低浓度组标本经 5、10、15min 离心后，结果偏移分别是 13.51%和 15.48%，大于中浓度组（5.78 %和 10.17 %）和高浓度组（1.88 %和 4.28 %）。不同溶血程度对结果的影响 在不同溶血程度的条件下，检测结果均呈现不同程度的增高（P < 0.0001）。L 组结果增高幅度最大，6 g/L、8 g/L、10 g/L 时结果偏移分别是 10.57%、15.45%和 20.65%；而 M 组仅在 8 g/L 和 10 g/L 时偏移大于 10%（10.72%和 16.29%）；H 组偏倚很小，不超过 1%。

PU-2925

基于时间节点监控的门诊血液采集流程管理

李梅
中国人民解放军空军军医大学第一附属医院

目的 探讨基于关键时间节点的监控在门诊血液采集流程管理中的应用，建立精确、有效的人员配置机制。
方法 实现血液采集系统的护士终端与 LIS 和 HIS 的无缝连接，设置关键时间节点并实时监控工作进度；采用 SPSS 20.0 统计学软件，t 检验比较时间节点监控前后 6 个月的平均分诊时间、等待时间、转运时间及 TAT 时间的差异性，χ2 检验比较误采率、试管差错率、漏采率及患者满意度。
结果 时间节点监控前后，分诊时间分别为（19.8±3.6）和（16.2±2.8）分钟，等待时间分别为（36.3±5.4）和（18.2±3.6）分钟，转运时间分别为（19.8±3.6）和（15.2±2.8）分钟，TAT 分别为（26.1±2.2）和（20.4±2.5）分钟，患者满意度分别为 93.17%和 99.17%，误采率、试管差错率、漏采率各项指标均明显降低（表 1），具显著性统计学意义（P＜0.05）。护理管理人员通过护士终端可直观获得各时段、各采血护理人员（窗口）所完成血液采集的患者人数以及待采血患者人数的实时动态信息（图 1、2），并以此为量化指标作决策性依据，及时作出响应，制定合理改进措施。
结论 实施时间节点监控，及时发现问题，采取改进措施，明显缩短分诊扣费时间、采血等待时间和检验 TAT 时间，降低采血错误率，提高患者满意度，为门诊血液采集流程管理提供决策性方案。

PU-2926

山东地区急性淋巴细胞白血病患者骨髓染色体核型的比较

王彦文[1]、王姣姣[2]、彭德志[1]、王佳佳[1]、张陈祎[1]、陈永新[3]
1. 济南金域医学检验中心
2. 山东大学生殖医学研究中心
3. 山东省千佛山医院检验科

目的 统计分析比较不同年龄段急性淋巴细胞白血病患者的核型表达。
方法 收集山东地区送检济南金域医学检验中心经流式细胞术检测和（或）骨髓组织活检确诊的急性淋巴细胞白血病的骨髓染色体核型 204 例。
结果 1.在异常核型中 t(9;22)和 t(9;22)伴其他异常最常见；且免疫表型 B-ALL 最常见，极少数为 T-ALL 表型。且年龄分布在 15-74 岁之间。2.不同年龄段骨髓染色体正常核型及骨髓染色体 t(9;22)和 t(9;22)伴其他异常核型具有统计学意义，P<0.05。且 ph 样骨髓染色体核型年龄范围锁定在 20 岁以上的成人，≦10 岁幼儿及儿童出现频率为 0。
结论 急性淋巴细胞白血病不论年龄范围，其免疫表型多为 B-ALL，T-ALL 少见；不同年龄段骨髓染色体核型的表现不同，其中 t(9;22)和 t(9;22)伴其他异常最常见，且具有年龄分布；≦10 岁患者正常核型检出率较高，但其正常核型中部分 FISH 检测出 TEL-AML1 融合基因阳性，可见在急性白血病中单一的骨髓染色体核检测不能全面了解其疾病性质，要结合其 MICM 综合考虑。

PU-2927

由戈登链球菌感染导致的急性心内膜炎——一种罕见的表现

田本顺
广东省人民医院
徐州医科大学

急性感染性心内膜炎(Acute 感染性心内膜炎，AIE)是一种严重威胁生命的急症，患者在短时间内死亡。因此，早期正确的发现是挽救患者生命的关键。戈登链球菌引起的亚急性心内膜炎已有文献报道。这里，我们首先报告一例年轻的经质谱(MS)鉴定出的戈登链球菌引起的急性心内膜炎病例，更重要的是，通过早期手术治疗和抗生素治疗，该年轻患者最终治愈。

PU-2928

基于 Top-Down 法评定临检常规项目测量不确定度

李明勇
四川省人民医院

目的 分别以室内质量控制数据与室间质量评价（EQA）数据以及校准品评定白细胞（WBC）、红细胞（RBC）、血红蛋白（Hb）、红细胞压积（HCT）、血小板（PLT）的测量不确定度，通过评价血液常规检验项目的测量不确定度，使临床检验项目更好地服务于临床。
方法 利用实验室内部的分析仪器日常工作中得到的复现性和参加卫生部临床检验中心室间比对结果， 分析检测中的测量不确定度，并计算合成不确定度和扩展不确定度。
结果 取 k＝2 时，包含概率 P＝95%，WBC 低、中、高值的扩展不确定度分别为（3.06 ± 0.27）、（7.35±0.49）、（18.32 ± 1.32）× 109/ L；RBC 低、中、高值的扩展不确定度分别为（1.37± 0.08）、（4.37 ±0.18）、（5.21 ±0.16）× 1012/ L； Hb 低、中、高值的扩展不确定度分别为

（58.97 ±3.09）、（121．89 ± 3.37）、（157.87 ±9.73）g/ L； PLT 的扩展不确定度分别为（57.72 ± 11.71）、（223.17 ± 31.35）、（515.63 ± 92.31）× 109/ L。基于校准品（中值）及校准过程中的测量不确定度分别为 WBC 0.424× 109/ L，RBC 0.15×1012/ L，Hb 3.4g/ L，HCT 1.62，PLT 27.9×109/ L.各项的扩展不确定度均包含于中华人民共和国卫生行业标准提出的临床血液学检验常规项目分析质量要求的允许总误差。

结论 利用实验室室间质量评价数据及校准品的不确定度对实验室血常规检测项目不确定度进行评定是合理可行的，且此方法比利用室间质评进行不确定度评估更方便、可靠。通过对不确定度的评价，可以提高实验室的检测水平，有助于临床更好地理解、使用检验结果。

PU-2929

15 号染色体 q11.2-q13 缺失病例 1 例

梁间芬
南方医科大学珠江医院

人类细胞染色体异常是遗传疾病的常见原因，而缺失、重复、易位、倒位、环状染色体等可产生严重的性状而引起各种染色体病。其中 15 号染色体长臂(15q11-q13)发生基因变异即 15 号染色体 q11.2-q13 缺失或该区域的父源性单亲二倍体 upd(15)pat 或母源性单亲二倍体 upd(15)mat，可导致普瑞德-威利氏综合症 PWS 和天使综合征 AS。

普瑞德-威利氏综合症 PWS 中 25%~30%为 upd(15)mat,1%~3%为印迹区域异常，70%~75%为父源性染色体 15q11.2-q13 的缺失。主要表现为新生儿肌张力减退、发育迟滞、智力低下、儿童期肥胖、身材矮小、性腺机能减退以及严重的行为异常。

天使综合征中 3%~7%为 upd(15)pat,,3%~5%为印迹区域的异常，5%~11%为 UBE3A 基因突变，68%~70%为母源性染色体 15q11.2-q13 的缺失，其余的 10%~15%则病因未明。天使综合征主要表现为严重智力低下、语言障碍、共济失调、癫痫、阵发性欢笑。现将我科检测儿科门诊病例 1 例报告如下：

PU-2930

抽丝剥茧，寻找真相

李丹、刘道林
隆回县人民医院

日常血液检验中，发现一血小板显著升高达 1314×109/L，嗜碱性粒细胞明显升高的病人，涂片镜检血小板成堆分布，其余各系数量、形态基本正常。查阅病史：青年女性，患鼻咽癌一年余，经系统放化疗后。查体肝脾淋巴结无肿大，实验室检查肝肾功能、凝血常规、自身抗体等正常。为明确诊断，行骨髓穿刺细胞形态学检查，同时外送 JAK2、CALR、MPL 突变基因检测。骨髓象巨核细胞显著增高，符合原发性血小板增多症。但病人骨髓象有核细胞增生明显活跃，粒系增生明显活跃，原始粒细胞占 3%，嗜酸、嗜碱性粒细胞增高，是否要考虑以血小板增高为主要表现的慢性粒细胞白血病？外检结果回馈 JAK2、CALR、MPL 基因均未检测到突变,也不支持 ET 的诊断。又加送 BCR-ABL1 融合基因检测。结果 P210 阳性。至此，基本可以确定此患者为慢性粒细胞白血病。

总结：1.骨髓增殖性肿瘤，一般有脾大甚至巨脾，而此患者无脾大。

2.慢性粒细胞白血病一般外周血白细胞显著增高，而此患者白细胞正常。

3.由于实验室条件限制，缺少必要的检查，如 NAP 积分，使结果难以判断。

4.慢性粒细胞白血病，部分初诊病人血小板明显升高，可达 1000×109/L，骨髓象巨核细胞数量增多或正常，易见小巨核细胞。原发性血小板增多症，血小板显著增高，血小板形态异常，大小不等，骨髓象巨核细胞明显增生，多为巨大的巨核细胞。

PU-2931

乌鲁木齐地区 0~18 岁人群 25 羟维生素 D 水平及其与季节相关性分析

崔彦杰、 刘红春
新疆维吾尔自治区人民医院

目的 了解乌鲁木齐地区 0~18 岁人群 25 羟维生素 D 水平及其与性别、年龄、季节的关系，为及时、科学的补充维生素 D 提供依据。
方法 回顾性分析 2018 年 1 月-2020 年 12 月间就诊于我院儿童保健室的 0~18 岁体检人群 3454 例为研究对象，根据其年龄将其分为学龄前组（0~3 岁），幼儿园组（4~6 岁），小学组（7~12 岁），初中组（13~15 岁），高中组（16~18 岁），采用雅培电化学发光仪检测其血清中 25 羟维生素 D 水平，根据其年龄、性别及季节因素分析比较其 25 羟维生素 D 水平的差异。
结果 3454 例 0~18 岁人群的 25 羟维生素 D 平均水平为（30.35±8.23），25 羟维生素 D 缺乏与不足者之和为 2161 例（占 62.57%）。随着年龄的增长 25 羟维生素 D 呈现降低的趋势，但同年龄段不同性别之间未发现存在显著差异（P>0.05）。夏季、秋季 0~18 岁人群的 25 羟维生素 D 水平明显高于春季、冬季，缺乏率及不足率明显低于春季、秋季，差异有统计学意义（P <0.05）。
结论 乌鲁木齐地区 0~18 岁人群 25 羟维生素 D 总体水平偏低，且与年龄、季节相关，应及时检测，并根据检测结果进行科学合理的补充。

PU-2932

检验科窗口工作的医患沟通

纵帅、冯倚帆、徐银海
徐州医科大学附属医院

目的 通过解读检验科窗口的工作特点和工作性质，并以此为依据、关注点和突破口，规范和提升检验科窗口工作医患沟通及其技巧。
方法 （1）指导患者正确做好标本采集前准备。做好标本采集前的准备是获取合格标本的前提,检验科窗口应该积极指导患者正确做好标本采集前准备，消除非疾病因素影响，消除患者顾虑，取得配合。（2）接收标本时做好必要的询问和告知。对患者送检标本，有必要主动与患者沟通获得信息，确保标本合格，并以适当的方式告知报告发出时间和可能延迟的情况进行合理解释，取得患者的理解，预防不必要的投诉或纠纷。（3）标本需要重新采集时做好合理解释。在临床检验中需要进一步确认结果需要复查的情况，应给患者合理的解释，向患者及家属耐心解释使其正确认识到需要重新采集标本的重要性。（4）认直谨慎对检验结果进行答疑。对于患者的咨询和疑问，既不可推卸责任，也不可武断给予解答或下结论，否则容易造成患者的心理负担乃至误导患者。要求检验科工作人员不仅要熟悉医疗法规，而且要了解本单位开展所有检验项目，不断加强结合临床内容的理解，给出合理合适的分析。
结果 通过上述四项主要沟通和注意事项，检验科窗口工作人员能够很好的从综合性，复杂性，专业性，服务性和危险性五个方面了解检验科的工作特点，明确在实际的临床工作中窗口岗位的特点，知道窗口工作既需要直接面对患者进行检验相关的操作和沟通，也需要专业技能，还需要有灵活机动的应变沟通能力和技巧，并且在沟通过程中保持足够的冷静和耐心，取得患者的理解和支持，消除医患矛盾。
结论 检验人员在做好检验本身工作的同时，也要做好耐心细致的解释工作，与患者在良好的沟通中取得理解和信任，对患者一视同仁，不冷淡、不歧视，不区别对待。与患者面对面交谈时善于运用语言艺术和身体语言，注意情感支持，就使患者充分感受到工作人员的耐心和关爱之意，赢得患者对检验科的认可，减少甚至避免不必要的医患矛盾。

PU-2933

2016-2020 年杭州地区单中心 EB 病毒感染患儿阳性率的统计与分析

徐旭栋[1]、周俊[1]、肖湘阳 2[2]、曾工博[1]、林先耀[1]、吴亦栋[2]
1. 杭州市儿童医院
2. 浙江省杭州市中医院丁桥院区

目的 了解杭州地区 2016 年至 2020 年间儿童 EB 病毒的感染情况、构成、流行趋势等信息。
方法 选取 2016 年至 2020 年期间，杭州市儿童医院病原体核酸检测的样本共 72526 例，将其中 EBV 核酸阳性的 1391 例纳入统计研究，并分析各年份杭州地区儿童 EB 病毒感染的人数、感染月份、性别比例及年龄构成等因素。
结果 2016-2020 年，报告 EB 病毒核酸阳性病例 1391 例，占全院儿童病原体检测数的 1.92%，五年间 EB 病毒感染阳性率分别为 1.56%，1.81%，1.89%，1.63%和 3.11%；性别方面，男性感染患儿报告 783 例，女性感染患儿报告 613 例，男女比例为 1.28：1；年龄分布方面，EB 阳性感染患儿 1-6 学龄前儿童累计报告 1184 例，占我院 1-15 岁患儿总阳性病例数的 85.12%。流行季节方面，夏秋季为感染高峰，冬春季不明显。
结论 2016 年-2019 年，杭州地区 EB 病毒感染比例相对平稳（x2 趋势检验，P>0.05），但在 2020 年，阳性率明显上升，这可能与新冠疫情有关；学龄前儿童为 EB 病毒的主要感染者，这与学龄前儿童的免疫水平以及淋巴细胞比例水平可能存在一定相关性，同时男童与女童的阳性感染率存在显著差异（P<0.05）且男童感染风险更高，此外 EB 病毒传播还具有一定季节规律。

PU-2934

境外输入新冠病毒感染者不同标本阳性检出率分析

杨勇卫、陈锡莲、林青、曲人亮、张帅、石建凤、刘静静
烟台市奇山医院

目的 探讨境外输入 2019-nCoV 感染者不同标本的阳性检出率，以期为新冠病毒变异相关研究和临床新冠肺炎诊治提供数据支持和理论依据。
方法 回顾性分析 2020 年 10 月至 2021 年 4 月烟台市奇山医院收治的 9 例境外输入新冠病毒感染者 36 次（108 份）新冠核酸检测实验的结果；每次实验采集标本类型均为痰、鼻咽拭子和粪便标本，运用荧光定量 PCR 方法检测，提取试剂和扩增试剂均购自上海之江生物科技股份有限公司，试剂均在有效期内，实验操作和结果判断均按照试剂说明书严格执行；运用 SPSS19.0 软件做卡方检验，P<0.05 具有统计学意义。
结果 108 份新冠核酸检测结果中，36 份痰标本检出阳性 11 份，检出率为 30.56%；36 份鼻咽拭子检出阳性 32 份，检出率为 88.89%；36 份粪便标本均未检出阳性；不同标本类型的新冠病毒核酸检出存在差异（Pearson 卡方 65.85，P<0.01）。
结论 境外输入新冠病毒感染者鼻咽拭子较痰标本阳性检出率高，粪便标本阳性检出率极低，对新冠肺炎轻症患者、新冠病毒无症状感染者以及健康筛查人员推荐优先采集鼻咽拭子标本，以提高检出率。

PU-2935

独立实验室葡萄糖检测流程优化研究

陈灿星[1]、胡志峰[1,2]、姚少濠[1,2]、张玲[1,2]、刘勇[1,2]、徐海超[1]、欧狄[1]、陶然[1,2]
1. 广州金域医学检验中心有限公司
2. 广州医科大学金域检验学院

目的 未使用专用抗凝管，葡萄糖因血细胞的糖酵解，每小时降低 5-7%，专用抗凝管能抑制糖的酵解过程。当医院、社康或独立透析中心等第三方医疗单位送检批量葡萄糖检测时，独立实验室复杂繁琐的检验流程，且要区分血清葡萄糖结果和葡萄糖专用抗凝管结果，需耗费人力，浪费时间和试剂，还增加检测者疲劳度的后果。本文以保证葡萄糖报告结果的准确性、减少员工疲劳程度、节约样品检测时间和降低样品检验成本为流程改造的目标，通过前期调查分析，研究并优化本实验室葡萄糖检测流程。
方法 以流程优化和“6S”管理的有关理论为优化的主导思路，整理既往数据，分析实验室葡萄糖检测周转时间，采用包括为社康等医疗单位提供专用抗凝管，定期到社康宣讲培训，增置新的为专用抗凝管检测的辅助设备和检测设备，优化葡萄糖标本接收检测流程，设计适合本实验室的葡萄糖检验方案，制作血糖检测操作卡，减少实验室人员对葡萄糖检测前的干预。
结果 2020 年葡萄糖检测量较 2019 年增长 25%，2020 年葡萄糖检测周转时间中位数为 5.1h，比 2019 年同期检测周转时间中位数提升 48%。
结论 本文的研究成果，不仅解决了本实验室现场管理混乱、员工素养不高、制度不完善的问题，还理顺了原来杂乱不清的检测程序、减少了繁琐的工作交接。葡萄糖检测程序运行的更加科学、合理、高效，也缩短其他检测业务的检测周转时间。对其它第三方实验室的葡萄糖检验业务或其他检验业务也有一定的借鉴意义。

PU-2936

术前外周血 NLR、PLR 及 NLR-PLR 评分与局部进展期胃癌新辅助化疗疗效及预后的相关性研究

刘亮华、赵明才
遂宁中心医院

目的 探讨局部进展期胃癌患者接受新辅助化疗前外周血 NLR、PLR 及 NLR-PLR 评分与临床疗效及预后的相关性。
方法 回顾性分析 2015 年 1 月至 2020 年 1 月在遂宁市中心医院就诊的 60 例胃癌患者的临床资料。根据 ROC 曲线确定 NLR、PLR 最佳截断值，将患者分别分为低 NLR (NLR＜2.62)组、高 NLR (NLR≥2.62)组，低 PLR (PLR＜169.0)组、高 PLR (PLR≥169.0)组；本研究根据 NLR-PLR 评分将患者重新分为 3 组，NLR、PLR 都低者为 0 分，一低一高者为 1 分，两者都高者为 2 分。采用卡方检验或 Fisher 精确概率法检验分析 NLR、PLR 与各临床特征之间的关系；利用 Kaplan-Meier 法对分类变量进行生存分析；采用 Cox 回归模型进行单因素和多因素生存分析。
结果 术前 NLR≥2.62 在高 CEA 值（P=0.01）、新辅助化疗无效（P=0.025）、cTNM 分期晚（P=0.04）、有脉管侵犯（P=0.021）、未能获得 pCR(P=0.044)的患者中较为常见。术前 PLR≥169.0 在 cTNM 分期晚（P=0.038）、新辅助化疗无效（P=0.006）、未能获得 pCR(P=0.039)的患者中较为常见。低 NLR 组的 PFS 明显优于高 NLR 组（P=0.015）；低 PLR 组的患者与高 PLR 组相比拥有更长的 PFS（P=0.032）；NLR-PLR 评分越低，患者的中位 PFS 越长（P＜0.001）。多因素 Cox 回归模型分析显示新辅助化疗效果差、未能获得 pCR、高 NLR 值、NLR-PLR 评分是影响胃癌患者预后的独立危险因素。NLR、PLR 的 AUG 值为 0.614（P=0.039）、0.559（P=0.026），均小于 NLR-PLR 评分的 AUG 值 0.696（P=0.007）。

结论 而 NLR-PLR 评分对胃癌患者的预后评估价值优于 NLR 及 PLR，但需要进一步的研究和验证。

PU-2937

Expression and prognostic analyses of TP53 family in human esophageal cancer

Lihua Yao、Xiaowu Zhong、Xiaolan Guo
Department of Laboratory Medicine, Affiliated Hospital of North Sichuan Medical College

Objective Esophageal cancer (ESCA) is one of the most common malignant tumor of digestive system, while the morbidity and mortality of esophageal squamous cell carcinoma were ranked fifth and fourth in China. It is high importance to identify more specific and sensitive biomarkers and understand the pathogenetic mechanisms of esophageal cancer is very helpful for clinicians to choose suitable treatments for esophageal cancer patients, which may further help to prolong the overall survival of patients. The TP53 family of transcription factors, including TP53, TP63, and TP73, plays key roles in both biological and pathological processes, including cancer and neural development. While the diverse expression patterns, prognostic value, and potential mechanism of TP53 family in esophageal cancer remain unclear. Thus, investigating the functions of TP53 family members and understanding their regulatory mechanism in esophageal cancer is crucial for the diagnosis and effective strategies to treat esophageal cancer.
Methods Expression data, Immune Infiltration Analysis and clinicopathological features of TP53 family genes for esophageal cancer patients were extracted from TIMER database and the Cancer Genome Atlas (TCGA). The prognostic value of TP53 family genes in esophageal cancer patients were explored using Kaplan–Meier plotter database. And validated the expression of TP53 in 65 pairs esophageal cancer tissues and corresponding adjacent tissues by qRT-PCR. Besides, Plasmid encoding knocked down the expression of TP53 and stably transfected in esophageal squamous cell carcinoma cells (Kyse150 and TE1), then the Transwell assay, Scratch test and Crystal violet assay were utilized to examine the effects of TP53 on esophageal squamous cell carcinoma cells migration and proliferation. Additionally, GSEA algorithm and Western Blotting were performed to explore the relationship between the TP53 and AKT-mTOR pathway.
Results In the present study, the mRNA expression of TP53 members (TP53, TP63, TP73) were significantly higher in esophageal cancer tissues compared with normal tissues, and high mRNA expression of TP53 members were associated with clinical cancer stages and nodal metastasis status in esophageal cancer patients. Moreover, additional experiments verified that the mRNA expression of TP53 was up-regulated in esophageal squamous cell carcinoma tissues. Furthermore, high expression of TP53 and TP73 were significantly correlated with shorter overall survival (OS) in esophageal cancer patients. Meanwhile, immune infiltration level analysis showed that the mRNA expression of TP53 were obviously related to tumor purity and neutrophil, and the correlation of mRNA expression of TP63 with B cells, CD8+ T cells and Dendritic cells was statistically significant, besides, the mRNA expression of TP73 had significant correlations with infiltrating levels of B cell and CD8+ T cells in esophageal cancer. Additionally, down-regulation of TP53 expression significantly retarded esophageal squamous cell carcinoma cells migration and proliferation, it may be involved in AKT-mTOR signaling pathway and TP53-dependent autophagy.
Conclusion Taken together, these results indicated that TP53 family members have the potential biological functionality and prognostic value in esophageal cancer, especially TP53 could be as a diagnostic marker and a valuable therapeutic target in esophageal squamous cell carcinoma.

PU-2938

IL-10 基因 rs1800872 位点多态性与宁夏回、汉族人群自发性早产的相关性

詹福寿
宁夏医科大学总医院

目的 探讨 IL-10 基因 rs1800872 位点多态性与宁夏回、汉族人群自发性早产（spontaneous premature delivery，SPTD）的相关性。
方法 收集 2013 年 1 月－2021 年 5 月，宁夏医科大学总医院和银川市妇幼保健院产科被确诊为 SPTD 患者 401 例（汉族 286 例，回族 115 例），正常足月分娩产妇 418 例（汉族 290 例，回族 128 例）作为对照组。采用聚合酶链反应-限制性片段长度多态性技术对研究对象 IL-10 基因 rs1800872 位点多态性进行检测，比较各组的基因型及等位基因频率，并分析其与 SPTD 的相关性。
结果 宁夏回、汉族人群 SPTD 组与对照组 IL-10 基因 rs1800872 位点的基因多态性分布差异均无统计学意义（P≥0.05）。宁夏回、汉族人群 SPTD 组 IL-10 基因 rs1800872 位点的基因多态性分布差异均无统计学意义（P≥0.05），将宁夏回、汉族群体合并，然后按照新生儿出生时的孕周大小分为早期 SPTD 组和中晚期 SPTD 组 2 组，早期 SPTD 组与对照组相比，CC 和 AC 基因型频率相似（P≥0.05），AA 基因型频率低于对照组（P<0.05），C 等位基因的频率高于对照组（P<0.05），A 等位基因的频率低于对照组（P<0.05），中晚期 SPTD 组与对照组 IL-10 基因 rs1800872 位点的基因多态性分布差异均无统计学意义（P≥0.05）。
结论 携带 AA 基因型的个体发生早期 SPTD 的风险显著降低，IL-10 基因 rs1800872 位点多态性可能与宁夏地区早期 SPTD 的发病存在相关性。

PU-2939

普陀区 6352 例妊娠中期孕妇全血微量元素结果分析

闫辉波
上海市普陀区妇婴保健院

目的 全面掌握上海市普陀区孕妇全血中微量元素的实际水平，为下一步合理补充微量元素以及妊娠期指导提供可靠的实验室依据。
方法 选取 2019 年 01 月至 2020 年 06 月在我院产科门诊就诊建卡的 6352 例孕妇作为研究对象，分析妊娠中期血中钙、镁、铁、铜、锌这五种微量元素的实验室检测结果，按年龄分为高龄组（≥35 岁）和适龄组（<35 岁），通过计算比较两组孕妇之间微量元素含量的差异。
结果 纳入分析的 6352 例孕妇中，钙、铁的缺乏最为普遍分别占比 21.76、21.39%，其次为锌缺乏占 8.66%，镁缺乏较少占 1.84%，铜缺乏者比较少见只有一例；随年龄的增加钙水平明显降低，镁、铁略有升高，铜、锌水平基本不随年龄发生变化。
结论 普陀区孕妇中钙、铁缺乏较为普遍，锌也存在一部分缺乏，在妊娠过程中要注意补充微量元素或者调整膳食结构以保证孕妇及胎儿的健康。

PU-2940

Analytical sensitivity comparison of 14 conventional and three rapid RT-PCR assays for SARS-CoV-2 detection

Xueliang Wang 、Zhongqiang Huang、Jian Song、Yanqun Xiao 、Hualiang Wang
Shanghai Centre for Clinical Laboratory

Purpose Recent reports have compared the analytical sensitivities of some SARS-CoV-2 RT-PCR assays, but differences in the viral materials used for these evaluations made comprehensive conclusions difficult. We aimed to conduct a direct comparison of the analytical sensitivities of 17 approved SARS-CoV-2 RT-PCR assays (14 conventional and three rapid detection assays).
Methods The comparison was performed utilizing a certified reference material for SARS-CoV-2 RNA that was serially two-fold diluted in RNA storage solution.
Results Our results show that the analytical sensitivities of the 17 assays varied within an 8-fold range (100–800 copies/mL). Moreover, a trend with some rapid assays yielding slightly higher analytical sensitivities (2- to 4-fold) compared with conventional assays was observed.
Conclusions We conclude that most of the RT-PCR assays can be used for routine COVID-19 diagnosis, but some assays with the poorest analytical sensitivities may lead to false-negative results when used to identify asymptomatic individuals who can carry a low viral load but still be infectious. These findings should be kept in mind when selecting high-sensitivity and rapid assays.

PU-2941

纳米酶及其在生物医学检测领域的研究进展

赵峰峰
东南大学附属中大医院

天然酶是高度特异性的生物催化剂，可通过选择性催化特定反应而达到识别和检测的目的。然而，天然酶制备成本高、易失活，限制了其实际应用。纳米酶是一类具有类酶活性的纳米材料，可通过无机材料自身的催化活性实现模拟酶的仿生催化功能，具有价格低廉、性能稳定、应用范围广泛等优点。基于纳米酶的生物医学检测具有灵敏度高、特异性强、检出限低等特点，展现出良好的发展前景。本文总结了目前主流的纳米酶材料，介绍了其在生物医学检测领域的研究进展，并展望了纳米酶在生物医学检测领域的发展方向。

PU-2942

结直肠癌患者合并大肠埃希菌血流感染的危险因素分析

张文芳
天津医科大学肿瘤医院

目的 研究结直肠癌患者大肠埃希菌血流感染的危险因素，进行临床分析。
方法 回顾性分析天津医科大学肿瘤医院 2011 年 1 月至 2020 年 12 月 2128 例血流感染的肿瘤患者临床资料，将病理诊断确诊为结直肠癌且合并大肠埃希菌血流感染的 33 例患者与同期 99 无血流感染的结直肠癌患者分为感染组和对照组；分析相关临床资料，采用 Whonet 5.6 软件和 SPSS 17.0 对数据进行统计学处理。
结果 引起肿瘤患者血流感染最主要的病原菌是大肠埃希菌 336 株（32.2%），引起大肠埃希菌血流感染第二多的肿瘤患者为结直肠癌患者 33 例（6.8%），均经病理诊断为结直肠癌。感染组患者男性 18 例，女性 15 例，平均年龄（59.7±26.7）岁；对照组患者男性 55 例，女性 44 例，平均年

龄（59.5±19.5）岁；通过单因素分析显示住院次数、使用≥2 种类型抗生素、住院天数、白细胞、中性粒细胞、PCT、化疗、和白蛋白为结直肠癌患者合并大肠埃希菌血流感染的潜在危险因素（P<0.1）;多因素 Logistic 回归分析显示住院天数、化疗和 PCT 为结直肠癌患者合并大肠埃希菌血流感染的独立危险因素（P<0.05）。

结论 尽可能缩短患者住院时间，严格控制院内感染以及化疗后的护理是在临床工作中应采取的有效治疗措施，以防止结直肠癌患者血流感染的发生。

PU-2943

群体感应系统介导的铜绿假单胞菌毒力因子研究进展

郝京臣
西南医科大学附属医院

铜绿假单胞菌是重要的医院获得性感染条件致病菌，属革兰阴性非发酵菌，可引起体弱、长期卧床者、各种医疗器械受检、皮肤组织感染、导管相关感染、尿路感染、血流感染及肺炎等，具有较高的致病性。铜绿假单胞菌的致病性与其产生的毒素和毒力因子密切相关,如弹性蛋白酶,生物膜,外毒素 A,蛋白分解酶和绿脓菌素等。细菌毒力可通过多种机制进行调节, 其中群体感应（quorum sensing,QS）系统是的主要机制之一。群体感应（quorum sensing,QS）作为最重要的一个信号途径，控制着众多致病因子的表达并且减弱宿主的免疫应答。研究表明群体感应系统参与铜绿假单胞菌各种毒力因子的调控，与其致病能力密切相关，且能激活生物膜的形成并调节外排泵的表达。近年关于铜绿假单胞菌中群体感应（quorum sensing,QS）系统的研究已成为研究者们的热点。而铜绿假单胞菌中的 QS 系统包括 LasI/LasR 和 RhlI/RhlR 两条主要的信号系统和喹诺酮信号系统。现对群体感应系统介导的铜绿假单胞菌相关的毒力因子作一综述。

PU-2944

不同年龄阶段患儿呼吸道病毒分布情况及 SAA、CRP 水平分析

尹姣姣、董雪梅、王临艳、孙朋、景萌萌、颜鲁伟、孙志鹏、张翀、赵翠生
甘肃省妇幼保健院

目的 探讨 974 例甘肃兰州地区不同年龄阶段（≤6 月，6 月-1 岁，1 岁-3 岁，>3 岁）呼吸道病毒感染阳性患儿呼吸道病毒的分布情况及 SAA、CRP 变化。

方法 选取 2020 年 3 月至 2021 年 3 月于甘肃省妇幼保健院行呼吸道病原血清 IgM 抗体检测（化学发光法）结果为阳性，并同时检测血清淀粉样蛋白 A（serum amyloid A ,SAA）、C 反应蛋白（C reaction protein,CRP）及细菌培养的患儿 1267 例。排除细菌培养阳性的患儿 293 例，分析 974 例患儿不同年龄阶段呼吸道病毒的分布情况，及 SAA、CRP 水平；进一步探讨感染不同种类的呼吸道病毒，患儿 SAA、CRP 的水平变化。

结果 974 例呼吸道病毒感染阳性患儿，各年龄阶段男女比例不同，3 岁以下男性（7.4%，29.6%，14.8%）明显大于女性（6.4%，14.4%，8.0%），3 岁以上女性（10.3%）大于男性（9.2%），差异具有统计学意义（P<0.05）。6 月-1 岁的患儿占总人数的 43.9%，更易感染呼吸道病毒；其中腺病毒 334 例（34.3%）、和肺炎支原体 252 例（25.9%）检出率高。各年龄阶段 SAA 的平均值（21.9mg/L，58.0mg/L，73.2mg/L，86.4mg/L），CRP 的平均值（9.1mg/L，14.9mg/L，20.4mg/L，20.8mg/L），均呈升高趋势，差异具有统计学意义（F=14.008，P=0.001；F=3.874，P=0.009），SAA 的变化率大于 CRP。感染 B 型流感病毒的患儿其 SAA 平均值 103.5mg/L，明显大于感染其他病毒的 SAA 水平（P<0.05）。

结论 6 月-1 岁的患儿更易感染呼吸道病毒，其中腺病毒、肺炎支原体检出率高；SAA、CRP 在各年龄阶段的平均值均呈升高趋势，其变化率 SAA 大于 CRP；不同的呼吸道病毒对应不同的 SAA 水平。

PU-2945

2020 年四川省细菌耐药性监测成人组结果分析

王潇、喻华
四川省医学科学院·四川省人民医院

目的 了解 2020 年四川省细菌耐药监测网成员医院成人段年龄组分离的细菌种类及对临床常用抗菌药物的敏感性和耐药性，为我省抗菌药物的合理使用提供依据。
方法 按照耐药监测方案,采用标准纸片扩散法或自动化仪器检测法,测定监测药物对细菌的敏感性,依据 CLSI 2020 年标准,使用 WHONET 5.6 软件进行数据统计分析。
结果 2020 年共纳入数据分析的非重复细菌总数为 98381 株，其中革兰阳性菌占 30.4%（29927/98381），革兰阴性菌占 69.6%（68454/98381）。革兰阳性菌分离率排名前五位的是：金黄色葡萄球菌 11007 株、粪肠球菌 2727 株、表皮葡萄球菌 2574 株、无乳链球菌菌 2376 株和屎肠球菌 2226 株。革兰阴性菌分离率排名前五位的是：大肠埃希菌 26890 株、肺炎克雷伯菌 13608 株、铜绿假单胞菌 7494 株、鲍曼不动杆菌 4432 株和阴沟肠杆菌 3010 株。金黄色葡萄球菌中 MRSA 的检出率为 28.4%，凝固酶阴性葡萄球菌中 MRCNS 的检出率为 76.0%，MRSA 和 MRCNS 对绝大多数测试药物的耐药率均显著高于甲氧西林敏感株(MSSA 和 MSCNS)。肠球菌属中粪肠球菌对多数测试抗菌药物(除外利奈唑胺)的耐药率均显著低于屎肠球菌,两者中均有少数万古霉素耐药株分别为 0.5%和 0.8%。三代头孢菌素、喹诺酮类及碳青霉烯类耐药大肠埃希菌的检出率分别为 48.7%、47.4%和 1.0%。三代头孢菌素及碳青霉烯类耐药肺炎克雷伯菌的检出率分别为 23.1%和 5.5%。碳青霉烯类耐药铜绿假单胞菌的检出率为 9.5%，铜绿假单胞菌对多黏菌素 B 耐药率高于 1.0%。碳青霉烯类耐药鲍曼不动杆菌的检出率为 47.1%。
结论 临床分离菌对常见抗菌药物的耐药率仍居高不下,在继续做好细菌耐药监测工作的同时加强实验室与临床的沟通,以发挥耐药监测工作的最大价值。

PU-2946

生化检测标本周转时间改进措施探讨

李杰、毛达勇、李转转、张吉才
十堰市太和医院

目的 探讨我院生化标本周转时间（TAT）实施持续改进措施的效果，为进一步流程优化提供依据。
方法 随机抽取 2019 年 3 月 1 日-3 月 15 日与 2021 年 3 月 1 日-3 月 15 日经实验室信息系统接收并审核的生化检测标本，统计各时间段 TAT 中位数及超时标本比例，分析 TAT 不合格原因及持续改进相关措施的成效。
结果 2021 年生化检测标本量较 2019 年明显增加，且集中在每周一至周四，以上午九点为标本送检高峰；采取检测设备升级改造、标本分类别集中签收、人员弹性排班等改进措施后，生化标本总 TAT 时间中位数由 236 分钟下降至 167 分钟，总 TAT 时间超过 120 分钟标本比例也由 78.16%降至 68.37%，其中以检验前 TAT 时间下降最为明显，实验室内 TAT 改善不显著。
结论 我院实施流程优化措施对降低生化标本 TAT 时间具有较好的效果，尤其是对降低检验前 TAT 时间成效显著，为提高我院及科室服务质量与管理水平提供了坚实基础，但仍需进一步优化改进措施以提高门诊标本 TAT 检测合格率。

PU-2947

项目开展前以贝叶斯公式计算某 NIPT 检测的阳性预测值

吕杨
海南金域医学检验中心有限公司

目的 在实验室开展 NIPT 检测前，在本实验室未累积数据情况下，根据试剂说明书和疾病流行率，从理论上计算评估本检测为阳性结果时真阳性的概率，为临床医生进行产前咨询提供指导数据。
方法 采用贝叶斯公式对阳性预测值进行计算评估。贝叶斯公式是 Thomas Bayes 于 1761 年提出的一个计算概率的公式。其具体公式为：$P(A|B)=P(B|A)\times P(A)/[P(B|A)\times P(A)+ P(B|A^C)\times P(A^C)]$。$P(A|B)$指检测结果阳性时被检测者患病的概率，即阳性预测值；$P(A)$为被检测者患病的概率，即某疾病的流行率；$P(A^C)$为被检测者未患病的概率，计算方法为 100%- P(A)；$P(B|A)$为已知患病的情况下检测为阳性的概率，即检测方法的敏感性；$P(B|A^C)$为已知未患病的情况下检测为阳性的概率，即检测方法的假阳性率。查询资料知新生儿中 21 三体综合征发病率为 1/800~1/600，18 三体综合征发病率为 1/8000~1/3500，13 三体综合征发病率为 1/25000。以上数据即为相应疾病的流行率，即 P(A)。查询本实验室所用试剂的说明书得知，此 NIPT 试剂的灵敏度为 100%，特异性为 99.93%，知 P(B|A)为 100%，$P(B|A^C)$为已知未患病的情况下检测为阳性的概率，此试剂盒的为 100%-99.93%即 0.07%。
结果 本检测对 21 三体综合征的阳性预测值为 64.13%~70.46%，对 18 三体综合征的阳性预测值为 15.15%~28.99%，对 13 三体综合征的预测值为 5.41%。
结论 实验室在检测开展前通过贝叶斯公式获得了理论的阳性预测值，结果与以往相关文献报道接近，可供临床产前咨询使用。后续可在实际工作中不断累积数据对阳性预测值持续进行修正。

PU-2948

临床化学室内质量控制数据分析对持续质量改进的作用

邱谷、张曙晴、戴世荣、刘培龙
南通市第二人民医院

目的 探讨周期性室内质量控制数据分析总结对持续质量改进的作用。
方法 回顾 2014-2018 年以来本实验室临床化学室内质量控制数据，对当月所有测定项目的失控情况及准确度、精密度改变超出允许范围的原因进行分析总结。
结果 2014-2018 年临床化学失控共 295 项次，其中，违反 1_{3s} 失控占 40.7%，违反 2_{2s} 失控 39.0%，违反 R_{4s} 失控 15.3%，三者总计占 94.9%。质控品因素、校准不当、试剂因素是失控的主要原因，占 67.5%，与其它原因比较差异有统计学意义($P<0.05$)。5 年中当月均值与设定均值比较，偏差超出实验室允许范围共 26 项，当月标准差或变异系数与设定值比较有明显改变，超出实验室允许范围共 21 项，试剂（包括水质）因素、仪器耗材因素、质控品因素等是引起准确度和精密度改变超出允许范围的主要原因。5 年来临床化学室内质量控制失控率呈逐年下降趋势，参加室间质评项目合格率逐年提高。
结论 认真进行室内质量控制数据的周期性分析总结对发现、排除质量环节中的不满意因素和持续质量改进，保证临床检验结果稳定可靠十分重要。

PU-2949

南昌地区 2019 年儿童流感样病例流感检测结果分析

梁振山
江西省儿童医院

目的 探讨 2019 年-2020 年期间南昌地区儿童流感的构成类型以及分布情况。
方法 收集流感流行期间前来我院就诊的儿童流感样病例（ILI）咽拭子，采用江苏硕士甲流/乙流流感抗原检测试剂盒（免疫层析法），行流感快速检测；应用 SPSS18.0 统计软件进行数据分析，采用描述性分析及×2 检验对两个流感流行季的流行特征及各亚型流感病毒感染患儿性别和年龄等特征进行比较分析。
结果 共采集 ILI 样本 38150 人次；阳性检出数 8589，阳性率 22.51%，其中甲流 6675 人次，甲流检出率 17.5%，乙流 1889 人次，乙流检出率 4.95%，甲流乙流同时感染患者 25 人；性别差异无统计学意义。
结论 本地区儿童流感发病主要集中在冬春季节，呈明显的双高峰流行；男女发病率无差异，学龄前和小中学儿童是高发病率人群。

PU-2950

省域应急检验人员储备能力建设的思考

宋建
四川省医学科学院·四川省人民医院

目的 探索由省、市、县（区）、基层社区等多级医疗机构检验人员参与的省域应急检验储备能力的形成方式，建设完整的应急检验人员储备体系，实现为卫生行政部门在应急救援情况下提供能力可靠的专业应急检验队伍的目的。
方法 成立省级检验专委会下辖的应急检验工作领导小组，由省级检验专家担任组长，市级专家担任副组长，县（区）检验科主任为组员的领导机构；依据国内及省内多发事件及偶发事件的不同类型建立相对应应急检验小组，编写管理文件；统计省内检验科相关仪器的型号和数量分布，确定满足应急检验使用需求的仪器类型；选择具有中级及以上专业职称检验人员进入后备人员数据库；开展应急检验工作技能、生物安全防护技能、户外生存技能、身心医学健康管理的培训。
结果 依据调查数据，省内具有应急检验工作经验的专家数名，具有领导该项工作开展的能力；我省参与新冠核酸应急检测的工作人员数千名，具备应急检验的初步能力储备，可以满足建立应急检验体系的人员要求；参照国家的法律法规可以编制应急检验工作的组织文件，包括应急事件的类型及响应程序；参照检验行业标准可以编制应急检验的质量管理文件，包括质量目标、检验工作制度、仪器设备的选择及维护、人员的培训考核及甄选、质量的评价及改进等内容；该体系的探索现局限在检验专业的局部领域内，未与卫生行政部门建立常规性联系，且缺少财政资金支撑，后期需要向行政部门寻求政策性支持。
结论 该“树状”结构的应急检验体系在专业技术层面具有可操作性，该体系的建立可以保证突发事件发生时我省可实时出动一支人员技术过硬、检验质量精准、持续作战能力强大的专业检验队伍，实现疾病的早发现、早诊断、早治疗，减少突发事件对人民群众生命健康的威胁；争取卫生行政部门及财政资金的支持是该体系作用发挥的关键因素。

PU-2951

黄腐酚通过抑制肝星状细胞的活化保护肝功

苏海翔、何贵山、张秀丽
甘肃省医学科学研究院，甘肃省肿瘤医院

目的 黄腐酚是啤酒花雌花序中的主要异戊二烯基黄酮。本文拟通过文献学习，了解天然黄酮类化合物黄腐酚是如何保护肝脏功能的。
方法 通过文献学习综述黄腐酚在肝脏功能保护中的作用。
结果 黄腐酚具有抗炎、抗氧化、降血糖、抗癌等多种药理作用，在抑制慢性肝病发生发展过程中，黄腐酚主要通过肝星状细胞的活化和促纤维化环节发挥作用。黄腐酚或富含黄腐酚的啤酒花提取物作为治疗剂在对抗慢性肝病进展中也具有潜在应用价值。除了具有保肝作用外，黄腐酚还有望作为治疗肥胖、糖代谢失调和代谢综合征的药物。
结论 治疗性黄腐酚应用似乎是一种很有前途的策略，特别是在肥胖患者中，黄腐酚可以抑制非酒精性脂肪肝的发展和进展。

PU-2952

黄腐酚和其相关的黄酮与健康

苏海翔、郭红云、王涛、张秀丽
甘肃省医学科学研究院，甘肃省肿瘤医院

目的 黄腐酚（3'-[3,3-二甲基烯丙基]-2'，4'，4-三羟基-6'-甲氧基查尔酮）是啤酒花雌性花序的主要异戊二烯基黄酮，啤酒花是啤酒的一种成分。人类接触黄腐酚和相关的异戊二烯类黄酮（如 8-异戊二烯柚皮素和异黄腐酚）的主要途径是通过啤酒消费。在体外研究中，黄腐酚被认为是一种"广谱"的肿瘤化学预防剂，而 8-丙炔柚皮素被誉为迄今为止最有效的植物雌激素。本文综述近年来啤酒花和啤酒中的黄腐酚和相关的黄酮在人类健康领域应用的研究进展。
方法 通过文献学习完成综述。
结果 啤酒花中的丙炔基黄酮类化合物在肿瘤预防和绝经后潮热和骨质疏松症预防和治疗方面有潜在的作用。黄腐酚和 8-异戊二烯柚皮素在体内被代谢成具有异戊二烯基结构的黄酮类化合物。黄腐酚是在羽扇豆素腺体中通过类黄酮生物合成的一个特殊分支形成的，该分支涉及聚酮中间体查尔康林素的异戊二烯基化和 O-甲基化。目前已知羽扇豆素腺体特异性查尔酮合酶，但尚未鉴定出参与黄腐酚的芳族丙氨酰转移酶和 O-甲基转移酶。
结论 黄腐酚在许多种人类疾病的预防和治疗方面有潜在价值，值得开展深入研究。

PU-2953

ISO15189 认可中实验室质量管理体系的建立与应用

任静
广元市中心医院

目的 探讨 ISO15189 实验室认可过程中实验室质量管理体系的建立及其在临床医学实验室中的应用价值。
方法 2018 年 7 月广元市中心医院检验科依据 CNAS－CL02:2012《医学实验室－质量和能力认可准则》和既往实验室质量管理的经验，建立临床实验室质量管理体系：确定实验室的质量方针和目标，完成各层文件的编写，并实施运行。

结果 实验室质量管理体系经过一年多的应用，实现了对人员、设备、试剂和耗材、环境、服务与供应等要素的全方位有效管理。同时建立质量管理体系质量指标和质量监督管理程序、质量体系管理评审程序等对质量管理体系进行控制，实现持续改进，确保质量管理体系的有效运行。
结论 建立的实验室质量管理体系效果好、效率高，满足了当前临床实验室质量管理需求，提高了管理水平和工作效率，创造了一个使员工充分参与的环境，保障了质量体系的有效运行和持续改进。

PU-2954

2020 年我院细菌耐药监测分析

谢扬虎
合肥市第二人民医院

目的 分析 2020 年我院临床标本常见细菌分布及耐药性。
方法 仪器法进行细菌鉴定和药敏试验，按 CLSI（2019）文件标准判断结果，采用 WHONET5.6 软件对数据进行分析。
结果 临床分离菌共 4126 株，其中革兰阳性菌占 25.3%，革兰阴性菌占 74.7%。革兰阳性菌居前 5 位的是金葡菌、屎肠球菌、粪肠球菌、表皮葡萄球菌和人葡萄球菌，革兰阴性菌前 5 位的依次为大肠埃希菌、肺炎克雷伯菌、铜绿假单胞菌、鲍曼不动杆菌和奇异变形杆菌。葡萄球菌中 MRSA 和 MRSCN 检出率分别为 49.7%和 75.7%；耐万古霉素粪肠球菌检出率为 0.7%；碳青霉烯类耐药肠杆菌（CRE）中，除大肠埃希菌为 1.7%外，碳青霉烯类耐药的肺炎克雷伯菌和黏质沙雷菌均高达 30.5%。碳青霉烯类耐药鲍曼不动杆菌（CRAB）为 57.1%，碳青霉烯类耐药铜绿假单胞菌（CRPAE）为 32.2%。
结论 细菌多重耐药仍然很严重，CRE 检出率有增高趋势，特别是碳青霉烯类耐药的肺炎克雷伯菌和黏质沙雷菌，应及时进行细菌耐药性监测。

PU-2955

The Clinical Application Value of Prognostic Nutritional Index for the Overall Survival Prognosis of Patients with Esophageal Cancer：a Robust Real-world Observational Study in China

guishu yang、huaichao luo
Sichuan Cancer Hospital & Institute, Sichuan Cancer Center, School of Medicine, University of Electronic Science and Technology of China

Background Esophageal cancer is a kind of cancer with high morbidity and mortality, which is accompanied by a profound poor prognosis. Prognostic nutritional index, based on serum albumin levels and peripheral lymphocyte count, has been confirmed to be significantly associated with various cancers. This study was aimed to explore the prognostic significance of PNI in overall survival prognosis of patients with esophageal cancer.
Methods As a real-world study based on the big database, clinical data of 2661 patients with esophageal cancer were evaluated retrospectively, and the individuals were randomly divided into training and testing cohort. In these two cohorts, patients are classified into high-risk group(PNI<49) and low-risk group(PNI≥49). The univariate and multivariate analyses were performed to analyze the independent risk factors for the prognosis of esophageal cancer patients by using the Cox proportional hazards regression model. A p-value of 0.05 was considered statistically significant.

Results In this study, whether in the training cohort or the test cohort, according to the univariate analysis, the gender, tumor size, tumor grade, T stage，N stage，M stage，TNM stage and PNI were significantly correlated with overall survival ($p<0.05$). Furthermore, the multivariate analysis showed that gender, T stage，N stage，M stage，TNM stage and PNI were independent prognostic risk factors of esophageal cancer($p<0.05$).
Conclusion PNI can be regarded as an independent prognostic factor combined with tumor size, T stage, N stage, M stage and TNM stage, and it might be a novel reliable biomarker for esophageal cancer.

PU-2956

1010 例女性泌尿生殖道支原体感染与耐药分析

高海强、刘艳飞、王真
杭州市妇产科医院

目的 分析本地区女性泌尿生殖道支原体感染情况并对常用抗菌药物进行耐药分析，为临床合理用药提供参考依据。
方法 对 2018 年 1 月 至 2019 年 12 月 1010 例疑似泌尿生殖道感染门诊患者的支原体感染情况病历资料进行收集，并对药敏结果进行回顾性分析。
结果 1010 例中有 566 例支原体阳性，占比 56.04 %，其中 Uu 阳性有 449 例 ，Mh 阳性有 13 例，Uu+ Mh 阳性有 104 例。女性感染主要集中在 20-30 岁，并且在耐药结果分析中，交沙霉素、强力霉素和美满霉素针对不同类型支原体感染的敏感率都高于 90% 。
结论 本地区女性泌尿生殖道支原体感染以单纯 Uu 感染多见，好发于 20-30 岁年龄段，支原体对常见药物产生较高耐药性，临床医生可以选用交沙霉素、强力霉素和美满霉素作为经验治疗首选药，但为了防止耐药情况加剧，临床医生应根据患者药敏培养结果合理选用抗菌药物，给足剂量，用足疗程，加强支原体耐药监测。

PU-2957

新型微管抑制剂克服肿瘤耐药

宁楠楠
山东大学齐鲁医院

目的 恶性肿瘤发病率逐年增加，治疗效果有待提高。作为一类化疗药，微管抑制剂在临床肿瘤治疗中应用广泛。但是，随着化疗的进行，肿瘤产生多药耐药，严重影响治疗效果。本研究旨在寻找能够克服肿瘤多药耐药的新型化疗药物。
方法和结果 通过高通量筛选，我们发现了一种小分子化合物 133，它能够抑制数百种肿瘤细胞株的增殖。流式细胞检测和免疫荧光染色表明，该化合物可将细胞阻滞在有丝分裂前中期。通过微管蛋白体外聚合试验，确定了 133 具有抑制微管聚合的作用。耐药细胞株增殖试验和小鼠模型说明 133 能够克服肿瘤耐药。
结论 我们发现了一种新型的微管抑制剂 133，在细胞水平和动物体内均能克服多药耐药，为临床肿瘤治疗研究提供帮助。

PU-2958

简析发热伴血小板减少综合征外周血涂片

曹选
江苏省人民医院（南京医科大学第一附属医院）

我们收集了 2019 年 5 月-2021 年 5 月期间在我院治疗的发热伴血小板减少综合征病人外周血涂片，发现血常规外周血涂片主要表现为白细胞和血小板进行性减少。少数患者白细胞降低不明显，红细胞正常，伴有核左移，浆细胞样反应淋增多，涂抹细胞增多，为发热伴血小板减少综合征比较特有的外周血表现，此时需要提醒临床做发热伴血小板减少综合征病毒检测。同时发现大多数患者特别是多器官功能衰竭危重症患者 ALT、AST、LDH、CK、APTT、TT、D-D 等指标均有不同程度异常，且升高程度与预后有一定的相关性。

PU-2959

多囊卵巢综合征患者血清抗缪勒管激素及血脂检测结果的分析

杨艳
江苏省连云港市第一人民医院

目的 多囊卵巢综合征(PCOS)是育龄女性一种很常见的内分泌紊乱的代谢性疾病，同时也是引起育龄女性不孕症的主要病因之一 ，其发病机制目前尚不清楚，其与环境和遗传及肥胖等多种因素相关联，其发病率占育龄期女性约 6％左右 。其对妇女身心健康及家庭造成非常严重的影响，本研究的目的是对多囊卵巢综合征患者血清抗缪勒管激素(AMH)及血脂检测结果进行分析。
方法 选取 2019 年 2 月到 2022 年 2 月在连云港市第一人民医院妇科确诊的 218 例多囊卵巢综合征患者作为观察组，选取同时期到本院体检中心进行健康体检的 218 例月经正常女性作为对照组,两组均测定三酰甘油(TG)、胆固醇（TC）、高密度脂蛋白胆固醇(HDL-C)、低密度脂蛋白(LDL-C）、血清抗缪勒管激素(AMH)。
结果 观察组的三酰甘油(TG)、、胆固醇（TC）、低密度脂蛋白(LDL-C）、血清抗缪勒氏管激素(AMH)均高于对照组（P<0.05）,观察组的高密度脂蛋白胆固醇(HDL-C)低于对照组（P<0.05），
结论 多囊卵巢综合征存在血清抗缪勒氏管激素和血脂的改变，现阶段对于多囊卵巢综合征 的诊断主要依据病人的临床表现和多囊卵巢超声检查及内分泌特征来判断，所以对于联合应用检测血清抗缪勒管激素和血脂对于多囊卵巢综合征具有相当高的临床诊断价值, 且各检测数值的变化有助于指导多囊卵巢综合征患者临床治疗。

PU-2960

北京协和医院定量生化和免疫检验报告取消审核现状分析及改进策略

李鹏昌、程歆琦、夏良裕、刘文静、王军、张强兴、鲁军、邱玲
中国医学科学院北京协和医院

目的 分析检验报告取消审核的原因，探索实验室信息系统改进方法，降低检验报告不正确率。
方法 回顾分析 2019 年 1 月 1 日至 12 月 31 日北京协和医院检验科定量生化和免疫检验报告取消审核的标本信息，计算取消审核率，分析取消审核原因、取消审核的时间和不正确报告打印率等指标。
结果 定量生化和免疫检验标本总数为 2134723 份，取消审核标本数为 1054 份，总体取消审核率为万分之 4.94。所有取消审核报告中，已打印率为 15.4%。最常见的取消审核原因为标本复检、

修改尿量、补录备注信息和样本需要稀释，占全部取消审核报告的比例分别为 43.8%、22.6%、14.2%和 6.1%。在信息系统中增加审核报告后延迟 10min、30min、60min、90min 或 120min 发送结果，将分别使不正确报告率下降 18.4%、27.5%、37.1%、43%和 45.9%。
结论 需要定期汇总和分析检验结果取消审核率，优化实验室信息系统的功能可以有效降低检验报告不正确率。

PU-2961

上海地区白细胞分类计数项目性能规范探索

缪颖波、王青、徐翀
上海市临床检验中心

目的 寻找一种适合白细胞分类计数能力验证项目的性能规范，帮助上海地区持续有效地提高白细胞分类计数项目的检测水平。
方法 收集 2015～2020 年 12 次共 60 批次白细胞分类计数能力验证活动数据，比较按照基于生物学变异和基于当前技术水平设定的性能规范评价各年份所有批次能力验证结果通过率，选择通过率均≥80%的性能规范作为该项目的性能规范。
结果 所有批次中性粒细胞计数（neutrophile，Neut）、嗜酸性细胞计数（eosinophil，Eos）、嗜碱性细胞计数（basophil，Bas）使用基于生物学变异设定的最佳性能规范（11.2%、18.6%和19.2%）时通过率均≥80%；所有批次淋巴细胞计数（lymphocyte，Lymph）使用基于生物学变异设定的最低性能规范（24%）时通过率均≥80%；所有批次单核细胞计数（monocyte，Mono）在使用基于当前技术水平设定的性能规范（＜1，±0.279；≥1，±27.9%）时通过率均≥80%。
结论 上海地区白细胞分类计数能力验证中 Neut、Lymph、Eos 和 Bas 可分别采用 11.2%、24%、18.6%和 19.2%的性能规范，Mono 可采用＜1 时，±0.279 和≥1 时，±27.9%的性能规范。

PU-2962

博鳌乐城国际医疗旅游先行区政策变化的研究

云天宝
海南博鳌金域国际医学检验中心有限公司

2013 年 2 月 28 日国务院正式批复海南设立博鳌乐城国际医疗旅游先行区，并给予九项支持政策“国九条”，加快先行区药品、医疗器械进口审批;对先行区范围内临床急需少量进口药品、医疗器械的符合要求的临床使用数据，可以用于进口药品、医疗器械注册申请;在患者备案承诺基础上，有条件允许先行区医疗机构患者带合理自用量的进口药品离开先行区使用;将卫生系列高级专业技术职称评审权下放先行区，试行社会化评价机制;建设国内一流的特许药械追溯管理平台。这标志着我国第一家以国际医疗旅游服务、医疗科技创新和国际组织聚集地为主要内容的国家级开发园区宣告成立。本文梳理了先行区的发展历程，通过政策的变化研究鳌乐城国际医疗旅游先行区内多家医疗机构的快速发展。结果证明，乐城国际医疗旅游先行区将有望破解游客对海南健康服务消费的刚性需求与健康服务供给不足的突出矛盾，并带动海南经济社会发展。乐城国际医疗旅游先行区“先行先试”将优化海南健康服务业的软硬环境，推动海南医疗、旅游、地产、会展、教育等产业融合。

PU-2963

海南省黎族新生儿地中海贫血基因特征分析

赵振东、王洁
海南省妇女儿童医学中心

目的 了解海南省黎族新生儿地中海贫血发病情况及基因特点。
方法 以海南省 1438 例黎族新生儿干血斑为样本，使用荧光 PCR 熔解曲线法检测中国人常见的地中海贫血基因，并对部分样本使用 PCR+导流杂交法进行验证。基因检测提示疑似新突变的样本外送基因公司以寻找未知突变。
结果 ①在筛查率达 94.8%（1438/1517）的情况下，检出地中海贫血基因 1024 例，黎族地中海基因贫血基因携带率高达 71.2%（1024/1438）。②检出地中海贫血男性 524 例和女性 500 例，男性和女性地中海贫血基因携带率分别为 70.5%（524/743）和 71.9%（500/695），经统计学分析男女间地中海贫血基因携带情况（X2=0.074,P=0.786）无统计学意义。③此次共检出 31 种已知基因型和 2 种疑似新基因型。经基因公司分析为-α4.2/HKαα 和 c.229G>C 少见型。
结论 海南省黎族新生儿人群中地中海贫血基因携带率高，以 α 地中海贫血基因型最常见，排在前三位的基因型为： -α4.2/αα、-α3.7/αα 和 αWSα/αα。

PU-2964

血清淀粉酶与血清脂肪酶的相关性研究

解春宝
电子科技大学附属医院•四川省人民医院

目的 探讨血清淀粉酶（AMY）与血清脂肪酶（LIPA）的相关性，为临床对检测结果的解读提供科学思路。
方法 对我院急腹症患者抽取静脉血液，分离血清后同时进行 AMY 与 LIPA 测定。分析比较单独结果阳性，两者同时为阳性的结果，同时分析两个项目的相关性。
结果 本研究中 114 例急腹症患者 AMY 的阳性率为 64.9%、LIPA 的阳性率为 71.9%。在研究对象中 AMY 与 LIPA 同时为阳性的比例为 27.2%，提示 AMY 与 LIPA 同时升高的比例较低、两者的相关性不高。
结论 AMY 与 LIPA 有各自的特性，其相关性较低。在分析临床结果时应综合多方面对患者做出诊疗。

PU-2965

湖南地区 1982 例脊髓性肌萎缩症携带者筛查结果与分析

梁雄伟、吴秋、陈鹏、余艳、代冰、唐春燕、朱加琳
长沙金域医学检验实验室有限公司

目的 对湖南地区 1982 名受检者进行脊髓性肌萎缩症(spinal muscular atrophy, SMA)携带者筛查，了解本地区人群脊髓性肌萎缩症 *SMN1* 基因拷贝数异常的携带频率，为遗传咨询以及进一步的产前诊断提供参考与依据。
方法 回顾性分析长沙金域医学检验实验室从 2018 年 1 月到 2021 年 4 月，应用荧光定量 PCR 技术，对 1982 例受检者进行 *SMN1* 基因中 exon 7 和 exon 8 拷贝数变异检测与诊断，并基于遗传平衡定律计算人群中各等位基因频率。

结果 在 1982 例筛查样本中，共检测出 SMA 携带者（即 *SMN1* 基因 exon 7 的拷贝数为 1）36 例，人群携带者频率为 1.82%。其中，exon 7 和 exon 8 的比值包含以下三种：exon 7:exon 8=1:1，exon 7:exon 8=1:2，exon 7:exon 8=1:3。正常人群中，*SMN1* 基因 exon 7 拷贝数为 2 共计 1868 例，频率为 94.3%，exon 7 的拷贝数大于等于 3 共检出 78 例，频率为 3.94%。exon 7 的拷贝数和 exon 8 的拷贝不一致，共检出 77 例，频率为 3.88%，表明 *SMN1* 和 *SMN2* 之间存在高频的相互转换。利用遗传平衡定律计算得，“0 拷贝”等位基因（5 号染色体上缺乏 *SMN1* exon 7）的频率为 9.40×10^{-3}，“1 拷贝”等位基因的频率为 9.71×10^{-1}，“2 拷贝”等位基因（5 号染色体上存在两个 *SMN1* exon 7）的频率为 1.97×10^{-2}。

结论 湖南地区 SMA 携带者频率为 1.82%（1/55），与不同人群携带波动频率 1/100~1/45 较为一致；SMA 作为一种高携带率、病情严重的遗传病，开展 SMA 携带者筛查对于预防 SMA 患儿的出生，提高出生人口质量有重要的价值和意义；qPCR 技术具有操作简单、成本低廉、结果准确等优势，可用于 SMA 患者的初步诊断和人群中大规模的携带者筛查。

PU-2966

拉萨某三甲医院儿科住院患者乙肝感染现状及分析

张子玉
拉萨市人民医院

目的 分析拉萨某三甲医院儿童住院患者乙肝（HBV）感染情况，为科学制定西藏地区乙肝免疫策略提供依据。

方法 统计 2017-2020 年拉萨市某三甲医院儿科住院患者乙肝表面抗原（HBsAg）检测结果，根据患儿性别、年龄、出生年份进行分组，分析儿童乙肝感染率。

结果 住院儿童乙肝感染率，男性为 2.74%，女性为 2.56%，两者之间无显著性差别。按照年龄分组，<1 岁组，1-5 岁组的阳性率分别为 2.16%、2.44%；6-10 岁年龄组的乙肝阳性率高达 7.30%，与其他两组具有显著性差异（$p<0.01$）。按照出生年份统计，2010 年、2011 年出生儿童乙肝阳性率分别为 8.70%、6.71%，逐渐降低至 2016 年的 1.44%。2017-2020 年的乙肝阳性率呈现窄幅波动。

结论 自 2010 年起西藏地区儿童乙肝感染率呈下降趋势，仍需加强西藏地区乙肝防控的宣传教育和措施，提高西藏地区乙型肝炎的防控意识。

PU-2967

Accuracy assessment of four blood glucose monitoring test systems against the accuracy requirements specified in different standards: A retrospective single center study

李润青
北京清华长庚医院

Background The aim of this study was to retrospectively evaluate the accuracy of four blood glucose monitoring test systems (BGMS) in comparison with the laboratory biochemical analyzer, and to explore the differences of comparison results against the requirements specified in five different criteria.

Methods The comparison between BGMS and the laboratory biochemical analyzer was conducted by laboratory technicians and nurses who performed blood glucose tests twice a year from 2015 to 2019. A total of 366 glucose meters with 10808 pairs of comparative results from four BGMS (Roche Accu-Chek® performa, Bayer Contour™TS, Sinomedisite Glupad® H1 Plus, and Sinocare® Gold-Accu) were retrospectively analyzed. The differences of the comparative

results of accuracy assessment were analyzed and compared applying five different criteria, the International Organization for Standardization (ISO) 15197:2003, Clinical Laboratory Standards Institute (CLSI) POCT12-A3, ISO 15197:2013, Chinese Society of Laboratory Medicine (CSLM) consensus, and the US Food and Drug Administration (FDA) guidance.
Results There was a very close correlation between the glucose results and the central laboratory hexokinase method Results The correlation coefficients were r = 0.995 for Roche Accu-Chek® performa, r = 0.994 for Bayer Contour™TS, r = 0.983 for Sinomedisite Glupad® H1 Plus, and r = 0.997 for Sinocare® Gold-Accu. Assessment of system accuracy varied significantly for one system of glucose meter when evaluated with five different accuracy criteria. BGMS of Roche Accu-Chek® performa, Bayer Contour™TS, Sinomedisite Glupad® H1 Plus, and Sinocare® Gold-Accu showed 99.26%, 88.07%, 58.62%, and 91.43% within the requirement of ISO15197:2013 by numbers of glucose meters, respectively. And the four BGMS showed 99.34%, 96.86%, 84.54%, and 97.83% within the requirement of ISO15197:2013 by number of pairs of comparative results, respectively. The Clarke and Parkes Error Grid analysis revealed both above 99.8% of the glucose results to be within the clinically acceptable areas (Clarke Error Grid: Zone A + B with Roche Accu-Chek® performa (99.83% + 0.13%), Bayer Contour™TS (99.67% + 0.33%), Sinomedisite Glupad® H1 Plus (96.08% + 3.87%), and Sinocare® Gold-Accu (99.71% + 0.14%.); Parkes Error Grid: Zone A + B with Roche Accu-Chek® performa (99.91% + 0.09%), Bayer Contour™TS (99.40% + 0.60%), Sinomedisite Glupad® H1 Plus (97.97% + 1.98%), and Sinocare® Gold-Accu (99.86% + 0.14%)).
Conclusions ISO15197:2013, with increased the technical accuracy and clinical accuracy requirements, was a high-level and feasible criterion for the system accuracy requirements of glucose meters. BGMS of Roche Accu-Chek® performa demonstrated more favorable accuracy than the other three BGMS

PU-2968

产前诊断免疫检验项目质量控制分析

廖琳
郴州市第一人民医院

目的 探讨采用质量控制措施对产前诊断免疫检验项目进行干预后获得临床效果。
方法 将我院 2017 年 05 月～2020 年 06 月收治的 60 例分娩孕妇数字奇偶法分组；干预组（30 例）：采用质量控制措施完成产前诊断免疫检验项目干预；常规组（30 例）：采用常规方式完成免疫检验工作；就组间甲胎蛋白、C-肽、Ca125、肿瘤标志物以及癌胚抗原展开对比。
结果 干预组分娩孕妇甲胎蛋白（31.35±3.99）、C-肽（56.79±7.25）、Ca125（25.29±2.85）、肿瘤标志物（31.03±2.49）以及癌胚抗原（40.03±2.69）同常规组分娩孕妇甲胎蛋白（65.69±2.79）、C-肽（36.39±2.03）、Ca125（59.03±5.69）、肿瘤标志物（60.85±5.69）以及癌胚抗原（64.88±3.03）比较差异显著（P<0.05）。
结论 质量控制措施的有效开展，可确保分娩孕妇产前诊断免疫检验项目开展价值获得显著提升，对于免疫检验结果可靠性以及准确性可以做出充分保证，并且管理期间不但需要将标本采集管理力度加强，而且针对阶段分析工作需要积极展开管理工作，就检验系列影响因素展开有效控制，针对甲胎蛋白、C-肽、Ca125、肿瘤标志物以及癌胚抗原等系列指标表现加以充分明确，最终对分娩孕妇身体状态进行充分了解，使检验结果准确性获得有效提高，对免疫检验项目检验质量做出充分保证，显著发挥质量控制措施应用价值。

PU-2969

急性脑梗死患者血清脂蛋白相关磷脂酶 A2 和超敏 C 反应蛋白的检验分析

廖琳
郴州市第一人民医院

目的 急性脑梗死患者机体的实验室指标可出现明显变化，本文主要对血清脂蛋白相关磷脂酶 A2 和超敏 C 反应蛋白的变化情况进行分析。
方法 本次实验的研究时间控制为 2019.1-2020.6，选取该期间内进行脑梗死患者 80 例作为实验组进行对比研究，且根据患者脑梗死面积的大小分为 45 例大面积组、35 例小面积组，同时，选择该期间内的健康体检人员 40 名作为对照组，均行血清脂蛋白相关磷脂酶 A2 和超敏 C 反应蛋白的检验，对比三组患者的不同检验结果。
结果 实验、对照二组患者的 Lp-PLA2、hs-CRP 对比，存在差异（P＜0.05）；对比 Lp-PLA2、hs-CRP 的变化情况，大面积组患者数据更高，统计学意义存在（P＜0.05）；不同严重程度急性脑梗死患者 Lp-PLA2、hs-CRP 的变化存在显著性差异（P＜0.05）。
结论 血清脂蛋白相关磷脂酶 A2 和超敏 C 反应蛋白是诊断、评估急性脑梗死的敏感指标，值得推广。

PU-2970

怀化地区男性患者人乳头状瘤病毒基因型分析

梁明星、廖晓敏、杨长顺
怀化市第一人民医院

目的 分析怀化地区不同年龄组男性人乳头状瘤病毒（HPV）感染亚型分布及流行病学特点，为男性 HPV 感染早期筛查、预防、诊断提供临床依据。
方法 采用 DNA 反向斑点杂交技术，回顾性分析了 742 例男性患者的 HPV DNA 亚型、感染率和年龄分布。
结果 742 例男性标本中检出 HPV 阳性者 376 例，总阳性率为 50.67%，其中单纯低危基因型 122 例（32.45%），单纯高危基因型 68 例（18.09%），低危型与高危型混合感染 186 例（49.47%）。低危型以 HPV6（27.40%）感染为主，其次为 HPV11（12.40%）。高危型以 HPV52（10.40%）感染为主。各年龄段均以单一感染为主，其次为双重感染。在 5 个年龄组中，≥51 岁男性 HPV 阳性率最高(70.21%)，其次为≤20 岁年龄组(57.50%)。
结论 怀化地区男性 HPV 感染率较高，感染情况以单一感染为主，低危亚型以 HPV6 和 HPV11 为主要感染亚型。高危亚型以 HPV52 和 HPV16 为主要感染亚型。

PU-2971

平均血小板体积在卵巢癌患者中的临床意义

施晶晶、束国防
东南大学附属中大医院

目的 探讨平均血小板体积（MPV）在卵巢癌患者中的临床意义，为卵巢癌的诊断提供新的依据。
方法 回顾性分析东南大学附属中大医院 2019-2020 年经病理确诊的卵巢良恶性肿瘤患者 110 例（良性 70 例，恶行 40 例），收集并记录相关临床资料，应用 t 检验比较两组 MPV 差异，应用 ROC 曲线计算 MPV 诊断卵巢癌的特异性、敏感性及曲线下面积，以评价 MPV 在卵巢肿瘤中的诊断价值。

结果 卵巢恶性肿瘤患者外周血 MPV 高于良性肿瘤患者，差异具有统计学意义（$p<0.05$）；MPV 对卵巢癌的诊断价值较低（AUC=0.550）。
结论 卵巢癌患者外周血 MPV 水平升高，MPV 可作为卵巢癌患者辅助诊断及病情监测的指标之一。

PU-2972

A novel LAMP2 p.G93R mutation associated with mild Danon disease presenting with familial hypertrophic cardiomyopathy

Jing Xu[1]、Qiming Dai[2]
1. 东南大学附属中大医院检验科
2. 东南大学附属中大医院心内科

Background Danon disease (DD) is an X-linked dominant multisystem disorder that is associated with cardiomyopathy, skeletal myopathy, and varying degrees of intellectual disability. It results from mutations in the lysosome-associated membrane protein 2 (LAMP2) gene.
Methods Herein, a proband with a mild DD case presenting with a familial hypertrophic cardiomyopathy (HCM) phenotype and additional family members were evaluated. Exome sequencing and Sanger sequencing were performed to explore the genetic basis of DD in the proband. Segregation, in silico, and functional analyses were carried out to explore potential pathogenicity in the candidate mutation.
Results Exome sequencing and Sanger sequencing identified one novel missense mutation (p.G93R) in the LAMP2 gene in the proband, and this mutation was also identified in three other family members. In silico analysis of LAMP2 predicted that the mutation causes a conformational change and subsequent protein destabilization. Furthermore, functional examination showed that mutation carriers have a significant reduction in LAMP2 expression, which supports that the mutation is pathogenic. Moreover, skewed X chromosome inactivation (XCI) was identified in one female mutation carrier, thus suggesting that skewed XCI may be the reason why this individual escaped the pathogenic influence of the mutation.
Conclusion These findings will aid in diagnosing DD patients carrying this LAMP2 mutation that presents with an HCM phenotype. Furthermore, this study illustrates the importance of utilizing a molecular diagnostic approach in HCM patients and is the first study to report a LAMP2 p.G93R mutation associated with mild DD and identify that XCI serves a protective role in DD etiology.

PU-2973

碘化造影剂对甲状腺癌患者治疗过程中尿碘检测的影响

张洁心、颜承靖
江苏省人民医院（南京医科大学第一附属医院）

目的 As3+-Ce4+催化分光光度法是我国国家卫计委推荐的尿碘定量检测方法，目前面向广大甲状腺疾病患者在临床实验室得到广泛应用。我们首次报道碘化造影剂与该方法中的过硫酸铵试剂会自发地发生非特异性化学反应，导致尿碘结果出现较大偏差，将可能误导甲状腺癌治疗方案的制定。
方法 对在我院首诊的甲状腺癌患者的生活史、病史、临床表现和临床检验项目进行分析，筛选得到在院尿碘检测结果极高的病例。从患者接受双能 CT 检查静脉注射碘化造影剂后第一份随机尿标本开始，收集至出院后一至两个月，着重比较研究尿碘检测反应曲线及检测结果。
结果 在院期间尿碘浓度极高的 24 位患者，其出院一至两个月尿碘结果示正常。进一步实验表明，即使人体内仅留存 0.01%的碘化造影剂，其仍对碘与过硫酸铵之间的生化反应产生干扰，导致尿碘检测结果不准确。

结论 本研究有助于提高我们检验人员对基于 As3+-Ce4+催化分光光度法的生物化学反应机制的认识，为临床医生在甲状腺疾病诊断和治疗过程中的尿碘检测项目提供必要的解释和辅助作用。本研究也提示应完善患者个体随访检测项目的评估体系。

PU-2974

加强血站实验室质量管理与血液检测不合格率的关系

张锋
苏州市中心血站太仓分站

目的 血站实验室的检测质量是在一个相对矛盾的环节中实施的。既要提高实验室的检测能力，将血液检测漏检率控制为零，又要合理保护珍贵的血源，要把假阳性率控制在最低，否则血液报废增多，造成血源浪费。这就要求我们在提高实验室质量管理能力，将血液漏检率降为零，血液检验不合格率控制在合理范围，确保临床用血安全。
方法 通过从标本管理，人员培训，设备的维护保养等方面加强管理，从而逐年统计分析血液检测不合格率的变化，查看加强实验室管理对血液检测不合格率变化的相关情况
结果 通过从标本管理，人员培训，设备的维护保养等方面加强管理，历年血液检测不合率变化如下:2011 年 3.45%,2012 年 3.60%,2013 年 2.44%,2014 年 1.69%,2015 年 1.67%,2016 年 1.71%,2017 年 1.70%,2018 年 1.60%,2019 年 1.17%,2020 年 0.96%.
结论 血站实验室分酶免技术和生化技术，随着医学实验科学技术的发展，酶免技术和生化技术以其迅速简便灵敏度高，特异性强等特点，在临床免疫和生化方面不断得到普及应用，特别是近年来，血站实验室基本都装备了全自设备，提高人对机器的控制管理优为重要，加强实验室质量管理尤为重要，实验室质量管理和血液检测不合格率息息相关。目前实验室质量管理主要表现在设备的运行状态、人员的素质培训、检测试剂等物料的控制、实验室全面质量管理体系的建立并不断完善和改进、生物安全等方面的管理环节。通过从标本管理，人员培训，设备的维护保养等方面加强管理，血液检测不合格率逐年下降.

PU-2975

ISO15189 监督评审工作做在日常

周海宁
沈阳金域医学检验所有限公司

目的 通过实验室认可准则后保证医学实验室始终处于能够让社会证相信其能力和公正性的状态顺利通过监督评审
方法 在日常工作中按照 ISO15189：2012《医学实验室质量和能力认可准则》的要求开展日常工作并将此种状态常态化。
结果 科室内宣贯准则要求，将科室工作合理进行模块划分并由合适的人员负责，科室人员间间互相监督提醒日常工作流程按照标准执行，遇到困难科室人员共同寻求解决方法，每人熟练掌握自己负责的工作同时，也了解其他同事的工作，能够做到临时顶替其他岗位工作，将准则贯要求穿到日常科室工作中。
结论 通过科室人员的共同努力，科室的工作流程清晰，要求明确，工作效率和完成质量都较高，对于即将到来的监督评审有十足的信心。

PU-2976

骨膜素通过激活外膜成纤维细胞来促进动脉硬化的外膜重构

雷小梅[2]、雷小梅[2]、王映芬[1]、刘巧突[1]、张巍[1]、李芬[1]
1. 郴州市第一人民医院检验科
2. 郴州市第一人民医院检验科

Objective In order to study the effect of adventitial remodeling of arteriosclerosis by periostin.
Methods We examined the effect of periostin by Immunofluorescence cell staining and collagen gel contraction assay.
Results Our data indicated that periostin is highly expressed in adventitia of atherosclerotic arteries. TGF-β1 induced the expression of periostin in fibroblasts of adventitia. While periostin can promote activation and enhance the contractility of adventitial fibroblasts. Periostin induces adventitial fibroblasts to produce collagen I and TGF-β1 and activate FAK and Src phosphorylation.
Conclusion These results suggest that periostin contributes to adventitial remodeling of arteriosclerosis by activating adventitial fibroblasts.

PU-2977

鼻咽癌免疫治疗临床试验进展

雷小梅[1]、谭潭[2]、王映芬[1]、张巍[1]、李芬[1]
1. 郴州市第一人民医院检验科
2. 郴州市第一人民医院检验科

鼻咽癌是高发于我国南方地区的头颈部恶性肿瘤，以放疗为基础的综合治疗是晚期鼻咽癌最主要的治疗模式。目前，以免疫检查点抑制剂单抗为代表的免疫治疗已成为目前临床试验和新药上市的热点候选实体。本文综述近年来已完成和正在进行的鼻咽癌免疫治疗临床试验，其代表性试验新药主要包括过继免疫治疗、肿瘤疫苗和免疫检查点抑制剂单抗。通过总结上述药物的治疗策略、疗效评价、不良反应、毒性和安全性，为寻找有效的治疗靶点提供线索。

PU-2978

南京地区血栓弹力图参考范围的研究

张敏
东南大学附属中大医院

目的 建立南京地区健康成年人血栓弹力图（TEG）正常参考值。
方法 研究对象：2017.4-5 进行健康体检的成年人，肝肾功能正常，排除孕妇、有出血病史或血栓病史者、服用影响凝血药物者(阿司匹林、氯毗格雷、华法林、双嘧达莫等)人群。共收集 45 例健康成年人标本（枸橼酸盐抗凝血）3 ml，进行 TEG 检测。主要检测四项指标：R(凝血因子反应时间，是指凝血过程开始到凝血酶激活所需的时间；K(即从凝血开始至描记图振幅达到 20 mm 的时间，反映纤维蛋白原功能)；Angle(是从血凝块形成点至描记图最大曲线弧度作切线与水平线的夹角，反映纤维蛋白原功能）；MA(最大振幅，表示血凝块绝对强度，反映血小板功能)。
结果 45 名健康成年人 TEG 各参数均值为 R：5.631min，K：1.709min，Angle：65.944，MA：63.062mm。标准差分别为 1.331、0.506、5.578、3.822，按照参考范围制定标准，参考值分别为 R：3.024-8.238 min，K：0.717-2.701 min，Angle：55.012-76.878，MA：55.573-70.551mm。本研究所得参考值与厂家提供参考值有一定差异。

结论 不同地区、不同环境的人群 TEG 参考值可能略有不同，实验室有必要根据当地人群特点建立自己地区的正常参考值。此外，本研究例数较少，应扩大调查例数后再进行进一步分析。

PU-2979

妊娠中期孕妇血细胞分析参考值的研究

张敏
东南大学附属中大医院

目的 观察孕中期全血细胞计数（CBC）参数的变化，为孕中期健康孕妇建立合适的参考间期。
方法 健康孕妇于孕中期进行血液检查。健康的成年女性同时接受测试。所有血样在 Sysmex XE-2100 上进行检测。分析以下 CBC 参数：红细胞计数、血红蛋白、红细胞压积、平均红细胞体积、平均红细胞血红蛋白、平均红细胞血红蛋白浓度、血小板计数、白细胞计数，白细胞分类。确定孕妇和健康成年妇女之间是否存在差异。参考区间的计算基于 x± 1.96s。
结果 孕妇红细胞计数、血红蛋白浓度、红细胞压积、血小板压积均显著低于健康成人（p<0.001）。孕妇平均红细胞体积、平均红细胞血红蛋白、平均红细胞血红蛋白浓度及白细胞计数均显著高于健康成人（p<0.001）。中性粒细胞百分率显著增加；单核细胞百分率略有上升；淋巴细胞、嗜酸性粒细胞和嗜碱性细胞的百分率均相应降低。红细胞的参考区间为 3.19–4.58×1012/L，Hb 为 100.04–139.43 g/L，HCT 为 0.32-0.38L/L，PLT 为 91.27-281.32×109/ L，MCV 的参考区间为 81.40-99.83fL，MCH 为 24.95-36.85pg，MCHC 为 320.90-358.90g/L，白细胞计数的参考区间为 5.20-13.59×109/L，中性粒细胞百分比%为 63.34%-84.51%，淋巴细胞百分比为 10.21%-29.18%，单核细胞百分比为 2.96%-7.91%，嗜酸性粒细胞百分比为 0%-2.36%，嗜碱性粒细胞百分比%为 0%-0.46%。
结论 孕妇与健康成年妇女血细胞计数有显著性差异。本文初步确定了妊娠中期血细胞计数的参考范围。

PU-2980

扩增效率受损时应用 Ct 值与 Cp 值定量检测 HCV-RNA 的比较分析

杨辉
中日友好医院

目的 应用阈值法的 Ct（cycle threshold）值与二阶求导法的 Cp（cross point）值分别对 HCV-RNA 的 PCR 扩增曲线（外标法）进行定量分析，比较两种分析法的精密度，比较扩增效率受损时定量值的变化特征。
方法 real-time PCR 重复检测中等浓度的核酸样本，分别应用 Ct 值和 Cp 值计算浓度，比较 CV(Coefficient of Variance)差异，另有 3 名工作人员对扩增曲线重新分析，观察 4 人之间的分析差异；重复检测已赋值的 HCV-RNA 标准品与血清样本，用 Ct 值和 Cp 值计算浓度，比较二者的 CV 差异；两种方法降低扩增效率（梯度减少扩增液体积；反应体系中梯度递加扩增抑制剂 IgG），用 Ct 值和 Cp 值计算浓度，比较二者定量值的变化趋势。
结果 重复检测中等浓度核酸样本，四位工作人员各自独立分析存储数据，用 Ct 值和 Cp 值计算浓度，使用 Ct 值计算时 CV 大；用 Ct 值计算浓度，人员间有显著差异，用 Cp 值计算浓度，无人员差异；重复检测 5 个标准品和 6 个血清核酸样本，用 Ct 值和 Cp 值分析浓度并比较 CV，前者 CV 均大于后者；扩增液减少时，用 Ct 值和 Cp 值计算浓度，均会低估，但 Cp 值计算浓度，下降趋势相对平缓；扩增抑制剂（16.50g/L）增加时，使用 Ct 值和 Cp 值分析，定量浓度均明显低估。

结论 real-time PCR（外标法）检测 HCV 病毒载量，用二阶求导法计算浓度，精密度优于阈值法，不同浓度均有优势，中高浓度优势明显；不同人员分析同一批扩增曲线，用二阶求导法无人员间差异，优于阈值法；因扩增液成分差异导致扩增效率降低时，用二阶求导法定量值变化较小，优于阈值法；因抑制剂 IgG 导致扩增效率降低时，应用二阶求导法与阈值法计算浓度均不准确。

PU-2981

非编码 RNA 在自身免疫性甲状腺疾病中的研究进展

徐海娈
郑州安图生物工程股份有限公司

非编码 RNA（non-coding RNAs，ncRNAs）是指不编码蛋白质的 RNA，其中参与基因调控的 ncRNAs 主要包括两种：微小 NRA (microRNAs，miRNA)和长链非编码 lncRNAs（long non-coding RNAs，lncRNAs）。lncRNAs 和 miRNAs 的异常表达与自身免疫性甲状腺疾病（Autoimmune thyroid disease ，AITD）的发生发展密切相关。桥本氏甲状腺炎（Hashimoto's disease，HT）及格雷夫斯病（Graves' disease，GD）是最常见的两种 AITD。有研究表明差异表达的 miRNAs 与 GD 的预后相关，可能是 GD 的新的生物标志物和治疗 GD 的潜在靶点。有些 miRNAs 在 HT 患者外周血浆中显著升高，可有潜力作为 HT 的潜在诊断标志物。已经有研究发现 lncRNA 与 TRAb 水平呈现正相关，可通过调节 B 细胞的增殖参与 GD 的致病机制，但目前关于 lncRNAs 与 AITD 的研究较少。在 AITD 的发展和进程中探索 lncRNAs 和 miRNAs 的表达特征及其潜在的分子机制，可以在分子水平上增加对该疾病的了解，进而明确其临床意义，并为 AITD 的诊断生物标志物和可能的治疗靶标提供理论基础。

PU-2982

亚低温培养对猪肝细胞形态与功能的影响

张世昌、黄蕾、梁婷婷
江苏省人民医院（南京医科大学第一附属医院）

目的 评价亚低温培养对猪肝细胞形态与功能的影响，探讨亚低温保存和运输肝细胞的可行性。

方法 将分离的新生猪肝细胞分别采用 25℃、28℃、33℃条件下培养 24 h 后，恢复至 37℃继续培养，观察亚低温培养肝细胞的形态及 LDH 和 AST 漏出量，检测复温前后肝细胞白蛋白合成、氨清除率和尿素合成率。

结果 亚低温培养 24 h 和复温 37℃培养能较好的维持肝细胞形态，各组肝细胞 LDH 和 AST 漏出量无显著差异。亚低温培养 24h，25℃组肝细胞活性显著低于对照组、28℃组和 33℃组，28℃组和 33℃组尿素和白蛋白合成率、氨清除率均显著低于对照组。复温 37℃后，28℃组和 33℃组肝细胞活性显著高于对照组；28℃组和 33℃组肝细胞活性、尿素合成率和白蛋白合成率均显著高于复温前、25℃组和对照组，28℃组肝细胞氨清除率与对照组无显著差异，33℃组的肝细胞氨清除率显著高于对照组。

结论 亚低温特别是 28℃和 37℃培养可有效的保持肝细胞形态和维持肝细胞功能，有望为临床生物人工肝治疗提供一种较好的肝细胞保存和运输方法。

PU-2983

真空采血管性能评价的探讨

蔡斌宏
东南大学附属中大医院

目的 通过真空采血管性能验证，确认本科室使用的真空采血管不会增加检测结果的差异。
方法 依据 WS/T 224-2018《真空采血管的性能验证》，同时结合 ISO15189 医学实验室质量和能力认可准则及采血管制造商使用说明书的要求依次对采血管的外观、抽吸量、管体强度、血清分离管纤维挂壁、溶血情况、抗凝管的抗凝情况，结果可比性等项进行验证。
结果 采血管的外观、抽吸量、管体强度、血清分离管纤维挂壁、溶血情况、抗凝管的抗凝均符合行标要求。
结论 本次真空采血管性能验证，所有操作都按照 WS/T 224-2018《真空采血管的性能验证》的操作步骤严格执行，验证的结果均符合行业标准的要求。说明本实验室使用的采血管不会影响检测结果的准确性，完全能够满足临床检验的需求。

PU-2984

针对抗磷脂抗体检测的标准化研究进展

丁亚辉、李忠信、王文强、张亚平
郑州安图生物工程股份有限公司

目的 近年来，随着国内外对抗磷脂综合征的研究的深入，抗磷脂抗体对抗磷脂综合征的诊断重要性已得到认可和重视，因此对于抗磷脂抗体检测标准化研究显得格外重要。
方法 通过研读近年来关于抗磷脂抗体检测相关文献以及相关共识，对标准化现状进行归纳总结。
结果 不同厂家试剂盒检测结果可能存在差异，这种情况不利于医生针对抗磷脂综合征的严重程度的诊断、用药指导、预后判断等，因此，实现抗磷脂抗体检测的标准化显得十分重要。
结论 随着检测技术的发展，新兴的化学发光等自动化检测方法提高了抗磷脂抗体检测的精密性和可重复性，在一定程度上为国内抗磷脂抗体检测的标准化提供了助力。

PU-2985

Effects of meropenem combined with moxifloxacin on clinicalphenotype, pulmonary function and systemic inflammation in patientswith COPD

Meng Huang
The Affiliated Hospital of Qingdao University

This paper discusses the effect of meropenem combined with moxifloxacin on COPD patients with infectious pneumonia. The patients in the control group were treated with moxifloxacin on the basis of routine treatment and empirical anti infection treatment, and the patients in the observation group were treated with meropenem and moxifloxacin on the basis of routine treatment and empirical anti infection treatment. The results showed that the clinical effect of the observation group was better than that of the control group ($P < 0.05$). The recovery time of body temperature, leukocyte count, rales and cough in the observation group were shorter than those in the control group ($P < 0.05$). The clearance rate of pathogenic bacteria in the observation group was higher than that in the control group. There was no significant difference in the levels of PCT, TNF-a and hs CRP between the two groups before and after treatment ($P > 0.05$). There

was no significant difference in the incidence ofadverse reactions between the two groups. Meropenem combined with moxifloxacin is effective in the treatment of COPD patients with infectious pneumonia. It can effectively shorten the time for clinical symptoms to return to normal / disappear, improve the clearance rate of pathogenic bacteria, improve lung function, reduce inflammatory reaction, and has high safety.PCT is a kind of glycoprotein without hormone activity. The level of serum PCT in normal people is very low. The level of serum PCT in patients with acute and chronic pneumonia is high, and it is positively correlated with inflammatory response . TNF-α is a kind of cytokine which can secrete various biological effects through monocyte macrophage. It can promote the expression of other inflammatory factors and cause systemic inflammatory response . Hs-CRP is a kind of non glycosylated polymer protein secreted by hepatocytes after being stimulated by IL-6 and other related cytokines during acute inflammatory reaction. The results showed that PCT, TNF-α, hs CRP in the observation group were lower than those in the control group, suggesting that moxifloxacin combined with meropenem can effectively reduce the inflammatory response of COPD patients with infectious pneumonia. The results of this study also showed that there was no difference in the incidence of adverse reactions between the two groups, indicating that moxifloxacin combined with meropenem did not increase the incidence of adverse reactions in COPD patients with infectious pneumonia.Key words: Chronic obstructive pulmonary disease; Bacterial; Meropenem; Moxifloxacin

PU-2986

邻苯三酚红钼络合法与双缩脲比色法测定胸腹水蛋白的比较

陈炜钢、裴银桃、孔莉、童兰庭、张露、夏慧、王建平、缪卫华
南京医科大学第二附属医院

目的 对邻苯三酚红钼络合比色法测定胸腹水蛋白方法进行评价。
方法 收集 130 例胸腹水标本，采用邻苯三酚红钼络合比色法检测体系：检测 M（罗氏仪器 Modular P 模块生化分析系统和德赛邻苯三酚红钼络合试剂及校准品）和 3 种双缩脲比色法检测体系：检测 C（罗氏仪器 Modular P 模块生化分析系统和配套双缩脲试剂及校准品）、检测 E（罗氏仪器 Cobas 602 生化分析系统和配套双缩脲试剂及校准品）和检测 P（西门子仪器 Dimension® EXL™ 综合化学分析系统和配套双缩脲试剂及校准品）测定胸腹水蛋白。共 520 个数据，采用单因素多水平方差分析的两两比较的 Games-Howell 检验；正态分布数据分别采用 Pearson 相关、非正态分布数据采用 Spearman 相关分析。偏倚分析采用根据回归方程分别计算 3 种不同的检测体系在 25g/L 的浓度的相对偏差及相对偏差的 95%可信区间，并以相对偏差和 95%可信区间作为评价目标。
结果 检测 M 和 3 种双缩脲比色法检测体系（检测 C、检测 E 和检测 P）的测定结果进行配对 T 检验．P=0.000，表示检测有显著差异；相关性分析结果显示，邻苯三酚红钼络合法测定值与 3 种双缩脲比色法测定值显著相关，检测 C、检测 E 和检测 P 与检测 M 的相关系数分别为 0.687、0.599、0.863；相关性检验的概率 P 都为 0.000。其值小于 0.05，说明存在一定的相关性；邻苯三酚红钼络合法与 3 种双缩脲比色法在总蛋白为 25g/L 处的相对偏倚分别为：33.1%、33.3%和 40.4%。
结论 邻苯三酚红钼络合比色法测定值与 3 种双缩脲比色法测定值之间虽然有较好的相关性，其测定值普遍比双缩脲比色法测定值低，且配对检验有显著差异，因此要引起临床重视。

PU-2987

院内三年来 POCT 比对结果

单洪丽、孙瑞营、续薇
吉林大学第一医院

目的 为了进一步加强了医学检验的质量管理，保证临床检验项目的技术规范与检验结果的准确度、一致性，提高检验队伍的整体专业水平及全院 POCT 检验的准确度和规范性。
方法 自 2018 年起每年两次开展 POCT 的比对工作。比对按照 CNAS-CL02《认可准则》实验室间比对（5.6.3）的要求。临床采集患者标本后立即进行测定并记录结果，同时采集患者同侧的静脉血送至检验科，申请比对条码后由检验科进行检测。比对结束后由各科室 POCT 管理员打印比对报告单，将检测结果和 POCT 仪器记录结果，填写比对记录后送至中心进行评价，由医务部备案，2020 年简化流程，借助信息化软件汇总相关数据。
结果 截止到目前共计进行五次 POCT 比对，参加比对的科室 57 个，检测标本 5418 份（血糖 4832 份、血气分析 503 份、HCG 25 份），血糖项目参加比对仪器共 908 台次，一次性符合率 100%为 241 台次（26.54%），一次性符合率 80%为 142 台次（15.64％），校准后一次性符合率 100%为 136 台次（14.98%），校准后一次性符合率 80%为 124 台次（13.66%）；血气分析项目参加比对仪器共 83 台次，均合格；HCG 项目参加比对仪器共 1 台，均合格；
结论 经过五轮比对后，目前 POCT 仪器的动态管理及时有效，随时追踪仪器使用情况，同时保证了 POCT 设备的检测质量，使院内 POCT 设备能够有效利用。

PU-2988

Association between ICAM-1 level and weight loss: a review and meta-analysis

陈曦、王清、黄猛、田清武
青岛大学附属医院

Recently, several pilot studies already investigated potential association between ICAM-1 and weight, but the findings have been inconsistent. It is possible that a single study may have a relatively inadequate sample size to draw a definite conclusion, and different types of study populations, study design or duration of intervention obviously may also contribute to the inconsistent Results

Given these inconsistencies, we conducted a comprehensive meta-analysis of all eligible studies to clarify the association between ICAM-1 and weight, in order to provide evidence for further experimental and clinical studies, to understand the role of ICAM-1 in weight loss and to assess and predict the effect of weight loss through ICAM-1.

PU-2989

差值校验在临床医学实验室中的应用

朱晶、邵文琦、王蓓丽、郭玮
复旦大学附属中山医院

目的 研究差值校验在临床医学实验室中的应用。
方法 围绕差值校验的发展历史、参数选择、在临床医学实验室质量控制和检验报告自动审核中的应用价值进行综述。

结果 差值校验的如今临床实验室应用了多种质量控制方案以监控分析前中后各阶段可能发生的检测误差，尤其在分析前阶段。与传统室内质量控制方案相比，基于患者数据的质量控制方案拥有实时监控、克服质控品基质效应、没有额外检测成本等特点，已在临床医学实验室中得到越来越多的应用。自上世纪 60 年代发展至今的差值校验，就是其中一种非常经典的基于患者数据的质量控制方法。此外在临床医学实验室的检验报告自动审核系统中，差值校验也作为一类重要的审核规则用于拦截变化异常的检验报告提交人工审核。
结论 差值校验可用于识别实验室检测各阶段中可能发生的错误，以及识别和监测疾病显著变化。尽管差值校验在实验室医学中得到了广泛的应用，但目前明确支持其有效性的研究数据并不够充分。临床实验室需要通过选择，实施，监控来谨慎均衡地对差值校验报警采取措施，已达到更好的实际应用效果。

PU-2990

一对分别携带倒位染色体夫妻的遗传学分析

伍仙
湖南中医药高等专科学校附属第一医院（湖南省直中医医院）

目的 对婚后自然流产一次的夫妻外周血和流产组织进行遗传学检测，探讨染色体倒位对生育后代的影响。
方法 双方行外周血淋巴细胞培养，G 显带及 C 显带后分析妻子的外周血染色体核型；利用 G 显带及荧光原位杂交(fluorescence in situ hybridization,FISH)技术分析丈夫外周血染色体核型；高通量测序技术检测流产组织。
结果 妻子染色体核型确定为 46，XX，inv(9)(p12q13)；丈夫染色体核型确定为 46，XY，inv(7)(q21.2q32)；流产胚胎组织结果显示为 14 号染色体和 22 号染色体三体。
结论 染色体倒位携带者生育染色体病患儿的风险，需要从倒位的类型和倒位染色体以及倒位片段进行综合分析，合理进行遗传咨询，指导生育。

PU-2991

IL-6 和 CRP 预测新型冠状病毒肺炎严重程度的 Meta 分析

倪艺芸
永州市中心医院

目的 探讨白介素-6（IL-6）和 C 反应蛋白（CRP）预测新型冠状病毒肺炎（COVID-19）严重程度的临床价值。
方法 计算机检索 PubMed、Web of Science、Scopus、Embase、中国知网（CNKI）、万方数据知识服务平台（Wanfang Data）、维普数据库（VIP）及中国生物医学文献数据库（CBM），搜集以 COVID-19 为主题的相关研究，检索时间为 2019-12-01 至 2021-01-16，由两名研究人员独立筛选文献、提取资料，采用 RevMan5.4 软件进行 Meta 分析。
结果 共纳入 18 篇文献，共计 4286 例 COVID-19 患者，其中轻症组 2662 例，重症组 1624 例。与轻症组比较，重症组 IL-6 水平显著高于轻症组患者，差异有统计学意义（SMD=0.92，95%CI：0.65~1.18，P<0.00001），重症组 CRP 水平也显著高于轻症组患者，差异有统计学意义（SMD=1.47，95%CI：1.03~1.91，P<0.00001）。
结论 IL-6 和 CRP 水平的升高与 COVID-19 的严重程度呈正相关，可作为临床 COVID-19 患者风险分层的炎症指标，为临床治疗提供有意义的依据。

PU-2992

定点医院输血科救治 COVID-19 患者防控感染实践

秦莹[1]、林国跃*[1]、段丽[1]、木尼热.库尔班[1]、蔺志强[1]、付玉华[2]、李菲[3]、陈苒[4]、邓茜[5]
1. 新疆医科大学第八附属医院(新疆新冠肺炎医疗救治定点医院) 输血科
2. 新疆维吾尔自治区儿童医院输血科
3. 新疆维吾尔自治区人民医院输血科
4. 新疆维吾尔自治区第三人民医院输血科
5. 新疆维吾尔自治区第八人民医院检验科

目的 总结定点医院输血科在保障新冠肺炎救治 COVID-19 中的防控经验。
方法 通过回顾性总结和统计分析新冠疫情期间输血科创新性防控做法和一些有益经验探索。
结果 明确了定点医院输血科采用三级安全防护措施，要加强输血科人员院感再培训和日常生活管控，多层次检查督导实验室生物安全，严格规定特殊疫情取血流程，严把进入输血科物品和工作环境消毒关、检测标本保存监管及废弃物处置关， 确保输血科新冠感染防控工作安全有效。
结论 定点医院输血科为防范新冠病毒高度传染保证绝对安全，应重点把好血液标本关、个人接触关、环境消毒关、制度流程关，可避免感染风险和职业暴露。

PU-2993

天然抗肿瘤化合物的筛选及其抗肿瘤机制的研究

高丹丹、续薇
吉林大学第一医院

目的 本研究以人宫颈癌 HeLa 细胞为研究对象，从来源于植物内生真菌 Phomopsis 的六种化合物中筛选出具有较强抗肿瘤活性的天然化合物并研究其抗肿瘤机制。
方法 MTT 方法检测来源于内生真菌 Phomopsis 中六种化合物在不同时间、不同剂量下对人宫颈癌 HeLa 细胞和人胃癌 MGC803 细胞的增殖抑制能力，从六种化合物中筛选出最佳抗肿瘤活性的化合物 HX06，即 Dicerandrol B。Annexin V-FITC /PI 染色法流式细胞仪检测 Dicerandrol B 作用的 HeLa 细胞发生凋亡的细胞百分比，用 Western blot 检测与细胞凋亡相关的蛋白质 cleaved-PARP 的表达水平。
结果 与其他五种化合物相比，Dicerandrol B（HX06）具有较强的抗肿瘤活性且对人良性乳腺上皮细胞增殖抑制能力较弱。用 Dicerandrol B 处理 HeLa 细胞 24h，48h 和 96h，其 IC50 值分别为 7.13μg/mL，3.00μg/mL 和 1.84μg/mL，Dicerandrol B 抑制 HeLa 细胞的增殖呈现剂量依赖性和时间依赖性。流式结果显示 Dicerandrol B 处理 HeLa 细胞 24h，3μg/mL 组细胞凋亡发生率为 30.9％，5μg/mL 组细胞凋亡发生率为 45％，与对照组相比，差异有统计学意义（$p<0.01$）。同时 Dicerandrol B 引起 HeLa 细胞中 cleaved-PARP 的表达水平上调，说明 HeLa 细胞在 Dicerandrol B 的作用下发生了细胞凋亡。
结论 从内生真菌 Phomopsis 代谢产物中筛选到具有较强的抑制 HeLa 细胞增殖能力、呈现剂量和时间依赖性、同时对人乳腺上皮细胞 MCF10A 无明显细胞毒性的 Dicerandrol B。 Dicerandrol B 抑制 HeLa 细胞增殖的机制是诱导 HeLa 细胞发生了细胞凋亡。

PU-2994

临床乙肝两对半五项报告自动审核的优化与验证

朱晶、周佳烨、邵文琦、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 探讨临床免疫乙肝两对半自动审核系统建立后的优化与验证。
方法 选取 2018 年至 2020 年经自动审核系统判断的临床免疫乙肝两对半五项报告，从两对半异常模式、灰区复检、HBsAg 与 HBcAb 定性结果 Delta check、HBsAb 定量结果根据大数据回顾分析优化 Delta check 范围和时间范围进行规则优化。以人工审核结果为标准，比较自动审核系统优化前后的性能参数。
结果 临床乙肝两对半五项报告自动审核系统通过率从 82.9%提高至 89.6%，灵敏度和特异性分别从 79.5%和 68.0%提高至 83.6%和 79.6%，阳性预期值和阴性预期值分别从为 74.9%和 83.2%提高至 89.7%和 93.2%。自动审核系统与两位实验室高年报告审核人员判断的一致性达到 98.68%。统计 kappa 分析结果为 0.99（P<0.001）。
结论 临床乙肝两对半五项报告自动审核系统优化后的性能参数显著提升，灵敏度和特异性更佳，同时与人工审核判断的一致性更高。使工作人员有更多的时间关注在疑难报告上。有效提高分析后环节的工作效率，进一步确保检验报告的准确性。

PU-2995

胎儿 9 号染色体臂间倒位与母体血清学筛查异常相关性研究

谢小雷
清远市人民医院

目的 研究胎儿 9 号染色体臂间倒位(inv9)与母体血清学筛查异常相关性。
方法 收集 2014 年 4 月至 2019 年 5 月来我院产前诊断中心因产前筛查高风险、高龄等进行产前诊断的孕妇病例及其妊娠结局数据。
结果 1865 例产前诊断样本中共检出 31 例 inv9 胎儿，检出率为 1.66%(31/1865)。87.10%(27/31)inv9 胎儿进行了血清学筛查，其中血清学筛查假阳性 13 例，临界风险 4 例，2 例单项指标异常，血清学筛查异常比例 70.37%(19/27)。free β-hCG 生化指标异常在 inv9 胎儿孕妇中所占比例最高达 52.63%(10/19)，其次为 PAPPA 占 26.32%(5/19)。Inv9 胎儿中，母体血清学筛查假阳性率明显高于同期人群筛查假阳性率(48.15%比 4.35%)，两者具有显著性差异(c2 =123.71，P <0.0001)。
结论 胎儿 9 号染色体臂间倒位通过影响母体血液中 free β-hCG 及 PAPPA 含量导致母体血清学筛查异常。

PU-2996

利用生物信息学技术初步筛选肺癌诊疗的潜在生物标记物

龙婷婷、陈月梅、江虹
四川大学华西医院

目的 利用生物信息学方法分析肺癌组织与正常组织之间差异基因的表达，筛选并评价肺癌相关分子标记物，挖掘潜在的肺癌诊疗靶标。
方法 提取 GEO 数据中肺癌相关的基因表达谱 (GSE19804)，利用 R 语言分析原始数据，经标准化处理后统计肺癌组织与正常组织之间基因在表达水平上的平均改变倍数（FC），满足|Log2 (FC)

|≥1 为差异表达基因（Differentially Expressed Genes，DEGs）。采用 DAVID 软件进行基因本体（GO）分析和京都基因和基因组百科全书（KEGG）信号通路分析。蛋白互作网络由 STRING 软件生成，并由 Cytoscape 软件构建蛋白互作网络，同时提取网络中的主要功能模块及关键蛋白进一步分析评价。

结果 通过生物信息学分析获得肺癌与正常组织间有 1970 个 DEGs，以下调基因为主，其中|FC|最大的是 AGER。这些 DEGs 涉及细胞增殖、粘附及迁移等多种生物学过程，并在细胞外基质受体相互作用、PI3K-Akt 信号通路等 77 条信号通路中存在明显富集。从 PPI 互作网络中挖掘出包括 EGFR 在内的 1770 个关键蛋白，涉及的主要功能模块包括趋化因子信号通路、细胞周期及癌症信号通路模块等。其中排名前十的关键节点分子有 EGFR，JUN ，FOS，IL6，MYC，MMP9，CDK1，CDH1，FYN，FGF2。

结论 通过生物信息学方法对肺癌差异基因进行分析，有助于增强对肺癌发生发展过程的认识。通过筛选肺癌关键基因、分子标记物（如 AGER 和 EGFR）及信号通路，将可能为肺癌的诊断与治疗提供线索。

PU-2997

Effects of co-infection with Clonorchiasis Sinensis on sex hormone levels in male patients with chronic hepatitis B

Huimin Dong、mei shang、Yuan Liao、Minqi Luo、Wenya Chen
Department of Clinical Laboratory, Third Affiliated Hospital, Sun Yat-Sen University

Objective The effects of co-infection with Clonochiasis Sinensis on sex hormone levels in male patients with chronic hepatitis B were statistically analyzed to explore the interaction between co-infection and sex hormone levels.

Methods Select 27 healthy male subjects,30 male patients mono-infected with Clonorichis Sinensis alone,18 male patients with post-hepatitis cirrhosis co-infected with Clonorichis Sinensis, 25 male patients with chronic hepatitis B co-infected with Clonorichis Sinensis,27 male patients with post-hepatitis cirrhosis with hepatitis B,and 18 male patients with hepatitis B alone. Measure their levels of sex hormone.

Results the levels of E2 in patients with post-hepatitis cirrhosis co-infected with Clonorichis Sinensis increased, while the levels of T and FSH decreased , compared with those in patients with hepatitis cirrhosis, and the difference were statistically significant（P<0.05)； the levels of E2 and T in patients with hepatitis B co-infected with Clonorichis Sinensis increased , compared with those in patients with hepatitis B alone, and the difference were statistically significant（P<0.05)；the levels of LH、PRL、E2、T、FSH and P in patients with post-hepatitis cirrhosis increased, compared with those in healthy male subjects; In contrast, the levels of PRL,E2 and T in patients with HBV decreased, compared with those in healthy male subjects; there was no statistically difference in the levels of LH、PRL、E2、T、FSH and P between the group of patients with only Clonorichis Sinensis and the healthy group.

Conclusion Co-infection with Clonorchiasis Sinensis would further aggravate sex hormone disorder in hepatitis B patients,whether in the chronic hepatitis stage nor the cirrhosis stage,the results of this study can guide the clinical medication and the selection of the correct treatment plan to prevent and control the diseases.

PU-2998

CircRNA 作为分子海绵在肿瘤发生发展中的研究进展

朱艺
清远市人民医院

环状 RNA （circular RNA,circRNA)是内源性非编码 RNA(non-coding RNA,ncRNA)中的一类，普遍存在于真核转录组中，与基因表达调控密切相关。circRNA 作为分子海绵是对传统基因表达调控方式的补充，其在肿瘤发生发展中的机制研究已成为热点，本文将对 circRNA 作为 miRNA 海绵在肿瘤研究中的现状、进展及前景进行总结。

PU-2999

柳州地区儿童过敏性鼻炎患者常见过敏原 sIgE 检测分析

戴钰
柳州市妇幼保健院

目的 分析柳州地区过敏性鼻炎患儿常见过敏原分布特征，为合理防治过敏性鼻炎提供依据。
方法 采用酶联免疫捕获法，对 2019 年 3 月至 2021 年 4 月间在柳州市妇幼保健院进行过敏原特异性免疫球蛋白 E（sIgE）筛查的 532 例过敏性鼻炎患者进行血清学检测，其中，男性 337 例，女性 195 例，按年龄将受试患者分为 0~2 岁（115 例）、3~5 岁 （233 例）、6~≤15 岁 （184 例）。采用 SPSS 25.0 分析受试者年龄、性别以及季节等因素对过敏原分布特征的影响。
结果 最常见的过敏原是屋尘螨，阳性率均为 63.72%（339/532），其次是粉尘螨、鸡蛋、牛奶、屋尘。受试者中过敏原组合数量以 2~3 种最为常见（44.17%，235/532）。男性患儿最常见的过敏原为屋尘螨 64.09%， 216/337；女性患儿最常见的过敏原有两种，分别是屋尘螨/粉尘螨,63.08%，123/195）。性别在过敏原种类中无显著差异（P＞0.05）。吸入性过敏原（如尘螨类）在 6~15 岁组阳性率较高，而食物性过敏原（如鸡蛋、牛奶）在 0~2 岁组阳性率较高，差异有统计学意义（P＜0.05）。尘螨类（粉尘螨、屋尘螨）过敏原在夏季阳性率较高，屋尘、虾阳性率在冬季最低，而牛奶阳性率则在秋季最高，虾阳性率在冬季最低，差异有统计学意义（P＜0.05）。
结论 柳州地区过敏性鼻炎患者最常见过敏原是屋尘螨，吸入性和食物性过敏原是导致过敏性疾病发生的重要原因，在不同的年龄段及不同季节均存在差异，为柳州地区过敏性鼻炎患者实施个体化干预策略提供客观证据，具有重要价值。

PU-3000

急性早幼粒细胞白血病初诊检测结果的分析

黄美群、贾雪、张敏、张嘉琳
广东省人民医院

目的 探讨急性早幼粒细胞白血病（APL）初诊时检测结果的特点。
方法 收集 70 例急性早幼粒细胞白血病患者初诊时检测结果，并应用 SPSS19.0 软件对其进行统计学分析。
结果 70 例患者中白细胞< 4.0×109/L 38 例（54.3%）、中位数 1.45×109/L, 血红蛋白<99g/L 51 例(72.9%)、中位数 69.0g/L ,血小板 7－50×109/L 51 例(72.9%)、中位数 26.0×109/L。D-二聚体 351－1000 ug/L30 例(42.9%),中位数 761ug/L，1001－3000 ug/L 22 例(31.4%),中位数 1618ug/L 。单核细胞比值 0.11－0.857 36 例(51.4%)、中位数 0.225。通过骨髓细胞检查，发现异常早幼粒细胞

白血病骨髓增生活跃，其胞浆内充满紫红色颗粒及柴束样奥氏小体。59 例患者中细胞免疫表型 $CD33^+$, $CD13^+$为 46 例（78.0%），MPO +为 44 例（74.6%）。
结论 检测结果表明 70 例急性早幼粒细胞白血病（APL）初诊患者的外周血中白细胞、血红蛋白、血小板偏低，且单核细胞以增高为主，D-二聚体检查结果均增高。因此，对于初诊为外周血细胞偏低的急性早幼粒细胞白血病患者，必须借助于显微镜进行细胞形态和特征的分析,才能准确无误地发出报告。

PU-3001

POCT 信息化管理系统在医院中的建设和应用

姚瀚鑫
吉林大学第一医院

目的 在当前新型冠状病毒疫情下，为应对快速检测的需求，医院各临床科室不同类型的 POCT 设备，特别是发热门诊，隔离病房等中的 POCT 设备被大量应用，由于操作人员的复杂化，试剂耗材的多元化，各类型 POCT 设备厂家繁多导致质量标准和操作标准不统一，因此需要 POCT 信息化管理系统规范医院 POCT 设备的应用和管理。
方法 依据吉林大学第一医院临床质控（检验）中心的要求，以检验科为管理中心，结合 POCT 人员、设备等特点制定质量指标，构建符合本地化的医院 POCT 信息化管理系统。
结果 对医院各临床科室不同类型的 POCT 设备实现了智能化、标准化和规范化管理，使 POCT 设备为临床诊疗提供优质的服务。
结论 POCT 信息化管理系统是 POCT 设备一体化管理的有效手段，特别在疫情下 POCT 设备诸如快速核酸检测设备、床旁血气分析仪、床旁免疫分析仪、便携式生化分析仪、床旁快速凝血分析仪被大量应用，信息化、智能化、标准化的管理系统值得推广应用，特别是在 POCT 信息信息系统中应用检测结果自动审核，危急值或异常值提示，报告推送等功能，能大大提高检测效率，异常状态识别情况，及时采取临床干预措施。

PU-3002

不同方法联合检测在梅毒血清学筛查中的应用

杨静
天津市泰达医院

目的 探讨梅毒血清学的不同方法联合检测在两个不同年龄段人群中的应用价值。
方法 使用 CLIA 法对两个不同年龄段的人群进行梅毒血清学的初筛试验，阳性标本使用 TPPA 法和 TRUST 法复检，对于检测结果不一致的血清标本使用蛋白印记法确认。
结果 1. TPPA 法和 TRUST 法与 CLIA 法的阳性符合率，≤60 岁人群为 94.29%和 50.17%， >60 岁人群为 85.00%和 25.00%。TPPA 与 CLIA 两种检测方法结果的差异，主要集中在 CLIA 检测系统 s/co＜5 的阳性低值区。2. 在 CLIA 检测系统 s/co 的阳性低值区，当 CLIA 检测系统 1≤s/co＜5，且 TPPA 为阳性时，≤60 岁人群，与 WB 方法的符合率为 96.42%，＞60 人群为 86.66%；当 CLIA 检测系统 5≤s/co＜10 且 TPPA 为阳性时，≤60 岁人群与 WB 方法的符合率为 98.15%，＞60 人群为 96.29%。
结论 三种方法联合检测有效的减少了检测结果的漏诊和误诊，但对于 CLIA 法检测系统 s/co＜5 的阳性低值区标本应结合临床资料分析，如有必要须做确诊试验。

PU-3003

168 例念珠菌血流感染患者的预后相关危险因素分析

赵越、叶龙、凌勇、张莉澉
广东省人民医院

目的 探讨临床念珠菌血流感染患者的预后相关危险因素，为防控及改善念珠菌血流感染患者预后情况提供依据。

方法 回顾性分析 2017 年 1 月-2019 年 12 月广东省某三级甲等医院所确诊的念珠菌血流感染病例 168 例，查询相关病例的基础资料（年龄、性别、住院时间、基础疾病、入住科室、病原菌分离等）、临床病程诊疗记录（住院期间侵入性操作、抗菌药物使用情况等）及患者预后情况等信息，并对数据整理分析。同时根据患者预后，将纳入研究的病例分为两组：即生存组（81 例）与死亡组（87 例），并对两组间相关危险因素进行比较分析。

结果 168 例患者主要分布于重症监护室（81 例）、血液科（30 例）、内科（23 例）及外科（22 例）等科室，以白念珠菌（71 例）、热带念珠菌（45 例）及近平滑念珠菌（30 例）为主。患者病死率为 51.79%，死亡组患者的平均年龄要高于生存组（t 值=4.459，P 值=0.000）。单因素分析显示：患有白血病、恶性肿瘤，入住过重症监护室，存在机械通气、中心静脉插管、留置尿管等侵入性操作可能会加大患者死亡风险,应用抗真菌药物可能会降低患者病死率。多因素 logistic 回归分析显示：患者有留置过尿管（OR 值=10.847,95%CI:3.175-37.061，P 值=0.000）是影响患者预后的重要危险因素，尽早应用抗真菌药物治疗（OR 值=0.307,95%CI:0.132-0.714，P 值=0.006）对患者生存率有所改善。

结论 念珠菌血流感染病死率高，影响患者预后的各种危险因素需要引起临床重视。在诊疗过程中，需尽早完善病原学送检，加强环境卫生学监测，强化对各使用级别抗菌药物监管，做到精准用药，以改善患者预后，降低病死风险。

PU-3004

血清样本经不同处理后对胃泌素释放肽前体稳定性的影响

万鹏、渠文涛
安图生物工程股份有限公司

目的 胃泌素释放肽前体（ProGRP）是小细胞肺癌（SCLC）的肿瘤标志物；目前国内外均有用于 ProGRP 检测的试剂盒。血清中存在降解 ProGRP 的酶，且 ProGRP 蛋白上不同抗原结构位点降解的先后顺序也不一致，不同厂家生产的试剂盒因为针对检测 ProGRP 抗原结构位点的不同，导致样本保存的时间不同；时间短的，样本放置 2-8℃一天之后降幅就会超过 10%，长的可在 2-8℃保存三天。本文主要是研究了血清样本经过不同处理后，ProGRP 降解速率的变化。

方法 取一份血清样本，分为 A,B,C,D 等量 4 份，A 不经过任何处理，B 经过去激素处理，C 在 56℃灭活半小时，D 添加 2%海藻糖。分别在 4 份处理后的血清样本中添加等量的 ProGRP 标准品。将 4 份样本放到 2-8℃保存，分别在第 0 天、第 1 天、第 3 天、第 5 天、第 6 天进行检测。其中试剂盒采用“郑州安图生物工程股份有限公司”厂家的。

结果 A 不经过任何处理的样本可在 2-8℃保存 3 天，降幅在 10%以内；B 经过去激素处理的样本在 2-8℃一天降幅就超过了 10%；C 经过灭活的样本在 2-8℃保存 6 天之后样本降幅依然保持在 10%以内；D 添加海藻糖的样本，2-8℃可保存 5 天。

结论 经过去激素处理后的样本加速了 ProGRP 的降解速度；血清样本灭活或者在血清样本中添加海藻糖可以降低 ProGRP 的降解速度。

PU-3005

实验室自动化与信息管理系统的建立和性能优化

廖建枫、刘胜男、张喜钦、李靖华、张娟、顾兵
广东省人民医院

目的 探讨实验室自动化与信息化管理系统对提升实验室检验工作效率的作用。
方法 收集广东省人民医院检验科 2019 年 6 月 9 号-6 月 15 号 Remisol 信息管理系统优化前、2019 年 12 月 8 号-12 月 14 号优化后生化、免疫样本的周转数据和自动审核的运行数据，与 2018 年 9 月自动质控启用前、2019 年 12 月自动质控启用后的质控数据分析差异。
结果（1）流水线和信息管理系统优化后平均检测周期降低了 34min；（2）优化后样本前处理人员减少 50%，仪器操作人员减少 33%；（3）应用自动质控后可使仪器提前 1 小时进入工作状态，且 21 个自动化免疫项目中 17 个项目的 CV 对比和靶值偏差的评价提高；（4）应用流水线和信息管理系统优化后自动审核总通过率提高 9%；（5）应用流水线和信息管理系统优化后减少检验人员与标本直接接触，降低检验人接触传染性阳性标本的风险。
结论 实验室自动化与信息化管理系统优化后明显提升了实验室检验工作的效率，突出优化流程的优势，实验室在检测周期、样本采集、检测效率上明显提高，质控评价也有所提升。

PU-3006

20 项常规生化指标应用自上而下法计算测量不确定度的评定报告

张娟、禄梦笛、陈秀贤
广东省人民医院

目的 探讨自上而下法评估测量不确定度在临床常规生化检验中的应用。
方法 收集本室 2019 年质控批号稳定至少 3 个月的 IQC 数据和国家卫生健康委临床检验中心 2017-2019 年的 EQA 回报结果，采用自上而下法评定 20 项临床常规生化指标的测量不确定度。
结果 CA、P、GLU、UREA、URIC、TC、TG、TBIL、ALT、AST、ALP、AMY、CK、LDH、GGT、MG、FE、HBDH、CHE19 项常规生化指标低水平质控品浓度的合成相对扩展标准不确定度分别为 4.91%，7.10%，6.94%，7.88%，6.45%，6.96%，7.73%，7.86%，8.96%，6.69%，17.52%，8.10%，8.44%，9.99%，6.11%，9.53%，9.56%，10.02%，10.40%；其高水平质控品浓度的合成相对扩展标准不确定度分别为 3.83%，6.19%，5.90%，5.79%，5.90%，6.22%，6.82%，8.41%，8.23%，6.17%，14.58%，6.39%，8.07%，8.56%，5.35%，7.12%，7.06%，9.85%，11.99%均小于 WS/T 403-2012《临床生物化学检验常规项目分析质量指标》要求的目标扩展不确定度；DBIL 低高两个质控水平的合成相对扩展标准不确定度分别为 11.41%和 9.06%，均小于基于生物学变异的适当质量规范。其中批间不精密度与相对扩展标准不确定度呈极强相关（r=0.857，P<0.001），偏移呈中度相关（r=0.528，P<0.001），批间不精密度分量在大部分生化指标中呈主要分量趋势。但 ALT、AMY、CK、FE（高浓度水平）、HBDH（高浓度水平）则受偏移分量影响相对较大。
结论 应用自上而下法评定测量不确定度适用于临床常规生化检验项目；且不同项目不同分量来源的主要占比不同，为实验室质量管理提供了改进方向。

PU-3007

探讨三种不同评定方法在临床生化检验测量不确定度中的应用价值

姚亚男、张娟、顾兵
广东省人民医院

目的 探讨三种不同评定方法在常规生化检验测量不确定度中的应用价值。
方法 采用依据 Nordtest 准则的自上而下法（方法 1）、澳大利亚临床生物化学家协会(AACB)建议方法（方法 2）以及国内文献参考法（方法 3）三种不同的评定方法对 26 项常规生化指标进行测量不确定度的评定，对三种方法的评定结果进行差异性和相关性分析。分析其不同分量来源与合成的相对标准不确定度之间的相关性并单独比较 26 项生化指标的主要不确定度分量。
结果 三种方法评定结果间差异无统计学意义（P>0.05），并且显著相关（r1,2=0.895，P<0.001；r1,3=0.988，P<0.001；r2,3=0.885，P<0.001）。在 Tea 达标率的比较上，三种方法没有差异，均为 100%；在 1/2Tea 达标率比较上，国内文献参考法与 AACB 法有统计学意义（Bonferroni 校正，P<0.0167）；1/3Tea 达标率比较无统计学意义（P>0.05）。批间不精密度分量和合成相对标准不确定度呈显著相关性（r>0.8，P<0.001）。26 项生化指标不确定度分量的分布图显示大部分生化指标的 CVB 最大。其中 NA 和 CREA 则是以 CVBias 为主，分别为 1.27%，1.36%；6.34%，2.96%。CK 和 ALT 的 CVCal 分别达到 5.17%和 3.55%。三个指标 CL、FE、AMY 则出现两个浓度水平不一致的结果。
结论 三种评定方法结果无差异并显著相关，AACB 法的质量目标达标率最高。批间不精密度是三种方法中最主要的不确定度分量，其次是偏移分量。以单个的指标的不确定度分量来看，CVBias 分量是 NA 和 CREA 测量不确定度的主要分量，CVCal 分量则是 CK 和 ALT 测量不确定度的主要分量。

PU-3008

常用抗肿瘤药物对胃泌素释放肽前体检测的干扰

万鹏、渠文涛
安图生物工程股份有限公司

目的 肺癌是目前严重威胁人类健康的一种恶性肿瘤，其发病率及死亡率均居恶性肿瘤之首。其中小细胞肺癌（SCLC）在肺癌中所占的比例约为 15% ～ 25% ，其恶性程度高、发展迅速、转移发生早、预后差，5 年总体生存率小于 10% 。胃泌素释放肽前体（ProGRP）是 SCLC 的肿瘤标志物，本文主要是验证常用抗肿瘤药物对 ProGRP 检测结果的影响。
方法 选用 8 支临床血清样本，混合后浓度为 210pg/ml，分为 16 份；其中 8 份实验样本中添加常用抗肿瘤药物，卡铂、顺铂、环磷酰胺、多西他赛、洛莫司汀、吉非替尼、厄洛替尼、地塞米松，添加浓度分别为 600ug/ml，180ug/ml、500ug/ml、115ug/ml、175ug/ml、250ug/ml、150ug/ml、20ug/ml。对照组 8 份添加等量体积的 PBS 缓冲液，用国产安图生物公司生产的“胃泌素释放肽前体检测试剂盒（磁微粒化学发光法）”进行检测。按照公式“干扰率=（实验结果-对照结果）/对照结果”计算干扰率。
结果 常用抗肿瘤药物卡铂、顺铂、环磷酰胺、多西他赛、洛莫司汀、吉非替尼、厄洛替尼、地塞米松对 ProGRP 检测的干扰率分别为-2.43%、2.14%、3.26%、4.89%、-3.64%、-2.49%、1.35%、0.89%。
结论 常用抗肿瘤药物卡铂、顺铂、环磷酰胺、多西他赛、洛莫司汀、吉非替尼、厄洛替尼、地塞米松对 ProGRP 的干扰率均在±5%之内。

PU-3009

Association of Cardiovascular Risk Burden and Subsequent Poor Cognitive Performance among Older People: the Mediating Role of Brain MRI Measures

Chong Chen
Tianjin Medical University Cancer Institute and Hospital

Our aim was to measure the association between cardiovascular risk profiles and subsequent cognitive performance and to examine whether brain magnetic resonance imaging (MRI) markers modify the relationship. We assessed cardiovascular risk profiles, brain volume and cognitive performance using baseline and 7-year follow-up data from Tianjin Longitudinal Study of Aging in China (n=1360) and the embedded MRI (n=318) studies. Framingham general cardiovascular risk score (FGCRS) was computed using baseline data. Cognition was assessed with a comprehensive test battery at least three times over seven years. Mixed-effect model and structural equation model were used to assess the association between FGCRS, MRI variables and longitudinal cognitive performance. High FGCRS was significantly associated with poor performance in global cognition, and other specific cognitive domains. Low baseline hippocampal volume was significantly associated with cognitive decline for all neuropsychological tests in MRI variables. Low cortical white matter volume at baseline was associated with poor performance in all tests except perceptual speed. Subjects with both small hippocampal and cortical white matter volumes had higher risk of cognitive decline. SEM analyses indicated that the direct path between high FGCRS and poorglobal cognition was significant. Increased hippocampal volume mediated the relationship of FGCRS on global cognition. In conclusion, high cardiovascular risk burden was associated with subsequent poor cognitive performance. Hippocampal volumes loss can mediate the association between FGCRS and global cognition. Cardiovascular risk profiles, as manifested into appropriate brain MRI markers, may be an important tool for identifying subjects at high risk of future dementia.

PU-3010

罗森沙门菌临床菌株的基因组分析及毒力研究

周爱萍、郭建、吴文娟
上海市东方医院同济大学附属东方医院南院

目的 近年来，罗森沙门菌感染呈现上升趋势，但目前关于该血清型的毒力研究尚未见报道。本研究通过对一株临床来源的罗森沙门菌的毒力研究及基因组分析，加深人类对沙门菌致病性的认识，为沙门菌感染的预防和治疗提供依据。
材料和方法 首先利用动物实验和细胞实验，对该菌株的毒力进行评估，随后为了探究其致病机制，本研究对该菌株进行了全基因组测序，测序结果提交 NCBI non-redundant (NR)蛋白数据库进行注释并进行 COG 分析和 KEGG 分析。利用 Genomic Epidemiology (CGE)对基因组进行深入分析。
结果 罗森沙门菌对小鼠的致病性及对 HeLa 细胞的入侵能力弱于鼠伤寒沙门菌。在鼠来源的巨噬细胞 Raw264.7 中罗森沙门菌的存活和复制能力弱于 14028S，但在人来源的巨噬细胞 U937 中，罗森沙门菌的存活和复制能力强于 14028S。基因组分析结果显示该菌株中存在 8 个 SPI（SPI1-6，SPI-8 和 SPI-9）5 个耐药基因(blaTEM-1b, addA1, addA2, tetA, sul3, cmlA1), 25 个移动基因元件(2 T3ss, 1 T6ss, 6 噬菌体和 16 基因岛)。MLST 分型为 ST469 型。
结论 罗森沙门菌对小鼠的致病性弱于鼠伤寒沙门菌，但仍然能够引起小鼠的血流感染。并且对人类的巨噬细胞有较强的适应性。进一步基因组分析发现，虽然罗森沙门菌中缺失了常见的沙门菌毒力因子如 spv 毒力质粒，sodCI 及 spoE 等基因中，但仍然存在 8 个 SPI 及 2 个对致病性非常重要

的 T3SS。对罗森沙门菌毒力及基因组的研究，有利于人类对沙门菌致病机制的认识和沙门菌病的防治。

PU-3011

炎症因子与白血病相关性研究及临床意义探讨

袁媛、曹方方、韩斌、马书丽
青岛大学附属医院

目的 通过检测白血病患者标本中 IL-6、IL-8、IL-10、TNF-α 以及 T 细胞亚群，还有炎症相关检测指标 C-反应蛋白、D-二聚体、降钙素原的变化，并与正常人血液标本进行对比、分析。通过分析以上检测指标与白血病的发生、发展存在的相关性，以探讨其临床意义及应用前景。
方法 分析我院收治的 60 例白血病患者的血液标本, 男 30 例, 女 30 例,平均年龄 42（10～70 岁）, 全部患者均经免疫学及骨髓细胞学确诊，且符合 FAB 分型标准。另收集我院体检中心正常人血液标本 60 例，男 30 例, 女 30 例, 平均年龄 35（23～50 岁），作为对照组。运用西门子 BNP 特定蛋白分析仪测得 CRP 的结果；运用 ACLTOP700 全自动血凝仪检测 D-二聚体的水平；运用罗氏 411 电化学发光全自动免疫分析仪检测降钙素原的变化；运用 ELISA 检测试剂盒检测 IL-6、IL-8、IL-10、TNF-α 细胞因子表达水平；运用贝克曼 FC500 流式细胞术检测以上标本的 CD3、CD4、CD8、CD4/CD8、NK、 CD19 等细胞亚群的变化。
结果 CRP、D-二聚体、PCT 的表达明显高于正常人(P < 0. 01)；且 CD3、CD4、CD8 阳性 T 细胞水平均明显低于正常人(P < 0. 01)；在 MDS、急、慢性白血病及再生障碍性贫血中 IL-6、IL-8、IL-10、TNF-α 均高于正常对照组的水平。
结论 白血病的病程发展与炎症因子及抗炎因子的表达水平存在相关性。说明炎症因子和抗炎因子之间相互作用和动态平衡与白血病的发生、发展密切相关，此研究将有助于发掘白血病的“促炎治疗”策略，使未来开展个体化治疗成为可能。此外，为探讨新的检测手段和新型检测试剂盒的开发奠定了理论基础。

PU-3012

Increased Serum Levels of Complement C1q in Major Depressive Disorder

Qian Yao
Renmin Hospital of Wuhan University

Background The complement system is involved in multiple biological processes including inflammation, synaptic pruning and apoptosis. However, it is not well understood whether peripheral complement C1q levels are altered major depressive disorder (MDD) patients.
Objective This study aimed at assessing serum levels of complement C1q in MDD patients using a cross-sectional, case-control design. Also, the correlations between complement C1q and inflammation and lipid profile in patients with MDD were also assessed.
Methods Serum complement C1q levels were measured by ADVIA 2400 biochemical analyzer in 160 patients with MDD diagnosed using International Classification of Diseases-10 criteria (ICD-10) and were compared with those of 159 healthy controls between January 2017 to May 2019. Then correlation analysis was carried out between the level of serum complement C1q among MDD patients with inflammation and lipid profile.
Results Serum complement C1q levels were higher in MDD patients than in controls (P<0.0001) and the difference between the two groups was small (r=0.239 [0.128 to 0.350]). We found that serum complement C1q concentrations was positively correlated with HAMD-24 score (r=0.234, P=0.003) and log hs-CRP (r=0.334, P<0.001).

Conclusion We found serum complement C1q levels were significantly higher in MDD patients than in controls. The current results suggest that the dysfunction of complement C1q may be involved in the pathophysiology of MDD.

PU-3013

CLSI EP06-A 和 EP06-Ed2 应用于定量测量系统线性验证程序的差别

谢轩波、刘洋洋、单汉明、李晓博
杭州迪安医学检验中心有限公司

目的 以部分项目为例，讨论美国临床和实验室标准协会（CLSI）EP06-Ed2 与 EP06-A 在定量测量程序线性验证应用中的差异。
方法 通过选择接近线性区间上下限的样本，按比例配制 7 例样本，各重复测定 2 次，测定结果分别以 EP06-Ed2 和 EP06-A 的方法进行分析，比较两者的差异。
结果 部分项目的线性区间验证，以 EP06-A 分析视为临床不可接受，但以 EP06-Ed2 分析可被临床接受。
结论 CLSI EP06-Ed2 相对于 EP06-A 等指南，对线性样本浓度选择的要求合理，更符合实际临床使用需求，是值得借鉴的新的定量测量程序线性区间验证指南。

PU-3014

探讨在常规化学项目质量管理中进行 σ 验证的必要性

刘洋洋、李晓博、谢轩波、单汉明
杭州迪安医学检验中心有限公司

目的 通过计算 12 个常规生化项目的 σ 度量值，探讨 σ 验证在临床实验室测量程序评价和个性化 westgard σ 质控规则的应用。
方法 统计 2019 年度杭州迪安医学检验中心卫健委临检中心常规化学项目室间质量评价、正确度评价数据及室内质量控制数据，计算绘制标准化西格玛性能验证图，对 σ 验证未能通过的项目进行测量程序分析性能的评价，对 σ 验证通过项目进行 Westgard σ 质控规则及质控方法性能特征误差检出率，假失控概率的评估。
结果 经两种不同来源偏倚，双水平浓度质控品变异系数的计算，确定每个项目最低 σ 水平，σ≥6（世界一流）包括 CK、AMY、CREA 3 个项目，5≤σ＜6（优秀）无，4≤σ＜5（良好）包括 GLU、TC、NA、K 4 个项目，3≤σ＜4（临界）包括 TP、TG 2 个项目，2≤σ＜3（欠佳）包括 ALT、UREA 2 个项目，σ＜2（不可接受）包括 CA 1 个项目；ALT、UREA、CA 3 个项目年度分析性能验证均通过，σ 验证提示 CA 分析性能为不可接受，ALT、UREA 分析性能欠佳，对应无质控规则可选，应努力改善或更换测量程序；对 σ 验证通过项目进行 Westgard σ 质控规则评估，其中 CK、AMY、CREA 已达到世界一流水平，可选择宽松的质控规则进而降低假失控概率；TP、TC、TG、NA、K 项目误差检出率分别为：0.925、0.940、0.900、0.900、0.977 较评价前得到显著提高，ALT、CREA 项目 σ 值水平较低无可选的质控规则，需更换或改进测量程序，可见基于不同 σ 水平可选择合适的室内质控规则。
结论 σ 验证与测量程序的分析性能评价起到良好的协同作用，对质控方法个性化质控规则的应用起到相应的指导作用。

PU-3015

阿尔茨海默症患者血清中核酸氧化损伤产物与抗氧化物质硒、维生素 A 和维生素 E 的质谱检测及相关性研究

房敬尧、牛文彦
天津医科大学朱宪彝纪念医院

目的 研究显示 DNA 氧化损伤产物 8-氧化脱氧鸟苷(8-oxo-7,8-dihydro- deoxyguanosine,8-oxo-dGsn) 和 RNA 氧化 产物 8- 氧化鸟苷（8-oxo-7,8- dihydroguanosin，8-oxo-Gsn)与阿尔茨海默症（Alzheimer's disease，AD）发病的密切相关。具有抗氧化功能的维生素 A（Vit A）和维生素 E（Vit E），硒元素（Se）被证明对 AD 患者的氧化损伤具有一定的保护作用。然而尚未有研究对 AD 患者血清中 8-oxo-Gsn、8-oxo-dGsn 和 Vit A、Vit E、Se 的关系进行探讨，本研究将综合比较 AD 患者与同年龄层表观健康对照组血清中上述物质，对上述氧化应激相关物质的差异性与相关性进行探讨。

方法 选取 55 例 AD 患者，同时选取 64 例年龄分层相近，性别匹配且生化指标正常的表观健康人群，分别采用高效液相色谱串联质谱（HPLC-MS/MS）对血清中的 上述物质进行检测，使用电感耦合等离子体质谱（ICP-MS）测定血清中 Se 含量。比较两组人群以上各指标的差异，不同年龄分层的差异以及各项目的相关性。

结果 病例组血清中 Se 含量显著低于对照组（P<0.01），在各年龄分层中与对照组相比也显著降低（P<0.01）。VitA 在<60 岁和 60-69 岁低龄分组 中，病例组含量显著低于对照组（P<0.01），但总体上与对照组无显著差异。 Vit E 在对照组与病例组中差异不明显。对照组与病例组血清 8-oxo-Gsn 无显著 差异，在<60 岁和 60-69 岁低龄分组中病例组血清中 8-oxo- dGsn 含量显著高于对照组(P<0.01)。通过相关性分析发现 8-oxo-Gsn 与年龄存在显著相关性 （P<0.01），8-oxo-dGsn 仅在表观健康人群中与年龄呈现显著相关性。血清 Se 分 别与 Vit A 和 Vit E 呈现显著相关性（P<0.01），但未发现 8-oxo-Gsn、8-oxodGsn 与两种维生素和 Se 之间存在显著相关关系。

结论 AD 患者血清含有显 著高水平的 DNA 氧化损伤产物 8-oxo-dGsn 和低水平的抗氧化物质 Se，血清 8- oxo-Gsn、8-oxo-dGsn 与 Vit A、Vit E 和 Se 关系需进一步研究。

PU-3016

新型冠状病毒核酸检测中单基因“假阳性”可能因素的探讨

王梓
天津医科大学肿瘤医院

实时定量 PCR(简称 qRT-PCR)技术是检测新型冠状病毒(简称“新冠病毒”)的主要手段。目前 qRT-PCR 试剂盒，多以新冠病毒 RdRP 基因(ORFlab 读码框)、N 基因和 E 基因为靶基因，实现对新冠病毒的检测。其检测结果是新冠病毒感染者确诊及治愈出院的重要依据。由于 qRT-PCR 灵敏度高其特异性强，其结果容易出现假阳性及假阴性的状况。在临床实践中，多次出现 E 基因阳性、N 基因和 RdRP 基因阴性的情况。使用不同厂商的 qRT-PCR 试剂盒对可疑样本复查，最终确定 N 基因和 RdRP 基因阴性。由此可知 E 基因在新冠病毒检测中易出现假阳性结果。其原因可能为新冠病毒的 E 基因为保守基因，存在于多种病原体中。

PU-3017

分离胶采血管制备血清某些特定情况下对 HBsAg 定性检测结果的影响

贾红基、王爱华
杭州迪安医学检验中心有限公司

目的 通过对科室工作中遇到的 26 例 HBsAg 异常阳性样本进行分析，了解分离胶采血管制备的血清是否会在某些特定情况下对 HBsAg 定性结果产生影响。
方法 收集科室在工作中遇到的 26 例 HBsAg 定性检测初步判定为假阳性的样本，进行重新检测、罗氏乙肝定量复测及分注管样本复测，来比较三者结果之间的差异。
结果 经过实验，对 26 例 HBsAg 定性检测异常阳性样本进行分离胶采血管制备的原管血清重测结果和罗氏乙肝定量复测结果均为阳性，而用分注管样本进行复测的 HBsAg 结果均为阴性。
结论 用分离胶采血管制备的血清标本在血清量低于 1 毫升时检测 HBsAg，会对北京万泰生物药业股份有限公司生产的 HBsAg（ELISA）定性结果产生假阳性反应。

PU-3018

幽门螺旋杆菌抗体、抗原检测与 14C 呼气试验的对比研究

罗曼
成华区第三人民医院

幽门螺旋杆菌（H.pylori）是一种存在于胃粘膜上皮表面和黏液底层的革兰阴性弯曲螺杆菌，全球一半以上人口被 HP 感染。幽门螺旋杆菌感染可引起消化性溃疡、慢性胃炎、胃癌等多种消化道疾病相关，其传染性很强，可通过口-口、粪-口在人与人之间传播，因此准确快速的检测出幽门螺旋杆菌对大众健康有重要的价值。目的比较幽门螺旋杆菌的血清学抗体检测、粪便抗原检测和 14C 呼气试验对于诊断幽门螺旋杆菌感染的可用性和准确率，并进行比较研究。方法选择一段时间内 100 例以上的胃幽门螺旋杆菌检测患者分别进行三种试验的检测，记录结果。结果血清学抗体检测、粪便抗原检测和 14C 呼气试验三种试验的阳性率、敏感性、特异性无显著差异。结论三种方法用于幽门螺旋杆菌均具有一定意义，各有优缺点，可以根据患者自身情况选择对应的检测方法，以帮助病情的治疗和预后。

PU-3019

Ginkgolide B Maintains Calcium Homeostasis in Hypoxic Hippocampal Neurons by Inhibiting Calcium Influx and Intracellular Calcium Release

Li Wang、Qinghai Shi
新疆军区总医院临床医学检验诊断中心

Ginkgolide B (GB), a terpene lactone and active ingredient of Ginkgo biloba, shows protective effects in neuronal cells subjected to hypoxia. We investigated whether GB might protect neurons from hypoxic injury through regulation of neuronal Ca2+ homeostasis.

Primary hippocampal neurons subjected to chemical hypoxia (0.7 mM CoCl2) in vitro exhibited an increase in cytoplasmic Ca2+ (measured from the fluorescence of fluo-4), but this effect was significantly diminished by pre-treatment with 0.4 mM GB. Electrophysiological recordings from the brain slices of rats exposed to hypoxia in vivo revealed increases in

spontaneous discharge frequency, action potential frequency and calcium current magnitude, and all these effects of hypoxia were suppressed by pre-treatment with 12 mg/kg GB. Western blot analysis demonstrated that hypoxia was associated with enhanced mRNA and protein expressions of Cav1.2 (a voltage-gated Ca2+ channel), STIM1 (a regulator of store-operated Ca2+ entry) and RyR2 (isoforms of Ryanodine Receptor which mediates sarcoplasmic reticulum Ca2+ release), and these actions of hypoxia were suppressed by GB.

Taken together, our in vitro and in vivo data suggest that GB might protect neurons from hypoxia, in part, by regulating Ca2+ influx and intracellular Ca2+ release to maintain Ca2+ homeostasis.

PU-3020

系统性红斑狼疮患者抗核抗体检测及临床特点分析

邹红云、晁亚妮、何华月、何江
中国人民解放军新疆军区总医院检验科

目的 探讨 263 例系统性红斑狼疮（SLE）患者抗核抗体（ANA）及首发临床表现在不同性别、年龄间的分布差异和特点。

方法 回顾性调查和分析 2015 年 1 月至 2018 年 12 月 SLE 住院患者 263 例，收集患者的临床资料信息，包括年龄、性别、起病时首发临床表现、抗核抗体（ANA）及荧光核型实验结果等信息。采用线性免疫印迹法进行 ANA 谱检测，间接免疫荧光法（IIF）进行 ANA 免疫荧光检测，荧光显微镜下判读荧光核型。对收集的资料信息进行统计学分析。

结果 SLE 患者 ANA 阳性率为 94.29%，不同性别、年龄组间 ANA 阳性率无显著性差异（P > 0.05）；ANA 免疫荧光核型以核颗粒型最为多见（64.64%）；核颗粒型和着丝点型 2 种核型阳性率在不同年龄组间差异具有统计学意义（P< 0.05），≤35 岁年龄组的核颗粒型阳性率明显高于≤50 岁年龄组及> 50 岁年龄组的阳性率；> 50 岁年龄组的着丝点型阳性率（8.00%）明显高于≤35 岁年龄组(3.27%）及≤50 岁年龄组（4.39%）；女性患者 Ro-52 和 NUC 抗体阳性率均显著高于男性患者阳性率（P < 0.05）；≤35 岁年龄组抗组蛋白抗体阳性率（39.34%）显著高于≤50 岁年龄组（21.98%）和 > 50 岁年龄组阳性率（20%）；SLE 患者首发临床表现中肾损害阳性率最高（34.60%），其次为皮肤损害（23.19%）和关节炎（19.39%）。男性患者皮肤损害（41.46%）和神经系统症状（7.31%）的阳性率显著高于女性患者（19.82%，0.45%），女性患者关节炎阳性率（21.62%）显著高于男性患者（7.31%），差异具有统计学意义（P < 0.05）。

结论 SLE 患者 ANA 核型、ANA 谱和首发临床表现分布具有性别和年龄差异性。SLE 患者抗核抗体和临床表现特点，可为 SLE 的早期诊断和治疗提供重要参考依据。

PU-3021

梅毒螺旋体阳性患者与其血清学检测结果相关性分析

黄进梅
南方医科科大学皮肤病医院

目的 探讨梅毒螺旋体阳性患者与血清学检测结果相关性。

方法 选择临床症状怀疑梅毒感染患者，对其进行梅毒螺旋体暗视野检查、梅毒螺旋体明胶颗粒凝集试验（TPPA）和甲苯胺红不加热血清试验（TRUST），部分患者进行 2 型单纯疱疹病毒核酸检测或抗体检测。

结果 怀疑梅毒感染的患者 953 例中 60 例暗视野检查可见梅毒螺旋体，其中 TPPA 阳性 35 例阳性率 58.3%、TRUST 阳性 24 例阳性率 40.0%。53 例一期梅毒患者 TPPA 阳性 28 例阳性率 54.7%、

TRUST 阳性 17 例阳性率 32.1%；7 例二期梅毒患者 TPPA 和 TRUST 均为阳性。41 例梅毒螺旋体阳性患者中有 16 例合并 2 型单纯疱疹病毒感染，阳性率达 39.0%。

结论 梅毒螺旋体阳性的一期梅毒患者其血清学检测结果阳性率较低，但 TPPA 阳性率明显高于 TRUST；一期梅毒患者出现临床症状时间与 TPPA、TRUST 阳性率和滴度呈正相关。梅毒螺旋体暗视野检查法对于一期梅毒（尤其早期）患者的及时诊断、及早治疗、减少传播具有重要意义。梅毒患者合并单纯疱疹 2 型感染率高，应引起临床的高度重视。

PU-3022

浅谈方舱医院检验组规划建设和管理

袁改玲、李蓉
新疆生产建设兵团第五师医院

背景 2020 年 2 月，为了应对武汉发生的新型冠状病毒蔓延，国家卫健委及相关单位在武汉建立了武汉火神山医院、武汉雷神山医院，以及 14 所方舱医院。[1]新型冠状病毒肺炎疫情在武汉暴发后，方舱医院在阻止疫情蔓延扩散、落实"应收尽收"战略方面发挥了重要作用。武汉东西湖方舱医院作为武汉市首批投入使用的 3 家方舱医院之一，由武汉大学附属中南医院托管，国家紧急医学救援队组建，通过明确定位、合理布局、完善组织架构、健全规章制度、加强院内感染防控、做好支撑保障等举措，有效完成了轻症患者的收治任务。本文作者就所参与的方舱医院检验组的管理，浅谈方舱检验组的规划建设和管理。就进一步完善应急救治体系提出建议，国内救援医学以及国外救援医疗建立方舱医院提供较完善的检测实验方案和布局。

新冠肺炎具有高传染性、潜伏期长的特性，致使在早期不容易引发重视，加上防控初期的措施不力，信息不畅通，导致医疗资源被不断挤压。当时，大量的轻症疑似患者无法确诊，只能居家隔离，易造成次生的家庭聚集性传染，重症患者也不能及时收入专科医院接受治疗。 在这种情况下，有关专家向中央建议建立方舱医院，将大量的轻症确诊患者集中收治。事实证明，方舱医院在控制疫情上发挥了关键作用。目前，武汉的方舱医院已经全部关闭，世卫组织表示，当前多个国家床位紧张，可以借鉴“方舱医院”的方式对轻症患者进行集中隔离。方舱医院的大规模使用，对于整个疫情的防控和逆转具有重要意义，也为今后的医改乃至社会治理提供了思路。作为新冠诊疗的重要辅助组－临床检验组，承担着初筛、鉴别、确诊、分型、治疗监测的重要职责。如何在传染病条件下能够更好更快更安全的开展检验工作，一直是我们研究的课题。总结方舱医院检验组运行规划、质量控制、实验室检查，对进一步完善传染病疫情暴发期的方舱医院医疗检测体系，具有重要的现实意义。

PU-3023

遗传代谢病氨基酸和酰基肉碱的方法学验证

张洋
吉林金域医学检验所有限公司

目的 本文对遗传代谢病氨基酸和酰基肉碱检测进行方法学验证，以保证检测结果的准确性，为人类健康保驾护航。

方法 应用仪器为 API3200 MD。室内质控品是自配质控。通过准确度、精密度、灵敏度等进行方法学验证。准确度选用集团临床样品比对和集团 PT 比对两种方式。精密度：批内精密度及批间精密度使用自配质控样品，分别以 QC-AA-L、QC-AA-H、QC-AC-L、QC-AC-H 作为低、高两水平氨基酸及酰基肉碱血片；计算 8 种氨基酸和 14 种酰基肉碱指标检测结果的平均值及相对标准偏差（RSD）；灵敏度：混合收集同批次处理好的样品溶液，用流动相将该样品溶液按：原倍、1：2、1：4、1：8、1：16、1：32、1：48、1：64 稀释，最终确定氨基酸和酰基肉碱内标的响应下限。

携带效应：选取自配高浓度水平样品，分别以 QC-AA-H 表示高浓度氨基酸样品，QC-AC-H 表示高浓度酰基肉碱样品，与空白样本一起进行处理，氨基酸及酰基肉碱分别按照空白-空白-高浓度样本-空白-高浓度样本-空白-高浓度样本-空白-高浓度样本-空白-高浓度样本-空白-高浓度样本-空白进行上机检测。

结果 所有临床样本临床判读与集团判读一致，PT 检测结果与参考物质来源机构提供的结果一致。批内精密度与批间精密度均小于 25%。氨基酸和酰基肉碱内标的响应下限。空白样本的响应信号低于参考下限的响应信号。

结论 通过对批内、批间精密度的验证实验，其准确度、精密度、灵敏度、携带效应等均满足检测要求。新生儿遗传代谢病的检测有助于实现早筛查、早诊断、早治疗；减少疾病对家庭带来的经济与精神的压力，减少疾病对患儿带来的疼痛，保证患儿的健康成长。

PU-3024

Application of the sigma metrics to evaluate the analytical performance of cystatin C and design a quality control strategy

Qian Liu、Fumeng Yang
The Second People's Hospital of Lianyungang

Background Sigma metrics are commonly used to evaluate laboratory management. In this study, we aimed to evaluate the analytical performance of cystatin C using sigma metrics and to develop an individualized quality control scheme for cystatin C levels.

Methods Bias was calculated based on the samples used for the external quality assessment. The coefficient of variation was calculated using 6 months of internal quality control (IQC) measurements at two levels, and desirable specification derived from biological variation was used as the quality goal. The sigma value for cystatin C was calculated using the above data. The IQC scheme and improvement measures were formulated according to the Westgard sigma standards for batch size and quality goal index (QGI).

Results The sigma values for cystatin C, for quality control levels 1 and 2, were 3.04 and 4.95, respectively. The 13s/22s/R4s/41s/6x multi-rules (N=6, R=1), with a batch size of 45 patient samples, were selected as the IQC schemes for cystatin C. With different levels of cystatin C, the power function graph showed a probability for error detection of 94% and 100% and a probability for false rejection of 4% and 2%, respectively. According to the QGI of cystatin C, its precision needs to be improved.

Conclusions With a "desirable" biological variation of 6.50%, the Westgard rule $1_{3s}/2_{2s}/R_{4s}/4_{1s}/6_{x}$ (N=6, R=1, batch size of 45) with high efficacy for determining the detection error is recommended for individualized quality control schemes of cystatin C.

PU-3025

Distribution of urinary N-acetyl-beta-D-glucosaminidase and the establishment of reference intervals in healthy adults

Qian Liu、Fumeng Yang
The Second People's Hospital of Lianyungang

Background Urinary N-acetyl-beta-D-glucosaminidase (NAG) plays an important role in the early diagnosis and progression of diseases related to renal tubular injury. We detected the urinary

NAG concentration, assessed the preliminary statistics of its distribution, and established reference intervals for healthy adults in China using the rate method.
Methods A total of 1,095 reference individuals (aged 20 to 79 years) met the requirements for inclusion in this study. Urinary NAG concentrations were detected using an AU5800 automatic biochemical analyser with its matched reagents. The Kolmogorov-Smirnov test was used to analyse the normality of the data. According to the guidelines of C28-A3 and WS/T 402-2012, the reference intervals of urinary NAG were established using the nonparametric percentile method (unilateral 95th percentile).
Results The urinary NAG data showed a non-normal distribution. The distribution of urinary NAG was significantly different by sex and age. Therefore, the reference intervals of urinary NAG were established using the rate Method males (aged 20-59 years) <19.4 U/L (90% CI: 18.0–20.3 U/L); males (aged 60-79 years) <22.3 U/L (90% CI: 20.2–22.6 U/L); females (aged 20-59 years) <15.7 U/L (90% CI: 15.2–16.5 U/L); and females (aged 60-79 years) <21.4 U/L (90% CI: 20.3–22.3 U/L).
Conclusions We established preliminary reference intervals of urinary NAG for healthy adults in China to provide guidance for health screening, auxiliary diagnosis and treatment monitoring of renal tubule-related diseases.

PU-3026

Application of a six sigma model to the evaluation of the analytical performance of the assays of enzymes in serum and the design of a quality control strategy: a multicentre study

Qian Liu、Fumeng Yang
The Second People's Hospital of Lianyungang

Background We aimed to apply a six sigma model to the evaluation of the analytical performance of the assays of enzymes in serum, design of individualized quality control schemes and development of the improvement measures for multicentre laboratories using the detection platform based on an automatic AU5800 biochemical analyser.
Methods The internal quality control (IQC) and external quality assessment (EQA) data were collected and analysed by calculating the sigma values for the assays of enzymes in the serum based on the coefficient of variation, bias and allowable total error. Normalized sigma method decision charts for the assays of enzymes in the serum were generated using these parameters. IQC schemes and improvement measures were defined using the Westgard sigma rule with batch size quality control (QC) at two levels. The quality goal index (QGI) was used to assist with identification of the reasons (bias problems, precision problems or their combination) that affect the analytical performance of the analytes (sigma<6).
Results Sigma values for the assays of enzymes in the serum were significantly different at various enzyme concentrations, and the differences between the laboratories in the levels of the same analytes were also observed. Individualized quality control schemes were designed for each laboratory; for example, the sigma values ALT (Lab A) were more than six sigma, and 1_{3s} (N=2, R=1) with a batch size of 1000 patient samples was selected. Additionally, improvement measures for the analytes (sigma<6) were provided for each laboratory.
Conclusions The six sigma model can visualize the performance of the assays of enzymes in the serum to design individualized IQC schemes and provide strategies for continuous quality improvement for each laboratory.

PU-3027

基于六西格玛模式评价糖化血红蛋白的分析性能及质控策略的设计

杨伏猛、刘倩
连云港市第二人民医院

目的 应用六西格玛模式评价糖化血红蛋白(HbA1c)的分析性能，并初步建立 HbA1c 项目的室内质控策略和质量改进措施。
方法 收集本实验室 HbA1c 项目 2020 年国家卫健委临检中心室间质评数据及 2020 年 1 月至 6 月两个浓度水平的室内质控数据，并结合四个不同来源的允许总误差(TEa)分别计算 HbA1c 项目的 σ 水平，同时应用标准化的西格玛性能验证图进行标示。并依据具有批长度的 Westgard 西格玛规则流程图和质量目标指数(QGI)，制定 HbA1c 项目的室内质控策略和质量改进方案。
结果 基于西班牙室间质评标准和德国 RiliBAK 标准作为质量目标时，HbA1c 的分析性能均处于“世界一流”水平，而基于“适当”生物学变异和我国室间质评标准作为质量目标时，则 HbA1c 的分析性能分别处于“不可接受”和“优秀”水平。本研究依据我国室间质评标准作为质量目标，同时结合具有批长度的 Westgard 西格玛规则，初步建立以下质控策略：选择 $1_{3s}/2_{2s}/R_{4s}$ 多规则(N=2)且分析批长度为 450 个患者的样本作为 HbA1c 的室内质控方案。且 QGI 计算结果显示，HbA1c 项目的偏倚是影响其分析性能的主要因素，需优先在正确度的提升方面制定相应的改进措施。
结论 6σ 模式能够客观评价 HbA1c 项目的分析性能，且在实验室质控策略的设计和检测质量的改进方面具有重要的指导意义。

PU-3028

基于六西格玛模式评价血常规项目的分析性能及质控策略的设计

刘倩、杨伏猛
连云港市第二人民医院连云港市肿瘤医院

目的 应用六西格玛(6σ)模式评价血常规项目的分析性能，并建立血常规项目个性化的质控方案和质量改进措施。
方法 收集本实验室血常规项目 2020 年江苏省卫健委临检中心室间质评数据及同期室内质控数据，以“适当”生物学变异导出的质量规范作为实验室允许总误差(TEa)，计算各项目的 σ 值，同时应用标准化的 σ 性能验证图进行标示。并依据具有批长度的 Westgard 西格玛规则和质量目标指数(QGI)，分别制定各项目个性化的室内质控方案和质量改进措施。
结果 以生物学变异数据作为质量目标，白细胞计数(WBC)项目的分析性能达到“世界一流”水平，其余项目则处于“临界”至“优秀”之间。依据具有批长度的 Westgard 西格玛规则，WBC 项目选择 1_{3s} 规则(N=2)且分析批长度为 1000 个患者的样本作为其室内质控方案；红细胞计数(RBC)项目选择 $1_{3s}/2_{2s}/R_{4s}/4_{1s}$ 多规则(N=4)且分析批长度为 200 个患者的样本作为其室内质控方案；血红蛋白(Hb)项目选择 $1_{3s}/2_{2s}/R_{4s}$ 多规则(N=2)且分析批长度为 450 个患者的样本作为其室内质控方案；血细胞比容(HCT)和血小板计数(PLT)项目选择 $1_{3s}/2_{2s}/R_{4s}/4_{1s}/6_X$ 多规则(N=6)且分析批长度为 45 个患者的样本作为其室内质控方案。此外，Hb 和 HCT 需要优先改进精密度；RBC 和 PLT 则需同时改进精密度和正确度。
结论 6σ 模式能够客观评价临床血常规项目分析性能，其在帮助实验室质控策略的设计和质量改进方面具有重要的指导意义。

PU-3029

食管癌淋巴细胞亚群的临床意义

韩景银
东营市人民医院

目的 探讨食管癌患者 CD3+细胞、CD4+细胞、CD8+细胞、NK 细胞的表达及临床意义。
方法 回顾性分析 2015 年 1 月至 2020 年 1 月东营市人民医院收治的 80 例食管癌患者资料,选取 40 名正常人作为阴性对照。运用流式细胞术仪检测食管癌及健康人群的外周血淋巴细胞亚群,探讨淋巴细胞亚群中 CD3+, CD4+, CD8+，NK 细胞与食管癌临床特征的关系。
结果 与阴性对照组相比，食管癌患者 CD4+细胞比例降低，[(31.38±3.62)%vs(37.23±4.01)% ,P=0.012] ，CD8+细胞比例升高[(41.52±4.21)%vs(32.31±4.12) %, P=0.002]。NK 细胞和 CD4/CD8 比值均降低。在不同分期的食管癌组中，I 期，II 期， III 期， IV 期食管癌中，CD3+、CD4+、NK 及 CD4+/CD8+呈现递减趋势,CD8+呈现递增趋势,差异具有统计学意义(P <0. 05). 单因素分析提示，CD3+细胞、CD4+细胞、CD8+细胞、NK 细胞及 CD4+/CD8+均与食管癌 T 分期及 N 分期呈显著相关(P <0. 05)。多因素分析提示，CD4+/CD8+与食管癌患者预后相关，CD3+细胞、CD4+细胞、CD8+细胞、NK 细胞无明显相关性。
结论 食管癌患者 CD3+细胞，NK 细胞及 CD4/CD8 比值降低提示存在免疫功能失调，随着肿瘤分期增加，免疫功能越差，预后越差。

PU-3030

广州市 2017—2019 年流感暴发疫情及病原学特征分析

李美霞、潘心红
广州市疾病预防控制中心

目的 对广州市 2017－2019 年流感暴发疫情和病原学特征进行分析，为流感防控策略制定提供依据。
方法 收集流感暴发疫情资料进行统计分析，采集流感暴发疫情标本,采用多重实时荧光定量 PCR 方法检测流感病毒核酸。
结果 2017—2019 年我市分别报告流感样病例暴发疫情 110、75 和 183 起。2017 年 110 起疫情采集咽拭子共 1250 份，经检测 B 型流感 76 起，A(H3N2)型流感 16 起，A(H1N1)和 A(H3N2)混合型流感 4 起，A(H1N1)型流感 3 起， B 型和 A(H1N1)型混合型流感 2 起， B 型和 A(H3N2) 型混合型流感 1 起，阴性 8 起。2018 年 75 起暴发疫情共采集咽拭子 915 份，经检测 A（H1N1）型流感 54 起，A（H3N2）型流感 2 起，B 型流感 12 起，阴性 7 起。2019 年 183 起疫情采集咽拭子共 2490 份，经检测 A(H1N1)型流感 15 起，B 型流感 37 起，A(H3N2)型流感 11 起，阴性 9 起，混合感染 11 起。2017 年和 2018 年疫情均呈现双峰流行的特点，其中 2017 年流行高峰出现在 4—6 月和 11 月—次年 1 月，2018 年流行高峰为 4—5 月和 9—12 月。2019 年疫情呈现三个高峰，分别发生在 1 月、3-6 月和 12 月。2017 年疫情流行株为 B 型流感病毒和甲型 H3N2 亚型，2018 年为甲型 H1N1 流感病毒，2019 年为 B 型和 A(H3N2)型流感病毒。疫情主要发生在中小学及托幼机构等人群密集场所，尤其是小学，是流感暴发疫情的高发场所。
结论 广州市 2017—2018 年流感疫情呈双峰流行，高峰期出现在 4—6 月和 10—12 月，2019 年呈三个高峰，分别发生在 1 月、3-6 月和 12 月。不同流感病毒型别交替流行, 学校和托幼机构等集体单位为暴发事件发生的高风险场所。加强集体单位培训、落实疫情报告、晨检、通风和隔离消毒各项防控措施，加强中小学学生和托幼机构儿童流感疫苗接种有利于疫情防控。

PU-3031

异嗜性抗体对自身抗体检测结果干扰的处理和分析

梁晓玲[2]、连鑫磊[1]
1. 济南金域医学检验中心有限公司
2. 青岛金域医学检验所有限公司

目的 分析及处理人体内异嗜性抗体对自身抗体干扰，导致测定结果的假阳性。
方法 分别采用更换检测系统和异嗜性抗体阻断剂对 1 例女性患者样本进行处理检测，比较更换检测系统和使用异嗜性抗体阻断剂前后自身抗体检测结果的差异。
结果 受异嗜性抗体干扰的自身抗体，主要是 ds-DNA、His、Jo-1、Nuclear、P0、SSA、PM-Scl、Sm、SSB/La、Scl-70、AMA-M2、nRNP/Sm、GBM、MPO、PR3、β2-G、β2-M 等检测结果在更换检测系统和使用异嗜性抗体阻断剂后结果为正常值。
结论 该患者血清自身抗体检测受到异嗜性抗体的干扰，导致结果假阳性，在更换了检测系统和使用了非特异性吸附特殊试剂处理样本解决了异嗜性抗体的对检测结果的干扰。

PU-3032

非标准磷脂抗体在不良妊娠患者中阳性率分析

梁晓玲
青岛金域医学检验所有限公司

目的 通过对不良妊娠患者血液中非标准磷脂抗体阳性率分析，了解非标准抗体在磷脂综合征中的临床意义，为标准抗体阴性的磷脂综合征的诊断提供科学依据。
方法 选取 2020 年我检验中心共接收的 15291 例样本进行研究，分析不同送检类型的医疗机构各类抗体的阳性率情况。
结果 15291 例样本中某不孕不育专科医院送检量为 629 例，磷脂非特异性抗体阳性率为 31.16%，其他类型医院送检量为 14662 例，阳性率为 7.50%。同一患者超过两项抗体阳性占比情况，某不孕不育专科医院为 21.94%，其他类型医院为 14.27%。某不孕不育专科医院，各类非特异性磷脂抗体阳性率为 PT-IgG 8.94%、PT-IgM 21.86%、PSPT-IgG 1.71%、PSPT-IgM 12.68%、PS-IgG 0.78%、PS-IgM 2.58%、PI-IgG 2.60%、PI-IgM 1.82%，其他类型医院，各类非特异性磷脂抗体阳性率为 PT-IgG 7.25%、PT-IgM 14.38%、PSPT-IgG 1.40%、PSPT-IgM 9.25%、PS-IgG 0.61%、PS-IgM 0.62%、PI-IgG 1.74%、PI-IgM 1.19%。
结论 磷脂非特异性抗体在不良妊娠患者中阳性率较高，不孕不育专科医院的阳性率显著高于其他类型医院，且多项抗体阳性率占比具有显著性差异，PT-IgG、PT-IgM 、PSPT-IgG、PSPT-IgM、PS-IgG 、PS-IgM、PI-IgG、PI-IgM 在不孕不育专科医院的阳性率均高于其他类型医院，其中 PT-IgM、PSPT-IgM、PS-IgM 具有统计学差异（P＜0.05）。

PU-3033

国际输血协会 3 个新增红细胞血型系统的研究回顾（2019）

何克宇、徐婧、张敏
东南大学附属中大医院

国际输血协会（International Society of Blood Transfusion，ISBT）在 2019 年 8 月注册了 3 个全新的血型系统：KANNO 血型系统、Sid 血型系统、CTL2 血型系统（待定）。ISBT 此次更新的主要原因是，2019 年研究者们通过全基因组关联研究和全外显子组测序，先后发现了 KANNO

血型系统（rs1800014）和 Sid 血型系统（rs7224888）表面抗原的重要单核苷酸多态性（single nucleotide polymorphism，SNP）位点，获得了这 2 种血型系统的遗传学证据支持，其结果也与目前的免疫学研究结论相一致。此外，在 2017 年研究者首次发现红细胞血影（细胞膜）上也存在 CTL2 抗原，但由于缺少血清学和遗传学证据，CTL2 血型系统目前仍为待定状态。三种血型系统中，Sid 血型系统对输血安全具有重要意义。极少数人红细胞膜表面存在一种 Cad 抗原，亦称 Sd（a^{++}）抗原，能够与抗-Sd^a 抗体产生强烈的作用，引起溶血反应。此次新增血型系统的最关键证据是血型抗原编码基因和重要 SNP 位点的发现和验证。随着基因测序、基因芯片等基因组学方法的普及，未来高频抗原和新抗原亚型的遗传学验证仍将是血型研究的重要突破口。

PU-3034

强直性脊柱炎患者 HLA-B27 基因及分型、T、B 及 NK 淋巴细胞亚群检测的临床意义

刘倩、马亮
中日友好医院

目的 探讨强直性脊柱炎(Ankylosing spondylitis ,AS)患者人类白细胞抗原 B27(HLA-B27)基因、T、B 及 NK 淋巴细胞亚群检测的临床意义。
方法 收集中日友好医院 2018～2020 年期间确诊的 121 例 AS 患者以及 120 例健康体检人群外周血样本，采用荧光定量 PCR 染料法检测 HLA-B27 基因及分型，流式细胞术方法检测其标记为 T、B 及 NK 的淋巴细胞亚群。
结果 121 例 AS 患者中 HLA-B27 基因阳性 101 例，其中 HLA-B2704 型 58 例，HLA-B2705 型 40 例，HLA-B2702 型 1 例，HLA-B2704*HLA-B2705 复合杂合子 2 例。AS 组 HLA-B27 基因阳性率明显高于健康对照组（83.5%vs2.5%,P<0.01）。AS 组 CD3+CD8+(Ts)%、CD3-CD16+CD56+(NK)%明显低于健康组（P<0.01），AS 组 CD3+CD4+(Th)%、Th/Ts、CD19+CD5+(B1)%、CD19+CD5-(B2)%明显高于健康组（P<0.01）。HLA-B2705 型 AS 组 T%、Th%、Th/Ts 明显高于 HLA-B2704 型 AS 患者（P<0.01），B1%、NK%明显低于 HLA-B2704 型 AS 患者（P<0.01）。101 例 HLA-B27 基因阳性与 20 例 HLA-B27 基因阴性 AS 患者 T、B 及 NK 淋巴细胞亚群差异暂无统计学意义（P>0.05）。
结论 AS 患者淋巴细胞分布异常，免疫功能紊乱。检测 AS 患者 HLA-B27 基因分型及 T、B、NK 淋巴细胞亚群对于强直性脊柱炎发病机制、诊断、评估免疫状态等具有重要意义。

PU-3035

Analysis of Influence Factors of Intra-laboratory Turnaround Time in Emergency Blood Routine specimens

Fengfeng Zhao
Department of Clinical Laboratory of Zhongda Hospital, Southeast University

Objective A COX proportional hazards regression model was established to analyze the factors influencing the intra-laboratory turnaround time in emergency blood routine specimens
Methods In the retrospective study, 3,986 emergency blood specimens from October 2015 to August 2016 in the Department of Clinical Laboratory of Zhongda Hospital, Southeast University were used to randomly select 4 weeks of data. The records of Samples included determination date, sample statuses, times of arrival, times of test, processing time, project portfolios, measurement period, operators, 10 minutes treatment results, and delay factors. SPSS 18.0 was used for statistical analysis. The COX single factor analysis was performed for each of the above indicators, and COX multi-factor regression analysis was performed step by step.

Results Within 10 minutes, 3789 reports were sent, accounting for 95.1%. The median actual processing time of the specimens was 7.3 min. The single factor analysis of the COX proportional hazards regression model showed that the sample status, times of arrival, measurement period, operator and delay factors had statistically significant delays in sample turnaround time (P values were all less than 0.05); COX multi-factor regression analysis showed that the appropriate time of arrival was the favorable factor for shortening the sample turnover time (Wald=34.101, P=0.001). The non-normal measurement period and the handover factor were the negative factors for shortening the sample turnover time (Wald=17.210, 21.184, P= 0.001, 0.000), No. 3, No. 4 and No. 8 operators are favorable factors for shortening the sample turnover time (Wald=11.018, 13.219, 9.225, P=0.001, 0.001, 0.000), No. 2 operator was the unfavorable factors to shorten the sample turnaround time (Wald=27.163, P=0.001). There were no significantly different among other operators (P values were greater than 0.05).
Conclusion Time of arrival, measurement period, operator and delay factors are independent risk factors leading to the delay in the turnover time of the specimens in the laboratory. Other hospitals can establish the COX proportional hazards regression model according to specimen transport, testing procedures, and main influencing factors. To achieve a significant reduction in the laboratory specimen turnaround time and ensure that emergency and critically ill patients receive timely diagnosis and treatment, a quantitative evaluation of the various factors in the process of specimen processing lead to the extension of the laboratory specimen turnover time can be achieved.

PU-3036

血清 microRNA-26、microRNA-122 对原发性胆汁性肝硬化的诊断价值

张帅
青海大学附属医院

目的 观察原发性胆汁性肝硬化（primary biliary cirrhosis, PBC）患者血清 miR-26 和 miR-122 的含量表达水平，探讨血清 miR-26 和 miR-122 对于原发性胆汁性肝硬化的诊断价值和意义。
方法 本研究选取 33 例 PBC 患者，另选取 10 例慢性乙肝患者（chronic hepatitis B,CHB）作为疾病对照组及 7 例健康对照者（healthy control, HC）作为健康对照组，采用实时荧光定量 PCR 方法检测患者样本中血清 miR-26 和 miR-122 的表达水平，比较血清 miR-26 和 miR-122 在 PBC 患者和健康对照组之间以及疾病对照组之间存在的表达差异，分析血清 miR-26 和 miR-122 对 PBC 患者的诊断价值，并与现有诊断指标进行比较，探讨血清 miR-26 和 miR-122 对于原发性胆汁性肝硬化的诊断价值。
结果 原发性胆汁性肝硬化 PBC 患者血清 miR-26 和 miR-122 表达水平明显低于健康对照组（分别为 P=0.001, P <0.001）和疾病对照组（P=0.006, P=0.001）。血清 miR-26 和 miR-122 对原发性胆汁性肝硬化具有较好的诊断价值（AUC=0.913，AUC=0.963）和鉴别诊断价值（AUC=0.809，AUC=0.857）。血清 miR-26 和 miR-122 与现有诊断指标谷丙转氨酶（ALT）、白蛋白（ALB）、碱性磷酸酶（ALP）、谷氨酰转移酶（GGT）和球蛋白（GLOB）等与肝功能相关的指标都具有很好的相关性。
结论 血清 miR-26 和 miR-122 有望成为 PBC 患者明确诊断的潜在诊断标志物。

PU-3037

Atorvastatin inhibits inflammation through the cysteine-rich motor neuron 1 (Crim1) pathway in human umbilical vein endothelial cells

Xuehui Liu[1]、Shaoguo Wu[1]、Yanwei Hu[2]
1. Guangzhou Twelfth People's Hospital，Guangzhou，Guangdong
2. 广州市妇女儿童医疗中心

Background and Aims Inflammation has been recognized to have a role in the process of atherosclerosis. Although evidence indicates that atorvastatin has anti-inflammatory effects besides cholesterol-lowering ability in atherosclerosis, the specific mechanisms of atorvastatin in inflammation requires further discussion.
Methods Here, we explored the effects and mechanisms of atorvastatin on inflammation in human umbilical vein endothelial cells through quantitative real-time PCR and western blot analyses. In addition, microarray analysis and immunohistochemistry were used to analyze the expression of Crim1 in atherosclerotic plaques.
Results Cysteine-rich motor neuron 1 (Crim1) mRNA was upregulated 36.68 fold ($P<0.001$), and Crim1 protein was upregulated 3.63 fold ($p<0.001$), in human atherosclerotic plaques compared with normal intima tissues. Bioinformatics analysis revealed Crim1 co-expression with IL-6, TNF-α and NF-κB. Atorvastatin dramatically downregulated the mRNA and protein levels of Crim1 and inhibited inflammation by decreasing the levels of IL-6, TNF-α and NF-κB. Knockdown of Crim1 significantly inhibited IL-6, TNF-α and NF-κB expression, whereas overexpression of Crim1 upregulated IL-6, TNF-α and NF-κB expression. In addition, the inhibitory effects of atorvastatin on inflammation were markedly offset by overexpression of Crim1.
Conclusion These results demonstrated that atorvastatin decreases inflammation via the Crim1 pathway in HUVECs, thus, providing a new prospect for the use of atorvastatin for non-lipid lowering functions, and new directions for the prevention and therapy of atherosclerosis.

PU-3038

Cut-off 值的建立与验证

谢屿平、曹颖平
福建医科大学附属协和医院

Cut-off 值，即临界值，是临床检验免疫中"阴性"与"阳性"间的分界线。厂家在供应检测试剂盒时，会提供本试剂盒的 Cut-off 值,他们提供的 Cut-off 值通常是一成不变的固定值，但即使是试剂盒批次之间生产工艺也存在不均一的情况，以及不同实验室环境，受检人群的种族、地域等多种影响因素下，都用同一 Cut-off 值是不合理的，因此，各个医院诊断实验室在投入之前未开展的检验项目前，应该在厂家提供的 Cut-off 值基础上，自行建立适合该实验室的 Cut-off 值，美国临床病理学会(College of American Pathologists, CAP)推荐每六个月验证一次，以减少漏诊与误诊的发生，达到较高的准确度。本文就 Cut-off 值的建立与验证方法作一综述，以供实验室的规范化与标准化管理。

PU-3039

细菌性肝脓肿患者的细菌感染情况及临床疗效分析

陈喻
自贡市第一人民医院

目的 调查细菌性肝脓肿患者的细菌感染情况，分析临床治疗效果情况，探究其对临床指导用药的意义。
方法 利用细菌分离培养技术和 VITEK 2-Compact 微生物鉴定药敏系统，对 2013 年 1 月-2019 年 4 月间于自贡市第一人民医院就诊的细菌性肝脓肿患者的临床表现、感染病原体种类和耐药性，进行回顾性分析。
结果 共有 132 例患者被诊断为细菌性肝脓肿，且多为老年男性常有其他的并发症，最为常见的是糖尿病。132 例患者，其中送检的有 108 例，送检率 81.8%，有 58 例检出病原菌，检出率为 53.7%。共分离出 65 株非重复菌株，包括肺炎克雷伯菌（46 株），大肠埃希菌（8 株）。
结论 大多数细菌性肝脓肿是由肺炎克雷伯菌引起的，其次是大肠埃希菌，其中大量的菌株都对常见的抗生素表现出敏感。细菌的感染情况与治疗效果有一定的相关性，在治疗细菌性肝脓肿时，需根据病原学和药敏试验特点选择合适的抗菌药物。

PU-3040

CKD 患者 25(OH)D3、骨密度情况及二者关系

邵茁
中日友好医院

目的 了解 CKD 人群 25(OH)D3、骨密度情况、二者关系及影响因素。
方法 对住院 CKD 患者的临床资料进行回顾性分析。分析 25(OH)D3 水平与骨密度的关系，并将骨密度与其他临床指标进行相关分析，应用 Logistic 方程寻找低骨量的影响因素。
结果 CKD5 期患者股骨颈、桡骨骨密度低于对照组及 CKD 余各期患者。CKD 各期患者各组之间股骨颈低骨量的发生率存在差异($\chi2=8.635$，$P=0.035$）。CKD5 期患者股骨颈低骨量的发生率高于健康对照，差异具有统计学意义。股骨颈骨密度 T 值与年龄、性别、心脑血管疾病、BMI、Hb、CRP、ALB、eGFR、TC、24 小时尿蛋白相关，年龄、性别，BMI 是股骨颈低骨量的影响因素。桡骨骨密度 T 值与年龄、DM、心脑血管疾病、CRP、FIB、BMI、ALP、eGFR 相关，年龄、ALP 是桡骨低骨量的影响因素。
结论 CKD 患者 25(OH)D3 水平处于较低状态，白蛋白、BAP、DM、P 是维生素 D 缺乏的独立危险因素。CKD5 期患者股骨颈骨密度下降，年龄、性别、BMI、ALP 是低骨量发生的独立危险因素。

PU-3041

2020 年吉林地区过敏原检测结果分析

陈超
吉林金域医学检验所有限公司

目的 近年来过敏性疾病逐渐增多，通过分析过敏原检测结果情况，对吉林地区针对过敏性疾病进行预防及干预进行提供帮助。
方法 采用免疫印迹法检测血清样本，收取吉林地区样本，针对对 20 种过敏原进行检测，包括 10 种食入性过敏原：榛子/开心果、蟹、虾、鳕鱼、西红柿、牛奶、大豆、蛋黄/蛋清、花生、小麦；

以及 10 种接触性过敏原**结果** 狗上皮、猫毛、普通豚草、艾蒿、律草、榆树、梧桐、霉菌混合、蟑螂、尘螨组合 1(屋尘螨/粉尘螨)；
结果 通过对吉林地区 2020 年过敏原结果进行整理及分析，发现食入性过敏原，牛奶的阳性率较高，其次是榛子/开心果、虾以及蟹等；接触性的过敏原，尘螨、狗上皮以及猫毛阳性率较高，但大都数过敏原在不同年龄组间的差异有统计学意义（P<0.05），随着年龄的增长牛奶、蛋黄/蛋清以及尘螨等的阳性率明显下降。
结论 伴随生态环境的变化，饮食结构与生活习惯有所不同，食品添加剂被广泛应用于日常食品中，室内装修材料的更迭换代，由此引发的各种过敏性疾病逐年增加，给患者个人及其整个家庭造成了困扰。过敏性疾病的病因复杂多样，不容易明确过敏原的种类，给临床治疗和疾病防控造成困扰。为了明确过敏原种类并及时避免接触，除了询问病史、了解日常接触物品、观察临床表现外，过敏原检测成为辅助诊断过敏性疾病的重要手段，对吉林地区荨麻疹、过敏性鼻炎、湿疹等过敏性疾病辅助诊断以及干预有显著临床意义。

PU-3042

染色体核型分析实验室建设方案探讨

陈振朋
西安金域医学检验所有限公司

目的 随着诊疗水平的不断提高，遗传性疾病尤其是染色体疾病逐渐被认知和重视，染色体核型分析作为染色体病的一项重要筛查手段，在临床诊断中发挥重要作用。染色体核型分析制片实验室对环境要求非常高，甚至决定着着制片技术的成败，同时制片过程中使用的挥发性化学品、废液等影响工作人员的健康。同时不间断电力供应也是细胞培养成败的前提。因此合理设计实验室，不仅关乎到制片技术的成败，同时也关乎工作人员的健康。
方法 染色体核型分析实验室装修设计方案从以下几个方面考虑：
1. 实验室通风系统和外排系统；
2. 实验室电力系统；
3. 实验室密闭性设计；
4. 实验室地面防渗漏；
5. 实验室化学品使用和环境净化。
结果 根据实验室实际环境要求，通过对不同厂家比对，测试送风和排风量选择性价比高的送风和排风系统；因细胞培养需要在 37℃培不间断养数天，因此培养箱需连接 UPS 电源，若条件允许尽量配备独立供电的 UPS 电源；由于染色体核型分析在制片时对环境温湿度要求非常严格，制片过程中需整个实验室空间湿度至少达到 40%，温度需达到 24℃，位于南方的实验室需配备大功率抽湿机，而地处北方的实验室，一般加湿器无法满足整体湿度要求，多台配置又会影响实验环境温度，因此建议配备加湿毯；同时实验室应尽量封闭式设计，避免在实验过程中与外界环境有较多的空气流通，影响室内温湿度；另外，应配备化学品柜和通风橱，严格规定化学平的保存和使用，还需定期对实验室内环境进行净化，清除残存环境里的化学品，降低工作人员伤害。
结论 染色体核型分析实验室在设计时，在满足细胞培养和制片条件的同时，还应考虑降低人员伤害。

PU-3043

Serum-soluble ST2 as a novel biomarker reflecting inflammatory status and illness severity in patients with COVID-19

Zhikun Zeng
Zhongnan Hospital of Wuhan University

Aim The authors studied the role of soluble ST2 (sST2) in COVID-19 and its relationship with inflammatory status and disease severity.
Materials & Methods Serum levels of sST2 and interleukin (IL)-33, C-reactive protein (CRP), serum amyloid protein (SAA), IL-6 and procalcitonin (PCT), and T lymphocyte subsets from 80 subjects diagnosed with COVID-19 including 36 mild, 41 severe and three asymptomatic cases were tested.
Results Serum sST2 levels were significantly increased in COVID-19 patients, which were positively correlated with CRP, but negatively correlated with CD4 + and CD8 + T lymphocyte counts. Serum sST2 levels in nonsurviving severe cases were persistently high during disease progression.
Conclusion Serum sST2 level test is helpful for reflecting inflammatory status and illness severity of COVID-19.

PU-3044

Risk assessment and biosafety experience: How to minimize the nosocomial SARS-CoV-2 infection in clinical laboratory?

Zhikun Zeng
Zhongnan Hospital of Wuhan University

The coronavirus disease 2019 (COVID-19) pandemic, caused by the novel severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), is still ongoing. Early on during the COVID-19 outbreak, the healthcare workers (HCWs) working in the department of clinical laboratory in hospital have been facing high risk of developing COVID-19. Their daily work is to receive, test and analyse different types of specimens from patients, and also direct contact with patients through fingerstick or venous blood draw. This review assesses the potential infection risk and summaries the biosafety processes in clinical laboratory in Zhongnan Hospital of Wuhan University during the COVID-19 outbreak, aiming to promote the adoptable experience to minimize the nosocomial SARS-CoV-2 infection in clinical laboratory.

PU-3045

加强独立医检实验室的化学危险品管理

张岩
吉林金域医学检验所有限公司

目的 加强独立医检实验室化学危险品的管理，提高独立医检机构安全意识，强化化学危险品安全意识。

方法 ①制定健全的化学危险品管理制度及存储制度，根据相应的法律法规对化学危险品本身特点进行分类；②建立化学危险品管理委员会，针对管理、使用化学危险品人员应每年至少两次针对性培训及考核；③制定化学危险品的风险评估，通过风险评估来识别潜在未发生的危害；④建立可行有效的化学危险品应急防范预案。

结果 ①确定了化学危险品的危险特点以及储存方式，其中常规的化学危险品进行集中存放、统一管理；特殊的化学危险品应单独存放；所有的化学危险品应实行双人双锁制管理，并对出入库进行检查、验收、登记，进入化学危险品区域的人员必须实行防火措施，不仅规范了化学危险品的存储，也使这些危险品在使用时方便拿取，避免长时间接触；②通过全员培训，考核合格率达到 98%，提升了全员对化学危险品的认知，完善了个人防护措施及应急处置措施。③确定潜在风险，全员知晓率达到 100%，避免了因化学危险品而带来对人员、财产、环境等带来的危害。④应急预案的实施，使全员在遇到紧急情况时有可以及时、有效的应对，将危险和损失降到最低。

结论 综合上述，随着经济不断发展，独立医检实验室越来越多，随之化学危险品的使用量也跟随提升。医检实验室应加强对化学危险品的管理，重视化学危险品的危害，降低不必要的化学危险品事故。

PU-3046

POCT 技术在检验医学领域的应用与研究进展

李进
重庆医科大学

近年来，随着检验新兴技术的迅猛发展，POCT 技术已广泛应用于临床生化检验、血液学检验、分子生物学检验、微生物学检验、免疫学检验等领域中，它可通过与其它检查技术相结合，为临床疾病的诊治提供强有力的依据，是检验医学学科发展不可或缺的一门新兴技术。本文立足于 POCT 技术在检验医学领域的临床应用，简要阐述了 POCT 的概念和演化，详细介绍了 POCT 技术在检验医学领域应用的技术发展及最新研究成果，同时还探讨了 POCT 技术在临床应用中存在的问题及发展前景。

PU-3047

Case Report: Disseminated Talaromyces (Penicillium) marneffei infection in a Chinese Patient with nephrotic syndrome

Chenli Rao、Jieying Zhou、Guizhen Xu、Qiang Huang、Lin Zhang、Ting Fang
The First People's Hospital of Chenzhou Affiliated to University of South China

Background Talaromyces (Penicillium) marneffei is an important pathogenic thermally dimorphic fungus causing systemic mycosis in Southeast Asia. It is now widely recognized that the infection is not limited to HIV-infected patients, and an increasing number of Talaromyces marneffei infections have been reported among non-HIV-infected patients with impaired cell-mediated immunity, including autoantibodies against interferon-gamma, systemic lupus erythematosis, and use of novel targeted therapies. In this study we describe a case of fatal T. marneffei infection in a patient with nephrotic syndrome.

Case presentation A 44-year-old female, previously diagnosed with nephrotic syndrome and treated with prednisolone and tacrolimus (FK 506), was admitted to our hospital presented with fever, oral ulcer and diarrhea. Beforehand, she had been placed on antibiotic treatment in local

hospital. Laboratory results on admission showed kidney injury, glucose homeostasis alteration and inflammation response. CT scans showed bilateral pulmonary infiltrates, pleural effusion, and enlargement of the mediastinal and right axilary lymph nodes. The blood routine test showed thrombocytopenia and some yeast-like cells were found within leukocyte from the peripheral blood smear. Blood cultures drawn on admission grew fungi after 2 days of incubation. Fungal hyphae were discovered under microscope, suggestive of a disseminated infection with T. marneffei. Although our laboratory discovered the yeast cells on her admission and informed clinicians the suspicion of T. marneffei timely. The patient became severely exhausted and even suffered cardiac arrest on the morrow. It was unfortunate that she quitted continued therapy and discharged from hospital in view of poor outcome.

Conclusion T. marneffei infection usually occurred when patients with various autoimmune diseases received high-dose or prolonged treatment with T-lymphocyte-depleting drugs, including corticosteroids, cyclosporine, and tacrolimus, just as our case showed. The major clinical manifestation of this patient was fever, which shows the importance of differentiation between T. marneffei infection and other diseases (eg, mycobacterial, intracellular bacterial diseases) which have symptoms and signs that significantly overlap with it in non-HIV-infected individuals. This is especially true when the response to initial antibacterial treatment is unfavorable. So it would be important for clinicians to have a high index of suspicion on rare fungal infections such as T. marneffei infection in patients receiving immunosuppressor, and be familiar with the clinical characteristics and management of the infection among those at-risk individuals to avoid delay in diagnosis and treatment.

The laboratory diagnosis is performed by identifying the fungus by microscopy and culture from a variety of specimens. As shown in our case, T. marneffei can be found on direct examination of a peripheral blood smear in patients with disseminated disease, and it's relatively earlier than other diagnostic Methods Early diagnosis and appropriate treatment should result in clinical success and microbiological eradication, but delays in a timely diagnosis may result in a fatal outcome. Maybe there is a need to design an algorithm to evaluate such patients with stepwise laboratory investigations.

PU-3048

Using FOCUS-PDCA to improve the management of hazardous chemicals

Huali Li
The First Affiliated Hospital of Xi'an Medical University

Objective To standardize the management of hazardous chemicals by scientific management methods, improve the accuracy of registration of hazardous chemicals in and out of warehouse, as well as ensure the safety and accurate use of hazardous chemicals in clinical work.

Methods According to the FOCUS-PDCA procedure, the problems existing in hazardous chemicals storage and registration were analyzed, the improvement measures were formulated, the management system was improved, hazardous chemicals files were established, and the management of hazardous chemicals in and out of the warehouse was standardized and improved continuously.

Results Through the application of FOCUS-PDCA, the registration accuracy of hazardous chemicals was increased from 12.5% to 98.9%; It improves the staff's understanding and familiarity of hazardous chemicals, so as to ensure using them in clinical laboratory safely, timely and accurately.

Conclusion FOCUS-PDCA has a good effect on standardizing the entry, classification, and storage of hazardous chemicals, and plays an important role in achieving continuous improvement of medical quality and safety, which is worth promoting.

PU-3049

上海市临床实验室 13 个常规化学检测结果互认项目检测质量分析

蒋玲丽
上海市临床检验中心

目的 通过分析上海市临床实验室 13 个常规化学检测结果互认项目室内质量控制（internal quality control，IQC）和室间质量评价（external quality assessment，EQA）数据，了解互认和非互认实验室的检测质量。
方法 计算 13 个常规化学检测项目包括总蛋白（TP）、清蛋白（ALB）、丙氨酸氨基转氨酶（ALT）、天门冬氨酸氨基转氨酶（AST）、γ-谷氨酰基转移酶（GGT）、肌酐（CRE）、尿酸（UA）、尿素（URE）、总胆红素（TBIL）、总胆固醇（TC）、三酰甘油（TG）、铁（Fe）和镁（Mg）2019 年 IQC 数据累积变异系数（coefficient of variation，CV），以 WS/T 403-2012 临床生物化学检验常规项目分析质量指标为标准，评价互认和非互认实验室各项目 CV 合格率。计算 2019 年常规化学 EQA 数据，统计互认和非互认实验室各项目合格率。
结果 互认和非互认实验室 13 个项目 CV 合格率分别为 44.44%～100%和 43.58%～89.86%。GGT,TG，Mg，UA,AST，URE,TC 和 CRE 项目 CV 合格率在互认和非互认实验室比较差异有统计学意义（c2=5.197-13.636，P 值均<0.05）。互认和非互认实验室各项目 EQA 合格率分别为 97.22%～100%和 96.62%～100%,各项目互认和非互认组实验室比较差异无统计学意义（P 值均>0.05）。
结论 互认实验室检测质量优于非互认实验室，检验结果互认可以从市级公立医疗机构试点实施，通过监测 IQC 和 EQA 数据可作为检验结果互认动态监管的依据。

PU-3050

医疗实验室的计算机管理设计与优化研究

宋银森
郑州人民医院

随着人们生活水平的提高和社会的进步，医疗实验水平的高低与医疗实验的应用程度成为衡量医院业务水平的重要标志。引入计算机管理管理系统，不仅能医院的实验活动更加系统化，规则化；同时亦能加强医院对各科室及人员的信息统筹管理与协调。为了对智慧医疗实验室服务的计算机管理进行优化，找到最优解，我们基于 RBF 神经网络对本市医院的实验室计算机进行实验，为其他研究者提供了参考。通过采集相关数据，取得本文对现有的医疗实验室研究进行了归纳分析，总结了现行的实验室存在的问题和发展方向，利用 RBF 神经网络对这些模型进行修正，创新性的从而实现了一种具有效率高、低能耗、反应快等特点的医院实验室计算机管理优化系统。实验结果证明，通过 RBF 神经网络对实验室服务的计算机进行管理优化，计算机管理设计与优化效率有极大的提升，其速度比其他的算法计算快 30%以上，准确值也有极大的提高，比传统医疗实验室提高 20%左右。这表明，RBF 神经网络设计的智慧医疗实验室服务的计算机管理设计与优化可以在医院实验室建设中起到重要作用。

PU-3051

西藏地区某三甲医院临床用血分析及管理对策

陈艳美、王国洪、贡布、索朗央金
拉萨市人民医院检验科

目的 通过 2019、2020 年全年临床用血数据，分析西藏地区某三甲医院临床用血和管理现状，为医院三甲复审和突发重大公共卫生制定相应的输血管理方案和持续改进措施。
方法 统计拉萨某医疗机构 2019-2020 年全年临床用血信息，分析同期 2020 年住院、门急诊患者、手术患者用血量进行比较分析。
结果 2020 年住院人数与 2019 年基本持平，但输血率增加 4.1%；全血、悬浮红细胞输注量分别下降 75.4%、21.0%，血浆使用量增加 38.4%。开展互助献血和加强医院输血质量管理能有效缓解临床用血压力。
结论 新冠疫情对本院临床用血产生明显影响，全血用量下降，血浆用血量上升。通过互助献血和加强医疗机构临床输血管理能有效保证临床用血需求。

PU-3052

宫颈液基细胞学对子宫内膜癌的诊断

张雪莲
南京金域医学检验所有限公司

目的 探讨宫颈液基细胞学对子宫内膜癌尤其是Ⅰ型子宫内膜癌的检出和诊断线索。
方法 回顾 2010 年 12 月至 2019 年 12 月由本中心组织病理诊断为子宫内膜癌患者的术前宫颈液基细胞学涂片（进口耗材 38 例，国产耗材 90 例），对这些涂片中存在的诊断子宫内膜癌的线索及特征进行分析。
结果 128 例中阴性 30 例，非典型子宫内膜细胞(atypical endometrial cells AEM)57 例，宫内膜腺癌 39 例，阳性病例占 75%。1 级子宫内膜样腺癌中高达 72.9 %（35/48）的病例出现了具有诊断价值的中心粒细胞口袋。两种液基产品的灵敏度分别为 65.2%（23/38）和 81.1%（73/90），两组检出率比较，差异有统计学意义($\chi^2 = 6.038$, $P < 0.05$)。
结论 宫颈液基细胞学可作为筛查子宫内膜癌重要方法，国产耗材优于进口新柏氏，除细胞形态的改变与组织结构碎片外中心粒细胞口袋可作为诊断子宫内膜癌的重要线索。

PU-3053

毛细血管内增生性肾小球肾炎患儿肾穿刺组织中 miR-194-5p 表达意义及与 eIF3f 的相关性

李胜涛、彭小友、徐玉娟、曹红、朱军民
郴州市第一人民医院

目的 观察微小 RNA-194-5p（MicroRNA-194-5p, miR-194-5p）在毛细血管内增生性肾小球肾炎（endocapillary proliferation glomerulonephritis, EnPGN）患儿穿刺组织中的表达，分析与真核翻译起始因子 3f（eukaryotic translation initiation factor 3f, eIF3f）的关系。
方法 选择 69 例 EnPGN 患儿作为观察组，同时选择 69 例微小病变性肾小球病患儿作为对照组，均行肾穿刺后行病理活检，应用实时荧光定量 PCR 法检测二组中 miR-194-5p 的表达，应用免疫组化法检测观察二组中 eIF3f 的表达。

结果 观察组肾穿刺组织的病变均呈典型的病理形态。观察组中 miR-194-5p 的表达明显低于对照组，观察组中 eIF3f 的表达明显高于对照组，观察组中 miR-194-5p 的表达在不同病程、是否伴有新月体及急性肾损伤的分组中差别有统计学意义。观察组中 eIF3f 的表达在有无急性肾损伤的分组中差别有统计学意义。相关分析显示 miR-194-5p 与 eIF3f 具有负相关性。
结论 miR-194-5p 在 EnPGN 患儿肾穿刺组织中的表达下降，并参与病变的进展。miR-194-5p 与 eIF3f 具有负相关性。

PU-3054

UBE2T is a prognostic biomarker and correlates with immune infiltration in thymoma, lung adenocarcinoma and gastric cancer

Yunliang Yu、Jiankai Feng
Department of Medical Laboratory, Yantai Affiliated Hospital of Binzhou Medical University, Yantai, Shandong 264000

Aims Ubiquitin-conjugating Enzyme E2T (UBE2T) has been described participated in the occurrence of many tumors. However, cross talk between UBE2T and cancer immunity in diverse cancers remains unclear. Here, we evaluated the clinicopathological significance of UBE2T in different cancers and investigated the correlations of UBE2T to prognosis and tumor-infiltrating lymphocytes in several cancers.
Methods Expression data of UBE2T was extracted from the Oncomine, Gene Expression Profiling Interactive Analysis (GEPIA) and Tumor Immune Estimation Resource (TIMER) databases. The Kaplan-Meier plotter and GEPIA databases were used to investigate the correlation between UBE2T expression and the clinical prognosis of cancer patients. Correlations between UBE2T expression level and tumor-infiltrating lymphocytes as well as gene marker sets of immune infiltrates were analyzed by TIMER.
Results The results revealed that the up-regulated expression level of UBE2T was significantly associated with poor overall survival in patients with breast cancer or lung adenocarcinoma. However, patients with high expression of UBE2T had a better prognosis than the low expression group in thymoma, gastric cancer and ovarian cancer. Moreover, high expression of UBE2T significantly influenced the prognosis of breast, lung and gastric cancer in patients with lymphatic metastasis. There were clear positive or negative correlations between the expression level of UBE2T and the level of infiltration of immune cells in lung, gastric and thymoma cancer.
Conclusions UBE2T may appreciate for having a dual role in human cancers and it may play an important role in recruitment and regulation of immune infiltrating cells in cancers.

PU-3055

浅谈全自动染色机 HE 染色程序调试

张淑正、张效娟
南京金域医学检验所有限公司

目的 探讨全自动染色机正式用于临床样本的染色之前，其染色程序的调试步骤、方法、及问题的解决。确保能稳定、高效、安全地将“手染”作业过渡到“机染”自动化。
方法 以手工染色程序为初始模板，以手工染色的的染色质量、染色用时为“基准”，通过反复进行单架染色、连续 10 架次以上染色，评估并比较染色效果、观察并记录染色时间、分析并解决问题，不断调试机染程序。

结果 调试后的切片机染效果同比手染：①染色质量：机染切片细胞核蓝色、核染色质清晰，细胞浆成红色，核浆对比清晰，切片色彩鲜亮；机染与手染质量比较，基本一致。②染色用时：手染单独进行一架次染色用时 40min，以每 5min 增加一架次切片的频率，连续 10 架切片染色用时共 85min；机染单独一架次染色用时 42min，以每 5min 增加一架次切片的频率，连续 10 架切片染色用时共 87min。两者染色用时上差异不大。③试剂耗用量：机染与手染同步进行，连续 5 天，共染色 3000 张切片，所用试剂的更换规则有所不同，但所耗用试剂量无明显区别。④人员工时耗用：连续 10 架切片手染，需固定 1 位技术员持续在岗，用时共 85min；连续 10 架切片机染，仅上下架切片时需要技术人员手动操作，技术人员不必持续在岗，连续用时共 3min。
结论 调试完成后，获得了一套稳定有效的机染程序，该程序可用于“徕卡-AUTO Stainer XL-1 型全自动染色机”全自动染色机替代“手染”作业，正式用于临床样本的染色工作。

PU-3056

HP 亚甲蓝染色法改善探讨

张淑正、张效娟
南京金域医学检验所有限公司

目的 寻找一种提升 HP 阳性率的亚甲蓝染色检测法。
方法 选取胃镜活检标本 100 例，经过固定、脱水、包埋制成蜡块，每个蜡块切片 3um 厚白片 2 张，分别设为实验组 100 张，对照组 100 张。对照组使用传统方式染色，实验组使用改进过的方法染色。
结果 经两名高年资主治病理医生双盲阅片，两组的 HP 诊断阳性率一致，但在切片质量方面实验组优于对照组。
结论 本研究通过在染色前或染色时进行染液的充分混匀，可以使沉淀物重新溶化于染液中，促使染色效价开始回升，HP 阳性率得到提升；同时发现此时使用高浓度酒精（95%、100%）进行脱水，并不会洗脱掉或极少洗脱掉已结合于 HP 上的染料，其着色强度与传统方法无明显差异；而经过高浓度酒精（95%、100%）脱水后的组织切片再经二甲苯透明，可使组织切片在整个实验过程中均保持湿润状态，组织和细胞未暴露在空气中，其切片透明度相较传统方法显著提升，且组织上无干扰诊断（甚至可能引起误诊）的强折光小点样物，无“碳核”现象。

PU-3057

石家庄应对新型冠状病毒大规模筛查经验总结分析

冯广东
南京金域医学检验所有限公司

2021 年 1 月初，新型冠状病毒肺炎疫情在河北省局部地区出现爆发，尤其以石家庄市藁城区为主，短短数日确诊病例数即出现了较大规模的增长。根据石家庄市疫情防控工作需要，金域医学组建了一批来自全国各子公司近 60 人的核酸检测团队赶赴石家庄，支援石家庄全市开展大规模筛查工作。本文主要针对疫情期间石家庄金域医学检验所大规模筛查所遇到的各类问题总结分析，为可能存在的局部大规模人群筛查提供参考。

PU-3058

独立医学实验室与基层医院共建病原学诊断中心的实践探索

冯广东
南京金域医学检验所有限公司

目的 以南京金域医学检验所与江苏省内 7 家二级医院（其中民营二级医院 5 家，公立二级医院 2 家）共建病原学诊断中心为案例，结合新型冠状病毒肺炎的长期防控趋势，探讨基层医院建设病原学诊断中心的难点及痛点，为基层医院建设病原学诊断中心提供借鉴及帮助。
方法 逐条分析目前独立医学实验室与医院合作共建病原学诊断中心在建设费用、检测设备及检测技术能力等方面所存在的问题，并提出相应的解决方案。
结果 解决了基层医院因短期内缺少资金而无法进行的病原学诊断实验室的建设、设备采购等方面问题，从前期病原学检测平台的场地选择、图纸设计、设备配备、人员培训等做到标准化和统一化，且均通过了生物安全二级备案及江苏省临检中心验收。
结论 合作共建实验室避免了基层医院在实验室建设方面缺经验、走弯路的情况出现，为基层医院建设一个标准的核酸检测实验室提供了一套标准化模板。

PU-3059

抗血小板抗体阳性的相关风险因素分析

李文敏
广东省人民医院

目的 探讨抗血小板抗体阳性的相关风险因素。
方法 采用荧光鼠抗人 IgG 和羊抗人 IgM、IgA，用流式细胞仪测定血小板相关免疫球蛋白（platelet associated immunoglobulin，PAIg）。对 2018 年 1 月-8 月来广东省人民医院拟诊特发性血小板减少性的 303 例患者外周血进行例用流式细胞术（FCM）检测抗血小板抗体（PAIg），同时收集患者的年龄、性别、基础疾病、血常规、凝血指标等资料，采用 spss20.0 数据处理软件分析不同因素对 PAIg 的影响因素，以 P<0.05 表示具有统计学差异。
结果 男性 142 例，女性 161 例，年龄在 0-99 岁之间，平均年龄 53±30.0 岁，性别和年龄对 PAIg 的影响差异无统计学意义。女性怀孕次数对 PAIg 影响差异有统计学意义（P<0.05）。在 PAIg 阳性病例中，抗血小板抗体三项 PAIgG、PAIgM 和 PAIgA 中有两项及以上阳性的占 43.9%；APTT、DDI、自身免疫性疾病（包括 ITP,系统性红斑狼疮，痛风，风湿性关节炎等）都是抗血小板抗体阳性的独立危险因素（P<0.05）。外周血血小板数量与抗 PAIg 具有负相关性（P<0.05）。
结论 外周血血小板数量减少、APTT 延长、DDI 增高是血小板抗体阳性的危险因素；ITP、系统性红斑狼疮、风湿性关节炎等免疫性疾病患者都应该特别注意进行血小板抗体的检测，以期及早发现及早对症治疗。

PU-3060

干/湿化学法对不同方式处理脂血样本检测结果的一致性研究

汤新乐[1]、达尼亚尔•泰来提[1]、刘子峰[2]、梁静[1]
1. 新疆医科大学第六附属医院
2. 新疆维吾尔自治区第三人民医院检验科

目的 探讨干式化学和经低温高速离心/生理盐水稀释降脂处理后的脂血样本湿式生化检测结果的一致性研究分析，探讨不同检测系统检验结果之间是否具有可比性。

方法 收集 2021 年 1 月-2 月新疆医科大学第六附属医院、新疆维吾尔自治区第三人民医院血脂异常患者样本 30 例为研究对象,将每例患者的脂血标本平均分成 3 份。对其中 1 份脂血标本进行干式生化检验，分别检测钙离子（Ca2+）、天门冬氨酸氨基转移酶（AST）、谷丙转氨酶（ALT）、血清葡萄糖（GLU）、淀粉酶（AMY）、肌酐（Cr）浓度；对其它 2 份脂血标本分别使用低温高速离心法、生理盐水稀释进行去脂处理后用湿式生化检验上述项目。观察用原脂血标本进行干式生化检验及用低温高速离心/生理盐水稀释处理后湿式生化检验各项指标的水平并分析其相关性。
结果 经低温高速离心降脂处理后的脂血样本，湿式生化检测 ca2+、AST、ALT、GLU、AMY、Cr 结果与干式生化相比均存在统计学差异（P＜0.05）；线性回归分析：Ca2+、GLU、Cr 湿式化学检测结果与干式化学结果相关性较低，AST、ALT、AMY 湿式化学检测结果与干式化学结果相关性较好。经生理盐水稀释降脂处理后脂血样本，湿式生化检测 ca2+、AST、AMY、Cr 结果与干式生化相比存在统计学差异（P＜0.05），ALT、GLU 结果无统计学差异（P＞0.05）；线性回归分析：GLU、Cr 湿式化学检测结果与干式化学结果相关性较低。
结论 面对严重脂血样本，使用低温高速离心/生理盐水稀释法进行去脂处理，可在一定程度上减少 ca2+、ALT、AST、AMY、GLU、Cr 项目湿式生化检验结果受到的干扰，使湿式化学和干式化学检测脂血样本时结果具有一致性；除 ALT 外，其余项目定量检测结果在不同检测系统之间存在统计学差异，无法保证脂血样本检测结果的准确性。

PU-3061

化疗前 D-dimer 值在预测转移性结肠癌患者治疗效果中的临床价值

杜娜
天津医科大学肿瘤医院

目的 化疗前 D-dimer 值在预测转移性结肠癌患者治疗效果中临床价值。
方法 回顾性收集 2019 年 1 月至 2020 年 12 月期间我院收治的 107 例首次化疗的转移性结肠癌患者病历资料和实验室指标，化疗前外周血 D-dimer 值、中性粒细胞/淋巴细胞比值（NLR）、血小板/淋巴细胞比值（PLR）、全身免疫炎症指数（SII）、CEA、CA199、ALB、FBG 等并对检测结果进行统计分析。
结果 低 D-dimer 组患者的 PFS 明显高于高 D-dimer 组(D-dimer=1004.87ng/ml)。生存分析也显示低 D-dimer 组患者的 PFS 明显高于高 D-dimer 组。NLR、PLR、SII、CEA、CA199、AFP、ALB 正常组与异常组生存期差异无统计学意义（P>0.05）。
结论 化疗前 D-dimer 值对转移性结肠癌患者一线治疗的 PFS 有预测作用。可能是独立于病理类型和临床分期的转移性结肠癌预后指标。D-dimer 值越高，PFS 越短。

PU-3062

独立医学实验室在实验室感染控制与管理方面的探讨

谢曙光、李玲
广州金域医学检验中心

在医改的推动下，独立医学实验室在国内的行业规模快速增长，有效缓解患者排队就医难的问题，有利于间接提升公立医院服务的水平，社会影响力突显，在 2020 年新冠核酸检测中发挥了较大的作用。国内独立医学实验室启步晚，迅速的发展加重风险存在，而规模化、自动化标本集中检测，多科室交叉共享样本，如果实验室感染控制的缺位、投入不够等都有可能引发实验室人员感染，甚至环境污染，引发公共生物安全事故。所以研究和规范独立医学实验室的实验室感染控制，对于保证实验室安全和社会安全都具有非常重要的意义，必须引起独立医学实验室的高度重视。我国在

相关法律法规中明确要求实验室设立单位应当承担实验室感染控制工作，但目前独立医学实验室感染控制缺乏相关研究工作，相关理论、标准、做法基本上是引用医院院感管理模式，然而，独立医学实验室往往都是独立于医院之外单独检测场地，无病房和诊室，不与患者接触，如何做好独立医学实验室感染控制工作值得深入研究和探讨，本文从独立医学实验室设计，特别是普通型和加强型二级生物安全实验室设计、院感体系建设和相关制度制定、实验室感染性物质及实验活动的风险识别与评估、院感监测的项目和周期、实验室工作人员生物安全和感染控制知识培训、环境与物品消毒与感染性病原微生物灭菌、生物安全设备设施投入、实验室感染控制监督检查与持续改进等八个方面系统性研究和规范独立医学实验室感染控制要求，确保独立医学实验室感染控制有效，降低生物安全事故发生。

PU-3063

1566 例围生期孕妇生殖道分泌物 B 群链球菌培养及耐药性分析

王迪
桂林医学院第二附属医院

目的 研究围生期孕妇生殖道分泌物中 B 群链球菌感染情况及耐药性分析。
方法 对桂林医学院第二附属医院就诊的 1566 例围生期孕妇生殖道分泌物进行病原菌培养，对检出的 B 群链球菌进行药物敏感性实验。
结果 1566 例围生期孕妇生殖道分泌物中检出 B 群链球菌 149 株，阳性检出率为 9.5%。各年龄段检出率从高到低依次为：36-40 岁（11.7%）、26-30 岁（10.7%）、41-45 岁（9.1%）、31-35 岁（8.9%）、18-25 岁（7.1%），各年龄段检出率之间比较差异没有统计学意义（P>0.05)。检出的 149 株 B 群链球菌中红霉素、四环素、克林霉素、复方磺胺、左氧氟沙星、莫西沙星、氯霉素的耐药率依次为 52.3%、48.3%、42.2%、38.9%、28.8%、15.4%、10.7%，对美洛培南、头孢噻肟、头孢吡肟、阿莫西林、青霉素、替考拉宁、万古霉素、利奈唑胺的耐药率为 0。
结论 B 群链球菌对碳青霉烯类、第三代第四代头孢类、青霉素类、糖肽类抗生素敏感性较高，对大环内酯类、四环素类、林可霉素类、磺胺类抗菌药耐药性较高，临床不建议使用。

PU-3064

血小板输注效果影响因素分析

张强、张敏
东南大学附属中大医院

目的 探究影响血小板输注效果的因素，寻求有效的规避策略。
方法 收集本院 2016 年 7 月至 2017 年 10 月收治的共 583 例血小板减少患者的身高、体重、血小板输注量等数据资料，对患者输注血小板前血小板计数以及输注后血小板计数进行检测并记录结果，根据 PTR 诊断标准(CCI、PR%)判断患者的血小板输注效果。对患者的性别、年龄、疾病类型、血型以及累计输注次数与血小板输注效果进行相关性分析。
结果 583 例接受血小板输注患者中发生血小板输注无效患者为 200 例，血小板输注无效率为 34.30%。不同性别输注效果不同，女性输注无效率明显高于男性（P<0.05）；不同年龄组输注效果也不相同，随着年龄增加无效率升高，差异具有统计学意义（P<0.01）；不同疾病和不同累计输注次数也导致血小板输注效果的不同（p<0.01）；血型与血小板输注效果无相关性。
结论 患者血小板输注效果与性别、年龄、疾病类型和累计输注次数密切相关，而血型不是影响血小板输注效果的因素。

PU-3065

90 例 D 组染色体多态性统计学分析

任伟丹、刘玉霞、丁利霞、岳文兵
郑州金域临床检验中心有限公司

目的 探讨 D 组染色体多态性在年龄、性别上的分布情况及对生长发育、生殖的影响和相应的临床效应。
方法 采用外周血淋巴细胞培养和 G 显带技术，对送检郑州金域临床检验中心有限公司的 13 500 例外周血标本进行培养、染色体制备及分析，从中筛选出 90 例 D 组染色体多态性标本进行统计学研究。
结果 在 90 例 D 组多态性标本中，共检出 6 种核型，其中 pstk+ 49 例，占 54.44%；ps- 14 例，占 15.56%；ps+ 13 例，占 14.44%；cenh+ 8 例，占 8.89%；inv 4 例，占 4.44%；pss 2 例，占 2.22%。在 D 组多态临床效应中不孕不育 45 例，占 50%，其次为发育异常 30 例，占 33.33%。D 组多态性的人群分布中女性略高于男性，年龄分布以 21~30 岁为主，共 45 例，占比 50%，其次为 0~10 岁，29 例，占 32.22%。
结论 在 90 例 D 组多态性标本中，共检出 6 种核型，以 pstk+最多见，其次从高到低依次为 ps-、ps+、cenh+、inv、pss；其临床表现多样，以不孕不育为主，其次为发育异常；人群分布女性略高于男性，年龄分布以 21~30 岁为主，其次为 0~10 岁。

PU-3066

全血微量元素五项参考区间验证

王伟佳
吉林金域医学检验所有限公司

目的 对全血微量元素五项的参考区间进行验证，以保证检测在免疫分析物的改变、分析方法的改变、患者群体的改变、检测系统的改变及临床反馈的情况下保证检测质量。
方法 仪器为 ICP-MS7900，校准品为国家有色金属及电子材料分析测试中心的商业品，根据健康状况调查表在每个参考区间设置的年龄段（16 岁）选取 20 份符合的样本进行检测，男女各 10 例。
结果 全血钙，正态-95%的置信区间计算范围为(53.1-65.5)mg/L，厂家声明的参考区间为（46.0-84.0）mg/L；全血铁（<16 岁），正态-95%的置信区间计算范围为（397.9-459.0）mg/L，厂家声明的参考区间为（373.5-557.2）mg/L、全血铁（>16 岁），正态-95%的置信区间计算范围为（400.9-552.5）mg/L，厂家声明的参考区间为（380.8-572.3 ）mg/L；全血镁，正态-95%的置信区间计算范围为（33.4-43.2）mg/L，厂家声明的参考区间为（26.4-50.4 ）mg/L；全血铜（<16 岁），正态-95%的置信区间计算范围为（880.0-1129.5）ug/L，厂家声明的参考区间为（800.0-1290.0）ug/L、全血铜（>16 岁），正态-95%的置信区间计算范围为（724-1453）ug/L，厂家声明的参考区间为（720.0-1750.0）ug/L；全血锌（<16 岁），正态-95%的置信区间计算范围为（4.3-6.0）mg/L，厂家声明的参考区间为（3.7-7.3）mg/L、全血锌（>16 岁），正态-95%的置信区间计算范围为（5.7-6.8）mg/L，厂家声明的参考区间为（4.8-9.3）mg/L。
结论 通过验证，以上参考区间 100%落入厂家声明，实验室可以使用参考区间对病人的结果进行报告。

PU-3067

血清 25-OHD 检测项目的影响因素研究

廉春晖
吉林金域医学检验所有限公司

目的 开展血清 25-OHD 检测平台，检测东北三省内血清维生素 D 情况，为临床干预提供理论依据。
方法 确定样本处理方法，采用蛋白沉淀及液液萃取等方法对样本进行前处理，采用 AB Sciex Triple Quad 4500 MPX 系统，将处理后的样本经过液相进样、分离进入质谱，在 MRM 多反应监测模式下，质谱一级四级杆对其分子母离子进行筛选通过，而后进入碰撞室被氮气分子打碎成相应子离子，最后在二级四级杆监测特异性的子离子，根据相应子离子在检测器产生的信号强度及所绘制的标准曲线来定量待测物的浓度。然后制定搭建平台计划：试剂耗材准备、辅助设备、预实验及方法学验证等。
结果 在预实验过程中，发现采用本实验室方法检测 25-OHD，受温度，震荡幅度，以及耗材本地等影响较大。最后通过不断的测试及预实验，确定蛋白沉淀步骤温度需要控制在 25℃±2，并且震荡幅度需达到约 2500rpm 效果最佳;前处理耗材采用进口 Axgen 的 1.5ml 及 2.0ml 离心管对待测物质影响较小;
结论 维生素 D 的主要生理作用是调节钙的代谢，从而维持骨骼健康。最新的研究指出，多种慢性病（如动脉硬化、高血压、冠心病、糖尿病、乳腺癌、结肠癌、前列腺癌，慢性感染性疾病、自身免疫病等）的发生均与维生素 D 缺乏有关。经过基质效应、基质效应、携带效应、分析灵敏度、分析测量范围、正确度分析测量范围精密度等方法学验证，成功搭建血清 25-OHD 检测平台，可检测人体维生素 D 情况，为临床干预提供指导。

PU-3068

尿液有机酸 GCMS-QP2020 检测的方法学验证

高洪宇
吉林金域医学检验所有限公司

目的 由于尿中含有的氨基酸，糖类，脂肪和其他代谢终末或中间产物，而这些代谢产物的定量水平反应身体的代谢情况，通过对这些相关代谢产物的测定，可以对血遗传代谢病进行辅助诊断与鉴别诊断。因此有必要对尿液有机酸测定的方法学进行验证。
方法 应用仪器为气相色谱质谱联用仪 GCMS-QP2020。阴阳性质控品均为自配质控品。通过中间不精密度、重复性不精密度、准确度、携带效应几方面对尿液有机酸的检测方法进行验证。
结果 中间不精密度：通过对仪器的每日质控数据进行分析，来评估仪器的精密度，分析的数据从开始进行方法学验证之时前一个月的质控数据，计算其均值 X、标准差 SD 与变异系数 CV，CV 小于 30%；重复性不精密度：通过选取加入有机酸标准品的阴性样本，按照方法平行处理 12 个样品后上机检测，监测有代表性指标的精密度，计算其均值 X、标准差 SD 与变异系数 CV，CV 小于 30%；准确度：通过对已发报告的临床样本进行留样复查，其阴阳性均符合；携带效应：通过 6 组高浓度阳性样品和空白样品的数据比较，阳性样品无残留，且不影响下一样品检测。
结论 以上中间不精密度、重复性不精密度、准确度、携带效应的验证，说明用该方法进行尿液有机酸检测可被接受，满足临床标本检测的要求。

PU-3069

2020 年长春地区孕妇尿碘监测结果分析

李飞
吉林金域医学检验所有限公司

目的 运用电感耦合等离子体质谱法(ICP－MS)直接测定孕妇尿中碘元素的含量，为长春地区孕妇的饮食结构和含碘食盐用量提供理论指导依据，保证合理的碘摄入，促进优生优育。
方法 采集不少于 5mL 尿液，置于聚乙烯塑料或玻璃试管中，严密封口。采用 0.25%四甲基氢氧化铵和 0.02%TritonX-100 混合溶液对尿样稀释 10 倍混匀后直接用等离子体质谱仪进行分析。收集长春地区 2020 年在吉林金域进行体检的孕妇尿中碘元素数据结果 491 例，进行结果分析。
结果 该方法检出限为 2.1μg/L，精密度＜3.6%，加标回收率为 96.1-109.2%。尿中碘化物中位数为 163.9μg/L，其中＜100μg/L 占有 9.2%，提示碘营养缺乏；＞500μg/L 占有 2.6%，提示碘营养过量。
结论 随着人们生活水平的提高，科学意识的增强，孕期保健工作彰显尤其重要。碘是甲状腺激素合成的重要原料，在大脑的生长和发育过程中甲状腺激素扮演的重要角色，碘是脑组织正常发育必不可少的营养物质，孕妇的碘营养水平及其重要。根据 WHO/UNICEF/ICCIDD 推荐的尿中碘化物标准，碘化物中位数在 150-250μg/L 之间为碘营养适宜，2020 年长春地区孕妇碘营养水平处于适宜状态，碘营养缺乏和过量状态占比较小，可能是由于饮食烹调方式导致不足或过量，或者由于孕早期妊娠反应、后期水肿、高血压并发症导致碘摄入不足。根据尿中碘元素的监测，可及时调整孕期饮食结构，最大程度保证孕妇和胎儿的健康水平。同时，ICP－MS 法测定尿中碘元素的含量，方法操作简便、稳定、灵敏，准确度高，可用于临床大数据量分析。

PU-3070

56℃灭活 30min 对胃功能三项检测结果的影响

渠文涛、张杰、万鹏、史小芹
郑州安图生物工程股份有限公司

目的 为保障临床实验室操作人员的生物安全，通过会对一些含有潜在传染源的血清样本进行灭活处理，即将样本在 56℃灭活处理 30min。但灭活后样本的检测结果是否受影响，一直是检验工作者关注的重点。本文研究了血清样本灭活前后胃功能三项指标（PGI、PGII 和 G-17）检测结果的变化，以指导临床实验室对检测胃功能三项的样本采取正确的处理方法。
方法 取 10 例进行胃功能三项检测的血清样本，等分成 2 份，一组作为对照，在 2-8℃保存，另一组样本在 56℃条件下灭活 30min。取出两组样本，待恢复至室温后，使用 AutoLumo A2000 检测系统和配套试剂盒，平行考核两组样本的胃功能三项检测结果，并进行灭活前后的结果进行比对分析，观察灭活对检测结果是否有影响。
结果 与对照组相比，样本灭活后，三个项目的检测结果均有不同程度的降低，其中部分样本在灭活处理之后，基本变成了零值，即待测物全部被破坏掉。对照组三项的检测结果分别是：PGI 61.46±38.51 ng/ml；PGII 14.18±6.72ng/ml；G-17 5.07±3.73 pmol/L；灭活组三项的检测结果分别是：PGI 0.08±0.04ng/ml；PGII 0.11±0.07 ng/ml；G-17 0.82±0.59 pmol/L；结果差异有统计学意义（P＜0.05）。
结论 血清样本在 56℃灭活 30min 处理后，胃功能三项的检测结果均有非常显著的降低，说明三种待测物在 56℃条件下较不稳定，推测可能是由于高温导致蛋白变性或蛋白结合位点变性，使结果有显著差异。因此，临床实验室在进行胃功能三项检测时，血清样本不能进行灭活处理，否则会导致检测结果的不准确。

PU-3071

2020 年长春地区儿童维生素 D 检测结果分析

曲丹
吉林金域医学检验所有限公司

目的 检测长春地区表现健康的儿童体内 25 羟基维生素 D 含量，为本地区儿童维生素 D 缺乏情况研究提供理论支持。
方法 选取 2020 年在我公司检测的表现健康的儿童 1000 例，根据年龄分为三组：0-1 岁，1-6 岁，6-14 岁，采用蛋白沉淀及液液萃取等方法对样本进行前处理，运用高效液相色谱串联质谱仪，经过三重四极杆对其进行筛选，根据相应子离子在检测器产生的信号强度及所绘制的标准曲线来定量待测物的浓度。
结果 1、在不同年龄段儿童维生素 D 检测中 1-3 岁组 270 人，3-6 岁组 360 人，6-14 岁组 370 人，分析不同年龄段儿童维生素 D 水平，结果发现不同年龄段儿童维生素 D 的平均值之间差异有统计学意义 (P＜0. 05)；2、不同年龄段维生素 D 缺乏率分别为：1-3 岁 54.44%，3-6 岁 68.74%，6-14 岁 80.04%，分析不同年龄段维生素 D 的缺乏率，对比参考标准值，发现不同年龄段儿童维生素 D 的缺乏率差异有统计学意义(P＜0. 05)；3、分析不同性别儿童维生素 D 缺乏率差异无统计学意义（P＞0.05）。
结论 在长春地区 1-14 岁儿童维生素 D 检测中，随着年龄的增长，缺维生素 D 的情况逐渐上升，在不同性别儿童中，钙缺乏率无显著差别。维生素 D 可调节钙的代谢，从而维持骨骼健康。若儿童存在维生素 D 缺乏情况，则可能造成骨质疏松、龋齿、儿童佝偻病,危害极大，家长和社会各方面应当对儿童合理膳食，科学补充，监测及维持儿童体内的维生素 D 处于正常水平，保证其健康生长发育。

PU-3072

鲍曼不动杆菌多重耐药机制和用药的研究

孙悦
吉林金域医学检验所有限公司

目的 鲍曼不动杆菌属于革兰阴性杆菌，近些年来，多重耐药鲍曼不动杆菌在院内检出率逐渐上升，由于其多重耐药机制复杂，使得临床治疗十分困难。本文主要就鲍曼不动杆菌的耐药机制和用药进行研究。
方法 选用不同的抗生素，如舒巴坦复合制剂、碳青霉烯类、多粘菌素类 E 或联合使用抗生素等治疗鲍曼不动杆菌感染，用药时严密观察药物疗效，同时收集鲍曼不动杆菌耐药机制的研究资料，对其进行总结和研究。
结果 鲍曼不动杆菌的耐药机制主要存在以下 5 个方面：耐药基因、药物灭活酶、16S rRNA 甲基化酶、整合子及药物主动外排泵与外膜蛋白的协同作用。
结论 近些年来，国内鲍曼不动杆菌多重耐药发生率逐年增长，特别是耐碳青霉烯类鲍曼不动杆菌，四环素类和碳青霉烯类药物的应用，使鲍曼不动杆菌多重耐药有增多的现象，多粘菌素类抗生素对其在体外有明显的抗菌作用，但目前临床应用报道有限，还需进行进一步的研究。因此，实时监控鲍曼不动杆菌的传染源及其耐药，通过强化医院内预防感染措施，能减少鲍曼不动杆菌的传播，减少其耐药发生概率。加强管理措施，能够有效控制医院性感染，合理使用抗生素是防止和减少鲍曼不动杆菌感染及多重耐药性出现的重要对策。

PU-3073

三种不同试剂对新型冠状病毒的方法学验证结果比较

宋丽影、迟忠雨、张馨月
吉林金域医学检验所有限公司

目的 针对不同厂家生产的新型冠状病毒 2019-nCoV 核酸检测试剂盒（荧光 PCR 法）对新型冠状病毒的方法学进行验证，主要包括正确度、重复性精密度及检出限。最终对三种不同试剂做的新型冠状病毒方法学验证结果进行比较。
方法 使用深圳亚能试剂及仪器对样本进行自动提取，分别使用圣湘、伯杰和达安三种试剂扩增,对其正确度、重复性精密度、检出限进行验证。选取圣湘试剂检测为阳性的 20 例样本，分别用伯杰和达安试剂重复检测，评估其正确度；使用购买的水平 2 质控品，厂家为郑州标源，批号为 20210129-1，分别用三种试剂在同一次实验中重复检测该质控品各 20 次，记录结果并计算均值、标准差和变异系数 CV（%）。评估其重复性精密度；使用购买的水平 2 质控品浓度为 3 次方，稀释至 2、1 次方。平行检测 5 次，检测结果是否符合试剂盒 CT 值≤40 为阳性的判断标准，分别验证三种试剂盒的检测下限。
结果（1）通过选取用圣湘试剂检测为阳性的 20 例样本，再用伯杰和达安试剂检测后仍为阳性，正确度验证为 100%。
（2）评估其重复性精密度的结果为：圣湘试剂的 N 基因 CV 值为 3.12%，O 基因 CV 值为 3.91%,; 伯杰试剂的 N 基因 CV 值为 2.32%，O 基因 CV 值为 1.13%；达安试剂的 N 基因 CV 值为 3.29%，O 基因 CV 值为 4.35%,均小于 5%；三种试剂均满足说明书上面的要求，验证通过。
（3）最终验证新冠检测试剂盒圣湘检测下限 200copies/ml；伯杰检测下限 500copies/ml；达安厂家检测下限 500copies/ml。均符合用途要求。
结论 通过对三种试剂的方法学进行验证比较，均与试剂说明书一致，能够满足其用途。

PU-3074

二甲基塞来昔布抑制乳腺癌他莫昔芬敏感和耐药细胞增殖的机制研究

王映芬、谭潭
郴州市第一人民医院

目的 获得性他莫昔芬耐药是乳腺癌内分泌治疗的主要挑战，对其耐药机制的研究始终是人们关注的热点。本研究旨在探讨 2,5-二甲基塞来昔布(DMC)对他莫昔芬(TAM)敏感以及耐药乳腺癌细胞增殖的影响，并探讨其可能的作用机制。
方法 1.MTT 法检测 TAM 对 MCF-7 及 MCF-7/TamR 的增殖抑制作用并使用 SPSS 计算各细胞系在 72h 的 IC50 值，得出 MCF-7/TamR 的 RF；采用蛋白印迹技术检测 MCF-7、MCF-7/TamR 的蛋白基础表达情况，评估 MCF-7/TamR 的耐药特性。
2.MTT 及细胞克隆实验检测 DMC 对细胞的增殖抑制作用，筛选后续实验的药物浓度和作用时间。
3.实验分组：对照组(control)、TAM 干预组(TAM)、DMC 干预组(DMC)、TAM 联合 DMC 干预组(TAM+DMC)，MTT 实验检测不同干预对细胞增殖的影响，采用蛋白印迹技术检测细胞增殖相关蛋白的变化情况。
4.流式细胞术检测不同干预对细胞凋亡的影响，采用蛋白印迹技术检测细胞凋亡相关蛋白的变化情况。
5.蛋白印迹、细胞免疫荧光、彗尾实验探讨 DMC 抑制细胞增殖的作用机制。
6.小鼠成瘤实验及免疫组化验证体外细胞实验结果。**结果** 1.MCF-7/TamR 的 RF 为 2.231；Rb、P-Rb 在 MCF-7/TamR 中低表达。

2.TAM+DMC 作用显著抑制细胞增殖，P-Rb、Rb、MCM7、PCNA 表达降低。
3.TAM+DMC 作用显著诱导细胞凋亡,Bcl-2、survivin 表达降低，Cleaved PARP、Caspase-3 表达增加。
4.DMC 降低 MCM7/Rb 表达，增加 γ-H2AX 表达，诱导 DNA 损伤及激活 DNA 损伤修复相关蛋白，与 TAM 联合后更显著。
5.DMC 显著抑制动物体内肿瘤生长及 Rb/MCM7 蛋白表达。
结论 DMC 或 DMC+TAM 在体内外抑制他莫昔芬敏感及耐药乳腺癌细胞增殖，其作用机制可能与 DNA 损伤相关。

PU-3075

某医学实验室质量不良事件的分析

陈振朋、张维、李永霞
西安金域医学检验所有限公司

目的 通过分析质量不良事件，识别实验室质量管理过程中的高风险环节并加以控制，从而提升实验室质量体系运行能力。
方法 统计了某医学实验室近 3 年产生的质量不良事件，不良事件的来源包括实验室日常质量监督，内部审核、管理评审，外部的第二方审核和第三方审核，并对所发生的质量不良事件进行了分类分析。
结果 2018 至 2020 年 3 年间总共发生质量不良事件 345 起，其中记录控制方面 63 起，占比 18.2%；文控管理方面 48 起，占比 13.9%；人员管理方面 43 起，占比 12.5%；实验室检验结果质量保证方面 42 起，占比 12.2%；试剂耗材管理方面 35 起，占比 10.1%；设施与环境方面 24 起，7.0%；检验过程方面 23 起，占比 6.6%；实验室设备方面 22 起，占比 6.4%；外部服务于供应方面 9 起，占比 2.6%；持续改进方面 8 起，占比 2.3%；其他 28 起，占比 8.1%。在 345 起不符合事件中，其中建议项 101 项，观察项 104 项，一般不符合项 139 项，严重不符合项 1 项。
结论 建立良好的质量管理体系，并保证其有效运行，对提升实验室服务质量和效率尤为重要。通过对以上质量不良事件的分析，加强实验室工作人员的质量培训和教育，提升人员的实验室质量管理能力和水平，对促进实验室质量管理体系高效、健康的运行至关重要。

PU-3076

医学实验室关键指标的建立和运行

陈振朋、张维
西安金域医学检验所有限公司

目的 医学实验室关键指标指与实验室质量管理、技术运作和客户运作相关的关键过程监控指标，包括质量指标、技术指标和服务指标，实验室建立完善的关键指标管理程序，保证其良好运行，有助于提高实验室质量管，促进实验室质量体系持续改进，提升临床服务能力和水平。
方法 建立实验室关键指标的管理程序，规定关键指标程序实施范围、职责、关键指标的来源，明确关键指标监测的目的、方法和采集程序。确定实验室监测的关键指标，其来源包括卫健委规定的关键指标、行业标准和技术规范、ISO15189、实验室识别出的重点关注点以及与临床服务和体验相关性较大的指标。建立之初，通过对往年相关指标在实验室的表现值及变化情况制定关键指标的目标值，针对不同指标的属性制定其监控周期。建立的质量指标从以下几个维度监控：当月是否达到目标值；当月数据与上月数据（或上一统计周期）是否有较大差异；连续几个月或统计周期数据是否有不良上升或下降趋势；分析当年数据与历年数据是否有较大差异（在定本年度质量指标时需重点考量）；采集的数据是否与实际情况相符。对发现的异常情况进行分析，找出根本原因加以控

制，并定期监测确保依从。以一年为周期，在下年度对本年的关键指标进行回顾性分析，依据分析结论制定下年度关键指标目标值。
结果 通过关键指标程序的运行，及时发现实验室质量管理体系运行过程中的不足和存在的问题，并及时进行纠正，有效的减少了质量事件的发生，提高了质量体系运行的效率。
结论 关键指标做为实验室质量管理体系的一部分，尤其是在质量体系持续改进过程中发挥着非常重要的作用，建立和运行关键指标体系程序，对实验室质量管理至关重要，值得推广。

PU-3077

流式细胞技术在临床微生物定量质控品中的应用研究

徐蓉
上海市临床检验中心

目的 采用流式细胞技术，建立细菌定量分析的质量控制方法，为细菌定量检测提供更好的质量控制方法。
方法 根据细菌感染临床诊断阈值，设计病原菌的种类和数量，采用流式细胞技术联合琼脂菌落计数法，对样品中细菌数量进行准确定量分析，建立细菌定量分析的质量控制方法。
结果 采用定量计数方法，能够确定流式细胞技术定量结果与琼脂菌落计数法两种计数方法的对应关系，建立细菌定量分析的质量控制方法。
结论 采用定量计数方法，能够更好评价临床微生物实验室病原菌的定量检测能力，促进细菌鉴定和药敏试验的标准化，从而进一步提高实验室的临床微生物检出能力。

PU-3078

新冠抗体检测两种方法的性能评价及临床应用探讨

黄玮
长治医学院附属和平医院

目的 采用胶体金法和荧光免疫层析法检测新型冠状病毒血清特异性抗体，对两种方法进行性能评价，并对新型冠状病毒血清特异性抗体临床应用进行探讨。
方法 收集 2020 年 1 月 23 日至 3 月 2 日我院住院患者血清样本共 20 例。分别使用胶体金法和荧光免疫层析法检测各样本 IgM+IgG 总抗体及 IgM 抗体，并计算两种抗体试剂的敏感性、特异性、阳性预测值、阴性预测值、符合率及 Kappa 值等指标。
结果 胶体金法：敏感性为 91.6%（11/12）；特异性为 62.5%（5/8）；阳性预测值为 78.6%（11/14）；阴性预测值为 83.3%（5/6）；符合率为 80%（16/20）；与 RT-PCR 法 Kappa 值 0.565。荧光免疫层析法：敏感性为 83.3%（10/12）；特异性为 87.5%（7/8）；阳性预测值为 90.5%（10/11）；阴性预测值为 77.8%（7/9）；符合率为 85%（17/20）；与 RT-PCR 法 Kappa 值 0.693。
结论 从符合率来看，两种方法检验效能相当，均可进行新冠抗体检测。两种方法 Kappa 值与 RT-PCR 法检测结果中度一致。但是仍应明确，抗体检测只能作为核酸检测的有效补充检测指标，或疑似病例诊断中与核酸检测协同使用，或用于聚集性疫情的溯源，不适用于低流行区人群的筛查。

PU-3079

幽门螺杆菌既往及现症感染与肥胖/超重间相关性探讨

郭长青
江苏省中医院（南京中医药大学附属医院）

目的 探讨幽门螺杆菌（Hp）既往及现症感染与肥胖/超重之间的相关性。
方法 选取江苏省中医院 2017 年 5 月至 2019 年 8 月间接收的体检者 285 例作为受试者，分别测定各例 Hp IgG 抗体与现症感染蛋白抗体(CIM)，另测量各例身高与体重，计算其体重指数（BIM）；统计超重与非超重受试者二种抗体阳性人数，组间比较；统计不同性别及年龄组超重与非超重受试者二种抗体阳性人数，组间比较。
结果 Hp IgG 抗体阳性率、CIM 阳性率、Hp IgG 抗体与 CIM 同时阳性率在超重与非超重二组间均有显著性差异（$P < 0.05$）；超重组 Hp IgG 抗体阳性率、CIM 阳性率、Hp IgG 抗体与 CIM 同时阳性率在不同年龄组间有显著性差异（$P < 0.05$）。
结论 幽门螺杆菌既往及现症感染可引起肥胖/超重，二者间具有明显相关性，在高龄人群尤其显著。

PU-3080

PCR 实验室的区域设计及各区域要求探讨

文少佳、梁建萍、赵婷、张强、李永霞、张维
西安金域医学检验所有限公司

目的 通过对 PCR 实验室的分区及各区域要求进行探讨从而使得对 PCR 实验室有充分的认识和了解，确保按照规范进行相关基因扩增实验，进而保证检测结果的准确可靠。
方法 通过国家相关的法律法规要求，对 PCR 实验室进行相应的分区及各区域要求进行探讨。
结果 PCR 实验室对检测结果的准确性，可靠性，安全性起到至关重要的作用，因此实验内部的分区，以及对各区的要求都显得尤为重要。根据 PCR 操作流程方向，PCR 室主要分为缓冲区，试剂准备区，样本制备及加样区，扩增区，产物分析区。为了防止交叉污染，对 PCR 实验室的各实验房间压差控制一定要严格处理，尤其是基因扩增和产物区的气流不能互相串通，以免引起检测提取数据的重叠失效。各区域要求也略有不同，试剂配制室及样品处理室宜呈微正压，以防外界含核酸气溶胶的空气进入，造成污染；可以通过控制进风风量大于排风风量达到正压效果；而核酸扩增室及产物分析室应呈微负压，以防含核酸的气溶胶扩散出去污染试剂与样品，可以通过控制排风风量大于进风风量达到负压效果；在理想情况下，PCR 实验室缓冲间内，可设置正压，使室内空气不流向室外，室外空气不流向室内。
结论 在实际实验工作中要严格按照 PCR 实验室的分区要求进行实验，避免造成不必要的污染，从而影响实验结果的准确性和可靠性。

PU-3081

第三方医学检验行业产业链及业务模式分析

文少佳、赵婷、张强、梁建萍、张维、李永霞
西安金域医学检验所有限公司

目的 通过对第三方医学检验行业的产业链和业务模式的分析，对行业发展的前景进行一定的预测。
方法 采用第三方医学检验行业报告及各医学检验公司的业务模式的了解，对其产业链及业务模式进行分析。

结果 第三方医学检测公司主要以承接医院及各类医疗服务机构的检验业务，借助专业化的医疗器械，试剂及检验人员对待检样本进行集中检验，并将检验结果，临床解释及建议报告于送检单位，通过检验结果进行相应的临床治疗和医学实验。其上游供应商包括各种仪器生产供应商及检验试剂生产供应商，下游主要是各种医院及医疗服务机构，结合临床诊断，提供相应的检测服务。因其处于产业链的中游，可与各医疗机构形成合作，因此其集中化处理模式使得其可在检测项目数量及检测成本方面均形成较大的优势。

目前全国各区域检验公司及中心也依托医院检验科的实验室和设备资源，提供精细化的医学检测检验服务，形成了“医保+医检”整合服务、组建医联体整合资源、与医联体牵头医院合作共建、与三级医院协作共建等一系列创新型服务模式，同时基于各检测公司的规模、渠道、研发、生产、科研等优势差异，形成集研发、生产、销售，服务于一体各具特色的业务模式。

结论 第三方医学检验实验室通过集中化检测及特色的临床服务，形成了低成本，短时间，高质量，优服务的优势，因此第三方医学检验行业极大可能会成为将来的医学诊断的新风口。

PU-3082

第三方医学检验中心实验室员工能力的培养及综合素质的提高

文少佳、梁建萍、张强、李永霞、张维
西安金域医学检验所有限公司

目的 随着第三方医学检验行业的高速发展，相关检验人员的专业能力和综合素质直接影响检验结果的准确性和可靠性，进而对临床治疗产生决定性的作用，因此对相关检验人员的专业能力和综合素质的培训显得尤为重要，本文主要结合本实验室的实践经验, 为科室人员培训和能力评估的具体实施提供建议。

方法 1.对新进入科室人员，首先进行实验室生物安全和应急预案演练, 消防安全培训等突发事件的培训。

2.具体科室根据岗位要求进行相关专业知识的带教培训，经过一定时间的培训后进行相应的考核和测评，达到一定要求后方可进行相应的检验工作；特殊岗位如基因扩增室，HIV 初筛等岗位需参加相关机构或部门组织的培训班和上岗培训；

3.定期对员工进行职业道德素养的培训；

4.定期进行专业能力的考核和评估，对不合格者重新进行相应的培训并停止相应的检测项目，直至考核通过方可重新回到岗位进行相应检测。

结果 按照以上的要求进行员工培训及考核后，科室员工整体专业能力和素质均有明显提高，科室的检验工作更加快速精准的完成。

结论 本实验室按照以上要求对检验人员进行培养，一方面对日常检验工作有了明显质量和速度上的提升，另一方面，为当突发重大社会公共卫生事件时，培养出了专业能力过硬，综合素质达标的公共卫生后备人才。

PU-3083

第三方医学检验行业现状分析及前景预测

文少佳、张强、梁建萍、张维、李永霞
西安金域医学检验所有限公司

目的 基于国内目前第三方医学检验行业的发展现状，分析行业产业链和市场竞争格局，进一步预测该行业的发展前景并提出合理的发展建议。

方法 通过对我国与美国，日本，欧洲等发达国家第三方医学检验行业的发展阶段以及市场渗透率的比较，结合我国的国家政策，对该行业的发展前景进行预测病提出合理化建议。

结论 美、日、欧等发达国家第三方医学检验行业起步早，目前均已进入稳定发展阶段，且市场渗透率均在 40%以上。与其相比，我国的第三方医学检验行业目前处于竞争沉淀期，市场渗透率还较低，距进入稳定发展期还有一段距离。但近年来随着国家政策的支持和市场的需求，我国的第三方医学检验行业快速发展，据不完全统计，截止 2020 年 3 月，国内在业第三方医学检验实验室从 2012 年的 129 家增长到 1570 家，且依然呈现较高的增长趋势。同时，此次新冠疫情爆发后，在医院面对巨大的核酸检测压力的前提下， 国家政策的扶持以及广阔的市场需求给第三方医学检测机构带来重大发展机遇。因此，在后疫情时代，我国的第三方医学检验行业在各个有力条件的推动和加持下将会迎来的更大的发展契机。

PU-3084

Profiling serum cytokines in COVID-19 patients reveals IL-6 and IL-10 are disease severity predictors

Huan Han
Department of Clinical Laboratory, Renmin Hospital of Wuhan University

Background Coronavirus disease 2019 (COVID-19), which is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), was first reported in December, 2019, and the affected countries has grown rapidly and recently WHO has been declared it as a pandemic. While the majority of patients were considered mild, critically ill patients involving respiratory failure and multiple organ dysfunction syndrome are not uncommon, which could result death. We hypothesized that cytokine storm is associated with severe outcome.
Method We enrolled 102 COVID-19 patients who were admitted to Renmin Hospital (Wuhan, China). All patients were classified into moderate, severe and critical groups according to their symptoms. 45 control samples of healthy volunteers were also included. Inflammatory cytokines profile of serum samples were analyzed by specific immunoassays.
Results showed that COVID-19 patients have higher serum level of cytokines (TNF-α, IFN-γ, IL-2, IL-4, IL-6 and IL-10) than control individuals. Within COVID-19 patients, serum IL-6 and IL-10 levels are significantly higher in critical group (n = 17) than in moderate (n = 42) and severe (n =43) group. Using univariate logistic regression analysis, IL-6 and IL-10 are found to be predictive of disease severity and receiver operating curve analysis could further confirm this result (AUC = 0.841, 0.822 respectively).
Conclusion Our result indicated higher levels of cytokine storm is associated with more severe disease development. Among them, IL-6 and IL-10 can be used as predictors for fast diagnosis of patients with higher risk of disease deterioration. Given the high levels of cytokines induced by SARS-CoV-2, treatment to reduce inflammation-related lung damage is critical.

PU-3085

Evaluation of Serum GDF15, AFP, and PIVKA-II as Diagnostic Markers for HBV-Associated Hepatocellular Carcinoma

Juanjuan Chen、pingan zhang
Renmin Hospital of Wuhan University

Objective To evaluate the potential diagnostic value of GDF15 alone and its combination with PIVKA-II and AFP for HBV-associated HCC.
Methods Serum levels of GDF15, PIVKA-II, and AFP were measured in 110 patients with HBV-associated HCC, 70 patients with HBV-related LC, 70 patients with CHB and 110 healthy subjects.

Results Serum GDF15 was positively related to the levels of PIVKA-II and AFP in HCC patients (r=0.352 and r=0.378, all P＜0.0001). When ROC curve was plotted for HCC versus all controls, serum GDF15 had diagnostic parameters of AUC 0.693, sensitivity 67.30%, and specificity 66.70%, which were lower than PIVKA-II and AFP (all P＜0.0001). When ROC curve was plotted for HCC versus LC, the combination of GDF15 and PIVKA-II had the highest diagnostic accuracy of AUC and specificity than other combinations (all P＜0.0001).
Conclusions GDF15 is a potent serum marker for the detection of HBV-associated HCC, and PIVKA-II combined with GDF15 can improve the diagnostic accuracy of HBV- associated HCC.

PU-3086

Elevated serum C1q levels in children with sepsis

Huan Li、Pingan Zhang
武汉大学人民医院

Objective To analyze the serum complement C1q levels in children with sepsis, and explore the suggestive effect of serum C1q levels on the condition of children with sepsis.
Methods The clinical and laboratory data of children with sepsis (n = 95) and healthy children (n = 71) in Renmin Hospital of Wuhan University from January 2019 to October 2019 were collected, and each index of the two groups was compared. Then we divided children with sepsis into three subgroups based on the Pediatric Critical Illness Score (PCIS): non-critical group, critical group, and extremely critical group. The serum C1q and PCT levels of the three subgroups were analyzed, and the correlation analysis was carried out between the levels of serum C1q and PCT levels as well as PCIS among children with sepsis. Finally, we analyzed the serum C1q levels of septic children infected by different pathogens.
Results The serum C1q levels of children with sepsis were significantly higher than those of healthy children (median 198.4 vs. 186.2 mg/L, P < 0.001). In the analysis of subgroups, the serum C1q levels of non-critical group, critical group, and extremely critical group septic children were 182.80 (166.75, 195.85) mg/L, 219.90 (209.10, 246.40) mg/L and 249.95 (239.10, 272.25) mg/L respectively, which were correlated with the severity of the disease. At the same time, we also found that serum C1q in children with sepsis was positively correlated with PCT levels (r = 0.5982, P < 0.001), and negatively correlated with PCIS score (r = -0.6607, P < 0.001). The serum C1q levels of septic children with bacterial infections, mycoplasma infections, viral infections, and co-infection were higher than those of the control group (P < 0.05).
Conclusion The serum levels of C1q in children with sepsis were increased and related to the severity of sepsis, suggesting that C1q may be involved in the occurrence and development of sepsis, which had reference value for the preliminary diagnosis and severity classification of sepsis.

PU-3087

糖尿病患者胰腺外分泌功能不全与腹部症状的原因

朱时帅
哈尔滨医科大学第一附属医院

胰腺有内分泌和外分泌两种功能，它们相辅相成，紧密合作，有助于食物的消化、吸收和新陈代谢。早在十多年前，就有研究表明，相当数量的糖尿病患者存在胰腺外分泌功能不全。糖尿病几乎影响到身体的每个器官系统，器官受累的程度取决于疾病的持续时间和严重程度，以及其他合并症。胃肠道副作用包括胰腺病、小肠细菌过度生长、食道动力障碍、胃食管反流病、胃瘫、神经病和非酒精性脂肪肝。

PU-3088

冷凝集素对血常规参数的影响及解决处理方法探讨

朱时帅、史永胜
哈尔滨医科大学附属第一医院

目的 探讨冷凝集素对血细胞分析参数的干扰以及处理方法。
方法 临床收集冷凝集患者 EDTA-K2 抗凝静脉血，根据标本的外观，将其分为无变化，果冻状，沙粒状。通过比较 37℃水浴法加热法前后，血浆置换法，以及预稀释法用 Beckman Coulter DXH 800 全自动血液分析仪对标本各种方法处理前后的血细胞参数进行检测，以手工镜检为金标准进行对照实验验证以上方法能否消除冷凝集素的影响，并采用统计学方法对检测参数进行评价。
结果 直接上机检测，冷凝集现象可导致 RBC、HCT 结果假性减低，MCH、MCHC 结果增高，并出现红细胞直方图，散点图异常，仪器报警提示 RBC 凝集及双峰 RBC 分布，但 WBC，PLT，Hb 结果无明显变化。对其进行温浴，血浆置换及预稀释处理后,即刻上机检测,可使红细胞凝集现象有所改善，从而得到正确的红细胞系列参数。
结论 冷凝集现象可导致多个血细胞检测参数失真, 传统 37℃水浴法检测对于高效价冷凝集处理效果不明显, 血浆置换法和预稀释法对红细胞系列参数则能起到明显改善结果, 从而使血细胞各项检测参数结果得以校正, 为临床提供准确参考数值。

PU-3089

临床用细胞培养的质量控制

刘军权
杭州金域医检验所有限公司

随着国家《“十三五”国家战略性新兴产业发展规划》以及《“健康中国 2030”规划纲要》的颁布。细胞药物的开发正在生物技术领域展开，许多以往难以治疗的疾病目前都得到了很好的控制甚至治愈。细胞产品的应用分为医疗级和消费级应用。这些产品的应用除了更加关注安全性以外，对细胞产品质量和有效性评估提出了更高的要求。由于细胞在应用之前必须经过实验室培养和扩增，每个相关的环节都需要明确质量标准。本文根据细胞培养制剂产品特点，提出细胞培养实验室质量控制的一些思路，从细胞生产质量管理规范、细胞制剂产品生产用原材料、制备工艺与过程控制、质量研究和质量控制等方面系统。基于细胞制剂产品的细胞来源、体外操作、临床应用等方面的不同而赋予产品不同的临床应用风险程度，在技术审评过程中，应该坚持基于风险等级的评价理念，减少不必要的冗余要求，减轻不必要的研究与检验负担，同时监管部门也应与研究单位通力合作，建立并不断完善、优化和更新相应的管理制度和技术指南及标准，推进细胞产业的健康发展。细胞制剂产品的研发技术日新月异，产品种类不断更新，细胞体外操作的复杂程度不断提升，适用的领域不断拓宽，基于现有的认知水平和人体经验，很难提出全面的、具体的、具有先见性的技术管理规范和要求，仍需遵循具体情况具体分析的原则进行质量研究和质量控制。基于细胞制剂产品的细胞来源、体外操作、临床应用等方面的不同而赋予产品不同的临床应用风险程度，在技术审评过程中，应该坚持基于风险等级的评价理念，减少不必要的冗余要求，减轻不必要的研究与检验负担，同时监管部门也应与研究单位通力合作，建立并不断完善、优化和更新相应的管理制度和技术指南及标准，推进细胞产业的健康发展。

PU-3090

参加美国病理家协会（CAP）非妇科细胞病理学能力验证计划经验分享

庞晓川
吉林大学第一医院

目的 通过参加美国病理学会(CAP) 非妇科细胞病理学能力验证计划，评价检验室细胞病理组非妇科细胞学诊断水平，根据对回报结果的分析，来进一步提高非妇科细胞学的检测质量。
方法 将收到的 CAP 非妇科细胞学样本按照常规涂片进行检测，按 CAP 的要求将结果上报，并及时对回报结果进行分析。
结果 参加 CAP 能力验证计划 10 次 55 张涂片中，10 次 PT 活动所得分数均大于 80 分。本室诊断良恶性能力较强，准确率 100%，但具体亚分类的诊断水平有待提高。
结论 通过参加 CAP 能力验证计划不仅了解美国细胞病理学诊断标准，开拓视野，并且能够了解薄弱之处，有的放矢，积极学习，增强了诊断水平。将个人能力评估标准化，从整体上提高了非妇科细胞学的检测质量。

PU-3091

人羊膜上皮细胞和人羊膜间充质干细胞的研究进展

谢军花[1,2,3]、刘军权[1,2,3]、薛玲玲[3]、陈锦阳[3]
1. 龙泉市人民医院
2. 杭州金域医学检验所有限公司
3. 浙江卫未生物医药科技有限公司

人羊膜上皮细胞和人羊膜间充质干细胞存在于人羊膜组织中，随着胎儿的娩出，人胎盘羊膜组织几乎是作为废弃物处理。但人羊膜细胞可塑性强，具有多向分化的潜能，能够分化为来自不同胚层的细胞；并且免疫原性低，移植不会发生免疫排斥反应。因此，成为近年来研究的热点。成为干细胞药物产品的标准是原料来源必须广泛，取材无创。人羊膜上皮细胞和人羊膜间充质干细胞具备以上条件，将其应用于诸多疾病的治疗中，如心肌梗塞、脑梗塞、肾损伤等，均已取得良好的疗效，此外还为许多疑难杂症提供了治疗方向。本文将从羊膜细胞的生物学特性、培养方法、表面标记物、分化潜能和临床应用等方面进行综述。

PU-3092

间充质干细胞治疗肺纤维化的研究进展

杨建兰[1]、刘军权[1,2,3]、冯欣丽[3]、庄盼[3]
1. 杭州市下城区中西医结合医院
2. 杭州金域医学检验所有限公司
3. 浙江卫未生物医药科技有限公司

肺纤维化是一种具有破坏性和不可逆性的弥漫性肺间质性疾病。研究发现，产生肺纤维化的原因是成纤维细胞灶的出现导致大量细胞外基质沉积，胶原积聚，肺基质逐渐破坏，肺泡结构破坏，同时肺泡上皮细胞不能进行正常的修复重建，最终导致正常肺组织结构的破坏等。目前在临床上，吡非尼酮和尼达尼布等西药以及部分中药能够改善患者的临床预后，但是它们并不能完全阻止肺功能的下降，或者逆转纤维化的病理改变，只能延缓疾病进展。间充质干细胞及分泌的外泌体或者细

胞因子对于特发性肺纤维化的发病机制有一定的改善作用，能减轻炎症反应、减少氧化应激、调节细胞外基质等作用。本文对肺纤维化的发病机制和间充质干细胞的治疗进行综述。

PU-3093

弹性工作制在临床微生物检验工作中的初探

弓艳娥
长治医学院附属和平医院

目的 回顾性分析我院 2013 年到 2020 年细菌培养标本送检及报告情况，为微生物室工作人员配置和排班提供科学依据。
方法 收集 2013 年到 2020 年细菌培养标本送检及报告数据，对我院微生物室特设的中午班和小夜班收检的标本量和发放的药敏报告量及 TAT 时间进行统计分析。
结果 在 2013-2020 年，中午班收检标本量占全年标本量的 13%-15%左右；小夜班收检标本量占全年标本量的 11%-13% 左右；2017-2020 年小夜班审核的药敏报告量占同年药敏报告总量量的 17%-22%，2017-2020 年药敏报告的实验室周转时间（TAT）比 2013-2016 年明显缩短。
结论 在临床微生物检验工作中，根据临床送检标本情况及时调整工作思路、实行弹性工作制，是一种有效提高微生物检验工作效率、缩短检验周期的手段。

PU-3094

实验室风险管理程序的建立和运行

陈振朋、张维
西安金域医学检验所有限公司

目的 风险管理作为一种常态化的实验室质量管理方法，已逐步走进实验室。建立完善的风险管理程序，对实验室日常风险管理具有非常重要的指导作用。
方法 首先建立实验室风险管理程序，说明风险管理的价值、原则、目的，规定风险管理的职责、风险评估时机和程序。在风险管理程序的指导下，建立实验室风险管理模式。对实验室包括人、机、料、法、环、测以及检验前、检验中、检验后整个检验环节进行全面的风险评估，识别各个环节可能存在的风险。风险评估的内容一般包括风险事件的识别、评价、控制和监控。风险评估采用的工具有头脑风暴法、专家指导、鱼骨图法、根源树法，矩阵法、5Why 法等多种方法联合使用。依据建立起来的风险评估报告，对实验室质量体系进行梳理和完善。在日常风险管理工作中，通过日常监督、质量检查、管理评审、临床反馈等识别出风险管理过程中出现的新风险和不受控的风险，并对该事件进行评价，确定其优先级别，制定对应的处置措施加以控制和记录，并持续跟踪确保依从。
结果 通过风险评估，预先识别出实验室质量体系中的不足和可能存在质量事件，及时发现及时处理，有效的预防实验室质量事件的发生，并通过日常风险监督，使整个风险管理形成一个闭环，减少了实验室质量事件的发生，保证实验室质量体系更加健康有效的运行。
结论 在实验室建立风险管理程序并规范运行，对减少实验室质量事件发生、财产损失，提高临床服务能力和水平有非常重要的价值。

PU-3095

克罗恩病发病机制和间充质干细胞治疗研究进展

廖雨琴[3]、吴小佳[2]、刘军权 Liu[1,2,3]、谢军花[1]
1. 龙泉市人民医院
2. 浙江卫未生物医药科技有限公司
3. 杭州金域医检验所有限公司

克罗恩病（CD）是一种易复发且发病症状多样性的慢性肠道疾病，目前发病机制尚不明确。CD 的常规治疗是通过药物、手术等方法以抑制炎性反应和调节局部免疫平衡为手段。近几年间充质干细胞（MSCs）疗法作为 CD 新的治疗手段越来越被重视。MSCs 来源于发育早期的中胚层多能干细胞，具有自我更新、复制和多向分化潜能的干细胞，有抗炎、免疫调节、组织修复和促进血管新生的作用，可实现肠道免疫重建，减少免疫介导的肠道炎症发生等功效，是 CD 最具潜力的新型治疗手段之一。本文根据近几年应用 MSCs 治疗 CD 的研究报道综述如下。

PU-3096

基于 HACCP 及 FMECA 的风险管理法在分析前不合格标本管理中的应用

王海燕、郭笑然、杜秋明
吉林大学第一医院

目的 探索运用 HACCP 及 FMECA 的风险管理法降低分析前不合格标本发生率，提高标本质量，以减少分析前错误对检验结果的影响。
方法 依据危害分析与关键控制点(HACCP)原理及失效模式、影响及其危害性分析（FEMCA）方法，经检验科与护理部共同设计、实践， 通过确定“吉林省不合格静脉血液样本量化指标管理”项目、建立小组、 明确标本分析前环节不合格错误类型、 运用 HACCP 系统确立关键控制点、 对关键控制点进行 FMECA、 对评分较高环节进行防范方案改进、对改进方案进行实施及评估 7 步， 进行不合格标本防范的风险管理。
结果 表明该风险管理法实施效果良好，且较为灵活实用，是适用于检验科与护理部等多部门对分析前不合格标本进行风险管理的方法体系。
结论 HACCP 及 FMECA 的风险管理法的应用,提高了分析前标本的质量,降低不合格标本发生率。

PU-3097

急性呼吸道感染患者中呼吸道合胞病毒感染的流行情况及临床特征

丁细霞
南方医科大学珠江医院

目的 了解急性呼吸道感染患者中呼吸道合胞病毒（respiratory syncytial virus, RSV）的流行特征及其相应的临床特点。
方法 以南方医科大学珠江医院 2009 年 11 月至 2016 年 6 月收治的有发热呼吸道症状患者为研究对象，采集鼻拭子标本 3494 份，提取标本 RNA，采用 qRT- PCR 方法进行 RSV 检测，并对 RSV 阳性标本进行临床上常见的 7 种（10 个亚型）呼吸道病毒的检测，以了解混合感染情况。

结果 共检测患者标本 3494 份，其中 RSV 阳性标本 675 份，总阳性率为 19.3%。四个季节中 RSV 检出率存在统计学差异（p＜0.001），并以春节最高，冬季次之，夏秋两季最少。RSV 感染患者随着年龄的增长检出率逐渐降低，并以 3 岁以下儿童检出率最高，占 RSV 阳性标本数的 90.5%（611/675），儿童患者检出率明显高于成年患者（p＜0.001），男性患者检出率明显高于女性患者（P =0.049），住院患者检出率明显高于门诊患者（p＜0.001）。混合感染标本 161 份，其中双病毒感染标本 144 份，三种病毒混合感染 16 份，四种病毒混合感染 1 份，并以鼻病毒和合胞病毒混合感染率最高，住院患者混合感染率明显高于门诊患者（P＜0.001）。RSV 感染组除了流涕和胸痛等临床症状不存在统计学差异外（P＞0.05），其他临床症状包括咽喉痛、咳痰、头痛、乏力、寒战/畏寒、肌肉酸痛、气促/呼吸困难等均存在统计学差异（P＜0.05），此外，RSV 组与非 RSV 组在临床诊断上也存在临床差异（P＜0.001）。
结论 RSV 是引起 3 岁以下儿童呼吸道病毒感染的主要病原体，也是引起 3 岁以下儿童呼吸道病毒感染住院的主要原因，临床上应加强对该年龄段儿童的防护。

PU-3098

嗜麦芽窄食单胞菌对复方新诺明耐药机制研究进展

杨勇文 Yang
中南大学湘雅医院

嗜麦芽窄食单胞菌（Stenotrophomonas maltophilia,SMA）现已成为重要的医院机会病原体。其引起的感染具有较高的发病率和死亡率，且对绝大多数抗生素天然耐药，是临床抗感染治疗的难题。复方新诺明（trimethoprim-sulfametoxasole,SXT）是临床治疗 SMA 感染的首选抗生素，国内外耐药监测显示已出现 SXT 耐药菌株，检出数量逐年升高，临床抗感染治疗将面临严峻的挑战。因此，本文将对耐复方新诺明的嗜麦芽窄食单胞菌的耐药机制进行综述。

PU-3099

临床医生如何选择检验项目及合理填写申请单

魏亚权、张维
西安金域医学检验所有限公司

目的 分析临床医生如何选择检验项目及合理填写化验申请单
方法 1.检验项目的种类越来越多，检验实验室应与临床医生交多流与沟通，介绍该项目的诊断实验的灵敏度，特异性，预测值等实验特性，使临床医生在选择化验项目时可供参考。
2.临床医生必须按照要求填写申请单上所有信息；包括姓名、性别、年龄、门诊或住院号、科别、临床诊断以及其他特定的识别等填写清楚，以保证实验结果的可靠性和准确，无年龄、性别，不同年龄和不同性别的人群有不同的参考范围。这些都是导致检验单或检验结果出现与临床偏差的重要原因。
3.送检标本应再申请单上注明标本类型、全血、血清、血浆、胸腹水、脑脊液或尿等，不同的标本类型对结果有不同的解释。比如内生肌酐清除率测定需要病员身高、体重及 24 小时尿量等信息，申请日期未填，无法确定标本送检时间。
4.申请单上临床医生签名未填或不清，当检验人员出具报告需要了解更多的临床资料或病史时，紧急情况下无法与临床医生取得联系，会延误对病人的抢救和治疗。
结果 保证检验实验数据的可靠性，为临床提供全面、快速，准确的循证资料。
结论 检验科室人员要加强与临床的沟通交流，增进相互理解，而要达到与临床科室互相学习、交流，两者架起基础医学和临床医学之间的友谊桥梁。

PU-3100

2016-2020 年郑州某三甲医院现患率调查分析

郭娟
郑州人民医院

目的 为了解本院乃至本地区医院感染现状和抗菌药物使用情况，针对总体趋势评价我院实际效果和问题不足，对 2016-2020 年连续 5 年住院患者感染率进行了调查，分析了解某三甲医院感染的实际情况和变化趋势及抗菌药物使用状况，评判医院感染的危险因素。
方法 采用横断面调查方法，调查当日以病区为单位，由管床医生按医院感染监控员要求，填写床旁调查表和调查登记表。调查内容包括患者一般情况、手术情况、感染情况（感染类型、感染部位、病原微生物、侵入性操作、危险因素、抗菌药物使用及微生物送检情况、感染相关的检验与检查结果。对 2016-2020 年每年所有住院患者进行医院感染横断面统计调查，分析 5 年现患率的医院感染情况。
结果 2016-2020 年共统计出 10422 例住院患者，其中医院感染 227 例（2.18%）、241 例次（2.31%）；连续 5 年感染部位均以下呼吸道为主，感染科室主要是重症医学科；医院感染病原体为革兰阴性菌居多，主要是肺炎克雷伯菌(34.95%)、鲍曼不动杆菌(12.62%)和铜绿假单胞菌(10.68%)；革兰阳性菌(9.71%)主要以金黄色葡萄球菌(2.91%)和粪肠球菌(2.91%)为主，连续 5 年病原菌中检出的多重耐药菌以肺炎克雷伯菌居多。抗菌药物平均使用率为 30.77%，联合用药均以一联用药为主。抗菌药物使用率比较差异无统计学意义，预防药物使用率和一联用药方面则有差异学意义，病原学标本送检差异也有统计学意义。
结论 连续 5 年该院院内感染现患率始终保持在较低水平，院内感染防控与抗菌药物管理取得一定成效。但医院仍需加强对重症医学科等重点科室的管理，科学制定医院感染的有效措施，加大对医护人员的无菌操作、手卫生的管理以及抗菌药物使用与环境清洁消毒防控，尽可能减少医院感染的发生。

PU-3101

开发 LIS 功能实现 2019 新型冠状病毒核酸及抗体自动审核和综合报告的尝试及探讨

李利娟[1]、丁利霞[1]、胡正川[1]、陶然[2,3]
1. 郑州金域临床检验中心有限公司
2. 广州金域医学检验中心有限公司
3. 广州医科大学金域检验学院

目的 实现新型冠状病毒核酸及血清学抗体结果自动审核和综合报告，提升临床服务
方法 根据新型冠状病毒检测流程的风险控制需求、检测结果意义，使用金域检验自行开发的自动审核系统设置 20 条自动审核规则，包括 3 条结果审核规则和 17 条结果解释规则。实验室信息管理系统（LIS）对新冠核酸和抗体结果自动审核并综合至一张报告单，实现自动报告
结果 LIS 成功进行结果审核和综合，结果解释类规则使用率占 99.7%，结果审核类规则使用率占 0.3%，自动审核缩减新型冠状病毒样本检测周转时间（TAT）2.7 小时，尚未发现任何 LIS 执行缺陷。
结论 通过自动审核和综合报告可以控制内部风险、提供结果解释，提升报告处理效率和临床服务质量，为检验临床的良性互动提供保障。

PU-3102

肠杆菌科与宿主健康的关联分析

吴凡
南方医科大学珠江医院

肠杆菌科细菌是常见的人类微生物组成员，是影响肠道微生态的重要菌科，并与多种营养代谢性疾病相关。然而目前对于肠杆菌科在人群中的流行率、丰度、结构组成、宿主疾病关联等基本信息的描述仍不清晰。因此，需要较大的样本量来揭示人群肠道中肠杆菌科的共性，并在此基础上进一步探究肠杆菌科与宿主生活方式、与其他肠道菌群的关系以及与宿主疾病之间的关联。

PU-3103

kit/D816V 基因突变阴性的 1 例慢性嗜酸性粒细胞白血病的病案讨论

陈月梅
四川大学华西医院

目的 探讨慢性嗜酸性粒细胞白血病（CEL）的临床特征以及临床诊疗方法，从而总结该类疾病的临床特征。
方法 回顾分析慢性嗜酸性粒细胞白血病(CEL)1 例病患的临床资料和诊断治疗方法。
结果 慢性嗜酸性粒细胞白血病除了白血病的临床特征外伴有嗜酸嗜碱性粒细胞的异常增生，并且浸润各脏器官的单克隆性增殖表现。
讨论 本文就我院临床收治的一位病人伴 MPN 未见基因突变、-kit/D816V 基因突变阴性。染色体为正常核型的临床表现讨论。病人进行伊马替尼治疗后缓解出院，因肝脾肿大再次入院，入院后发热采用达沙替尼治疗，停用伊马替尼。症状缓解后进行父系 HLA 5/10 相合异基因外周血造血干细胞移植，粒细胞植活后。因肺部感染再次入院治疗。酪氨酸激酶抑制剂(比如伊马替尼) 成为治疗 CEL 患者的首选方案，且效果显著。然而，不同重组基因类型对伊马替尼的敏感性及疗效差别显著。

PU-3104

BCR-ABL1 阳性伴 FLT3-ITD 及多种基因突变的原发性急性髓系白血病的实验室检测及临床特征分析

陈月梅
四川大学华西医院

目的 探讨 BCR-ABL1 阳性伴 FLT3-ITD 及多种基因突变的原发性急性髓系白血病（AML）的诊断和治疗，为研究这种罕见 AML 亚型的临床特征及预后意义提供临床参考。
方法 对伴有 BCR-ABL1、FLT3-ITD 和其它多种基因错义突变的原发性 AML 患者进行实验室临床诊断，并总结其临床及实验室特征。
结果 细胞形态学示原始细胞。原始细胞免疫表型为 CD13+、CD33+、CD34+（部分）、CD117+和 HLA-DR+。染色体核型分析示存在 t（9；22）形成的费城（Ph）染色体。髓系白血病 34 种高频基因筛查示 FLT3-ITD 阳性，且 DNMT3A、BCOR、IDH2、BCORL1 和 RUNX1 基因均检测到错义突变。结合历史实验室检查结果，该病例符合 BCR-ABL1 阳性 AML。患者接受伊马替尼、地西他滨、高三尖杉酯碱及盐酸阿糖胞苷化疗方案及抗感染治疗，总体生命体征平稳，出院随访。

结论 BCR-ABL1 阳性的原发性 AML 病例报道较少，尚未形成标准化的诊断和治疗方案，MICM 分型，尤其是细胞遗传学和分子生物学相关检测对其诊断和预后评估极为重要。本病例能够为 BCR-ABL1 阳性 AML 的临床和实验室特征提供资料。

PU-3105

血清炎性因子及血小板参数与肺癌的相关性研究

金亚雄
四川大学华西医院

目的 为探讨肺癌患者血清各炎性因子水平变化、血小板相关参数变化以及血清炎性因子与血小板相关参数之间的相关性。
方法 本研究回顾性纳入 2018 年 1 月~2020 年 1 月来华西医院就诊的 100 例肺癌患者，选择同期来华西医院健康体检中心体检的 100 例健康人做对照组，分别测定血清炎性因子水平及血小板相关参数，分析肺癌患者血清炎性因子与血小板相关参数的相关性。
结果 肺癌患者血清降钙素原、C 反应蛋白以及白介素 6 水平显著高于健康对照组（P 均<0.001）；肺癌患者血小板计数显著升高（P<0.001），而平均血小板分布宽度较低（P<0.001）；肺癌患者血清降钙素原、C 反应蛋白以及白介素 6 水平与血小板计数呈明显正相关（P 均<0.001），血清降钙素原和 C 反应蛋白水平与平均血小板体积及血小板分布宽度未见明显相关关系（P 均>0.05），血清白介素 6 水平与平均血小板体积未见明显相关关系（P=0.154），血清白介素 6 水平与血小板分布宽度呈显著负相关关系（P=0.041）。
结论 肺癌患者血清降钙素原、C 反应蛋白、白介素 6 水平显著升高，血小板计数也显著升高，且血清降钙素原、C 反应蛋白、白介素 6 水平与血小板计数呈明显正相关，血清炎性因子水平以及血小板参数可共同作为肺癌预后判断指标，为患者进一步治疗方案的选择以及治疗疗效的判断提供更准确的参考。

PU-3106

应用 ISO20914 将常规化学项目不确定度应用于检验报告的探讨

曲波、高昕、尹晓雪、张云丽、赵红梅
中国医科大学人民医院辽宁省人民医院

目的 探讨不确定度应用于检验报告的可行性。
方法 应用 ISO20914 提供方法计算实验室不确定度，评价不确定度是否满足行标要求，并计算每日不确定度以报告形式提供给临床。
结果 长期不确定度满足行标要求，并且葡萄糖项目的不确定度在临床决定水平附近时可以给内分泌科医生提供帮助。
结论 不确定度在具有临床决定水平的项目上可以帮助临床医生作出更恰当的诊治。

PU-3107

2 型糖尿病患者血清游离脂肪酸水平以及与空腹血糖的相关分析

林妍榕
南方医科大学第二附属医院珠江医院

目的 探讨 2 型糖尿病患者血清中游离脂肪酸（FFA）的水平，并探讨其与空腹血糖（FBG）的相关性。

方法 采取在珠江医院确诊为 2 型糖尿病的患者血样 82 份和正常对照血样 30 份，进行空腹血糖和游离脂肪酸检测，并进行相关性分析。
结果 2 型糖尿病组 FFA 水平较对正常对照组明显升高（P<0.01）；相关性 2 型糖尿组 FFA 与 FBG 成明显正相关（r=0.303，P<0.01）
结论 FFA 可以很好地反映 2 型糖尿病患者血糖情况，为该疾病提供新的诊断依据。

PU-3108

胸苷激酶 1 在癌性胸腹水方面的探讨

邓智铭
南方医科大学珠江医院

目的 目前针对胸腹水性质的鉴别诊断是医学难题，本次研究通过检测胸腹水中的胸苷激酶 1 的水平，来评估胸苷激酶 1 是否能用于鉴别诊断癌性胸腹水，进而为临床探索出一种新型的，可靠的鉴别诊断癌性胸腹水的方法。
方法 于 2014 年 10 月-2015 年 1 月，收集广州市珠江医院住院部临床胸腹水标本共 92 例，其中 42 例癌性胸腹水标本为实验组，50 例良性胸腹水标本为对照组,两组同时采用免疫点印迹化学发光法进行胸苷激酶 1 水平的测定并对其进行相关性分析；根据所得数据，绘制 ROC 曲线初步确定胸苷激酶 1 对癌性胸腹水的鉴别界限。
结果 与对照组相比，实验组胸腹水中胸苷激酶 1 的水平明显高于对照组（P＜0.05），差异有统计学意义；根据绘制的 ROC 曲线，本次研究初步确定以大于 3.10pg/ml 为诊断界限，其敏感度为 71.4% 特异性为 74.0% 。
结论 本次研究中癌性胸腹水中胸苷激酶 1 的水平显著升高，其在鉴别癌性胸腹水方面具有一定的临床意义和应用前景。

PU-3109

小剂量兔抗胸腺细胞免疫球蛋白在肾移植中的应用

潘沅
南方医科大学珠江医院

目的 评价小剂量兔抗胸腺细胞球蛋白(rATG)在同种异体肾移植术中应用的临床价值。
方法 回顾性分析我院 2016 年 1 月至 2017 年 1 月肾移植术后小剂量应用 rATG 临床病例患者共 107 例。
结果 84 例预防性应用 rATG 患者，81 例肾功能恢复正常。23 例急性排斥反应（AR）经 rATG 治疗后 22 例逆转，有效率 95.65%。术后出现移植肾功能延迟恢复（DGF）预防性应用 rATG 37 例（34 例恢复），32 例未使用 rATG (27 例恢复)，两组差异没有统计学意义 (P＞0.05)。DGF 平均恢复时间 rATG 组（18.22±13.74）d、非 rATG 组（24.76±16.34）d，差异有统计学意义(P<0.05)。小剂量应用 rATG 患者术后 3 年内感染率为 8.4%，而未使用 rATG 患者术后 3 年内感染率为 6.2%，差异无统计学意义(P＞0.05)。
结论 术后小剂量 rATG 能有效预防、控制 AR，且能逆转大部分对甲强龙冲击无效及短期内连续发生 AR 的难治性 AR，对于 DGF 患者应用 rATG 能有效平稳过渡，缩短 DGF 时间。在合理使用免疫抑制方案的情况下应用 rATG 的受者术后 1-3 年内继发感染风险较未使用 rATG 组无统计学差异。

PU-3110

浅谈检验危急值与患者安全

任建平
山西省中医药研究院 山西省中医院

危急值是表明患者可能正处于有生命危险的边缘状态的异常结果；既然是关系到患者的生命和安全，那么危急值的预警和预防是非常的重要，他不仅可以有效规避医疗风险的发生，显著降低纠纷和投诉率，缓和医患矛盾，而且最重要的挽救患者的生命。因此，危急值的管理：进无止境！

PU-3111

自动粪便分析仪在医院实验室使用过程中的流程优化及经验

张春莹、陈月梅、谢恒、邓山鹰、熊明、蒋能刚
四川大学华西医院

临床实验室检查中，粪便检验是常规检验三大项目之一，对消化系统疾病及寄生虫病等的诊断、治疗有十分重要的作用。由于粪便标本易采集、无创的特点，易被患者接受。但对于粪便的常规检测技术，目前国内外仍主要依赖手工操作方法（生理盐水湿片法），操作中易造成交叉污染且检出率较低，同时由于粪便的特殊气味严重影响工作环境，易引起医护人员抵触心理，由此而引发的生物安全问题突出。近些年，国内很多企业投入到粪便分析仪的研制中，粪便检验自动化得到了蓬勃发展，新的自动粪便分析装置层出不穷。

我院在多方面考察及对比多种粪便自动分析仪/自动粪便分析工作站的基础上，选择了一款自动粪便前处理分析系统。该仪器为全自动一体机，带有专用的多功能样本采集管和专门与仪器配套使用的粪便隐血试验卡（胶体金法），因而与本实验室之前手工检测方法使用的样本采集和隐血试剂有所不同，可替代人工操作涂片和显微镜检查，并自动判读隐血结果，大大解放人力，提高了工作效率。但是，检测方法的改变意味着工作流程的变化，在检测方法从手工转换为仪器的过程中，伴随着病人采样容器的改变和实验室隐血试剂的更换。作者所在医院于 2016 年开始使用自动粪便前处理分析仪，在因检测方法而改变工作流程中，涉及到门诊病人、住院病人、医生、护士以及检验人员的沟通与合作。本文就自动粪便前处理分析仪在我院使用过程中的流程优化以及使用经验作一个简要的总结。

PU-3112

296 例多发性骨髓瘤 mSMART 细胞遗传学预后分布的研究

华佳敏
上海金域医学检验所有限公司

目的 分析国内多发性骨髓瘤（MM）细胞遗传学预后分布情况，并与国外的数据进行比较。
方法 回顾性分析 296 例确诊的 MM 患者间期荧光原位杂交（FISH）检测（样本经过浆细胞富集）的结果，统计 MM 预后分层体系中各种细胞遗传学异常(CA)频率，并与国外的相关数据进行比较。
结果 296 例 MM 标本通过 FISH 检测分析，211 例阳性，阳性率为 71.28%。296 例标本中存在 1q21 扩增拷贝的总共 153 例，占 51.69%；存在 13q14 缺失的共 125 例，占 42.37%(295)；存在 17p13.1 缺失共 31 例，占 10.47%；存在 t (11; 14)的共 31 例，占 11.00%(282)；存在 t (4; 14)的总共 42 例，占 14.89%(282)；存在 t (14; 16)的共 5 例，占 1.77%(282)。根据 mSMART3.0 的定义标准，296 例 MM 样本中存在至少一项高危遗传异常的 170 例，占 57.43%，占所有阳性标本的

80.57%。双打击 57 例，占 19.26%，三打击 3 例，占 1.01%。结合近年文献报道的 MM FISH 细胞遗传学异常频率数据进行了讨论。
结论 根据 mSMART3.0 的定义标准，本组 MM 细胞遗传学高危与极高危病例比例总体上较高，高于文献报道的欧美国家数据。

PU-3113

PLT 与肝脏疾病严重程度的相关性分析

陈钰静、卢舜均
南方医科大学珠江医院

目的 分析 PLT 与肝脏疾病严重程度的相关性。
方法 收集在 2013 年 8 月到 2019 年 1 月期间被诊断为肝炎的 111 例病人、肝硬化的 118 例病人、肝癌的 113 例病人和健康体检者 122 例进行回顾性分析。分析各组的 PLT 水平及 PLT 与肝脏疾病严重程度的关系。以 ALT 超过正常值 2 倍以上，即 ALT≥80IU/L 作为判定肝损伤的诊断标准[1]，把三组中的患者再各自细分为是否有肝损伤，分析血小板计数与肝损伤之间的相关性。
结果 与对照组（236.52±49.37×109/L）比较，肝炎组（213.65±70.72×109/L）、肝硬化组（110.44±76.04×109/L）和肝癌组（153.62±57.85×109/L）的 PLT 都有下降（P＜0.5）。肝硬化组 PLT 最低，肝癌组次之，肝炎组 PLT 轻微下降,经方差分析差异具有统计学意义（F=93.22，P＜0.05）。各组之间的 PLT 总体均数不等或不全相等。进一步进行多个均数的两两比较，四组两两之间的总体均数差异都有统计学意义。采用 Spearman 相关性分析发现，PLT 与肝脏疾病严重程度呈负相关（rS=-0.517，P=0.01）。肝炎患者肝损伤组与非肝损伤组经近似 t 检验分析得差异不具有统计学意义（t=0.392，P＞0.05），肝硬化患者肝损伤组与非肝损伤组经两独立样本 t 检验分析得差异不具有统计学意义（t=0.621，P＞0.05），肝癌患者肝损伤组与非肝损伤组经两独立样本 t 检验分析得差异不具有统计学意义（t=0.277，P＞0.05）。
结论 PLT 与肝脏疾病损伤程度有一定的相关性，血小板数量在对肝脏疾病损害程度进行评估时，可以作为一项参考的指标。肝癌患者与肝硬化患者相比，其 PLT 增多，这种变化可以作为肝癌诊断的辅助依据。但同一肝脏疾病随着病情进程的加深，肝炎患者、肝硬化患者和肝癌患者 PLT 水平与肝功能损伤程度关系不大。

PU-3114

抗凝血酶在临床中的应用

杨萌
南方医科大学珠江医院

目的 抗凝血系统是人体内重要的功能系统，它与纤溶系统共同组成完整的防御体系。抗凝血酶是抗凝系统中重要的组成部分。在早期研究中ＡＴ可吸附凝血酶的纤维蛋白被称为为ＡＴⅠ，肝素辅助因子被称为ＡＴⅡ，促ＡＴ被称为ＡＴⅢ。其中 ATⅢ起决定性作用。它是一种球蛋白，由 3 个 β 折叠结构、9 个 α 螺旋结构和 1 个反应中心环。主要由肝脏合成，肺、脾、肾、心、肠、脑、血管内皮细胞和巨核细胞也可合成。本篇文章将系统性阐述抗凝血酶的结构及其在各系统疾病中的应用。
方法 通过 pubmed、万方、知网等数据库，检索抗凝血酶的相关研究，以综合阐述抗凝血酶在疾病方面的价值。
结果 抗凝血酶在抗凝系统中起关键作用，因此在多种疾病中广泛应用。在脓毒血症中，炎症细胞大量激活，释放各种因子损害机体，同时也破坏了人体的凝血系统，AT 活性明显下降。在脑梗死中，因机体处于高凝状态，从而消耗各种凝血因子，导致 AT 活性亦下降。在 DIC 中，，血管内的

抗凝系统被启动，导致ＡＴ被大量消耗，使ＡＴ水平明显低于发病前。在易栓症中，ＡＴ活性水平与易栓症的严重程度呈负相关关系，其活性水平越低易栓症的风险就越大。在肿瘤、习惯性流产中，AT 活性也是降低的。

结论 抗凝血酶在抗凝系统中起关键作用，通过测量抗凝血酶的活性，尤其是抗凝血酶Ⅲ的活性，并结合凝血四项，可很好的了解患者体内凝血系统状态，从而达到对疾病的早期干预，以防出血或再出血的风险。

PU-3115

儿童异型淋巴细胞检测结果分析

凌永基
南方医科大学珠江医院

目的 探讨全自动血液分析仪 Sysmex XT-2000i 对儿童外周血异型淋巴细胞(异淋)警示的可信性,以及儿童异型淋巴细胞增高症的临床意义。
方法 对 284 例各类疾病患儿进行血常规检测和人工显微镜检查（人工镜检），比较所得结果;对 49 例手工确认异淋阳性（人工镜检中异型淋巴细胞>5%者）标本中异淋的比率及患儿所患疾病进行统计。
结果 Sysmex XT-2000i 提示异淋阳性 90 例标本中人工镜检异淋阳性 17 例,其敏感性为 34.69%，阳性预测值为 82.02%；194 例未提示异形阳性的标本中人工镜检异淋阳性 31 例,特异性为 68.94%，阴性预测值为 83.94%；仪器提示异淋阳性与未提示异淋阳性的患儿标本中,人工镜检淋巴细胞和单核细胞百分比均值间均无统计学差异 (P>0.05)；其中，仪器提示异淋阳性和未提示异淋阳性标本，人工分类单核细胞>8%的频数符合度无统计学差异（P>0.05）。手工确认 49 例异淋阳性的患儿，传染性单核细胞增多症、上呼吸道感染和急性毛细支气管炎分别占 30.61%、16.32%和 10.20%。
结论 全自动血细胞分析仪对异型淋巴细胞提示的敏感性不高,阳性预测值低,因此对异淋的检测，此 Sysmex XT-2000i 不能作为过筛工具,外周血中单核细胞量对仪器判断是否有异淋无影响；同时异淋增高不是 EB 病毒感染特异现象,在各种感染性疾病中都有出现,异淋检测可为临床提供辅助诊断，用于疾病的鉴别诊断，临床应注重儿童异淋的显微镜检查。

PU-3116

一例 Rh 血型结果与历史不符的病例分析

周祺淇
南方医科大学珠江医院

患者女性，年龄 21 岁，为血液内科病区病人，临床诊断为急性淋巴细胞白血病。于 10 月某天早晨送来一份血型标本做检测，经过常规操作流程离心上机检测，第一次检测结果为：正定型 Anti-A 柱 4+，Anti-B 柱阴性；Anti-D 柱报 MF 警；Ctrl 阴性；反定型 A1-Cells 柱阴性，B-Cells 柱 4+。点开仪器的标本血型卡快照，显示 Anti-D 柱中有两群细胞，离心后沉下去的细胞数量较少。查看病人送检血型的结果历史，发现病人最近一次检测为同年 3 月份，Rh 血型结果为阴性。此时出现了 Rh 血型结果与历史不符的情况，在等待与联系临床医生的时间里，与同事几番讨论，提出输血、移植等几种可能性。后经与医生沟通了解到，该病人早前往当地血站送过血型鉴定，结果为 Rh 阳性（DEL 阳性），谜底逐渐揭开。

PU-3117

血清基质金属蛋白酶 16 表达水平在神经胶质瘤辅助诊断中的应用

张佳佳
河南省肿瘤医院

目的 分析基质金属蛋白酶 16 (Matrix metalloprotease 16)在神经胶质瘤患者血清中的表达水平，并探讨其在神经胶质瘤诊断中的应用价值。
方法 将 2019 年 1 月至 2020 年 6 月于河南省肿瘤医院就诊的 40 例神经胶质瘤患者纳入神经胶质瘤组,统计患者的年龄、性别、病理分级、肿瘤直径、体质指数等，另选同期 20 名健康受试者作为对照组。收集受试者空腹静脉血，通过酶联免疫吸附法测定两组血清中的基质金属蛋白酶 16 水平,经受试者工作特征曲线评价所观察指标对神经胶质瘤的诊断价值,并分析其与神经胶质瘤临床病理特征的关系。两组间比较采用 Wilcoxon 秩和检验，多组间比较采用 Kruskal-Wallis H 检验。
结果 神经胶质瘤组血清基质金属蛋白酶 16 水平（中位数）均高于健康组,且差异具有统计学意义(P<0.05)；受试者工作特征曲线结果显示,血清基质金属蛋白酶 16 对神经胶质瘤的诊断效能高，曲线下面积(AUC)为 0.938；基质金属蛋白酶 16 水平与病理分级呈正相关(P<0.05)，与肿瘤直径呈正相关(P<0.05)。
结论 神经胶质瘤患者血清中基质金属蛋白酶 16 水平呈高表达,且与 TNM 分期、肿瘤直径等病理特征密切相关,可作为诊断神经胶质瘤的潜在标志物。

PU-3118

性激素六项检查对多囊卵巢综合征的诊断价值

崔思洋
吉林金域医学检验所有限公司

目的 探讨性激素六项检查对多囊卵巢综合征的诊断价值。
方法 选取 2020 年 6 月至 2020 年 12 月确诊的多囊卵巢综合征患者 100 例，同期进行体检的健康女性 100 例作为对照组，回顾多囊卵巢综合征患者与所有对照组女性的性激素六项的检测结果，对两组性激素六项（睾酮，孕酮，泌乳素，促黄体生成素，雌二醇，促卵泡雌激素）水平进行分析对比结果，检测设备为雅培化学发光分析仪 i2000SR，方法为磁微粒化学发光法，使用雅培原装试剂进行检测。
结果 与对照组相比较，多囊卵巢综合征患者，促黄体生成素、促黄体生成素/促卵泡雌激素、睾酮水平显著升高，（P＜0.05）；促卵泡雌激素水平显著降低（P＜0.05）泌乳素、孕酮、雌二醇水平无明显差异（P＞0.05）
结论 多囊卵巢综合征是育龄妇女较常见的内分泌症候群，一种多病因、表现极不均一的临床综合征。性激素六项水平可以作为多囊卵巢综合征患者的辅助诊断手段，但对于不确定的多囊卵巢综合征患者，仍需进行阴道彩超等进一步的诊断。

PU-3119

TCT 与 HPV 联合阴道镜下用于宫颈癌筛查临床应用

付玉华
内蒙古科技大学包头医学院第一附属医院

目的 评价人乳头状瘤病毒（HPV）与液基薄层细胞学检查(Thinprep cytologic test TCT)并联合阴道镜下活检在妇女宫颈癌筛查中的诊断价值。
方法 临床妇科大夫采集宫颈细胞标本分别做 TCT 和 HPV 定量检测，TCT 用液基薄层技术制片。HPV 采用人乳头状瘤病毒核酸试剂盒的杂交捕获-化学发光法。收集我院 2017 年 1 月年到 2019 年 1 月接受 TCT、HPV 及阴道镜检查患者共 450 例。
结果 病理结果为正常的共计 380 例，低级别病变的 51 例，高级病变及原位癌 15 例，鳞状细胞癌为 4 例。
结论 以病理为金标准，TCT 阳性，HPV 阳性联合检测阳性率明显高于 TCT 或 HPV 单一检测。

PU-3120

与维生素 D 缺乏相关的气象条件和空气污染：一项基于中国西部人群的横断面研究

何訸、曾玉萍、王霞、杨礼丹、张玫、安振梅
四川大学华西医院（四川省国际医院）

目的 本研究旨在了解该地区人群维生素 D 缺乏状况及环境因素对维生素 D 水平的影响，为促进该地区公众健康工作提供理论支持。
方法 选择 2018 年 4 月至 2020 年 5 月在四川大学华西医院中心体检的 22387 名受试者为研究对象。对其性别、年龄、检查日期、血清 25-羟基维生素 D (25-(OH)D)、甲状旁腺激素(PTH)、总钙数据进行回顾性分析。比较不同性别、不同年龄组维生素 D 的水平，并描述维生素 D 水平随环境变化的变化情况。对维生素 D 缺乏的危险因素和保护因素进行单变量和多变量线性回归分析。
结果 本地区维生素 D 缺乏率为 42.17%，女性维生素 D 缺乏的患病率为 51.6%，高于男性的 34.1%，差异有统计学意义；不同年龄组中比较结果显示 20-30 岁人群维生素 D 不足患病率为 48.7%，维生素 D 缺乏患病率为 10.7%。50-60 岁人群微生素 D 不足和维生素 D 缺乏的患病率分别为 29.4%和 3.2%。在全年内 25-羟基维生素 D 水平的波动趋势与温度和太阳辐射一致，与空气质量相反。回归分析显示 25-羟基维生素 D 水平与甲状旁腺激素、空气质量呈负相关；与温度、太阳辐射呈正相关。
结论 亚热带地区(如四川盆地)维生素 D 普遍缺乏，可能与太阳辐射和空气污染有关。

PU-3121

尿白蛋白排泄率与肾小球滤过率在 2 型糖尿病肾病诊断中的关系与价值

吕献敏[1]、吕火烊[2]、陈铮铮[1]
1. 桐乡市第一人民医院
2. 浙江省人民医院

目的 探讨尿白蛋白排泄率与肾小球滤过率在 2 型糖尿病肾病诊断中的关系与价值。

方法 回顾分析已有数据，根据尿白蛋白排泄率（UAER）分组,比较各组估计肾小球滤过率（eGFR）的变化；根据 eGFR 分组，比较各组 UAER 的变化;分别比较 UAER 与 eGFR 各组的关系及 UAER 各组与 eGFR 的相关性以深入挖掘 UAER 与 eGFR 间的关系，以及在 2 型糖尿病患者中的变化情况，探讨其临床应用价值。
结果 不同 UAER 组，随着 UAER 升高，eGFR 降低，各组差异具有统计学意义(P<0.05）；不同 eGFR 组，随着 eGFR 下降，UAER 升高，各组差异具有统计学意义（P<0.05）；微量白蛋白尿组、大量白蛋白尿组患者肾功能异常率（分别为 13.5%和 37%）显著高于正常白蛋白尿组（7.8%），而肾功能异常组尿白蛋白（包括尿微量白蛋白和尿大量白蛋白）发生率 51.5%（35/68）显著高于肾小球高滤过组 10.2%（13/127）、正常滤过组 24.8%（34/137）和轻度滤过降低组 32.4%（83/256）；全部患者的 eGFR 与 UAER 呈负相关（r=-0.488 P<0.01），UAER 各组与 eGFR 相关性以大量白蛋白尿组最强（r=-0.572 P<0.01）。
结论 UAER 与 eGFR 是从不同角度较好反应肾功能早期变化的敏感指标，二者呈负相关，但单一检测均存在不能全面反映糖尿病肾病患者肾脏受损情况。联合检测能较全面了解肾小球器质性损伤情况和肾功能的损伤程度，能较好地对 2 型糖尿病肾病作出早期诊断。

PU-3122

原发性胆汁性胆管炎患者自身抗体的聚类分析

赵丹彤[1]、韩莹[2]、张海萍[1]、黄春洋[2]、刘燕敏[2]、廖慧钰[2]、张伟明[3]、赵艳[1]、闫惠平[1]
1. 首都医科大学附属北京佑安医院 临床检验中心
2. 首都医科大学附属北京佑安医院 肝病中心二科
3. 首都医科大学附属北京佑安医院 临床检验诊断学系

目的 比较不同自身抗体特征的 PBC 患者临床、预后的差别，为进一步了解疾病特点，加深对疾病的认识提供证据支持。
材料与方法 对 2009 年 7 月至 2019 年 7 月间 537 例 PBC 患者自身抗体检测结果进行聚类分析。包括：ANA, AMAs 和/或抗 AMA-M2、ACA 和/或 CENP-B、抗 Ro52、抗 SSA、抗 SSB、抗 Sm、抗 nRNP、抗 dsDNA、抗 Rib、抗 His、抗 Nuk、抗 Scl-70、抗 Jo1、抗 gp210、抗 sp100、抗 SLA、抗 LKM-1 和抗 Lc1。采用二阶聚类进行分析、Kaplan-Meier 法进行单因素生存分析，组间生存率比较采用 log-rank 检验；生存预后多因素分析采用 Cox 回归。
结果和结论 (1)共得 5 个聚类：聚类 1（n=107），主要为 ANA(100%)、AMA 和或 AMA-M2（84.1%）、ACA 和/或抗 CENP-B（28%）、抗 Ro52（15%）、抗 gp210（100%）；聚类 2（n=120），主要为 ANA（94.2%）、AMA 和或 AMA-M2（96.7%）、抗 Ro52（47.5%）、抗 SSA（47.5%）、抗 SSB（14.2%）、抗 gp210（34.2%）、抗 sp100（51.7%）；聚类 3（n=124），主要为 ANA（63.7%）、AMA 和或 M2（100%）、ACA 和/或抗 CENP-B（100%）；聚类 4（n=101），主要为 ANA（100%）、AMA 和或 AMA-M2（94.1%）、ACA 和/或抗 CENP-B（98%）、抗 Ro52（54.5%）、抗 SSA（18.8%）、抗 sp100(21.8%）；聚类 5（n=85），主要为 ANA（84.7%）、AMA 和或 AMA-M2（100%）、抗 Ro52（100%）、抗 gp210（47.1%）。(2)聚类 1 生存率明显低于聚类 2、聚类 3 和聚类 4（P<0.005）；抗 gp210 是影响 PBC 患者生存预后的主要危险因素。

PU-3123

2 型糖尿病患者血清非酶类抗氧化物水平的研究

吕献敏[1]、吕火烊[2]、陈铮铮[1]、虞国其[1]、肖龙[1]、姜黎花[1]
1. 桐乡市第一人民医院
2. 浙江省人民医院

目的 探讨 2 型糖尿病（T2DM）患者血清中非酶类抗氧化物水平，分析其与氧化应激的关系及与血糖的相关性。
方法 选择符合纳入条件的 588 例 T2DM 患者作为研究组，检测血清白蛋白、胆红素及尿酸，与同期健康体检者进行比对，统计分析二者的差异，并分析研究组非酶类抗氧化物与空腹血糖水平的相关性。
结果 T2DM 患者血清白蛋白、胆红素水平明显低于对照组，差异有统计学意义（P <0.05），血清白蛋白、胆红素水平与空腹血糖呈二者呈负相关（P <0.05）；尿酸水平明显高于对照组，差异有统计学意义（P <0.05），尿酸与空腹血糖呈正相关（P <0.05）。
结论 T2DM 患者血清白蛋白、胆红素、尿酸水平有显著变化，发生变化的原因可能与氧化应激有关，检测上述非酶类抗氧化物有助于 T2DM 的诊断及可为 T2DM 的治疗提供参考。

PU-3124

某院实验室危急值指标不同年度间的回顾性分析

李鹏、韩素丽、闫慧
长治医学院附属和平医院

目的 对临床实验室不同年度危急值报告指标进行统计分析并做出科学评价，使科室的危急值报告合理运行。
方法 对我院 2016-2019 年的危急值报告内容中的危急值发生率、危急值报告及时率、危急值发生的项目和危急值发生的科室等指标进行回顾性分析并提出改进性措施。
结果 2016-2019 年间危急值发生率升高，危急值报告及时率明显提高，危急值报告时间缩短，无需向临床发放的危急值率上升，危急值发生的科室构成比和发生率出现了相应的变化。
结论 对临床实验室危急值报告指标进行合理有效的分析对于临床危急值报告的运行具有重要价值。

PU-3125

类风湿因子对类风湿关节炎合并结核患者预后的影响

吕梦媛、赖红历、周妍冰、王义莉、唐婕希、陈雪融、应斌武
四川大学华西医院

目的 探究类风湿因子(rheumatoid factor, RF)对类风湿关节炎合并结核患者的结核相关预后的影响，并且建立预测两月痰涂片转化(2-month sputum smear conversion, 2m-SSC)的模型。
方法 收集 2013 年 12 月至 2019 年 9 月期间在四川大学华西医院住院的类风湿关节炎合并结核患者的初始医疗记录和随访数据（每半年随访一次）。通过 logistic 回归和 cox 回归识别 2m-SSC 及结核复发的危险因素，并计算相对危险度(odds ratio, OR)或风险比(hazard ratio, HR)和相应的 95%置信区间(confidence interval，CI)。使用 Logistic 回归和弹性网络回归构建预测模型，计算敏感性、特异度及曲线下面积(area under curve, AUC)以评估模型效能。
结果 纳入 434 例类风湿关节炎合并结核的患者。以纳入人群 RF 值的中位数（24）为截断值，将其分为 RF 高值组和低值组。回归分析显示 RF 分级(OR=9.548, 95%CI: 5.390-16.913, p<0.001)是

2m-SSC 的独立危险因素；结核复发风险在两组间无明显差异(p=0.292)。三个 2m-SSC 预测模型均纳入了 RF 分级这一变量。在训练集中，Logistic 回归模型的敏感度、特异性和 AUC 分别为 57.0%, 78.3% 和 66.6%；在验证集中，分别为 53.8%, 92.9% 和 74.9%。在弹性网络回归中应用 K 折叠交叉验证筛选变量时，模型在训练集中的敏感度为 81.2%，特异性为 70.0%，AUC 为 80.8%；在验证集中敏感度和 AUC 分别降至 62.1%和 78.0%，特异性升高至 89.3%。使用最小均方根误差选择变量时，模型在训练集中的敏感度、特异性和 AUC 分别为 70%, 80.5% 和 80.8%，在验证集中分别为 89.3%, 62.7% 和 78.1%。

结论 对类风湿关节炎合并结核的患者而言，RF 分级是 2m-SSC 的独立危险因素，并且对构建性能良好的 2m-SSC 预测模型做出了重大贡献。对 RF 水平进行分级可以帮助临床医生预测结核相关结局，及时采取措施，以改善患者预后。

PU-3126

2019 至 2020 骨髓涂片镜检与流式免疫分型结果不相符分析

金咏梅、刘雨涵、蒋能刚、廖红艳、粟军
四川大学华西医院

目的 探讨同时进行了骨髓涂片细胞学检查与流式细胞免疫分型两种检查结果不相符的情况，分析二者分型结果不相符的原因，并进一步分析其对于造血系统疾病的诊断价值，同时对如何提高实验室骨髓涂片镜检准确率进行探讨。

方法 回顾四川大学华西医院 2019 年 3 月 1 日至 2020 年 3 月 31 日内送至临检血液室骨髓组的骨髓涂片细胞学检查及流式细胞术免疫分型结果，并对其进行统计学分析。

结果 四川大学华西医院临检血液室骨髓组在 2019-2020 一年零一个月内共计接收 5373 例同时进行了骨髓涂片细胞学检查与流式细胞免疫分型的病例，其中两种检查结果不相符为 746 例，占总病例数的 13.88%。在分型结果不相符的病例中，急性髓系白血病分型结果不相符为 116 例(占总不相符数的 15.55%，下同)；混合型白血病分型结果不相符为 3 例（0.40%）；急性淋巴细胞白血病分型结果不相符为 82 例(10.99%)；上述两例之中形态学结果为急性淋巴细胞白血病而流式免疫分型结果为急性髓系白血病病例数为 6 例（0.80%）；慢性髓系白血病分型结果不相符为 5 例(0.67%)；异常细胞检测结果不相符病例数为 331 例（44.37%）；由形态学诊断为 MDS 的病例总数为 74 例，其中不相符 12 例(1.61%)；MM 诊断结果不相符病例数为 3 例(0.40%)；白血病预后检监测结果不相符病例数为 129 例(17.29%)；贫血类疾病检测结果不相符病例数为 74 例（9.92%）；由于取材或制片问题造成的结果不相符为 188 例(由于其为外在因素因此未计入不相符病例数中)。

结论 (1)形态学检查对于细胞典型特征病例(例如 MM、LPD)以及贫血类疾病(例如 AA,PRCA)的识别度较高，并能够诊断出 MDS；流式细胞数对于肉眼无法判别的异常细胞、以及淋巴细胞类分型的识别度较高，并在白血病分型与预后检测方面优于形态学。(2)二者的主要区别主要表现在异常细胞计数分类及红系细胞的识别两方面，一方面可提高形态学检查的准确性，另一方面可增加流式细胞术对红系表面抗原的检测。

PU-3127

2 型糖尿病合并肥胖病人中 Irisin 水平的研究

张诗田、王雅茹、刘影、张亚南、刘蕊、王爽、李宣、牛文彦
天津医科大学朱宪彝纪念医院

目的 近年来，由于人们高脂饮食增多，体力活动减少，生活压力增加，肥胖人群逐年扩大。糖尿病是以高血糖为特征的慢性代谢性疾病，90%以上为 2 型糖尿病。中心性肥胖是 2 型糖尿病发病的关键因素。Irisin 是纤维连接蛋白Ⅲ型域包含蛋白 5（FNDC5）112 号位氨基酸的裂解产物，由肌

肉和脂肪分泌故而称之为肌肉脂肪因子。Irisin 可上调产热以及白色脂肪棕色化相关基因的表达，促进能量消耗进而导致体重降低。同时，Irisin 还可以降低血中葡萄糖和胰岛素水平进而改善胰岛素抵抗。大多数研究发现 Irisin 与肥胖以及肥胖相关指标呈正相关。然而，在糖尿病人群中 Irisin 水平降低。Irisin 在糖尿病合并肥胖这一特定人群中水平如何相关文献报道较少。本研究旨在比较单一糖尿病以及糖尿病合并肥胖人群中 Irisin 水平，探讨 Irisin 与肥胖和糖尿病相关临床指标的关系，进而为临床诊断和治疗肥胖和糖尿病提供新视角。

方法 测量 2 型糖尿病组以及 2 型糖尿病合并肥胖组身高体重并计算、全自动生化分析仪及糖化血红蛋白分析仪检测肥胖和 2 型糖尿病相关的血液生化指标（甘油三酯、总胆固醇、低密度脂蛋白、高密度脂蛋、空腹血糖、糖化血红蛋白）、ELISA 试剂盒检测血中 Irisin 水平，分析血中 Irisin 水平与肥胖和 2 型糖尿病相关指标的相关性。

结果 2 型糖尿病合并肥胖组体重和 BMI 显著高于 T2DM 组。甘油三酯、总胆固醇、低密度脂蛋白、高密度脂蛋、空腹血糖、糖化血红蛋白水平在两组间无显著差异。2 型糖尿病合并肥胖组组血中 Irisin 水平显著升高，BMI 与 Irisin 水平呈正相关。

结论 在 2 型糖尿病病人中血中 Irisin 水平与肥胖密切相关。

PU-3128

不同方法学检测类风湿因子的比较

姚军、王文强、李忠信、谢茜、孙萌
郑州安图生物工程股份有限公司

目的 探讨不同检测方法学检测类风湿因子对临床诊断的辅助作用。

方法 采用散射比浊法、乳胶凝集法比浊法 、酶联免疫吸附法(ELISA)检测类风湿关节炎患者 104 例，系统性红斑狼疮患者 4 例及健康体检病患者 196 例。

结果 散射比浊法检测类风湿关节炎患者、非类风湿关节炎患者 RF 阳性率分别为 100%、100%,196 例健康者 9 例为阳性结果，诊断效率为 95.72%。乳胶凝集法检测类风湿关节炎患者、非类风湿关节炎患者 RF 阳性率分别为 98.1%、100%，196 例健康者 7 例为阳性结果，诊断效率为 99.01%。ELISA 法 IgA/G/M 诊断效率分别为 90.13%、66.90%、78.62%。

结论 乳胶凝集法检测类风湿因子的效果最好，虽然检出率低于散射比浊，但是其特异性较好，诊断效率总分最高。

PU-3129

Expression and prognosis analyses of Dectin-1 cluster genes in patients with lung adenocarcinoma (LUAD) and the association with immune checkpoint molecules

Liting You、Feifei Na、Juan Zhou、Lin Jiao、Yi Zhou、Binwu Ying
West China Hospital, Sichuan University

The Dectin-1 cluster comprises seven members: CLEC-12A, CLEC-12B, CLEC-1A, CLEC-7A, CLEC-2, CLEC-9A and OLR1. These members have been demonstrated to be involved in the tumorigenesis, progression, and metastasis of several cancers. However, little is known about their roles in human lung adenocarcinoma (LUAD). The expression patterns of the Dectin-1 cluster were analyzed via the ONCOMINE and GEPIA databases. We evaluated the prognostic value of the Dectin-1 cluster in patients with LUAD using the Kaplan-Meier plotter and GEPIA. Differential expression was validated with the EMBL-EBI database, and protein expression was analyzed with the HPA database. In addition, protein-protein interaction network, GO, and KEGG analyses were conducted. Finally, the correlations between CLEC-12A and immune molecules

(immune inhibitors and MHC molecules) were investigated via TISIDB and GEPIA. The expression levels of Dectin-1 cluster genes were downregulated in LUAD tissues compared to those in normal lung tissues. The expression levels of CLEC-12A, CLEC-12B, CLEC-2, and CLEC-9A correlated with tumor stage, and CLEC-12A and CLEC-12B were significantly associated with survival in patients with LUAD. The seven genes mostly participated in immune regulation processes and were involved in autoimmune disorders and hematological malignancies. Finally, correlation analyses revealed CLEC-12A expression was associated with most immune inhibitors and MHCs. CLEC-12A was positively related to PD-1, PD-L1, PD-L2, CTLA4, TIM3, and LAG3. In conclusion, our findings suggest that CLEC-12A and CLEC-12B can be used as prognostic biomarkers in LUAD. CLEC-12A expression was associated with immune checkpoint molecules, and CLEC-12A may be a potential assistant target to improve the efficacy of immune checkpoint inhibitors immunotherapy.

PU-3130

灯盏乙素调控同型半胱氨酸缓解 2 型糖尿病中肝脏损伤的分子机制研究

王依雨
四川省八一康复中心（四川省康复医院）

目的 灯盏乙素（SCU）是从灯盏花（Erigeron breviscapus（Vaniot）Hand.-Mazz）中提取的有效成分。它的主要生理功能是消炎和抗氧化剂。在这项研究中，我们建立了 STZ 诱导的 2 型糖尿病（T2DM）模型和同型半胱氨酸（Hcy）诱导的 LO2 凋亡模型，以研究 SCU 是否可以通过调节 2 型糖尿病中的 Hcy 减轻肝脏损害。
方法 用小剂量的链脲佐菌素（35 mg/kg）诱导大鼠 2 型糖尿病模型。SD 大依次分为正常组、2 型糖尿病模型组、灯盏乙素低剂量治疗组（100 mg/kg/d）、灯盏乙素高剂量治疗组（200mg/kg/d）和罗格列酮治疗组（5 mg/kg/d）；各治疗组进行灌胃治疗；各治疗时间段完成后，进行糖耐量实验分析；检测大鼠血清 CHO、TG 血脂指标，ALT、AST 肝功指标，血清及肝脏组织中 SOD 水平、MAD 水平以及肝脏组织中 GSH 水平；用 ELISA 检测 Hcy、Insulin、VitB 6 、VitB 12 、叶酸水平并计算胰岛素抵抗指数。用 HE 染色来观察肝脏细胞形态学改变；TUNEL 染色观察细胞凋亡情况，Western blot 和免疫组化学检测 CBS、CSE、MTR、MTHFR、Caspase-3 酶原和活性片段的蛋白表达水平。采用不同浓度 Hcy 诱导 LO2 肝细胞建立细胞凋亡模型，检测细胞凋亡情况；用灯盏乙素预处理后，流式细胞技术和 Western blot 检测灯盏乙素对 Hcy 诱导细胞凋亡模型的影响及关键的凋亡因子（caspase3）的改变。
结果 生化分析表明，SCU 可以通过下调甘油三酸酯（TG），胆固醇（CHO），低密度脂蛋白（LDL），丙氨酸转氨酶（ALT）和天冬氨酸转氨酶（AST），上调高密度脂蛋白（HDL）的水平来改善糖尿病大鼠的脂质代谢紊乱和肝功能。有趣的是，SCU 还可以下调 Hcy 和胰岛素的水平，并增强 2 型糖尿病大鼠调节血糖的能力。从机制上讲，我们的结果表明 SCU 可能通过调节肝脏组织中的 β-胱硫醚酶（CBS），γ-胱硫醚酶（CSE）和 5,10-亚甲基四氢叶酸（MTHFR）的水平来控制 Hcy 的水平，并上调叶酸，血清中的 VitB6 和 VitB12 水平。此外，SCU 抑制 T2DM 大鼠肝脏和 Hcy 处理的 LO2 细胞的凋亡。
结论 我们的发现表明 SCU 可能通过下调 T2DM 大鼠的 Hcy 水平来减轻肝脏损伤。

PU-3131

基于贝叶斯网的检验科标本采集风险分析研究

郭笑然、王海燕、杜秋明
吉林大学第一医院

目的 本文针对我院检验科采血室现状,对标本采集过程中发生的风险因素进行全面分析, 并基于贝叶斯网络理论构建标本采集风险分析研究模型,以识别标本采集过程中发生问题的影响因素，进行相应的风险分析，从而为降低标本采集风险采取针对性措施提供帮助。
方法 综合近年来对检验科采血室标本采集过程中发生风险研究的文献，基于贝叶斯网络的相关理论，通过事件回顾的方式，对我院检验科采血室采集标本过程中发生问题的事件作为样本，建立标本采集风险分析研究模型。
首先通过相关文献综述，对采血室标本采集风险进行了系统分析，选择患者因素、护士因素、管理因素、医生因素等作为标本采集风险发生的影响因素，利用因果关系构建出风险研究评估模型拓扑结构，依据事件回顾对情境因素节点的参数进行分析确定；
1、为获得给定条件下标本采集风险发生节点的概率，本文基于联合树算法对标本采集风险分析模型进行了详细的推理。首先，将护理风险分析模型转化为联合树，然后通过联合树消息传递来进行风险发生概率的确定，并通过样本数据进行节点概率学习。 3、为验证所构建护理风险研究模型的准确性，本文进行了相关的实验研究,并基于实验数据分析护理风险各因素的影响因子，测算各影响因子的导致发生护理风险的概率。
结果 第一、检验科作为主要科室，在标本采集过程中，由于数量大、情况复杂，随着样本扩大，发生风险概率也在扩大。
第二、根据本文得出的贝叶斯网络模型在根据样本训练后，可以判定标本采集过程中，护理人员失误操作造成的标本采集风险的概率最大。
第三、标本采集风险发生影响因素中，护士注意力指标为最主要影响指标。护士执业时间越长，发生护理风险概率越低。
第四、患者检验标本采集前的指导，尤其是采血护士采血前的叮嘱，可有效降低护理风险发生概率。
结论 该分析模型可以有效分析检验科标本采集过程中发生风险的概率，并根据采集到的影响因素给予预警，计算结果符合经验性认知，模型允许在更多数据支撑下逐步逼近真实值。

PU-3132

质量管理体系历年不符合项分析及改进

张青杨
中国医科大学附属第一医院

目的 依据 CNAS-CL02《医学实验室质量和能力认可准则》，对体系成立至今的所有内部审核和外部审核中识别的不符合项进行统计分析，以持续改进的宗旨，指导下一步质量监督工作。
方法 依据 CNAS-CL02:2012《医学实验室质量和能力认可准则》，对本实验室自 2009.09 体系运行至今，13 次内部审核识别的 123 项不符合项和 7 次 CNAS 外部审核识别的 37 项不符合项，进行统计分析。
结果 对所有 160 项不符合项统计分析发现：
1. 不符合项年度和部门分布：体系建立初期不符合项最多，2011 年为 41 个，占总数的 25.6%；部门分布中，临检室为 30 项次，占总数的 18.8%，为各部门最高。
2. 不符合项条款分布：发生不符合项覆盖要素 18 个，其中识别不符合项最多的要素是 5.3（34 个，占总数的 21.3%），其次为 5.6（27 个，占总数的 16.9%）。
3. 具体条款分析：依据 CNAS-CL02:2012《医学实验室质量和能力认可准则》对所有不符合项对应的条款号重新识别，然后对识别不符合项最多的两个要素（5.3、5.6）进行条款的具体分析，发

现 5.3 中识别最多的是 5.3.1.7 设备记录（12 个，占比 32.4%）和 5.3.1.2 设备验收（7 个，占比 20.6%），5.6 中识别最多的是 5.6.2.3 质控数据（14 个，占比 51.9%）和 5.6.2.2 质控物（6 个，占比 22.2%）。

结论 通过对既往不符合项的统计分析，发现实验室质量管理工作的薄弱环节，针对性地制定下一阶段质量监督的工作重心和具体细则，认真分析、定期监督，从根本上实现实验室的持续改进。

PU-3133

应用 PDCA 循环法提高门诊检验科自动贴标签机产生的弃用采血管利用率

白璐、王珂、蒋梨
陆军军医大学第一附属医院（西南医院）

目的 应用 PDCA 循环法，提高门诊检验科自动贴标签机产生的弃用采血管利用率。

方法 通过鱼骨图分析，找出门诊检验科抽血室真空采血管贴标签后被弃用的主要原因:患者未满足静脉采血要求；取号前缺乏相关指导和咨询；自动贴标机仪器故障，分析影响因素，制定计划，采取相应的干预措施。观察贴标后弃用真空采血管的产生率、利用率的变化。通过口头、书面、标识牌告知等形式，依托科室信息化建设，加强取号前咨询，减少无效取号；对已排号但不符合采血条件患者，及时取消贴管打印信息；定期进行仪器维护和系统升级，采用综合措施减少弃用机贴真空管的产生。定期整理弃用真空采血管，将试管原有的条码信息用记号笔涂写覆盖，摆放整齐后搁置于手工贴管位置，便于采血护士再使用。按时查看试管的有效期，联系并转送至其它采血量较大的科室使用。

结果 运用 PDCA 循环法后，使自动贴标机产生的无效真空采血占使用试管总数由 7.0%～7.3%减少到 4.5%～5.2%，弃用真空采血管的利用率从改进前的 25%提高到改善后 53%。

结论 应用 PDCA 循环法，提高了弃用真空采血管的利用率，节省科室成本，减少耗材浪费。

PU-3134

区域医学检验中心发展现状及展望

陈洪卫
上海市松江区中心医院

区域医学检验中心建设是落实国家医疗卫生改革、实行分级诊疗、推动医联体建设的重要环节，在提升区域医学检验质量、推动优质医疗资源下沉、降低医疗机构运营成本、减少政府财政重复投入、实现区域医学检验结果互认及区域医学检验资源共享等方面发挥重要作用。近年来，随着国家医改的深化和分级诊疗制度的不断推进，独立医学实验室和公立医院检验科的发展开始转型升级，我国区域医学检验中心建设进入快速发展期，出现多种新模式。未来，区域医学检验中心将呈现规模化、专科化、平台化、信息化、一体化的发展趋势。

PU-3135

浅析医学检验实验室质量管理体系

魏亚权、张维
西安金域医学检验所有限公司

探讨医学检验实验室质量管理体系的建。质量管理体系文件是质量管理体系存在的基础和证明，也是对质量管理的评价，执行文件者容易得到并能充分理解所有文件，同时要让技术人员认识到实验室的质量管理现状与先进管理模式之间的差异，认识到先进质量管理体系的意义。

PU-3136

IL-17 在急性痛风性关节炎大鼠中作用机制的研究

王国镇
中日友好医院

目的 探讨 IL-17 在痛风性关节炎中的作用机制。
方法 通过动物痛风性关节炎模型来验证 IL-17 对痛风性关节炎组织损伤的作用。分别在大鼠踝关节腔内注射纯化 IL-17、MSU、MSU+IL17 抑制剂或生理盐水，观察关节周径，关节腔周围软组织的炎性病理学改变、关节滑膜及骨组织的病理学改变、主要的血液炎性及生化指标等，以明确 IL-17 在痛风性关节炎发病过程中的作用。
结果 结果显示，大鼠踝关节腔内注射纯化 MSU 结晶或 IL-17，均可以诱导大鼠关节局部明显肿胀，大量炎性细胞浸润，血清各项炎性因子水平显著升高，可用于制备痛风性关节炎大鼠模型。MSU+IL-17 抑制剂组，大鼠关节局部肿胀明显减轻，组织病理显示炎症反应较轻，各项炎性因子水平（如 PGE2、MPO、CRP、IL-6、IL-8 和 TNF-α）显著低于单独注射 IL-17 或 MSU 组（$P<0.05$）。分别采用 IL-6 抑制剂、IL-8 抑制剂或 TNF-α 抑制剂与 IL-17 联合注射大鼠踝关节腔，所造成的大鼠关节炎症反应明显弱于 IL-17 单独注射组。
结论 IL-17 在痛风性关节炎中发挥了重要的促炎作用，并且 IL-17 可能促进 IL-6、IL-8、TNF-α 的表达与分泌从而参与痛风性关节炎的发病过程；抑制 IL-17 或下游炎性因子（如 IL-6、IL-8、TNF-α）对痛风性关节炎有较好的治疗效果。

PU-3137

甲状腺疾病实验室诊断现状与进展

王晨、陶庆春
北京中医药大学第三附属医院

目的 研究整理归纳总结甲状腺疾病主要的实验室诊断项目，列出其检测指标正常参考范围与检测方法，并探讨今后仍需思考和解决的，比如根据多种因素划分更细的分组建立各指标的正常范围等问题。
方法 应用文献搜集整理文献综述。
结果 目前临床常用的 12 个甲状腺疾病实验室诊断项目共包括 12 个，具体包括甲状腺功能测定：促甲状腺激素（TSH)、游离三碘甲状腺原氨酸（FT３)、游离甲状腺素（FT４)、三碘甲状腺原氨酸（T３）、甲状腺素（T４）；甲状腺相关自身抗体：抗甲状腺球蛋白抗体（TGAb）、抗甲状腺过氧化酶抗体（TPOAb）、促甲状腺素受体抗体（TRAb）；甲状腺激素合成功能测定：甲状腺吸131I 试验；甲状腺球蛋白(thyroglobulin, TG)测定；降钙素（calcitonin，CT）；甲状腺激素在机体组织中效应评价：基础代谢率、跟腱反射松弛时间测定、无创性心功能检查；下丘脑-垂体-甲状腺

轴评价：促甲状腺激素兴奋试验、促甲状腺激素释放激素兴奋试验、促甲状腺激素测定、甲状腺激素抑制试验；尿碘检测；五肽胃泌素激发试验；血清微小 RNA：血清 miR-451a、miR-25-3p、GAS8-AS1；外周血液白细胞分化抗原 195（CD195）、单核细胞趋化蛋白 1（MCP-1）；甲状腺细针穿刺活检（fine needle aspiration biopsy；FNA）。
结论 现在实验室检测项目与方法日新月异，有单一检测特异性高者，亦有联合检测敏感性增加者，查阅文献后能够发现全自动化学发光免疫分析仪在甲状腺疾病实验室诊断中现有很高的临床价值，具有准确度高且操作简便、快速等多种优点，但因为多种因素的影响，很多甲状腺实验室诊断项目并未确定好明确的指标正常范围，所以我们可以根据多种因素划分更细的分组，建立各指标的正常范围，是我们今后研究的重点，有待我们进一步探讨。

PU-3138

药物对临床医学检验结果的影响分析

刘恭序
中国人民解放军联勤保障部队第 900 医院(原福州总医院)

在新时代背景下，我国经济水平逐步提高，医疗事业也在逐步完善。临床医学检验在现代医学治疗过程中扮演着重要的角色，而药物在临床医学的检验中也有着很大的影响。本文首先简述了药物对临床医学检验的具体影响，然后列出了防范药物干扰在临床医学检验结果上的主要措施，最后说明临床医学检验结果有助于医师诊断患者的病情，为患者确定更为妥善合适的治疗方法。

PU-3139

一种 21 分型 HPV 检测试剂盒的性能验证和评价

冯倚帆、张帅、刘志坚、宋子威、李世宝
徐州医科大学附属医院

目的 对硕世生物科技股份有限公司的 21 型 HPV 检测系统进行性能验证。
方法 采用实时荧光定量 PCR 法对待启用的 21 型 HPV 检测试剂盒的准确度、测定下限、精密度、特异性、抗干扰能力等性能参数进行验证及评价。
结果 准确度实验结果与已知结果一致，符合率 100%；最低检测下限 104copies/ml；21 种 HPV 亚型和阳性参照物批内精密度 CV 范围为 0.22%~3.40%，均小于 5%，符合行业标准（CV≤5%）；21 种 HPV 亚型和阳性参照物批间精密度 CV 范围为 0.31%~0.91%，均小于 5%，符合行业标准（CV＜5%）；HPV40、白色念珠菌、大肠杆菌和解脲支原体与试剂盒 21 种 HPV 亚型不存在交叉反应；干扰物质对检测结果无明显影响。
结论 本研究所用的 HPV 分型检测系统的主要性能指标满足相关标准的要求，可常规应用于临床。

PU-3140

鲍曼不动杆菌黏菌素耐药机制的研究进展

樊轩扬、李荷楠
北京大学人民医院

目的 多重耐药鲍曼不动杆菌的出现与全球感染率和病死率的升高有关，黏菌素成为对抗其感染的最后一线抗菌药物。但是近几年，黏菌素耐药的鲍曼不动杆菌被多次报道，了解其耐药机制，有利于控制耐药的播散，对研发新型抗菌药物有重要意义。

方法 通过整理和阅读 PubMed 上近二十年关于鲍曼不动杆菌和黏菌素相关文献资料，综述了鲍曼不动杆菌黏菌素耐药机制的最新进展，包括 2001～2017 年的流行病学调查，黏菌素抗菌作用机制和耐药机制，以及有效减少耐药菌株出现的方法和对新型抗菌药物的展望。
总结 鲍曼不动杆菌与大多数革兰阴性菌黏菌素耐药机制不同。除了共同的双组份系统 PmrAB 突变对脂质 A 进行修饰改变膜电位外，其最特殊的耐药机制是脂质 A 生物合成基因 lpxC/A/B 突变导致外膜表面的脂多糖完全丧失表现较高水平的耐药。但最近的研究发现质粒、转座子、插入序列（IS）等可移动的遗传元件也在黏菌素耐药播散中发挥重要作用。除了基因组水平的变化，表达水平的变化也会对黏菌素耐药产生很大影响，比如 Emb 类外排泵表达增加，增强了菌株黏菌素的耐药。
结论 我国黏菌素耐药率仍比较低，但是需要引起临床医生的关注；黏菌素耐药机制最为常见的就是菌体外膜脂质 A 的修饰；黏菌素耐药的鲍曼不动杆菌在表型上会发生很大变化，菌落形态的改变，毒力的改变和适应性的改变，这些改变使得菌株更能适应黏菌素环境；联合用药，特别是黏菌素和利福平联合，有利于减少黏菌素的使用，减少耐药性的产生。

PU-3141

包皮龟头炎患者真菌分离鉴定结果分析

杨阳
电子科技大学附属医院•四川省人民医院

目的 对疑似包皮龟头炎患者进行真菌学检查，了解念珠菌、马拉色菌在包皮龟头部的感染情况及菌种结构。
方法 刮取包皮垢或分泌物分别接种于沙堡斜面培养基和含菜子油沙堡斜面培养基，同时涂片染色作滴虫、霉菌、线索细胞检查。根据培养物菌落形态及镜下结构特征和生理生化特点，采用血清出芽试验，科玛嘉显色培养基（CHROMagar Candia），吐温生长试验，过氧化氢试验及七叶苷分解试验对培养物进行鉴定。
结果 从 86 例标本中分离白色念珠菌 33 株（38.37%），光滑念珠菌 1 株（1.16%）；分离出 27 株菌马拉色菌，其中糠秕马拉色菌共 10 株（11.63%），合轴马拉色菌共 8 株（9.30%），钝形马拉色菌 5 株（5.81%），球形马拉色菌 3 株（3.49%），限制性马拉色菌 1 株（1.16%）。在同一标本中同时分离白色念珠菌和马拉色菌有 6 例标本（6.98%），有 1 例标本同时分离出了两株马拉色菌菌，分别是糠秕马拉色菌和合轴马拉色菌。
结论 白念珠菌是念珠菌致真菌性龟头炎的主要菌群；马拉色菌感染也是重要的致病因素。

PU-3142

探索 HPLC-MS/MS 在快速检测耐碳青霉烯类肠杆菌目产 KPC 型和金属酶型碳青霉烯酶中的应用

李根、叶致含、张雯雁、叶扬芹、陈念贞、范列英
上海市东方医院（同济大学附属东方医院）

目的 碳青霉烯酶的产生是肠杆菌目细菌耐碳青霉烯类抗生素的主要原因，它可水解碳青霉烯类药物，导致药物失效。肠杆菌目细菌产生的常见碳青霉烯酶型主要为 KPC 型和金属酶型，在体外条件下，KPC 酶活性可被苯基硼酸抑制，而金属酶活性能被 EDTA 抑制。临床中针对产不同碳青霉烯酶酶型的肠杆菌目细菌引起的感染，其治疗方案不同，而目前实验室使用的碳青霉烯酶型检测方法耗时过长，难以满足临床需要。HPLC-MS/MS 是检测小分子物质的金标准，具有快速、稳定、准确的特点，因此我们开发了一种基于 HPLC-MS/MS 快速检测耐碳青霉烯类肠杆菌目产 KPC 型和金属酶型碳青霉烯酶的技术方法。

方法 本实验共收纳 241 株分离于临床的产碳青霉烯酶肠杆菌目细菌（肺炎克雷伯菌 217 例，产酸克雷伯 4 例，产气克雷伯 1 例，阴沟肠杆菌 10 例，大肠杆菌 8 例，粘质沙雷 1 例），经过测序得知，产 KPC 酶 212 例，产金属酶 29 例（26 例 NDM，3 例 IMP）。将受检菌+美罗培南共孵育作为对照管；受检菌+美罗培南+苯基硼酸共孵育作为检测管 A；受检菌+美罗培南+EDTA 作为检测管 B，以测序结果作为金标准，通过 HPLC-MS/MS 检测对照管与 AB 管之间美罗培南药物峰面积之比的变化，计算出用于检测产 KPC 酶以及金属酶的 cutoff 值。
结果 通过 HPLC-MS/MS 检测，对照管与 A 检测管美罗培南药物峰面积之比<0.4 时，待测菌为产 KPC 型碳青霉烯酶，敏感性为 93.70%，特异性为 95.60%；对照管与 B 检测管美罗培南药物峰面积之比<0.5 时，待测菌为产金属酶型碳青霉烯酶，敏感性为 100.00%，特异性为 92.86%。
结论 在本次实验中，HPLC-MS/MS 展现出了对耐碳青霉烯类肠杆菌目产 KPC 型和金属酶型碳青霉烯酶极佳的检测能力，整个检测过程，操作简单快速，结果准确性高，有望未来应用于临床。

PU-3143

碳青霉烯耐药肺炎克雷伯菌临床分析

许鑫悦
沈阳金域医学检验所有限公司

目的了解碳青霉烯耐药肺炎克雷伯菌（carbapenem-resistant Klebsiella pneumoniae,CRKP）的流行病学特征以及抗菌药物敏感性，临床开展相关治疗提供理论依据。
方法 收集 2017 年 6 月至 2019 年 9 月的临床标本中非分离的 236 株碳青霉烯耐药肺炎克雷伯菌菌株，使用安图 AUTO 1000 进行菌种鉴定，VITEK 2 Compact 微生物自动分析仪、和 K-B 法进行药物敏感性试验。
结果 从 2017 年 6 月至 2019 年 9 月住院患者中筛选出的 236 例 CRE 菌株进行分析。其中尿液标本 110 个、血液 50 个、胆汁 11 个、引流液 19 个、脑脊液 14 个、胸水 4 个、分泌物 12 个、腹水 1 个、其他 15 个。据药敏结果显示 CRKP 菌株对碳青霉烯类药物亚胺培南和厄他培南的耐药率分别为 90.82%,100.00%，对头孢类药物头孢唑林、头孢西丁和头孢曲松的耐药率均为 100.00%，对氨曲南的耐药率也较高为 95.64%，对环丙沙星和左氧氟沙星的耐药率可达 90%以上。而对阿米卡星,庆大霉素和妥布霉素的耐药率相对较低,分别为 54.23%,70.17%,74.17%。
结论 近年来 CRKP 菌株呈现出多重耐药的现象,且耐药趋势的发展也日趋严重,加强重点科室的感染控制,对于控制医院内耐药菌株传播至关重要。研究其耐药现象及耐药机制、做好对医院内感染的控制、对抗菌药物的管理合理使用抗生素和联合用药，对于临床的治疗来说至关重要。

PU-3144

The determination of gyrA and parC mutations and the prevalence of plasmid-mediated quinolone resistance genes in carbapenem resistant Klebsiella pneumonia ST11 and ST76 strains isolated from patients in Heilongjiang Province, China

Lingyi Zeng、Jisheng Zhang
Yongchuan Hospital of Chongqing Medical University

Background There is increasing resistance to carbapenems among Klebsiella pneumoniae,and fluoroquinolones (FQ) are increasingly used to treat infections from extended-spectrum β-lactamase(ESBLs) and carbapenemase-producing Klebsiella pneumoniae. However, the

acquisition of plasmid-mediated quinolone resistance (PMQR) or the spontaneous mutation of the quinolone resistance-determining regions (QRDR) of the gyrA and parC genes can severely affect the therapeutic effect of quinolones. The goal of this study was to investigate the molecular determinants of FQ resistance(FQ-R) in carbapenem-resistant Klebsiella pneumoniae (CRKP) isolates from Heilongjiang Province,China.

Materials and Methods We isolated 40 strains of CRKP from a treatment center in the eastern part of Heilongjiang Province from January 2016 to December 2018. The VITEK2 Compact analyzer was used to identify and detect drug sensitivity. Different types of drug resistance genes were detected by polymerase chain reaction (PCR). PCR and DNA sequencing were used to assess the presence of qnrA, qnrB, qnrS,qepA and acc(6′) Ib-cr genes,which are plasmid-encode genes that can contribute to resistance. The sequences of gyrA and parC genes were sequenced and compared with the sequences of standard strains to determine if mutations were present.Multi-site sequence typing (MLST) and pulsed-field gel electrophoresis (PFGE) were performed on the strains to assess homology.

Results The isolated CRKP strains showed rates of resistance to fluoroquinolones of 22.5% to 42.5%. The resistance rate of ciprofloxacin was significantly higher than that of levofloxacin.Nine CRKP strains (22.5%) showed co-resistance to ciprofloxacin and levofloxacin.The quinolone resistant strains were screened for plasmid-encoded genes that can contribute to resistance (PMQR genes).Among the 17 quinolone resistant strains,one strain contained no PMQR genes,twelve strains contained two PMQR genes,and four strains contained four PMQR genes.Acc (6′)Ib-cr was the most frequently detected PMQR gene, detected in 95% of strains tested (38 of 40) and in 94.1% of the quinolone-resistant strains (16 of 17). The qepA gene encoding an efflux pump was not detected in any strains.No isolate carried five different PMQRs simultaneously.Changes of S83I and D87G changes in gyrA, and the S80I change in parC,which were mediated by QRDR,were identified in two isolates,which showed resistance to both ciprofloxacin and levofloxacin.Most of the FQ-R strains(58.8%,10/17) belong to ST(sequence type) 76, which is dominant in the local area, while all the mutant strains (100%,2/2),that differ in at least one site from standard bacteria, belong to the ST11 group. The strains were isolated from a hospital where there had been a recent outbreak of ST76 type CRKP in the neurosurgery ward and intensive care unit.

Conclusion CRKP strains were identified that were insensitive or even resistant to quinolones,and this resistance is common in Heilongjiang Province of eastern China;fluoroquinolone-resistance in these clinical CRKP strains is a complex interplay between PMQR determinants and mutations in gyrA and parC.The resistance level caused byQRDR mutation is higher than that caused by PMQR, however, the high frequency of PMQR genes in the isolated CRKP strains suggests the potential for impact of these genes.PMQR determinants are often found in carbapenemase-producing or ESBLs-producing Klebsiella pneumoniae,and some resistance genes,such as:SHV,TEM, CTX-M-15,and OXA-1 are closely associated with FQ-R. Finally, geographical factors can affect the emergence and spread of PMQR and QRDR.Some genetic lineages have higher potential risks, and continuous close monitoring is required.

PU-3145

Autof MS 1000 质谱鉴定系统对临床分离病原菌的鉴定能力评价

陆丹、周雪婷、陈雨婷、魏望、曹宇杰、薛魁
江苏省邳州市人民医院

目的 分析 Autof MS 1000 质谱鉴定系统和 VITEK 2 Compact 全自动微生物分析系统对临床分离病原菌鉴定的一致性和准确率，评价 Autof MS 1000 质谱鉴定系统对病原菌的鉴定能力。

方法 收集我院 2020 年 9 月-2021 年 5 月分离自临床的非重复菌株共 190 株，分别采用 Autof MS 1000 和 VITEK 2 Compact 两种细菌鉴定仪进行鉴定，鉴定结果不一致或未鉴定出结果的菌株以 16SrDNA 或真菌 ITS 区测序结果为准，分析比较两种仪器鉴定结果的一致性和准确率。
结果 本次研究共纳入 190 株菌株，其中革兰阳性需氧菌 58 株，革兰阴性需氧菌 93 株，厌氧菌 6 株，酵母样真菌 33 株。在种水平上鉴定一致的有 166 株（87.4%），不一致的有 24 株（12.6%）。鉴定结果不一致的菌株经 16SrDNA 或真菌 ITS 区测序确认，Autof MS 1000 的准确率为 70.8%（17/24），明显高于 VITEK 2 Compact 的准确率 45.8%（11/24）（P<0.05）。Autof MS 1000 鉴定的总准确率为 93.2%（177/190），略高于 VITEK 2 Compact 鉴定的总准确率 90.0%（171/190）（P>0.05），其中 Autof MS 1000 鉴定革兰阳性需氧菌的总准确率（94.8%）略高于革兰阴性需氧菌的总准确率（89.2%），鉴定厌氧菌的总准确率为 100%（6/6），鉴定酵母样真菌的总准确率为 100%（33/33）。
结论 Autof MS 1000 与 VITEK 2 Compact 鉴定结果较为一致，差异无统计学意义（P>0.05）；但对于临床少见菌，Autof MS 1000 较 VITEK 2 Compact 具有更高的准确率（P<0.05），且快速经济，适合临床分离病原菌的常规鉴定。

PU-3146

多粘菌素体外药物敏感性试验方法探讨

王珏
江苏省人民医院（南京医科大学第一附属医院）

近年来,抗菌药物不合理使用,使得细菌耐药问题越来越严重，抗感染治疗药物选择变得越来越棘手，特别是多重耐药（MDR）菌出现，尤其是产碳青霉烯酶的革兰阴性杆菌的感染，往往面临无药可用的境地，已成为威胁全球公共卫生健康的重要问题之一。在新抗菌药物研发鲜有突破的形势下，一些“老抗菌药” 重新被临床启用以应对抗感染治疗需求，黏菌素就是其中 之一，成为当前临床治疗多重耐药，尤其是产碳青霉烯酶的革兰阴性杆菌感染的最后手段。

日益突出的多重耐药菌问题给临床抗感染治疗带来了严峻挑战[1]。随着抗菌药物的广泛应用，细菌的耐药形式愈演愈烈，根据中国细菌耐药性监测网数据显示，2018 年 CRE 分离率为 28.6%，CRAB 分离率为 78.1%;我院 2018 年 CRE 分离率为 19.8%，CRAB 分离率为 78.6%；多重耐药的细菌已逐渐成为医院感染重要的病原菌，其引起的感染是导致患者病死率增加的主要因素[2，3] 。替加环素和黏菌素是治疗多重耐药革兰阴性杆菌的挽救性治疗措施[4];近年国内外逐渐分离出替加环素耐药革兰阴性杆菌，使得多粘菌素成为抗击泛耐药革兰阴性杆菌感染的最后一道防线，临床上迫切需要提供多粘菌素的药敏结果。

PU-3147

Antimicrobial resistance of Pseudomonas aeruginosa isolated from the clinical laboratory of the First hospital of Jilin University from 2020 to 2021

Chun Yang、Xufeng Ji
First hospital of Jilin University

Objective The main objective of this study is to investigate the antimicrobial resistance of Pseudomonas aeruginosa. To provide the theoretical guidance for the rational use of antimicrobial agents and the scientific basis for control the drug-resistant strains.
Methods 1. The Pseudomonas aeruginosa were isolated from the clinical laboratory of the First hospital of Jilin University.

2. The resistance of Pseudomonas aeruginosa for 20 antimicrobial agents were determined using paper disk method and minimum inhibitory concentration（MIC）method, analyzed the drug-resistant spectrum. The results were evaluated based on Clinical and Laboratory Standards Institute (CLSI-M100-S29).WHONET-5.6 software was used to analyze the drug resistance data.
Results 1. Most of 1104 Pseudomonas aeruginosa strains were collected from abdominal fluid (10 strains), broncho-alveolar lavage (25 strains), bile (10 strains), blood (39 strains), ear (6 strains), sputum (881 strains), urine (49 strains), shunt fluid (17 strains), secretion (6 strains) during the whole year.
2. The drug-resistant rates of the 1104 isolated strains to meropenem and imipenem were 11.8% and 12.4% respectively. 11045 strains were all resistant to ceftriaxon, cefotaxim, cefuroxim. The rates of Pseudomonas aeruginosa resistant to ceftazidime, cefepime, were 7.6% and 6.1% respectively. The rates of Pseudomonas aeruginosa resistant to levofloxacin and ciprofloxacin were 6.8% and 8.2% respectively. The rates of Pseudomonas aeruginosa resistant to piperacillin/tazobactam and amikacin were 4.7% and 6.8% respectively.
3.One thousand one hundred and four strains of Pseudomonas aeruginosa mainly from the surgical ward, 114 case from ICU, 2 case of infectious diseases department, 78 from neurology, 4 from pediatric respiratory medicine, 188 strains from department of respiration, 76 strains from neurosurgery, 50 strains from emergency department, 17 strains from oncology department, 23 strains from hepatobiliary pancreatic surgery, 22 strains from urinary surgery, 65 strains from gastrointestinal surgery, three strains from the outpatient department, five strains from trauma department of orthopedics, two strain from obstetrical department and only one strains from thyroid surgery.
Conclusions 1. One thousand one hundred and four strains of Pseudomonas aeruginosa were screened by analyzing the drug resistance spectrum in the research, which has different resistant rates to different antimicrobial agents.
2. Most of the 1104 Pseudomonas aeruginosa were isolated from sputum. Department of respiration is the department that isolated most numbers of Pseudomonas aeruginosa. The rate of Pseudomonas aeruginosa resistant to amikacin is lowest. Monitoring of the antimicrobial resistance of Pseudomonas aeruginosa should be strengthened. The change of the antimicrobial resistance should be investigated in order to direct rational drug usage in clinic.

PU-3148

厄他培南诱导铜绿假单胞菌耐药性变化的研究

许一筠[1]、蔡淑梅[1,2]、李卫滨[1,2]、张胜行[1,2]
1. 福建医科大学福总临床医学院检验科
2. 联勤保障部队第九〇〇医院福建省适配体技术重点实验室

目的 通过体外实验，研究厄他培南反复刺激耐 2 类碳青霉烯类铜绿假单胞菌和敏感铜绿假单胞菌对亚胺培南及美罗培南耐药性的变化及可能的机制。为预防和治疗临床铜绿假单胞菌所致的感染以及合理使用厄他培南提供依据。
方法 收集耐 2 类碳青霉烯类铜绿假单胞菌 10 株和敏感铜绿假单胞菌 2 株，用高浓度（10mg/ml、5mg/ml、2.5mg/ml）及低浓度（125μg/ml、62.5μg/ml、31.25μg/m）的厄他培南持续刺激及传代并将高浓度刺激后的菌株再用低浓度刺激。在刺激后的不同时间对待测菌株用 K-B 法进行美罗培南、亚胺培南药敏检测，分析厄他培南的使用对耐 2 类碳青霉烯类铜绿假单胞菌的影响。
结果 10 株耐 2 类碳青霉烯类铜绿假单胞菌经刺激后对亚胺培南、美罗培南及其他临床常用药耐药性未发生变化，但亚胺培南及美罗培南抑菌圈有所缩小，其中对美罗培南的药敏结果由中介变为耐药的有 3 株，菌株对亚胺培南的药敏结果由中介变为耐药有 1 株。2 株敏感铜绿假单胞菌经高浓度厄他培南刺激后无变化，由低浓度厄他培南刺激后由敏感变为耐药（亚胺培南分别由 26 到 6mm、22 到 10mm），且出现异质性耐药现象。药敏实验过程中，亚胺培南与哌拉西林/他唑巴坦药敏纸片相邻时可出现“D”圈，表现出拮抗作用。

结论 高浓度厄他培南的使用可能使耐 2 类碳青霉烯类铜绿假单胞菌对第 2 类碳青霉烯类药物的敏感性下降；7-14 天低浓度使用可能导致铜绿假单胞菌发生对美罗培南以及亚胺培南耐药；厄他培南的使用可能引起铜绿假单胞菌产生异质性耐药；亚胺培南与哌拉西林/他唑巴坦联合使用可对 PA 表现出拮抗作用。

PU-3149

质谱技术快速鉴定临床分离丝状真菌的应用探讨

曹敬荣、王岩、谢威、李文军、陈典典、段园园、刘云屹、闵嵘、王培昌
首都医科大学宣武医院

目的 探讨质谱（MALDI-TOF MS）在临床分离的丝状真菌快速鉴定的应用。
方法 收集某三甲医院 2017 年 1 月-2019 年 1 月经形态学鉴定为丝状真菌的菌株,分别采用双甲酸夹心法和甲酸乙腈萃取法提取真菌蛋白行 MALDI-TOF MS 鉴定，并与聚合酶链反应（PCR）内转录间隔区(ITS)基因序列测定结果比较；采用 SPSS20.0 软件统计分析丝状真菌菌种分布和标本来源。
结果 共收集临床分离的丝状真菌 90 株，其中曲霉菌属 70 株（77.78%），青霉菌属 6 株（6.67%），链格孢霉 5 株（5.56%），镰刀菌属 4 株（4.44%），赛多孢菌和接合菌各 2 株（2.22%）；曲霉菌以烟曲霉 47 株(52.22%)、黄曲霉 13 株（14.44%）和黑曲霉 4 株(4.44%)为主。标本主要来源于呼吸道标本（90.0%）（包括痰标本和肺泡灌洗液），其次为角膜和耳道分泌物（3.33%），其中分离率最多的为曲霉菌 59 株（65.56%）。MALDI-TOF MS 鉴定到种 82 株，与基因测序结果一致率为 92.11%，鉴定准确率远高于形态学（68.89%）鉴定结果（x2=12.02，p=0.01）；质谱鉴定丝状真菌中的曲霉菌（烟曲霉、黄曲霉、黑曲霉）、镰刀菌、赛多孢菌和链格孢霉时准确率高（98.57%-100%）；双甲酸夹心法和甲酸乙腈萃取法前处理的质谱鉴定丝状真菌到种水平的比率分别为 91.11%和 90%，鉴定曲霉菌种水平分别为 98.57%和 97.14%，鉴定准确率无明显差异（x2=0.34，p=0.95）；两种前处理方法均可 100%鉴定烟曲霉、黄曲霉、赛多孢菌和链格孢霉到种水平，其中 88.57%烟曲霉和 76.92%黄曲霉鉴定得分≥2.0 分，但前者操作更简单快速。
结论 MALDI-TOF MS 技术鉴定丝状真菌快速准确，双甲酸夹心法前处理操作更简便，适合实验室常规检测，可用于实验室常规鉴定曲霉菌等常见丝状真菌。

PU-3150

NDM-1 阳性大肠埃希菌分子生物学特征

李彬
福建医科大学附属协和医院

目的 探讨产 blaNDM-1 大肠埃希菌临床分离株的耐药机制及分子分型。
方法 收集 2014 年 8 月-2015 年 8 月福建医科大学附属协和医院临床分离非重复大肠埃希菌 700 株，采用 PCR 检测 blaNDM-1 基因；采用法国梅里埃 Vitek-2 Compact 系统检测 blaNDM-1 基因阳性菌株及其接合子药物实验；对 blaNDM-1 基因阳性菌株，采用 PCR 检测其毒力基因、O 抗原分型、系统发育分型以及其他 b 内酰胺基因；通过接合试验验证 blaNDM-1 基因能否水平转移，利用肠杆菌基因重复一致序列分析（ERIC-PCR）和多位点序列分型（MLST）进行菌株同源性分析。
结果 700 株大肠埃希菌中有 4 株（0.6％）blaNDM-1 基因阳性菌株；药敏结果显示 blaNDM-1 阳性菌对 β 内酰胺类抗生素高度耐药，系统发育分型显示 2 株属于 B1 群，A 群和 D 群各一株；blaNDM-1 阳性菌中检测到七种不同的毒力基因；EC12 菌株血清型分型为 O8，其余未能分型；blaNDM-1 阳性分离株共同携带其他 β 内酰胺酶基因（blaTEM-1、blaCTX-M-14 和 blaCTX-M-15）。接合实验有 3 株菌是成功的，质粒分型结果显示含有 blaNDM-1 基因的质粒属于 Inc FIB、

Inc I1 和 Inc P。ERIC-PCR 显示四种 blaNDM-1 阳性菌株被分为三种不同的型别；MLST 显示，四株 blaNDM-1 菌株分为四种不同类型：ST156、ST167、ST405 和 ST648。
结论 该院产 blaNDM-1 大肠埃希菌阳性菌株流行率较低，但具有广泛的耐药谱，同时携带多种耐药基因和毒力基因，以非克隆播散方式在该院流行。

PU-3151

基于 CRISPR-Cas12a 检测碳氢酶烯酶的新方法以及临床应用

徐华铭、徐华铭
安徽医科大学第四附属医院

碳青霉烯酶类耐药基因对抗生素的耐药性是目前全球关注的热点问题，这类耐药菌在医院内传播力强，引起的感染临床治疗手段有限，且效果不佳。如何快速、有效、方便的进行分子检测至关重要，是目前急需解决的问题。因此，我们开发了一种针对 KPC、NDM 碳青霉烯酶新型核酸检测**方法** 基于环介导等温扩增、CRISPR-Cas12a 和免疫层析条的检测系统（CRISPR/Cas-LAMP-lateral flow strip）。其原理是通过等温扩增的方式扩增目的基因再以 gRNA 靶向识别并引导 Cas12a 切割目标 DNA，同时切割反应体系内的任一条单链 DNA 为特征，并将切割后产物通过免疫层析条显示结果。这种方法有几个明显的优点。首先，LAMP 扩增强调了所需仪器简单或者无仪器要求，灵敏度也较传统 PCR 技术高,CRISPR/Cas12a 技术可特异性地反式切割报告基因，避免 LAMP 扩增假阳性的影响，使其结果可在横向侧流条上肉眼可见。其次，与传统繁琐、耗时的检测方法相比，该方法既大大地缩短了检测时间。全程四十分钟分钟即可完成检测，也不需要反复训练的操作人员，而且可精确地对不同耐药基因进行精确分型。最后，通过该技术可建立快速检测平台，该平台可应用于其他引起重大公共卫生问题的病原体，如新冠病毒、人乳头瘤病毒、新布尼亚病毒，且只需要改动其中的 LAMP 扩增引物和 crRNA 即可完成，在低医疗资源环境条件下，也可提供了更多的诊断结果。因此它可以广泛应用于医院院感防控和耐药菌的鉴定与治疗，管此方法刚刚起步，我们仍有理由相信该技术对病原体的诊断能力。它可以适用于大规模的人群筛查控制爆发感染，正在引领一场生物技术革命。

PU-3152

铜绿假单胞菌 T6SS clpV1 基因缺失株的构建及对相关功能的影响

邹雅如
上海市宝山区吴淞中心医院

铜绿假单胞菌是一种广泛存在于各种环境中的革兰阴性菌，是医院感染最常见的病原菌之一，常感染免疫力低下的人群，是临床引起患者发病和死亡的主要因素，特别是囊性纤维化(cystic fibrosis, CF)的患者。

细菌通过蛋白质分泌系统，与外界环境及宿主真核细胞相互作用。VI型分泌系统(Type VI secretion system, T6SS)广泛存在于革兰阴性菌中，是一种重要的毒性因子分泌系统，与病原菌的致病性和对外界环境的适应性密切相关，但目前对于 T6SS 生物学功能的了解仍很少。
铜绿假单胞菌几乎编码所有已发现的蛋白质分泌系统，包括三种不同类型的 T6SS 基因簇，即 H1-T6SS，H2-T6SS 和 H3-T6SS，这使它成为研究 T6SS 最理想的模式细菌之一。铜绿假单胞菌中，T6SS 的基因结构中约有 13 个保守的基因片段是其核心部件，包括 clpV 等。它们编码的胞外蛋白，如溶血素共调节蛋白(Hemolysin co-regulated protein, Hcp)和缬氨酸-甘氨酸重复蛋白 G (VgrG)，是 T6SS 最重要的两个效应蛋白。我们前期研究发现，PAO1 菌株生物被膜菌 Hcp1、Hcp2 和

Hcp3 基因的相对表达量均明显高于浮游菌，提示 T6SS 可能参与了生物被膜形成。clpV 是 T6SS 重要的功能元件，它属于 T6SS 的分子伴侣蛋白，具有 AAA+ ATP 酶活性，为 Hcp 蛋白的分泌提供必需的能量来源。因此，如果将 clpV1 基因敲除，铜绿假单胞菌将丧失分泌 Hcp1 的能力。VgrG1a 和 VgrG1c 蛋白的分泌也依赖于 clpV1。

基因敲除术是研究基因功能的重要方法，本研究中，我们通过同源重组法和融合 PCR 技术成功构建铜绿假单胞菌模式菌株 PAO1 的 clpV1 基因缺失株，为进一步在体外对铜绿假单胞菌的 H1-T6SS 的生物学功能进行研究奠定基础。

PU-3153

广州禾信 CMI-1600 全自动微生物质谱检测系统与 VITEK 2 Compact 全自动微生物鉴定仪对临床常见病原菌鉴定的一致性分析

李世荣
复旦大学附属华山医院虹桥院区

目的 分析广州禾信 CMI-1600 全自动微生物质谱检测系统与 VITEK 2 Compact 全自动微生物鉴定仪对临床常见病原菌鉴定的一致性。并评估两种方法的鉴定时间和经济成本。
方法 收集复旦大学附属华山医院 2021 年 3 月-2019 年 5 月来自临床不同标本分离的非重复菌株 292 株。
采用广州禾信 CMI-1600 全自动微生物质谱检测系统和 VITEK 2 Compact 全自动微生物鉴定仪对病原菌进行鉴定，比较两种鉴定方法的一致性。
结果 292 例临床菌株中，两种方法鉴定至种水平一致的样本 276 例，占比 94.5%；鉴定至属水平以上一致的样本 291 例，占比 99.6%，鉴定不一致的样本 1 例，占比 0.4%。
结论 CMI-1600 与 VITEK 2 Compact 对于临床常见病原菌的鉴定结果较为一致，但 CMI-1600 全自动微生物质谱检测系统在时间和经济成本上明显优于 VITEK 2 Compact 鉴定仪，且操作简便，易于使用，给临床微生物的鉴定带来了方便。

PU-3154

2016-2020 年安徽医院念珠菌血流感染患者临床特点及危险因素分析

叶乃芳、刘周、周强
安徽医科大学第二附属医院

目的 探讨安徽医院念珠菌血流感染患者临床特点及影响其预后的危险因素。
方法 收集 2016 年 1 月至 2020 年 12 月安徽医科大学第二附属医院全部念珠菌血流感染患者临床资料及抗真菌药物药敏结果进行回顾性分析,采用单因素、多因素回归分析对念珠菌血症患者预后危险因素进行分析。
结果 共检出念珠菌血症患者 85 例，其中 2016 年至 2020 年，分别为 12 株、11 株、20 株、12 株及 20 株。念珠菌血流感染的发生与年龄性别无明显相关性，菌株主要为热带念珠菌 28 株(32.9％),白色念珠菌 26 株(30.6％),光滑念珠菌 14 株(16.5％), 近平滑念珠菌 12 株(14.1％),克柔念珠菌 2 株(2.4％),其他念珠菌 3 株(3.5％)。对抗真菌药物的敏感率依次为氟胞嘧啶(100.0％)、两性霉素 B(100.0％)、伏立康唑(94.1％)、伊曲康唑(82.4％)和氟康唑(74.1％)。30 天死亡与念珠菌血症直接相关的归因病死率为 32.9％。Logistic 单因素回归分析显示，30 天内使用抗生素、2 个月内使用激

素及机械通气是归因死亡危险因素。Logistic 多因素回归分析显示，2 个月内使用激素及机械通气是其归因死亡独立危险因素。
结论 引起我院念珠菌血流感染病原体最常见为热带念珠菌，已经超过白色念珠菌。三唑类药物是抗真菌药物的主力军，其念珠菌对伏立康唑、氟康唑、伊曲康唑均有不同程度的耐药。2 个月内使用激素及机械通气是念珠菌血流感染死亡独立危险因素。

PU-3155

2015-2020 长沙地区泌尿生殖道支原体感染现状及药敏分析

肖金红、李江、徐文、胡一敏、谢良伊、刘琼
湖南省人民医院

目的 了解长沙地区泌尿生殖道支原体感染情况并进行药敏分析,为临床合理使用抗菌药物提供实验参考依据。
方法 对 2015—2020 年本院 50362 例疑似泌尿生殖道支原体感染患者的感染情况和药敏试验结果进行回顾性分析。
结果 50362 例标本中共检出支原体阳性标本 24677 例，感染率为 48.99%，其中解脲脲原体（Uu）感染 14267 例，感染率 28.33%，人型支原体（Mh）感染 2862 例 感染率为 5.68%，Uu+Mh 混合感染 7548 例，感染率为 14.99%。男性 Uu、Mh、Uu+Mh 感染率分别为 18.23、0.72%、6.25%，明显低于女性的感染率 42.24%、1.43%、10.61(P＜0.05）。对药敏实验结果分析表明，Uu、Mh 和 Uu+Mh 对强力霉素、美满霉素耐药率均低于 3%，对喹诺酮类抗生素耐药率较高；Uu 对大环内酯类抗生素中的阿奇霉素、红霉素耐药率较高，分别为 30.25%和 55.72%，而对交沙霉素、环酯红霉素和克拉霉素耐药率均低于 3%； Mh 对大环内酯类抗生素（除交沙霉素）耐药率均大于 90%。2015 至 2020 年，Uu 对阿奇霉素的耐药率呈逐年上升趋势，对加替沙星和甲砜霉素的耐药率呈下降趋势；Mh 对甲砜霉素、加替沙星的耐药率呈下降趋势。
结论 泌尿生殖道支原体对强力霉素、美满霉素和交沙霉素的敏感率较高，可首选用于本地区泌尿生殖道支原体感染的临床治疗。长沙地区泌尿生殖道支原体感染率呈上升趋势，且女性高于男性，应加强泌尿生殖道感染的监测和防控，同时规范临床抗菌药物的合理使用。

PU-3156

尿培养阳性标本中大肠埃希菌的耐药性分析

杜娜、尧静、李玉海
云南省中医医院（云南中医药大学第一附属医院）

目的 探究尿培养阳性标本中大肠埃希菌的耐药性，为临床治疗尿路感染提供合理的用药指导。
方法 通过 Vitek 2 Compact 系统对 2012-2018 年尿培养阳性标本进行细菌鉴定及药敏试验，使用 WHONET 5.6 软件进行分析。
结果 总的分离到 1419 株大肠埃希菌，前三位感染病区为内分泌科病区、肿瘤科病区和针灸科病区，构成比为 16.5%、15.5%和 14.8%。大肠埃希菌对氨苄西林、头孢唑啉、头孢他啶、头孢曲松、氨曲南、庆大霉素、环丙沙星、左旋氧氟沙星、复方新诺明及四环素呈现不同水平的耐药，但是对阿莫西林/克拉维酸、头孢吡肟、厄他培南、亚胺培南、美洛培南、阿米卡星及呋喃妥因还保留较高敏感活性。在统计的肠杆菌科细菌中，产 ESBLs 肠杆菌科细菌中所占比例最高的为大肠埃希菌(74.4%),碳青霉烯类耐药肠杆菌科细菌中所占比例最高的为肺炎克雷伯菌(67.8%)。
结论 引起尿路感染最常见的细菌为大肠埃希菌，其因产 ESBLs 对临床常用的青霉素类和头孢菌素类抗生素耐药，因此临床应根据细菌培养和药敏试验结果制订合理的抗生素用药方案，避免抗生素滥用，导致耐药菌的产生。

PU-3157

孕 35-37 周产妇外阴和肛周双部位采样进行 B 群链球菌筛查的必要性分析

陈涌泉、王世杰
厦门弘爱医院

目的 通过比较 B 群链球菌筛查中阴道分泌物和肛周拭子的阳性率，分析双部位同时采样送检的必要性。
方法 回顾性分析 2020 年 1 月—2020 年 12 月就诊于福建医科大学附属厦门弘爱医院的 3534 例孕 35-37 周产妇的 B 群链球菌筛查结果，用运送显色培养管分别采集阴道分泌物和肛周拭子，置 5%二氧化碳培养箱孵育 36-48 小时，记录显色的阳性结果。所有显色培养后样本再接种血平板中 5%二氧化碳培养过夜，挑选可疑菌落进行 CAMP 试验，必要时采用 VITEK MS 飞行质谱仪鉴定。
结果 B 群链球菌双部位采样筛查的阳性率为 22.84%，仅采集阴道分泌物阳性率为 16.77%，敏感性为 73.42%；仅采集肛周拭子送检阳性率为 16.44%，敏感性为 72.00%，以上差异均具有统计学意义 （P＜0.05）。与血平板细菌培养法对比，运送显色培养管法敏感性 96.68%，特异性 96.78%，此差异没有统计学意义（P>0.05）。
结论 同时采集阴道分泌物和肛周拭子双部位进行 B 群链球菌筛查，能提高 B 群链球菌筛查的阳性率；运送显色培养管的敏感性和特异性均较高，能达到作为筛查试验的基本要求。

PU-3158

深圳市罗湖区铜绿假单胞菌感染现状 及耐药性分析

付汉维、莫云均、覃俊龙、张宇英、张智耀、何婷、钟如燕、陈璐
深圳市罗湖医院集团医学检验中心

目的 研究罗湖区铜绿假单胞菌感染部位的分布特点及对常用抗菌药物的耐药性，为临床医师合理选用抗菌药物抗感染治疗提供依据。
方法 对我检验中心 2018-2020 年实验室常规分离培养并进行药敏实验分离的 161 株铜绿假单胞菌进行回顾性统计分析，分析临床分布情况和病人易感染部位，评价抗菌药物的体外抗菌活性。
结果 铜绿假单胞菌在呼吸道的检出率较高，对多粘菌素 B、哌拉西林/他唑巴坦、美洛培南、亚胺培南、左氧氟沙星等抗生素的敏感性较高，对氨苄西林/舒巴坦、复方新诺明、头孢噻肟耐药率较高，对其它抗生素出现不同程度的耐药。
结论 铜绿假单胞菌感染部位较多，感染率较高，耐药性呈上升趋势；对碳青霉烯类氨基糖甙类、多粘菌素 B、喹诺酮类、部分头孢类、β－内酰胺酶抑制剂复合药物保持较好的敏感性，耐药性逐渐上升，应加强对铜绿假单胞菌感染率和耐药性有计划地连续监测，加强耐药菌的隔离。

PU-3159

基于 ACE/ACE2 平衡的 COVID-19 治疗思路

李思进、任碧琼
湖南省第二人民医院

COVID-19 的全球流行已导致数十万人死亡，迄今为止尚未找到有效的治疗方法，严重威胁着世界公共健康和生命安全。因此我们迫切需要找到降低死亡率的有效方法。 ACE2 是 ACE 的同工酶，两者都是 RAS 的重要组成部分，但它们的生理作用却相反。 新型冠状病毒通过 ACE2 进入人

体，导致 ACE / ACE2 失衡，并导致各种病理变化。 本文综述了 ACE / ACE2 的双重作用，并讨论了基于 ACE / ACE2 平衡的药物对 COVID-19 引起的 ALI 和 ARDS 患者的潜在治疗作用。

PU-3160

血培养主要病原菌分布及耐药性分析

赵梅娥、王春霞
兰州市第一人民医院

目的 了解兰州市第一人民医院血培养病原菌分布及其对抗菌药物的耐药情况。
方法 对 2016 年 1 月 至 2020 年 12 月 的住院患者血培养的常规鉴定及药敏试验进行分析。
结果 2760 例血培养标本中共检测出病原菌 196 株，阳性率为 7.1％。其中革兰阴性菌占 63.8%（125 / 196），以大肠埃希菌为主、其次为肺炎克雷伯菌、阴沟肠杆菌、1 例耐碳青霉烯类药物的鲍曼不动杆菌等；革兰阳性菌占 32.7％（64 / 196），并以表皮葡萄球菌为主；真菌 7 株，占 3.57％。药敏结果显示大肠埃希菌和肺炎克雷伯菌对氨苄西林耐药率最高（83.2％ ~100％），对哌拉西林 / 他唑巴坦、头孢哌酮 / 舒巴坦、头孢吡肟、头孢他啶耐药率均较低（0~10％），对亚胺培南、阿米卡星 100.0%敏感；革兰阳性菌对青霉素、红霉素耐药率较高（80.5%-93.6%），对万古霉素、利奈唑胺、替考拉宁 100.0％敏感；
结论 兰州市第一人民医院血培养病原菌以革兰阴性菌为主，首选抗生素哌拉西林 / 他唑巴坦或头孢哌酮 / 舒巴坦，由于地区环境不同，病原菌及耐药情况应做定期监测分析，为临床合理使用抗菌药物提供客观、准确的依据。

PU-3161

新型冠状病毒疫情爆发前后西安某医院呼吸道病毒发病情况调查及分析

姚子淳
西安医学院第一附属医院

目的 分析新型冠状病毒疫情爆发前后西安某医院呼吸道病毒发病情况调查及分析。
方法 回顾性分析 2018 年 2 月～2021 年共 7893 例呼吸道感染的患者，抽取鼻咽部分泌物，采取胶体金法、直接免疫荧光法检测 7 种常见呼吸道病毒。分析比较常见呼吸道病毒季节分布特征以及在新冠疫情前后发病情况。
结果 7 种病毒中呼吸道合胞病毒（RSV）检测阳性例数最多，其次为 A 型流感病毒。从季节分布情况来看，，以春、夏季多发。从年龄段分析，1 岁以下的婴幼儿组阳性率在各年龄组中最高，其次是 1 ～ 3 岁的患儿，阳性率随年龄增长逐渐下降。总病毒阳性率与性别无关。不同疾病的病毒检出率不同，在肺炎、支气管肺炎患儿中，病毒阳性率最高，各组疾病检出的最主要病毒均为 RSV。新冠疫情爆发后，各种病毒阳性率均下降。
结论 呼吸道病毒发病具有明显的季节性，集中趋势明显。疫情爆发后，呼吸道病毒阳性率明显下降。

PU-3162

2016 年-2018 年某院血培养标本中病原菌分布及耐药性分析

吴玲玲
泰安市中心医院

目的 分析血流感染主要病原菌种类及耐药情况。
方法 对医院 2016 年 1 月-2018 年 12 月临床送 检成人血培养标本的培养和药敏结果进行回顾性统计分析，对阳性标本进行病原菌统计分析。
结果 2016 年 1 月-2018 年 12 月医院共送检成人血培养标本 17140 份，阳性标本 1753 份，阳性率 10.2%，共检出病原菌 1737 株。 其中, 革兰阴性菌 1120 株占 64.48%， 革兰阳性菌 550 株占 31.66%， 真菌 49 株占 2.82%， 专性厌氧菌 18 株占 1.04%。 病原菌分布占前 3 位的科室分别是重症医学科（ICU）、急诊科和血液内科。 检出率较高的病原菌依次为：大肠埃希菌、肺炎克雷伯菌和凝固酶阴性葡萄球菌。
结论 该院血流感染的病原菌以革兰阴性菌为主，定期对血培养 病原菌的分布及耐药情况进行分析，对临床合理用药有重要意义。

PU-3163

Xpert Mtb/RIF、γ-干扰素释放试验、荧光定量 PCR 在结核病诊断中的对比研究

刘爱波、王京梅
四川省医学科学院·四川省人民医院

目的 比较结核分枝杆菌/利福平耐药快速检测法(Xpert Mtb/RIF)、荧光实时定量 PCR、γ-干扰素释放试验检测结核分枝杆菌的价值。
方法 纳入 2018 年 4 月 1 日至 2019 年 4 月 1 日在四川省人民医院就诊的结核分枝杆菌培养阳性的患者 151 例。利用 Xpert Mtb/RIF、荧光实时定量 PCR 技术对其痰液（或体液）标本进行 DNA 检测，并抽血送检 γ-干扰素释放试验，利用统计分析方法比较这三种检测技术对结核分枝杆菌的检出率以及结核培养阳性患者的 r-干扰素的集中范围。
结果 以结核培养为金标准，用 γ-干扰素释放试验辅助检测结核分枝杆菌的阳性率高于荧光实时定量 PCR 法与 Xpert Mtb/RIF 法，P＜0.05，差异有统计学意义。
结论 与用荧光定量 PCR 技术和 Xpert Mtb/RIF 相比，用 γ-干扰素释放试验辅助诊断结核分枝杆菌的阳性率更高，但可能存在假阳性，在临床诊断中应结合多方面考虑。

PU-3164

糖尿病足溃疡的细菌分布及药物敏感试验分析

方慧
上海市杨浦区中心医院（同济大学附属杨浦医院）

目的 分析糖尿病足溃疡患者病原菌分布、特点及药物敏感性，指导医生选择性用药。
方法 选择 50 例糖尿病足溃疡患者，进行溃疡部位病原菌检测及药物敏感试验。
结果 50 例患者，共检出 65 株病原菌， 33 株革兰氏阳性菌（50.77%），30 株革兰氏阴性菌（46.15%），2 株白色念珠菌（3.08%）。排在前三位的分别为金黄色葡萄球菌、凝固酶阴性葡萄球菌（第二位）、大肠埃希菌（第二位）、阴沟肠杆菌。其中，革兰氏阳性菌中有金黄色葡萄球菌、凝固酶阴性葡萄球菌、粪肠球菌、屎肠球菌。有 6 株为耐甲氧西林的金黄色葡萄球菌(MRSA)

（35.29%），有 10 株耐甲氧西林的凝固酶阴性球菌（MRSCN）（100%）。革兰氏阳性菌对替加环素、替考拉宁、利奈唑烷、万古霉素全敏感。革兰氏阴性菌中有大肠埃希菌、阴沟肠杆菌、铜绿假单胞菌、奇异变形杆菌。革兰氏阴性菌对阿米卡星，亚胺培南、美罗培南全敏感。另外，铜绿假单胞菌对妥布霉素的敏感率也是 100%。

结论 DFU 患者在诊断和治疗过程中，要进行病原菌检验，在细菌培养和药敏试验结果出来以前，可参考以上细菌的药物敏感性数据选择性用药，待明确病原菌后，就选择窄谱抗菌药物，并注意多重耐药菌。

PU-3165

鸟分枝杆菌分泌的 EVs 调节宿主巨噬细胞的炎性反应

王静宇
南方医科大学南方医院

细胞外囊泡可以携带蛋白，核酸，脂质，毒素以及酶等生物活性物质的膜型囊泡。并且细菌分泌的 EVs 会携带菌体抗原，诱发靶细胞产生免疫反应，从而影响细菌的感染及致病机制。在本研究中，M.avium 可以分泌 EVs，建立了 EVs 密度梯度分离纯化的方法。并且通过 TEM 和 NTA 对 M.avium-EVs 进行了表征。随后证实，M.avium-EVs 可以被巨噬细胞捕获并促进巨噬细胞分泌 ROS 和 NO 的能力。M.avium 分泌的 EVs 促进巨噬细胞 IL-6、IL-10、TGF-β、TNF-α 细胞因子的分泌及抗原共刺激分子 CD80, CD83, CD86, MHC-II 的表达。蛋白质谱对 M.avium 分泌的 EVs 内容物进行深入分析，筛选到 EVs 内含有分枝杆菌的关键毒力蛋白脂蛋白、ESAT6 及 antigen 85B 等，并初步探索了携带生物活性的 EVs 可能通过 TLR2 信号通路，激活宿主的免疫炎性反应。这些发现可以为分枝杆菌的感染致病机制和疫苗的开发提供新的视角。

PU-3166

耐碳青霉烯类鲍曼不动杆菌耐药基因的检测在重症医学中的应用

马亚楠、王素梅、刘树业、张建东
天津市第三中心医院

目的 耐碳青霉烯类鲍曼不动杆菌已经成为引起院内感染的一大重要致病菌。本文针对重症监护病房内患者感染鲍曼不动杆菌对碳青霉烯类药物的耐药情况，探究 CRAB 耐药基因的检测在重症医学中的应用价值，从而快速指导临床用药。

方法 收集重症医学科疑似感染鲍曼不动杆菌患者的痰标本共 285 份；统计传统培养与耐药基因检测两种方法对 AB 及 CRAB 的阳性菌株数；筛选 PCR 基因检测 OXA-51 阳性的标本，将传统培养与荧光定量 PCR 两种方法对 CRAB 的检出率做统计学分析；并探讨 OXA-23 基因阳性的患者标本其他抗生素的耐药情况。

结果 鲍曼不动杆菌对碳青霉烯类药物耐药率为 72.20%。利用实时荧光定量 PCR 方法检测 OXA-51 基因检出 AB 的符合率为 92.28%(P>0.05)，OXA-23 基因检出 CRAB 的符合率为 86.62%(P>0.05)。在 108 株鲍曼不动杆菌感染 OXA-23 阳性标本中，耐药率明显较低的药物有米诺环素、头孢哌酮/舒巴坦、粘菌素、替加环素。

结论 近年来，临床上分离的鲍曼不动杆菌对碳青霉烯类药物的耐药率逐渐上升。与传统培养方法相比，qRT-PCR 法针对 AB 及 CRAB 检出结果的符合率高达 92.28%、86.6%，由于该方法简便、快速，特别是对重症患者可以及时救治，值得临床广泛应用。针对 qRT-PCR 方法检测 OXA-23 阳性标本的米诺环素、头孢哌酮/舒巴坦、替加环素、粘菌素的耐药率低，可为临床用药提供建议。

PU-3167

临床诊断肺隐球菌病的方法探究

朱波、郑港森、洪国斧
厦门大学附属第一医院

目的 初步探讨临床诊断肺隐球菌病的体系的建立。
方法 2020 年 1-4 月采集厦门大学附属第一医院确诊肺隐球菌病患者 50 例，根据临床表现，肺部影像学，病理穿刺，balf 培养，血培养，血清及 Balf 隐球菌荚膜多糖抗原检测，Balf NGS 测试数据综合分析各方法学在诊断肺隐球菌病中的作用。
结果 50 例患者中,经病理活检或培养阳性确诊为肺隐球菌病 14 例,血培养阳性 4 例，Balf NGS 检测阳性 10 例，血清和 balf 隐球菌荚膜多糖抗原阳性 49 例，上述方法中检测灵敏度最高的是隐球菌荚膜多糖抗原为 98%，高于其他方法。
结论 临床可以结合临床表现，肺部影像学，病理穿刺，Balf 培养，血培养，血清及 balf 隐球菌荚膜多糖抗原检测，Balf NGS 测试数据综合建立诊断肺隐球菌病的体系，其中胶体金隐球菌荚膜多糖抗原检测是临床诊断肺隐球菌病的灵敏度较好且经济快速的方法,临床应注意筛查。

PU-3168

临床微生物室两种常用血培养系统的性能评估

张学林、陈艳芝
保山市人民医院

目的 评估微生物室常用的两种血培养系统：BD BACTEC FX 和梅里埃 BacT/ALERT 3D 性能是否满足临床要求，并进一步判定两种血培养系统的优势。
方法 采用留样验证的方法对菌株进行一系列稀释，最终接种至培养瓶的细菌浓度为 5-30CFU/瓶；苛养菌添加适量的新鲜无菌血液（成人瓶 5-10ml，儿童瓶 1-3ml）后置于血培养系统上进行培养、检测。比较两种血培养系统配套的需氧瓶、厌氧和兼性厌氧瓶、儿童瓶的报阳时间和 3 天的检出率。
结果 BD BACTEC FX 和梅里埃 BacT/ALERT 3D 配套的培养瓶对 30 株病原菌的阳性率均为 100%，BD BACTECTM Plus 需氧瓶和 BacT/ALERT FA 需氧瓶阳性报警时间（h）和 BD BACTECTM Peds 儿童瓶和 BacT/ALERT PF 儿童瓶阳性报警时间（h）的 P 值分别为 0.13 和 0.16，两者差异无统计学意义（P>0.05），BD BACTECTM Lytic 厌氧瓶和 BacT/ALERT SN 厌氧瓶阳性报警时间（h）的 P 值为 0.03，两者差异显著（P<0.05），有统计学意义。
结论 两种血培养系统的性能能检出血液中的大部分病原菌，能满足临床需求和 CNAS-GL28《临床微生物检验程序验证指南》关于血培养系统性能验证的要求。

PU-3169

多重 PCR 方法检测血流感染常见病原菌的临床应用

井发红
西安医学院第一附属医院

目的 建立一种能够应用于临床检测血流感染患者常见病原菌的多重 PCR 方法。
方法 针对血流感染 7 种主要病原菌鲍曼不动杆菌、大肠埃希菌、金黄色葡萄球菌、铜绿假单胞菌、肺炎克雷伯菌、表皮葡萄球菌及屎肠球菌设计多重 PCR 体系，对其敏感性及特异性进行验证，然后对临床标本进行检测并与培养方法进行比较。

结果 采用优化后的多重 PCR 体系对 200 份血液标本和 60 份穿刺引流液标本进行检测，血液标本中共检出 21 例阳性，其中表皮葡萄球菌 5 例，大肠埃希菌 3 例，屎肠球菌 3 例，鲍曼不动杆菌 3 例，金黄色葡萄球菌 3 例，铜绿假单胞菌 2 例，肺炎克雷伯菌 2 例；穿刺引流液标本中共检出 24 例阳性，其中大肠埃希菌 5 例，表皮葡萄球菌 5 例，屎肠球菌 4 例，鲍曼不动杆菌 2 例，铜绿假单胞菌 3 例，金黄色葡萄球菌 3 例，肺炎克雷伯菌 2 例；经统计学分析表明多重 PCR 的敏感性高于培养方法。

结论 利用多重 PCR 体系可以在一个反应中同时检测 7 种血流感染常见病原菌，且有较高的特异性和灵敏度，可同时检测、鉴别出多种病原菌，在临床混合感染的鉴别诊断上具有其独特的优势。该方法稳定可靠，成本低，操作简单、快速，整个检测过程受污染风险小，具有很高的临床应用价值。

PU-3170

结核分枝杆菌感染后宿主细胞外泌体内容物的改变

简苗苗
德阳市人民医院

结核病（tuberculosis，TB）是由结核分枝杆菌（Mycobacterium tuberculosis，Mtb）感染引起的慢性传染病，严重威胁着人类的健康。结核病人外泌体浓度与细菌负荷相关，且 Mtb 感染修饰外泌体的组成。然而，参与结核病进展的具体外泌体内容物与机制尚未完全清楚。本文旨在总结 Mtb 感染后外泌体内容物的变化，并对外泌体作为结核病检测生物标志物的可能性进行介绍以及探索外泌体在结核病中的作用有利于新型结核病疫苗的开发及应用。

Mtb 感染的巨噬细胞中分离的外泌体中一共鉴定出 41 种分枝杆菌蛋白质，也包含脂阿拉伯甘露聚糖和其他分枝杆菌脂类。从受感染的巨噬细胞释放的外泌体中鉴定出 57 种 miRNA，但与未感染的细胞相比，Mtb 感染导致 miRNA 掺入外泌体普遍受抑制。在来自感染细胞的外泌体中检测到大量用于编码核糖体蛋白质以及 RNA 结合蛋白的转录物。实验发现 Mtb 感染的巨噬细胞释放的外泌体含有 9 种分枝杆菌转录物，TB 感染个体的血清外泌体中存在 Rv2796 和 Rv1369c。

外泌体是动态的，外泌体对于鉴定细胞内病原体尤其重要，因为细菌产物并不总是存在于用于病原体检测和诊断的流体中。与大多数免疫生物标志物不同，Mtb 产物对结核病是特异性的。呼出气中的外泌体包裹的 miRNA 被认为具有成为肺结核病患者生物标志物的潜能。通过多重反应监测质谱平台使用来自 GlcB7、HspX、Mpt51、Mpt63、Mpt64 蛋白的 7 个肽的生物标志物可以正确诊断出 83%的结核患者。在 LTBI 病人中，一些 Mtb 细胞被破坏并且许多 Mtb RNAs 和蛋白被外分泌进入血清外泌体。患者血清中外泌体内容物有望成为诊断和区分潜伏性结核和活动性结核的工具。

来自 Mtb 感染细胞的外泌体可以促进巨噬细胞和 T 细胞的趋化性。研究发现，使用 Mtb CFP 处理的巨噬细胞衍生的外泌体接种小鼠后，可以保护小鼠免受用低剂量的 Mtb 气溶胶感染。Mtb CFP-外泌体可以在体内引发保护性免疫应答，又能强化先前接种的 BCG 免疫反应，其保护作用优于或等于卡介苗。这些结果表明外泌体可能为新型结核病疫苗和 BCG 加强疫苗的开发提供独特的方向。

PU-3171

The mechanism and current situation of phage used in the treatment of multi-drug resistant bacteria

Dandan Tie
Department of Laboratory Medicine, Sichuan Provincial People's Hospital, University of Electronic Science and Technology of China, Chengdu, China.

The emergence of drug-resistant "super bacteria" will enable us to enter the "post-antibacterial era". In the face of increasing bacterial resistance, finding new treatment options has

become an urgent problem to be solved.In this article, by consulting a large number of successful cases of phage clinical treatment at home and abroad, the advantages of phage treatment are elaborated in detail.It fully shows that the use of phages to lyse drug-resistant strains is an effective way to treat bacterial diseases.

With the more and more widespread application of antibiotics, clinical multi-drug resistant bacteria are gradually increasing, and the current research and development speed of antibiotic drugs is far less than the speed at which bacteria acquire antibiotic resistance, The emergence of multi-drug resistant bacteria has brought great challenges to clinical anti-infective treatment.In order to overcome the dangers of drug-resistant bacteria and the diseases they cause, researchers are forced to turn their attention to alternatives to antibiotics-phages. Compared with antibiotics, phage preparations have the advantages of strong specificity, fast self-proliferation, and short development time .

PU-3172

血液来源表皮葡萄球菌生物被膜形成及分子特征研究

胡洪华
四川省医学科学院·四川省人民医院

目的 分析临床血液来源表皮葡萄球菌的生物被膜形成能力，探究生物被膜形成与相关基因携带的分子生物学特征。
方法 收集临床分离血液来源的表皮葡萄球菌 68 株，用 96 孔聚苯乙烯培养板分析生物被膜形成能力，用 PCR 法检测 psm-mec，icaA，IS256， aap，agrA 和 atlE 基因的携带，采用 fisher 检验分析这些基因与生物被膜形成的相关性。
结果 68 株表皮葡萄球菌中生物被膜阳性的有 36 株，占 52.94%；psm-mec，icaA，IS256， aap，agrA 和 atlE 基因的检出率分别为 38.24%，60.29%，67.65%，82.35%，82.35%，88.24%；其中 icaA，psm-mec 和 IS256 基因的携带与生物被膜形成相关，差异有统计学意义（$P<0.05$）。
结论 临床分离血液来源的表皮葡萄球菌具有较高的产生物被膜能力，icaA，psm-mec 和 IS256 基因是表皮葡萄球菌形成生物被膜的重要因素。

PU-3173

布鲁菌感染的实验室指标与临床特征分析

张秀芳
安徽亳州市人民医院

目的 总结并分析我院检出的布鲁菌感染患者的实验室指标及临床特征，提高非疫区检验人员对该病的检测能力，为布鲁菌病的早期诊断提供依据。
方法 收集我院 2016 年至 2020 年收治的 17 例布鲁菌病患者分析其实验室指标、临床资料、流行病学特点。
结果 布鲁菌病患者各年龄段均可感染，主要为中年人，最低 4 岁，最高 75 岁；75%以上有明确的、与牛羊相关的密切接触史，大多为农民及无职业的个体经营者；实验室检查 40%以上患者的白细胞（WBC）减低，80%以上患者的超敏 C-反应蛋白（CRP）和谷丙转氨酶（ALT）升高，90%以上患者降钙素原（PCT）升高。另外，90%以上患者会出现反复高热，部分病人会伴随关节痛、肌肉痛、腰痛等症状。
结论 布鲁菌病实验室检查及临床特征无特异性，非疫区医务人员均应提高对该病的认识，避免误检漏检。

PU-3174

急性与慢性细菌性关节炎病原菌组成及炎症指标比较

高玉红、郑瑞、李艺坤
云南省第一人民医院

目的 分析急性与慢性细菌性关节炎病原菌组成差异及炎症指标差异。
方法 回顾性分析 2016 年至 2020 年五年间云南省第一人民医院关节液培养阳性的患者资料，比较 90 例急性细菌性关节炎与 40 例慢性细菌性关节炎的病原菌组成，及炎症指标包括 C 反应蛋白、降钙素原、铁蛋白、血沉差异。
结果 急性细菌性关节炎病原菌主要以金黄色葡萄球菌为主，而慢性细菌性关节炎以马耳他布鲁菌感染为主。急性细菌性关节炎组的 C 反应蛋白和降钙素原均高于慢性细菌性关节炎组，两组结果有显著差异；而慢性细菌性关节炎组的血沉指标高于急性细菌性关节炎组，差异有显著性；两组的铁蛋白均有显著升高，差异无显著性。
结论 急性与慢性细菌性关节炎病原菌组成不同，且临床有效治疗用药也完全不同，及时送检关节液培养有重要的临床意义。

PU-3175

胶体金法测隐球菌荚膜多糖抗原在肺隐球菌病诊断中的应用

朱波、徐和平、洪国斧
厦门大学附属第一医院

目的 探讨胶体金检测隐球菌荚膜多糖抗原诊断肺隐球菌病的价值。
方法 2020 年 1-4 月采集厦门大学附属第一医院疑似肺隐球菌病患者 200 例的血液,采用胶体金法（美国 Immuno Mycologics 公司）检测隐球菌荚膜多糖抗原并评价效果.
结果 200 例患者中,经病理活检或培养阳性确诊为肺隐球菌病 36 例,非肺隐球菌病 164 例。上述两组分别采用胶体金法检测，其中 36 例肺隐球菌病患者中隐球菌抗原阳性 32 例，检测灵敏度为 88.89%，164 例非隐球菌病患者检测结果均为阴性，检测特异度 100.00%。
结论 胶体金隐球菌荚膜多糖抗原检测是一种简单快速的肺隐球菌病筛查方法,具有一定的临床应用价值。

PU-3176

基于 Mp 模拟表位的 MAP 的制备、纯化与鉴定

王阿金、张文瀚、宋然、李章勇、周杰英、张林、史文元
郴州市第一人民医院

目的 制备含有肺炎支原体 (Mp) 模拟表位的多抗原肽(MAP) ，为研制基于模拟表位的 MAP 用于 Mp 的诊断与预防提供前期实验基础。
方法 肺炎支原体感染患者的血清用饱和 (NH4)2SO4 法进行纯化，以此为靶分子应用噬菌体展示技术筛选出 2 条 7 肽 CS1：T-V-N-F-K-L-Y 和 CS2：L-P-Q-R-L-R-T；以多聚赖氨酸为核心基质，采用 Fmoc 方法合成含有 Mp 模拟表位的八分枝 MAP，反向高效液相色谱(ＲP-HPLC) 分析 MAP 的纯度，质谱分析法测定 MAP 的分子量并对其进行鉴定。
结果 分别制备了含有肺炎支原体 2 个模拟表位的 MAP，ＲP-HPLC 分析的结果表明合成的 2 个 MAP 的纯度都在 90%以上，质谱分析的结果表明所合成的 MAP 的分子量与预期的理论分子量基本相符。

结论 成功制备、纯化并鉴定了 2 个含有 Mp 模拟表位的 MAP。

PU-3177

低出生体重儿希木龙念珠菌血流感染的临床特征及同源性分析

朱波、房丽丽、洪国斧
厦门大学附属第一医院

目的 探讨低出体重儿希木龙念珠菌血流感染的临床特点。
方法 回顾性分析我院 NICU 极低出体重儿希木龙念珠菌血流感染 3 例患儿临床资料，并对菌株进行同源性分析。
结果 3 例患儿出生体重均小于 1200g。临床表现为呼吸暂停、发热、腹胀、黄疸等，感染初期多有血小板计数下降，C 反应蛋白升高，G 试验阳性。3 例患儿先后均有脐静脉置管和经外周中心静脉置管（PICC）；发生感染前使用广谱抗生素和氟康唑预防真菌治疗。3 例希木龙念珠菌对氟康唑、两性霉素 B、伊曲康唑、伏立康唑、5-氟胞嘧啶高度耐药。3 例用米卡芬净治疗均治愈。2 例为同源性最近。
结论 低出生体重儿，尤其是辅助生殖婴儿应警惕泛耐药希木龙念珠菌真菌感染的发生，及时监测感染性指标，尽快送检标本，早期治疗并采取合理院感防控措施以防爆发流行。

PU-3178

2016-2020 年某院碳青霉烯类耐药肺炎克雷伯菌分析

韩云港、赵悦、王伟
河南省胸科医院

目的 分析某院 2016-2020 年碳青霉烯类耐药肺炎克雷伯菌(CRKP)的流行趋势、分布特点及耐药性，为 CRKP 的防治提供临床诊疗依据。
方法 通过医院 HIS 系统调查 CRKP 患者的抗菌药物使用情况，采用纸片扩散法或自动化仪器法进行抗菌药物敏感性试验，按照 CLSI 2019 年标准判读结果，对科室来源、标本来源及药物敏感性进行分析，数据统计分析采用 SPSS25.0 软件及 WHONET 5.6 软件。
结果 5 年共分离肺炎克雷伯菌 1657 株，其中 376 株为 CRKP，2016-2020 年 CRKP 检出率分别为 24.2%、22.6%、29.7%、31.3%、12.4%。CRKP 分离株最多的科室重症监护室(ICU)为 63%，明显高于普通病房（$p<0.05$）,CRKP 标本来源最多为呼吸道标本（痰液 77%，肺泡灌洗液 8%），其次为血液 8%，静脉导管尖端 5%。CRKP 株的检出与第三代头孢菌素、碳青霉烯类和酶抑制剂复方制剂使用强度呈正相关($P<0.05$)。CRKP 株对大多数抗菌药物的耐药率超过 90%，耐药率较低的为替加环素 1.1%、多粘菌素 1.5%、头孢他啶/阿维巴坦 7.5%。
结论 该院 CRKP 分离率 2019 年之前较高，2020 年有明显下降趋势，CRKP 分离株与来源于呼吸道标本以及患者入住 ICU 有关、同时与广谱 β-内酰胺类、碳青霉烯类的用量有关。应加强抗菌药物管理，强化院感意识，做好消毒、隔离等措施，减少耐药菌株在院内感染的发生。

PU-3179

ICU 多重耐药鲍曼不动杆菌的产生及耐药性分析

朱薇、石红、顾振东
宝鸡市中心医院

目的 分析我院重症监护室（ICU）临床分离到的多重耐药不动杆菌的产生及耐药特点，为临床合理应用抗生素提供依据。
方法 采用法国梅里埃公司的 VITAIKE—2 对重症监护室（ICU）送检的标本进行细菌培养、鉴定和药敏试验,药敏试验结果判定依据 CLSI 颁布标准,采用 WHONET 5.4 软件进行数据分析。
结果 近一年我院重症监护室（ICU）分离到的多重耐药鲍曼不动杆菌 90%来自呼吸道标本，对抗生素耐药率最低的是米诺环素和多粘菌素 B,对碳青霉烯类抗生素的耐药性急速增长。
结论 我院所分离到的多重耐药鲍曼不动杆菌耐药性呈上升趋势，区分定植与感染对临床治疗及合理用药至关重要。

PU-3180

革兰阴性杆菌检出率及耐药性分析

肖慈然[1]、吴悦[2]
1. 四川省医学科学院·四川省人民医院东院
2. 成都医学院检验学院

目的 探讨四川省人民医院城东病区革兰氏阴性杆菌的检出率及耐药情况，为抗菌药物的使用提供理论依据。
方法 提取四川省人民医院城东病区 2019 年至 2021 年第一季度间革兰阴性杆菌的检出数据，使用 WHONET5 软件对上述数据进行分析。
结果 本次试验共检出 1268 株细菌，革兰阴性杆菌 871 株，占 68%；革兰阴性杆菌包含：大肠埃希菌 402 株、肺炎克雷伯菌 304 株、阴沟肠杆菌 37 株、奇异变形杆菌 19 株、沙门氏菌 18 株；革兰阴性杆菌的标本来源主要是：痰液 344 例、尿液 167 例、血液 124 例、分泌物 155 例、其他类型 81 例；主要送检科室是：呼吸内科 139 例、胃肠外科 100 例、ICU 94 例、肾脏内科 94 例；分离细菌对各类药物的最高耐药率：青霉素类的氨苄西林耐药率 92.2%：β 内酰胺合剂类氨苄西林/舒巴坦耐药率 48.2%、头孢菌素类的头孢唑啉耐药率 72.2%、碳青霉烯类的亚胺培南耐药率 4.6？、氨基糖苷类的庆大霉素耐药率 28.3%、喹诺酮类的莫西沙星耐药率 48.9%、四环素类的四环素耐药率 52%；敏感率超过 90%的药物有： 头孢替坦、亚胺培南、美洛培南、厄他培南、阿米卡星。
结论 革兰阴性杆菌在四川省人民医院城东病区检出率及耐药情况均较严重，需要引起临床重视，应更加合理规范性使用抗生素，实时监测耐药水平。

PU-3181

Identification of host cell proteins that interact with Chlamydia trachomatis T3SS effector CT622

Wenbo Lei[1,2]、Binfeng Peng[1]、Mingyi Shu[2]、En Chen[1]、Shuangquan Liu[1]、Zhongyu Li[2]
1. 南华大学附属第一医院检验医学中心
2. 南华大学衡阳医学院原生物学研究所

As a kind of obligate intracellular pathogen, Chlamydia trachomatis (C. trachomatis) infections are an important cause of public health diseases and there is no effective vaccine to prevent it. However, the pathogenic mechanism of C. trachomatis is still unclear. Previous studies

have demonstrated that C. trachomatis interacts with host cells by secreting effector proteins to complete its growth and development. Type III secretory system (T3SS) has emerged as the key device for the virulence of C. trachomatis, which mediates the interaction of Chlamydia with host cells through secretion of effector proteins, The T3SS effector protein CT622, which localizes in the host cell cytoplasm, is crucial for C. trachomatis growth and infection. To further understand the role of CT622 protein in the pathogenic mechanism of C. trachomatis, here, we screened the host cell proteins that interact with C. trachomatis T3SS effector CT622 by using co-immunoprecipitation combined with mass spectrometry, and we constructed the CT622 interaction host proteins database based on the Unused score of LC-MS/MS. We further identify several candidate host proteins (Myo1c， TPM1, ARP2, CAPZB， Rab4) through co-immunoprecipitation and GST-pulldown assays, our results confirmed the interaction between Myo1c and CT622 protein. However, the contribution of the interaction between Myo1c and CT622 in C. trachomatis infection needs to be further clarified. Collectively, these findings may further promote our focus on the role of CT622 in Chlamydial pathogenic mechanisms.

PU-3182

铜绿假单胞菌血流感染耐药机制研究及预后分析

李霜
成都市第三人民医院

目的 探讨血流感染中碳青霉烯耐药而头孢敏感的铜绿假单胞菌的耐药机制，致患者感染的危险因素及预后，为临床预防感染及治疗提供理论依据。
方法 收集我院 2011 年至 2017 年间血流感染患者的病历资料及致病菌株，定义感染碳青霉烯耐药而头孢敏感的铜绿假单胞菌患者为病例组 I，按 1：1：2 的比例随机选取感染碳青霉烯和头孢敏感的铜绿假单胞菌患者作为病例组 II，未患血流感染的患者作为对照组，进行病例-病例-对照研究。采用聚合酶链反应 (PCR)和实时逆转录 PCR (RT-PCR) 对铜绿单胞菌的耐药机制进行研究，同时采用卡方检验和 logistic 回归模型对患者病历资料进行危险因素和临床预后分析。
结果 PCR 结果显示 63 株碳青霉烯耐药而头孢敏感的铜绿假单胞菌均不产 ESBLs 和碳青霉烯酶相关基因，但 RT-PCR 结果显示外排泵的表达上调和孔蛋白 OprD 的表达下降与碳青霉烯耐药有关。预后分析显示病例组 I 的 30 天死亡率为 27% (17/63)，显著高于病例组 II (12.7%, 8/63)，差异有统计学意义（P <0.05）。危险因素分析显示 30 天之内再次入院、中央静脉置管和碳青霉烯的使用为病例组 I 的独立危险因素， 患血液肿瘤为病例组 II 的独立危险因素，完全肠外营养为两种表型血流感染的共同危险因素。入住 ICU 和休克为感染两种表型铜绿假单胞菌患者死亡的独立危险因素。
结论 碳青霉烯的使用为铜绿假单胞菌耐药的高危因素，同时头孢类药物应作为治疗此表型血流感染的一个重要选择。

PU-3183

6 例人型支原体血流感染的临床特征和耐药性分析

曾童、张小团、刘卓然
南华大学附属第二医院

目的 分析人型支原体引发血流感染患者的临床特征及耐药情况
方法 回顾性分析南华大学附属第二医院 2018 年 1 月－2020 年 12 月人型支原体血流感染患者的临床及微生物学资料。
结果 6 例人型支原体血流感染患者纳入研究，主要临床症状为不明原因且难以用临床经验性抗生素控制的发热，外周血白细胞升高或正常，以中性粒细胞升高为主。发热前行泌尿生殖道手术者占 50%（3/3），车祸后多发性外伤占 33.3%（2/6）；行导尿操作患者占 100%（6/6）。血液分离的

人型支原体对多西环素、米诺环素、交沙环素耐药率最低，为 0%（0/6），对罗红霉素、红霉素、克拉霉素耐药率最高，为 100%（6/6）。6 例患者中，发热完全控制大于 50 天 3 例（3/6），死亡 1 例（1/1）。

结论 人型支原体血流感染症状不典型；免疫缺陷的患者人型支原体血流感染症状更难控制；临床常用抗生素难以控制的高热应积极留取血培养，警惕人型支原体入血可能。

PU-3184

碳青霉烯类耐药大肠埃希菌的流行病学研究

梁树梅
成都市第三人民医院

目的 近年来对碳青霉烯类抗生素耐药的肠杆菌科细菌(Carbapenem-Resistant Enterobacteriaceae,CRE)不断出现,给临床治疗的用药选择带来了巨大挑战。本研究旨在了解大肠埃希菌的药物敏感性变迁,确定 CRE 菌株的产酶情况和科室分布情况等，为院内感染控制及临床治疗提供基础数据。

方法 收集 2018 年 1 月到 2020 年 4 月成都市某三甲院临床分离的碳青霉烯类耐药大肠埃希菌共 30 株进行回顾性分析，采用 Microsan WalkAway plus 96 全自动微生物鉴定仪进行细菌鉴定及药物敏感试验;采用碳青霉烯酶抑制剂增强试验对大肠埃希菌的耐药机制进行表型检测。

结果 30 株感染患者临床诊断大肠埃希菌感染的标本来源以尿液、痰液及血液多见，分别占 50.0%、26.7%和 16.7%；感染的病区主要集中在呼吸科、ICU、泌尿科和血液科，分别占 20.0%、16.7%、13.3%和 10.0%，碳青霉烯酶抑制剂增强试验结果表明已产 NDM 酶为主。

结论 对碳青霉烯类药物耐药的机制主要是携带 blaNDM-1 基因并呈现多重耐药，给临床治疗带来了困难。加强对碳青霉烯耐药菌株基因型和耐药基因的检测，将对减缓或阻断耐药菌的传播具有重要意义。

PU-3185

耐碳青霉烯类大肠埃希菌流行病学研究及耐药性分析

陈曦
中国人民解放军南部战区总医院

目的 了解南部战区总医院耐碳青霉烯类大肠埃希菌(CREC)药物耐药情况和流行趋势，为落实医院感染防控措施提供理论依据。

方法 1.收集 2015 年 10 月～2020 年 7 月期间本院耐碳青霉烯类大肠埃希菌。2.使用 mCIM 和 eCIM 方法快速筛查产酶情况。分析 26 株 CREC 的病区分布、标本来源分布和对临床常用 14 种抗生素耐药性。3.运用多位点序列分析(MLST) 方法分析待测菌株的 7 个管家基因，获得菌株的 ST 型；采用聚合酶链反应(PCR) 鉴定血清型。

结果 1. 我院住院患者临床标本中分离到耐碳青霉烯类大肠埃希菌共 26 株,其中 25 株均产金属酶。从临床标本分布来看，主要分离自中段尿(46.2%)；从临床科室分布来看，分离率最高的是泌尿外科病区(26.92%)。2.从药物敏感性来看，亚胺培南和厄他培南均耐药，其他各种药物的耐药率也较高，仅阿米卡星耐药率较低(23.1%)。3.多位点序列分型和血清型分型均获得 13 个型别，其中 ST167 、ST131 和 H4:O25、H9:O101 是本院最主要的流行型别，均为 4 株；且 MLST 分型与血清型分型结果基本一致。

结论 本院中段尿标本耐碳青霉烯类大肠埃希菌检出率高；泌尿外科病区流行情况最为严重；ST 型别及血清型种类较多且散在分布于各临床科室且均与标本类型无相关性；同一病人不同时间可出现不同 MLST 型和血清型，甚至同一标本中可出现不同型别；本研究中血清型和 MLST 分型表现出

较高一致性；同时高耐药率也提示临床应合理用药并加强消毒隔离措施，防止此类耐药菌的传播扩散。

PU-3186

2020 年四川地区尿路感染病原菌分布和耐药分析

钟敏
四川省医学科学院·四川省人民医院

目的 总结分析四川省细菌耐药监测网成员单位 2020 年尿液标本病原菌分布及耐药情况，为本省临床合理应用抗菌药物提供依据。
方法 收集 2020 年四川省细菌耐药监测网数据合格的 94 家成员单位中门诊和住院患者临床尿液标本中分离的非重复病原菌，按照监测方案，采用标准纸片扩散法、E-test 法或自动化仪器检测法，测定监测药物对细菌的敏感性，并依据美国临床和实验室标准协会(CLSI)2020 年标准，使用 WHONET 5.6 软件进行数据统计分析。
结果 按患者首次分离菌株进行统计分析，从尿液标本中共分离出 39797 株病原菌，其中革兰阴性菌 30307 株占 76.2%，革兰阳性菌 9490 株占 23.8%，检出率前 5 位的病原菌依次是大肠埃希菌（50.8%）、屎肠球菌（9.9%）、肺炎克雷伯菌（8.1%）、粪肠球菌（6.6%）、奇异变形杆菌（2.8%）。主要革兰阴性菌对碳青霉烯类抗菌药物耐药率较低，对头孢呋辛、头孢曲松、头孢噻肟耐药率较高。屎肠球菌和粪肠球菌对万古霉素、替考拉宁、利奈唑胺耐药率较低。未发现对万古霉素、利奈唑胺耐药的葡萄球菌。
结论 尿液标本病原菌多样化，以大肠埃希菌和肠球菌为主，临床应根据药敏结果合理用药，达到最佳治疗效果； 同时应充分利用本地细菌耐药监测结果进行感染控制管理，促进抗菌药物合尿路感染；病原菌分布；耐药分析理应用。

PU-3187

Xpert 诊断结核性脑膜炎的 Meta 分析

张杰
电子科技大学附属医院·四川省人民医院

目的 系统评价 Xpert 诊断结核性脑膜炎的价值。
方法 计算机检索 PubMed、EMbase、The Cochrane Library、Web of Science、CNKI、CBM、WanFang Data 和 VIP 数据库，搜集 Xpert 诊断结核性脑膜炎的诊断性试验，检索时间从建库截止至 2018 年 8 月 30 日。经过独立筛选文献、提取资料，并评价纳入研究的偏倚风险后，采用 Meta-Disc 软件进行 Meta 分析，计算其合并敏感度（Sen）、特异度（Spe）和绘制受试者工作特征曲线（SROC）并计算曲线下面积（AUC）。
结果 共纳入 10 个研究。Xpert 诊断结核性脑膜炎的合并敏感度、合并特异度和 AUC 分别为 0.57［95%CI（0.52，0.71）］、0.96［95%CI（0.95，0.98）］和 0.9135。根据是否离心进行亚组分析，其结果显示：未离心组的合并敏感度和特异度是 0.56(0.49, 0.61)，0.96(0.94, 0.97)，离心组的合并敏感度和特异度是 0.58(0.51, 0.65)和 0.98(0.96, 1.00)。
结论 Xpert 诊断结核性脑膜炎具有一定的诊断效能。将来需要更多的研究来验证本研究结果。

PU-3188

blaNDM-1 基因敲除对阴沟肠杆菌致病性和毒力的影响

代鹏飞、杜艳
昆明医科大学第一附属医院

目的 评估 blaNDM-1 基因对阴沟肠杆菌致病性和毒力的作用。
方法 比较携带 blaNDM-1 基因阴沟肠杆菌与 blaNDM-1 基因敲除阴沟肠杆菌（△NDM-1）感染小鼠后致病性和毒力的差异，包括小鼠生存率、脾脏载菌量、肝肺肠病理特征、肝肺脾产生的细胞因子等。
结果 blaNDM-1 基因敲除后，阴沟肠杆菌导致的腹膜炎小鼠在生存率、脾脏载菌量、肝肺肠病理特征、肝肺脾产生的细胞因子未见统计学差异。
结论 blaNDM-1 基因可能并不增加阴沟肠杆菌的毒力。

PU-3189

2020 年四川省细菌耐药监测网胆道标本病原菌分布及耐药

杨盛慧
电子科技大学附属医院•四川省人民医院

目的 对 2020 年四川省细菌耐药监测网成员单位胆道标本中的细菌分布与耐药情况进行统计分析，为临床合理使用抗菌药物提供依据。
方法 选取 2020 年四川省细菌耐药监测网数据合格的 94 所成员单位从临床患者胆道标本中分离的病原菌，经纸片扩散法或自动化仪器法检测细菌对抗菌药物的耐药性，并使用 WHONET 5.6 软件进行统计分析。
结果 从胆道标本共分离出病原菌 3502 株，其中革兰阳性菌 1049 株，占 30.0%，革兰阴性菌 2453 株占 70.0%，检出率排名前 6 位的细菌是大肠埃希菌、肺炎克雷伯菌、屎肠球菌、粪肠球菌、阴沟肠杆菌、铜绿假单胞菌。碳青霉烯类耐药大肠埃希菌、肺炎克雷伯菌、铜绿假单胞菌、鲍曼不动杆菌的检出率分别为 2.1%、4.0%、15.8%、30.0%。大肠埃希菌对头孢菌素类和喹诺酮类药物的耐药率较高，分别为 20%-70%，50%-70%，对碳青霉烯类药物的耐药率较低，小于 2%。肺炎克雷伯菌和阴沟肠杆菌对氨基糖苷类、喹诺酮类药物的耐药率低于大肠埃希菌。屎肠球菌和粪肠球菌对万古霉素、利奈唑胺、替考拉宁耐药率很低，屎肠球菌对多种抗菌药物的耐药率普遍高于粪肠球菌。
结论 四川地区 2020 年胆道分离的病原菌以肠杆菌目细菌和肠球菌为主，存在对多种抗菌药物耐药菌株，尤其是耐碳青霉烯类菌株，临床应根据药敏试验合理选择抗菌药物。

PU-3190

培养阳性的时间可以区分表皮葡萄球菌脑膜炎以外的神经外科手术后凝固酶阴性葡萄球菌与污染：病例对照观察性研究

郑光辉
首都医科大学附属北京天坛医院

目的 探讨表皮葡萄球菌（Nse-CoNS）脑膜炎以外的凝固酶阴性葡萄球菌（Nse-CoNS）脑膜炎的特点，应用脑脊液（CSF）时间阳性培养（TTPC）准确鉴别脑膜炎与污染。
方法 我们进行了病例对照研究来完成。首先，我们回顾性审查了 2019 年 1 月至 10 月在北京天坛医院产生 Nse-CoNS 的神经外科手术后患者的 CSF 记录；审查了 17 项临床特征和 12 项实验室

特征。其次，我们研究了 Nse-CoNS 的 TTPC、临界值和相应的参数，以区分 Nse-CoNS 脑膜炎与污染。
结果 本研究共纳入 146 名 Nse-CoNS CSF 培养阳性患者。 Nse-CoNS 脑膜炎组的平均 TTPC 明显短于污染组（分别为 20.2 ± 5.0 小时和 30.2 ± 12.6 小时，P < 0.05）。该模型的曲线下面积 (AUC) 为 0.802。 20.0 小时的 TTPC 具有 94.3% 的灵敏度和 90.2% 的负值，用于预测 Nse-CoNS 脑膜炎。
结论 Nse-CoNS 脑膜炎常引起临床诊断的混淆。在本研究中，我们评估了 Nse-CoNS 脑膜炎的临床预测因素，并确认 Nse-CoNS 脑膜炎组的中位 TTPC 显着短于污染组。 TTPC 短于 20.0 小时与 Nse-CoNS 脑膜炎有关，而 TTPC 长于 20.0 小时与 Nse-CoNS 污染有关。这些信息将有助于快速诊断 Nse-CoNS 脑膜炎。

PU-3191

耐碳青霉烯肠杆菌引起神经外科细菌性脑膜炎/脑炎的流行病学及危险因素

郑光辉
首都医科大学附属北京天坛医院

目的 这是在中国最大的神经外科临床中心之一进行的回顾性观察研究。我们的目的是确定碳青霉烯类耐药肠杆菌科 (CRE) 相关脑膜炎/脑炎的流行病学特征，并阐明 CRE 神经外科感染的危险因素。
患者和方法 我们在 2012 年 1 月至 2017 年 12 月期间对接受神经外科手术的患者进行了回顾性研究。对每位患者的病历进行审查，并通过 CRE 脑膜炎/脑炎的多变量逻辑分析提取和评估危险因素的 20 个临床变量。
结果 2012-2017 年神经外科脑膜炎/脑炎阳性率为 7.9%（2947/29605），肠杆菌科占所有细菌感染的 6.3%（185/2947）。本研究共获得 133 株肠杆菌科细菌，包括 26 株 CRE。其中，单因素分析显示 CRE 脑膜炎的危险因素为呼吸机、菌血症、重症监护病房（ICU）入院、医院获得性肺炎和感染致死率。多因素 logistic 分析显示，医院获得性肺炎和感染导致的死亡率是 CRE 脑膜炎的独立危险因素。
结论 CRE 是世界卫生组织（WHO）2016 年公布的最严重的耐药菌之一，CRE 引起的脑膜炎/脑炎是神经外科手术失败的重要标志，需要医生立即关注.

PU-3192

用于诊断中枢神经系统感染的微/纳米流体芯片平台的评估：多中心前瞻性研究

郑光辉
首都医科大学附属北京天坛医院

中枢神经系统感染 (CNSI) 是一种严重的感染类型，困扰着神经病学和神经外科科学领域。及时准确地诊断 CNSI 是临床和实验室评估的主要挑战；然而，开发新方法可能有助于改进诊断协议。本研究评估了第二代微/纳米流体芯片平台（MNCP-II），该平台克服了诊断中枢神经系统细菌和真菌感染的困难。 MNCP-II 操作简单，可在 50 分钟内识别 44 个属或种目标和 35 个遗传抗性决定簇。在多中心研究中评估用于 CNSI 的第二代微/纳米流体芯片平台的诊断准确性。使用第二代微/纳米流体芯片平台的检测限 (LOD) 首先使用六种不同的微生物标准确定。使用 MNCP-II 平台评估了总共 180 份含细菌/真菌的脑脊液 (CSF) 培养物和 26 份从微生物培养阴性的 CNSI 患者收集的 CSF

样本，以鉴定微生物和遗传抗性的决定因素。将结果与使用常规鉴定和抗菌药物敏感性测试方法获得的结果进行比较。发现用 MNCP-II 测试的各种微生物的 LOD 在 250-500 个 DNA 拷贝的范围内。对于 180 份 CSF 微生物阳性培养物，平台与常规鉴定方法的一致率为 90.00%；八个物种达到了 100% 的一致性。在碳青霉烯酶、ESBLs、氨基糖苷类、万古霉素相关基因、mecA 等 9 种抗生素耐药基因的检测中，与常规药敏试验方法的符合率超过 80.00%。对于碳青霉烯酶和 ESBLs 相关基因，平台检测的敏感性和阳性预测值均较高（>90.0%），完全可以满足临床诊断的要求。 MNCP-II 是一个非常有效的分子检测平台，可以辅助 CNSI 的诊断，可以显着提高诊断效率。

PU-3193

肠杆菌目细菌粘菌素耐药性机制研究进展

涂尚宇、张雅薇、王辉
北京大学人民医院

多重耐药的肠杆菌目细菌出现使得粘菌素重新被投入临床使用，并成为治疗此类难治性革兰阴性杆菌感染的最后防线。粘菌素主要通过与细菌外膜脂多糖上的脂质 A 成分结合，引起外膜结构紊乱，最终通过破坏细菌膜结构导致细菌死亡。肠杆菌目细菌对粘菌素耐药机制主要体现在对外膜脂质 A 的修饰，这种修饰大多数受双组分调节系统控制。最常见的是通过 L-Ara4N 和 PEtN 两种阳离子基团的修饰，来实现降低净负电荷，从而阻碍粘菌素的结合，这种改变源自于细菌的基因突变或质粒介导的水平转移。此外，外排系统与细菌粘菌素耐药性的相关性已被明确报道。对粘菌素天然耐药的细菌，其耐药机制源自于脂质 A 修饰相关基因 arnBCADTEF 操纵子的结构性表达。值得注意的是，已有许多研究者发现一些药物具有协同增强粘菌素抑菌作用，甚至逆转细菌对粘菌素耐药性的能力，包括 CCCP、SLAP-S25、氯硝柳胺等，但其机制尚不明确。本文主要以肠杆菌目细菌为例，概述关于粘菌素作用机制、耐药性情况及其他药物联合使用方面的研究进展。然而，目前存在许多未知的耐药机制和耐药性逆转机制，若能进一步研究透彻，将对我们理解如何克服粘菌素耐药性大有裨益。

PU-3194

耐亚胺培南的肺炎克雷伯菌（IMPKpn）的分布及流行病学研究

杨柳扬
中国人民解放军总医院第一医学中心

收集了本院 2009-2020 年分离到 29 株耐亚胺培南的肺炎克雷伯菌（IMPKpn），经全基因组测序分析，ST 型比较散发，存在 16 种不同的 ST 型，其中 4 型为新发现的 ST 型。同源分析结果显示，IMPKpn 在某些科室可能已经形成局部爆发，例如 ST5423 和 ST5422。IMP 酶型主要是 IMP-4（14 株）和 IMP-79（10 株），部分为 IMP-8（3 株）和 IMP-26（2 株），同时鉴定出一种新型的 IMP 酶（IMP-90）。

PU-3195

由产 ESBL 肠杆菌科引起的术后脑膜炎的表型、分子特征和危险因素分析：一项持续 6 年的比较队列研究

郑光辉
首都医科大学附属北京天坛医院

目的 为了确定在中国由产 ESBL 肠杆菌科引起的术后脑膜炎的表型、分子特征和危险因素分析。
方法 我们对 2014 年 1 月至 2019 年 12 月中国 4 个神经外科中心中发生术后脑膜炎感染患者进行了多中心对比队列研究，对分离菌株的分子生物学特性进行了回顾和检测，，并用二元 Logit 模型对脑膜炎 EPE 的独立危险因素进行了分析。
结果 在这项研究中，总共有 220 种肠道细菌，其中包括 78 种 EPE。85.6% (67/78)的 esbl 相关基因被检测，其中 blaSHV (14.9%) 和 blaSHV + blaTEM + blaCTX-M-9 (20.9%)是肠道细菌最常见的单基因和联合基因。二元逻辑分析，开颅手术/n(2.583,95% CI. 1.274-5.235，p = 0.008)和恶性肿瘤(OR)。2.406,95% CI. 1.299-4.456，p = 0.005)为/n 是脑膜炎相关的独立危险因素。
结论 就我们所知，这是 中国开展的最大的关于 EPE 脑膜炎的危险因素的研究，开颅手术和恶性肿瘤是发生脑膜炎的独立危险因素。确定的危险因素可在将来进一步用于临床实践和研究，以避免和降低死亡率

PU-3196

生物膜和细菌耐药的研究进展

刘青宇
湖南中医药大学第一附属医院

细菌一直以来是感染性疾病的重要来源。细菌分泌的胞外多糖以及胞外 DNA 等，形成致密的生物膜，是抗生素难以发挥其效应。生物膜的形成加重了细菌耐药，给临床治疗细菌感染性疾病增加了难度。本文从生物膜的结构和形成、生物膜的耐药机理和生物膜抑制药物等方面进行论述，为研究细菌耐药以及生物膜的控制提供理论基础。

PU-3197

2016 年-2020 年我院临床分离细菌种类分布及耐药性监测

彭利群、郑康
衡阳市中心医院

目的 了解 2016 年-2020 年我院临床分离细菌的种类分布和耐药性，为临床合理使用抗菌药物提供参考依据。
方法 分析我院 2016 年-2020 年各临床科室门诊和住院患者培养标本分离的细菌菌株，包括菌种名称、来源标本和药敏情况，应用 WHONET 5.6 和 SPSS20.0 软件对数据进行统计分析。
结果 2016 年-2020 年共分离细菌 15747 株，其中革兰氏阴性（G-）菌 11489 例，占 72.96%，革兰氏阳性菌 4258 例，占 27.04%。检出主要细菌排名前五的细菌分别为大肠埃希菌（3259 株，占 20.70%）、肺炎克雷伯菌（2159 株，13.71%）、铜绿假单胞菌（1511 株，占 9.60%）、金黄色葡萄球菌（1140 株，占 7.24%）和鲍曼不动杆菌（1039 株，占 6.60%）；肠杆菌目对美罗培南总的耐药率为 2.9%，仍高度敏感，大肠埃希菌和肺炎克雷伯菌分别为 0.8%和 4.7%，都低于 5%。铜绿假单胞菌对美罗培南的耐药率为 21.2%。鲍曼不动杆菌对美罗培南的耐药率较高，为 53.8%。

金黄色葡萄球菌对苯唑西林的耐药率为 33.5%，未检出对万古霉素和利奈唑胺耐药的菌株；检出耐万古霉素屎肠球菌和粪肠球菌（VRE）为 4 例；
结论 细菌对抗菌药物的耐药率呈增长趋势，特别是碳青霉烯类耐药肠杆菌科细菌，及时全面地了解耐药现状与趋势、细菌耐药谱的组成与变化对临床合理使用抗菌药物有指导性作用，并指导医院加强院内感染管理。

PU-3198

肺结核患者结核分枝杆菌的四种临床检验方法比较

梁桂亮、李晓非
昆明市第三人民医院

目的 通过对结核分枝杆菌四种临床检验方法的比较，以评价不同方法在肺结核病诊断中的临床应用价值。
方法 回顾性分析 2017 年某院接收的 418 例肺结核患者痰标本，以临床诊断肺结核为标准，对比 Xpert MTB/RIF 与 BACTEC MGIT 960(结核培养)、PCR-反向点杂交法、聚合酶链反应(PCR)四种检测方法的阳性检出率。
结果 418 例送检的痰标本中，结核分枝杆菌阳性检出率为 41.38%(173/418)；检出的 173 例阳性标本中，药物敏感性实验利福平(RF)敏感率为 61.27%(106/173)；耐药率为 38.73%(67/173)。72 例标本 Xpert MTB/RIF 与结核培养结果比较，检出率无统计学差异(Kappa=0.584, P=0.000<0.005; McNemar 检验=0.057>0.05)；50 例标本 Xpert MTB/RIF 与 PCR-反向点杂交法比较，检出率无统计学差异(Kappa=0.795, P=0.000<0.005; McNemar 检验=0.063>0.05)；186 例患者同时使用 Xpert MTB/RIF 与 PCR 比较，检出率有统计学差异(Kappa=0.535, P=0.000<0.005; McNemar 检验=0.013<0.05)。
结论 使用 Xpert MTB/RIF 能准确和快速检测痰标本中结核分枝杆菌，是适合基层医院开展结核病诊断的检测手段。

PU-3199

嗜麦芽窄食单胞菌菌血症感染的危险因素及临床预后分析

艾子译、孟涵、王启、王辉
北京大学人民医院

目的 探讨嗜麦芽窄食单胞菌菌血症感染和感染后死亡的风险因素。为临床嗜麦芽窄食单胞菌菌血症防治提供数据基础。
方法 对北京一家三级甲等临床医院 10 年中出现的嗜麦芽窄食单胞菌菌血症进行一项回顾性病例对照研究，以 53 例嗜麦芽窄食单胞菌菌血症感染病人作为病例组，53 例其他革兰阴性杆菌菌血症感染病人作为对照组。通过单因素分析和多因素 logistic 回归分析嗜麦芽窄食单胞菌菌血症感染的风险因素及临床结果。
结果 单因素分析显示：患有中性粒细胞缺乏症（OR=2.309,95%CI：0.920-5.794，P=0.071）、感染前 30 天内接受腰部穿刺（OR=2.136,95%CI：1.889-9.950，P=0.067）、感染前 30 天内接受中心静脉插管（OR=4.336,95%CI：0.943-4.836，P<0.001）、激素类药物使用史（OR=2.019,95%CI：0.923-4.418，P=0.077）两组间具有显著性差异，感染前 30 天内接受喹诺酮类药物（OR=2.136,95%CI：0.943-4.836，P=0.067）、碳青霉烯类药物（OR=3.559,95%CI：1.483-8.539，P=0.004）、头孢哌酮舒巴坦（OR=2.606,95%CI：1.076-6.310，P=0.031）、氨曲南（OR=1.128,95%CI：1.024-1.242，P=0.027）、替加环素（OR=4.365,95%CI：1.142-16.685，P=0.022）在两组间的差异具有统计学意义。多因素分析显示：感染前 30 天内中心静脉插管

（OR=13.679,95%CI：4.144-45.147，P<0.001），以及激素使用史（OR=4.416,95%CI:1.575-12.385,P=0.005）是嗜麦芽窄食单胞菌菌血症感染的独立危险因素。感染中毒性休克（OR=14.305,95%CI:3.014-67.899,P=0.001)是嗜麦芽窄食单胞菌菌血症感染后死亡的独立危险因素。

结论 减少感染前 30 天内中心静脉插管等侵入性操作以及激素的使用可能会降低嗜麦芽窄食单胞菌菌血症感染的概率。预测和预防感染中毒性休克的发生将有助于降低患者的死亡风险。

PU-3200

高通量宏基因组测序技术检测病原微生物的研究进展

曹啟新、赵亚楠
内蒙古自治区内蒙古人民医院

目的 分析研究高通量宏基因组测序技术在检测病原微生物上的最新进展和临床应用，对该项技术在检测病原微生物方面的进展综合论述。

方法 我们利用 PubMed/Medline、Scopus、Web of Science 和知网等检索了已有的基于高通量宏基因组测序技术用于微生物种类鉴定和抗菌药物敏感性鉴定的文献。

结果 随着医疗技术的快速发展，各种侵入性诊疗技术的大力应用，广谱抗生素的广泛使用，免疫抑制剂等的应用以及环境的变化，感染性疾病发生率逐年上升，已经成为临床治疗的重大难题。然而传统的检测病原微生物的方法存在阳性检测率低、周期长等弊端，已经无法满足临床需求，急需要一项快速准确率高的技术服务于临床。目前，高通量宏基因组测序技术已经开始应用于临床，研究显示，其能够快速、准确、高效地获得整个病原体群体的基因组信息。宏基因组测序不依赖于病原体的分离培养，可以得到环境中丰度较低甚至是痕量病原体的信息。同时宏基因组测序可以对任何类型的病原体进行鉴定，甚至可以用于识别新的病原体，这可能会替代许多目标病原体检测。随着高通量测序技术的发展，采用宏基因组测序技术可以突破传统检测方法的局限性。针对难以培养的病原体和不明病因无法预判的感染病患，利用高通量宏基因组测序技术和专业的病原体数据库，可直接对样本中的病原体 DNA 进行检测，通过软件分析得出覆盖齐全、准确可靠的样本病原体遗传信息。但是，高通量宏基因组测序技术也存在着一定的不足：如参考数据库不完整、测序结果复杂多样，缺乏统一的指南、测序成本高等等，这些问题还需我们进一步去克服。

结论 希望在不久的将来，高通量宏基因组测序技术发展的越来越完善，能够满足临床各方面的需求，更好的为临床服务。

PU-3201

某院 2020 年肺炎链球菌的标本来源、科室分布及耐药性分析

曹身云
泰安市中心医院

目的 了解我院 2020 年临床分离肺炎链球菌的标本来源、科室分布及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。

方法 对 2020 年 1 月 1 日～2020 年 12 月 31 日间临床标本中分离的肺炎链球菌，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。

结果 2020 年我院临床标本共分离出肺炎链球菌 169 株。主要科室分布为儿内科（46.83%）、神经外科（12.87%）、老年科（7.17%）、重症医学科（5. 52%）和耳鼻喉科（5.34%）。主要标本来源为痰液（83.77%）、分泌物（8.99%）和咽拭子（4.43%）。肺炎链球菌对红霉素耐药率

100%，克林霉素和四环素耐药率 90%以上，复方新诺明耐药率 72.3%,其余抗菌药物耐药率较低，均低于 3%。未发现对青霉素、美罗培南、万古霉素、利奈唑胺和三代头孢菌素耐药的菌株。
结论 我院肺炎链球菌主要科室分布为儿内科、神经外科、老年科、重症医学科和耳鼻喉科。主要标本来源为痰液、咽拭子和分泌物。肺炎链球菌对红霉素、克林霉素和四环素耐药较高，其余抗菌药物耐药率较低，未发现对青霉素、美罗培南、万古霉素、利奈唑胺和三代头孢菌素耐药的菌株。临床医生应及时关注本医院本病区细菌耐药监测报告，选取敏感性高的药物进行经验治疗，并及时送检相关培养，尤其是血培养等无菌体液的培养，根据药敏结果及时调整合理的抗菌药物。同时医护人员要注意手卫生和院感的防控。

PU-3202

某院 2020 年流感嗜血杆菌的标本来源、科室分布及耐药性分析

曹身云
泰安市中心医院

目的 了解我院 2020 年临床分离流感嗜血杆菌的标本来源、科室分布及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。
方法 对 2020 年 1 月 1 日～2020 年 12 月 31 日间临床标本中分离的流感嗜血杆菌，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。
结果 2020 年我院临床标本共分离出流感嗜血杆菌 276 株。主要科室分布为儿内科（26.83%）、神经外科（10.87%）、神经内科（7.97%）、呼吸内科（6. 52%）和肿瘤外科（5.84%）、。主要标本来源为痰液（89.77%）、咽拭子（5.43%）和分泌物（3.99%）。流感嗜血杆菌对氨苄西林和复方新诺明耐药率较高，分别为 69%和 66%。氨苄西林舒巴坦的耐药率 36%，头孢呋辛的耐药率 35%，阿莫西林克拉维酸耐药率 19%，未发现对三代头孢菌素、喹诺酮类药物、碳青霉烯类药物和阿奇霉素耐药的菌株。
结论 我院流感嗜血杆菌主要科室分布为儿内科、神经外科、神经内科、呼吸内科和肿瘤外科。主要标本来源为痰液、咽拭子和分泌物。流感嗜血杆菌对氨苄西林和复方新诺明耐药率较高，未发现对三代头孢菌素、喹诺酮类药物、碳青霉烯类药物和阿奇霉素耐药的菌株。临床医生应及时关注本医院本病区细菌耐药监测报告，选取敏感性高的药物进行经验治疗，并及时送检相关培养，尤其是血培养等无菌体液的培养，根据药敏结果及时调整合理的抗菌药物。同时医护人员要注意手卫生和院感的防控。

PU-3203

某院 2020 年金黄色葡萄球菌的标本来源、科室分布及耐药性分析

曹身云
泰安市中心医院

目的 了解我院 2020 年临床分离金黄色葡萄球菌的标本来源、科室分布及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。
方法 对 2020 年 1 月 1 日～2020 年 12 月 31 日间临床标本中分离的金黄色葡萄球菌，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。
结果 2020 年我院临床标本共分离出金黄色葡萄球菌 535 株。主要科室分布为儿内科（11.83%）、耳鼻喉科（9.11%）、重症医学科（5.74%）、神经外科（4.10%）、和血液病诊疗中心

（3.39%）。主要标本来源为痰液（32.77%）、分泌物（23.1%）、穿刺液（4.39%）和血液（2.97%）。金黄色葡萄球菌对青霉素和红霉素耐药率高，分别为 93%和 71%，其余抗菌药物耐药率低，苯唑西林的耐药率 23%，环丙沙星和左氧氟沙星的耐药率 13%，未发现对万古霉素、利奈唑胺、替考拉宁、达托霉素耐药的菌株。

结论 我院金黄色葡萄球菌主要科室分布为儿内科、耳鼻喉科、重症医学科、神经外科和血液病诊疗中心。主要标本来源为痰液、分泌物、穿刺液和血液。金黄色葡萄球菌对青霉素和红霉素耐药率高，其余抗菌药物耐药率低，未发现对万古霉素、利奈唑胺、替考拉宁、达托霉素耐药的菌株。临床医生应及时关注本医院本病区细菌耐药监测报告，选取敏感性高的药物进行经验治疗，并及时送检相关培养，尤其是血培养等无菌体液的培养，根据药敏结果及时调整合理的抗菌药物。同时医护人员要注意手卫生和院感的防控。

PU-3204

某院 2020 年肺炎克雷伯菌的标本来源、科室分布及耐药性分析

曹身云
泰安市中心医院

目的 了解我院 2020 年临床分离肺炎克雷伯菌的标本来源、科室分布及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。

方法 对 2020 年 1 月 1 日～2020 年 12 月 31 日间临床标本中分离的肺炎克雷伯菌，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。

结果 2020 年我院临床标本共分离出肺炎克雷伯菌 933 株。主要科室分布为重症医学科（13.83%）、神经外科（9.11%）、神经内科（5.04%）、血液病诊疗中心（4.50%）、和呼吸重症科（4.39%）。主要标本来源为痰液（60.77%）尿液（15.43%）、、血液（6.97%）、分泌物（7.72%）和穿刺液（5.57%）。肺炎克雷伯菌对临床常用抗菌药物敏感性较好，一二代头孢菌素的耐药率 38%；头孢曲松和头孢噻肟耐药率 35%；头孢他定耐药率 21%；酶的抑制剂类药物敏感性较好，耐药率低于 34%，其中氨苄西林舒巴坦的敏感性略差，耐药率 33%，哌拉西林他唑巴坦敏感性较好，耐药率 11%；对碳青霉烯类药物耐药率 7%。未发现对替加环素和多粘菌素耐药的菌株。

结论 我院肺炎克雷伯菌主要科室分布为重症医学科、神经外科、神经内科、血液病诊疗中心和呼吸重症科。主要标本来源为尿液、痰液、血液、分泌物和穿刺液。肺炎克雷伯菌对临床常用抗菌药物敏感性较好，未发现对替加环素和多粘菌素耐药的菌株。临床医生应及时关注本医院本病区细菌耐药监测报告，选取敏感性高的药物进行经验治疗，并及时送检相关培养，尤其是血培养等无菌体液的培养，根据药敏结果及时调整合理的抗菌药物。同时医护人员要注意手卫生和院感的防控。

PU-3205

某院 2020 年大肠埃希菌的标本来源、科室分布及耐药性分析

曹身云
泰安市中心医院

目的 了解我院 2020 年临床分离的大肠埃希菌的标本来源、科室分布及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。

方法 对 2020 年 1 月 1 日～2020 年 12 月 31 日间临床标本中分离的大肠埃希菌，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。

结果 2020 年我院临床标本共分离出大肠埃希菌 1124 株。主要科室分布为肾病科（10.41%）、重症医学科（6.76%）、血液病诊疗中心（5.78%）、儿内科（5.43%）和儿外科（4.80%）。主要标本来源为尿液（47.42%）、痰液（14.95%）、血液（11.57%）、分泌物（10.50%）和穿刺液（13.26%）。大肠埃希菌对氨苄西林耐药率高（91 %）；对氟喹诺酮类耐药率在 54%～58%；复方新诺明的耐药率 58%；一二代头孢菌素的耐药率 53%～55%；头孢曲松和头孢噻肟耐药率 51%；头孢他定耐药率 21%；酶的抑制剂类药物敏感性较好，耐药率低于 31%，其中氨苄西林舒巴坦的敏感性略差，耐药率 31%，哌拉西林他唑巴坦敏感性较好，耐药率 4%；对碳青霉烯类药物耐药率 1%。未发现对替加环素和多粘菌素耐药的菌株。

结论 我院大肠埃希菌主要科室分布为肾病科、重症医学科、血液病诊疗中心、儿内科）和儿外科。主要标本来源为尿液、痰液、血液、分泌物和穿刺液。大肠埃希菌对氨苄西林耐药率高，对酶的抑制剂类药物敏感性较好，未发现对替加环素和多粘菌素耐药的菌株。临床医生应及时关注本医院本病区细菌耐药监测报告，选取敏感性高的药物进行经验治疗，并及时送检相关培养，尤其是血培养等无菌体液的培养，根据药敏结果及时调整合理的抗菌药物。同时医护人员要注意手卫生和院感的防控。

PU-3206

Impact of subinhibitory concentrations of tedizolid and linezolid on gene transcription in Staphylococcus aureus strain Newman and N315

Han Yang [1]、Wen Lin[1]、Chunyan He[1]、Wen Shu[1]、Qingzhong Liu[2]
1. Shanghai General Hospital
2. 上海市中医医院

Aim To access the impact of subinhibitory concentrations (sub-MIC) of tedizolid and linezolid on gene transcription in Staphylococcus aureus Newman and N315 strain.
Methods When the bacteria grew into exponential phase (3 h), 1/8, 1/4 and 1/2 MIC of tedizolid and linezolid were added into the cultures. After 4 h, the expression of 23 virulence factors and regulatory genes was determined by qRT-PCR.
Results Our findings show that tedizolid could significantly increase the most of gene's expression including clfA, lukE, nuc and agrA. In the Newman strain, 1/8 MIC of tedizolid up-regulated the mRNA levels of sasG, fnbA and sdrD by 3.5, 1.5 and 2.2 folds compared with the control group. The mRNA levels of hla, lukE and psmα in Newman were increased by 2.5 to 5 times, 3.2 to 7.9 times and 5.6 to 16.6 times with different sub-MIC of tedizolid. As for N315 isolate, tedizolid at different subinhibitory concentrations increased the expression levels of icaA, fnbA and sdrD 6.8 to 21.4 folds, 3 to 8.8 folds and 1.7 to 2.2 folds. 1/8 and 1/2 MIC of tedizolid up-regulated clfA mRNA by 2.1 and 1.8 folds. Linezolid could promote some gene gene's expression including clfA, psmα, sea and seaS but inhibit gene's expression including icaA, spa, coa and agrA in Newman strain. The mRNA of icaA was down-regulated by 2.9 to 4.2 folds by sub-MICs of linezolid. 1/4 and 1/2 MIC of linezolid inhibited spa mRNA transcription 1.7 to 2.3 folds. The antibiotic required to alter gene expression was strain-dependent.
Conclusion Sub-MIC of tedizolid and linezolid promote gene transcription in S. aureus and the finding is helpful to the rational use of tedizolid and linezolid in staphylococcal infection.

PU-3207

某院 2021 年第一季度痰液培养细菌的菌株分布及耐药特点

曹身云
泰安市中心医院

目的 了解我院 2021 年第一季度痰液培养细菌的菌株分布及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。
方法 对 2021 年 1 月 1 日～2021 年 3 月 30 日间临床痰液标本中分离的细菌，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充和复核，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。
结果 2021 年第一季度我院临床共送检痰液培养 2607 人份，痰液标本共分离出非重复细菌 994 株，分离前五位的细菌主要是肺炎克雷伯菌（17.30%）、鲍曼不动杆菌（15.49%）、铜绿假单胞菌（10.46%）、金黄色葡萄球菌（9.39%）和纹带棒杆菌（8.35%）。肺炎克雷伯菌对氟喹诺酮类耐药率在 24%～30%；一二三代头孢菌素的耐药率 19%～34%，其中头孢曲松和头孢噻肟耐药率 32%；头孢他定耐药率 19%；酶的抑制剂类药物敏感性较好，耐药率低于 31%，其中氨苄西林舒巴坦的敏感性略差，耐药率 31%，阿莫西林克拉维酸敏感性较好，耐药率 12%；对碳青霉烯类药物耐药率 8%。未发现对替加环素和多粘菌素耐药的菌株。鲍曼不动杆菌耐药率较高，对头孢菌素类、酶的抑制剂类、碳青霉烯类和喹诺酮类药物的耐药率均在 90%以上，呈现多重耐药。只有米诺环素、替加环素和多粘菌素敏感性较好。
结论 痰液培养细菌主要是肺炎克雷伯菌、鲍曼不动杆菌、铜绿假单胞菌、金黄色葡萄球菌和纹带棒杆菌。肺炎克雷伯菌对酶的抑制剂类药物敏感性较好。未发现对替加环素和多粘菌素耐药的菌株。鲍曼不动杆菌耐药率较高，呈现多重耐药。临床医生应及时关注本医院本病区细菌耐药监测报告，选取敏感性高的药物进行经验治疗，并及时送检相关培养，尤其是血培养等无菌体液的培养，根据药敏结果及时调整合理的抗菌药物。同时医护人员要注意手卫生和院感的防控。

PU-3208

某院 2021 年第一季度血培养细菌的菌株分布及耐药特点

曹身云
泰安市中心医院

目的 了解我院 2021 年第一季度血培养细菌的菌株分布及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。
方法 对 2021 年 1 月 1 日～2021 年 3 月 30 日间临床血液标本中分离的细菌，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充和复核，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。
结果 2021 年第一季度我院临床共送检血液培养 1625 人份，血液标本共分离出非重复细菌 141 株，主要是大肠埃希菌（40.43%）、肺炎克雷伯菌（17.02%）、金黄色葡萄球菌（4.26%）和人葡萄葡萄球菌（4.26%）。大肠埃希菌对氨苄西林耐药率高（84 %）；对氟喹诺酮类耐药率在 56%～60%；复方新诺明的耐药率 60%；一二代头孢菌素的耐药率 47%～49%；头孢曲松和头孢噻肟耐药率 47%；头孢他定耐药率 26%；酶的抑制剂类药物敏感性较好，耐药率低于 27%，其中氨苄西林舒巴坦的敏感性略差，耐药率 26%，哌拉西林他唑巴坦敏感性较好，耐药率 4%；对碳青霉烯类药物耐药率 2%。未发现对替加环素和多粘菌素耐药的菌株。
结论 我院 2021 年第一季度血培养细菌主要是大肠埃希菌、肺炎克雷伯菌、金黄色葡萄球菌和人葡萄葡萄球菌。大肠埃希菌对氨苄西林耐药率高，酶的抑制剂类药物敏感性较好，未发现对替加环素和多粘菌素耐药的菌株。临床医生应及时关注本医院本病区细菌耐药监测报告，选取敏感性高的药

物进行经验治疗，并及时送检相关培养，尤其是血培养等无菌体液的培养，根据药敏结果及时调整合理的抗菌药物。同时医护人员要注意手卫生和院感的防控。

PU-3209

我院 2021 年第一季度尿培养细菌的菌株分布及耐药特点

曹身云
泰安市中心医院

目的 了解我院 2021 年第一季度尿培养细菌的菌株分布及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。
方法 对 2021 年 1 月 1 日～2021 年 3 月 30 日间临床尿液标本中分离细菌，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。
结果 2021 年第一季度我院临床共送检尿液培养 1446 人份，尿液标本共分离出非重复细菌 357 株，主要是大肠埃希菌（56.02%）、肺炎克雷伯菌（12.61%）、屎肠球菌（8.40%）、粪肠球菌（6.16%）和奇异变形菌（4.48%）。大肠埃希菌对氨苄西林耐药率高（89 %）；对氟喹诺酮类耐药率在 60%～66%；一二三代头孢菌素的耐药率 42%～43%；酶的抑制剂类药物敏感性较好，耐药率低于 29%；对碳青霉烯类药物均敏感。肺炎克雷伯菌对一二三代头孢菌素的耐药率 29%～47%；对氟喹诺酮类耐药率在 33%～40%；对碳青霉烯类药物的耐药率 9%。屎肠球菌对环丙沙星、青霉素、左氧氟沙星和氨苄西林耐药率高，分别为 93%、90%、90%和 87%，其余抗菌药物耐药率低，未发现对万古霉素、替考拉宁和杜托霉素耐药的菌株。
结论 我院临床尿液标本的细菌分布以大肠埃希菌、肺炎克雷伯菌和屎肠球菌为主。肺炎克雷伯菌对抗菌药物的耐药率略低于大肠埃希菌，两者对酶的抑制剂类药物敏感性均较好。屎肠球菌对环丙沙星、青霉素、左氧氟沙星和氨苄西林耐药率高，未发现对万古霉素、替考拉宁和杜托霉素耐药的菌株。临床医生应根据药敏结果选择并及时调整合理的抗菌药物。

PU-3210

2021 年第一季度临床分离的耐碳青霉烯类肠杆菌科细菌的分布及耐药特点

曹身云
泰安市中心医院

目的 了解我院 2021 年第一季度临床分离的耐碳青霉烯类肠杆菌科细菌（CRE）的菌株分布、科室来源及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。
方法 对 2021 年 1 月 1 日～2021 年 4 月 30 日间临床标本中分离的 CRE，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。
结果 2021 年第一季度我院临床标本共分离出 29 株 CRE，主要是肺炎克雷伯菌（62.07%）、大肠埃希菌（17.24%）和粘质沙雷菌（13.79%）。主要科室分布为重症医学科（31.03%）、医养结合区（13.79%）、急诊内科病房（10.34%）、呼吸重症科（10.34%）和神经外科（10.34%）。CRE 对大多数临床常用抗菌药物耐药率高，呈现多重耐药甚至泛耐药。对头孢菌素类耐药率 100%，对酶的抑制剂类耐药率大于 90%，对喹诺酮类耐药率大于 70%，替加环素和多粘菌素耐药率最低。
结论 我院 CRE 检出率较高，以肺炎克雷伯菌、大肠埃希菌和粘质沙雷菌为主。主要来源于重症医学科、医养结合区、急诊内科病房、呼吸重症科和神经外科。CRE 耐药情况严峻，对大多数临床常用抗菌药物耐药率高，呈现多重耐药甚至泛耐药。临床医生应关注本医院本病区耐药监测报告，

选取敏感性高的药物进行经验治疗，并及时送检相关培养，根据药敏结果选择并及时调整合理的抗菌药物。医护人员要注意手卫生和院感的防控，防止 CRE 暴发流行。

PU-3211

2021 年第一季度我院临床标本病原菌检出情况及前三位细菌的耐药性

曹身云
泰安市中心医院

目的 了解 2021 年第一季度我院临床标本的病原菌检出情况及前三位细菌的耐药性，为临床合理使用抗菌药物提供理论依据。
方法 回顾性分析我院 2021 年 1 月 1 日～2021 年 4 月 30 日期间各临床标本中检出的细菌。利用 Microscan WalkAway 96plus 全自动微生物鉴定药敏系统进行菌株鉴定和药敏试验，部分药敏试验采用纸片扩散法进行补充。菌株分布及耐药率使用 WHONET5.6 软件进行统计分析。
结果 2021 年第一季度我院临床标本共分离出非重复细菌 2014 株，分离前五位的细菌分别为：大肠埃希菌（17.38%）、肺炎克雷伯菌（13.06%）、金黄色葡萄球菌（11.27%）、鲍曼不动杆菌（8.69%）和铜绿假单胞菌（6.01%）。主要科室分布为重症医学科（13.56%）、儿内科（8.292%）、血液科（7.55%）、呼吸重症科（6.36%）和耳鼻喉科（5.16%）。大肠埃希菌对氨苄西林耐药率高（89 %），对氟喹诺酮类耐药率在 59%～64%，一二三代头孢菌素的耐药率 45%～47%。酶的抑制剂类药物敏感性较好，耐药率低于 30%。肺炎克雷伯菌对抗菌药物的耐药率较低，均低于 32%。金黄色葡萄球菌对青霉素和红霉素耐药率高，分别为 93%和 71%，其余抗菌药物耐药率低，未发现对万古霉素和利奈唑胺耐药的菌株。
结论 我院临床标本的细菌分布以大肠埃希菌、肺炎克雷伯菌和金黄色葡萄球菌为主。主要科室分布为重症医学科、儿内科、血液科、呼吸重症科和耳鼻喉科。肺炎克雷伯菌对抗菌药物的耐药率低于大肠埃希菌，两者对酶的抑制剂类药物敏感性均较好。金黄色葡萄球菌对青霉素和红霉素耐药率高，未发现对万古霉素和利奈唑胺耐药的菌株。临床医生应根据药敏结果选择并及时调整合理的抗菌药物。

PU-3212

高毒力肺炎克雷伯菌的研究进展

曹身云
泰安市中心医院

目的 为了解高毒力肺炎克雷伯菌的流行现状、毒力影响因素及耐药性，为医院感染控制和临床治疗提供理论依据。
方法 肺炎克雷伯菌分为普通肺炎克雷伯菌和高毒力肺炎克雷伯菌。高毒力肺炎克雷伯菌致病性强，导致的感染多以严重的原发性肝脓肿为首发症状，并可合并眼内炎、败血症等其他部位的迁徙性感染。感染患者死亡率高。近年来发现了对多种抗生素耐药的高毒力肺炎克雷伯菌，高毒力与高耐药的重叠给临床带来了极大挑战。本文通过查阅国内外大量相关文献，对高毒力肺炎克雷伯菌的流行现状、毒力影响因素及耐药性方面的研究现状进行综述，以期为高毒力肺炎克雷伯菌的预防和治疗提供理论依据。
结果 分析发现高毒力肺炎克雷伯菌感染流行性传播的国家仍主要集中在亚洲。荚膜、菌毛、摄铁系统、脂多糖等毒力相关因子与其致病性密切相关。已发现对 ESBL 耐药，甚至对碳青霉烯耐药的高毒力菌株。高毒力肺炎克雷伯菌已成为威胁人类健康一大杀手。

结论 目前临床对于高毒力肺炎克雷伯菌检测方法有限，早期、灵敏的检测技术有待研发。许多具体的致病机制和耐药机制尚不清楚，需要我们进一步去研究。对于耐药的高毒力肺炎克雷伯菌，我们更应该提高警惕，做好感染预防和控制，防止多重耐药菌的产生和耐药菌的院内播散。

PU-3213

肠杆菌科碳青霉烯类传播方式的研究进展

邢小平
安徽省铜陵市人民医院

目的中国是抗菌药物的生产和使用大国，细菌耐药性已经成为全世界关注的问题，尤其是对碳青霉烯类抗生素的耐药。肠杆菌科是一大类革兰氏阴性细菌，包含许多重要的病原体，碳青霉烯类抗生素是杀死肠杆菌科的最后手段，已在我国广泛使用，既往的研究主要集中在耐药机制方面研究，本篇综述主要从流行病学、传播途径及防控措施来阐述。

PU-3214

耐碳青霉烯肺炎克雷伯菌的碳青霉烯酶基因携带情况及分子流行病学特点

曹身云
泰安市中心医院

目的 了解耐碳青霉烯肺炎克雷伯菌（CRKP）的碳青霉烯酶基因携带情况及分子流行病学特点,为医院感染控制和临床治疗提供理论依据。
方法 收集我院 2019 年 1 月～12 月临床分离的 CRKP 31 株, 采用 Microscan WalkAway 96plus 全自动细菌鉴定药敏仪进行菌株鉴定和药敏试验，同时用纸片扩散法和 E-test 法进行药敏试验的补充和复核；采用聚合酶链式反应（PCR）扩增相关碳青霉烯类耐药基因 KPC、NDM、 IMP-1、OXA-48 并测序；采用多位点序列分型（MLST）调查菌株的克隆相关性并进行流行病学比较。
结果 31 株 CRKP 主要标本来源为痰液（80.65%）和尿液（9.68%）,主要科室来源为各监护室病房。CRKP 耐药率高，酶的抑制剂和头孢菌素的耐药率为 100%。氟喹诺酮的耐药率在 90%以上。氨基糖苷耐药率略低，在 77%～81%。复方新诺明和多粘菌素的耐药率较低，分别为 12.90%和 3.23%。替加环素的耐药率为 0。经 PCR 测序确认,碳青霉烯耐药基因总检出率为 100%，其中 KPC-2 基因检出率为 93.55%（29/31），NDM-5 检出率为 6.45%（2/31）, OXA-48 和 IMP-1 检出率为 0。未发现同时携带两种碳青霉烯耐药基因的菌株。表明该院 CRKP 对碳青霉烯类药物耐药的机制是产碳青霉烯酶，主要携带是 KPC-2 基因，其次为 NDM-5 基因。菌株有 3 个 MLST 序列类型，分别属于三种克隆复合群。ST11 型是主要型别，通过 MLST E-burst 聚类分析，属于 CC258 克隆复合群，检出率为 93.55%（29/31）。与我国流行的 MLST 型别一致。
结论 碳青霉烯酶基因 KPC-2 基因和 NDM-5 基因是引起该院肺炎克雷伯菌对碳青霉烯类抗生素耐药的主要原因,ST11 是主要的克隆类型,医院需尽快强化医院感染预防控制措施。

PU-3215

2016—2020 年某三甲医院尿路感染细菌分布及耐药性分析

何盼、许心怡、李达明、姚冬梅、蒋传好
中南大学湘雅二医院

目的 了解本院 2016—2020 年引起尿路感染的常见病原菌分布以及临床常用的抗菌药物，为本院尿路感染患者临床选择用药的药物以及防治提供参考。
材料与方法 收集 2016—2020 年 5 年本院尿路感染患者的中段尿标本或尿液标本分离培养出来的革兰阴性菌、革兰阳性菌以及真菌（剔除同一患者同一部位同一菌种）。以微量肉汤稀释法为主，纸片扩散法和琼脂稀释法为辅进行抗菌药物敏感性实验。按照当年最新的 CLSI 原则进行药敏结果的判读：敏感（S）、中介（I）、耐药（R）。
结果 尿路感染病原菌以革兰阴性菌为主且呈上升趋势，分离出的 10616 株菌里检出率居前 5 位者分别是大肠埃希菌（34.2%~38.6%）、屎肠球菌（8.3%~12%）、白色念珠菌（6.9%~12.2%）、肺炎克雷伯菌（6.4%~10%）和粪肠球菌（4.8%~6.2%）。分离出的大肠埃希菌对头孢吡肟的耐药率均〉40%，对氨苄西林/舒巴坦耐药率〉44%,对左旋氧氟沙星、环丙沙星、复方新诺明耐药率均〉50%，肺炎克雷伯菌对氨苄西林/舒巴坦耐药率较高，耐药率均在 55%以上。屎肠球菌对左氧氟沙星、呋喃妥因、利福平高度耐药。白色念珠菌、热带念珠菌、光滑念珠菌对卡泊芬净、氟康唑、泊沙康唑、伏立康唑等抗生素低耐药。金黄色葡萄球菌、表皮葡萄球菌和溶血葡萄球菌中未发现对万古霉素、替考拉宁、利奈唑胺的耐药株，对青霉素高度耐药。
结论 本院尿路感染患者病原菌以革兰氏阴性菌为主，且多重耐药菌检出率较高。临床应继续规范抗菌药物的合理使用，加强院感防控。

PU-3216

2011-2020 新生儿分离病原菌分布及耐药性分析

黄佳怡、许心怡、李达明、曹伟、蒋传好
中南大学湘雅二医院

目的 了解本院 2011-2020 年新生儿患者感染病原菌的分布及其对常用抗菌药物的耐药性变化，为新生儿患者的抗感染治疗提供参考。
方法 采用回顾性方法，收集我院 2011 年 1 月 1 日～2020 年 12 月 31 日新生儿专科送检各类标本分离的病原菌和抗菌药物敏感性试验结果，应用 WHONET5.6 软件分析新生儿患者病原菌数据。
结果 从新生儿专科细菌标本中共分离出细菌 2245 株。其中革兰阴性菌共 1650 株占 73.7%，革兰阳性菌 588 株占 21.3%，革兰阴性菌的占比整体呈上升趋势。2020 年标本主要来自痰标本(59.8%)、血液标本(27.8%)、胃液标本(8.4%)。2011-2020 年临床分离菌株中前五位的菌分别为肺炎克雷伯氏菌、大肠埃希菌、溶血葡萄球菌、表皮葡萄球菌、鲍曼不动杆菌。金黄色葡萄球菌对青霉素的耐药率逐年上升（60.0%~100.0%），对庆大霉素保持较高的敏感率（70.0~100.0%）。凝固酶阴性的葡萄球菌对阿米卡星的耐药率逐年下降（12.5%~0.0%）。出现利奈唑胺的葡萄球菌属菌株。屎肠球菌对万古霉素、替考拉宁的敏感率均高于粪肠球菌。肺炎克雷伯菌对左旋氧氟沙星的耐药率为 0.0%～到 43.0%。大肠埃希菌对部分头孢类药物都有一定的耐药性，对亚胺培南的耐药率在 4.3%～25.0%。铜绿假单胞菌对大多数抗菌药物的敏感度都比较高，对亚胺培南的耐药率为 37.5%～80.0%。鲍曼不动杆菌对环丙沙星的耐药率从 2011 年的 44.4%下降到了 2019 年的 5.6%，对亚胺培南和美罗培南的敏感率有所上升，分别为 44.4%～89.5%、44.4%～100.0%。白色念珠菌仅对伊曲康唑产生了一定的耐药性。
结论 新生儿患者临床分离细菌以革兰阴性菌为主，且多重耐药菌检出率较高，应加强新生儿感染的预防和控制。

PU-3217

COVID-19 患者主调节子分析和单细胞测序揭示锌指蛋白抗 SARS-CoV-2 的潜在机制

杨阳、夏欣一
中国人民解放军东部战区总医院

目的 研究表明不同性别 COVID-19 患者的感染率相差不大，但死亡率和严重程度均存在显著差异。通过生物信息学从分子层面和单细胞层面分析不同性别的患者在抗 SARS-CoV-2 病毒机制中的差异。
方法 临床数据来自于 2020 年 2 月 4 日至 2020 年 4 月 13 日期间在武汉市火神山医院的 3059 例 COVID-19 患者，排除了病历不完整的患者后，共纳入 3044 例患者；430 份 SARS-CoV-2 阳性鼻咽拭子和 54 份阴性对照的转录组数据来自 GEO 数据库（GSE152075），生信分析包括差异表达分析和主调节子分析、基因功能分析和基因集活性计算、单细胞数据分析等。
结果 一方面，通过临床数据分析发现 COVID-19 女性患者的预后显著高于男性，女性患者比男性有更多的淋巴细胞与更少的中性粒细胞，单核细胞，白介素 6 和 C 反应蛋白等。另一方面，通过生物信息学分析确定了许多重要的主调控子，如 STAT1/STAT2 和锌指(ZNF)蛋白，且女性患者在 SARS-CoV-2 感染后，比男性患者表达更多的 ZNF 蛋白且有着更强的转录活性；ZNF 蛋白活性与 COVID-19 患者的 SARS-CoV-2 病毒载量存在显著负相关，作为转录因子也可激活其靶基因参与抗 SARS-CoV-2 感染过程；进一步分析发现 ZNF 蛋白活性与 COVID-19 患者的多重免疫细胞的丰度呈正相关，提示高 ZNF 蛋白活性可提高多种免疫细胞的丰度与抗病毒活性，有效抑制 SARS-CoV-2 感染。
结论 本研究发现 ZNF 家族的 MRs 在 SARS-CoV-2 感染后高度活化且与病毒载量和疾病分级呈负相关，暗示其可能具有抗病毒作用。此外，女性比男性有更多和更高活性的 ZNF 蛋白，这可能是女性新冠患者临床预后更好的原因之一。（本文部分内容已被 Brief Bioinform， IF=8.99 接受）

PU-3218

大疱性类天疱疮患者并发鼻疽诺卡菌引起右肺感染及胸壁脓肿一例

赵俊琴、王晖、何鸿绯、郑礼瑶
阳泉市第一人民医院

目的 探讨一例大疱性类天疱疮患者右肺上叶炎性占位的病原菌鉴定，为临床诊疗提供可靠依据。
方法 将患者送检痰液标本和右侧胸壁肿物穿刺标本分离得到的菌株，采用标本原始涂片革兰染色、抗酸染色、弱抗酸染色、细菌形态学观察、菌落涂片、微生物质谱技术、16S rRNA 基因测序鉴定等方法进行鉴定。
结果 痰液及右侧胸壁肿物穿刺液标本涂片，经革兰染色均可见到革兰阳性、纤细、杆状、90 度角交叉的菌丝体，抗酸染色阴性，弱抗酸染色阳性；痰液分离菌株及右侧胸壁肿物穿刺液分离菌株在血琼脂、巧克力琼脂均生长缓慢，约三天后长出细小淡黄色菌落，十天后变为黄色、粗糙有褶皱、质地坚硬、不易挑取的菌落；菌落涂片因乳化不良，多为聚集成簇的菌丝体，或散落的短杆菌，革兰染色阳性，弱抗酸染色有阳性有阴性，抗酸染色阴性；经外院布鲁克 Microflex 质谱仪鉴定为鼻疽诺卡菌，分值 1.500；经 16S rRNA 基因测序鉴定为鼻疽诺卡菌（Nocarida farcinica）。临床及时排查脑 CT 未见播散，应用磺胺类药物、米诺环素、左氧氟沙星等，症状缓解，肿块消退，出院随诊。

结论 诺卡菌为临床不常见病原菌，免疫力地下人群易感染，实验室鉴定时因其生长缓慢容易漏检，可通过原始标本涂片进行多种染色、延长标本培养时间，菌落形态观察，因其生化反应不易，可通过微生物质谱仪鉴定或借助分子生物学方法得到鉴定。临床明确诊断后，治疗有效。

PU-3219

孕中期母体泌尿系感染与子痫前期发生危险性的关系

杜伟平
延安大学附属医院检验科

目的 有理论认为孕期炎症因素在子痫前期的发生中起一定作用,探讨孕中期母体泌尿系感染与子痫前期发生的相关性。
方法 选取 2018-10 月-2020-12 月在延安大学附属医院诊治，1430 例单胎孕妇，于孕中期（22w-27w）无菌中段尿尿培养检测，观察孕妇子痫前期的发生率。
结果 ①孕中期，67(4.7%)例确诊为泌尿系感染；在孕末期，119(8.3%)例诊断为子痫前期。②孕中期单纯泌尿系感染的孕妇与孕末期泌尿系感染合并子痫前期的孕妇人数比较有统计学差异（29 VS 38，P=0.042）；伴有泌尿系感染阳性体征的子痫前期患者与泌尿系感染阴性体征的子痫前期患者比较有显著统计学差异（13 VS 5，P=0.008）③采用 Logistic 回归分析子痫前期发生的危险性，孕妇年龄［OR=3.91，（95％置信区间 2.76-5.38）］,体重指数［OR=5.37，（95％置信区间 4.01-5.85）］，孕中期伴有阳性体征的泌尿系感染［OR=3.27，（95％置信区间 2.33-4.25）］。
结论 孕中期伴阳性体征泌尿系感染与子痫前期发生有关。

PU-3220

流感合并细菌感染患者的临床和实验室特点

吴思颖、黄家旺、谢轶、康梅
四川大学华西医院

目的 探讨流感合并细菌感染患者的临床和实验室特点，以期为流感合并细菌感染患者的临床诊断和治疗提供一定的依据。
方法 纳入 2018 年 1 月至 2019 年 4 月，四川大学华西医院流感病毒核酸检测阳性的住院患者 1249 例，其中合并细菌感染的患者 211 例，随机筛选出 241 例流感未合并细菌感染的患者作为对照组。使用 lis 和 his 系统查询实验组和对照组的临床资料和实验室检查指标，使用 SPSS 软件进行统计学分析。
结果 流感合并细菌感染的发生率为 16.9%（211/1249）。211 例流感合并细菌感染的患者中，男性 143 例，女性 68 例，平均年龄 59±16 岁，平均住院天数 25±20 天，有 64.2%的患者入住 ICU。与对照组相比，实验组平均年龄高于对照组，住院天数增加，咳痰和呼吸困难症状的患者较多，差异具有统计学意义。实验组伴基础疾病的患者 201 例（95.3%），对照组伴基础疾病的患者 203 例（84.2%），其中基础疾病主要包括高血压、糖尿病、心脏病、肾脏病、肝脏疾病、慢性阻塞性肺疾病、肿瘤等。实验组患高血压、糖尿病、心脏疾病、肾脏疾病和慢性阻塞性肺疾病的患者比对照组多，差异具有统计学意义。实验组危重和死亡患者较对照组多，差异具有统计学意义。实验组白细胞计数，中性粒细胞百分比，降钙素原，C 反应蛋白和白介素-6 高于对照组，差异具有统计学意义。 211 例流感合并细菌感染患者中分离到 294 株细菌，共 28 个菌种，以鲍曼/溶血不动杆菌为主，占 35.4%，其他的主要菌种有铜绿假单胞菌（11.9%）、肺炎克雷伯菌肺炎亚种（11.2%）、大肠埃希氏菌（7.8%）、金黄色葡萄球菌（5.4%）。社区获得性感染中，主要为鲍曼/溶血不动杆菌（43%），其他的主要菌种为金黄色葡萄球菌（13.1%）、肺炎克雷伯菌肺炎亚种（9.3%）、大肠

埃希氏菌（5.6%）等。医院获得性感染中，以鲍曼/溶血不动杆菌为主（31.7%），其他的主要菌种为铜绿假单胞菌（15.8%）、肺炎克雷伯菌肺炎亚种（12.6）、大肠埃希氏菌（9.3%）等。
结论 流感合并细菌感染在临床上较为常见，多见于老年人，病人多有基础疾病，预后较差，相关实验室检查指标数值升高，分离菌株以鲍曼/溶血不动杆菌为主。

PU-3221

ICU 与非 ICU 血培养病原菌组成及耐药性差异

陶晓燕[1,2]、闵昌航[2]、于婷[2]、王海晨[2]、李军[2]、胡咏梅[2]、邹明祥[2]
1. 电子科技大学附属医院·四川省人民医院
2. 中南大学湘雅医院

目的 探讨重症监护病房（ICU）与非 ICU 住院患者血培养病原菌组成及耐药特点，为临床合理使用抗菌药物提供实验依据。
方法 对某大型三甲医院 2015 年 1 月-2019 年 12 月 ICU 与非 ICU 血培养检出的病原菌的组成及耐药性进行分析，并对 6 种关键多重耐药菌（MDRO）的检出情况进行比较。
结果 共分离非重复病原菌 3301 株，革兰阴性菌 2066 株，占 62.59%。ICU 共分离病原菌 734 株，鲍曼不动杆菌最多（19.75%）；非 ICU 分离病原菌 2567 株，大肠埃希菌最多（22.59%）。在监测的 6 种主要病原菌中，MDRO 占 33.46%（631/1886）。其中，鲍曼不动杆菌中 CRAB 最高（94.42%），大肠埃希菌中 CREC 最低（5.02%）。ICU 6 种病原菌中 MDRO 占 61.88%（276/446），高于非 ICU 的 24.65%（355/1440）。ICU 分离的肺炎克雷伯菌、大肠埃希菌、鲍曼不动杆菌、铜绿假单胞菌、金黄色葡萄球菌和凝固酶阴性葡萄球菌对多种抗菌药物的耐药率高于非 ICU（P<0.05）。
结论 我院血流感染病原菌以革兰阴性菌为主，且耐药十分严重。ICU 血培养分离菌株 MDRO 检出率高，对多种抗菌药物的耐药率高于非 ICU。临床应根据相应流行病学数据，制定针对性的经验治疗策略，并及时根据患者病原学检测结果，调整治疗方案。

PU-3222

抗菌药物莫西沙星联合益生菌培菲康治疗伴有细菌移位的 IBS-D 临床疗效观察

王勇
四川绵阳四 0 四医院

目的 探讨抗菌药物莫西沙星联合益生菌培菲康治疗伴有细菌移位的腹泻型肠易激综合征(IBS-D)临床疗效影响。
方法 选择 2017 年 1 月-2018 年 1 月在我院收治的 160 例 IBS-D 患者，按照随机数表法将其分为两组，各 80 例；其中对照组单纯采用抗菌药物莫西沙星进行治疗；观察组在服用莫西沙星 4 周后，口服培菲康治疗。比较两组患者治疗前后的免疫细胞因子、临床疗效、肝功能指标。
结果 ①两组患者治疗后 IL-6、IL-8、TNF、CD8+均降低(t=2.989，P=0.003；t=10.600，P=0；t=11.142， P=0；t=23.583，P=0；t=13.483，P=0；t=47.851，P=0；t=7.583，P=0；t=10.375，P=0)；CD4+/CD8+升高(t=14.013，P=0；t=16.663，P=0)，且观察组治疗后 IL-6、IL-8、TNF、CD8+低于对照组(t=14.583，P=0.00；t=21.934，P=0；t=33.217，P=0； t=12.484，P=0)，CD4+/CD8+高于对照组(t=11.465，P=0)。②对照组治疗有效率远低于观察组，差异具有统计学意义(t=112.624， P=0)。③两组患者治疗后

腹痛与腹泻症状评分低于治疗前(t=16.435，P=0；t=29.584，P=0；t=18.937，P=0；t=45.764，P=0)，且观察组患者评分均明显低于对照组(t=54.586，P=0；t=52.412，P=0)。

结论 抗菌药物莫西沙星联合益生菌培菲康治疗伴有细菌移位的 IBS-D 临床疗效显著，能够有效改善细胞炎症因子水平，改善腹痛、腹泻症状情况，值得临床广泛应用。

PU-3223

首次发现一株大肠埃希菌中 IS26 介导的三种喹诺酮耐药基因位于一个多重耐药质粒

陶颖[2]、孙景勇[1]
1. 上海交通大学医学院附属瑞金医院微生物科
2. 上海交通大学医学院附属瑞金医院临床检验中心

目的 喹诺酮类药物常用于肠杆菌科细菌感染的治疗,然而世界范围内喹诺酮类药物耐药性的上升构成临床和公共卫生风险。本研究旨在探究一种新的同时存在三种喹诺酮类耐药基因的多重耐药质粒以及分析大肠埃希菌 RJ749 耐药基因的遗传环境。

方法 Etest 法检测 RJ749 和接合子 c749 对头孢曲松、头孢吡肟、头孢他啶、环丙沙星以及左氧氟沙星的 mic 值。以叠氮化钠耐药的大肠埃希菌 J53 株为受体菌进行接合实验。全基因组测序探究多重耐药区的形成及其遗传环境。

结果 RJ749 对喹诺酮类药物表现为高水平耐药，c749 表现为低水平耐药。S1-PFGE 显示 RJ749 和 c749 均含有质粒。c749 中存在质粒 pRJ749，其包含 3 种质粒介导的喹诺酮类耐药(PMQR)基因(aac(6′)-Ib-cr、qnrS2 和 oqxAB)和 10 个其他种类的获得性耐药基因。qnrS2 基因首次发现存在两侧有两端为插入序列 IS26 的遗传环境。

结论 我们发现了 3 种 PMQR 基因在一个多重耐药质粒上共存，并发现了一个新的 qnrS2 的遗传结构，其两侧是 IS26 元件。IS26 在喹诺酮类药物耐药的水平传播中起重要作用。

PU-3224

粪便样本蓝氏贾第鞭毛虫、溶组织内阿米巴双重实时荧光 PCR 检测方法的建立

孟妍明、张春莹、易凡莉、马莹
四川大学华西医院

目的 本研究计划建立针对蓝氏贾第鞭毛虫以及溶组织内阿米巴的双重实时荧光聚合酶链式反应（RT-PCR）分子诊断方法。

方法 两种原虫基因序列比对后确定保守区，使用 Primer5 进行引物设计，Beacon Designer 软件进行探针设计。在 nr（non-redundant）数据库进行 Primer blast 分析确定其特异度。以 ATCC 标准株 DNA 梯度稀释液为模板进行扩增，筛选灵敏度较好引物对。使用较好引物进行双重 PCR 的体系建立，并使用临床样本进行性能验证。将目标序列导入 pUC57 质粒，梯度稀释用于测定最低检测限。收集临床粪便样本，首先镜检法筛查其原虫滋养体或包囊。随后提取 DNA 进行双重 taqman RT-PCR 检测，验证建立的所建方法效能。

结果 构建了蓝氏贾第鞭毛虫、溶组织内阿米巴双重 taqman RT-PCR 方法。8 例蓝氏贾第鞭毛虫镜检阳性样本 PCR 扩增结果均阳性，204 例蓝氏贾第鞭毛虫镜检阴性样本中 1 例 PCR 扩增结果为阳性，其余为阴性。3 例溶组织内阿米巴镜检阳性患者样本 PCR 扩增结果均为阳性，209 例溶组织内阿米巴镜检阴性的患者样本 1 例 PCR 扩增结果阳性，其余为阴性。通过扩增产物测序和 blast 分析确定了镜检阴性 PCR 阳性患者样本中扩增序列属于目标病原体，且临床信息也支持该诊断。

结论 设计了蓝氏贾第鞭毛虫、溶组织内阿米巴特异性引物、探针，建立了双重 taqman RT-PCR 检测体系。对引物进行 primer blast 分析，并使用其他致腹泻原虫及常见致腹泻细菌菌株进行 DNA 扩增，确定所建立方法与这些病原体不存在交叉反应。通过质粒确定两原虫最低检测限均约 30 拷贝。临床样本检测显示该方法可以检测出镜检阳性样本以及镜检漏检样本。

PU-3225

2013-2019 年上海某三级综合性医院重症监护室肺炎克雷伯菌分布及耐药性分析

尧荣凤
上海市杨浦区中心医院
同济大学附属杨浦医院

目的 了解上海某三级综合性医院重症监护室（Intensive Care Unit，ICU）肺炎克雷伯菌（Klebsiella pneumoniae，KPN）的分布和耐药性变迁，为临床合理使用抗菌药物提供参考。
方法 对同济大学附属杨浦医院重症监护室 2013 年 1 月-2019 年 12 月临床分离的肺炎克雷伯菌分布及耐药性进行回顾性分析。
结果 2013-2019 年共分离出肺炎克雷伯菌 653 株，主要来自呼吸道标本（80.7%）。主要分离自急诊科重症监护室（Emergency Intensive Care Unit，EICU） (37.5%) 和外科重症监护室（Surgery Intensive Care Unit，SICU）（38.6%）的患者。2013-2019 年该院 ICU 肺炎克雷伯菌中耐碳青酶烯类肺炎克雷伯菌(Carbapenemase resistant Klebsiella pneumoniae, CRKPN)共检出 199 株，检出率为 30.5%，从 2013 年至 2019 年肺炎克雷伯菌对亚胺培南和美罗培南的耐药率呈现逐年上升的趋势，从 2013 年的 10.2%和 11.3%，到 2019 的 58.6%和 60.0%。其中，MICU 病区 CRKPN 检测率（68.8%）最高。亚胺培南和美洛培南同时耐药肺炎克雷伯菌对多数抗菌药物的耐药率>80%，且对多数抗菌药物的耐药率明显高于非碳青霉烯类耐药菌株（P<0.05）。在不同病区中，CCU 和 SICU 病房患者中分离的肺炎克雷伯菌对受试的所有抗菌药物耐药率均明显低于 EICU、RICU 和 MICU（P<0.05）。从>65 岁患者分离的肺炎克雷伯菌对受试的所有抗菌药物耐药率均显著高于≤65 岁患者分离的肺炎克雷伯菌（P<0.05）。不同标本中，从尿液中分离的肺炎克雷伯菌对受试的大多数抗菌药物耐药率均明显的高于呼吸道标本和血液标本（P<0.05）。
结论 医院重症监护室分离的肺炎克雷伯菌耐药情况非常严峻，分离自不同年龄段、科室和标本的菌株对抗菌药物的耐药性相差较大，必须加强抗菌药物管理，继续开展病原菌分布及其耐药性监测，用于指导临床医师合理使用抗菌药物，控制耐药菌株在病区中的流行。

PU-3226

长沙某地区儿童艰难梭菌定植的相关研究

李艳明、刘文恩
中南大学湘雅医院

目的 了解长沙某地区健康儿童肠道艰难梭菌定植率及分子流行特征，为预防儿童艰难梭菌感染提供依据。
方法 收集 2020 年 3-6 月长沙市某地区小学 369 名儿童粪便标本各一份作为实验组，厌氧培养获得艰难梭菌的阳性定植率。回顾性分析 2017 年 1 月 1 日至 2020 年 1 月 30 日某大型教学医院住院儿童腹泻送检艰难梭菌筛查的数据，计算艰难梭菌的感染率。将临床分离的艰难梭菌非重复菌株 35 例作为对照组，对比分析实验组与对照组的毒素基因型、多位点序列分型。
结果 实验组 369 份标本中共分离到艰难梭菌 14 株，阳性定植率为 3.84%。分离得到的菌株主要为两类，其中 tcdA+tcdB+cdtA-cdtB-菌株占 57.14%（8/14），tcdA-tcdB-cdtA-cdtB-菌株占 42.86%

（6/14），产毒率为 57.14%（8/14）；2017 年 1 月 1 日至 2020 年 1 月 30 日共有 336 例腹泻儿童送检艰难梭菌筛查，共筛查出艰难梭菌 45 株（其中 10 株为重复菌株），阳性率为 13.4%。35 株非重复菌株中，tcdA+tcdB+cdtA-cdtB-菌株占 68.57%（24/35），tcdA-tcdB-cdtA-cdtB-菌株占 31.43%(11/35)，产毒率为 68.57%（24/35）。MLST 分型的分析结果表明，49 株艰难梭菌共检测出 16 种 ST 型别。其中 ST3(8 株)、ST2（7 株）、ST26（5 株）是主要型别，分别占 16.33%、14.29%、10.20%。在实验组分离的 14 株菌株中，共检测出 7 种 ST 型别，其中 ST2（4 株）、ST3（3 株）、ST8（3 株）为主要型别；在对照组分离的 35 株菌株中，共检测出 15 种 ST 型别，其中 ST3（5 株）、ST26（4 株）、ST35（4 株）ST37（4 株）为主要型别。

结论 长沙某小学健康儿童肠道艰难梭菌定植率远低于住院儿童腹泻患者的艰难梭菌定植率，但健康儿童和艰难梭菌感染儿童检出产毒株阳性率均较高，健康儿童与艰难梭菌感染儿童检出的艰难梭菌型别类似，艰难梭菌可能在儿童之间互相传播，无症状定植儿童可能作为移动传染源引起其他儿童的艰难梭菌感染。

PU-3227

利用实时荧光定量 PCR 快速检测肺炎克雷伯菌亚胺培南敏感性的方法

赵芯米、黄建胜、赵志钢
丽水市中心医院

目的 建立一种可在 2-3h 内快速检测肺炎克雷伯菌对亚胺培南敏感性的新方法。

方法 针对 4 种耐药基因 KPC、NDM、IMP、OXA48 以及膜孔蛋白 ompK36 突变序列设计 qPCR 引物及 Taqman 探针。收集丽水市中心医院分离的肺炎克雷伯菌 259 株，以 PCR 扩增产物测序结果为参考标准，验证 qPCR 检测目的基因的灵敏度和特异性；以微量肉汤稀释法测定菌株对亚胺培南的 MIC 值，结合 qPCR 结果，建立 qPCR 检测肺炎克雷伯菌对亚胺培南敏感性的判断标准。从丽水市疾控中心收集肺炎克雷伯菌 159 株，验证所建立方法的可靠性。

结果 丽水市中心医院的 259 株菌中，qPCR 检测 5 种目的基因的特异性和灵敏度均为 100%。比对药敏结果与 qPCR 结果发现，4 种耐药基因阴性的菌株 98.2%对亚胺培南敏感；KPC 阳性而 ompK36 突变阴性的菌株，96.8%MIC 值落在 4-16μg/mL；KPC 与 ompK36 突变双阳性的菌株，89.1%MIC≥32μg/mL。以此作为判断标准，丽水市疾控中心 159 株菌的检测结果显示，未检测出 4 种耐药基因的菌株 100%敏感；KPC 阳性而 ompK36 突变阴性的菌株，95.5%符合 MIC 值为 4-16μg/mL；KPC 与 ompK36 突变双阳性的菌株中，98.3%符合 MIC≥32μg/mL。

结论 本研究成功建立了一种肺炎克雷伯菌对亚胺培南敏感性快速检测的新方法，其操作简单，准确度高。

PU-3228

某医院肠杆菌科细菌耐药性及碳青霉烯类耐药菌株的分布

吴亚洲
上海市杨浦区中心医院（同济大学附属杨浦医院）

目的 了解我院 2015-2018 年临床分离肠杆菌科细菌耐药性，以及耐碳青霉烯类肠杆菌科细菌的分布及检出率变迁，为临床合理用药及医院感染防控提供依据。

方法 收集 2015-2018 年我院患者感染性标本中分离的肠杆菌科细菌，采用全自动细菌鉴定药敏系统对细菌进行鉴定和药物敏感性试验，并采用纸片扩散法（K-B）法进行补充药敏试验。

结果 近 4 年共检测出肠杆菌科细菌 6666 株，其中位列前 5 位的分别为大肠埃希菌 3189 株、肺炎克雷伯菌 1725 株、奇异变形杆菌 522 株、阴沟肠杆菌 358 株、粘质沙雷菌 297 株。大肠埃希菌中

产 ESBLs 菌株为 1897 株，产酶率 59.4%；肺炎克雷伯菌中产 ESBLs 菌株为 493 株，产酶率 28.6%。大肠埃希菌对氨苄西林及头孢唑林耐药率较高，分别为 84.6%和 76.6%；肺炎克雷伯菌对头孢唑林耐药率最高，为 60%。共检测出耐碳青霉烯类肠杆菌科细菌（ Carbapenem-resistant Enterobacteriaceae，CRE）498 株，检出率为 7.5%，其中肺炎克雷伯菌 339 株、大肠埃希菌 75 株、粘质沙雷菌 22 株、阴沟肠杆菌 16 株、奇异变形杆菌 11 株、其他 35 株;主要科室分布为神经外科（130 株），EICU（65 株），急诊观察室（53 株），SICU（43 株）。

结论 医院感染细菌中仍以肠杆菌科细菌为主，大肠埃希菌的 ESBLs 检出率较高且显著高于肺炎克雷伯菌，耐碳青霉烯类肠杆菌科细菌分离率逐年升高，且以肺炎克雷伯菌为主。

PU-3229

234 例甲型流感病毒感染调查

牛雷
东部战区总医院秦淮医疗区

目的 了解南京地区住院及社区甲型流感病毒的感染及分布情况。

方法 对 2017 年 3 月至 2019 年 3 月收治的 234 例疑似甲流感染患者咽拭子标本,采用免疫渗滤技术结合双抗体夹心法原理检测甲型流感病毒抗原。

结果 在 234 例咽拭子中, 甲型流感病毒抗原阳性 26 例, 甲型流感病毒感染率为 11.1%，其中男性为 14/166（8.4%），女性为 12/68（17.6%）；10 岁以下阳性 12 例；11～20 岁 2 例；21～30 岁 10 例；31～40 岁 2 例，41 岁以后未有检出阳性。

结论 甲型流感病毒感染男女有性别差异，年龄多分布在 10 岁以下和 21～30 岁的年轻人,并且春季 1～3 月感染为主。

PU-3230

EV71 致儿童手足口病患儿的肠道菌群分析

王珂、周红平、朱春晖、柯江维、刘发娣
江西省儿童医院

目的 探讨 EV71 感染后不同的临床类型的手足口病患儿肠道菌群的丰度、种群结构、群落等变化，以获取 EV71 感染的轻症与重症患儿肠道菌群差异，为手足口病的治疗和特效药物的研发提供理论依据。

方法 筛选经核酸检测 EV71 阳性的手足口病确诊患儿，根据疾病的严重程度分为重型组 S、和轻型组 M、以及健康对照组 N，采集患者发病 3 天内的大便标本，提取其基因组 DNA，经二代测序对合格样本建立文库，并分析测序结果。

结果 儿童肠道微生物群中含量最多的菌群在门水平上包括拟杆菌门(Bacteroidetes)、厚壁菌门(Firmicutes)、变形菌门(Proteobacteria)、放线菌门(Actinobacteria)、疣微菌门(Verrucomicrobia)、梭杆菌门(Fusobacteria)、TM7、广古菌门(Euryarchaeota)、互养菌门(Synergistetes)、蓝藻菌门(Cyanobacteria)，其中拟杆菌门、厚壁菌门、变形菌门是儿童肠道微生物群落中最丰富的菌群。拟杆菌门相对丰度在正常儿童中均值为 47.72%，而手足口病患儿中轻症为 57.33%，重症为 67.44%，呈逐渐上升的趋势；而厚壁菌门和变形菌门的相对丰度则是随着疾病严重程度的加重，相对丰度逐渐降低。

结论 随着手足口病患儿的临床症状加重，拟杆菌门比例增加，厚壁菌门和变形菌门比例减少，其肠道菌群多样性降低，菌群失调加重。

PU-3231

艾滋病合并马尔尼菲篮状菌病的体外药敏试验及临床治疗效果分析

高丽、张桂仙、樊红丽、李正伦、谢祺
云南省传染病医院

目的 分析艾滋病（AIDS）合并马尔尼菲篮状菌（TM）感染的体外药敏试验结果及临床治疗效果，为临床合理用药提供依据。
方法 收集 2016 年 2 月至 2018 年 11 月云南省传染病医院收治的 119 例 AIDS 合并 TM 感染患者的临床病历资料，分析患者的人口学特征、标本类型、TM 体外药敏试验结果及临床治疗效果。
结果 119 例病人中，男性病人人数是女性病人人数的 2.61 倍。平均年龄为 37.08 岁，年龄范围为 3~70 岁，以青壮年为主。病人感染 HIV 的传播途径中性传播人数居多，共 105 人，占总人数的 88.24%。检出最多标本类型是血液和骨髓，共占总样本数的 88.24%。CD4+T 淋巴细胞计数为 39±40cells/μl，大多数病人处于 AIDS 晚期。两性霉素 B、伊曲康唑和伏立康唑对马尔尼菲篮状菌的敏感性均为 100%。119 例患者中有 8 例未接受抗真菌治疗患者均死亡，111 例接受了抗真菌治疗，其中 105 例治疗好转，治疗好转率 94.59%（105/111）。两性霉素 B 治疗组和伏立康唑治疗组好转率比较差异无统计学意义（P=0.317，χ2=0.859）。
结论 AIDS 合并 TM 感染好发于 CD4+T 淋巴细胞计数低于 50cells/μl 的患者，临床表现复杂多样。云南省艾滋病合并马尔尼菲篮状菌病推荐选择两性霉素 B、伏立康唑和伊曲康唑治疗，尽量避免使用氟康唑和氟胞嘧啶。

PU-3232

肺炎链球菌抗原快速检测在痰液中的临床价值

蒋瑶[1,2,3]、郭杨柳[1,2,3]、廖涛[1,2,3]、岳瑾熙[1,2,3]、谢宁[1,2,3]
1. 川北医学院附属医院
2. 川北医学院医学检验系
3. 川北医学院转化医学研究中心

目的 社区获得性感染（CAP）是验证严重威胁人类健康的感染性疾病之一，其中肺炎链球菌是首要致病菌，但其常规痰培养检出率并不高，故探讨利用免疫层析法检测痰液中肺炎链球菌抗原对肺炎链球菌感染的诊断价值。
方法 分离痰标本中与肺炎链球菌同属的草绿色链球菌、星座链球菌，和呼吸道标本分离菌中前五位菌种包括肺炎克雷伯菌、鲍曼不动杆菌、铜绿假单胞菌、金黄色葡萄球菌和嗜麦芽窄食单胞菌，以及 CAP 中常见的流感嗜血杆菌和卡他莫拉菌，后配成菌悬液验证 BinaxNOW 试剂盒的特异性；利用 BinaxNOW 试剂盒检测 20 例肺炎链球菌培养阳性的原始痰液标本，比较两种方法的一致性。
结果 免疫层析法检测痰标本中分离得到的草绿色链球菌、星座链球菌、肺炎克雷伯菌、鲍曼不动杆菌、铜绿假单胞菌、金黄色葡萄球菌和嗜麦芽窄食单胞菌、流感嗜血杆菌和卡他莫拉菌结果均为阴性；免疫层析法检测 20 例肺炎链球菌培养阳性的原始痰液标本的阳性率为 95%（19/20）。
结论 免疫层析法在 CAP 中的肺炎链球菌抗原检测中具有较好的特异性，并且与痰培养结果有较好的一致性。

PU-3233

革兰阴性杆菌与真菌感染患者血小板参数变化的对比分析

梅秋雁、姜波
昆明医科大学第一附属医院

目的 探讨革兰阴性杆菌、真菌感染对血小板的影响 ，为感染性疾病的临床诊断、病情评估 、预防治疗提供试验依据。
方法 收集 2018 年 1 月-2018 年 12 月昆明医科大学第一附属医院革兰阴性杆菌感染患者 30 例 、真菌感染患者 30 例的病例资料；另外选择同期参加健康体检者 60 例病历资料为对照组，比较血小板的参数，包括血小板数量、血小板平均体积 (MPV)、血小板压积 (PCT)、血小板体积分布宽度(PDW)四项的变化，从而探讨革兰阴性杆菌、真菌感染对血小板的影响。
结果 试验组患者均出现血小板数量减低 、MPV 增大、PCT 减低 、PDW 增大，与对照组比较 ，差异均有统计学意义 (P<O.05)，比较革兰阴性杆菌 、真菌感染患者血小板数量、PCT、MPV、PDW 的变化具有统计学差异(P< O．05)，革兰阴性杆菌感染患者变化尤为明显；各试验组 PLT 数目与 MPV 均呈显著负相关，且相关系数均有降低，其中革兰阴性杆菌下降最明显。
结论 革兰阴性杆菌、真菌感染不单只会造成血小板的数量减低 ，还会造成 MPV 增大 、PCT 减低 、PDW 增大，且革兰阴性杆菌感染患者变化较明显。血小板计数简便而且容易操作，能比较正确以及敏感地反映出感染状态，可借助血小板计数以及相关参数检测为临床感染性疾病的诊断及鉴别诊断提供有效参数。

PU-3234

重庆市 2011-2019 年尿路感染肺炎克雷伯菌耐药趋势分析

丁艳辉
重庆医科大学附属第一医院

目的 分析自尿路感染（UTIs）患者尿液标本中分离的肺炎克雷伯菌（K.pneumoniae）对临床常用抗生素的耐药特点以及趋势。
方法 收集重庆市某教学医院 2011 年至 2019 年 UTIs 分离 K.pneumoniae 的实验室数据进行回顾性分析。
结果 自 UTIs 患者尿液样本分离的 17966 株非重复菌株中，共鉴定出 1543 株 K.pneumoniae，感染率仅次于大肠埃希菌（E.coli），并在 2013 年出现 K.pneumoniae 的感染高峰。自 2011 年至 2019 年，产超广谱 β-内酰胺酶（ESBL）的 K.pneumoniae 占比从 2011 年的 48.4%下降到 2019 年的 32.9%，而对碳青霉烯类抗生素的耐药率自 2.2%急升至 18.0%，其中 2017 年分离到的耐碳青霉烯 K.pneumoniae 高达 22.6%，伴随较低的 ESBL 产生率（30.9%）；K.pneumoniae 对哌拉西林/他唑巴坦和头孢吡肟的耐药率分别从 4.4%和 18.2%上升到 25.7%和 30.5%；此外，K.pneumoniae 对碳青霉烯类和丁胺卡那霉素的耐药率在 2017 年达到高峰后逐年下降，而对头孢他啶和氨曲南的耐药率相对稳定，分别在 21.8% - 35.6%和 32.2% - 39.4%之间波动。
结论 自 UTIs 患者尿液标本中分离的 K.pneumoniae 对碳青霉烯类抗生素的耐药率呈上升趋势伴随 ESBL 产生率的下降，需对其进行持续监测。

PU-3235

CRISPR-Cas9 基因编辑技术在念珠菌中的应用研究进展

于淑颖、徐英春
中国医学科学院北京协和医院

近年来，念珠菌感染已经成为严重威胁全球健康的疾病，亟需深入理解真菌病原体的生物学和病理生理学，并阐明耐药机制。因此，对于高效基因操作工具的需求十分迫切。本文旨在对 CRISPR-Cas9 系统的工作原理和其在念珠菌中的应用进行系统的综述，希望 CRISPR 的发展和应用能够有助于微生物学家解决念珠菌的致病机理和耐药机制等多方面问题，从而进一步促进新的治疗策略的开发。本文提供了 CRISPR-Cas9 基因编辑技术在念珠菌中应用的最新进展，灵活、有效的 CRISPR-Cas9 系统对医学真菌学领域产生了巨大的影响。在实验室方面，通过促进基因操作技术的发展，为探究真菌生物学和致病机制、剖析毒力因子的作用、调查新的药物潜在靶点以及研究宿主和病原体间的相互作用奠定了基础；在临床方面，进一步改善了真菌感染的诊断策略和抗真菌耐药的监测手段。此外，目前该系统在模式真菌中应用可以进一步推广至其他致病真菌，从而研究宿主和真菌间的相互作用或者解决念珠菌耐药等问题。

PU-3236

糖尿病肾病患者肠道菌群变化及生物标志物

伦恒忠
泰安市中心医院

人体拥有一个非常复杂的共生微生物群落，它们定殖在肠道、泌尿生殖道、呼吸道和其他屏障组织中，参与机体的发育以及人体生理功能的形成和维护，维持体内稳态，被称作人体的另外一个器官。肠道拥有人体内数量最多、构成最复杂的微生物群落。研究表明，肠道菌群在人体能量摄入、营养支持、代谢平衡、炎症、神经激素反应、免疫系统发育和免疫调节中起着重要作用。糖尿病肾病是由糖尿病所致的慢性肾脏疾病, 是糖尿病的主要微血管并发症之一，也是终末期肾病最常见的病因。大量研究指出：肠道微生物菌群与许多疾病有关，包括肥胖、2 型糖尿病和非酒精性脂肪性肝病等。最近研究表明糖尿病肾病 的发生发展与肠道菌群密切相关。

研究目的 本课题拟利用分子生物学方法探索糖尿病肾病患者肠道菌群的改变，识别与糖尿病肾病相关的标志性菌属,为进一步研究通过调节肠道菌群治疗糖尿病肾病提供理论基础。

研究方法 1. 招募糖尿病肾病患者和健康志愿者，收集入组者新鲜粪便标本，使用试剂盒提取粪便基因组 DNA，进行高通量测序。

2. 使用物种组成分析、主成分分析线性判别分析效应尺寸分析等多种生物信息分析方法来比较糖尿病肾病患者和正常人群肠道菌群的差异。

3. 制作受试者工作特征曲线鉴别糖尿病肾病患者和正常人群差异肠道菌属中最好的生物标志物。

研究结果 糖尿病肾病患者和健康人群的肠道菌群结构存在差异。糖尿病肾病患者肠道菌群分布发生了显著变化，硬壁菌门占比明显降低，拟杆菌门（Bacteroidetes）和变形菌门占比显著增加。

研究结论 与健康人群相比糖尿病肾病患者肠道菌群结构发生了改变。

PU-3237

Histone Acetylation Regulator Gcn5 Mediates Drug Resistance and Pathogenicity in Candida glabrata

Shuying Yu 、Yingchun Xu
Peking Union Medical College, Chinese Academy of Medical Sciences

Background Candida glabrata was the common pathogen causing invasive candidiasis. C. glabrata displayed an inherently reduced susceptibility to azoles, meanwhile, with a staggering rising in echinocandin resistance. Gcn5 is one of the most characterized fungal KATs, which is necessary for transcription regulation in eukaryotes. Here, we explore the role of GCN5 in antifungal resistance and pathogenicity in C. glabrata by genetic ablation of GCN5, as well as the expression dynamics of critical genes and pathways.
Methods The GCN5 gene in C. glabrata strain ATCC 2001 were knocked out and restored by using the Alt-R CRISPR-Cas9 system. Antifungal susceptibility testing and serial dilution growth assays were performed to detect the susceptibilities against antifungal drugs and stress agents of C. glabrata lacking GCN5. Time-kill kinetics of WT (ATCC 2001) strain and gcn5Δ strain against micafungin and fluconazole were carried out. Fungicidal and fungistatic activity were calculated, and resistant colony frequency and resistance-conferring mutations were evaluated. For western blot analysis, the effect of GCN5 deletion for the level of histone acetylation was detected. By transcriptomic analysis, we explored the regulatory mechanism of GCN5 deletion on drug resistance and virulence for C. glabrata. THP-1 macrophage infection assays were performed for detecting the viability of C. glabrata inside THP cells.
Results Deletion of GCN5 in WT Background increases 2 to 4-fold susceptibility for echinocandins, 2-fold for azoles and SCY048, more importantly, more than 8-fold for FK506 (4 μg/ml) + micafungin and APX001A. Deletion of GCN5 appeared to complete or near complete reverse the Fks-mediates echinocandins resistance by FK506 in 4 μg/ml. Disruption of GCN5 dramatically enhanced the fungicidal or fungistatic activity of micafungin and fluconazole. Reduced colony frequency and gain-of-function mutations detected from this dynamic experiment. Compared to the WT and gcn5Δ::GCN5 strain, the acetylation level of H3K9 and H3K14 in gcn5Δ strain were around 0.6-fold and 0.45-fold to those in WT strain. GCN5 deletion changes the landscape of several transcriptional networks by regulating specific functional gene group. The distribution of genes corresponding to GCN5 deletion major enriched in transmembrane transport, transmembrane transporter activity, component of membrane and plasma membrane and cell wall. Lack of GCN5 unable to drive the expression of transmembrane transporter activity genes, cell wall component synthesis genes and multidrug resistance transporters genes. Cells lacking GCN5 need to mobilize much more genes to sustain life upon micafungin pressure. Most of the significantly changed genes in gcn5Δ are down-regulated in response to micafungin treatment, which are major associated with cell wall biosynthesis. gcn5Δ cells were much more sensitive to killing by THP cells. Loss of GCN5 significantly reduced the viability of C. glabrata inside THP cells.
Conclusions C. glabrata histone acetyltransferase GCN5 plays a critical role in the antifungal resistance, stress response and pathogenesis. Loss of GCN5 attenuated antifungal drug resistance and pathogenicity in C. glabrata. We propose Gcn5 could be a promising candidate target for new drug discovery or therapeutic intervention to combat fungal infections.

PU-3238

基于 16S rDNA 测序分析血吸虫感染对宿主肠道菌群的影响

宋秋月
襄阳市第一人民医院

目的 研究日本血吸虫不同感染程度对小鼠肠道菌群的影响，寻找日本血吸虫感染潜在的肠道菌群标志物。
方法 将 15 只 6 周龄雄性 BALB/c 小鼠随机分为正常对照组（n=5）、轻度感染组（n=5）、重度感染组（n=5）。其中，轻度感染组每只小鼠感染 5±2 条日本血吸虫尾蚴，重度感染组每只小鼠感染 60±2 条日本血吸虫尾蚴。感染第 7 周处死小鼠，剖开腹腔切下一块肝左叶和一段结肠组织用于制作病理切片，同时在无菌条件下收取小鼠结肠内容物，提取 DNA 后利用 16S rDNA 测序技术进行微生物多样性分析。
结果 日本血吸虫感染小鼠肝脏、结肠中可见明显的虫卵肉芽肿和纤维化病变。小鼠肠道菌群的 α 多样性分析显示，重度感染组 Shannon 指数显著低于正常对照组或轻度感染组，差异有统计学意义（P = 0.0068；P = 0.015）；轻度感染组或重度感染组 Simpson 指数显著高于正常对照组，差异有统计学意义（P = 0.047；P = 0.012）。PCoA 分析显示，轻度感染组与正常对照组小鼠肠道菌群的群落组成比较接近，而重度感染组则与正常对照组的群落组成明显不同。小鼠的肠道菌群主要由厚壁菌门、拟杆菌门和变形菌门组成，随着感染程度的加重，变形菌门的相对丰度增加。Lachnospiraceae_NK4A136_group 菌属的相对丰度随着感染程度的加重而降低；Alistipes 和 Bacteroides 菌属的相对丰度随着感染程度的加重而增加。LEfSe 分析显示，Lachnospiraceae_NK4A136_group、 Desulfovibrio、Alistipes、Lactobacillus 菌属是正常对照组与感染组之间具有显著差异的菌属。
结论 日本血吸虫感染小鼠肠道菌群的物种分布、多样性和群落组成均发生了改变，而且这种改变会受到感染程度的影响； Lachnospiraceae_NK4A136_group 、 Desulfovibrio 、 Alistipes 、 Lactobacillus 菌属可作为日本血吸虫感染的潜在的生物标志物。

PU-3239

淋病奈瑟菌耐药性分析及蛋白质谱聚类应用初探

卢赞
昆明市第一人民医院

目的 了解本地区淋病奈瑟菌常用抗菌药物敏感性，探索蛋白聚类在细菌同源性分析中的应用；
方法 回顾分析该院 2018 年 5 月至 2020 年 12 月分离的 154 株淋病奈瑟菌药物敏感性，利用质谱仪配套软件 Biotyper3.4 对 65 株淋病奈瑟菌进行聚类分析，比较引入标准菌株和数据库内淋病奈瑟菌 MSP 后聚类图变化；
结果 未发现头孢曲松耐药菌株，头孢菌素类敏感性较好，青霉素均不敏感，环丙沙星耐药率为 96.8%，四环素耐药率为 83%。65 株临床分离淋病奈瑟菌聚类形成 3 个大簇，不同时间分离株散在分布于各簇。引入 ATCC19424、ATCC49226 和一株随机数据库内 MSP 后，聚类图无明显变化，上述 3 株菌分别聚类入已形成的 3 大簇。随机引入多株数据库内 MSP 后，聚类图明显改变，将所有菌株聚类为 2 个大簇；
结论 头孢曲松可做为本地区淋病奈瑟菌感染的首选用药，青霉素、喹诺酮类和四环素类应避免使用。利用 MALDI-TOF MS 进行细菌蛋白质谱聚类，可以反映菌株之间的相对差异，但不能量化差异大小。

PU-3240

2018-2020 年我院细菌耐药检测结果分析

吴迪[1]、吴亚洲，尧荣凤，方慧，任圣洁[2]
1. 上海市杨浦区中心医院（同济大学附属杨浦医院）
2. 同济大学附属杨浦医院

目的 对我院近两年细菌耐药监测结果进行统计分析，为本院临床合理使用抗生素及院内感染防控提供理论依据。
方法 收集 2018 年至今我院患者感染性标本中分离的病原菌，采用全自动细菌鉴定药敏系统对细菌进行鉴定和药物敏感性试验，并采用纸片扩散法（K-B）法进行补充药敏试验。用 WHONET 5.6 软件进行分析。
结果 2018 年至今剔除同一患者同一部位重复菌株共分离病原菌 7802 株，其中革兰阴性菌 5736 株（73.5%），革兰阳性菌 2066 株（26.5%）。耐甲氧西林金黄色葡萄球菌(MRSA)和耐甲氧西林凝固酶阴性葡萄球菌(MRCNS)的检出率分别为 67.8%和 81.1%，检出率较 2017 年均有所上升，未发现万古霉素、利奈唑胺和替考拉宁不敏感的葡萄球菌。大肠埃希菌、肺炎克雷伯菌和铜绿假单胞菌分别为 1402 株(24.4%)、1126 株(19.6%)和 1060 株(18.5%)，为革兰阴性菌分离率前 3 位。大肠埃希菌，肺炎克雷伯菌和奇异变形杆菌的 ESBLs 检出率分别为 58.9%，21.6%和 55.4%，产 ESBLs 株对测试药物的耐药率均比非产 ESBLs 株高。大肠埃希菌对三代头孢菌素中的头孢噻肟和头孢曲松的耐药率分别为 63.7%和 65.2%；肺炎克雷伯菌对三代头孢菌素中的头孢噻肟和头孢曲松的耐药率分别为 45%和 46.5%，较大肠埃希菌稍低。肠杆菌科细菌对亚胺培南和美罗培南的耐药率为 10.5%和 10.2%，虽仍是很敏感，但较 2017 年的 8.5%和 8.2%有所升高。鲍曼不动杆菌对亚胺培南和美罗培南的耐药率为 45.9%和 46.5%。与 2017 年耐药数据相比，铜绿假单胞菌中广泛耐药株的检出率有所上升。
结论 我院临床分离菌的耐药性仍呈增长趋势，应加强医院感染防控措施和抗菌药物临床应用管理措施，继续做好细菌耐药性监测工作。

PU-3241

分离胶离心法结合 MALDI-TOF MS 直接鉴定阳性血培养物的研究

卢赞
昆明市第一人民医院

目的 评价分离胶离心法结合 MALDI-TOF MS 直接鉴定阳性血培养物的结果符合性。
方法 对 204 份阳性血培养物分别用传统培养法和离心处理后 MALDI-TOF MS 直接鉴定法检测，以传统法结果为标准，观察直接法结果的符合性。
结果 204 份阳性血培养物经传统法检测包括 189 份单一微生物生长瓶、10 份复数菌生长瓶及 5 份假阳性瓶，共检出微生物 41 种，鉴定分值均数为 2.299。分离胶离心法结合 MALDI-TOF MS 直接检测，199 份给出了鉴定结果，5 份无结果。其中种符合占 68.6%，鉴定分值中位数 2.054；属符合占 6.4%，分值中位数 1.588；染色符合占 7.8%，分值中位数 1.295；完全不符合占 14.7%，分值中位数 1.182；无结果占 2.5%。染色及以上符合结果鉴定分值均数 1.916，与培养后鉴定得分均值差异有统计学意义（P<0.05）。结果符合性分布与培养瓶类型无关（P>0.05），阴性菌与阳性菌之间差异无统计学意义（P>0.05），微生物类型总体间差异有统计学意义（P<0.05）。
结论 分离胶离心法结合 MALDI-TOF MS 直接鉴定阳性血培养物与传统培养法结果有较好的符合性，实验室建立标准的操作和结果评价程序并结合培养液涂片结果，该方法可为临床血流感染的早期精准治疗带来帮助。

PU-3242

感染科 312 例血流感染患者病原菌分布及耐药性分析

金菲
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨感染科血流感染患者病原菌分布及其药物敏感性，指导临床合理使用抗生素。
方法 回顾性分析南京医科大学第一附属医院感染科 312 例血流感染患者临床资料、实验室指标（白细胞计数、中性粒细胞百分比、C-反应蛋白、降钙素原）及血培养结果。
结果 2014 年-2018 年感染科患者共送检血培养标本 6370 份，同一患者相同菌株只分析第一株菌，共分离病原菌 312 株，血培养阳性率为 4.90%。312 株病原菌中革兰阴性菌 194 株，占 62.2%；革兰阳性菌 109 株，占 34.9%；真菌 9 株，占 2.9%。病原菌分离前五位分别为大肠埃希菌（77 株，24.7%）、肺炎克雷伯菌（46 株，14.7%）、链球菌（43 株，13.8%）、布鲁氏菌（35 株，11.2%）、金黄色葡萄球菌（28 株，9.0%）。G-菌血流感染患者血清 PCT 水平高于 G+菌患者，差异有统计学意义（P=0.028）。大肠埃希菌和肺炎克雷伯菌的抗菌药物敏感性较好，二者对亚胺培南、美罗培南的敏感性均在 95%以上。分离到耐甲氧西林的金黄色葡萄球菌（MRSA）12 株，占 42.86%（12/28），未发现对万古霉素和利奈唑胺耐药的链球菌和金黄色葡萄球菌药物。
结论 感染科血流感染患者以 G-菌为主，但布鲁菌和链球菌分离率高，G-菌感染患者血清 PCT 水平高于 G+菌患者。感染科发热血流感染患者总体耐药率不高。

PU-3243

MALDI-TOF-MS 快速鉴别 MRSA 和 MSSA 的临床研究

白秀伟[1]、曾春回[2]
1. 北京华信医院（清华大学第一附属医院）
2. 河北北方学院

目的 探讨基质辅助激光解吸/电离飞行时间质谱仪（MALDI-TOF-MS）快速鉴别甲氧西林耐药金黄色葡萄球菌（MRSA）及甲氧西林敏感的金黄色葡萄球菌（MSSA）的可行性，为临床提供一种快速简便的方法，方便指导临床用药。
方法 用 MALDI-TOF-MS 鉴定的 48 株金黄色葡萄球菌，经 Kirby-Bauer 法确认为 MRSA 和 MSSA 后，从质谱仪上查看各个菌株的特征峰，然后利用 SPSS 软件对特征峰进行聚类分析，聚类分析后随机选取 59 株金黄色葡萄球菌对其进行外部验证，验证其符合率。
结果 经 Kirby-Bauer 法确证经质谱仪鉴定为金黄色葡萄球菌的 48 株菌株，其中 16 株是 MSSA，32 株是 MRSA，48 株菌株的特征峰经过 SPSS 软件聚类分析后，聚类为 2 类，能够将 MRSA 和 MSSA 区分开来，外部验证的 59 株金黄色葡萄球菌，经 Kirby-Bauer 法确证为 37 株为 MRSA，22 株为 MSSA，与仪器鉴别结果符合率为 MRSA 72.97%（27/37），MSSA 68.18%（15/22）。
结论 MALDI—TOF—MS 能够快速鉴别 MRSA 和 MSSA，具有操作简便、耗时短等优点。

PU-3244

白念珠菌和非白念珠菌血症的流行病学、危险因素与预后

金菲
江苏省人民医院（南京医科大学第一附属医院）

目的 本研究旨在探讨白念珠菌和非白念珠菌血症的流行病学、危险因素和预后。

方法 回顾分析南京医科大学第一附属医院 2016 年 1 月-2020 年 12 月 171 例念珠菌血症患者临床资料。通过卡方检验和二元 Logistic 回归分析对白念组和非白念组血流感染患者的临床危险因素进行比较，确定与念珠菌感染有关的危险因素，且进一步分析与念珠菌血症预后相关的独立危险因素。
结果 光滑念珠菌是最常见的分离菌（28.65%），其次为白念珠菌（28.07%）、热带念珠菌（21.64%）、近平滑念珠菌（18.13%）和其他念珠菌（3.51%），非白念珠菌占 71.93%（123/171）。多因素分析显示机械通气（OR 2.588; 95%CI:1.119-5.987; P=0.026）是白念珠菌血症的独立危险因素。所有念珠菌对两性霉素 B 均敏感，白念珠菌、光滑念珠菌和近平滑念珠菌对氟康唑的敏感率分别为 91.8%、91.7%和 90.3%，热带念珠菌的耐药性相对较高。171 例念珠菌血症患者中，有 48 例死亡，病死率为 28.07%。多因素分析显示年龄（OR 1.027; 95%CI:1.004-1.050; P=0.022）、深静脉置管（OR 2.489; 95%CI:1.033-5.996; P=0.042）和入住 ICU（OR 2.921; 95%CI:1.020-8.362; P=0.046）是与死亡率相关的独立危险因素。
结论 我院念珠菌血症的念珠菌分布与其他医院存在差异。除热带念珠菌外，绝大多数念珠菌对抗真菌药物敏感性较高，为经验抗真菌药物的选择提供有用的信息。

PU-3245

替加环素耐药外排泵 tmexCD-toprJ 在不同物种中多种传播机制的探究

孙世俊、王启、靳龙阳、王辉
北京大学人民医院

目的 探究不同菌株替加环素耐药菌株中的耐药机制，以及不同物种中 tmexCD-toprJ 的传播结构，以及流行趋势。
方法 2018 年至 2019 年收集全国 26 个省市多家教学医院内收集碳青霉烯耐药的肠杆菌科细菌，从中分离替加环素耐药肠杆菌科细菌。通过 PCR 筛选其中 tmecXD-oprJ 阳性菌株，提取完整基因组 DNA，高通量短读长测序通过 Illumina 平台进行，同时利用 ONT 平台对长读长进行测序，测序结果利用 unicycler 混合二三代数据进行组装。耐药基因通过 resfinder 进行确认。对比下载数据库中数据，建立进化树。利用 BLAST 对发现的 tmexCD-oprJ 外排泵进行分型，并利用吉普森组装构建表达质粒，并在大肠杆菌 DH5α 中验证其功能。
结果 共在全国四个省市病人身上分离到 5 株不同分型的 tmexCD-oprJ 阳性菌株，其中在 kpn 和 kox 中新分离出两种 tmexCD1-toprJ1 和 tmexCD2-toprJ2 的新的亚型，实验证明新的亚型同样可以介导大肠杆菌对替加环素药品水平有四到八倍提升；另外有两株与 blaNDM 共存于同一质粒上，通过对比其遗传背景鉴定出主要的两条不同的耐药传播途径，并通过对于数据库对其不同分型的耐药传播进行分析。
讨论 替加环素耐药基因的传播，大大降低了临床重症感染患者可选择的抗生素用药范围。质粒介导的替加环素耐药外排泵 tmexCD-toprJ 自首次发现至今已被广泛报道，其耐药性的传播机制也多有不同，探究其耐药机制的传播途径对于耐药防控意义深远。

PU-3246

我院常见念珠菌快速鉴定与药敏分析

任圣洁
同济大学附属杨浦医院

目的 了解临床念珠菌的菌种分布及耐药谱，为合理使用抗真菌药物提供依据。
方法 对 2015 年~2019 年临床标本中分离出的念珠菌采用真菌快速培养鉴定药敏试剂进行鉴定和测定菌株对 10 种抗真菌药物的敏感性。

结果 共分离出 12848 株念珠菌，最常见的菌种依次为白色念珠菌占 67.62%，光滑念珠菌占 19.95%，热带念珠菌占 10.26%， 克柔念珠菌占 1.66%。以痰液最多，占全部标本 69.87%，其次是尿液占 14.94%。在痰液中主要是白色念珠菌（72.32%），其次是光滑念珠菌（18.53%），而尿标本主要是白色念珠菌（59.38%），其次是热带念珠菌（18.59%）和光滑念珠菌（17.86%）。粪便和血液标本是以白色念珠菌和光滑念珠菌为主。药敏结果显示两性霉素 B、制霉菌素和 5-氟胞嘧啶对四种常见念珠菌抗菌活性好，耐药率均<4%(除克柔念珠菌)；三唑类对四种常见念珠菌平均耐药率>35%；咪唑类（除酮康唑外）对四种常见念珠菌平均耐药率>53%。白色念珠菌对大多数的抗真菌药物的耐药率要明显低于非白念珠菌 P<0.05）。痰液中的白色念珠菌对伊曲康唑和咪唑类（益康唑、咪康唑、克霉唑）耐药率和热带念珠菌对三唑类耐药率均明显低于粪便标本（P<0.05），克柔念珠菌对制霉菌素、伏立康唑、伊曲康唑、酮康唑和克霉唑耐药率均明显低于尿标本（P<0.05）。

结论 本院临床分离的念珠菌以白色念珠菌为主，其次为热带念珠菌。非白念珠菌对大多数的抗真菌药物的耐药率要明显高于白色念珠菌，不同来源的同种念珠菌对常用抗真菌药耐药性也有不同，所以实验室应加强对真菌菌种的鉴定和耐药性的持续监测。临床一旦发生真菌感染，应尽早监测真菌的耐药性，按抗真菌药敏结果，合理使用抗真菌药物，减少医院感染、多重耐药和深部真菌感染的发生。

PU-3247

Cefazolin and Imipenem Enhance AmpC Expression and Resistance in NagZ-dependent manner in Enterobacter cloacae

Xianggui Yang[1]、Yuanxiu Zhong[2]、Fuying Wang[2]、Ying Xu[1]
1. the First Affliated Hospital of Chengdu Medical College
2. 成都医学院

Enterobacter cloacae (EC) is one of the most common opportunistic pathogens causing various infections in human, which is inherited resistant to the 1st- and 2nd- generation cephalosporins due to its inducible chromosomal AmpC β-lactamase (AmpC). However, whether β-lactams antibiotics enhance EC resistance remains unclear. In this study, we found that subinhibitory concentrations (SICs) of cefazolin (CFZ) and imipenem (IMP) can promote the expression of AmpC and enhance resistance to β - lactams through b-N- acetylglucosaminidase (NagZ) in EC clinical isolate. Our data indicated that AmpC was significantly up-regulated in EC in response to SICs of CFZ and IMP. In nagZ knockout EC (ΔnagZ EC), we found that the resistance to β - lactam antibiotics was attenuated and the effect of CFZ and IMP on induction of AmpC was completely abrogated, ectopic expression of NagZ can rescue the induction of CFZ and IMP on AmpC and enhance resistance in ΔnagZ EC model. More interestingly, CFZ and IMP could induce the expression of other target genes of AmpR (a global transcriptional factor that regulates hundreds of genes including ampC) in NagZ-dependent manner, which suggested that the promotion of AmpC by CFZ and IMP is mediated NagZ-AmpR pathway. Our data highlights that NagZ is the key factor for CFZ and IMP to induce AmpC expression and enhance resistance and that CFZ and IMP must be used carefully because they might aggravate the resistance of EC. At the same time, this study further improves the mechanism of resistance of EC.

PU-3248

Antimicrobial resistance of Acinetobacter baumannii isolated from the clinical laboratory of the First hospital of Jilin University from 2020 to 2021

Xufeng Ji、Chun Yang
The first hospital of Jilin University

ObjectiveThe main objective of this study is to investigate the antimicrobial resistance of Acinetobacter baumannii. To provide the theoretical guidance for the rational use of antimicrobial agents and the scientific basis for control the drug-resistant strains.
Methods1. The Acinetobacter baumannii were isolated from the clinical laboratory of the First hospital of Jilin University.
2. The resistance of Acinetobacter baumannii for 20 antimicrobial agents were determined using paper disk method and minimum inhibitory concentration（MIC）method, analyzed the drug-resistant spectrum. The results were evaluated based on Clinical and Laboratory Standards Institute (CLSI-M100-S29).WHONET-5.6 software was used to analyze the drug resistance data.
Results1. Most of 912 Acinetobacter baumannii strains were collected from abdominal fluid (14 strains), broncho-alveolar lavage (54 strains), bile (4 strains), blood (15 strains), ear (1 strains), sputum (765 strains), urine (17 strains), shunt fluid (7 strains), secretion (2 strains) during the one year.
2. The drug-resistant rates of the 912 isolated strains to meropenem and imipenem were 52.8% and 51.9% respectively. 912 strains were all resistant to cefazolin, cefotetan, cefuroxim. The rates of Acinetobacter baumannii resistant to cefatriaxone, cefepime, were 99.3% and 51% respectively. The rates of Acinetobacter baumannii resistant to levofloxacin and ciprofloxacin were 19.3% and 50.6% respectively. The rates of Acinetobacter baumannii resistant to piperacillin/tazobactam and amikacin were 54.8% and 36.4% respectively.
3. Nine hundred and twelve strains of Acinetobacter baumannii mainly from the surgical ward, 259 case from ICU, 2 case of infectious diseases department, 82 from neurology, 7 from pediatric respiratory medicine, 62 strains from department of respiration, 105 strains from neurosurgery, 40 strains from emergency department, 14 strains from oncology department, 21 strains from hepatobiliary pancreatic surgery, 10 strains from urinary surgery, 33 strains from gastrointestinal surgery, 9 strains from neonatal department, three strains from the outpatient department, three strains from trauma department of orthopedics, two strain from obstetrical department and only one strains from otolaryngology.
Conclusions1. Nine hundred and twelve strains of Acinetobacter baumannii were screened by analyzing the drug resistance spectrum in the research, which has different resistant rates to different antimicrobial agents.
2. Most of the 912 Acinetobacter baumannii were isolated from sputum. And the ICU is the department that isolated most numbers of Acinetobacter baumannii. The rate of Acinetobacter baumannii resistant to levofloxacin is lowest. Monitoring of the antimicrobial resistance of Acinetobacter baumannii should be strengthened. The change of the antimicrobial resistance should be investigated in order to direct rational drug usage in clinic.

PU-3249

Serum ceramide concentrations are associated with depression in patients after ischemic stroke-A two-center case-controlled study

Hong Lv
首都医科大学附属北京天坛医院

Background and aims: The present study aims to correlate the severity of post-stroke depression (PSD) and serumceramide concentration.
Materials and Methods In this two-center case-control study, we prospectively collected clinical and demographical information from age and gender-matched 51 PSD patients, 56 non-post-stroke depression (Non-PSD)patients, and 39 patients with major depression (MD) to perform the suitable biochemical analysis to bring acorrelation in causing depression in patients soon after the stroke. The ROC curve method was used to evaluateceramide's diagnostic effcacy in all three groups of patients. A follow-up analysis was also conducted based onPSD severity to associate serum ceramide levels and neuropsychiatric symptoms. The severity of the patient'sdepressive symptoms was assessed by using the self-rating depression scale (SDS).
Results In comparison between PSD and MD patients, three serum ceramide species were found to be signifcantly different. Compared with Non-PSD patients, PSD patients had signifcantly higher levels of all the fourserum ceramides, and increasing levels ofC16:0, C18:0(VS MD) and C16: 0(VS Non-PSD) serve as a diagnostictool and an independent risk factor in all three categories of patients. Moreover, the follow-up analysis resultsshowed that, as the treatment progressed, the differences in the 3 serum ceramide species were statisticallysignifcant.
Conclusion There was a stage-specifc association between serum ceramides and PSD, and the potential pathophysiological mechanism has to be investigated in future research.

PU-3250

核心基因多位点序列分型对鲍曼不动杆菌爆发的流行病调查

孙晓军
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 核心基因多位点序列分型技术对 ICU 耐碳青霉烯鲍曼不动杆菌爆发进行分子流行病学调查。
方法 2016.12-2017.3 从 7 名 ICU 患者中分离出 13 个 CRAB 菌株，rep-PCR 进行基因分型，全基因组测序数据（GWS）进行多位点序列分型（MLST）结果的计算机分析以鉴定抗性基因和核心基因组 MLST 分析。
结果 所有分离物均存在碳青霉烯抗性谱并携带 blaOXA-23 碳青霉烯酶基因，rep-PCR 和 MLST 分型显示这些分离株为一种基因型；cgMLST 方法使用 2390 个基因靶标表征等位基因谱，证明了该基因型有两种表现型。
结论 cgMLST 基础上的 WGS 分析与传统的分类方法相比具有较高的区分性，更适合于迅速的流行病学调查。

PU-3251

免疫功能正常青少年肺隐球菌病的案例

杨芳、刘文恩
中南大学湘雅医院

目的 隐球菌的感染在临床并不罕见，但免疫功能正常青少年出现肺部隐球菌病极其少见。本文报道一例免疫功能正常青少年肺隐球菌病的病例报道。
方法 患者江某，男，18 岁，学生。因“发热、左侧胸痛近 2 月，咳嗽 43 天，咯血 8 小时”入院。
结果 患者 2 个月前受凉后出现发热，最高体温 38.5℃，发热以夜间为主，胸痛，左侧胸部持续性胀痛，深呼吸时明显加重，疼痛不向他处放射。无畏寒、寒战，无头痛、鼻塞、流涕、咽痛、咳嗽、咳痰等症状，在当地卫生院就诊，诊断不详，予抗感染（具体药物不详）治疗 8 天左右胸痛明显减轻后出院。出院后患者仍有低热，出院 2 天后开始患者出现阵发性咳嗽，偶有咳痰，痰液为白色泡沫样，量少，仍有夜间低热，再次至当地卫生院予抗感染治疗 6 天后无好转，并出现咯血，患者遂来我院就诊，门诊拟诊“左下肺感染？”收入呼吸内科。血常规：白细胞 18.4×109/L，血红蛋白 142g/L，血小板 407×109/L，中性粒细胞百分比 80.7%；肺部 CT 示：左肺下叶前内基底段实变，感染性病变可能性大，肿瘤性病变待排除。入院后痰液涂片抗酸染色镜下检查阴性，痰培养示正常咽喉杂菌。考虑患者肺部病变为感染可能性大，先予莫西沙星 0.4g qd 静滴抗感染治疗。入院第 2 天在 CT 引导下行肺穿刺活检，送肺组织标本做病原培养培养第 4 天初步报告见隐球菌，检验科将初步结果电话报告给临床，并建议抽血查隐球菌抗原，抽血查隐球菌抗原结果为阳性。予氟康唑经验性抗真菌治疗。肺组织标本送检第 7 天肺组织细菌培养鉴定结果为新型隐球菌，氟康唑敏感，此时患者体温恢复正常 2 天，要求回当地医院继续治疗，嘱继续使用氟康唑氯化钠注射液 0.4g 静滴 qd。1 个月后门诊复查肺部 CT，显示左肺下叶病灶有所减小，嘱患者继续用药。
根据患者血清隐球菌抗原检测阳性、肺组织培养结果及治疗效果，患者左下肺病变确诊为肺隐球菌病。
结论 本案例患者为免疫功能正常的青少年男性，无基础疾病，无明显真菌感染的高危因素，因此诊断疾病时未考虑到肺隐球菌病，因而未及时进行血清隐球菌荚膜抗原检测，实验室提示为隐球菌后抽血检测隐球菌荚膜抗原阳性，在得到病原学证据后积极采取持续强有力的抗真菌治疗，患者症状明显好转，足疗程治疗后患者痊愈。因隐球菌生长缓慢，痰培养时常被口咽正常杂菌覆盖，若能早日行血清学检查检测隐球菌抗原，对其早期诊断肺隐球菌病具有重要作用。提示临床合理选用辅助检查手段，对疾病的及时诊治具有重要的价值。

PU-3252

Rhodosporidiobolus fluvialis 作为一个新发病原体引发真菌血症

黄晶晶、徐英春
中国医学科学院北京协和医院

目的 报道一例目前尚未在人类临床样本中分离到的 *Rhodosporidiobolus fluvialis* 所致真菌血症。
方法 作为中国医院侵袭性真菌监测网（CHIF-NET）项目的一部分，在此报道国际首例由 R. fluvialis 引起的真菌血症。患者出现真菌血症前接受了中心静脉置管，并处于免疫低下状态。入院第 98 天，患者因发热、寒战抽取外周血进行培养，同时 C 反应蛋白检测值为 120.7mg/L。对血培养分离株进行基质辅助的激光解吸/电离飞行时间质谱（MALDI-TOF MS）和 rDNA 内部转录间隔区（ITS）测序鉴定，采用 Sensititre YeastOne YO10 进行提外抗真菌药物敏感性检测。
结果 在念珠菌显色培养基上，*R. fluvialis* 分离株呈珊瑚色至橙红色，比沙堡弱培养基上的菌落颜色略深。API 20C AUX 将该分离株错误鉴定为黏红酵母（*Rhodotorula glutinis*）。在两个 MALDI-

TOF MS 鉴定系统中，Vitek MS 和 Autobio MS 无法将其鉴定至属水平。该分离株的 rDNA ITS 区域和 D1 / D2 结构域序列与 *R. fluviali* 参考菌株 CBS 6568T 相似性≥99.18％。体外药敏显示，棘白菌素类药物对其无体外活性，氟康唑 MIC 值≥256 mg/L。菌株可在 37℃下生长，并在 35∽37℃孵育温度下形成假菌丝。

结论 本研究报道了 *R. fluvialis* 这一新兴病原体在接受了中心静脉置管的患者中引发的感染，并且其对棘白菌素类药物和氟康唑的低敏感性应值得注意。

PU-3253

全球范围内碳青霉烯耐药鲍曼不动杆菌流行克隆 ST208 的起源、系统发育与时空传播

高悦、李荷楠、王辉
北京大学人民医院

目的 研究全球范围分布的碳青霉烯耐药鲍曼不动杆菌（CRAB）流行克隆 ST208 的起源、地理分布与时空传播轨迹。

方法 收集 2005 年至 2018 年中国教学医院住院患者的 CRAB ST208 菌株，使用 Pacbio 平台测序，从 NCBI GenBank 非冗余数据库和全基因组测序数据库中获得了完整的鲍曼不动杆菌 ST208 基因组，并在 NCBI BioSample 数据库检索了相关的临床原始数据进行比较。使用 ResFinder 数据库鉴定抗生素耐药基因，Kaptive 数据库鉴定血清分型，VFDB 数据库鉴定毒力基因。分别使用 Prokka、Roary、Raxml 等生信分析软件进行基因组的注释、提取核心基因组以及建立系统发育树。使用 Beast2 软件分析 CRAB 流行克隆 ST208 的起源时间与进化速率，以研究全球范围分布的 CRAB 流行克隆 ST208 起源、地理分布与时空传播轨迹。

结果 共纳入鲍曼不动杆菌 ST208 基因组 239 个（本研究新测序 45 个, NCBI 数据库 194 个），包括中国（n = 124）、美国（n = 62）、加拿大（n = 9）、泰国（n = 7）、韩国（n = 6）、希腊（n = 4）、印度（n = 3）、巴基斯坦（n = 3）、西班牙（n = 3）、澳大利亚（n = 2）、丹麦（n = 2）、日本（n = 2）、墨西哥（n = 2）、德国（n = 1）、伊朗（n = 1）、瑞士（n = 1）。CRAB 流行克隆 ST208 地域分布广泛，内部发生 KL 重组。CRAB ST208 Bayesian 推测起源时间为 1976 年，进化速率为 6.4x10-4 substitutions per nucleotide site per year，且随时间推移，耐药基因携带有增加趋势，碳青霉烯酶 OXA 有地域分布差异。CRAB ST208 内部毒力基因差异与分离部位、血清分型无明显关联。中国 ST208 分离株的质粒多携带 OXA-23，且存在 OXA-23 在质粒和染色体上同时定位的菌株。

结论 全球范围内 CRAB 流行克隆 ST208 的起源时间为 1976 年，存在耐药基因的洲际传播现象，且中国 CRAB ST208 分离株的质粒多携带 OXA-23，因此应予以更多关注和监测。

PU-3254

Phenotypic and Genotypic Characterization of Carbapenem-resistant Enterobacter cloacae Complex in 11 cities of China

Yanning Ma
Chinese PLA General Hospital

Background Carbapenemase-resistant Enterobacter cloacae complex (CREL) were rapidly increasing in many regions of China. But the molecular epidemiology and clonal relateness of

CREL was not clarify. Especially with the development of bioinformatics, the research would be convenient.
Methods Using clinical CREL isolates detected in 12 hospitals of China over 4 years. Genome sequencing was performed with a paired-end library with an average insert size of 350bp on a HiSeq X Ten sequencer. The tree file was visualized by iTOL. Molecular epidemiological analyses were conducted with multilocus sequence type (MLST).
Results Among the 87 non-duplicate CREL isolates, 57 strains were identified as carbapenemase producers: 35 isolates carried blaNDM−1; 6 isolates possessed blaNDM-5 and blaKPC-2, respectively; 5 isolates contained blaIMP-26; 4 isolates had blaIMP-4, 2 isolates were blaOXA-48 positive. Besides, there were also two isolates coexisting of blaNDM-1 and blaKPC-2 simultaneously. Totally the MBLs genes accounted for 57.47% and existed in plasmids. Among them, the blaNDM-1 gene was mainly carried in IncX3 plasmid, secondly was the IncHI2/IncHI2A plasmid. The blaNDM-5 was mostly carried in IncX3 plasmid. The blaIMP and KPC-2 gene were all in IncHI2/IncHI2A plasmid. There were still 30 isolates without the carbapenemase resistance genes were 74.71% and 98.85% (86/87) positive for ESBLs and AmpC genes, respectively. In addition to β-lactam resistance, the CREL isolates also harbored a variety of multi-class antibiotic resistance genes. MLST showed subtype diversity. Isolates were distributed across 43 different sequence types (STs). The most prevalent was ST78, followed by ST93, ST171. The phylogenetic tree revealed six major clades. Different clades had different sequence types. Despite the ST types were sporadicly in geographically distribution, there might be a local outbreak in some districts, like the ST1001 in Chengdu and ST528 and ST182 in Beijing.
Conclusions Carbapenemase NDM-1 were the primary mechanisms responsible for CREL. It highlighted an urgent need to develop effective measures to monitor and control the further spread of it in China. Further understanding of the molecular epidemiology of CREL and investigation of carbapenemase gene-carrying plasmids, which was the most important resistance mechanism of transmission, are needed to for steps to prevent their further dissemination.

PU-3255

首例由 Candida sorboxylosa 引发的深部皮肤感染

黄晶晶[1]、胡仁静[2]、徐英春[1]
1. 中国医学科学院北京协和医院
2. 南京医科大学附属无锡第二医院

目的 报道一例由 Candida sorboxylosa 引发的深部皮肤感染病例。
方法 一名来自南京医科大学附属无锡第二医院的 51 岁女性患者，于 2019 年 11 月因小腿 10cm * 5cm 大小的皮肤缺损入院，在外科医生切开皮肤表面采集的深部肌肉组织拭子中培养出酵母样真菌。该患者因患有类风湿关节炎和高血压，接受泼尼松治疗长达 25 年，长期处于免疫低下状态。 临床医生根据体外抗真菌药敏试验结果，采用伊曲康唑治疗。
结果 在念珠菌显色培养基上，该菌株呈湿润、粉色菌落。MALSI-TOF MS 鉴定显示为：无鉴定结果；rDNA D1/D2 测序获得的序列与 NCBI 数据库 C. sorboxylosa 序列相似度≥98.95%。使用 YeastOne YO10TM 微量肉汤稀释法进行体外药物敏感性检测发现，其对氟康唑、伏立康唑、伊曲康唑、泊沙康唑的最小抑菌浓度（minimal inhibitory concentrations，MICs）分别为 16, 0.12, 0.25 and 0.12 μg/mL，对棘白菌素类药物和两性霉素 B 敏感性高（MIC 分别为≤0.03 和＜0.12 μg/mL），对 5-氟胞嘧啶的 MIC 值为 4 μg/mL。
结论 C. sorboxylosa 作为一机会致病性真菌病原体，其下降的敏感性需引起关注。

PU-3256

Molecular Characterization of Carbapenem-resistant clinical Citrobacter spp. isolates in China: a multicenter study

Liyan Ye
Center for Clinical Laboratory Medicine, Chinese PLA General Hospital

Background Carbapenem-resistant Citrobacter spp. (CRC) are increasingly recognized as healthcare-associated pathogens but systematic syudies on the clinical epidemiology, genetic diversity, and resistant mechanisms of CRC are relative limited. Herein, we first individually analyed the Chinese nationwide multicenter study about CRC in China.
Methods The prevalence of resistance rates and genes, STs and plasmid replicon types was investigated of CRC strains collected from five provinces between Oct. 2014 and Dec. 2017. All the isolates were identified by MALDI-TOF MS and rMLST. Antimicrobial susceptibility test was determined by the broth microdilution method. Molecular characterization research was done with genome sequencing, plasmidFinder, ResFinder, SNPs and phylogenetic analysis.
Results From the CRE monitoring work, 31 CRC isolates were received from 31 unique patients at 5 distributed hospitals in different provinces. Obvious differences existed in the geographical distribution of CRC. The identification of Citrobacter spp. by MALDI-TOF MS and rMLST were consistent at the genus level, but there were still some differences in species-level identification. There were highly resistant to the most common antimicrobial agents, except amikacin (12.12%), colistin (3.03%), and tigecycline (0%). KPC-2(25.81), NDM (41.94%), and IMP (19.35%) are the most frequent carbapenemases of CRC in China. One isolate co-harbored blaIMP-4 plus blaVIM-1 simultaneously, but four isolates did not detect any known carbapenemase. ST85 (12.90%) and ST116(12.90%) were the predominant ST and we detected 5 novel STs (ST551, ST552, ST553, ST554, ST555). Phylogenetic major lineages are characterized by high levels of core genome diversity and polyclonal spread of CRC across several Chinese geographical areas.
Conclusions The spread of carbapenem-hydrolyzing Citrobacter spp. has emerged in some regional hospitals in China. The small-scale clonal and polyclonal spread of CRC across hospitals in different geographical areas. Therefore, the extremely high antimicrobial resistance rates and the emergence of CRC represented a significant health threat in terms of both disease and treatment.

PU-3257

Xpert 联合液基夹层杯检测对结核病的诊断价值

曾玲
湖南省人民医院

目的 探讨 Xpert 联合液基夹层杯检测对结核病的临床诊断价值，区分结核杆菌和非结核杆菌所引起的肺部感染，为临床治疗提供理论依据。
方法 回顾性分析湖南省人民医院 2020 年 7 月-2020 年 12 月 300 例同时经过 Xpert 检测和液基夹层杯抗酸染色镜检的疑似结核病患者的临床资料，将研究对象分为三组：第一组为 Xpert 联合液基夹层杯检测组；第二组为单独使用 Xpert 检测组；第三组为单独使用液基夹层杯检测组；分别统计三组检测的阳性检出率、灵敏度和特异度，比较 Xpert 联合液基夹层杯检测与临床诊断的一致性。
结果 300 例患者中 51 例为活动性结核病患者，249 例为非结核患者，Xpert 联合液基夹层杯检测的阳性检出率 17.67%（53/300）明显高于单独使用液基夹层杯检测的阳性检出率 6.67%（20/300），差异有统计学意义（$\chi 2=7.98$, $P<0.05$）。以临床诊断为金标准，Xpert 联合夹层杯法检测的敏感度、特异度分别为 100%、99.19%，Xpert 检测的敏感度、特异度分别为 100%、100%,

夹层杯法检测的敏感度、特异度分别为 35.29%、99.19%，Xpert 联合液基夹层杯检测与临床诊断在结核病的诊断上有较好的一致性（Kappa=0.976）。
结论 Xpert 联合液基夹层杯检测与临床诊断在结核病的诊断上具有高度的一致性，并且能够同时检测出结核分枝杆菌及是否对利福平耐药,区分结核病患者是否为结核分枝杆菌感染，对肺结核及肺外结核病的早期诊断具有重要意义,减少不必要的抗结核药物应用。

PU-3258

Xpert MTB/RIF 检测对结核的辅助诊断价值研究

杨芳[1]、陈宜[2]、刘文恩[1]
1. 中南大学湘雅医院
2. 中南大学湘雅医学院

目的 本项目为研究利福平耐药实时荧光定量核酸扩增技术（Xpert MTB/RIF）在抗酸染色阳性涂片标本中结核分枝杆菌的诊断价值。
方法 回顾性调查分析湘雅医院 2020 年 01 月 01 日至 2021 年 01 月 01 日疑似结核患者病史资料，对其进行 Xpert MTB/RIF 检测、自动涂片抗酸染色、结核感染 T 细胞检测及结核抗体检测等分析，比较各自检测情况、灵敏度、特异度、阴性预测值，分析方法间一致性情况。
结果 共分析进行 Xpert MTB/RIF 标本 2381 例，阳性率 19.2%。标本以肺泡灌洗液为主，送检科室多来源于呼吸内科。除呼吸道标本以外，Xpert MTB/RIF 在非呼吸道标本中阳性率较高，提示在肺外结核诊断中具有良好价值。在 1903 例同时进行 Xpert MTB/RIF 与自动涂片抗酸染色标本中，Xpert MTB/RIF 阳性率为 16.29%,高于涂片法（4.89%）。以涂片法为参考，Xpert MTB/RIF 灵敏度为 94.62%,特异度 87.73%。以培养或综合参考标准（composite reference standard, CRS）为确诊结核金标准，Xpert MTB/RIF 灵敏度为 44.50%，阴性预测值为 85.75%，高于涂片法（16.14%、81.05%）；特异度为 83.71%，具有较好表现。
结论 Xpert MTB/RIF 具有较高的灵敏度、特异度、阴性预测值，可用于结核分枝杆菌感染临床早期快速筛查。

PU-3259

昼夜节律失调对 BALB/c 小鼠肠道菌群的影响

李月红
襄阳市第一人民医院

目的 肠道微生物群参与胃肠道等多种生理过程，在调节宿主新陈代谢过程中起着核心作用。人类几乎所有的生理功能都与昼夜节律有关，昼夜节律紊乱会引发疾病。那么昼夜节律的变化对哺乳动物的肠道菌群会造成什么影响呢？本研究旨在观察昼夜节律的破坏对 BALB/c 小鼠肠道菌群的影响。
方法 1. 实验研究对象：
选取 4 窝同一天出生的健康 BALB/c 小鼠，每窝选出 4 只雄性小鼠，一共 16 只。在 SPF 级环境中，正常昼夜（日夜 12:12）节律下养至 8 周的大小。
2. 实验分组：
分别标记 4 窝小鼠分别为 B1、B2、B3、B4，每窝 4 只小鼠分别标上 BX-1、BX-2、BX-3、BX-4。其中 BX-1、BX-2 为正常光照节律（日夜 12:12）。BX-3、BX-4 为昼夜节律破坏组（每 2 天日夜 12:12 周期提前 6 小时）。先把这两组在不同环境下饲养 3 周。
3. 样本采集：
（1）原始组：在小鼠 6 周、7 周、8 周时采集小鼠新鲜粪便。
（2）对照组：在小鼠 9 周、10 周、11 周时采集 BX-1、BX-2 小鼠新鲜粪便。

（3）实验组：在小鼠 9 周、10 周、11 周时采集 BX-3、BX-4 小鼠新鲜粪便。
4. 各实验样本采集后的粪便培养
尽量安排在同一时间，采集新鲜无污染粪便，做粪便培养。分别选用 XLD、哥伦比亚血平板、巧克力平板培养。
5. 观察粪便培养 72 内小时菌群的生长情况，记录情况。
结果和结论 为了探究昼夜节律破坏对 BALB/c 小鼠肠道微环境的影响，本研究记录了每一次粪便培养的细菌结果，并进行细菌种类及细菌数量的统计。由于粪便培养接种时取样没有做到统一的定量，且粪便内细菌数量杂，所以，未能对菌群种类及数量进行系统规范的比较。结果，本研究对正常昼夜节律下和昼夜节律破坏的 BALB/c 小鼠肠道菌群的比较，未能得出有统计学意义的差异。
改进措施，若研究对象采用荷瘤小鼠，对其进行昼夜节律破坏肠道菌群的研究，有望能更深入更详细的了解昼夜节律对肠道菌群的影响。

PU-3260

605 例脓液培养回顾性分析

马金霞
江苏省人民医院（南京医科大学第一附属医院）

目的 为了提高脓液培养的阳性率，更好的为临床诊治提供依据，探讨培养时间与阳性率的关系。
方法 PDCA 循环法，对 605 例脓液培养标本进行回顾性分析，按培养时间分为 A 组和 B 组，A 组 5%CO2 孵育箱培养 1-3 天，B 组 5%CO2 孵育箱培养 4-6 天，分别对可疑菌落分纯、格兰染色涂片镜检，用 Viteck2 细菌鉴定仪进行鉴定，报告临床。
结果 A 组阳性菌 32 例，阳性率 5.29%， B 组阳性菌 71 例，阳性率 11.73%，B 组阳性率明显高于 A 组（P<0.05）。
结论 延长培养时间有助于提高脓液培养的阳性率，尤其是一些慢性生长菌、厌氧菌的检出率，为临床诊治从经验治疗转为目标治疗提供参考依据。

PU-3261

“相识布君”一例布鲁菌病例的诊疗思考

汪文玉
娄底市中心医院

主要内容：病史摘要、诊疗经过、微生物培养及鉴定、讨论、经验积累。
患者中年女性，49 岁，湖南省涟源市湄江镇跑马村人，农民。
主诉：腰痛伴右下肢胀痛麻木伴发热 2 月余。
经验积累：1.询问病史时要注意尽量做到详尽。2.感染性疾病的诊断思路要清晰。

PU-3262

宏基因组测序在中老年女性泌尿系感染病原体检测的临床价值

付晓蕊、康蓓佩、周磊、刘家云
空军军医大学第一附属医院

目的 分析比较临床泌尿系感染患者宏基因组测序与常规培养检测结果，探讨宏基因组测序在中老年女性泌尿系感染病原体检测的临床应用价值。

方法 将我院近半年来临床泌尿系感染患者尿液标本分别进行宏基因组测序与常规培养检测感染病原体，分析其检出病原情况并做一致性分析。并对检出病毒样本进行 PCR 方法验证做一致性分析。
结果 宏基因组测序 20 例（83.33%）患者的尿液标本中检测到具有病原学意义的病原体 49 株，其中细菌 19 株（38.76%）、病毒 19 株（38.76%）。 微生物病原体分离培养培养出病原 8 例，阳性率为 33.33%。两种检测方法的一致性为 50.00%（12/24）。其中两种方法检出肺炎克雷伯菌、粘质沙雷菌的一致性较高（kappa=1.000）。2 例出现脲原体培养阳性，宏基因组测序出现 8 例人型支原体和细小脲原体感染。高通量测序法与普通培养法检测时间相差不大，但高通量测序检测检出阳性率 83.33%，阳性率极高，且检测出常规尿培养无法培养出的病毒、支原体和部分细菌，其中以 JC 多瘤病毒检出株数最多。
结论 宏基因组测序能更快更准确更全面的检出病原体，尤其是中老年女性有症状的尿液感染患者在排除细菌感染的情况下，宏基因组测序可以作为帮助明确病原体感染的又一有力的检测技术。

PU-3263

利奈唑胺耐药粪肠球菌的耐药机制与感染危险因素调查

夏云
重庆医科大学附属第一医院

目的 研究利奈唑胺耐药粪肠球菌（linezolid-resistant Enterococcus faecalis, LRE）的耐药机制并分析其感染的临床特征及危险因素。
方法 收集 2014-2018 年从住院病人的无菌体液标本中分离的 LRE（MIC≥8mg/L），利用 PCR 及测序技术检测菌株中的 optrA 基因，cfr 基因，poxtA 基因，23S rRNA V 区突变以及核糖体蛋白 L3、L4 的突变。回顾性收集 LRE 感染病人的临床和实验室资料，通过病例对照研究对 LRE 感染的危险因素进行分析。
结果 5 年内共检出 85 株(4.5%) LRE, 耐药机制主要包括获得 optrA(98.9%)， 核糖体蛋白 L4 突变(36.5%)，L3 突变(4.7%)。85 例 LRE 病例组和 85 例利奈唑胺敏感粪肠球菌（linezolid-susceptible Enterococcus. faecalis, LSE）对照组被纳入本研究。多因素分析表明，从外院转入（OR，2.8; 95％CI，1.3-6.1; P = 0.007），高龄（≥60 岁）（OR，2.3; 95％CI，1.1-5.0; P = 0.034），恶性肿瘤（ OR，5.5; 95％CI，2.5-12.5; P < 0.000），气管内插管（OR，3.8; 95％CI，1.7-8.3; P = 0.001）、碳青霉烯类（OR，0.1; 95％CI， 0.0-0.5; P = 0.003）和氟喹诺酮类抗生素的使用（OR，4.3; 95％CI，1.4-13.7; P = 0.013）为 LRE 感染的危险因素。
结论 本研究中携带 optrA 是 LRE 的耐药主要机制，而从外院转入，高龄，恶性肿瘤，气管插管，碳青霉烯类及氟喹诺酮类抗生素的使用是 LRE 感染的独立危险因素。

PU-3264

重症急性胰腺炎合并感染耐碳青霉烯类肠杆菌科细菌的危险因素分析

夏吉荣
重庆医科大学附属第一医院

目的 分析重症急性胰腺炎（SAP）合并感染耐碳青霉烯类肠杆菌科细菌(CRE)的危险因素。
方法 选取本院 2011-2019 年期间收治的 105 例 SAP 患者为研究对象。按照是否合并感染 CRE，分为病例组（35 例）和对照组（70 例），结合患者感染的临床特点，采用单因素和多因素 Logistic 回归分析 SAP 合并感染 CRE 的危险因素。

结果 病例组的病原菌包括肺炎克雷伯菌（42.86%），大肠埃希菌（31.43%），阴沟肠杆菌（20.00%），弗氏柠檬酸杆菌（5.71%）。单因素分析结果显示，SAP 合并感染 CRE 与患者检出 CRE 前住院天数，合并胃肠、肾脏等基础疾病，以及进行气管切开、血液滤过、穿刺引流等治疗措施和并发休克、腹腔积液、腹腔感染、皮肤及软组织感染有关(P<0.05)。多因素分析结果显示，腹腔感染、皮肤及软组织感染和血液滤过是 SAP 合并感染 CRE 的独立危险因素(P<0.05)。
结论 SAP 合并感染 CRE 受多种危险因素的影响,临床治疗时应针对合并腹腔感染和皮肤及软组织感染患者采取积极预防治疗措施, 尽量减少血液滤过等侵入性操作，降低感染发生率。

PU-3265

南非诺卡菌致颅内感染病例分析并文献复习

王玉霞
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 通过对南非诺卡菌所致的颅内感染及治疗并回顾性查阅文献复习该菌的流行病学情况及相关研究为临床对该菌的诊治提供理论支持。
方法 通过文献分析及常规药敏检测对南非菌进行研究分析。
结果 南非菌是一种在环境中存在的可导致人类患病的一种条件致病菌，该菌大量分布于土壤中可致患者肺部或皮肤及全身性播散感染。
结论 南非诺卡菌是一种条件致病菌，常导致人类肺部及全身性感染，且具有临床症状不典型等特点，结合既往文献对该菌的感染应当引起重视，可有效防止病情恶化。

PU-3266

侵袭性真菌感染的实验室诊断技术以及面临的挑战

郁谨菡
中国医学科学院北京协和医院

侵袭性真菌感染（Invasive fungal infection ,IFIs）具有较高的发病率和死亡率，尤其在免疫系统受损的患者中，如血液恶性肿瘤患者、造血干细胞移植（HSCT）患者、实体器官移植（SOT）患者，以及重症监护室（ICU）的危重症患者。早期诊断与真菌感染预后息息相关。传统的真菌病诊断方法包括临床样本直接镜检、培养和组织病理学诊断。一些新的诊断方法包括抗原检测、分子生物学和基于蛋白质组学的诊断方法也逐渐被用于真菌病的诊断。这些新的方法显著提高了疾病的早期诊断水平。本文旨在对目前侵袭性真菌感染的实验室诊断技术以及临床研究的问题和现状给予总结，拟从诊断方法学角度对真菌病诊断进行概述。

PU-3267

厌氧菌血流感染的病原菌分布及临床特征分析

朱以军、单小云、卜黎红、方寅飞、陈科强
金华市中心医院

目的 分析厌氧菌所致血流感染的病原菌分布及临床特征，为临床抗感染治疗提供依据。
方法 对 2018 年 5 月-2021 年 1 月金华市中心医院微生物实验室分离的厌氧菌应用 Maldi-Tof（质谱）技术进行鉴定，并对患者的临床特征、感染指标进行统计分析。
结果 共有 84 例患者检出厌氧菌，其中单一厌氧菌感染 82 例，2 株厌氧菌混合感染、3 株厌氧菌混合感染各 1 例。患者男女比例为 1.05（43：41），平均年龄 55.67 岁。菌种分布以革兰氏阴性杆

菌为主，占 61%，其他依次为革兰氏阳性杆菌（23%）、革兰氏阳性球菌（11%）、革兰氏阴性球菌（4%）。革兰氏阴性杆菌中最常见的菌种为拟杆菌和普雷沃菌。厌氧菌血流感染患者的科室分布以外科、妇产科为主，两者之和占所有患者的 61.9%。61.9%（52/84）患者有基础疾病（高血压、冠心病、糖尿病、恶性肿瘤）。57.1%（48/84）患者有手术史（以子宫切除或宫腔手术、肠道及阑尾手术为主）。厌氧菌血流感染患者中 CRP、WBC、PCT 的异常增高率分别为 84.5%、63.1%和 44%。

结论 厌氧菌血流感染以革兰氏阴性杆菌，尤其是拟杆菌为主；患有基础疾病且进行腹部手术的患者是厌氧菌血流感染的高危人群，临床对于该类患者应加强厌氧菌感染的预防和治疗工作。

PU-3268

肿瘤患者念珠菌感染的危险因素及药敏分析

辛娜、陈燕
福建省肿瘤医院

目的 分析福建省肿瘤医院肿瘤患者念珠菌感染的临床特点、流行病学特征及导致感染发生的可能危险因素，为临床念珠菌感染的预防和诊疗提供参考依据。

方法 回顾性分析我院 2015-2017 年恶性肿瘤患者念珠菌感染的 60 例临床资料，对可能的危险因素进行单因素及多因素 logistic 回归分析，估计各危险因素的 OR 值并统计病原菌药敏试验结果作进一步分析。

结果 在念珠菌感染中，根据单因素卡方检验分析结果显示，应用广谱抗生素、住院天数（≥14 天）、术后引流管留置数量（≥4 个）及天数（≥7 天）、放化疗和是侵入性操作是发生念珠菌感染的危险因素（P＜0.05）。Logistic 分析中，应用广谱抗生素、术后引流管留置天数（≥7 天）、住院天数（≥14 天）和侵入性操作的 OR 值分别为 11.177、1.925、15.154、4.613 均是发生感染的独立危险因素（P＜0.05）。白色念珠菌仍是最主要的病原菌（73%），常见真菌对常见抗真菌药物的敏感性由高到低依次为：两性霉素 B,5-氟胞嘧啶，伊曲康唑，伏立康唑，氟康唑。

结论 肿瘤患者住院治疗的周期长，放化疗，术后引流管插管数量多时间长，侵入性操作，术后广谱抗生素应用不规范等是引起念珠菌感染危险因素，临床应对存在危险因素的患者重点预防感染并掌握引起真菌感染病原菌的分布及耐药性，同时合理应用抗真菌药物以及同时注意及时送检合格标本。

PU-3269

探讨妇科恶性肿瘤患者局部感染及围手术期预防用药选择

辛娜、陈燕
福建省肿瘤医院

目的 分析我院妇科恶性肿瘤患者宫颈非厌氧菌感染菌种分布及耐药性，为多重耐药菌管理提供依据，探讨妇科恶性肿瘤患者围手术期预防用药的选择。

方法 回顾性分析 2016-2017 年 482 例妇科恶性肿瘤患者感染情况，并收集临床分离株，采用 K-B 纸片扩散法结合 VITEK II MIC 法进行病原菌药敏试验，按照美国临床实验室标准化委员会（CLSI）标准判断结果,采用 WHONET5.5 进行统计。

结果 宫颈部位发生感染率为 59.43%，其中大肠埃希菌检出率占居首位，构成比为 64.9%，其次是粪肠球菌、肺炎克雷伯菌、铜绿假单胞菌，前四位构成比合计高达 91.50%。大肠埃希菌和肺炎克雷伯菌对头孢唑啉、头孢呋辛、头孢曲松耐药率均高于 50%，两者产超广谱 β-内酰胺酶（ESBL）菌检出率分别为 62.47%和 41.94%。肠球菌对红霉素耐药率为 88.37%，对环丙沙星和左旋氧氟沙

星耐药率高于 30%，屎肠球菌对多数抗菌药物耐药率均保持较高水平，金黄色葡萄球菌耐药率相对较低，本实验室未检出耐碳青霉烯类的肠杆菌科细菌和耐万古霉素及利奈唑烷的阳性球菌。
结论 妇科恶性肿瘤患者宫颈感染率较高，且耐药现象严重，需加强多重耐药菌管理及防治。妇科恶性肿瘤患者宫颈感染主要病原菌为大肠埃希菌、粪肠球菌、肺炎克雷伯菌、铜绿假单胞菌，其对第一、二代头孢菌素、头孢曲松及头孢噻肟耐药率高，是否可应用其他抗菌药物作为妇科恶性肿瘤围手术期预防用药值得探讨。

PU-3270

降钙素原在非霍奇金淋巴瘤患者伴感染中的诊断价值

陈丽妹、陈燕
福建省肿瘤医院

目的 分析降钙素原(Procalcitonin，PCT)在非霍奇金淋巴瘤（NHL）患者中的影响因素、评估感染诊断价值，探讨其在临床中的合理应用。
方法 收集 2017 年 1 月 1 日至 2020 年 12 月 31 日入住福建省肿瘤医院 736 例 NHL 患者病例，根据临床特点划分感染组与非感染组，并对两组患者的血清 PCT 水平进行比较；分析 NHL 非感染组基础血清 PCT 水平与肿瘤病理分型、肿瘤分期、肿瘤进程以及中性粒细胞数等影响因素，并进行多因素及独立影响因素分析；分析 80 例 NHL 患者在基础状态、感染状态、有效抗感染治疗后的三个阶段血清 PCT 检测值；分析感染组血清 PCT 水平与感染部位和致病菌类型之间关系。
结果 血清 PCT 水平在组织病理学类型、IPI 评分（0-2 与 3-4 分）、肿瘤分期、肿瘤进展和性别等方面有明显差异（P<0.05），与患者年龄无显著性差异（P>0.05），肿瘤转移和肿瘤进展是非感染 NHL 患者血清 PCT 水平升高的独立影响因素。I-III 与 IV 期比较，血清 PCT 诊断肿瘤 IV 期转移的 ROC 曲线下面积为 0.6532，最佳临界值为 0.065ng/mL，敏感度、特异性分别为 61.1%、59.9%，阳性预测值、阴性预测值分别为 56.3%、64.6%。血清 PCT 诊断感染 ROC 曲线下面积为 0.7885，最佳临界值为 0.120ng/mL，敏感度、特异性分别为 54.9%、89%，阳性预测值、阴性预测值分别为 65.6%、83.8%；在 80 例 NHL 患者中，其基础值、抗感染有效治疗后与感染阶段比较，血清 PCT 水平统计学均具有显著差异（P<0.001）。血清 PCT 水平在血流感染和局部感染之间统计学有显著差异（P<0.001）；在血流感染中血清 PCT 水平在 G+和 G-之间统计学存在差异（P=0.012，<0.05），凝固酶阴性葡萄球菌（coagulase-negative staphylococcus，CNS）血流感染组与污染组的血清 PCT 水平差异具有统计学意义（P=0.007，<0.05），诊断 CNS 感染的 ROC 曲线下面积为 0.7143，最佳临界值为 0.165ng/mL，患者 PCT 诊断指标敏感度、特异性、阳性预测值、阴性预测值分别为 60%、85.71%、75%、60%。
结论 血清 PCT 水平有望作为诊断 NHL 患者是否转移的参考指标；可作为 NHL 伴感染诊断和抗感染治疗监测指标，诊断感染 cut-off 值为 0.12ng/mL；同时对区分 NHL 患者血流感染与局部感染、区分血流感染 G+与 G-菌、血浆 CNS 血流感染与污染具有一定价值；建议 NHL 患者入院进行常规 PCT 检查，建立患者的 PCT 基础值，作为后续感染诊断对照。

PU-3271

鼻咽癌患者鼻咽溃疡医院感染及临床分析

辛娜、陈燕
福建省肿瘤医院

目的 调查分析鼻咽癌患者放疗过程中鼻咽溃疡发生医院感染的菌种分布、耐药性及其临床特征，总结临床经验，为医院感染的预防工作提供理论依据。

方法 随机选取医院 184 例鼻咽癌发生鼻咽溃疡的住院患者作为研究对象，通过对临床资料的回顾性分析，研究患者医院感染的临床特征与病原菌类型。
结果 184 例鼻咽癌鼻咽溃疡的住院患者中有 64 例发生医院感染，感染率高达 37%，共检出病原体 90 株 ，以肺炎克雷伯菌（26.9），铜绿假单胞菌（19.2%），金黄色葡萄球菌（15.4）为主，真菌比例较低。鼻咽癌患者行放化疗过程中鼻咽腔黏膜发生发射性反应 ，形成鼻咽溃疡，易造成医院感染 。肿瘤分期晚，肿瘤体积大，激素类药物的应用并发感染的概率高。发生医院感染的危险因素包括住院时间、鼻咽黏膜完整性、体内白细胞水平、抗菌药物。
结论 为预防医院感染，鼻咽癌患者在行放化疗时，应积极关注其鼻咽黏膜完整性，预防性保护，及时送检分泌物标本，合理用药。

PU-3272

G 试验在肿瘤患者侵袭性念珠菌感染中的临床价值

辛娜、陈燕
福建省肿瘤医院

目的 讨论 G 试验在恶性肿瘤患者侵袭性念珠菌(invasive candidiasis, IC) 感染中的临床早期诊断价值及其临床特征之间的关系。
方法 选取福建省肿瘤医院 2019 年 1 月至 2020 年 12 月期间 64 例侵袭性念珠菌感染(invasive candidiasis, IC)患者、58 例念珠菌粘膜定植者，采用免疫比浊法分别检测两组 G 试验与 pct 浓度，分析 G 试验早期诊断恶性肿瘤患者 IC 的灵敏度、特异度、阳性预测值、阳性预测值等指标，以受试者工作特征（ROC）曲线评估 G 试验在恶性肿瘤患者 IC 早期诊断中的价值，并比较 G 试验阳性率与患者临床特征之间的关系，以及与 PCT 联合检测对肿瘤患者 IC 的诊断价值。结果用 SPSS 26.0 分析。
结果 IC 组 G 试验浓度与粘膜定植组相比显著增高；64 例 IC 组患者中，白色念珠菌比例高于非白色念珠菌；G 试验诊断总体灵敏度为 56.25%，特异度为 87.9%，阳性预测值为 85.71%，阴性预测值为 67.1%，阳性似然比为 4.648，阴性似然比为 0.498，约登指数为 0.44；G 试验 ROC 曲线下面积 AUC 为 0.628；IC 患者 G 试验阳性率与病原菌、粒细胞、体温、合并感染的情况、治疗方法等临床特征无关；G 试验与 PCT 联合检测的灵敏度及特异度（分别为 75%、65.31%）高于二者单独检测（P＜0.05），但阴阳预测值并未明显改变。
结论 G 试验对于恶性肿瘤患者 IC 的早期诊断具有一定临床可用性，能区分定植和感染，但其在恶性肿瘤的患者临床应用价值准确性一般，实验室应优化检测方法，临床连续检测 G 试验以减少假阳性和假阴性的发生，提高 IC 诊断的准备性。

PU-3273

Development of a Droplet Digital Polymerase Chain Reaction (ddPCR) for Sensitive detection of Pneumocystis jirovecii in the Respiratory Tract Specimans

Jie Yi
Peking Union Medical College Hospital

Background Pneumocystis jirovecii Pneumonia (PJP) is a life-threatening and opportunistic lung infection that affects the immunocompromised patients. As the Pneumocystis colonization may be linked to the development or transmission of disease, the detection of Pneumocystis in immunocompromised patiesnts has become particularly important. The low fungal biomass and the presence of PCR inhibitors limits the usefulness of quantitative PCR (qPCR) for accurate absolute quantification of Pneumocystis in specimens from the human

airway. Droplet digital PCR (ddPCR), however, presents an alternative methodology allowing higher sensitivity and accuracy, which can be used for early detection and subsequent monitoring of treatment of low-load pathogenic microorganisms. Here, we developed an in-house method with ddPCR in detecting Pneumocystis in the diseased airway from respiratory specimens, and evaluated its sensitivity compared to qPCR.
Methods 82 BALF from 82 suspected PJP patients were collected to detect Pneumocystis jirovecii DNA using both ddPCR and qPCR, and the inconsistent results were confirmed by mNGS(metagenomics next generation sequencing). 37 sputum from 16 PJP patients, as well as continuous respiratory tract specimens from 9 patients with PJP and treated with sulfonamides, were also collected to detect Pneumocystis jirovecii DNA using both ddPCR and qPCR.
Results In BALF, 93.90% (77/82) results of both two Methods were coincident but there were results from 5 specimens were inconsistent. The 5 specimens were positive using ddPCR while negative using qPCR, and confirmed to be positive by mNGS. Detection results of 78.37%(29/37) sputum were coincident, but there were results from 8 specimens were inconsistent, which were positive using ddPCR while negative using qPCR. Pneumocystis biomass of PJP patients have decreased after treatment according to qPCR, even to 0, but they were still canbe detected using ddPCR.
Conclusions DdPCR importantly demonstrates better sensitivity especially at low abundance compared to qPCR. Considering the importance of Pneumocystis in patients with immunologic deficiency, ddPCR represents a useful, viable and reliable alternative to qPCR in such patients.

PU-3274

Genomic and pathogenic insights into the diversification of colony morphology in closely Related Clinical Isolates of Acinetobacter baumannii

Hongwei Pan、enhua sun、yi zhang
Qilu Hospital of Shandong University

Objective Acinetobacter baumanniiis a gram-negative, nonmotile, aerobic coccobacillus that is commonly found in natural environment and susceptible to most antibiotics in the 1970s. However, A. baumanniiis a fast-evolving organism, which exhibits a remarkable ability to rapidly acquired resistance to a vast array of antimicrobials that led to multidrug resistance (MDR) strains. Multidrug resistance (MDR)A. baumanniihas become a particularly problematic nosocomial pathogen during the past decades.The strains are frequently found to cause infections in hospitalized patients and resulted in disease such as bacteremia, pneumonia, septicemia, urinary tract infections, wound sepsis, endocarditis and meningitis, which highly increases the mortality of the immune compromised hospitalized patients. Thus, the emergence and rapid spreading of MDR A. baumanniistrains has become a big and growing public health threat worldwide. The ability of MDR A. baumanniito form variant morphology colonies was frequently observed in clinical microbiology lab. However, little has been done to analyze the pathogenic or biological importance of this phenomenon.The phenotype and genome differences analysis could provide us better understanding of the relationship between genome evolution and phenotype diversification of the closely related strains in the same hospital environment.
Methods Three closely related clinical isolates of A. baumanniithat show different colony morphology were collected for the analysis. All three strains were isolated from the respiratory samples of patients admitted to ICU the intensive care unit within a 6-month interval. Strains were cultured and purified in Columbia blood agar at 37oC. The strain identification and antimicrobial susceptibility testing were carried out by Vitek 2 system (bioMérieux, Marcy l' Étoile, France). The pathogenic ability of the strains was analyzed by biofilm formation and cell adhesion assay.

Whole genome sequencing and comparisons of the three clinical isolates were carried out for the genetic evolution analysis.
Results Based on the colony morphology, the three isolates were designated A.b-WT, A.b-mu, M.A.b, respectively. A.b-WT forms white and raised colonies that are similar to that of the wild type strain. A.b-mu forms gray white and flat colonies that are quite different with the wild type strain, while M.A.b forms mucoviscous colonies that areassociated with viscous, sticky strings when lifted with a toothpick. Similar antibiotic resistance profiles of the three closely related strains were revealed by antimicrobial susceptibility analysis. Detailed phenotype characteristic show that the three strains had different biofilm formation and cell adhesions ability in vitro. In order to better understand the evolutionary processes that contribute to the three closely related strains diversification, genome sequencing was carried out.A. baumanniiA.b-WT was assembled into 68 contigs and approximately 3,914 kb long with 38.84% GC content. A.b-Mu was assembled into 103 contigs and approximately 4,000 kb with 38.95% GC content. M.A.b was assembled into 56 contigs and approximately 3,920 kb with 38.81% GC content. All the three sampled A. baumanniistains are classified into International clone II. A total of 24 putative antibiotic resistance related genes in A.b-WT genome, 31 putative antibiotic resistance related genes in A.b-Mu genome and 25 putative antibiotic resistance related genes in M.A.b genome were identified, while 67 putative virulence factors related genes in A.b-WT genome, 65 putative virulence factors related genes in A.b-Mu genome and 67 putative virulence factors related genes in M.A.b genome were identified. Further single-nucleotide polymorphisms (SNPs) analysis reveals genes that may responsible for the phenotype diversification of the strains.
Conclusion Overall, we analyzed the relationship between genome evolution and phenotype diversification of the closely related clinical strains. The results demonstrated the microscale genome modification between the closely related A. baumannii strains, which expanded our understanding of the evolutionary processes that contribute to strain diversification and pathogenic in the same hospital environments.

PU-3275

Evaluation of an in-house rapid diagnostic method for direct identification of different panel of organisms from positive blood culture broths using MALDI-TOF MS

Hongwei Pan、enhua Sun、yi Zhang
Qilu Hospital of Shandong University

Objective Matrix-assisted laserdesorption-ionisation time-of-flight mass spectrometry (MALDI-TOF MS) is a fast and accuracy method for bacteria identification, which offers the potential for micro-organisms identification directlyfrom positive blood culture broths within an hour. Recently, we published an easy and accurate in-house (IH) developed lysis-centrifugation-wash sample preparation method that can facilitate the direct identification of bacteria in positive blood cultures. In order to further evaluate the IH method, we compared the accuracy and practical performance of the IH method and the Sepsityper™ kit (Bruker Daltonics, Bremen, Germany) for micro-organisms identification directlyfrom positive blood culture broths by MALDI-TOF MS in this study.
Methods Blood cultures positive for gram-positive bacteria, gram-negative bacteria, yeast and anaerobic bacteria from 112 patients were employed for analysis using the IH method and Sepsityper™ kit.
Results We observed 92.86% concordance with traditional culture-dependent colony identification Methods for IH and 87.50% for Sepsityper™ kit. Little difference was observed in the identification of regular gram-negative (100% and 97.5%) bacteria. The IH method demonstrated better identification rate than Sepsityper™ kit for gram-positive bacteria (95% and 87.5%). For identification of yeast, the Sepsityper™ kit works better than IH method (94.74% and 84.21%). However, identification ability was greater for anaerobic bacteria when the IH method

was applied, as the identification rated was 100% for IH method and 33.33% for Sepsityper™ kit. In addition, IH method constantly takes less time than the Sepsityper™ kit for samples processing. Finally, the viability of the isolated organisms from blood cultures using the two Methods was compared. The IH sample preparation method does not affect the viability of the isolated organisms from blood cultures, while the Sepsityper™ kit killed most isolates. Thus, microbial samples obtained from IH method could be used for the following direct susceptibility testing, while samples obtained from Sepsityper™ kit were not applicable for susceptibility testing.
Conclusion Both systems allowed for more rapid determination, compared to the classical culturing Methods However, our IH method displayed higher accuracy and cost-effectiveness than the commercial kit.

PU-3276

肿瘤患者尿路感染病原菌分布及常见细菌的耐药性分析

王国婧、朱宇、冯莎娜、魏葆珺、崔巍
中国医学科学院肿瘤医院

目的 了解引起恶性肿瘤患者尿路感染的病原菌分布和常见菌株的药敏特点，为临床的早期治疗提供实验室依据。
方法 对中国医学科学院肿瘤医院 2015 年 1 月至 2017 年 5 月恶性肿瘤患者送检的尿液标本进行常规培养，并对分离的菌株进行鉴定和 MIC 法药敏试验。
结果 2403 例尿液标本中，共检出病原菌阳性 334 例（13.90%），其中革兰阴性杆菌 207 例（占 61.98%），革兰阳性球菌 73 例（占 21.85%），酵母样真菌 54 例（16.17%）。207 例革兰阴性杆菌中以大肠埃希菌（119 例，占 57.49%）、肺炎克雷伯菌（31 例，占 14.98%）和铜绿假单胞菌（16 例，7.73%）为主；73 例革兰阳性球菌中以粪肠球菌（33 例，占 45.2%）、屎肠球菌（24 例，占 32.88%）和表皮葡萄球菌（8 例，占 10.96%）为主；54 例酵母样真菌中，以白色念珠菌为主（37 例，68.52%）。药敏试验结果显示，革兰阴性杆菌中大肠埃希菌和肺炎克雷伯菌产超广谱 β-内酰胺酶（ESBLs）的检出率分别为 49.58%和 29.03%，对阿米卡星和亚胺培南保持较高的敏感率（均>90%）；革兰阳性球菌对万古霉素的敏感率为 100%。
结论 引起恶性肿瘤患者尿路感染的病原菌以大肠埃希菌、肠球菌和白色念珠菌为主，临床应根据药敏结果合理选用抗菌药物，减少耐药菌株的产生。

PU-3277

Xpert 难辨梭菌分子检测方法对难辨梭菌感染的诊断效能评价

白媛媛
山东第一医科大学附属省立医院

目的 目前迫切需要快速准确的分子诊断检测方法来诊断难辨梭菌感染(Clostridium difficile infection ,CDI)。我们评估了 Xpert 难辨梭菌分子检测方法（Xpert Clostridium difficile assay, Xpert CD）对 CDI 的诊断准确性并对之前的分析进行了数据更新。
方法 根据制定的入选标准全面检索 PubMed, EMBASE， Cochrane 数据库，中国知网及万方医学网。RevMan 5.2 软件实现诊断试验质量评价体系-2 对入选文献的质量评价。STATA 13.0 软件实现敏感度、特异度、阳性似然比、阴性似然比、诊断比值比及拟合诊断受试者曲线等指标。Meta 回归，亚组分析及斯皮尔曼相关系数评价异质性。稳健性分析评价合并数据的稳定性。
结果 总共 26 个研究纳入了本项研究，Xpert CD 诊断难辨梭菌的合并敏感性（95%可信区间）为 0.97（0.95-0.99）；合并特异性为 0.96（0.94-0.96）。诊断曲线下面积为 0.99（0.98-1.00）。研

究间存在显著异质性。Meta 回归和亚组分析显示，样本量、样本类型、种族类型、患病率可能是异质性的显著来源。敏感性分析显示数据有很好的稳定性。
结论 Xpert CD 对于诊断难辨梭菌感染是一种有用的诊断工具，灵敏度高，特异性高，由于它的快速和简单性，具有良好的可用性。

PU-3278

孕妇 B 链球菌的筛查及耐药情况分析

刘莹、张桂华
中国医科大学附属第一医院鞍山医院

目的 调查 431 例妊娠晚期孕妇Ｂ族链球菌感染情况，，对Ｂ族链球菌的耐药情况进行检测分析。
方法 选择 2018 年 1 月～2020 年 1 月在本院门诊产检的妊娠 35～37 周的孕妇 431 例，筛查孕妇Ｂ族链球菌感染情况，并进行药敏试验。
结果 2018 年 1 月～2020 年 1 月该院门诊及住院产妇共分离Ｂ族链球菌共 31 株。Ｂ族链球菌的药敏试验显示，妊娠晚期孕妇感染的Ｂ族链球菌对万古霉素、头孢曲松、头孢丙烯、庆大霉素、氨苄西林、、替考拉宁、呋喃妥因、利奈唑胺以及磷霉素敏感，耐药率均为 0；青霉素耐药率为 6.45％（2／31），左氧氟沙星 35.48％（11／31），阿奇霉素和克林霉素耐药率分别为 77.42％（24／31）和 67.74％（21／31）(P＜0.05）。
结论 Ｂ族链球菌定植孕妇更容易出现不良妊娠结局，因此，应加强孕期和产前Ｂ族链球菌的筛查力度，以降低新生儿感染风险及时预防和治疗，以减少Ｂ族链球菌的定植感染，为母婴安全提供更多保障。

PU-3279

2016-2020 年肿瘤患者铜绿假单胞菌感染及耐药趋势的回顾性研究

崔兆磊、霍然、陈燕
福建省肿瘤医院/福建医科大学附属肿瘤医院

目的 回顾分析肿瘤患者临床标本分离的铜绿假单胞菌（PA）菌株相关信息，研究肿瘤患者感染 PA 的临床分布、耐药趋势，为临床上治疗肿瘤患者 PA 感染提供相关依据。
方法 回顾性分析 2016-2020 年福建省肿瘤医院临床标本分离的 PA 及相关数据，采用 WHONET5.6 和 SPSS22.0 统计软件对数据进行分析。
结果 从 2016 年 1 月到 2020 年 12 月，5 年共检出 PA 926 株，每年 PA 占临床分离菌株的比率分别为 8.61% （163/1893）、7.68%（170/2213）、7.62%（201/3637）、6.33%（182/2876）、7.36%（210/2852）； 2018-2020 年 PA 分离率与 2015-2017 年的 PA 分离率相比有所降低，但无显著差异（p=0.084）。临床患者标本来源主要为呼吸道标本（65.12%），各类来源之间具有显著差异。ICU 患者、腹部肿瘤患者、胸部肿瘤患者和头颈部肿瘤患者的 PA 分离率有显著差异（p＜0.05）。抗生素药敏试验表明，在 2016-2020 年，我院分离 PA 菌株对亚胺培南的耐药率大于 30%，；对庆大霉素、环丙沙星、头孢他啶的耐药率在 25%-3%之间，具有较大波动；对美罗培南的耐药率大于 20%；对头孢吡肟、左氧氟沙星、哌拉西林、哌拉西林/他唑巴坦的耐药率均小于 20%。我院肿瘤患者临床标本 PA 分离率与全国平均水平无显著差异，但分离的 PA 菌株对亚胺培南（31.43% vs 23.2%, χ2=10.416, p<0.05）的耐药率高于全国平均水平，对左氧氟沙星（13.82% vs 17.47%, χ2=10.262, p<0.05）、头孢吡肟（10.48% vs 14.78%, χ2=13.532, p<0.001）、哌拉西林（12.20% vs 16.4%, χ2=29.917，p<0.001）、哌拉西林/他唑巴坦（13.07% vs 15.55%, χ2=13.867, p<0.001）的耐药率低于全国平均水平，具有显著差异。

结论 肿瘤病人对某些药物的耐药率高于全国平均水平，但对某些药物的耐药率低于全国平均水平，这可能与肿瘤病人病种特殊性有关。研究结果提示我们，我们应该密切监测肿瘤患者 PA 感染及耐药情况，同时在临床 PA 感染治疗中应合理使用抗菌药物，预防耐药菌株的产生。

PU-3280

血清降钙素原（PCT）、Presepsin (sCD14-ST)和血培养联合应用对脓毒症的诊断价值

王芳、黄声雷、林见敏、邓燕燕、陈辉凤、王金金
复旦大学附属中山医院青浦分院

目的 探讨血清降钙素原（PCT）、可溶性白细胞分化抗原 14 亚型(sCD14-ST，Presepsin)和血培养联合应用对脓毒症的诊断价值。
方法 收集 2017 年 1 月至 2018 年 12 月门诊、急诊住院患者 127 例，根据脓毒症诊断标准分为住院患者中非脓毒症患者 50 例，住院患者确诊脓毒症感染者 47 例，同期选择 30 例健康体检者作为对照组；所有收集患者都进行 PCT 及 Presepsin 的检测。同时把住院患者确诊脓毒症感染者，根据血培养检测结果分为真菌组、革兰阳性细菌组、革兰阴性细菌组，血培养阴性组进行分析。
结果 通过对实验组（血培养阳性、血培养阴性）和对照组（正常健康人）的 PCT 检测绘制出 ROC 曲线，发现 PCT 的 ROC 曲线下的面积为 0.982，P=0.000(p<0.01),两组有显著统计学差异，PCT 在检测脓毒血症方面有诊断价值；通过对实验组（血培养阳性、血培养阴性）和对照组（正常健康人）的 presepsin 检测绘制出 ROC 曲线，发现 presepsin 的 ROC 曲线下的面积为 0.716，P=0.000(p<0.01),两组有显著统计学差异，presepsin 在检测脓毒血症方面有诊断价值；通过两组临床试验检测结果显示，PCT 检测的 CUT-OFF 值为 0.02ng/ml，其灵敏度为 97.8%，特异度为 90%，阳性预测值为 93.9%，阴性预测值是 96%。
结论 PCT 和 presepsin 在检测脓毒血症方面均有诊断价值，但 PCT 的诊断价值要高于 presepsin，可能是由于 presepsin 试剂盒检测灵敏度不够等原因引起。

PU-3281

An Outbreak of Carbapenem-Resistant Klebsiella pneumoniae of K57 Capsular Serotype in an Emergency Intensive Care Unit of a Teaching Hospital in China

Chunhong Shao [1]、Yan Jin[1]、Meijie Jiang[2]
1. Shandong Provincial Hospital affiliated to Shandong University
2. 泰安中心医院

The emergence of carbapenem-resistant hypervirulent K. pneumoniae (CR-hvKP) strains has increased the threat posed by K. pneumoniae. Here, we described an outbreak of 32 CR-hvKP isolates from the emergency intensive care unit (EICU) of a teaching hospital in China. 32 CRKp isolates were collected from 6 patients and their surrounding environment in EICU. Antimicrobial susceptibility testing was performed using VITEK 2 compact system, E-test or the broth microdilution method. All isolates were serotyped, antimicrobial resistance genes and virulence-associated genes were screened using PCR. Multilocus sequence typing (MLST) and pulse-field gel electrophoresis (PFGE) were employed to characterize the genetic relationships among the CPKP isolates. The virulence capability of 11 CRKp isolates from 6 patients was evaluated through Galleria mellonella larva infection assay. PFGE showed that all 32 isolates belonged to one cluster, and MLST revealed that belonged to ST11. All isolates exhibited high resistance to β-lactam antibiotics, quinolones, and aminoglycosides. They were susceptible to

ceftazidime/averbatan, tigecycline, and colistin. All 32 isolates harbored blaKPC-2, blaSHV-11, blaTEM-1, rmtB, and qnrD. The serotype of all 32 isolates was K57. All 32 isolates contained 6 virulence genes, namely, fimH, iucB, mrkD, rmpA, uge, and wabG. Infection assays demonstrated high mortality in the Galleria mellonella model. Following measures implemented by the hospital, the outbreak was controlled. The mortality rate was 83.3%. The epidemiology of CR-hvKP should be monitored closely to detect early indications of this emerging public health threat.

PU-3282

耐碳青霉烯类铜绿假单胞菌耐药机制研究

胡咏梅[1]、邹明祥[1]、李军[1]、祁瑄[2]
1. 中南大学湘雅医院
2. 中南大学湘雅医学院

目的 检测和分析临床分离耐碳青霉烯类铜绿假单胞菌携带的耐药基因，明确其耐药机制。
方法 收集 2018 年 12 月至 2019 年 4 月中南大学湘雅医院临床分离的 54 株耐碳青霉烯类铜绿假单胞菌，采用改良碳青霉烯灭活试验（mCIM 法）初步筛查碳青霉烯酶，通过聚合酶链反应(PCR)法检测铜绿假单胞菌的耐药基因。
结果 54 株耐碳青霉烯类铜绿假单胞菌对碳青霉烯类抗菌药物 100.0%耐药，但对氨基糖苷类及喹诺酮类抗菌药物的敏感性较高；经 mCIM 试验初筛，发现 5 株铜绿假单胞菌为阳性，阳性率为 9.3%；对 8 种常见的耐药基因进行 PCR 检测，发现 7 株菌携带碳青霉烯酶耐药基因，其中 2 株检出 blaKPC 基因，3 株检出 blaIMP 基因以及 2 株检出 blaVIM 基因，余下 5 种耐药基因（NDM-1、SIM、SPM、GIM、OXA-48）未检出阳性菌。
结论 产碳青霉烯酶是 54 株铜绿假单胞菌对碳青霉烯类抗菌药物耐药的重要机制，但同时还存在其他耐药机制，应加强院内感染预防措施，防止该类细菌的传播和流行。

PU-3283

碳青霉烯肺炎克雷伯菌的毒力基因携带情况及感染患者的临床特点

姜梅杰
泰安市中心医院

目的 了解耐碳青霉烯肺炎克雷伯菌（CRKP）的毒力基因携带情况及感染患者的临床特点,为医院感染控制和临床治疗提供理论依据。
方法 收集我院 2019 年 1 月～12 月临床分离的 CRKP 31 株, 采用 Microscan WalkAway 96plus 全自动细菌鉴定药敏仪进行菌株鉴定和药敏试验，同时用纸片扩散法和 E-test 法进行药敏试验的补充和复核；采用聚合酶链式反应（PCR）扩增相关毒力基因包括黏液表型调控基因 A（rmpA）、I 型菌毛粘附相关基因（fimH）、III 型菌毛粘附蛋白基因（mrkD）、铁载体相关的基因（iucB）、脂多糖编码基因（uge），阳性扩增产物送测序测序。
结果 该院 CRKP 的主要标本来源为痰液（80.65%）和尿液（9.68%）,主要科室来源为各监护室病房。有两种及以上基础疾病的患者和住院天数在 15 天以上的患者均占 90.32%（28/31）。接受过有创操作的患者占 96.77%（30/31）。使用过广谱抗菌药物的患者占 80.65%（25/31）。毒力基因的总检出率为 100%。其中 mrkD、fimH、uge 检出率均为 100%，iucB 检出率为 77.42%（24/31），rmpA 检出率为 70.97%（22/31）。mrkD + fimH +uge +rmpA +iucB 五种毒力基因同时检出率为 67.74%（21/31）。

结论 CRKP 感染患者大多基础疾病多，住院时间长。有创操作和抗菌药物暴露史可能是其感染率较高的原因。该院多株 CRKP 均同时携带多种毒力基因，可能是其致病性较高的原因。

PU-3284

2020 年山东某三甲医院的耐药性分析

赵书平
泰安市中心医院

目的 了解 2020 年我院临床标本的病原菌检出情况及前三位细菌的耐药性，为临床合理使用抗菌药物提供理论依据。
方法 回顾性分析我院 2020 年 1 月～2020 年 12 月各临床标本中检出的细菌。利用 Microscan WalkAway 96plus 全自动微生物鉴定药敏系统进行菌株鉴定和药敏试验，部分药敏试验采用纸片扩散法进行补充。菌株分布及耐药率使用 WHONET5.6 软件进行统计分析。
结果 2020 年我院临床标本共分离出非重复细菌 7058 株，分离前三位的细菌分别为：大肠埃希菌（15.98%）、肺炎克雷伯菌（13.22%）、金黄色葡萄球菌（9.00%）。主要科室分布为重症医学科（15.68%）、神经外科（10.16%）、儿内科（9.62%）。大肠埃希菌对氨苄西林耐药率高（91.00 %），对氟喹诺酮类和一、二、三代头孢菌素耐药率在 51%～58%，酶的抑制剂类药物敏感性较好，耐药率低于 30%。肺炎克雷伯菌对抗菌药物的耐药率较低，均低于 38%。金黄色葡萄球菌对青霉素和红霉素耐药率高，分别为 91%和 70%，其余抗菌药物耐药率低，未发现对万古霉素和利奈唑胺耐药的菌株。
结论 我院临床标本的细菌分布以大肠埃希菌、肺炎克雷伯菌和金黄色葡萄球菌为主。主要科室分布为重症医学科、神经外科和儿内科。肺炎克雷伯菌对抗菌药物的耐药率低于大肠埃希菌，两者对酶的抑制剂类药物敏感性均较好。金黄色葡萄球菌对青霉素和红霉素耐药率高，未发现对万古霉素和利奈唑胺耐药的菌株。临床医生应根据药敏结果选择并及时调整合理的抗菌药物。

PU-3285

耐碳青霉烯类肠杆菌科细菌的分布及耐药分析

赵书平
泰安市中心医院

目的 了解临床分离的耐碳青霉烯类肠杆菌科细菌（CRE）的菌株分布、科室来源及耐药特点，为临床合理使用抗菌药物提供理论依据与数据支持。
方法 对 2020 年 01 月-2020 年 12 月间临床标本中分离的 CRE，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充，应用 WHONET 5.6 软件对菌株分布及耐药率进行统计和分析。
结果 2020 年我院临床标本共分离出 104 株 CRE，主要是肺炎克雷伯菌（65.38%）和大肠埃希菌（12.50%）。主要科室分布为重症医学科（42.31%）、神经外科（10.58%）和儿科监护病房（10.58%）。CRE 对大多数临床常用抗菌药物高度耐药，对头孢类耐药率 100%，对酶的抑制剂和氨曲南耐药率大于 90%，对喹诺酮类耐药率大于 70%，替加环素和多粘菌素 B 耐药率最低。
结论 我院 CRE 检出率较高，以肺炎克雷伯菌和大肠埃希菌为主。主要来源于各监护室病房。CRE 耐药情况严峻，临床医生应根据药敏结果选择并及时调整合理的抗菌药物。医护人员要注意手卫生和院感的防控，防止 CRE 暴发流行。

PU-3286

Anti-psychotic drug thioridazine acts as a potent anti-microbial agent for multidrug-resistant bacteria: a clinical strains-based study

印琳
湖南省第二人民医院

Purpose The aim of the study was to comprehensively investigate the effect of anti-psychotic drug thioridazine on common MDR clinical isolated strains, and provide new strategies for the therapeutics of MDR infections.
Methods Bacteria were isolated from the clinical patients. The identification and susceptibility testing of isolated strains in this study were completed by MALDI-TOF mass spectrometry and VITEK 2 Compact analysis system, respectively. The antibacterial efficacy of thioridazine in vitro was assessed by agar dilution method.
Results MRSA and CRAB were significantly inhibited by thioridazine at low concentrations (20 μM). CRPA and CREO were inhibited by thioridazine at middle concentration (40 μM). CRKP were inhibited by thioridazine at high concentration (100 μM).
Conclusion The present study shows that thioridazine is an effective drug against common MDR clinical isolated strains, which provides an alternative strategy for MDR and has a highly translational value.

PU-3287

微生物检验技术研究

李思齐
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 大多致病源来自于食品，所以对食品微生物安全的检查是至关重要的，检测技术是至关重要的。
方法 从微生物的角度出发，代谢学技术，抗体的方法，分子生物学技术、仪器法。
结果 发现许多电阻抗法、快速酶处法及代谢产物检验、微量升华法、ATP 生物发光法、放射检测技术；乳胶凝集反应，酶联免疫吸附法；核酸探针技术，PCR 技术；流式细胞术，免疫磁性微球，电阻电导检测器，VITEK-AMS，VIDAS 全自动免疫分析仪，质谱技术，拉曼光谱仪等微生物检验技术。
结论 由于微生物种类复杂，也可能有所改变，随着科技的发展，对微生物检验技术，进行总结，发现了许多新的微生物技术，为临床提供了方便。

PU-3288

鲍曼不动杆菌外膜囊泡（OMVs）通过携带 adeB、adeJ 外排泵相关分子介导耐药性传递的机制研究

姜红烨[1]、胡秀梅[2]、郑磊[2]、吕伟标[1]
1. 南方医科大学顺德医院(佛山市顺德区第一人民医院)
2. 南方医科大学南方医院

目的 近年来鲍曼不动杆菌耐药形势越来越严峻，研究发现外膜囊泡（OMVs）可以传递抗生素抗性，但其是否可介导鲍曼不动杆菌耐药性传递及其与外排泵相关机制尚不清楚，本研究旨在探讨外膜囊泡（OMVs）介导鲍曼不动杆菌耐药性传递的外排泵机制。
方法 首先利用密度梯度离心法提取鲍曼不动杆菌 OMVs，并通过纳米颗粒追踪分析（NTA）和透射电镜（TEM）对其进行鉴定表征；接着利用纸片扩散法探讨鲍曼不动杆菌 OMVs 是否具有介导耐药性传递的作用；进一步利用 PCR、qRT-PCR 和蛋白质组学分析对鲍曼不动杆菌敏感株和耐药株 OMVs 中的外排泵相关基因在不同水平检测外排泵分子的表达情况，最后加入外排泵抑制剂 PAβN 反向验证 OMVs 中外排泵在介导耐药性传递中的作用。
结果 从鲍曼不动杆菌菌液中可提取出粒径较均一、大小在 100-250 nm 之间的 OMVs，TEM 证实其具有典型的囊泡结构。介导耐药性传递的实验证实 OMVs 确实可以介导耐药性的传递。PCR 检测耐药菌和敏感菌及其外膜囊泡中 2 个外排泵基因 adeB、adeJ，结果证实 OMVs 可以携带相关基因，且耐药菌 OMVs 中相关基因水平高于敏感菌 OMVs。qRT-PCR 检测耐药菌和敏感菌的菌液和 OMVs 中上述耐药基因的 mRNA 表达水平，发现耐药组显著高于敏感组（$P<0.05$），而且 adeB、adeJ 在 OMVs 中实现了富集，升高的倍数达到几百倍。蛋白质组学相对定量分析结果显示，耐药菌 OMVs 中外排泵相关蛋白较敏感菌 OMVs 中多。加入外排泵抑制剂 PAβN 后，发现其可有效逆转耐药菌 OMVs 与敏感菌共培养后的耐药性传递的趋势。
结论 本研究表明鲍曼不动杆菌外膜囊泡（OMVs）可以通过携带 adeB、adeJ 外排泵相关分子介导耐药性的传递。

PU-3289

抗菌药物的使用与铜绿假单胞菌和鲍曼不动杆菌耐药率的相关性分析

乔秀强、彭海英、高春海
临沂市人民医院

目的 分析医院近几年抗菌药物使用情况以及对铜绿假单胞菌和鲍曼不动杆菌耐药的影响，为临床合理使用抗菌药物，降低细菌耐药率提供指导依据。
方法 对我院 2017-2020 年常用抗菌药物使用频度和强度及同期分离的铜绿假单胞菌和鲍曼不动杆菌耐药情况进行回顾性调查分析。
结果 医院抗菌药物使用强度（AUD）从 2017 年-2018 年逐年上升，2019 年有所下降。铜绿假单胞菌和鲍曼不动杆菌对常用抗菌药物的耐药率也在缓慢上升。2019 年铜绿假单胞菌耐药率有所下降，而鲍曼不动杆菌的耐药率，特别是对头孢类、碳青霉烯类的耐药率仍居高不下。抗菌药物使用频度（DDDS）分析，铜绿假单胞菌耐药率与左氧氟沙星和头孢他啶的使用频度呈高度正相关、与头孢曲松、亚胺培南和哌拉西林/他唑巴坦呈正相关、与头孢哌酮/舒巴坦、头孢呋辛、头孢吡肟和庆大霉素呈负相关。鲍曼不动杆菌耐药率与美洛培南使用频度呈显著的正相关，有统计学意义（$r=0.938$，$P=0.018$）、与头孢吡肟和庆大霉素呈正相关、与亚胺培南、加酶抑制剂抗生素、左氧氟沙星、头孢他啶、头孢呋辛呈负相关。

结论 铜绿假单胞菌和鲍曼不动杆菌对临床常用抗菌药物耐药率高。鲍曼不动杆菌除对头孢哌酮/舒巴坦较敏感外，对其它抗菌药物的耐药率均明显高于铜绿假单胞菌，细菌与临床常用抗菌药物的使用频度有一定的相关关系，为避免细菌耐药的快速发展,应加强抗菌药物的监管。

PU-3290

Evaluation of GeneXpert vanA/vanB in the early diagnosis of vancomycin-resistant enterococci infection

zhuolei li[1,2]、qibing luo[1,2]、shanshan xiao[1,2]、zehong lin[1,2]、yeling liu[1,2]、mengyi han[1,2]、jinghua zhong[1,2]、tianxing ji[3]、xuguang guo[1,2]
1. Guangzhou Medical University
2. 广州医科大学附属第三医院
3. 广州医科大学附属第二医院

Purpose Vancomycin-resistant enterococci (VRE) infection is a worrying worldwide clinical problem. To evaluate the accuracy of GeneXpert vanA/vanB in the diagnosis of VRE, we conducted a systematic review in the study.
Methods Experimental data were extracted from publications until May 03, 2021 related to the diagnostic accuracy of GeneXpert vanA/vanB for VRE in PubMed, Embase, Web of Science and the Cochrane Library. We used the summary receiver to operate characteristic curve (SROC curve), pooled sensitivity, pooled specificity, PLR(positive likelihood ratio), NLR (negative likelihood ratio), and DOR(diagnostic odds ratio) to evaluate the accuracy of GeneXpert vanA/vanB for VRE.
Results We divided the 9 studies into 3 groups according to two golden standard references, vanA and vanB group, vanA group, vanB group, including 6 researches, 5 researches and 5 researches, respectively. The pooled sensitivity and specificity of group vanA and vanB were 0.96 (95% CI, 0.93–0.98) and 0.90 (95% CI, 0.88–0.91) respectively. The DOR was 440.77 (95% CI, 37.92–5123.55). The pooled sensitivity and specificity of group vanA were 0.86 (95% CI, 0.81–0.90) and 0.99 (95% CI, 0.99–0.99) respectively, and those of group vanB were 0.85 (95% CI, 0.63–0.97) and 0.82 (95% CI, 0.80–0.83) respectively.
Conclusion GeneXpert vanA/vanB can diagnose VRE with high-precision and shows greater accuracy in diagnosing vanA.

PU-3291

High prevalence of Extended-spectrum beta-lactamases in Escherichia coli strains collected from strictly-defined community-acquired urinary tract infections in adults in China: a multicenter clinical microbiological study

Peiyao Jia、Ying Zhu、Xue Li、Yang Yang、Ge Zhang、Jingjia Zhang、Yingchun Xu、Qiwen Yang
Department of Clinical Laboratory, Peking Union Medical College Hospital, Peking Union Medical College, Chinese Academy of Medical Sciences

Objectives To investigate the susceptibility and Extended-spectrum beta-lactamases (ESBL) rates of community-acquired urinary tract infection (CA-UTI) Escherichia coli in Chinese hospitals.
Methods A total of 809 E.coli isolates from strictly- defined CA-UTIs in 10 hospitals (5 tertiary hospitals and 5 secondary hospitals) from different regions of China during 2016 to 2017 were collected and antimicrobial susceptibility testing was carried out by standard broth microdilution method. ESBL confirmation was conducted by the third generation cephalosporin +/- clavulanic acid test recommended by CLSI.

Results The ESBL positive/ ESBL negative/ ESBL uncertainty rate was 38.07%/ 58.96%/ 2.97% against E. coli strains isolated from CA-UTIs. The antimicrobial agents with susceptibility rates of greater than 90% included imipenem (99.9%), colistin (99.6%), ertapenem (98.9%), amikacin (98.3%), cefmetazole (97.9%), nitrofurantoin (96%), and fosfomycin (95.4%). However, the susceptibilities to first-, third- and fourth-generation cephalosporins were relatively low, varying from 58.6%-74.9%. Antimicrobial susceptibilities of imipenem, cefmetazole, colistin, ertapenem, amikacin and nitrofurantoin against ESBL-producing Escherichia coli strains were greater than 90%. The percentage of ESBL-producing strains was much higher in male patients (53.6%) than in female patients (35.2%) ($p<0.001$). The incidence of carbapenem-resistant E. coli from CA-UTI was 0.25% (2/809).
Conclusion Our study indicated high prevalence of ESBL in E. coli strains collected from strictly-defined community-acquired urinary tract infections in adults in China. Imipenem, colistin, ertapenem, amikacin and nitrofurantoin were the most active antimicrobials against ESBL positive E. coli isolates. The use of cephalosporins for empiric treatment of CA-UTIs should be based on local ESBL prevalence and the use of fluoroquinolone need to be restricted.

PU-3292

侵袭性真菌血流感染的分布情况及其危险因素的分析

史永胜、金英玉
哈尔滨医科大学附属第一医院

目的 了解哈尔滨医科大学附属第一医院侵袭性真菌血流感染的分布情况及其危险因素分析，为临床预防侵袭性真菌血流感染提供参考依据。
方法 收集哈尔滨医科大学附属第一医院 2016 年 1 月至 2019 年 1 月 12 例血培养结果为侵袭性真菌血流感染的标本的资料进行菌种分布、送检科室、年龄分布、感染的危险因素进行回顾性分析。
结果 在侵袭性真菌血流感染中，白色念珠菌和光滑念珠菌最多，各占 33.3%（4/12），其次为近光滑念珠菌 16.7%（2/12）。科室主要分布在新生儿科和 ICU 重症监护室，各占 33.3%（4/12）。年龄段最集中在婴幼儿，占 41.7%（5/12），其次是免疫力低下的中老年。侵袭性真菌血流感染的高危因素主要是广谱抗生素的使用以及气管插管，分别占 33.3%（4/12）和 25%（3/12），其次是外科手术 16.7%(2/12)。
结论 白色念珠菌和光滑念珠菌是我院侵袭性真菌血流感染中重要的病原菌，年龄、广谱抗生素的使用、气管插管、免疫力低下、外科手术等都是我院主要的侵袭性真菌血流感染的危险因素。

PU-3293

Development of a combined immunochromatographic lateral flow assay for accurate and rapid Escherichia coli O157:H7 detection

Yuanyuan Ye
the Second Affiliated Hospital of Chongqing Medical University

Escherichia coli O157:H7 (E. coli O157:H7) is an important pathogenic Bacterium that threatens human health. A convenient, sensitive and specific method for the E. coli O157:H7 detection is necessary. We developed two pairs of monoclonal antibodies through traditional hybridoma technology, one specifically against E. coli O157 antigen and the other specifically against E. coli H7 antigen. Using these two pairs of antibodies, we developed two rapid test kits to specifically detect E. coli O157 antigen and E. coli H7 antigen, respectively. The detection sensitivity for O157 positive E. coli is 1x103 CFU ml-1 and for H7 positive E. coli is 1x104 CFU

ml-1. Combining these two pairs of antibodies together, we developed a combo test strip that can specifically detect O157: H7, with a detection sensitivity of 1x104CUF ml-1, when two detection lines are visible to the naked eye.This is currently the only rapid detection reagent that specifically detects O157: H7 by simultaneously detecting O157 antigen and H7 antigens of E. coli. Our product has advantages of simplicity and precision, and can be a very useful on-site inspection tool for accurate and rapid detection of E. coli O157:H7 infection.

PU-3294

耐碳青霉烯酶肠杆菌科细菌表型检测方法的评价分析

陈弟、邓德耀、徐红云、杨宝瑞、刘春林、马众仙
云南大学附属医院

目的 探讨耐碳青霉烯酶肠杆菌科细菌各表型检测方法的敏感性、特异性。
方法 选取碳青霉烯酶耐药的肠杆菌科细菌（CRE）50 株，碳青霉烯酶敏感的肠杆菌科细菌 20 株，采用改良 Hodge 试验（MHT）、纸片筛选及协同试验、Carba NP 试验、改良碳青霉烯灭活试验(mCIM)分别对菌株进行检测，以 PCR 检测碳青霉烯酶基因为金标准，评估每种表型检测方法的能力。
结果 50 株 CRE 菌株中，44 株携带碳青霉烯酶耐药基因。以 PCR 试验为金标准，表型筛选试验结果显示，MHT 试验、纸片筛选及协同试验、Carba NP 试验、mCIM 试验的敏感性分别是 79.5%（35/44）、90.9%(40/44)、93.2%(41/44)和 97.7%（43/44），特异性分别是 80.8%（21/26）、92.3%(24/26)、96.2%(25/26)和 100%（26/26）。
结论 纸片筛选及协同试验、Carba NP 试验、mCIM 试验均具有较高的敏感性和特异性，但 mCIM 相较与其他俩种方法，具有更高的检出率和一致性，且该方法操作简单、结果容易判读，是耐碳青霉烯酶肠杆菌科细菌表型筛选的有效方法。

PU-3295

铜绿假单胞菌的临床分布及耐药性分析

史永胜、金英玉
哈尔滨医科大学附属第一医院

目的 讨论哈尔滨医科大学附属第一医院感染铜绿假单胞菌的各科室分布及对抗生素的耐药性特点，对临床正当运用抗生素以及干预措施进行正确指导，及时切断多重耐药菌株的传播。做法，收集哈尔滨医科大学附属第一医院 16 年和 17 年这两年哈尔滨医科大学附属第一医院分离拿到的 490 株铜绿假单胞菌，并且分别在血平板、伊红平板、巧克力平板和沙宝弱培养基上进行 24 小时培养，观察其菌落形态，并用纸片扩散法进行药敏试验，同时做细菌涂片，并用显微镜镜检，观察其结构特点。
结果 经过培养观察共分离鉴定出 490 株铜绿假单胞菌，其中来源于呼吸道的标本痰液、咽拭子总共 359 株；490 株铜绿假单胞菌大多分布在呼吸科、重症监护室，共 213 株，占总数的 43.47%；根据药敏结果显示，我们对铜绿假单胞菌用的 14 种药物都有不同的耐药结果表现，在所有的结果上看耐药性都比较低，不高于 16%，其中耐药率最低药物是阿米卡星，为 3.1%，其次是妥布霉素，为 4.9%；敏感性最低的是氨曲南和左旋氧氟沙星，分别是 15.5%，13.6%。
结论 铜绿假单胞菌分布广泛，遍及各种科室，来源于各种标本，呼吸道最易感染此菌，加强呼吸道的保护，注重呼吸科相应仪器设备的消毒灭菌，避免感染此菌。

PU-3296

Epstein Barr virus regulates the expression of PD-L1 in EBV Associated-gastric carcinoma and EBV positive cell lines through methylation

Zhongxin Jiang、Mengyang Liu
The Affiliated Hospital of Qingdao University

Objective Epstein Barr virus (EBV) is an important DNA virus, which is closely related to a variety of B cell or epithelial cell-derived tumors, with the carcinogenesis of epigenetics on gene and protein expression of the cells and their biological behaviors. Immunosuppressive tumor immunotherapy based on the negative regulatory pathways of CTLA-4/B7 and PD-1/PD-L1 is a hot topic in the field of tumor therapy in recent years, and improving its efficiency is the key point. The purpose of this study is to explore the mechanism of PD-L1 expression in EBV positive gastric cancer and corresponding cell lines, and to provide a theoretical basis for improving the efficiency of tumor immunotherapy.
Method PD-L1 expression in EBV positive and negative gastric cancer tissues was detected by in situ hybridization and immunohistochemistry, and the expression of PD-L1 in EBV positive and negative gastric cancer tissues and cell lines were detected by high-throughput sequencing and real-time quantitative PCR (RT-qPCR); MSP(Methylated Specific PCR) was used to detect the methylation of CpG sites of PD-L1 gene in EBV positive tumor tissues and cell lines, and BSP(Bisulfite Sequencing PCR) was used to detect the methylation status of 24 CpG sites in CpG island in the promoter region of PD-L1 gene.
Results (1) The expression of PD-L1 in EBV positive gastric cancer was significantly lower than that in EBV negative gastric cancer ($P < 0.05$); (2) High throughput sequencing and RT-qPCR showed that the expression of PD-L1 in EBV positive gastric cancer tissues and cell lines was significantly increased than that in EBV negative gastric cancer tissues and cell lines ($P < 0.001$); (3) MSP showed that the CPG site of PD-L1 gene was hypomethylated (U-type) in EBV positive tumor tissues and cell lines, while it was hypermethylated (M-type) in EBV negative tumor tissues and cell lines, BSP detection of 24 CpG islands in PD-L1 promoter region further verified the MSP results($P < 0.05$).
Conclusion EBV regulates the expression of PD-L1 by regulating the methylation status of PD-L1 gene promoter in EBV associated-gastric cancer and cell lines. This study provides a theoretical basis of epigenetic for the regulation of PD-L1 expression and improving of the effect of tumor immunotherapy.

PU-3297

耐碳青霉烯肺炎克雷伯菌(CRKP)的耐药性及耐药基因类型研究

谢印容、廖蕴惠
厦门市中医院

目的 分析耐碳青霉烯肺炎克雷伯菌(CRKP)的耐药性，并研究其耐药基因类型。
方法 以 2019 年 1 月-2019 年 12 月我院肺炎患者中分离出的 CRKP 共 31 株为研究材料，通过改良碳青霉烯类失活试验(mCIM)对其中碳青霉烯酶进行检测，并经聚合酶链反应(PCR)、测序法分析耐药基因的具体类型。
结果 31 株 CRKP 对亚胺培南、哌拉西林、氨苄西林/舒巴坦、替卡西林/棒酸表现出 100%耐药；mCIM 试验显示 CRKP 菌株阳性率 61.29%；碳青霉烯酶基因检测 KPC 型、IMP 型、NDM 型基因的检出率分别为 19.35%、16.13%、38.71%，ESBLs 基因检测 TEM 型、SHV 型、CTX-M3 型基因的检出率分别为 61.29%、77.42%、61.29%，Amp C 酶基因检测 DHA 基因的检出率为 12.90%。

结论 CRKP 对多种抗菌药物均存在比较高的耐药性，KPC-2、NDM-1 是主要耐药基因类型，必须强化做好院感防控工作，做好这类菌株播散的预防控制。

PU-3298

Chlamydia psittaci inclusion membrane protein CPSIT_0844 elicits inflammatory cytokines in human monocytes via TLR2/TLR4 signaling pathways

Xiaoliang Yan[1]、Dan Luo[2]、Kang Zheng[1]、Wenheng Qing[1]
1. Affiliated HengYang central Hospital，Southern Medical University
2. 南华大学附属南华医院

The respiratory disease caused by Chlamydia psittaci infection may be associated with inflammation. However, the molecular mechanisms of C. psittaci leading to the production of proinflammatory cytokines have not been thoroughly elucidated. In our study, we demonstrated that the C. psittaci inclusion membrane protein CPSIT_0844 induced THP-1 cells to express IL-6 and IL-8. Moreover, silencing of Toll-like receptor 2 and Toll-like receptor 4 genes and transfection with the dominant negative plasmid encoding MyD88 were found to reduce the expression of IL-6 and IL-8 in THP-1 cells stimulated with CPSIT_0844. Furthermore, we found that CPSIT_0844 induces IL-6 and IL-8 production through MAPK and NF-κB signaling pathways by Western blotting. These results showed that CPSIT_0844 recognized by TLR2 and TLR4 promoted the expression of IL-6 and IL-8 in THP-1 cells through MyD88 mediated the activation of MAPK and NF-κB signaling pathways, which will promote our understanding of the pathogenesis of C. psittaci.

PU-3299

基于语言模型的原核病毒结构蛋白识别

方臻成、周宏伟
南方医科大学珠江医院检验医学部

目的 病毒与其宿主的相互作用是影响人体微生态的重要因素之一。因传统研究均依赖于培养菌株，人体微生物组中相当一部分的原核病毒以“暗物质”的形式存在。宏基因组测序理论上提供了病毒组序列的全景数据，但该数据中大量无法识别的结构蛋白成为病毒检测与研究微生物群落病毒组成、病毒宿主相互作用的瓶颈。本研究旨在开发高效的原核病毒结构蛋白识别算法，以促进病毒对微生物群落调控机制的研究。
方法 我们利用人工智能领域中自然语言处理的“分布式表示”数学模型对蛋白序列进行刻画。该方法将相邻的三个氨基酸映射为一“词向量”，蛋白序列中所有三氨基酸“词向量”的平均向量为该蛋白的特征向量。我们用基于该特征向量的随机森林算法对原核病毒结构蛋白进行识别。
结果 基于 t-SNE 的可视化结果显示，结构蛋白与非结构蛋白的“分布式表示”特征向量具有显著不同的空间分布。在基准测试集的性能评估中，我们提出的方法对结构蛋白的识别性能，比目前已有的 iVIREONS、PVPred、PVP-SVM、PVPred-SCM、Meta-iPVP、PhANNs、VirionFinder 工具高出约 8%-24%。此外，我们观察该方法对细菌蛋白的判断情况，结果显示，尽管在构建算法的训练集数据中不包含细菌蛋白，但算法仅将 2.09% 的细菌蛋白误判为病毒的结构蛋白。这表明词向量能对病毒蛋白进行良好的表征，使该方法在实际使用中不受非病毒蛋白的影响。
结论 利用语言模型对蛋白序列进行刻画显著提升了病毒结构蛋白的识别，为病毒组大量未知的结构蛋白注释提供了更好的技术保障，并有望进一步帮助生物学家认识病毒群落的物种结构及病毒对宿主的相互作用。

PU-3300

秀丽隐杆线虫感染产碳青霉烯酶肺炎克雷伯菌的转录反应

曹玲
南昌市第一医院

目的 建立秀丽隐杆线虫－产碳青霉烯酶肺炎克雷伯菌感染模型，并通过观察感染过程中线虫状态确定时间点，为了进一步理解线虫感染产碳青霉烯酶肺炎克雷伯菌的宿主防御机制。
方法 将产碳青霉烯酶肺炎克雷伯菌与线虫共培养，建立线虫－产碳青霉烯酶肺炎克雷伯菌感染模型，使用高通量 RNA 测序（RNA-seq）来量化产碳青霉烯酶肺炎克雷伯菌感染后的宿主 mRNA 水平。
结果 产碳青霉烯酶肺炎克雷伯菌能够感染线虫并致其死亡，CRKP 感染激活线虫中 p38-MAPK 途径的先天免疫防御反应，且 ROS 可能介导 CRKP 感染线虫的致死作用。
结论 通过对线虫感染后不同时间点基因表达谱的研究了解 CRKP 感染线虫后，寿命调控因子 daf-2 通过激活 FoXo 途径产生过氧化物等 ROS 介导对线虫的致死作用。

PU-3301

一例疑似棒孢霉菌感染的实验室菌株分离鉴定及蛋白指纹图谱数据库的建立

张婷、程建军
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 对 1 株疑似棒孢霉菌感染的病原菌进行分离鉴定，并应用 MALDI-TOF-MS 自建棒孢霉菌蛋白指纹图谱数据库，实现对该细菌的快速鉴定。
方法 研究和比较记录体外分离棒孢霉菌在不同培养条件下的菌落形态、染色形态、产孢特征。采用甲酸萃取法进行棒孢霉菌蛋白指纹图谱的添加,并用不同培养条件下的棒孢霉菌株对图谱进行验证。
结果 体外分离棒孢霉菌在 35℃和 28℃均可生长，37℃时生长更好。在固体培养基上比液体培养基内生长更好，更有利于产孢。在寡营养琼脂上比富营养琼脂更有利于产孢。采用新的棒孢霉菌蛋白指纹图谱鉴定时，甲酸萃取法鉴定准确率为＞90%。
结论 临床分离疑似棒孢霉菌时，可选取寡营养琼脂分离纯化，35℃培养后进行形态学鉴定或质谱鉴定。添加的棒孢霉菌蛋白指纹图谱能快速准确地鉴定棒孢霉菌,此图谱可以应用于棒孢霉菌的临床快速准确诊断。

PU-3302

2020 年四川地区腹水标本检出细菌的分布及其耐药性分析

常凡
电子科技大学附属医院·四川省人民医院

目的 了解 2020 年四川地区腹水送检标本中细菌检出的分布及其耐药情况，为本省临床合理应用抗菌药物提供实时依据。
方法 对四川省细菌耐药监测网成员单位 2020 年度腹水标本的细菌分布及耐药情况进行回顾性分析，参照美国临床实验室标准化研究协会(CLSI)2020 年标准，采用纸片扩散法、E-test 法或自动化仪器检测法进行药敏试验, 使用 WHONET 5.6 软件进行数据分析。

结果 2020 年度四川地区腹水标本共分离出 3363 株非重复细菌,其中革兰阳性菌 936 株,占比 27.8%,革兰阴性菌 2427 株,占比 72.2%。 前五名最常见的细菌依次为大肠埃希菌、肺炎克雷伯菌、屎肠球菌、铜绿假单胞菌、粪肠球菌。金黄色葡萄球菌中耐甲氧西林金黄色葡萄球菌 (MRSA)的检出率为 32.9%，凝固酶阴性葡萄球菌中耐甲氧西林凝固酶阴性葡萄球菌(MRCNS)的检出率为 78.1%，未发现万古霉素、替考拉宁及利奈唑胺耐药菌株；粪肠球菌和屎肠球菌对氨苄西林耐药率分别为 3.7%和 75.4%。碳青霉烯类耐药铜绿假单胞菌的检出率为 5.0%，碳青霉烯类耐药鲍曼不动杆菌的检出率为 47.1%，三代头孢菌素、喹诺酮类及碳青霉烯类耐药大肠埃希菌的检出率分别为 45.2%、51.4%和 1.0%。

结论 四川地区腹水标本送检分离细菌对常见抗菌药物的耐药形势仍较严峻,临床科室应进一步重视腹水等无菌体液标本的细菌学检查，积极主动与微生物检验室进行沟通，充分利用本地区细菌耐药监测结果进行感控管理,促进抗菌药物合理应用，加强感染预防控制。

PU-3303

2020 年四川地区胸水标本检出细菌的分布及其耐药性分析

常凡
电子科技大学附属医院·四川省人民医院

目的 了解 2020 年四川地区胸水送检标本中细菌检出的分布及其耐药情况，为本省临床合理应用抗菌药物提供实时依据。

方法 对四川省细菌耐药监测网成员单位 2020 年度胸水标本的细菌分布及耐药情况进行回顾性分析，参照美国临床实验室标准化研究协会(CLSI)2020 年标准，采用纸片扩散法、E-test 法或自动化仪器检测法进行药敏试验, 使用 WHONET 5.6 软件进行数据分析。

结果 2020 年度四川地区胸水标本共分离出 849 株非重复细菌,其中革兰阳性菌 462 株,占比 54.4%,革兰阴性菌 387 株,占比 45.6%。 前五名最常见的细菌依次为大肠埃希菌、金黄色葡萄球菌、肺炎克雷伯菌、表皮葡萄球菌和屎肠球菌。金黄色葡萄球菌中耐甲氧西林金黄色葡萄球菌 (MRSA)的检出率为 27.8%，凝固酶阴性葡萄球菌中耐甲氧西林凝固酶阴性葡萄球菌(MRCNS)的检出率为 73.4%，未发现万古霉素、替考拉宁及利奈唑胺耐药菌株；屎肠球菌和粪肠球菌对氨苄西林耐药率分别为 95.7%和 5.9%，均未发现万古霉素和利奈唑胺耐药株。碳青霉烯类耐药铜绿假单胞菌的检出率为 7.7%，碳青霉烯类耐药鲍曼不动杆菌的检出率为 40.5%，三代头孢菌素、喹诺酮类及碳青霉烯类耐药大肠埃希菌的检出率分别为 67.4%、62.5%和 5.2%。

结论 四川地区胸水标本送检分离细菌对常见抗菌药物的耐药形势仍较严峻,MRSA 检出率较 2019 年有所下降，但碳青霉烯类耐药肺炎克雷伯菌(CR-KPN)、三代头孢菌素和喹诺酮类耐药大肠埃希菌检出率仍明显高于整体检出率。临床科室应进一步重视胸水等无菌体液标本的细菌学检查，充分利用本地区细菌耐药监测结果进行感控管理,促进抗菌药物的合理使用。

PU-3304

抗具核梭杆菌多抗血清的制备、应用及评价

王昆
重庆市人民医院（三院院区）

目的 制备抗具核梭杆菌(Fusobacterium nucleatum，其抗原简写为 Fn)多抗血清，评价不同处理方式对抗原免疫原性的影响。

方法 采用甲醛灭活、热灭活、超声破碎 3 种方式处理细菌抗原接种新西兰兔和 c57 小鼠，检测不同抗原免疫动物抗血清的 ELISA 效价[1][k1] 。

结果 (1)ELISA 方案最佳条件：兔抗 Fn 抗体，二抗稀释度为 1 / 5000，抗原包被浓度为 4ug / ml ；小鼠抗 Fn 抗体，二抗稀释度为 1 / 5000，抗原包被浓度为 10ug / ml； (2)超声破碎抗原(UT-Fn)免疫新西兰兔和小鼠的抗血清 ELISA 效价分别高达 1 / 128000 与 1/256000。热灭活抗原(HT-Fn)抗血清 ELISA 效价达 1 / 64000。 (3)甲醛灭活抗原（FT-Fn）抗血清 ELISA 效价达 1 / 64000。 (3) UT-Fn 具有较强的免疫原性，HT-Fn 与 FT-Fn 在小鼠与新西兰兔中的免疫原性相对较弱(P<O，05)。
结论 建立了抗具核梭杆菌多克隆抗体的检测方法，制备了高效价的具核梭杆菌多抗血清；甲醛灭活和热灭活细菌具有较好的免疫原性，为下一步具核梭杆菌的原位检测打下了基础 。

PU-3305

9 株分离自住院患者 CA-MRSA 基因型菌株的分子特征及耐药性研究

王院霞、姚锂凤、陈旭
上海交通大学医学院附属第九人民医院

目的 分析自住院患者分离的社区获得耐甲氧西林金黄色葡萄球菌（community-associated methicillin-resistant Staphylococcus aureus, CA-MRSA）菌株的分子水平特征和耐药性，为治疗、控制 CA-MRSA 感染提供研究依据。
方法 收集 2014 年 4 月到 2015 年 12 月临床住院患者入院后 48h 内获取的标本中分离的金黄色葡萄球菌，检测其 mecA 基因以区分耐甲氧西林金黄色葡萄球菌（methicillin-resistant Staphylococcus aureus,MRSA）与甲氧西林敏感的金黄色葡萄球菌（methicillin-sensitive Staphylococcus aureus,MSSA），并根据葡萄球菌染色体基因盒 mec（Staphylococcal cassette chromosome mec,SCCmec）的携带情况筛选基因型 CA-MRSA 菌株，采用金黄色葡萄球菌 A 蛋白（Staphylococcus protein A,spa）基因分型、多位点序列分型（multilocus-sequence typing,MLST）等方法分析 CA-MRSA 菌株的分子水平特征，根据美国临床实验室标准化研究所（Clinical and Laboratory Standards Institute,CLSI）指南，采用纸片扩散法检测 CA-MRSA 菌株的药物敏感性，并对 CA-MRSA 菌株是否携带杀白细胞素基因（panton-valentine leukocidin gene,pvl 基因）进行检测。
结果 共收集到 147 株金黄色葡萄球菌，其中 MRSA 58 株，根据 SCCmec 分型结果,共有 CA-MRSA 9 株，包括 SCCmecIV 3 株、SCCmecV 6 株；9 株 CA-MRSA 菌株均有对不同的非 β-内酰胺类抗生素均耐药，其中有 8 株对红霉素和克林霉素耐药，主要是由 erm(B)基因介导；有 8 株对氨基糖苷类药物（主要为卡那霉素）耐药；对其进行分子流行病学特征分析后发现，CA-MRSA 主要以 t437-ST59 为主，其他还有 t034-ST804、t127-ST1、t008-ST8、t437-ST338 等，9 株 CA-MRSA 菌株中有 5 株携带毒力基因 pvl。
结论 致病性较强的 CA-MRSA 菌株逐渐进入医疗环境中，且对非 β-内酰胺类药物的耐药性也逐渐增加，应加强对住院患者 CA-MRSA 分离株的监控。

PU-3306

艰难梭菌肠道外感染

赵海
陕西省人民医院

Clostridioides (Clostridium) difficile is the major cause of healthcare antibiotic-associated diarrhoea. However, extra-intestinal manifestations of Clostridioides (Clostridium) difficile infection (CDI) (including bacteremia and tissue infection) are extremely rare. We report a case of extraintestinal CDI after surgery. The isolate of C. difficile was not the PCR ribotype 027.

However, this isolate produced toxins A and B. The patient underwent a follow-up examination 30 days after discharge, which showed complete recovery. This case report adds to existing knowledge of CDI.

PU-3307

分子生物学检测方法与传统方法检测结核病的比较研究

乔相练
庆云县人民医院

目的 对比传统方法与分子生物检测方法检测结核病的效果。
方法 选取 2020 年 1 月~2020 年 12 月在本院就诊的疑似结核病患者 80 例作为研究对象，所有患者均采用传统方抗酸杆菌涂片、分枝杆菌培养法和分子生物检测方法，对比三种检测方法的实施效果。
结果 传统方法的抗酸杆菌涂片检查诊断阳性率 62.5%，分枝杆菌培养诊断阳性率 70%。分子生物检测方法诊断阳性率 82.5%，分子生物检测方法高于传统方法的抗酸杆菌涂片和分枝杆菌培养的诊断阳性率，三种检测方法差异具有统计学意义（P<0.05）。
结论 在结核病的检测中，分子生物检测方法简便快捷，灵敏度高，具有较高的诊断和鉴别诊断价值，适合在临床推广应用。

PU-3308

单细胞测序在病原学发展中的价值

蔡阳
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 单细胞测序（Single-cell Sequencing，SCS）可用于探索未知病原微生物或者已知病原体的未知功能基因，通过分析核酸序列检测和鉴定物种，监测耐药株的出现，甚至在分子水平研究病原微生物的进化机制和感染动力学。然而，目前单细胞测序技术在临床应用中面临很多难题。
方法 查阅近 5 年的文献，归纳和总结单细胞测序技术在病原学发展中的价值。
结果 单细胞测序的技术过程包括单细胞分离、核酸序列扩增、基因测序和数据分析。其技术难点在于分离单个细胞及核酸序列扩增策略的选择。
可有较多信息产出的单细胞分离技术的主要方法有 FACS、MACS，但是会存在偏倚，可以收集的参数主要有细胞表面标志物的表达等。同时，需要对单细胞 RNA 序列谱和表型进行联合分析以得到特定的细胞表型与转录特征之间的联系，有助于识别针对病毒表型的新生物标记。
随着科技的发展，在扩增策略方面近些年的理念正不断更新完善。如，Christoph 等对六种单细胞测序常用的方法的性能进行比较，为方法的选择提供了依据。Yin 等对传统的单细胞基因组测序方法进行改进，提出一种结合了组合索引和线性扩增的单细胞测序方法-sci-L3，提升了通量和均匀性的水平。Guo 及其团队开发了一个可对单个细胞中的病毒感染进行动力学分析的基于微流体的高通量平台。通过该平台，研究了上千名脊髓灰质炎患者的病毒感染动力学，发现由于突变负荷，抗病毒药物对每个病毒的消灭能力不同，解释了为何病毒感染动力学与模型推测不符的原因，阐明了病毒种群逃避药物的作用机制。
除此之外，近些年使用单细胞测序技术检测真菌的试剂盒也已问世，填补了这一方面的空白。
结论 然而，单细胞测序费用高昂，若想在临床推广还有很多路要走。除此之外，该技术还有以下几方面需要注意：①在检测前的样本采集和保存阶段，要注意样本的新鲜，如果无法及时检测，可根据需要加入适宜的保护剂；②单细胞分选阶段仍旧存在细胞交叉污染、细胞损伤的可能，目前的技术尚无法完全避免该问题；③DNA 或 RNA 扩增过程中依旧会出现扩增失败及产生大量非特异性

产物的情况，严格控制实验条件以减少此类事件的发生，当然，我们相信过不断改进的扩增技术也会逐步降低该类事件的发生。

PU-3309

肿瘤医院妇科患者支原体和衣原体检查结果分析

周友全[1]、宴君[2]
1. 昆明医科大学第三附属医院（云南省肿瘤医院）
2. 昆明医科大学 2017 级医学检验技术专业

目的 为了明确肿瘤医院的妇科患者生殖道分泌物标本中支原体和衣原体的检出率；支原体、衣原体阳性患者的年龄和疾病的分布情况；以及不同类型支原体对抗菌药物的敏感情况。
方法 收集云南省肿瘤医院检验科细菌室从 2018 年 2 月到 2020 年 9 月的女性阴道支原体、衣原体检查结果。标本检测采用安图生物支原体培养鉴定药敏试剂盒、安图生物沙眼衣原体检测试剂盒。统计分析标本中支原体和衣原体检出情况及支原体的药敏结果。
结果 1557 份标本的检测结果中，沙眼衣原体的阳性率为 13.49%（210/1557），支原体的阳性率为 53.63%（835/1557），其中支原体计数＞104cfu/ml 的占比为 59.9%。单纯人型支原体感染构成比为 4.43%，人型支原体与解脲脲原体混合感染的比例为 15.69%，单纯解脲脲原体感染比比例为 79.88%。支原体、衣原体阳性标本中，妇科患者的年龄分布最大占例为≤44 岁，其次为年龄在 45-54 岁，年龄≥65 岁占比最小。支原体阳性患者中临床诊断为宫颈癌的概率较高，达 74.38%，其他良性疾病概率不高，如子宫肌瘤占 6.09%。人型支原体对红霉素、克拉霉素耐药率较高，对交沙霉素、多西环素敏感率较高。解脲脲原体对克林霉素耐药率较高，对多西环素、米诺环素敏感率较高。人型支原体和解脲脲原体混合感染时对红霉素、克拉霉素耐药率较高，对米诺环素、多西环素敏感率较高。
结论 女性泌尿生殖道支原体和衣原体有混合感染或单纯感染。不同妇科疾病、不同年龄阶段与支原体感染相关性不同，临床可以根据患者的相关情况进行支原体检查，以便及时进行治疗。不同类型支原体感染对抗菌药的敏感性也不同，临床可根据感染类型的差异和药敏结果，选用合理的抗菌药，来保证患者治疗的高效性和减少耐药菌株的出现。

PU-3310

血清 IFI27mRNA 监测甲型流感病毒感染进程的临床意义

韦栋、于德敏、张东华、张欣欣
上海交通大学医学院附属瑞金医院

目的 甲型流感病毒（IAV）感染进程的实时监测长期以来一直缺乏有效的技术手段，临床仅能通过常规炎症指标及影像学结果进行大致评估。本研究通过针对临床样本的回顾性研究分析与体外研究验证，尝试探究甲型流感病毒感染患者外周血干扰素刺激因子 IFI27 作为一种新型宿主生物标志物用于监测病毒感染进程的可行性。
方法 通过综合 261 例临床呼吸道感染患者（包括甲型流感患者组 148 例，非甲流呼吸道病毒感染患者组 55 例，细菌性感染患者组 58 例）的临床信息，分析各类感染患者血清 IFI27 mRNA 的表达水平及动态变化，并与 103 例健康人对照进行比较。比较血清 IFI27 mRNA 表达水平与甲型流感病毒感染患者感染进程之间的相关性，评估其作为 IAV 感染进程监测指标的临床应用价值。
结果 通过分析瑞金医院 2018-2019 年 261 例呼吸道感染住院患者的外周血样本、上呼吸道样本及临床资料，发现甲流病毒感染患者的血清 IFI27mRNA 表达水平显著高于其他各组。使用血清 IFI27mRNA 用于区分住院患者中 IAV 感染与细菌感染及非甲流呼吸道病毒感染的 ROC 曲线下面积分别可达 81.8%与 77%。针对其中 87 例 IAV 感染住院患者选取五个时间点进行持续监测（入院

后 1 天、3 天、5 天、7 天及出院时），结合血清外泌体及细胞感染模型的 RNA-Seq 分析结果，发现在 IAV 感染中血清 IFI27 的 mRNA 水平相比较于其他分子具有更好的特异性和相关性，，可以随患者住院时间点不同保持动态变化，其变化趋势在入院 1-5 天内同患者体温及 CRP 一致性较差，但与肺部影像学结果一致。当血清 IFI27 mRNA 水平下降到较低水平时，患者体温及 CRP 通常也伴随性回落，特别是出院时，绝大多数甲型流感病毒感染患者的血清 IFI27 mRNA 均下降到极低水平。上述结果表明血清 IFI27 mRNA 表达水平可以随着患者的感染进程而动态变化。此外，IAV 感染导致重症肺炎患者血清 IFI27 mRNA 峰值水平显著高于轻中度感染患者。进一步利用体外细胞及动物感染模型的验证实验结果与临床观察结果一致。

结论 血清 IFI27mRNA 水平不仅可以显著区分甲型流感病毒感染与其他病毒及细菌性感染，同时还可以直接反映甲型流感病毒感染患者的感染进程。

PU-3311

Study on the characteristics of intestinal microorganism disorder in patients with lung cancer

Xingbing Lu 、Xie Yi
Department of Laboratory Medicine,West China Hospital,Sichuan University

Objective Lung cancer is a malignancy with high morbidity and mortality worldwide. More evidences indicated that gut microbiome plays an important role in the carcinogenesis and progression of cancers by metabolism, inflammation and immune response. However, the study about the characterizations of gut microbiome in lung cancer is limited.

Method In this study, the fecal samples were collected from 20 healthy individuals and 40 lung cancer patients who were analyzed using 16S rRNA gene amplicon sequencing.There were 20 cases of adenocarcinoma and 20 cases of squamous cell carcinoma, including 7 cases of metastases and 33 cases of lung metastases.

Result the number of OTUs in each sample is between 448 and 1837.At the phylum level, Bacteroidetes (45.61%), Firmicutes (33.19%), Proteobacteria (15.83%), Actinobacteria (2.91%) and Fusobacteria (1.72%) were the most common in lung cancer patients, accounting for 99.27% of the total intestinal bacteria. At the genus level, Bacteroides (28.43%), Faecalibacterium (6.96%), Prevotella_9 (6.64%), Escherichia-Shigella (5.76%) and Klebsiella (4.90%) are the most common in lung cancer patients, accounting for 52.71%of the total intestinal bacteria.Species with higher ADC abundance correlation are Armatimonadetes and Caldiserica; species with higher SCC abundance correlation are Synergistetes and Thaumarchaeota; Nonmetastasis species with higher abundance correlation are: Planctomycetes, Caldiserica, Elusimicrobia, WPS-2 and Synergistetes ; Species with higher correlation of metastasis abundance are: Thaumarchaeota; Control: Zixibacteria, Dependentiae and Entotheonellaeota.No significant difference was observed in alpha diversity between LC patients and healthy controls.The result indicates that alpha diversity of the gut microbiota in ADC (and Metastasis) groups was higher than that of healthy control in terms of good coverage (P=0.016).Metastasis was lower than that of healthy control in terms of chao1 and PD whole tree (P=0.041,P=0.041).The alpha diversity of the gut microbiota was no differences between each SCC group and healthy control group. The principal coordinates analysis (PCoA) and ADONIS test based on unweighted uniFrac distance and binary jaccard distance indicated the stool microbiome composition and abundance of lung cancer patients clustered significantly separately from that of healthy controls ($p < 0.05$) .With a standardized importance value of 2.0-bit threshold, Subdoligranulum (MDG=2.130) and Parabacteroides (MDG=2.027) are the characteristic microbial flora of the healthy control group, which can be completely distinguished from LC patients.At the same time, Lachnospira and Parabacteroides can well screen out SCC patients.The Kyoto Encyclopedia of Genes and Genomes (KEGG) and COG annotation demonstrated decreased abundance of some dominant metabolism-related pathways in the lung cancer.

Conclusion This study explored the characteristics of the gut microbiota in patients with lung cancer for the first time. The systematic and multi-level assessment of the role of gut microbes in laparoscopic cholecystectomy provided basic guidance, suggesting that the gut microbiota may be a microbial marker It has the potential for early prevention and targeted intervention.

PU-3312

耐碳青霉烯类抗菌药物的铜绿、肺克及鲍曼的医院感染特征分析

李愿
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 探讨耐碳青霉烯类抗菌药物的铜绿假单胞菌、肺炎克雷伯菌及鲍曼不动杆菌的医院感染特征，推动医院感染耐药细菌的防治工作。
方法 选取苏州市独墅湖医院 2020 年 1 月至 2021 年 5 月，经临床检测中心微生物实验室鉴定临床样本培养结果为阳性的 129 个病例。采用质谱仪鉴定菌株，M50 药敏仪检测耐药情况。统计对碳青霉烯类抗菌素亚胺培南和美罗培南“耐药”的菌株作为耐碳青霉烯类抗菌药物菌株。
结果 在 129 个病例中，感染铜绿假单胞菌 55 例，其中碳青霉烯类耐药铜绿假单胞菌 23 例，占 41.82％；肺炎克雷伯菌共 51 例，碳青霉烯类耐药肺炎克雷伯菌 12 例，占 23.53％；鲍曼不动杆 23 例，碳青霉烯类耐药鲍曼不动杆菌 13 例，占 56.52％。所有耐碳青霉烯类药物共 48 例，其中 23 例为铜绿假单胞菌感染，12 例为肺炎克雷伯菌感染，13 例为鲍曼不动杆菌感染。其中耐亚胺培南有 48 例，耐美罗培南者 46 例，二者全部耐药 46 例。48 例均为下呼吸道感染病例，耐药菌株均从痰液及支气管灌洗液样本中分离，其中从痰液中分离的有 46 例，从支气管灌洗液中分离的有 2 例。
结论 本医院作为 2020 年 1 月新开设的医院，在开业半年内出现如此多的耐碳青霉烯类抗生素的菌株，一方面可能由于病人和医护人员在苏州市各医院之间的流动性导致，另一方面不排除敏感菌的耐药突变，产生的原因值得深入分析为新医院的感染控制提供理论支持。同时，医院应加强管理，执行严格的隔离预防措施，积极控制，及时遏止其在医院内的传播和流行。

PU-3313

Gut Microbiota Dysbiosis in Patients with Preeclampsia: A Systematic Review

卿维、史艺雅、周宏伟、陈慕璇
南方医科大学珠江医院

Currently, the etiology of preeclampsia (PE) has not been comprehensively clarified. Accumulating evidence indicated that gut microbiota is associated with the onset of PE. Herein, a systematic review was conducted to explore the dysbiosis of gut microbiota in PE patients compared with healthy controls (HCs). Publications were retrieved from Medline, EMBASE, Web of Science and Scopus. Studies comparing the composition of gut microbiota in PE patients to HCs using culture-independent Methods were included. In total, six studies with an overall sample size of 416 PE patients and 704 HCs were included. In terms of alpha- and beta-diversity, consistent results reflecting the dysbiosis of gut microbiota were observed in PE patients. Furthermore, Fusobacterium enriched, while Lachnospira, Akkermansia, Faecalibacterium and Alistipes were depleted in PE. This systematic review demonstrates significant dysbiosis of gut microbiota in PE patients, and confirms that that the possible correlations between gut microbiota dysbiosis and PE onset.

PU-3314

Inflammasomes restrain cytosolic Chlamydia trachomatis growth through GSDMD-mediated pyroptosis in macrophages

Ping Jiang、Xiaojing Feng、Yiyuan Fang、Lingli Tang
Second Xiangya hospital

Purpose Chlamydia trachomatis (Ct), an obligate intracellular Gram-negative bacterium, is a major cause of human sexually transmitted disease. Activation of inflammasomes plays a crucial role in the immune responses generated during C. trachomatis infection. However, the mechanism of inflammasome-mediated defense against C. trachomatis remains unclear. Thus, we aimed to explore anti-Ct effector mechanisms triggered by the inflammasome activation in macrophages.

Methods RAW264.7 cells were infected and uninfected with Ct. The morphological changes of macrophages after Ct infection were observed by inverted optical microscopy and transmission electron microscopy. PI fluorescence staining intensity and LDH release were used to evaluate the membrane permeability of macrophages infected with Ct. The secretion of IL-1β and IL-18 in the cultured supernatant, the activation of GSDMD, the canonical inflammasome NLRP3/caspase-1and non- canonical inflammasome caspase-11, and the expression of the Ct mark protein cHSP60 in the cell lysate were detected by Western Blot. Indirect immunofluorescence was used to detect the number and size of intracellular Ct inclusions. Intracellular Ct survival was evaluated by reinfection of Hela cells with the lysate of macrophages infected with Ct. To investigate the mechanisms by which inflammasomes defend against Ct infection in macrophages, the NLRP3 inhibitor MCC950, caspase-1 inhibitor Ac-YVAD-cmk and caspase-11 inhibitor Wedelolactone were used to pretreat macrophages. To study the effect of GSDMD-mediated pyroptosis during Ct infection, GSDMD-NT inhibitor Necrosulfonamide was used to pretreat macrophages.

Results Compared with uninfected macrophages, infected macrophages showed typical morphological changes of pyroptosis: cell swelling, characteristic large bubbles, fragmented cell membranes and organelle damage. High PI fluorescence intensity, the elevation of LDH release and IL-1β and IL-18 secretion suggested that membrane permeability of macrophages increased after infection with Ct. Both Canonical inflammasome NLRP3/caspase-1 and non-canonical inflammasome caspase-11 were activated in macrophages infected with Ct, which subsequently cleaved GSDMD into GSDMD-NT then induced pyroptosis. Blocking the activation of canonical and non-canonical inflammasomes significantly reduced GSDMD-mediated pyroptosis and increased Ct yield in macrophages. Consistently, direct inhibition of membrane perforation activity of GSDMD-NT significantly promoted the Ct growth in macrophages, including increased inclusion number and size, and infectious yield.

Conclusions The results demonstrate that GSDMD-dependent pyroptosis triggered by both canonical inflammasome NLRP3/caspase-1 and non-canonical inflammasome caspase-11 plays a critical role in restricting Ct infection in macrophages. This study reveals novel therapeutic targets for treating Ct infection.

PU-3315

胶体金免疫层析法快速检测 CRE 菌株碳青霉烯酶的应用评估

姚锂凤、郑巧平、杨蒙、罗清琼、陈旭、陈福祥
上海交通大学医学院附属第九人民医院

目的 评估胶体金免疫层析法快速检测耐碳青霉烯类肠杆菌科（Carbapenem-Resistant Enterobacteriaceae, CRE）菌株中碳青霉烯酶类别的临床应用价值。
方法 收集上海交通大学医学院附属第九人民医院 2016 年分离自临床标本的 CRE 菌株 73 株，采用聚合酶链反应（PCR）技术鉴定碳青霉烯酶的基因型，并采用胶体金免疫层析法（Colloidal Gold Immunochromatograohic Assay, GICA）对这些菌株的碳青霉烯酶进行快速检测，同时以 PCR 法为参考方法评估 GICA 法在快速检测碳青霉烯酶的准确度和临床应用价值。
结果 PCR 法结果显示 73 株 CRE 菌株中有 51 株为 blaKPC 基因阳性（69.9%），19 株为 blaNDM 基因阳性（26.0%），2 株为 blaIMP 基因阳性（2.7%），1 株为 blaVIM 基因阳性（1.4%），未检测到 blaOXA 基因阳性菌株；采用胶体金免疫层析法对这些菌株进行碳青霉烯酶检测，结果显示 GICA 法对 blaKPC 阳性菌株酶型检测准确度为 100% (51/51)，对 blaNDM 阳性菌株酶型检测准确度为 100%（19/19），对 blaIMP 阳性菌株酶型检测准确度为 100%（2/2），对 blaVIM 阳性菌株酶型检测准确度为 100%（1/1）。
结论 GICA 法与 PCR 方法在检测 CRE 菌株碳青霉烯酶类型中的一致性为 100%。 GICA 法具有简便快速、准确度高等特点，在早期监测临床耐碳青霉烯类菌株和抗感染治疗中具有重要的应用前景。

PU-3316

427 株无乳链球菌的临床分布及耐药性分析

陈坤[1]、黄程鑫[2]、张胜行[1]、李卫滨[1]
1. 联勤保障部队第九〇〇医院
2. 福建医科大学福总临床医学院检验科

目的 分析无乳链球菌的临床分布及其对常用抗生素的药物敏感性情况，为临床防治孕妇或新生儿无乳链球菌感染提供依据。
方法 回顾性分析 2018 年 1 月~2020 年 12 月自中国人民解放军联勤保障部队第九〇〇医院门诊和住院患者的标本中分离出的无乳链球菌。分离株均经 VITEK-MS 全自动微生物鉴定质谱分析仪鉴定为无乳链球菌，而后使用 ATB 半自动微生物鉴定及药敏分析系统对经分纯培养后的无乳链球菌进行药物敏感性试验。
结果 共收集 427 株无乳链球菌临床分离株，主要分离自阴道分泌物（46.1%）、精液（24.4%）、中段尿（15.9%）。患者主要来自妇产科（41.9%）、生殖助孕中心/不孕不育专科（24.4%）、泌尿外科（7.3%）。药敏结果显示，无乳链球菌对四环素、红霉素和克林霉素有较高的耐药率，分别为 77.7%、68.6%和 57.7%。对左旋氟氧沙星中等耐药（28.6%），偶见对青霉素（1.5%）和头孢噻肟（0.5%）不敏感的菌株。本次试验未发现对万古霉素和利奈唑胺耐药的分离株。对阴道分泌物中检出的无乳链球菌的患者按照年龄分组分析，分析结果表明各年龄段的分离率差异无统计学意义（$\chi2=3.654$，$P>0.05$），表明年龄不是本院阴道分泌物中无乳链球菌分离率的影响因素。
结论 无乳链球菌主要寄生于人类泌尿生殖道，孕妇是无乳链球菌感染的高风险人群。在药敏结果未报告之前，青霉素和其它 β-内酰胺酶类药物可以作为防治其感染的经验用药。其对四环素、红霉素和克林霉素的耐药率较高，临床需根据药敏结果合理选用抗菌药物。

PU-3317

布氏杆菌病以及布氏杆菌的微生物学检验的相关进展

宋威、关秀茹
哈尔滨医科大学附属第一医院

布氏杆菌病是世界上最为严重的人畜共患病之一，目前已成为我国发病数增长速度最快的传染病之一。近年来，布氏杆菌病呈现由牧区向非牧区转移，由职业人群向非职业人群扩散的趋势，我国布病疫情防治形势严峻。本病临床表现变化多端，可影响全身各个系统、器官，与多种疾病难于鉴别。因此，在流行区高度怀疑本病且正确的诊治对降低发病率有重要意义。其中在布氏杆菌病的相关诊断中，分离培养鉴定布氏杆菌是诊断布氏杆菌病最可靠的方法，因此通过细菌学检验检查到布氏杆菌对于布氏杆菌病的诊断是至关重要的。本综述将对布氏杆菌病以及布氏杆菌的微生物学检验相关进展做总结。

PU-3318

一例通过空调通风系统传播的嗜军团菌肺炎感染病例研究

秦诗睿
三峡大学附属仁和医院

目的 通过对一例本市新闻报道中通过空调通风系统传播造成感染的军团菌肺炎的病例的分析对嗜军团菌肺炎的传播特征和抗感染治疗进行探讨
方法 对该病例进行分析对军团菌的传播特点和药敏特征进行分析。
结果 通过对该病例进行分析，确定在空调滤芯中的湿润环境中滋生的军团菌通过空调通风系统进行传播，该患者出现急性上呼吸道感染及发热症状并迅速发展为呼吸衰竭和肾衰竭。该患者出现急性纤维蛋白化脓性肺炎及多器官损伤，符合嗜军团菌肺炎的典型病理特征。
结论 嗜军团菌肺炎主要感染部位为肺泡巨噬细胞，培养结果为阳性，是诊断军团菌感染的金标准。但其培养条件苛刻，阳性率较低。所以，关于军团菌肺炎的确诊，一般通过以下几种**方法** ①胸腔积液、痰液、血液或支气管肺泡灌洗液培养阳性，但需注意，嗜军团菌肺炎的培养需要特殊培养基，营养要求高，生长缓慢，阳性率一般不高。②军团菌血清学实验，通过免疫层析技术快速检测尿液中嗜军团菌 1 型抗原，但此方法只针对 1 型血清型，对于其它嗜军团菌以及非嗜肺军团菌阳性率很低。③双份血清抗体 4 倍升高或减低，但是血清抗体检测受检测方法的影响，其中 IFA 检测是公认比较好的办法，需注意的是，IFA 方法在结果判读时存在一定的主观性。关于嗜军团菌肺炎的治疗，由于军团菌在细胞内寄生，所以容易进入肺组织，气道分泌物并且细胞内药物浓度高的药物是比较好的选择。大环内酯类是治疗军团菌肺炎的常用药物，阿奇霉素、克拉霉素在目前一般比红霉素使用的更为广泛。氟喹诺酮类，如莫西沙星、加替沙星也有很好的抗军团菌的活性。利福平在临床上厂与大环内酯类抗生素联合使用，用于重症嗜军团菌肺炎的治疗。此类病例一般首先考虑为社区获得性肺炎，一般耐药性不高，但对于常用于社区获得性肺炎的抗生素，包括左氧氟沙星，头孢呋辛，青霉素等治疗无效后，应当考虑其耐药性发生变化或其它特殊感染。

PU-3319

流感病毒感染与急性心肌梗死关系的研究

杜柏岩、关秀茹
哈尔滨医科大学附属第一医院

目的 探讨流感病毒（influenza virus, IV）感染与急性心肌梗死（acute myocardial infarction, AMI）之间的关系。
方法 采用 EL ISA 法检测 74 例 AMI 患者与 77 例正常对照组血清中 IV-A 及 IV-B 抗体水平，同时检测两组的 IL-18、hsCRP 的水平，并对冠心病危险因素进行调查。
结果 AMI 组 IV-A IgG 抗体阳性率（86.48%）、IV-B IgG 抗体阳性率（75.67%）显著高于对照组（66.23%, 16.88%, p<0.01）。AMI 组 IL-18(0.98±0.26)、hsCRP (23.71±33.26)水平与对照组(0.46±0.12，2.10±1.81)比较明显增高，差异具有统计学意义，并且 IgG 水平与 IL-18 和 hsCRP 呈正相关。校正冠心病危险因素前后，IV-A 和 IV-B IgG 抗体阳性均与 AMI 有相关性(IV-A：OR = 3.2 , P = 0.025；OR =4.18 , P = 0. 001。IVB：OR = 15.31 , P = 0.01；OR =19.44 , P = 0. 001) 。
结论 IV 感染可能激发或加重冠状动脉内炎症反应，IL-18 和 hsCRP 参与 AMI 的病理过程。

PU-3320

148 例沙门菌血清型分布和耐药性分析

陈娟[1]、陈慧珍[2]、李卫滨[1]、张胜行[1]
1. 第九〇〇医院检验科
2. 福建医科大学

目的 分析联勤保障部队第九〇〇医院 2016 年 1 月-2021 年 4 月所检出的沙门菌的血清型分布、抗菌药物的耐药率及耐药变迁趋势，为临床利用抗生素治疗沙门菌提供指导。
方法 收集上述时间段内临床分离的沙门菌，对其进行血清学分型，采用 Walkaway 96 Plus 全自动细菌鉴定和药敏分析仪检测沙门菌的耐药情况，以 CLSI 为标准对药敏结果进行判读，应用 Excel 2007 与 SPSS 26.0 软件对数据进行整理分析。
结果 2016 年 1 月-2021 年 4 月共收集有效菌株 148 株，患者年龄分布以儿童（＜14 周岁 44.6%）与老人（＞60 周岁 28.4%）为主，标本类型以粪便（74.3%）为主，血清学分型中鼠伤寒沙门菌（20.9%）最多见，其次是肠炎沙门菌(11.5%）；药敏结果显示沙门菌对氨苄西林的耐药率最高为 57.6%，复方新诺明耐药率(26.4%)居于第二位，喹诺酮（环丙沙星 3.4%、左氧氟沙星 0.7%）和氨基糖苷类药物（妥布霉素 9.4%、庆大霉素 9.4%、阿米卡星 1.3%）的耐药率呈现下降趋势，对三代头孢（头孢曲松 7.4%、头孢噻肟 7.4%、头孢他啶 3.4%）表现出低耐药率，有 12 株产超广谱 β 内酰氨酶，3 株出现对碳青霉烯类药物（亚胺培南与美罗培南）耐药。
结论 本院儿童群体的沙门菌检出率最高，鼠伤寒沙门菌检出数量最多，夏秋季节（5-10 月）的检出量明显高于春季与冬季；对氨苄西林药物的耐药率最高，有多重耐药菌株出现且在儿童中占比大。综上建议临床医生应根据微生物实验室的培养结果并结合当地流行病学特点，合理地选择与使用抗生素，增加对儿童与老人患者的关注，控制多重耐药菌株的产生和增加。

PU-3321

（1-3）-β-D 葡聚糖临床研究

宋熙瑶、刘文博
哈尔滨医科大学附属第一医院

（1-3）-β-D 葡聚糖是酵母和丝状真菌的细胞壁脂多糖成分，可从真菌细胞壁释放至血液、肺泡灌洗液、脑脊液等。鲎的凝血系统中凝血酶原 G 因子能识别这种葡聚糖，所以被称为 G 试验。目前，临床上用比浊法和显色法来测定。在临床试验中，应该严格按照操作规程，无菌操作，必须确保使用试管等器具无菌、无热原的专用管。

G 试验<60pg/ml 为阴性结果不推荐抗真菌治疗，存在宿主因素，72 小时需再次检测。60-100pg/ml 时属于灰区，有可能发生侵袭性真菌感染的可能。存在宿主因素，48 小时需再次检测。当结果 100-500pg/ml 很可能会发生全身侵袭性真菌感染，此时建议进行抗真菌治疗，但也需要 6-24 小时复查确认。>500pg/ml，则发生全身侵袭性真菌感染可能性极大，建议治疗，G 试验结果还需要动态监测。

注意事项：G 试验的阳性阈值仅适用于成人，儿童和婴儿体内含量较成人高。脑脊液（1-3）-β-D 葡聚糖检测可用于中枢神经系统真菌感染的诊断，由于真菌无法通过血脑屏障，患者脑脊液中（1-3）-β-D 葡聚糖远高于血清。脑脊液含量随真菌治疗进行而逐渐下降。

PU-3322

不同感染性指标在血流感染早期诊断中的应用价值探讨

伏改芬
昆明市第一人民医院

目的 以血流感染患者为研究对象，分析不同感染性指标在病情早期诊断中的应用价值。
方法 以 193 例自 2018 年 8 月至 2020 年 4 月进行治疗的疑似血流感染患者为研究对象，将 76 例血流感染患者纳入研究组，将 117 例未确诊为血流感染者纳入对照组，检测两组患者 WBC、N 、CRP、PCT、IL-6、FIB 及体温等不同感染性指标并对各项指标水平进行对比。
结果 研究组 WBC、N%等各项外周血感染性指标水平均高于对照组，两组各项指标水平差异均有统计学意义，P<0.05。以血培养结果作为金标准分析各项指标单独检查以及联合检测在血流感染早期诊断价值，结果表明各项指标联合检测特异度及敏感度均明显高于各项指标单独检测，差异有统计学意义，P<0.05。各项感染性指标在血流感染及非血流感染鉴别中的效能均较高，具有一定的检测价值。
结论 血流感染患者不同感染性指标均存在一定程度的异常现象，早期联合检测能够为临床进行病情严重程度判断及预后评估提供重要指导和参考。

PU-3323

哈尔滨医科大学附属第一医院 ICU 细菌分布和耐药性分析

宋熙瑶、俞晓晨
哈尔滨医科大学附属第一医院

目的 分析本院 2018 年 ICU 分离菌的总体情况及其耐药性。
方法 使用梅里埃全自动细菌鉴定/药敏鉴定仪对临床有意义的分离菌进行鉴定和药敏试验，细菌药敏结果根据 2017 版临床和实验室标准协会 CLSI-M100 文件判读。

结果 2018 年本院共培养出 2603 株分离菌，约占全院分离菌的 25%（2603/10401）。占前五位的分别为鲍曼不动菌（694 株，占 26.7%）、肺炎克雷伯菌（281 株，占 10.8%）、金黄色葡萄球菌（181 株，占 7.0%）、铜绿假单胞菌（161 株，占 6.2%）、大肠埃希菌（126 株，占 4.8%）。与去年（2017 年 2008 株）相比，菌株数量明显增加。而前 5 位细菌分布变化不大。2017 年分别为鲍曼不动菌（653 株，占 32.5%）、肺炎克雷伯菌（265 株，占 13.2%）、金黄色葡萄球菌（163 株，占 8.1%）、铜绿假单胞菌（133 株，占 6.6%）、大肠埃希菌（120 株，占 6.0%）。
结论 2018 年 ICU 细菌耐药率与往年相比略有不同。总体而言，鲍曼不动杆菌在菌株去重之后，依然超过 1/4，且耐药严重，但可能很多细菌为定植株。另外，肺炎克雷伯菌紧随其次，而且肺炎克雷伯菌毒性大，所以更应引起临床重视。

PU-3324

鼠疫菌与酸应激相关转录组学和代谢组学研究

王敏
泰安市中心医院

鼠疫菌通过跳蚤叮咬进入人体被巨噬细胞吞噬后进入了一个低钙、弱酸、低镁、高渗的胁迫环境，并快速启动一系列应对机制存活下来从而发挥致病性。本研究将从鼠疫菌对酸性刺激在基因转录水平及代谢水平的变化探讨其可能存在的致病机制。研究**方法** 将鼠疫菌在 pH 值为 6、37℃无钙 TMH 培养基中进行培养（模拟鼠疫菌在巨噬细胞溶酶体内环境），运用 RNA-Seq 技术研究它们在转录水平上的差异，利用 GO 分析、 KEGG 通路富集分析发现影响显著的功能分类及代谢通路。运用气相色谱-飞行时间质谱联用技术 GC-TOFMS（气相色谱-飞行时间质谱联用技术）和 UHPLC-QTOFMS（超高效液相色谱-四极杆飞行时间质谱联用技术）检测酸刺激培养条件下的鼠疫菌在代谢物水平上的变化，经 PCA 及 OPLS-DA 多元统计分析方法找到对实验条件改变响应较强且稳定的差异代谢物。与在中性环境培养的鼠疫菌相比较，鼠疫菌在 pH 为 6 的弱酸环境下有 785 个基因发生了转录水平上调， 551 个基因发生了转录水平下调。差异表达基因在二元调控系统，TCA 循环，核糖体代谢，脂肪酸， T3SS 和无机盐代谢途径富集显著。联合运用 GC-TOF MS 和 UHPLC-QTOF MS 两个平台对 pH 为 6 且 37℃无钙离子培养条件下的鼠疫菌代谢物检测， 总共鉴定到 630 种物质，酸刺激培养环境下总差异代谢物 87 种。经代谢通路富集分析，发现嘧啶代谢通路被显著富集，同时发现脯氨酸明显累积，有研究表明脯氨酸积累可促进细菌对乳酸的耐受能力，改善应激下的细胞活力。我们通过转录组学和代谢组学分析，揭示了鼠疫菌胞内低 pH 环境下的转录与代谢规律，为该菌致病早期应对宿主抵抗的策略，为深入揭示分子机制提供了数据基础和新的研究思路。

PU-3325

CRISPR 技术在艰难梭菌研究中的应用进展

伏改芬
昆明市第一人民医院

艰难梭菌（Clostridium difficile，CD）是医院治疗腹泻获得性较高的病原菌之一，与抗生素治疗相关性腹泻、致命性的伪膜性结肠炎密切相关。随着广谱抗生素的应用、质子泵抑制剂、化疗药物等，艰难梭菌感染 （Clostridiumdifficile-infection CDI）的发生率明显增加，推测其与肠道菌群失调密切相关。CRISPR 免疫系统技术是广泛存在于人类细菌和其他古生菌细胞中的一种高度适应性自体免疫系统，CRISPR 技术已被广泛的应用到基因敲除、基因替换等基础基因细胞编辑方式、基因激活、疾病模型构建、甚至是基因治疗。由 II 型 CRISPR/Cas 系统改造而成的 CRISPR/Cas9 技术已经被开发成一种强大的基因组结构编辑和基因表达调控工具，应用最广泛。本文从艰难梭菌

感染的致病机制，治疗策略，CRISPR 基本结构、工作原理、CRISPR 技术在艰难梭菌中的应用进行综述总结及展望。

PU-3326

通过重组腺病毒介导的颗粒溶素的联合治疗提高结核病的清除率

马记磊
郑州大学第一附属医院

目的 结核病（TB）仍然是全世界传染病中主要的死亡原因。结核病患者对长期治疗的依从性差会增加复发的风险，并导致出现耐多药和广泛耐药的结核病（MDR-TB 和 XDR-TB）。迫切需要更有效的结核病治疗方法。我们假设细胞内外表达颗粒溶素，清除感染宿主肺泡巨噬细胞内外结核分枝杆菌，增强对 TB 的化学治疗功效。
方法 分别开发基于重组腺病毒 5 型（rAd5）的治疗性疫苗 rAdhGLi 和 rAdhGLs（rAds），以表达细胞内和细胞外颗粒溶素。在 U937 和 RAW264.7 细胞上评估了 rAdhGLi 和 rAdhGLs 的离体杀菌作用。进一步评估了使用 rAdhGLi 和 rAdhGLs 对结核分枝杆菌感染的 SCID 小鼠进行免疫治疗或对药物敏感的 TB 或 MDR-TB 小鼠模型进行免疫治疗联合化疗的疗效。
结果 rAdhGLi 和 rAdhGLs 分别对细胞外或细胞内结核分枝杆菌 H37Rv 和 MDR-TB 临床菌株表现出直接的杀菌作用。与单独使用 rAdhGLi 或 rAdhGLs 相比，用 109 PFU 的 rAdhGLi 和 109 PFU 的 rAdhGLs 进行免疫治疗对结核分枝杆菌 H37Rv 感染的 SCID 小鼠具有更显着的杀菌作用，并延长了它们的生存期。更重要的是，化学疗法与 rAds 免疫疗法相结合将结核分枝杆菌 H37Rv 感染小鼠的化学治疗时间缩短至 4 个月，并防止了复发。 rAds 与 MDR-TB 小鼠化学疗法的联合使用也比单次使用显着降低了器官细菌负荷。
结论 重组腺病毒将颗粒溶素递送至受感染的肺可提高体内结核的清除率，可能是一种有前途的结核和耐多药结核病辅助治疗疫苗。

PU-3327

耐碳青霉烯类肠杆菌科细菌的流行病学特点及耐药性分析

朱军
资阳市第一人民医院

目的 分析该院耐碳青霉烯类肠杆菌科细菌(CRE)的检出情况和耐药性,以期能够合理使用抗菌药物,更好地预防和治疗 CRE 感染.
方法 收集 2018-2020 年该院检出的肠杆菌科细菌,使用全自动微生物测定仪对菌株进行培养、鉴定、药敏试验,分析 CRE 的检出情况,统计 2018-2020 年主要 CRE 的检出率,比较各类型标本中 CRE 的检出情况,统计主要 CRE 对常用抗菌药物的耐药率.
结果 共分离肠杆菌科细菌 8139 株,其中 CRE 菌株为 180 株(2.2％),主要是肺炎克雷伯菌(54.2％)、大肠埃希菌(18.0％)和产气肠杆菌(12.0％)等菌株,主要来自痰液(57.8％)、尿液(27.7％)、静脉血(8.4％)和腹腔引流液(3.6％)等标本;检出的 CRE 中,肺炎克雷伯菌、大肠埃希菌和产气肠杆菌检出率总体呈现逐年递增趋势,尤其是肺炎克雷伯菌在 2019 年高达 47.2％;CRE 对所有常用抗菌药物的耐药率均＞60％,特别是对 β-内酰胺类和喹诺酮类的耐药率高达 100.0％.
结论 2018-2020 年该院 CRE 主要为肺炎克雷伯菌、大肠埃希菌和产气肠杆菌等,检出率总体呈逐年递增趋势,对临床常用抗菌药物的耐药性较高,特别是对 β-内酰胺类和喹诺酮类抗菌药物全耐药.

PU-3328

2018—2020 年资阳某医院血培养分离菌的耐药性分析

杨祺
资阳市第一人民医院

目的 了解 2018-2020 年该院血培养阳性细菌的分布及耐药情况.
方法 根据全国细菌耐药监测网技术要求,对血培养阳性分离菌进行鉴定和药敏试验,按照 2018 年美国临床和实验室标准化协会(CLSI)标准进行结果判读，结果 2018-2020 年自血培养中共分离得病原菌 1352 株,其中革兰阳性菌 224 株,占 16.6%;革兰阴性菌 1128 株,占 83.4%,前五位分离菌依次为大肠埃希菌、克雷伯菌属、金黄色葡萄球菌、肠球菌属和凝固酶阴性细菌.金黄色葡萄球菌和凝固酶阴性葡萄球菌中甲氧西林耐药株(MRSA、MRCNS)的检出率分别为 31.6%和 81.4%.除四环素外,粪肠球菌对其他抗菌药物的耐药率均低于屎肠球菌,肺炎链球菌对青霉素 G 的耐药率仅为 1.6%,未检出耐万古霉素和利奈唑胺的细菌.碳青霉烯类耐药大肠埃希菌和肺炎克雷伯菌检出率分别为 4.4%和 21.5%.
结论 血培养分离菌以革兰阴性菌为主,MRSA 仍然是革兰阳性菌感染中的主要问题.碳青霉烯类耐药的肠杆菌科细菌逐年增加,应加强医院感染防控和抗菌药物临床应用管理,以遏制此类菌株的传播扩散.

PU-3329

2020 年资阳市某三甲医院细菌耐药性监测结果分析

宋旭辉
资阳市第一人民医院

目的 探讨 2020 年资阳市某三甲临床分离菌株对常用抗菌药物的耐药率，为临床经验性抗感染治疗提供依据。
方法 收集 2020 年 1 月至 12 月我院检验科分离的非重复细菌，按统一方案进行菌株鉴定及药敏检测，应用 Whonet5.6 软件对数据进行分析。
结果 2020 年共分离出有临床意义的细菌 4801 株，其中，肺炎克雷伯菌共 1248 株（25.99%），大肠埃希菌 818 株（17.04%），金黄色葡萄球菌 512 株（10.66%），铜绿假单胞菌 469 株（9.77%），鲍曼不动杆菌 431 株（8.98%），阴沟肠杆菌共 254 株（5.30%）；本年度多重耐药菌的检出率中，耐甲氧西林金黄色葡萄球菌（MRSA）检出 180 株（35.16%），产超广谱酶 β-内酰胺酶细菌（ESBLs）检出大肠杆菌 308 株（37.65%）、肺炎克雷伯菌 142 株（11.38%），耐碳青霉烯肠杆菌（CRE）75 株（3.63%），耐碳青霉烯鲍曼不动杆菌（CRABA）115 株（26.68%），耐碳青霉烯铜绿假单胞菌（CRPAE）15 株（3.20%）。
结论 本院临床分离的常见细菌对不同抗菌药物呈不同耐药率，应充分了解细菌耐药监测结果，合理使用抗菌药物并加强医院感染管理。

PU-3330

Detection of a clinical carbapenem-resistant Citrobacter portucalensis strain and the dissemination of Citrobacter portucalensis in clinical settings

xiaoli cao
Nanjing Drum Tower Hospital'

Objective A clinically isolated carbapenem-resistant Citrobacter portucalensis was characterized by whole genome sequencing (WGS).
Methods Strain 3839 was identified by Vitek 2.0 and matrix-associated laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS). Antibiotic susceptibility testing was performed by microbroth dilution method. WGS followed by bioinformatics analysis was conducted.
Results Strain 3839 was initially identified as C. freundii by Vitek and MALDI-TOF MS, and later was demonstrated as C. portucalensis by WGS analysis. Through average-nucleotide identity analysis, we further detected 55 C. portucalensis genomes which were misidentified as C. freundii in GenBank, and at least 22 were clinical-associated, suggesting that the occurrence of C. portucalensis in the clinical setting might be underestimated by the conventional method. Strain 3839 was extremely drug-resistant, and the presence of multiple resistance determinants was detected by WGS, including blaNDM-1, blaSHV-12, blaCMY-150, blaOXA-1, qnrB9, qnrA1, aac(6')Ib-cr; aph(6)-Id_1, aph(3")-Ib, aac(6')Ib-cr, tetA, tet34, and catB3. Forty-five insertion sequences, 8 phages, and 1 integron gene cassette were identified in this strain. The blaNDM-1 gene was carried by an IncX3 plasmid, which was identical to a plasmid detected in a C. freundii strain. The genetic context of blaNDM-1 was IS30-blaNDM-1-bleMBL-trpF-dsbD-cutA1-groES-groEL-IS91.
Conclusion To our knowledge, this is the first report of carbapenem-resistant C. portucalensis isolated from clinical samples. The blaNDM-1 gene carried by C. portucalensis may transmit among Citrobacter spp. mediated by plasmids. Together with the underestimation of clinical occurrence caused by the misidentification, our study warrants the necessity of preventing the dissemination of such emerging drug-resistant species in clinical settings.

PU-3331

某三甲医院 2018-2020 年 ICU 病原菌分布及耐药性分析

龙绮云
资阳市第一人民医院

目的 了解四川省资阳市某三甲医院 2018-2020 年重症监护病房（ICU）分离所得病原菌的耐药性，为细菌耐药性监测提供基础数据。
方法 四川省资阳市某三甲医院 2018-2020 年分离所得病原菌的类型及耐药性进行回顾性分析。
结果 2018-2020 年 ICU 分离所得革兰阴性菌以大肠埃希菌 (12.67%、13.12%、13.2%)和肺炎克雷伯菌（13.4%、14.2%、14.51%）为主，革兰阳性菌以金黄色葡萄球菌（6.5%、7.3%、9.1%）为主。
结论 我院 ICU 病房分离所得病原菌耐药性较强，呈逐年递增趋势，ICU 应进一步强化无菌操作意识，应充分利用和重视细菌培养结果进行感控管理，有效控制细菌耐药率，促进抗菌药物的合理应用。

PU-3332

PfAP2-G2 介导恶性疟原虫配子体发育的研究

许瑶征
中国医科大学

目的 研究 PfAP2-G2 在恶性疟原虫配子体发育阶段的角色和作用并探讨其内在调控机制。
方法 通过 CRISPR-Cas9 技术获得 PfAP2-G2 敲除型以及标签型虫株，经间接免疫荧光（IFA）以及逆转录定量 PCR（RT-qPCR）检测 PfAP2-G2 的表达水平以及定位情况。通过生长试验以及诱导配子体检测敲除 PfAP2-G2 对于无性期疟原虫和配子体的生长状况的影响。通过 IFA 检测敲除 PfAP2-G2 对于恶性疟原虫从无性期转向有性发育比例的改变情况。通过 RNA-seq 以及 RT-qPCR 检测敲除 PfAP2-G2 影响何种基因转录改变。通过染色质免疫共沉淀-实时荧光定量 PCR（CHIP-qPCR）检测 PfAP2-G2 的直接作用靶点，从而分析 PfAP2-G2 影响恶性疟原虫配子体发育的具体机制。
结果 成功获得 PfAP2-G2 的基因修饰性虫株，发现 PfAP2-G2 在无性阶段中环状体期表达量最高并且定位在细胞核内。敲除 PfAP2-G2 对于无性期疟原虫的原虫率没有影响，但是使配子体感染率降低且使得配子体发育停滞在Ⅲ期。敲除 PfAP2-G2 使得恶性疟原虫从无性期转向配子体发育的转化率降低，并且雌雄配子体比例升高。敲除 PfAP2-G2 后，PfMDV-1 的表达量在环状体期以及裂殖体期均降低；PfAP2-G 在环状体期的表达量无变化，但在裂殖体期表达量降低。通过 RNA-seq 结果分析，PfAP2-G2 敲除型虫株在环状体期表达量下降的基因有 12 个，表达量上升的基因有 113 个；PfAP2-G2 敲除型虫株在裂殖体期表达量下降的基因有 102 个，上升的基因有 41 个。PfMDV-1 是 PfAP2-G2 的靶基因之一。
结论 PfAP2-G2 在无性阶段中环状体期表达量最高并且定位在细胞核内。PfAP2-G2 对于配子体的产生及发育有重要作用，尤其是雄配子体。PfMDV-1 是 PfAP2-G2 的靶基因之一，PfAP2-G2 是通过调控 PfMDV-1 的基因表达，从而影响配子体的发育。

PU-3333

衡阳地区某三甲医院微生物培养细菌分布及耐药性分析

陈聪
南华大学附属第一医院检验科

目的 了解衡阳地区某三甲医院患者医院感染病原菌分布及耐药性分析，为助力于临床合理使用抗生素提供有力依据。
方法 收集我院 2020 年 1 月至 2020 年 12 月所有临床科室送检标本，回顾性分析其临床科室分布特点及耐药性。
结果 2020 年 1 月至 2020 年 12 月临床送检细菌培养标本约 53315 份，送检标本检出病原菌约 10737 株，阳性率为 20%。其中革兰阳性菌 2311 株，占 22%；革兰阴性菌 6447 株，占 60%；真菌株 1979，占 18%。主要病原菌为大肠埃希菌、鲍曼不动杆菌、肺炎克雷伯菌、铜绿假单胞菌、金黄色葡萄球菌和白色假丝酵母菌。革兰阴性杆菌对亚胺培南、美诺培南的敏感率约为 85%。革兰阳性球菌对万古霉素敏感率约为 86%。
结论 衡阳地区某三甲医院临床分离菌种分布及耐药率与中国细菌耐药检测结果趋势大致相同，目前临床上细菌对抗菌药物的耐药趋势仍然较为严重，为应对多重耐药细菌所致感染，应加强并做好细菌耐药监测工作，积极主动与临床进行沟通，促进抗菌药物合理应用，加强感染预防控制。

PU-3334

MALDI-TOF MS 快速鉴定阳性血液培养物的快速方法

王月玲[1,2]、金炎[1]、白媛媛[1]、宋真[1]、初文君[1]、郝莹莹[1]
1. 山东第一医科大学附属省立医院临床医学检验部
2. 山东省立医院临床医学检验部

基质辅助激光解吸电离飞行时间质谱（MALDI-TOF MS）在阳性血液培养物鉴定中的应用是临床微生物实验室中鉴定微生物的一场革命。尽管有几种商业预处理方案，但是它们的成本很高。在这里，我们评估了本地生产的 Bioyong 预处理试剂盒的性能，该试剂盒通过 MALDI-TOF MS 方法直接鉴定阳性血液培养物（BCs）中的微生物。使用 200 个 Thermo 有氧血培养瓶和 200 个 Scenker 有氧血培养瓶进行模拟的阳性血培养。总共感染了 200 种生物，包括 91 株革兰氏阳性菌，97 株革兰氏阴性菌和 12 株念珠菌。将阳性 BC 传代培养，并通过经典生化 Vitek II 测试鉴定为鉴定的金标准。Bioyong 预处理试剂盒可以分别成功鉴定 189（94.5％）个热阳性 BCs 和 189（94.5％）Scenker 阳性血液培养物中的微生物。 94（96.9％）革兰氏阴性细菌中分离出 86 种（94.5％）革兰氏阳性细菌和 9 种（75.0％）念珠菌。正确鉴定出热阳性 BC 到物种水平。从 Scenker 阳性 BC 分离出的 95 种（97.9％）革兰氏阴性细菌，86 种（94.5％）革兰氏阳性细菌和 8 种（66.7％）念珠菌已正确鉴定到物种水平。此方法可在阳性血液培养物中在一小时内快速，准确地鉴定细菌和念珠菌。这项技术的常规应用将改善菌血症和念珠菌血症患者在 24 小时内的抗菌治疗。

PU-3335

健康儿童肠道产 ESBLs 大肠埃希菌的分子流行特征分析

钟一鸣[1]、殷雯钰[2]、刘文恩[1]
1. 中南大学湘雅医院
2. 中南大学湘雅医学院

目的 研究湖南长沙某幼儿园内健康儿童肠道产 ESBLs 大肠埃希菌的分子流行特征以及 ST38 型产 ESBLs 大肠埃希菌与非 ST38 型大肠埃希菌的耐药性和传播危险因素的差异。
方法 收集湖南长沙某幼儿园健康儿童的粪便标本，分离培养出产 ESBLs 大肠埃希菌，采用特异性引物扩增 7 对管家基因进行多位点序列分型；采用多重 PCR 检测耐药基因 CTX-M 并分型；采用特异性引物扩增检测碳青霉烯类耐药相关基因 OXA-48；采用 χ2 检验或 Fisher 确切概率法检验分析 ST38 型产 ESBLs 大肠埃希菌与非 ST38 型大肠埃希菌的耐药性和传播危险因素的差异。
结果 共检出产 ESBLs 大肠埃希菌 63 株，多位点分型成功分型 63 株，其中 ST38 占 12.70%（8/63）；ST1193，占 7.94%（5/63）；ST69 占 6.35%（4/63）；ST12、ST131 各占 4.76%（3/63）；发现 6 株大肠埃希菌具有新的序列类型。63 株大肠埃希菌中有 56 株大肠埃希菌成功扩增检测出 CTX-M 基因，其中 CTX-M-14 占 35.71%（20/56）、CTX-M-55 占 26.79%（15/56）、CTX-M-27 占 17.86%（10/56）。8 株 ST38 型产 ESBLs 大肠埃希菌中未检测出 blaOXA-48 基因阳性的菌株。ST38 型大肠埃希菌与非 ST38 型大肠埃希菌在耐药性和传播的危险因素方面并没有具有统计学意义的差异。
结论 长沙某幼儿园内健康儿童肠道携带的产 ESBLs 大肠埃希菌以 ST38 型为主，占 15.68%，其携带的耐药基因 CTX-M 以 CTX-M-14 为主，占 38.64%。ST38 型大肠埃希菌与非 ST38 型大肠埃希菌在耐药性和传播的危险因素方面并没有具有统计学意义的差异。

PU-3336

中年人脱发人群肠道菌群变化特点

强永杰
南方医科大学珠江医院

目的 研究通过分析脱发人群与正常人群肠道菌优势菌群变化与菌属组成结构变化，为未来脱发治疗方法提供一定的思路。
方法 实验组通过采集 10 例脱发人群（30-40 岁）大便样本，进行细菌、真菌涂片染色，细菌真菌培养（稀释后培养）鉴定，找到优势菌群；通过二代测序方法分析肠道菌群组成种类对照 10 例，为健康未脱发人群（30-40 岁）。提取粪便样本总 DNA;根据细菌 16SrDNA V3~V5 区设计引物进行扩增,利用 Illumina Miseq 平台进行高通量测序;测序结果经过 Reads 拼接,OTUs(operational taxonomic units)聚类,物种注释,α 多样分析,主成分分析,最终得到样品物种信息。
结果 涂片：实验组大便涂片革兰氏染色球/杆菌比例明显高于对照组；细菌、真菌培养：实验组双歧杆菌、消化链球菌、乳杆菌、产气荚膜梭菌、肠杆菌检出比例低于对照组；二代测序：实验组其中拟杆菌门(Bacteroidetes)占比 46.94%，厚壁菌门(Firmicutes)占比 30.58%，对照组实验组其中拟杆菌门占比 60.96%，厚壁菌门占比 41.51%包含幽门螺杆菌的螺杆菌属检出比例升高，实验组平均占比比对照组高 0.03%。
结论 表明实验组（脱发组）和对照组（未脱发组）菌群结构存在显著差异。这些结果表明,脱发人群与未脱发人群在肠道菌群多样性方面没有明显差异,但在菌群结构上存在较大差异;同时脱发人群肠道菌群致病菌数量多于健康人群,而拟杆菌类有益菌低于健康人群。由于有研究表明，脱发与生物素合成相关，未来可进一步细菌对生物素合成情况进行研究。

PU-3337

Dental plaque microbial resistomes of periodontal health and disease and their changes after scaling and root planing therapy

Yutong Kang[2]、Yongliang Lou [2]、Meiqin Zheng[1]
1. Eye Hospital of Wenzhou Medical University
2. 温州医科大学

Background The human oral microbial community has been considered to be reservoirs of antibiotic resistance, which constitute a direct threat to human health. Currently, the effects of the periodontitis and scaling and root planning (SRP) treatment on the performance of antibiotic resistance genes (ARGs) and metal resistance genes (MRGs) in the dental plaque microbiota are not well characterized. This is the first analysis of the profile of the microbial community, antibiotic and metal resistance genes in dental plaque by the metagenomic approach, to the best of our knowledge.
Methods To explore this problem, we selected 48 (healthy state), 40 periodontitis state (before treatment) and, 24 resolved state (after scaling and root planing treatment) metagenomic data from the Sequence Read Archive (SRA) database. This is the first analysis of the profile of the microbial community, antibiotic and metal resistance genes in dental plaque by the metagenomic approach.
Results NetShift analysis identified Fretibacterium fastidiosum, Tannerella forsythia, and Campylobacter rectus as key drivers during dental plaque microbiota alteration in the progression of periodontitis. The periodontitis group and SRP group had a significantly greater number for both ARGs and MRGs than the health group. PCoA analysis based on Bray–Curtis distance and Jaccard distance showed that the comprehensive composition for both ARGs and MRGs of the three groups was very different. In this study, 269 ARG subtypes of 18 ARG types and 240 MRG

subtypes of 18 MRG types were found in dental plaque. Bacitracin, beta−lactam, macrolide-lincosamide-streptogramin (MLS), tetracycline, and multidrug resistance genes were the main classes of antibiotic resistance genes (ARG) types with high relative abundance, whereas multi-metal, iron, chromium, and copper were the primary metal resistance gene (MRG) types. Procrustes tests indicated that the variation of microbial community composition was the determinant for the ARG and MRGs profile. Variation partitioning analysis also demonstrated that the Microbial community was the main driver shaping the resistome compared with mobile genetic elements (MGEs). The co-occurrence pattern network implied that 32 species might be potential hosts of 25 ARG subtypes and 35 species were speculated to be the possible hosts of 40 MRG subtypes. The co-occurrence of ARGs, MRGs, and MGEs indicated a co-selection phenomenon may exist in the resistome of the microbiota on the dental plaque.
Conclusions Overall, our data provide new insights into the standing of the distribution of ARGs and MRGs in oral microbiota of periodontitis patients. Monitoring the profile of these resistomes, has huge potential to provide reference regarding proper antibiotics use and the development of new antimicrobial strategies in periodontitis therapy and thereby improve actual efficacy of the treatment regimens.

PU-3338

人型支原体腰椎手术后切口感染一例

唐艳
湖南株洲市三三一医院

1 病历摘要
患者，男，64 岁。2018 年 11 月 28 日因“腰椎退行性变，继发性椎管狭窄，腰椎不稳”步行入院。于 11 月 20 日在全麻下进行腰椎后路减压椎间盘摘除骨内固定术手术。术后一周伤口无红肿，精神食纳明显好转。12 月 1 日下午突然出现不明原因的发烧，患者诉伤口胀痛，精神食纳差，感四肢无力。体查：伤口上部有明显渗出，渗出液较浑浊，伤口周围压有波动感，压痛明显，临床考虑伤口深部感染。12 月 6 日晚急诊脓肿清除引流术+腰椎后路伤口感染病灶清除灌洗引流术，给予万古霉素+美罗培南联合抗感染治疗，效果不佳，手术切口不愈合。期间取四块坏死组织培养，其中一块组织在血平板上培养出 Mh，另外中心静脉血也培养出 Mh。依据药敏结果临床给予左氧氟沙星、强力霉素治疗后，体温、血常规和 CRP 逐渐恢复正常，伤口愈合出院。
2.细菌培养及鉴定
12 月 2 日至 7 日共送 5 份脓液分泌物及脓液处组织物做细菌培养及涂片，细菌培养接种于痰三格平皿，其中一管脓液处组织物 3 天后在血平皿上长出细小菌落，倾斜平皿可见针尖大小、圆形、不溶血、半透明的菌落，革兰染色、抗酸染色均不着色。12 月 2 日分别送了中心静脉导管、中心静脉血、外周血做细菌培养，其中中心静脉血和外周血注射在血培养瓶中，在血培养仪中进行培养，中心静脉血在第 8 天报阳。其涂片和培养出来的菌落与分泌物中菌落一致。将该细菌接种在支原体培养液中，培养出人型支原体，药敏显示强力霉素、美满霉素、交沙霉素、司帕沙星敏感，左氧氟沙星中介。将该细菌送至广州金域医学研究所进行基因测序鉴定结果为 Mh，鉴定值为 100%。
3、讨论
人型支原体通常在宿主抵抗力低下时可引起非淋病性尿道炎，偶尔可穿透到黏膜下层，侵入血液并播散到全身各器官和组织。因此，对于患者手术后出现切口感染、持续发热，广谱抗生素治疗切口不愈合、效果不佳并且对其分泌物及无菌部位样本涂片革兰染色未发现细菌时，有必要考虑人型支原体感染，［实验室可采用专门的支原体培养基进行分离培养予以确认，并通过其药敏分析指导临床用药。由于人型支原体无细胞壁，革兰染色未见细菌形态，在血平板或哥伦比亚琼脂平板上至少 3 天才能长出针尖样小菌落，然而，针尖样半透明的小菌落很容易被人为的忽略或在 Mh 生长所需的时间（3 天甚至更长）到达之前就已经把培养基丢弃了，所以对于无菌部位标本或切口分泌物的培养，应延长培养时间至 4d，密切观察可疑菌落。患者发热时双份采集血培养标本，适当延长

血培养时间至 7-8 天，有助于人型支原体血液感染的检出。最后取菌落进行 16S rDNA 聚合酶链反应检测其是否为人型支原体。

PU-3339

Ceftazidime is the Key Diversification and Selection Driver of KPC-Type Carbapenemases

Siqiang Niu
Department of Laboratory Medicine, The First Affiliated Hospital of Chongqing Medical University

Objectives To explain the selection driver of KPC-Type Carbapenemases.
Methods KPC phylogroups analysis were conducted according to the results of the maximum-likelihood (ML) tree obtained using the nucleotide sequences by MEGA-X software, and 31 and 8 variants in nature and artificiality, respectively, were obtained by overlap extension PCR and expressed in an isogenic context. Drug susceptibility assays were performed by a standard broth microdilution method. Enzyme kinetics assays were conducted to compare the hydrolytic activities of KPCs, and molecular modeling and ITC assay were also employed to compare the interaction between AVI and different KPC variants.
Results The phylogenetic ancestral reconstruction revealed that the diversifications of blaKPC-2 and blaKPC-3 nodes were mainly the results of single, nonsynonymous mutations. The first was formed by blaKPC-2 with 24 members (blaKPC-2, -4, -5, -6, -11, -12, -14, -16, -17, -18, -20, -21, -22, -24, -25, -26, -30, -33, -34, -35, -37, -42, -43 and -44), the second corresponded with blaKPC3 with 18 members (blaKPC-3, -7, -8, -9, -10, -13, -15, -19, -27, -28, -29, -31, -32, -36, -38, -39, -40 and -41). The common characteristic of KPC-3 variants are a single amino acid substitution (H272Y) of KPC-2 type variants due to a single nucleotide substitution (C814T), which increased resistance to ceftazidime. When ceftazidime was considered as the selector antibiotic in different approaches, KPC-4, -5, -6, -14, -33 and -35 were always selected. Three positions, P103R (corresponding to KPC-5), V239G (corresponding to KPC-6) and D178Y(corresponding to KPC-31) with high frequency , were selected in the evolution experiments with ceftazidime. MICs of E. coli clones expressing KPCs enzyme were consistent with clinical isolates producing KPCs, both showed an increasing resistance to ceftazidime. The docking results showed that these interactions of KPC-14, -28 and -31 with AVI demonstrated by ITC were weaker than KPC-2 and KPC-3, which could result in lower inhibition of AVI on KPC.
Conclusions We first systematically analyzed the effect of amino acid mutation on the resistance of KPC enzyme and further identified ceftazidime as a driver drug of the KPC subtype outbreak.

PU-3340

中性粒细胞 / 淋巴细胞比值与 C 反应蛋白对新生儿血流感染的预测价值

吴琼、易斌
中南大学湘雅医院

目的 研究中性粒细胞 / 淋巴细胞比值（NLR）与 C 反应蛋白(CRP)在新生儿血流感染早期的预测价值，以及鉴别常见皮肤定植菌血流感染与污染的临床价值。
方法 收集本院 2013 年 1 月-2020 年 3 月发生血流感染的新生儿患者 70 例和未发生血流感染的新生儿患者 71 例，根据临床诊断及培养结果分为感染组、污染组和对照组，比较各组中 NLR、CRP 和 WBC 计数、中性粒细胞百分数（NEU%）、淋巴细胞百分数(LYM%)和报阳时间有无差异，并用受试者工作特征（ROC）曲线分析其预测及鉴别诊断价值。

结果 新生儿血流感染组 CRP、NLR、WBC、NEU%显著高于对照组，LYM%低于对照组，差异均有统计学意义（P<0.05）。在感染组中，革兰阴性细菌组引起的血流感染患者 CRP、NLR、NEU%显著高于革兰阳性组，LYM%显著低于革兰阳性组，而 WBC 计数无统计学差异。常见皮肤表面定植菌引起的血流感染与血流污染相比，患者 CRP、NLR、NEU%和报阳时间比较差异均有统计学意义（P<0.05），而 WBC 与 LYM%无明显差异（P>0.05）。ROC 曲线分析结果显示，NLR、CRP 诊断新生儿血流感染的曲线下面积（AUC）分别为 0.786 和 0.785，检测灵敏度分别为 64.9％和 67.10％，特异度分别为 74.6％和 69.0％，NLR 联合 CRP 检测后诊断新生儿血流感染的曲线下面积（AUC）达 0.846。NLR、CRP 鉴别常见皮肤表面定植菌引起新生儿血流感染与污染的曲线下面积（AUC）分别为 0.664 和 0.858，检测灵敏度分别为 70.8％和 83.3％，特异度分别为 79.40％和 85.90％。NLR 联合 CRP 检测后鉴别血流感染与污染的去线下面积（AUC）达 0.888。
结论 NLR 联合 CRP 检测对新生儿血流感染具有较好的预测价值，并对鉴别血培养常见皮肤表面定植菌阳性的患者为血流污染或血流感染有一定的应用价值。

PU-3341

Association of Ocular Surface Diseases with SARS-CoV-2 Infection in Six Districts of China: An Observational Cohort Study

Shengjie Li、wenjun cao
Eye & ENT Hospital, Shanghai Medical College, Fudan University

Purpose The association between SARS-CoV-2 and ocular surface diseases is poorly described.
Methods An observational cohort study. A total of 2, 0157 participants from six districts of China were enrolled. Serum samples were tested for immunoglobulin G and M (IgG and IgM) antibodies against the SARS-CoV-2 spike protein and nucleoprotein using magnetic chemiluminescence enzyme immunoassays. Throat swabs were tested for SARS-CoV-2 RNA using RT-PCR assays in a designated virology laboratory.
Results Of 2, 0157 serum samples tested, 1, 755 (8.71%) were from ocular surface diseases, 1, 2550 (62.26%) from no-ocular surface diseases, 5, 852 (29.03%) from no-ocular diseases. SARS-CoV-2 prevalence for the combined measure was 0.90% (182/2, 0157). Seroprevalence of SARS-CoV-2 was significantly (p<0.05) higher in the population with ocular surface diseases (2.28%, 40/1755) compared with no-ocular surface diseases (0.70%, 88/1, 2550), and no-ocular diseases (0.92%, 54/5, 852). The proportions of positive tests by sex, age, region, and times also show markedly higher proportions in ocular surfaces diseases than others (p<0.05). Logistic regression analyses revealed that ocular surface diseases [ocular surface diseases vs. no-ocular diseases (p=0.001, OR =1.467, 95% CI=1.174-1.834); ocular surface diseases vs. no-ocular surface diseases (p<0.001, OR =2.170, 95% CI=1.434-3.284)] were associated with increased risk of susceptible to SARS-CoV-2 infection.
Conclusions Ocular surface diseases may be a risk factor for getting COVID-19.

PU-3342

评估 EDTA 改良碳青霉烯灭活试验和碳青霉烯酶抑制增强试验鉴定肠杆菌目细菌产碳青霉烯酶型别的临床价值

王芳、邓燕燕、林见敏、王金金、龚倩、黄声雷
复旦大学附属中山医院青浦分院

目的 评估 EDTA 改良碳青霉烯灭活试验和碳青霉烯酶抑制增强试验检测肠杆菌目细菌产碳青霉烯酶型别的临床价值。
方法 收集临床标本分离的肠杆菌目细菌共 130 株，其中产碳青霉烯酶菌株（CPE）100 株，首先使用微量肉汤稀释法进行体外药敏试验，然后分别用 EDTA 改良碳青霉烯灭活试验和碳青霉烯酶抑制增强试验检测对肠杆菌目产生的碳青霉烯酶进行检测并分型，同时使用 PCR 作为金标准检测碳青霉烯酶基因型。
结果 耐碳青霉烯类的肠杆菌目细菌对常见的抗菌药物敏感率均<50%，除了对替加环素和粘菌素的敏感率>95%外。和 PCR 结果比较，碳青霉烯酶抑制剂增强试验检测丝氨酸碳青霉烯酶的灵敏度为 98.61%(71/72)，特异性为 100%(58/58)；检测金属 β-内酰胺酶的灵敏度为 100.0%(27/27)，特异性为 100%(103/103)。碳青霉烯酶抑制剂增强试验还能够准确鉴定同时产丝氨酸碳青霉烯酶和金属 β-内酰胺酶的菌株。 mCIM 和 eCIM 试验检测产丝氨酸碳青霉烯酶的灵敏度为 97.2%(70/72)，特异性为 100.0%(58/58)；检测金属 β-内酰胺酶的灵敏度为 96.3%(26/27)，特异性为 100.00%(103/103)，但 eCIM 试验无法检测同时产两种酶的菌株。
结论 EDTA 改良碳青霉烯灭活试验和碳青霉烯酶抑制增强试验都能较好区分不同类型的碳青霉烯酶，其中碳青霉烯酶抑制增强试验操作更加简易，结果更易观察，但试验成本较高，总之不同层级的微生物实验室可以根据自身需求选择性的常规开展 CRE 的快速表型检测。

PU-3343

儿童碳青霉烯类耐药肺炎克雷伯菌分子流行病学和耐药机制研究

周颖、孔子艳、杨晋
连云港市第一人民医院

目的 碳青霉烯类耐药肺炎克雷伯菌（CRKP）引起的感染具有高发病率和高死亡率，给临床抗感染治疗带来了严峻的挑战，尤其对于儿童患者。但有关儿童患者中 CRKP 感染的数据有限，因此本研究旨在阐明江苏省儿童 CRKP 的分子流行病学和耐药机制。
方法 本研究收集 2018 年 7 月-2019 年 5 月南京市儿童医院患儿分离的 CRKP 菌株。微量肉汤法检测菌株对临床常用药物的敏感性，PCR 检测菌株是否携带相关耐药基因，MLST 以及 PFGE 分析耐药菌株的同源性。
结果 本研究收集 94 株 CRKP，药敏结果发现菌株均为多重耐药菌，对美罗培南、头孢菌素类、哌拉西林/他唑巴坦均耐药。CRKP 均携带碳青霉烯酶耐药基因，以 blaKPC-2（79.8%）为主。值得警惕的是有 2 株 CRKP 同时携带 blaKPC-2 和 blaNDM-5，2 株 CRKP 同时携带 blaKPC-2 和 blaIMP-4。MLST 发现 CRKP 属于 14 种 ST 型，以 ST11 （75.5%, 71/94）为主，另外发现 2 株新型 ST 型（ST4854 和 ST4855）。PFGE 结果显示，产 KPC-2 酶 ST11 型菌株分为 4 个克隆型（E、D、O、S），以 PFGE-E 型为主，该型菌株主要分布在 PICU 和 CCU；非 ST11 型菌株可分为 15 个克隆型，其中存在 5 种脉冲型在院内不同科室进行小范围的克隆播散（C、L、M、N、R）。
结论 南京市儿童医院患儿分离的肺炎克雷伯菌对碳青霉烯类药物的耐药机制主要产 KPC-2 酶，并且院内多个科室存在产 KPC-2 酶 ST11 型肺炎克雷伯菌的克隆传播以及其他一些脉冲型菌株的小范围克隆播散，医院应及时制定有效感控措施, 防止耐药菌在病房进一步的暴发流行。

PU-3344

The relationship between mycoplasma infection in female genital tract and serum vitamin D level

Na An 、bitao wu、jun luo、chunmei dai、yarong liu
Mianyang Central Hospital, School of Medicine, University of Electronic Science and Technology of China

Objective To explore the relationship between female genital tract mycoplasma infection and serum vitamin D (Vit D) levels in Mianyang area.
Methods 1 776 women who attended the Obstetrics and Gynecology Department of Mianyang Central Hospital from January 2018 to December 2020 participated in the study. Vaginal secretions were collected for mycoplasma culture, and serum 25-(OH)VD2 and 25-(OH)VD3 levels were detected by high performance liquid phase mass spectrometry tandem mass spectrometry.
Results From January 2018 to December 2020, 791 people were diagnosed with mycoplasma infection, mainly 21-30 years old. The detection rate in 2018 was as high as 46.96%. The resistance rate of Mycoplasma genitalium to ofloxacin and josamycin is increasing year by year; among 220 women with complete data, 84 cases (38.18%) were infected with Mycoplasma genitalia. The serum 25-(OH)VD2 level (1.95±2.35 ng/ML) of the infection group was lower than that of the control group (2.14±2.56 ng/ML), and the difference was not statistically significant (t=-0.535, P=0.593) The serum 25-(OH)VD3 level (21.93±8.66 ng/ML) was lower than the control group (23.67±9.52 ng/ML), the difference was not statistically significant (t=-1.361, P=0.175). Serum 25-(The OH)VD level (23.88±9.00 ng/ML) was lower than the control group (25.81±9.71 ng/ML), and the difference was not statistically significant (t=-1.466, P=0.144). The positive rate of genital mycoplasma infection in the 25(OH)VD reduced group (42.68%) was higher than that in the 25(OH)VD normal group (26.98%), and the difference was statistically significant (χ2=4.690, P=0.033). Among the 84 cases of mycoplasma infection, the drug resistance rate of the 25(OH)VD reduced group (26.87%) was lower than that of the 25(OH)VD normal group (35.29%) (χ2=0.472, P=0.552); 25(OH)VD There was no statistically significant difference in the resistance rate of a single drug between the reduced level group and the 25(OH)VD level normal group (P>0.05).
Conclusion The situation of mycoplasma infection in female genital tract in Mianyang area still needs attention. Decreased serum Vit D levels are related to mycoplasma infection in the genital tract.

PU-3345

由须癣毛癣菌引起的儿童头部脓癣一例及文献阅读

胡中兰
郑州大学第一附属医院

脓癣是一种具有明显炎症性反应的头癣类型，由头皮毛囊及周围组织对感染真菌的强烈的炎症反应或不正规治疗导致，常伴有细菌感染。典型的损害是炎性毛囊丘疹、形成炎性肿块或囊肿，可伴局部疼痛、压痛及全身性反应。近年脓癣发病率有上升趋势，既往主要发生在城郊地区，随着饲养宠物的流行，城市人群发病率亦不断增加。此病因炎症反应过重或处理不当，往往治疗时间过长或治疗有效率低，给患者身心健康带来严重伤害。临床诊断脓癣主要由嗜动物真菌感染引起，在中国主要为须癣毛癣菌及犬小孢子菌。

须癣毛癣菌是临床上除红色毛癣菌外最常见的皮肤癣菌，可以引起人很动物包括毛发、趾甲、皮肤在内的多部位感染。由于须癣毛癣菌感染易发生误诊漏诊，正确治疗的延迟使得患者出现瘢痕、秃发及继发感染等危害，且须癣毛癣菌感染治疗时间长，容易反复感染。传统诊断主要通过刮取皮损皮屑、脓液或者活检组织进行真菌直接镜检或培养。

PU-3346

1140 例泌尿生殖道解脲脲原体和人型支原体感染情况及药敏分析

杨勇文
中南大学湘雅医院

目的 研究本地区解脲脲原体（Uu）和人型支原体（Mh）感染情况以及对常用抗生素的耐药情况，为临床合理用药治疗提供参考。
方法 收集 2017 年 1 月至 2019 年 12 月中南大学湘雅医院解脲和人型支原体培养的相关结果，采用 Excel 以及 SPSS 22.0 对结果进行统计分析。
结果 在 1140 例支原体检测结果中，Uu 感染、Mh 感染以及 Uu+Mh 混合感染的比例分别为 73.5%、3.9%、22.6%；其中女性 1086 例（95.3%），男性 54 例（4.7%）。70%的支原体感染患者集中 26～40 岁之间。药敏结果显示，交沙霉素、美满霉素和强力霉素的敏感率分别为 96.1%、96.8%、96.3%，其次左氧氟沙星和氧氟沙星的敏感率为 21.4%和 11.8%。
结论 Uu 是长沙地区泌尿生殖道感染的主要支原体类型，并且存在一定数量的混合感染，主要集中于中青年人群。交沙霉素、美满霉素和强力霉素可作为治疗 Uu 和 Mh 感染的首选药物，同时需要关注喹诺酮类药物的耐药变迁，防止耐药情况进一步恶化。

PU-3347

铜绿假单胞菌 ISCR1 分布及 ERIC-PCR 分型

孙静静
郑州大学第一附属医院

目的 研究临床分离铜绿假单胞菌的 ISCR1 的分布情况,并对其进行基因分型.
方法 分离临床 123 株铜绿假单胞菌,用 WHONET5.4 分析菌株药敏情况,PCR 检测 ISCR1 以及 ISCR1 携带的耐药基因.ERIC-PCR 进行基因分型.
结果 铜绿假单胞菌对阿莫西林/克拉维酸,氨苄西林,氯霉素,头孢唑啉,米诺环素,氨苄西林/舒巴坦高度耐药,对环丙沙星,头孢他啶,头孢哌酮/舒巴坦,阿米卡星,亚胺培南,美洛培南较敏感, 2 株 ISCR1 和 ISCRI 携带的耐药基因阳性.123 株铜绿假单胞菌分为 92 个基因型.
结论 ISCRI 携带率较低,ERIC-PCR 可用于临床分离铜绿假单胞菌的基因分型.

PU-3348

微生物形态学检验用于感染性疾病诊断的应用价值

熊阁
资阳市乐至县人民医院

目的 分析感染性疾病诊断中应用微生物形态学检验的价值。
方法 在 2019-3 至 2020-2 期间院内选取 134 例患感染性疾病的患者，分为 2 组。对照组分离出来的 134 例菌株不做任何处理和检查，形态学组也分离出来 134 例菌株，对其进行微生物形态学检验。然后对比各组病人感染程度，以及免疫力下降情况。
结果 形态学组患者中度和重度等感染率低于对照组，且形态学组免疫力下降率也比对照组低，差异有统计学意义（P＜0.05）。
结论 应用微生物形态学检验感染性疾病具有重要诊断价值，值得应用。

PU-3349

微生物检验在尿路感染预防和诊断治疗中的意义评价

陈敏
资阳市乐至县人民医院

目的 分析在尿路感染预防与诊断中应用微生物检验的意义。
方法 在 2019-3 至 2020 年 2 月期间选取 78 例尿路感染患者，将其分为 2 组。常规组实施常规检验，实验组实施微生物检验，然后对比各组检验结果。
结果 实验组治疗有效率、病情诊断准确率均比常规组高，且实验组无效患者感染率低于常规组，差异有统计学意义(P＜0.05)。
结论 使用微生物检验尿路感染患者能准确知晓感染情况，进而加以预防和治疗，能取得显著的治疗效果，值得应用。

PU-3350

2020 年度淋球菌耐药监测结果分析

梁艳华
广州市皮肤病防治所

目的 监测 2020 年收集的淋球菌耐药性，为淋病防治提供策略。
方法 采用琼脂稀释法，检测 2020 年本单位门诊临床分离培养的 100 株淋球菌，测定青霉素、四环素、环丙沙星、大观霉素、 阿奇霉素、头孢曲松、头孢克肟的最低抑菌浓度(MIC)，分析淋球菌耐药性，判定质粒介导的高度耐四环素淋球菌(TRNG)，同时用纸片碘量法检测 ß-内酰胺酶，筛查产青霉素酶淋球菌(PPNG)。
结果 PPNG 阳性率为 46%(46/100)；TRNG 阳性率为 35%(35/100)；青霉素、四环素、环丙沙星和阿奇霉素耐药率分别是 95％(95/100)、88％(88/100)、97％ (97/100)、16％ (16/100)。头孢克肟和头孢曲松未见耐药菌株，低敏率分别为 11％(11/100)和 4％(4/100)，大观霉素未发现耐药菌株和低敏菌株。
结论 广州市淋球菌临床分离株普遍对青霉素、环丙沙星、四环素耐药，治疗淋病的首选药仍是大观霉素、头孢曲松和头孢克肟，淋球菌耐药监测应定期进行。

PU-3351

微生物检验在感染性疾病临床诊断治疗中的应用价值

李阳
资阳市乐至县人民医院

目的 分析在临床上感染性疾病诊断治疗中应用微生物检验的价值。
方法 在 2019.3-2020.2 月期间选出 70 例(2 组)患上感染性疾病的患者，对照组患者不实施检验，根据患者的临床症状和医生的经验选择相应的抗生素进行治疗。检验组患者先进行微生物检验，然后根据结果选择针对性抗生素进行治疗。最后对比各组患者治疗效果以及病情诊断准确性。
结果 检验组治疗有效率、诊断准确率均比对照组高，差异有统计学意义(P＜0.05)。
结论 在临床上使用微生物检验判断感染性疾病能准确诊断出患者的病情，并给予针对性治疗，能获得显著的治疗效果，值得应用。

PU-3352

碳青霉烯耐药基因在肺炎克雷伯菌中的分布特点分析

刘畅
南京大学医学院附属鼓楼医院

目的 分析碳青霉烯耐药基因 KPC 在全球肺炎克雷伯菌中的分布规律和特点。
方法 从 NCBI 中下载全球肺炎克雷伯菌的基因组，分析 KPC 基因在这些细菌中的分布，产 KPC 肺炎克雷伯菌细菌基因组进行多位点序列分析，确定其序列分型（Sequence type,ST），进一步分析 KPC 基因在不同克隆菌株中分布，并使用 SPSS 软件分析主要 KPC 变异体 KPC-2 和 KPC-3 的流行与主要流行克隆 ST11、ST258 及 ST512 的相关性。
结果 我们检出了 14 个 KPC 的变异体，KPC 在全球的流行主要以 KPC-2（n=959）和 KPC-3（n=952）为主。产 KPC 肺炎克雷伯菌的克隆有 115 个 ST 型，以 ST258 (n=996)、ST11 (n=285)和 ST512(n=259)为主。KPC-2 分布在 87 个不同的 ST 菌株中，以 ST258 (n=413)和 ST11 (n=274)为主；KPC-3 分布在 45 个不同的 ST 菌株中，以 ST258 (n=570)和 ST512 (n=259)为主。ST11 携带的 KPC 变异体主要为 KPC-2(n=274)；ST258 携带的 KPC 变异体主要为 KPC-2(n=413)和 KPC-3(n=570)。ST512 携带的 KPC 变异体主要为 KPC-3 (n=259)。
结论 从全球范围来看，KPC 的流行以 KPC-2 和 KPC-3 为主，KPC-2 的流行克隆菌株以 ST11 和 ST258 为主，KPC-3 的流行克隆菌株以 ST258 和 ST512 为主，加强该类细菌的监测对于预防院内感染控制具有重要的作用。

PU-3353

精胺与 β-内酰胺类抗生素联合抗菌作用功能研究

刘畅
南京大学医学院附属鼓楼医院

目的 研究精胺与 β-内酰胺类抗生素联合应用时对于多重耐药细菌的协同治疗作用。
方法 实验菌株选取我院临床多重耐药革兰阴性杆菌，采用微孔稀释法测定 MIC 值，评估精胺与 β-内酰胺类抗生素的协同作用。
结果 β-内酰胺类抗生素与精胺联合使用时具有协同作用，抗菌效果增强，MIC 值大幅度下降，部分菌株 FICI 比值<0.5。
结论 β-内酰胺类抗生素与精胺联合用药方案可以有效提高临床抗感染治疗的效率。

PU-3354

基于荧光素酶报告基因的细菌外膜囊泡标记方法的建立

刘畅
南京大学医学院附属鼓楼医院

目的 建立一种基于荧光素酶报告基因的细菌外膜囊泡标记方法。
方法 利用细菌外膜囊泡表面携带高丰度外膜蛋白的特点，构建外膜蛋白-荧光素酶融合蛋白，实现细菌外膜囊泡的“自发光”以用于后期检测。
结果 通过构建 OmpA-NanoLuc 融合蛋白的方式实现细菌外膜囊泡的荧光素酶标记，表达该融合蛋白的细菌所分泌的外膜囊泡具有明确的荧光素酶活性，因此可通过检测荧光素酶活性的方式对细菌外膜囊泡进行检测。

结论 成功构建了一种基于荧光素酶报告基因的细菌外膜囊泡标记方法，可在不使用细胞膜染料的情况下对细菌外膜囊泡进行检测。

PU-3355

通过 mNGS 诊断鹦鹉热衣原体肺炎的患病、诊断和控制情况分析

卢秋然、葛虎、代冰、曹媛、刘昌霖、彭千、余艳（通讯作者）
长沙金域医学检验实验室有限公司

目的 了解湖南省各地级市地区居民鹦鹉热衣原体肺炎患病、诊断和控制情况，为鹦鹉热衣原体肺炎的防治工作提供科学依据。
方法 回顾性分析长沙金域实验室从 2020 年 10 月-2021 年 5 月，应用宏基因组高通量测序技术（metagenomic next-generation sequencing，mNGS），基于 20 例临床已经确诊为鹦鹉热衣原体肺炎的患者中进行总结其临床特征及诊治要点，比较不同地区人群鹦鹉热衣原体肺炎的患病、诊断及控制情况。
结果 在 20 例临床确诊为鹦鹉热衣原体肺炎的患者，共检测出永州市 6(7.69%)，长沙市、邵阳市均 3 例 (0.56%,6.12%)，岳阳市、郴州市均 2 例 (5.26%,2.90%)，吉首市、怀化市均 1 例 (1.64%,1.08%)。其中调查对象中男女性别比为 13：7。本研究中鹦鹉热衣原体肺炎的患者均有家禽接触史，其中男性患病率（65%）高于女性（35%），差异有统计学意义（P<0.05）。送检呼吸道样本（痰、肺泡灌洗液、肺组织）通过 mNGS 检测出鹦鹉热衣原体核酸序列，结合临床表现及接触史以明确诊断。其中肺泡灌洗液 mNGS 检出的病原体序列数较痰标本多，且没有口腔定植菌的干扰，还可以识别是否合并其他细菌、病毒等感染，大大缩短了鹦鹉热衣原体肺炎的诊断时间和病程，减少不必要抗菌药物的使用。
结论 湖南省居民鹦鹉热衣原体肺炎以永州市、邵阳市患病率较高，而诊断率和控制率较低，应进一步采取综合措施提高人群诊断率和控制率水平。据统计两地呼吸道标本送检总量分别是 78 例、50 例，随着 mNGS 更广泛的应用，会对该地区的鹦鹉热衣原体肺炎患病率有更全面的认识。同时，相信 mNGS 逐渐应用于临床后，越来越多的非典型病原菌被发现，特别对于肺部感染病原体不明的人群，做到及早发现，及时诊断、规范治疗。

PU-3356

重症监护病区接受肠道营养患者艰难梭菌感染的危险因素分析

王道盛、彭奕冰、董丹凤
上海交通大学医学院附属瑞金医院

研究目的 艰难梭菌感染（Clostridioides difficile infection, CDI）是住院病人医源性腹泻的主要原因，在重症监护病区（Intensive care unit, ICU）接受肠道营养的病人是 CDI 的潜在高发人群。本研究旨在揭示在 ICU 病区接受肠道营养病人 CDI 的发生率与 CDI 发生相关的危险因素。
研究方法 收集 2018 年 7 月至 2019 年 12 月期间于上海交通大学医学院附属瑞金医院 ICU 病区接收肠道营养至少一周的患者，自患者启动肠道营养后每周收集其粪便，使用培养法和毒素抗原检测法筛查其艰难梭菌携带状态，记录患者临床特征并分析其相关危险因素。
研究结论 研究期间共收集 168 名 ICU 病区接受肠道营养治疗至少一周的患者，18 名被确诊为 CDI，发病率为 10.7%。脑梗死个人史是肠道营养病人 CDI 的显著风险因素（OR, 9.759; 95% CI, 2.140-44.498）；预先使用甲硝唑是肠道营养病人 CDI 的显著保护因素（OR, 0.287; 95% CI, 0.091-0.902）。

PU-3357

Bacteraemia caused by Tsukamurella tyrosinosolvens in an immunocompromised patient in China

Lifeng Wang、Liyan Ye、Kun Ye、Qiang Zhao、Jiyong Yang
Chinese PLA General Hospital

We reported case of Tsukamurella tyrosinosolvens bacteraemia in an immunocompromised patient who was successfully treated with a ten days course of single Cefoperazone sulbactam. The identification of Tsukamurella tyrosinosolvens were by 16S rRNA sequence and Whole genome sequence. Antimicrobial susceptibility testing showed that the strain was susceptible to amikacin, ciprofloxacin, imipenem, Cefotaxime. Bioinformatic analysis showed that the G+C content and genome size of this isolate is 71.02% and 4.99 Mb. Single-nucleotide polymorphism (SNP) analysis was performed on Tsukamurella tyrosinosolvens genomes from our strain and seven international strains A maximum likelihood phylogenetic tree constructed on the basis of 10,300 core genome single nucleotide polymorphisms (cgSNPs) showed that TY201901 isolate in this study clustered in the same branch with GCA_001575225.1 and GCA_001623895.1 isolates from Subsurface soil and chemical hydrocarbon sludge, respectively. Therefore, the possible route of infection in our patient was environmental exposure in an immunocompromised status.

PU-3358

宏基因组高通量测序技术辅助诊断血流结核感染 1 例

刘昌霖、葛虎、代冰、曹媛、卢秋然、彭千、余艳
长沙金域医学检验实验室有限公司

目的 探索宏基因组高通量测序技术（metagenomic next-generation sequencing，mNGS）在临床检验技术中的应用，将 mNGS 检验技术更好的服务于临床，为 mNGS 检验技术更好的应用于血流感染的临床检验提供潜在价值。
方法 回顾性收集本实验室采用外周血 mNGS 技术辅助确诊的血流感染病例临床资料，采用 Illumina NextSeq™ 550 测序平台对外周血进行病原微生物测序，综合分析病例的临床、实验室和辅助检查结果。
结果 在送检的外周血标本中，发现 1 例老年男性患者，检出结核分枝杆菌复合群阳性，其中血常规检查白细胞 12.6X10^9/L 严重偏高、中性粒细胞比例 97.30%严重偏高、淋巴细胞比例 1.80%严重偏低；痰液抗酸染色（+++）；痰液结核分枝杆菌及利福平耐药检测(Xpert MTB/RIF Assay)阳性。外周血 mNGS 检测，结核分枝杆菌复合群 reads 数为 2，结核分枝杆菌 reads 数为 1，属的基因覆盖率为 0.208%，提示血流感染结核分支杆菌，临床确诊结核感染。在血流中检出结核分支杆菌，究其原因可能是由于感染部位的结核分枝杆菌经淋巴细胞播散传播进入血流，从而使其被检测到。
结论 mNGS 检验技术对血流感染病原微生物的鉴定具有一定的优势，有助于血流感染的诊断，扩展了人们对结核分枝杆菌感染在血流检测的认识，为结核分枝杆菌感染的诊断提供了一个新的检测方向，也为检验医学和临床治疗提供了参考。

PU-3359

碳青霉烯类耐药肺炎克雷伯菌药敏及流行病学分析

罗雪丹
资阳市安岳县中医医院

目的 研究碳青霉烯类耐药肺炎克雷伯菌的检测方法，对常用抗生素药物进行临床实践中敏感性的测定，分析其在临床上的流行特点为如何有效地控制医院感染提供了依据。
方法 搜集医院临床上分离出的非重复的 CRKP 进行筛选，应用上机与纸片法结合来测定临床上常用抗生素的敏感性，然后用改良 Hodge 试验与 EDTA 协同试验对碳青霉烯酶进行检测以及筛选。。
结果 发现 CRKP 菌株对多粘菌素几乎完全敏感，对四环素、米诺环素、替加环素、氯霉素均较敏感，对头孢菌素类和 β-内酰胺类抗菌药物均表现为高度耐药，而对阿米卡星、庆大霉素、妥布霉素的耐药率较低。 在收集到的这些 CRKP 菌株中，出现病区的分布以 ICU 病区占比重最多，其次是呼吸科病区。收集到的 CRKP 主要来源于呼吸道标本，尤其痰液最多，占一半以上。其次分别是血液、尿液、粪便等。CRKP 在临床疾病中的分布情况发现患者所患疾病以慢性阻塞性肺疾病和重症肺炎为主，其次是肺部感染、脓毒血症、尿路感染、肿瘤疾病等，与肺炎克雷伯菌的传播途径密切相关。
结论 CRKP 的治疗可以多粘菌素、四环素、氯霉素等为主，联合使用抗生素常强于单一使用某种抗生素的效果，ICU 的病患出现 CRKP 的风险更高，且肺炎克雷伯菌的主要传播途径是通过呼吸道。

PU-3360

临床微生物检验和细菌耐药性监测的应用价值研究

王阳
资阳市安岳县中医医院

目的 研究临床微生物检验和细菌耐药性监测的应用价值。
方法 抽取 2019 年 1 月-2020 年 12 月到我院接受住院诊疗的患者作为本次的研究对象，从他们的血液样本、尿液样本以及分泌物样本中剔除重复菌株提取 428 株致病菌作为本次的研究样本，对每个样本分别实施药敏试验，并对结果进行详细的分析，然后对细菌的耐药性进行监测。
结果 在本次研究的 428 株致病菌中发现革兰氏阴性杆菌有 256 株、革兰氏阳性球菌有 172 株，多重耐药菌 171 株，检出率达 40%。有许多临床医学中比较常见的致病菌，其中耐药性比较严重的几种致病菌包括鲍曼不动杆菌、铜绿假单胞菌、金黄色葡萄球菌以及凝固酶阴性葡萄球菌。耐甲氧西林金黄色葡萄球菌以及耐甲氧西林凝固酶阴性葡萄球菌检出率分别达 40%和 80%，而耐碳青霉烯的鲍曼不动杆菌检出率高达 87.5%，多重耐药的铜绿假单胞菌检出率也高达 42.5%。

结论 细菌的耐药性升高比较明显，多重耐药菌的检出率也越来越高，因此对临床微生物进行检验和耐药性监测的措施十分重要，能够帮助医院更加了解流行的致病菌分布情况以及细菌的耐药性，有效的对这些感染病菌进行预防，为患者的身体健康筑起一个屏障，是一项值得推广的应用。

PU-3361

临床微生物关于对临床泌尿系统感染病原菌的构成与耐药情况分析

李辉
资阳市安岳县中医医院

目的 分析临床患者泌尿系统感染病原菌分布特点及耐药情况，为临床合理用药提供依据。
方法 采集 2019 年 5 月 1 日至 2021 年 4 月 30 日我院临床病人的中段尿标本，了解病原菌分布情况及主要病原菌对抗菌药物的耐药性及其变化。
结果 共分离病原菌 335 株，其中革兰氏阴性杆菌占 69.6%，以大肠埃希菌（51.0%）为主，革兰氏阳性菌占 22.4%，以屎肠球菌（13.7%）为主，真菌占 6%，以副热带假丝酵母菌（3.9%）为主。病原菌分离率最高的科室为外一科。通过对比 2 年的药敏结果发现，大肠埃细菌中产超广谱 β-内酰胺酶的菌株比例较高，且呈逐年上升的趋势，头孢唑啉，头孢曲松，左氧氟沙星，氨苄西林及氨苄西林舒巴坦的耐药率较高，屎肠球菌对万古霉素和利奈唑胺耐药率较低，副热带假丝酵母菌对抗真菌性药物敏感性较好，耐药率不到 5%。
结论 我院泌尿系统感染患者的病原菌主要以革兰氏阴性杆菌为主，以大肠埃希氏菌最常见，其中 ESBLs 的菌株比例呈上升趋势，临床上应重视抗生素的合理使用，减少耐药菌的产生。

PU-3362

痰涂片与结核抗体检验在诊断肺结核中的应用

陈焦
四川省安岳县人民医院

目的 探讨痰涂片与结核抗体检验在诊断肺结核中的应用价值。
方法 选择 2019 年 2 月-2019 年 3 月在我院明确诊断为肺结核的患者 86 例，按照检验方法不同分为 A 组与 B 组，每组 43 例，分别行痰涂片检验、结核抗体检验，检验过程均严格按照试剂盒说明书进行，比较两组阳性检出率。
结果 A 组阳性检出率为 74.42%，B 组阳性检出率为 93.02%，B 组阳性检出率明显高于对照组，P＜0.05，差异有统计学意义。
结论 结核抗体检验在肺结核诊断中的阳性率更高，临床应用价值优于痰涂片检验，值得临床推广。

PU-3363

一种鉴定申克氏孢子丝菌的质谱方法

叶家美
四川金域医学检验中心有限公司

目的 探索申克氏孢子丝菌复合体的鉴定方法，寻找简单、快捷、准确的鉴定方法。申克氏孢子丝菌是一种子囊菌类的双相真菌，会引起一种世界范围的皮肤或皮下孢子丝菌菌病，偶尔也可向内脏和骨骼播散，严重者甚至可引起全身的播散感染。本病在我国东北地区相对多发，且部分区域可成

批发生，对人们的健康造成严重威胁。该菌在 SDA 上 25℃培养生长缓慢，7 天以上呈褐色有皱褶短绒毛菌落，棉兰染色镜下分生孢子梗直立，分生孢子呈梨花样排列；35℃培养可见卵圆形至雪茄形酵母样孢子。传统的培养方法至镜检周期较长（真菌生长缓慢），且需要丰富的经验来进行判断和鉴别。

方法 选用一例皮肤科感染了申克氏孢子丝菌的脓液样本，通过在 SDA 上 25℃和 35℃的条件进行培养，培养时间 3 天，有菌落成形生长，再利用郑州安图 Autof ms1000 飞行质谱仪进行鉴定，前处理方法为裂解法，在 1.5ml 离心管中加入 30 微升甲酸裂解液，挑取少量菌体至甲酸裂解液中，震荡裂解 1-3min，取 1 微升悬液滴加到样品靶上，晾干后，滴加 1 微升基质溶液，晾干后进样打靶。用第二代 DNA 测序加以证实结果的准确性。

结果 实验显示：郑州安图 Autof ms1000 飞行质谱仪总分值为 10 分，申克氏孢子丝菌质谱鉴定分值为 9.384 分，第二代 DNA 测序显示分辨率较好，与质谱鉴定结果一致。

结论 综上所述，Autof ms1000 飞行质谱仪开启了申克氏孢子丝菌新的鉴定方法，大大缩短了传统培养方法至镜检的报告周期，大大降低了其他方法的鉴定成本。同时，也开启了孢子丝菌鉴定研究的新领域，以期为临床孢子丝菌病的诊疗工作提供可靠依据。

PU-3364

2015～2019 年真菌血流感染菌种分布及抗真菌药物敏感性分析

王盛华
山东第一医科大学附属省立医院

目的 分析真菌血流感染菌种分布和抗真菌药物的敏感性，为临床诊治提供依据。

方法 回顾性分析山东省立医院 2015 年 1 月～2019 年 12 月血培养鉴定结果为真菌的临床资料，对菌种分布、抗真菌药的敏感性、阳性报警时间、科室分布等进行分析。

结果 血培养中共分离非重复真菌 156 株。排在前 3 位的真菌分别为白色念珠菌 59 株（37.8%），热带念珠菌 26 株（16.7%）和近平滑念珠菌 20 株（12.8%）；少见菌包括季也蒙念珠菌、毕赤酵母菌、新生隐球菌、酿酒酵母和红酵母等。我院真菌血流感染好发于 60 岁以上的老年患者 68 例（43.5%），男性 83 例（53.8%）。真菌血流感染前 3 位的科室为内科 ICU33 株（21.2%），急诊科 31 株（19.9%），和外科 ICU28 株（17.9%）。阳性报警时间从长到短依次为：光滑念珠菌（55.8±28.3）h，近平滑念珠菌（52.3±40.7）h，白色念珠菌（44.1±37.5）h 和热带念珠菌（22.6±19.2）h。白色念珠菌、近平滑念珠菌、光滑念珠菌和热带念珠菌对氟康唑敏感率分别为 100%、100%、93.8%和 73.1%。

结论 本院真菌血流感染以白念珠菌为主，绝大多数真菌对抗真菌药具有较高敏感性，热带念珠菌的耐药率相对较高。

PU-3365

耐碳青霉烯类肺炎克雷伯菌抗生素耐药性及毒力的分子进化研究

朱威南、沈立松
上海交通大学医学院附属新华医院

背景 耐碳青霉烯肺炎克雷伯菌(CRKP)是世界范围内的一种严重的致病菌，给公共卫生带来了严重的问题。本研究对我院分离的 CRKP 菌株进行了长时间回顾性地流行病学和基因组研究(2009-2018 年)，涵盖菌株早期出现到克隆菌株暴发的完整过程，用于评估 CRKP 和高毒力 CRKP (hv-CRKP)的流行和演变。

方法 本研究在住院患者中连续收集了 1181 株非重复 CRKP 分离株，采用 wzi 测序、基因组测序、rmpA/rmpA2 筛选、质粒追踪等，对菌株的荚膜类型、遗传亲缘关系、毒力特征和质粒传播特征进行鉴定。同时，对其中具有代表性菌株进行了生物膜形成、黏度和大蜡螟感染模型中毒力等进行了分析。
结果 wzi209-CRKP 和 wzi64-CRKP 被发现是主要存在的群别，均属于 ST11 且在进化关系上关系密切。blaKPC 被发现存在于 IncFII-IncR 耐药杂交质粒上。通过质粒上 blaKPC 周围的耐药环境(blaSHV-12/TnAs1)和接合环境(traN/traC)标记，我们确定了 wzi209-CRKP 与 K14.K64-CRKP 在我院不同患者之间的转移。hv-CRKP 主要存在于 K14.K64-CRKP 中。其中两种不同的毒力质粒，非结合的 IncFIB(k)-IncHI1B-rmpA/rmpA2 和接合型 IncFIB-IncHI1B-rmpA2-only 被发现在我院流行。IncFIB-IncHI1B-rmpA2-only 的发生率高于 IncFIB(k)-IncHI1B-rmpA/rmpA2。
结论 深入了解 CRKP 特别是 hv-CRKP 的流行和演变，对公共卫生控制策略的合理设计和实施是非常必要的。

PU-3366

无乳链球菌在临床不同类型标本中的分子分型分布

高珮菁、孙景勇
上海市交通大学医学院附属瑞金医院 临床检验中心

目的 明确临床不同标本类型中无乳链球菌的分子分型分布特征，了解临床上从阴道分泌物和中段尿标本中是否存在具有生存优势或更易引起感染的无乳链球菌分型。
方法 从无乳链球菌阳性的不同标本中分离无乳链球菌，冻存菌种并提取 DNA；通过 PCR 扩增 cpsG、cpsI、cpsJ、cpsN，检测分离株表面的荚膜多糖，进行血清型分型；通过 PCR 扩增 7 个管家基因，测定其序列后与数据库中基因序列比对，对分离株进行多位点序列分型（MLST）；主要分析临床上从阴道分泌物和中段尿标本中分离得到的无乳链球菌的分子分型分布情况，分析其是否具有统计学差异。
结果 本课题中采用收集的无乳链球菌 114 株，其中 41 株来自中段尿标本，73 株来自阴道分泌物标本。未采用的其余分离株来自前列腺液、白带等其他类型标本，但由于同种标本数量较少，结果随机性不足，故不进行分析。在对中段尿标本和阴道分泌物标本进行荚膜多糖血清分型后，发现在中段尿标本、阴道分泌物标本中分离株都以Ⅴ型为主，分别占 36.58%和 36.99%。在对中段尿标本和阴道分泌物标本进行 MLST 分型后，发现其中中段尿标本以 ST-10 和 ST-19 为主，分别占 17.07%和 19.51%，阴道分泌物标本以 ST-19 和 ST-24 为主，分别占 20.55%和 19.18%。
结论 本课题的 114 株 GBS 分离株中，分离株的血清型分型在中段尿及阴道分泌物标本中都以Ⅴ型为主，分离株的 MLST 分型在在中段尿及阴道分泌物标本中都以 ST-19 为主。

PU-3367

A ceftazidime-avibactam resistant and carbapenem susceptible Klebsiella pneumoniae strain harboring blaKPC-14

Siqiang Niu
Department of Laboratory Medicine, The First Affiliated Hospital of Chongqing Medical University

Objectives Here we report a novel KPC-14 allele found in the K. pneumoniae isolate (designated BK13048) in New York City.
Methods Drug susceptibility assays were performed by a standard CLSI broth microdilution method. And sequencing and characterization of the blaKPC-14 was achieved by first

segregating the plasmid into an E. coli host as described previously. Then the plasmid and whole genome sequencing was performed. Then the KPC-14- , KPC-2- and KPC-3-encoding open reading frames were cloned in E. coli DH10B with pET28a-kpc_pro vector.
Results Drug susceptibility assays showed that BK13048 was resistant to ceftazidime-avibactam but susceptible to ertapenem, imipenem and meropenem. The blaKPC-14-harboring plasmid was successfully transferred to E. coli J53 by conjugation. Sequencing the blaKPC gene in BK13048 revealed a novel KPC-type carbapenemase that differed from blaKPC-3 by a 6-bp deletion at position 721-726 and a transition T814C, leading to a two-amino acid (242Thr and 243Ala) deletion and a Tyr272His change relative to KPC-3, respectively. The transformant BK51985 harboring kpc-14 gene showed ceftazidime-avibactam MIC of 16 μg/ml, which is 64-folds higher than BK51982 and BK51984 transformant, more than 512-folds higher than native E. coli DH10B cells.
Conclusions we have isolated and characterized a novel KPC variant from K. pneumoniae BK13048, designated KPC-14. The data presented here show that KPC-14 is mainly responsible for the ceftazidime-avibactam resistance of this strain.

PU-3368

多种表型检测方法在耐碳青霉烯肠杆菌科中的应用评价

贾珉
武汉市第一医院

目的 评价三种方法对肠杆菌科细菌碳青霉烯酶表型的筛选能力。
方法 收集 59 株耐碳青霉烯肠杆菌科细菌和 22 株碳青霉烯类敏感菌，分别用 Carba NP 试验、mCIM 与 eCIM 试验、KPC 显色培养基三种方法进行表型检测。以 PCR 检测结果为金标准，比较三种方法对 CRE 表型检测的灵敏度和特异度等。
结果 基因检测中，共 58 株检出耐药基因，包括 KPC 型 35 株，NDM 型 21 株，IMP 型 2 株，有 1 株耐药菌未检测到相关基因。表型检测中，Carba NP 的灵敏度和特异度分别为 96.6%、100%；mCIM 的灵敏度和特异度均为 100%；eCIM 在 B 类金属酶的筛查中的灵敏度和特异度分别为 92%、100%；KPC 显色培养基的灵敏度和特异度分别为 100%、95.5%；其中有一株携带 KPC 基因的肺炎克雷伯菌 eCIM 为阳性。Carba NP 分别与 mCIM 与显色培养基之间进行一致性比较，其 Kappa 值分别为 0.94、0.91。
结论 三种方法均有较好的灵敏度和特异度，且有较好的一致性。其中 mCIM 的筛查效果最好，与 eCIM 联合使用可以有效的筛查丝氨酸酶和金属酶。

PU-3369

接受恩替卡韦或 peg-干扰素治疗的慢性乙型肝炎患者血清 HBV RNA 水平的动态变化

俞晓琦、于德敏、龚启明、张欣欣
上海交通大学医学院附属瑞金医院

目的 本研究旨在研究血清 HBV RNA 与其他生物标志物的相关性及其在抗病毒治疗过程中的动态变化和临床意义。
方法 回顾性分析 136 例接受恩替卡韦或 peg-干扰素抗病毒治疗慢乙肝患者的血清 HBV RNA 水平。使用实时荧光定量聚合酶链式反应（PCR）进行定量检测，受试者工作特征曲线（ROC）用以评估其对 HBeAg 阴转的预测价值。

结果 基线血清 HBV RNA 的平均值为 6.41 copies/ml，其中 HBeAg 阳性患者的平均值为 7.20 copies/ml，显著高于 HBeAg 阴性患者的平均值 4.60 copies/ml (p<0.001)。基线 HBV RNA 水平与 HBV DNA 水平显示出较强的相关性(r=0.82, p<0.001)，与 HBsAg 水平也呈现出一定的相关性(r=0.69, p<0.001)，但与 ALT 的相关性较弱(r=0.28, p<0.05)。和恩替卡韦单药治疗相比，peg-干扰素治疗的患者第 4 周、24 周和 48 周的 HBV RNA 水平下降更显著。接受恩替卡韦治疗后，获得 HBeAg 血清学转换的患者第 4 周、12 周、24 周和 48 周血清 HBV RNA 水平的下降更为显著。接受恩替卡韦治疗的患者基线 HBV RNA, HBV DNA 及 HBsAg 预测 HBeAg 血清学转换的受试者工作特征曲线下面积分别为 0.68，0.66 和 0.64；而在 peg-干扰素治疗患者中，HBV DNA 的曲线下面积最大为 0.66，其次是 HBV RNA 及 HBsAg，分别为 0.63 和 0.60。在抗病毒治疗过程中，恩替卡韦治疗组患者 HBeAg 血清学转换的最佳预测指标是第 4 周的 HBV RNA 水平 (AUC=0.71)，其预测的截断值、敏感度、特异性、阳性预测值、阴性预测值分别为 7.95 log10copies/mL, 83%, 56%, 40%, 91%；而在接受 peg-干扰素治疗的患者中则是第 24 周的 HBV RNA 水平(AUC=0.70)，其预测的截断值、敏感度、特异性、阳性预测值、阴性预测值分别为 3.55 log10copies/mL, 89%, 62%, 44%, 94%。

结论 血清 HBV RNA 水平可在慢乙肝患者抗病毒治疗期间作为一项新的生物标志物预测疗效。

PU-3370

Ribokinase screened from T7 phage displayed Mycobacterium tuberculosis genomic DNA library had good potenital for the serodiagnosis of tuberculosis

Dan Luo[1,2]、Jun He[2]、XiaoLiang Yan[1]、Yanhua Zeng[1]
1. Affiliated NanHua Hospital, University of South China
2. 南华大学附属南华医院

Tuberculosis (TB) caused by Mycobacterium tuberculosis is the leading cause of death among infectious diseases in the worldwide. Lack of more sensitive and effective diagnostic reagents has increased the awareness of rapid diagnosis for TB. In this study, T7 phage displayed genomic DNA library of M. tuberculosis was constructed to screen the antigens that specially bind with TB–positive serum from the whole genome of M. tuberculosis and to improve the sensitivity and specificity of TB serological diagnosis. After 3 rounds of biopanning, results of DNA sequencing and BLAST analysis showed that 19 positive phages displayed 4 different proteins and the occurrence frequency of the phage which displayed ribokinase (RK) was the highest. The results of indirect ELISA and dot immunoblotting indicated that representative phages could specifically bind to TB–positive serum. The prokaryotic expression vector containing the DNA sequence of RK gene was then constructed and the recombinant protein was expressed and purified to evaluate the serodiagnosis value of RK. The reactivity of the recombinant RK with different clinical sera were detected, and the sensitivities and specificities in TB serodiagnosis were 90% and 86%, respectively by screening sera from TB patients (n=90) and uninfected individuals (n=90) based on ELISA. Therefore, this study demonstrated that RK had good potential for the serodiagnosis of TB.

PU-3371

血培养联合质谱快速鉴定在肠炎沙门氏菌引起食物中毒公共事件中的应用

李晟彬、哈依努尔、刘洁
新疆自治区第三人民医院

应对一起疑似群体食物中毒公共卫生事件进行实验室检测分析，明确中毒原因，利用基质辅助激光解析电离飞行时间质谱（MALID-TOF MS）鉴定技术，实现病原体快速鉴定，进而指导后续的应急处理。

方法 根据临床《WST640-2018 微生物学检验标本的采集和转运行业标准》以及《WST498-2017 细菌性腹泻临床实验室诊断操作指南》对中毒病人粪便、血液标本进行细菌培养采样和实验室检测分析。

结论 从患者血液及粪便标本培养物中均分离检测出肠炎沙门氏菌。且血培养联合微生物质谱快速鉴定相较传统培养及鉴定结果提前 24～48 h ，时效性更高，第一时间为临床明确诊断、快速治疗提供有效病原学证据。

PU-3372

微生物检验泌尿系统的病原菌结果临床分析

杨姗
资阳市雁江区中医医院

目的 探讨采用微生物检验方法检验泌尿系统疾病患者的泌尿系统病原菌分布情况。

方法 选取本院于 2018 年 7 月至 2019 年 7 月收治泌尿系统疾病患者 200 例，患者均行微生物检验与细菌培养，分析检验结果。

结果 200 例泌尿系统感染患者尿液样本检出致病菌 287 株，包括单一病原菌感染 113 例、病原菌混合感染 87 例，单一感染几率相比混合感染更高（P<0.05）；单一病原菌感染者大肠埃希菌感染占比相比于白色尿球菌、尿肠杆菌占比明显更高（P<0.05）；病原菌混合感染患者的支原体+其他类型致病菌感染的占比较高，且多见为解脲支原体+其他类型细菌感染。

结论 临床针对泌尿系统疾病患者采用微生物检验方法检验有助于了解患者感染微生物类型，以此明确选择合理的治疗方案治疗，以降低误诊、误治几率，提高临床疗效。

PU-3373

利奈唑胺耐药头状葡萄球菌生物膜形成能力分析

周万青[2]、高硕[1]、陆瀚文[1]、张燕[1]、康怡[1]、沈瀚[1]
1. 南京大学医学院附属鼓楼医院
2. 南京大学医学院附属鼓楼医院

目的 分析临床分离利奈唑胺耐药头状葡萄球菌生物膜形成能力。

方法 收集 2017-2020 年间临床分离头状葡萄球菌共 104 株，采用 VITEK MS 质谱分析仪进行鉴定，VITEK 2 Compact 分析仪进行药敏试验并用 E-test 法复核利奈唑胺最低抑菌浓度（MIC）；PCR 及测序分析耐药基因 cfr， optrA 及 23S rRNA 耐药突变；96 孔板及结晶紫染色检测菌株生物膜形成能力，PCR 检测生物膜形成相关基因 icaAD，bap，fnbA 及 cna 的携带情况。

结果 44 株利奈唑胺耐药菌株中 35 株携带 cfr 基因（79.5%），44 株菌均存在 23S rRNA V 区 G2576T 突变。利奈唑胺耐药菌株均能形成生物膜（44/44，100%）。60 株利奈唑胺敏感株有 30

株生物成膜阳性（30/60，50%）。生物膜定量结果显示利奈唑胺耐药菌株明显强于敏感株（ U=658, P<0.0001）。生物膜阳性菌株均检出 icaAD 基因（74/74，100%），生物膜阴性菌株中有 93% icaAD 基因阳性（28/30）。bap 基因在产生物膜菌株中阳性比例为 86.5%，生物膜阴性菌株中有 40%菌株未检出 bap 基因。fnbA 和 cna 在所有菌株中均未检出。
结论 临床分离头状葡萄球菌对利奈唑胺耐药由 23S rRNA 突变及 cfr 基因导致；利奈唑胺耐药菌与敏感株相比具有更强的生物膜形成能力，并与黏附相关基因 icaAD 和 bap 有关。

PU-3374

股疝术后切口感染的病原菌分布特点及其危险因素分析

赵晓杰
徐州医科大附属医院

目的 探讨和分析股疝无张力修补术后切口感染的病原菌分布特点及其危险因素。
方法 选取 2015 年 1 月至 2019 年 12 月期间在医院进行腹股沟疝无张力修补术的 312 例患者作为临床研究对象，并分别对股疝无张力修补术后切口感染患者的病原菌分布特点和耐药情况，以及诱发感染的相关危险因素进行统计和分析。
结果 本次 312 例行股疝无张力修补术患者中发生切口感染 28 例，感染率为 8.97％。28 例腹股沟疝无张力修补术后切口感染患者中共检出病原菌 42 株，股疝无张力修补术后切口感染患者病原菌分布为革兰阴性杆菌 30.94％，革兰阳性球菌 66.68％，真菌 2.38％。感染病原菌中革兰阳性球菌对青霉素、红霉素均表现出较高的耐药性，耐药率均处于 70％以上；而对替考拉宁则均表现出较低的耐药性，耐药率均处于 20％以下。感染病原菌中革兰阴性杆菌对头孢唑林、氨苄西林均表现出较高的耐药性，耐药率均处于 70％以上；而对阿米卡星、庆大霉素则均表现出较低的耐药性，耐药率均处于 20％以下。年龄≥60 岁，合并糖尿病，低蛋白血症，手术时间≥30 min，均为腹股沟疝无张力修补术后切口感染的危险因素，差异具有统计学意义(P<0.05)。
结论 股疝修补术后切口感染的病原菌分布以革兰阳性球菌为主，其次为革兰阴性杆菌，且切口感染与年龄，合并糖尿病，低蛋白血症，手术时间相关，临床治疗过程中应结合病原菌分布特点及其危险因素给予针对性干预。

PU-3375

产 NDM-1 酶阴沟肠杆菌耐药性与毒力基因检测

余艳[1,2,3]、牛敏[1,2,3]、杜艳[1,2,3]、任玉吉[1,2,3]、代鹏飞[1,2,3]、何秋月[1,2,3]、刘淑敏[1,2,3]
1. 昆明医科大学第一附属医院检验科
2. 云南省检验医学重点实验室
3. 昆明医科大学第一附属医院临床检验诊断省创新团队

目的 了解产新德里金属 β-内酰胺酶-1（NDM-1）阴沟肠杆菌（ECL）耐药性与毒力基因分布情况。
方法 收集 2017 年 1 月至 2020 年 11 月昆明医科大学第一附属医院分离的阴沟肠杆菌，实验组为 29 株产 NDM-1 酶的耐碳青霉烯类阴沟肠杆菌(CR-ECL)，对照组为 32 株不产 NDM-1 酶 CR-ECL 和 35 株碳青霉烯类敏感阴沟肠杆菌（CS-ECL）。采用基质辅助激光解吸电离飞行时间质谱仪（MALDI-TOF MS）、全自动微生物分析系统进行菌株鉴定和药敏试验，PCR 方法检测 NDM-1 耐药基因、24 对毒力基因，χ 2 检验比较毒力基因分布差异。
结果 本院分离的 CR-ECL 菌株 NDM-1 基因检出率为 47.5%，产 NDM-1 酶的 CR-ECL 对常用抗菌药物表现为多重耐药。所有 96 株 ECL 菌株中，毒力基因 acrA、tolC、wcaA、wcaM、wza 的检出率较高，分别为 80.2%、90.6%、87.5%、75.0%、92.7%, clpB、icmf、VasD/Lip 基因的检出率也均在 60%以上，未检出 escV、nleB、pet、hlyA 等毒力基因。统计学分析显示产 NDM-1 酶 CR-

ECL 组 clpB、icmf、VasD/Lip 、acrA 基因检出率高于不产 NDM-1 酶 CR-ECL，CR-ECL 组 clpB、icmf、VasD/Lip 基因检出率高于 CS-ECL 组，差异具有统计学意义（P＜0.05）。
结论 产 NDM-1 酶 CR-ECL 耐药形势严峻而且部分毒力基因的携带率也增高，临床用药应兼顾细菌的耐药性和毒力基因分布情况。

PU-3376

小分子 STK-35/66 对革兰阴性致病菌的广谱抗菌活性研究

徐兰兰、佘鹏飞、刘亚倩、伍勇
中南大学湘雅三医院

目的 研究小分子 STK-35 及 STK-66 对大肠杆菌、铜绿假单胞菌、肺炎克雷伯菌和鲍曼不动杆菌及其持留菌的体内和体外抗菌活性。
方法 通过微量肉汤稀释法检测 STK-35/66 的抗菌谱；通过 K-B 纸片扩散法验证 STK-35/66 对革兰阴性菌的生长抑制能力；通过摇菌培养和菌落稀释计数绘制 STK-35/66 对革兰阴性菌的时间-杀菌曲线；通过人红细胞溶血试验和 CCK-8 细胞毒性实验检测 STK-35/66 的红细胞溶血率和细胞毒性；通过棋盘稀释法检测 STK-35/66 和传统抗生素联用对革兰阴性菌的抗菌效果；通过持留菌杀菌实验检测 STK-35/66 对革兰阴性菌持留菌的杀菌效果；通过小鼠腹膜炎模型检测 STK-35/66 对大肠杆菌的体内抗菌效果。
结果 STK-35/66 对四种革兰阴性菌具有较好的抗菌作用，但具有一定的菌株依赖性，其 MICs 范围在 0.0625-16μg/ml 之间，其中，对大肠杆菌的 MIC 值为 0.0625μg/ml；K-B 实验结果表明，相比对照组，STK-35/66 可明显增大对革兰阴性菌的抑菌圈直径范围，表现出较好的抗菌能力；STK-35/66 对人红细胞、人支气管上皮细胞（HBE）、人非小细胞肺癌细胞系（A549）的的溶血率和细胞毒性较低；此外，棋盘稀释法结果表明,洗必泰与 STK-35 联用对革兰阴性菌的协同抑菌指数值为 0.281-0.625，表现为协同或部分协同作用，其中，对大肠杆菌的抑制作用最强；利奈唑胺和 STK-66 联用对大肠杆菌和肺炎克雷伯菌的协同抑菌指数值分别为 0.125 和 0.375，表现为协同抗菌作用；STK-35/66 在 4h 时可明显降低鲍曼不动杆菌和大肠杆菌的持留菌数量，差异有统计学意义；此外，STK-35/66 可明显提高小鼠生存率，使小鼠肝脾肾细菌数量相比对照组下降约 5 个 Log10，达到和多粘菌素 B 相似的体内抗菌效果。
结论 STK-35/66 对革兰阴性菌具有较好的抗菌潜能，为我们治疗革兰阴性菌感染提供了新的思路。

PU-3377

血流感染播散源头及病原学分析

赵晓杰
徐州医科大附属医院

目的 通过对 723 例血流感染病原菌侵袭性及病原学感染特点进行分析，寻找血流感染病原菌的侵袭途径，查找播散源头，降低患者死亡率。同时对血流感染病原菌的菌群分布，耐药特点，耐药表型进行分析，指导临床合理用药，减少耐药菌的产生，为临床对血流感染的防控及治疗提供依据。
方法 收集我院 2018 年 1 月到 2019 年 12 月血培养阳性病原菌，用 Phoenix100 全自动细菌鉴定/药敏系统对其做出准确的分离鉴定及药敏试验。同时及时了解患者病情，查找病原菌侵袭性特点、临床耐药性特点、病原菌构成特点，并进一步分析病原菌及科室分布，结合相关实验室检查和病原菌侵袭特点，查找病原菌感染源头。同一时间段内感染灶培养菌株与血培养检出的菌株相同，且除外其他感染来源，认为该感染灶为血流感染的播散源头。
结果 1 血流感染病原菌播散源头情况：两年间共检出 723 株血流感染病原菌，分离率位于前五的病原菌依次为肺炎克雷伯菌（18.8%）、大肠埃希菌（15.3%）、鲍曼不动杆菌（10.7%）、凝固

酶阴性葡萄球菌（8.0%）和金黄色葡萄球菌（7.8%）。主要分布科室为重症医学科、泌尿外科和肾内科；腹腔感染来源 114 株（16.0%），以肠杆菌科细菌和链球菌为主，主要分布科室为重症医学科和普通外科；下呼吸道感染来源 86 株（11.9%），以肺炎链球菌（32 株）为主，主要分布科室为呼吸内科；外伤感染来源 57 株（7.9%），以金黄色葡萄球菌（33 株）为主，主要分布科室为骨科。其他不明途径 53 株（7.3%）。

结论 1 血流感染病原菌检出率位于前五位的依次为肺炎克雷伯菌、大肠埃希菌、鲍曼不动杆菌、凝固酶阴性葡萄球菌、和金黄色葡萄球菌。2 病原菌主要分布科室为重症医学科和神经外科；泌尿系感染来源的以大肠埃希菌为主，主要分布科室为重症医学科、泌尿外科和肾内科；腹腔感染来源以肠杆菌科细菌和链球菌为主，主要分布科室为重症医学科和普通外科；下呼吸道感染来源以肺炎链球菌为主，主要分布科室为呼吸内科；外伤感染来源以金黄色葡萄球菌为主，主要分布科室为骨科。

PU-3378

梅里埃 FAN Plus 瓶与 BD 树脂需氧瓶和溶血素厌氧瓶抗生素吸附能力评估

申芳芳[1]、李子尧[2]、纪爱芳[1]
1. 长治医学院附属和平医院
2. 中日友好医院

目的 本实验对梅里埃 FAN Plus 瓶与 BD 树脂需氧瓶和溶血素厌氧瓶对抗生素中和能力进行了评估。
方法 实验中所使用的抗生素包括亚胺培南、美罗培南、万古霉素、哌拉西林/他唑巴坦、左氧氟沙星、阿米卡星、替加环素。根据 CLSI 推荐的菌种与相应的抗生素进行组合并结合临床实际，分别用 ATCC25922 和亚胺培南、哌拉西林/他唑巴坦、阿米卡星、替加环素组合，以及 ATCC29213 和美罗培南、万古霉素、左氧氟沙星组合对试验所选用的血培养瓶进行了抗生素中和能力的评估。
结果 梅里埃 FAN Plus 瓶对于实验 7 种抗生素都可以吸附 ；BD 树脂需氧瓶和溶血素厌氧瓶均不能吸附亚胺培南、美罗培南、万古霉素 ；BD 厌氧瓶不能吸附哌拉西林/他唑巴坦、左氧氟沙星、替加环素； BD 需氧瓶对于左氧仅 80%吸附，且慢于梅里埃 FA PLUS 瓶 6.16h；BD 需氧瓶对于阿米卡星仅 50%吸附，且慢于梅里埃 FA PLUS 瓶 5.58h。
结论 梅里埃 FAN Plus 瓶对亚胺培南、美罗培南、万古霉素吸附性能显著优于 BD 树脂需氧瓶和溶血素厌氧瓶，梅里埃 FA PLUS 厌氧瓶对哌拉西林/他唑巴坦、左氧氟沙星、替加环素的吸附性能显著优于 BD 溶血素厌氧瓶，梅里埃 FA PLUS 需氧瓶对阿米卡星吸附性能显著优于 BD 树脂需氧瓶。

PU-3379

不同药敏实验评价流感嗜血杆菌对三种 β-内酰胺类药物的药敏结果一致性的研究

王战豪
成都市第三人民医院

目的 对比研究三种体外药敏试验在测定流感嗜血杆菌（haemophilus influenzae，Hi）对氨苄西林、阿莫西林克拉维酸、头孢呋辛等三种 β-内酰胺类药物药物敏感的可靠性及实用性。
方法 采用肉汤稀释法、纸片扩散法（K-B 法）和自动化微量肉汤稀释法（ATB 法）检测 Hi 对氨苄西林、阿莫西林克拉维酸、头孢呋辛的药物敏感度。以肉汤稀释法为参考方法，分析比较 K-B 法和 ATB 法结果间的一致性和误差率。
结果 K-B 法与肉汤稀释法对氨苄西林、阿莫西林克拉维酸、头孢呋辛的药敏一致率分别为 77.19%、91.58%、69.16%，ATB 法与肉汤稀释法的一致率分别为 70.18%、73.16%、51.98%，K-B 法对

阿莫西林克拉维酸、头孢呋辛这两种药物的一致率显著高于 ATB 法。结果误差方面，K-B 法对氨苄西林和头孢呋辛的重大误差率和极重大误差率都显著低于 ATB 法，K-B 法对阿莫西林克拉维酸的重大误差率也显著低于 ATB 法。

结论 检测 Hi 对 β-内酰胺抗生素药敏实验方面，K-B 法和肉汤稀释法的一致性较好；ATB 法对 Hi 药敏试验产生的误差较大。临床工作中报告 ATB 法药敏结果时，应结合 β-内酰胺酶试验，出现异常药敏表型，或者对 ATB 药敏结果有疑问时，建议联合使用其他药敏方法，对 ATB 法结果进行修正。

PU-3380

应用基质辅助激光解析电离飞行时间质谱鉴定金黄色葡萄球菌

罗慧娴
南方医科大学珠江医院

目的 应用基质辅助激光解析电离飞行时间质谱（Matrix Assisted Laser Desorption Ionization Time of Flight Mass Spectrometry，MALDI-TOF-MS）快速鉴定金黄色葡萄球菌。

方法 将经过 VITEK-2 系统鉴定为葡萄球菌的 234 株临床分离株进行 MALDI-TOF-MS 鉴定，鉴定结果不一致的菌株通过基因序列测定来确证，导出指纹图谱，采用自由距离计算的方法对他们进行聚类分析。

结果 MALDI-TOF-MS 鉴定的 234 株葡萄球菌中有 229 株与 VITEK-2 结果相符，有 5 株结果不一致。结果不一致的菌株采用 16S rDNA 测序分析，测序结果与 MALDI-TOF-MS 相符。将所有的葡萄球菌进行聚类分析，系统树状图示可将所有的葡萄球菌区分到种。

结论 基质辅助激光电离飞行时间质谱方法鉴定葡萄球菌可达到种的水平，能对金黄色葡萄球菌进行快速鉴定，具有准确、灵敏的特点，且实验时间短，是金黄色葡萄球菌分析鉴定的重要工具。

PU-3381

评价自建立飞行质谱仪检测肺炎克雷伯菌对亚胺培南耐药性的方法价值的研究

张子馨[1]、蔡淑梅[1,2]、李卫滨[1,2]、张胜行[1,2]
1. 福建医科大学福总临床医学院检验科
2. 联勤保障部队第九 OO 医院福建省适配体技术重点实验室

目的 利用基质辅助激光解吸电离飞行时间质谱(MALDI-TOF-MS)检测肺炎克雷伯菌（KP）对亚胺培南(IPM)的水解能力，以期检测产碳青霉烯酶肺炎克雷伯菌(CRKP)，建立一种利用 MALDI-TOF-MS 可以快速、准确检测产碳青霉烯酶肺炎克雷伯菌的方法。收集临床肺炎克雷伯菌株 40 株，和仪器 walkaway 96 plus MIC 法检测结果进行对比，评价自建立的方法检测能力。

方法 通过实验探寻本实验室合适的亚胺培南浓度、孵育时间以及温度，再利用检测 KP 对 IPM 的水解能力，建立基质辅助激光解吸电离飞行时间质谱(MALDI-TOF-MS)检测肺炎克雷伯菌（KP）对亚胺培南(IPM)的水解能力方法。在此基础上，收集临床肺炎克雷伯菌株 40 株，进行双盲随机编码，利用自建立的方法检测其肺炎克雷伯菌株水解 IPM 能力。将结果和 MIC 法结果进行比对，从而评价自建立的方法检测的敏感性和特异性。

结果 在实验中探索亚胺培南水解实验，亚胺培南浓度为 1mg/ml,菌悬液比浊度为 1McF,37℃条件下孵育 60min，有部分待测菌的亚胺培南质谱峰明显下降（70%以上）；在 37℃条件下孵育 120min,产碳青霉烯酶菌株的亚胺培南质谱峰均有明显下降（70%以上）。亚胺培南浓度为 1mg/ml，

菌悬液比浊度为 1McF，37℃条件下孵育 120min 下检测结果与 MIC 法结果进行比对结果，自建立的方法检测的敏感性和特异性分别为：82.76%，81.82%。

结论 KP 对 IPM 的水解能力与其产生碳青霉烯酶能力和酶的活力呈正相关,通过检测 KP 对 IPM 的水解能力可以筛查 CRKP。自建立的方法检测的敏感性和特异性较高，可适用于临床筛选 KP 是否水解 IPM, 指导临床合理用药，早期治疗，控制 CRKP 传播扩散。

PU-3382

徐州市 C 群流行性脑脊髓膜炎病病例病原学分析

赵树龙
徐州医科大学附属医院

目的 对江苏省徐州市 2021 年 3 月发现的 1 例青少年 C 群流行性脑膜炎（流脑）病例进行病原学分析。

方法 采集患者脑脊液接种于血培养瓶，对培养出的菌株采用生化鉴定、血清学分型和普通聚合酶链反应（polymerase chain reaction,PCR）技术鉴定进行基因分型；同时进行多位点序列分型（multilocus sequence typing，MLST）以及临床常见 14 种抗生素敏感性试验。

结果 从临床标本中分理出的菌株经生化鉴定、血清学分型与 PCR 技术鉴定、基因分型结果一致，均是 C 群脑膜炎奈瑟菌。该菌株的 MLST 分型为 ST-4821 型。该菌株对临床常见 14 种抗生素均敏感。

结论 徐州市发现 C 群流行性脑膜脊髓膜炎病例，应加强病原菌的检测与研究，方便指导进一步进行的防治与治疗。

PU-3383

老年神经内科患者感染肺炎克雷伯菌整合子耐药基因分析

刘唯
湖南省人民医院马王堆院区/湖南师范大学第一附属医院

目的 探讨在老年神经内科患者中感染产超广谱 β－内酰胺酶(ＥＳＢＬｓ)肺炎克雷伯菌整合子基因的分布及耐药率，为临床合理使用抗菌药物提供依据。

方法 运用法国生物梅里埃公司的 VITEK-2 微生物自动鉴定系统,对我院 2015 年 1 月至 2017 年 12 月老年神经内科患者患者的所有临床标本进行细菌鉴定和药敏试验,对产 ESBLs 肺炎克雷伯菌 214 株用 PCR 分析整合子基因,并通过测序明确基因.

结果 收集的肺炎克雷伯菌 524 株中产 ESBLs 检出率为 40.83%;非产 ESBLS 菌株耐药率明显低于产 ESBLS 肺炎克雷伯菌菌株;整合子阳性检出率 61.19％;检出全为Ⅰ类整合子; 整合子可变区扩增出为 TEM 基因、SH Ⅴ基因和 CTX-M 型 ESBLs 完整基因.

结论 老年神经内科患者感染产ＥＳＢＬｓ肺炎克雷伯菌和整合子基因密切相关，在细菌的耐药上整合子起着重要作用。

PU-3384

老年尿路感染耐碳青霉烯类大肠埃希菌整合子分布情况及耐药性分析

徐艳
湖南省人民医院

目的 研究老年尿路感染（UTI）患者耐碳青霉烯类大肠埃希菌（CREco）的耐药情况，以及整合子的分布与耐药性的关系。
方法 收集湖南省人民医院 2016 年 1 月至 2020 年 1 月老年尿路感染患者尿液分离大肠埃希菌（E.coli），采用 VITEK-2 系统鉴定及检测药敏情况。采用改良 Hodge 试验确证产碳青霉烯酶菌株表型，聚合酶链反应（PCR）方法检测整合子分布情况。
结果 共分离 610 株 E.coli，主要分布在重症病房（22.63%）、泌尿外科（16.23%）、康复科（13.93%）内分泌科（13.13%）、老年科（11.64%）。检出 CREco 共 68 株，占 11.15%。CREco 菌株耐药性均明显高于非 CREco 菌株（P＜0.05）。筛选多重耐药的 284 株 E.coli 中，检出Ⅰ类整合子阳性 163 株，检出率 57.39%，未检出Ⅱ、Ⅲ类整合子，其中 68 株 CREco 全部检测出Ⅰ类整合子。Ⅰ类整合子在 CREco 中的分布明显高于非 CREco 组（P＜0.01）。
结论 老年 UTI 患者 CREco 耐药情况严重，这与整合子在其分布较高有关系，临床需严格合理用药，避免 CREco 的传播与爆发。

PU-3385

血清降钙素原检测对血培养预测价值研究

刘梦婕
湖南省人民医院

目的 探讨血清降钙素原(PCT)对血培养结果的预测价值。
方法 采用回顾性分析研究，以 2016 年 1 月~2016 年 12 月我院收治的疑似菌血症的 304 例患者为研究对象，根据血培养结果分为阳性组和阴性组，比较两组间 PCT 水平的差异。绘制受试者工作特征曲线(ROC) 并计算曲线下面积分析 PCT 诊断菌血症的价值。
结果 PCT 检测血培养阳性的敏感性和特异性分别为 61.3%（73/119）和 73.0（135/185）。血培养阳性组 PCT 明显高于血培养阴性组，差异有统计学意义(P < 0.001)；血培养检出革兰阴性菌组 PCT 明显高于检出革兰阳性菌组，差异有统计学意义(P < 0.001)。PCT 检测血培养阳性的 ROC 曲线下面积为 0．700，最佳诊断临界值为 0.87 ng /ml，灵敏度为 0．538，特异度为 0．843。
结论 PCT 预测血培养阳性有很好的实用价值，临床上检测血清 PCT 可比血培养更快了解患者是否存在菌血症并预测病原菌种类，提示临床初步抗生素的使用方向，值得应用和推广。

PU-3386

高毒力肺炎克雷伯菌中 KPC-2 型碳青霉烯酶对细菌毒力 的影响

祝俊英[1]、沈震[1]、李敏[2]
1. 上海交通大学医学院附属仁济医院
2. 上海交通大学医学院附属仁济医院(东院)

目的 了解高毒力肺炎克雷伯菌获得 blaKPC-2 型碳青霉烯酶 后对细菌毒力的影响。
方法 收集 3 株碳青霉烯类敏感的高毒力肺炎 克雷伯菌野生株(hvKP)作为实验菌株并调查其临床信息,采用 PCR 方法检测其毒力基因、荚膜血清分型及 ST 分型等。采用过表达实验 将 blaKPC-2 克隆至 pHSG396 质粒并转化至 hvKP 野生株构建 blaKPC-2 转化株,采用血清抵抗试验和生物膜实验比较 hvKP 野生株和 blaKPC-2 转化株对血清中杀菌物质的抵抗能力及生物被膜形成能力, 低速度离心沉降实验及糖醛酸测定比较二者黏液性及荚膜多糖(CPS) 含量,荧光定量 PCR 检测 CPS 结构基因及调控基因转录水平。
结果 3 株 hvKP 野生株中 1 株为 ST23,K1 型,所检测的 10 种毒力基因均 为阳性。另外两株为 ST65,K2 型,毒力基因中 rmpA、rmpA2、iroB、iutA、ybtS、entB、mrkD 均为阳性,magA、allS 及 kfu 均为阴性。与 hvKP 野生株相比,blaKPC-2 转化株对血清中杀菌物质的抵抗能力明 显下降,生物被膜形成能力明显下降,细菌黏液性下降,CPS 含量下 降,CPS 结构基因及调控基因转录水平下降。
结论 hvKP 野生株获得 blaKPC-2 型碳青霉烯酶后可导致细菌荚膜多糖产生减少,细菌毒力降低。

PU-3387

肠道微生物在高脂饮食促进胰腺癌发生中可能会发挥关键作用

高惠茹
山东大学第二医院

目的 胰腺癌是目前消化系统最恶性的肿瘤，其死亡率接近发病率，预后极差。然而，胰腺癌的发病机制尚不完全清楚。许多研究表明，高脂饮食、肥胖、超重和糖尿病是胰腺癌的高危因素。作为一个公共健康问题，高脂饮食已被证明与多种消化疾病和肿瘤有关。它可以通过改变机体的炎症和代谢，促进胰腺癌的发生。肠道微生物是近年来的研究热点，肠道微生物的组成受饮食、地域、性别、环境等多种因素的影响。近年来，肠道微生物已被证实通过免疫系统直接或肠外作用促进胰腺癌的发生发展。本文旨在探讨高脂饮食、肠道微生物与胰腺癌发生发展的关系。
方法 作者使用各种搜索词组合从 PubMed 数据库中检索信息，包括高脂饮食、西式饮食、肠道微生物、胰腺癌、胃肠道肿瘤。选择了与评审主题相关的研究性文章和综述性文章。探讨并总结了高脂饮食与肠道微生物变化与胰腺癌发生发展的关系。
结果 高脂肪饮食通过促进上皮细胞的增殖，抑制上皮细胞抵抗癌症、炎症、DNA 损伤和代谢重编程的能力，从而促进胰腺癌的发生。肠道和胰腺微生物的变化，如 Firmicuts/Bacteroides 比值的增加，与胰腺癌的发生发展有关，同时，高脂饮食会促进肠道微生物的失衡。基于上述研究基础，我们提出“高脂饮食可通过改变肠道微生物组成促进胰腺癌的发生发展”的观点，并提出了三者相互作用的可能机制。.
结论 本文综述了近年来高脂饮食、肠道微生物与胰腺癌关系的研究现状，以及胰腺癌的主要治疗方向。同时，我们提出了高脂饮食改变肠道微生物组成促进胰腺癌发生发展的观点，为胰腺癌的发病机制和治疗研究提供了新的思路。

PU-3388

毛霉菌的质谱分析方法探析

涂杉
四川省人民医院城东病区

毛霉菌病致死率高达 50%，对免疫力低下的人群致死率甚至达 80%。当前在实验室诊断中霉菌病通过组织病理学发现组织中具有毛霉目典型结构结构的微生物，并经培养确诊，但培养经常无真菌生长，并且带有一定的主观性 [1],不能满足临床上对致病菌进行快速诊断的需要，而基质辅助激光解吸电离飞行时间(MALDI-TOF)质谱分析可以用来识别培养标本中的致病菌种，以达到精确高效检测毛霉菌的实验诊断方法，具有灵敏度高、准确度高及分辨率高等特点，其原理是不同的微生物样品与过量的基质溶液点在样品板上，溶剂挥发后形成样品与基质的共结晶，利用激光作为能量来源辐射结晶体，基质从激光中吸收能量使样本吸附，基质与样本之间发生电荷转移使得样本分子电离，样本离子在加速电场下获得相同的动能，经高压加速、聚焦后进入飞行时间质谱分析器进行质量分析，检测器检测到不同质荷比（m/z）的离子，并以离子质荷比为横坐标，以离子峰为纵坐标形成特异性的病原菌蛋白质组指纹图谱，进而与毛霉菌图谱库中进行对比，得到鉴定结果并最终确定细菌种类。在毛霉菌的 MALDI-TOF 分析中，从样本制备到获取准确的鉴定结果，每个步骤都决定了医技人员能否及时为临床医生提供准确结果。现就待测样品的制备及 MALDI-TOFMS 技术对毛霉菌分析(包括鉴定,分型,抗真菌敏感性测试方面)的应用及前景作一系统综述,也将对其一些未来发展进行展望。

PU-3389

某三级医院鲍曼不动杆菌的临床分布及耐药性分析

苏小燕
重庆市人民医院

目的 分析重庆市某三级医院鲍曼不动杆菌的临床分布及耐药情况，对医院感染预防和抗生素的选用提供实验室依据。
方法 对该院 2020 年 1 月至 2021 年 3 月所分离的 174 株非重复鲍曼不动杆菌临床病区分布、来源标本类型、感染者年龄及性别、抗生素的耐药性进行回顾性分析；用 VITEK 2 Compact 全自动细菌鉴定及药敏分析系统进行初步细菌鉴定和药敏检测，用 K-B 法及浓度梯度稀释法确认药敏结果。
结果 2020 年 1 月至 2021 年 3 月住院患者中共分离鲍曼不动杆菌 174 株，其中重症医学科共 73 株（41.95%），呼吸科 24 株（13.79%），肝胆胰腺外科 22 例（12.64%）；标本主要来源于呼吸道的痰和肺泡灌洗液，共 127 株（72.99%）；感染人群年龄广泛分布在 18 岁到 79 岁之间，男性（118 例）多于女性（56 例）；药敏结果显示呋喃妥耐药率为 99.43%，其他耐药率均在 60%以下；多粘菌素 b 敏感率为 99.42%，替加环素敏感率为 90.23%，米诺环素为 80.17%，复方新诺明为 65.23%，其余敏感率都低于 60%。
结论 本院鲍曼不动杆菌感染的高发人群未见明显年龄分布倾向，以呼吸道标本为主，危重症患者感染鲍曼不动杆菌的概率更大，说明基础疾病严重及免疫力低下患者更易感该菌，年龄分布没有特殊性；本院检测出的鲍曼不动杆菌大多对呋喃妥因耐药，对多粘菌素 b，替加环素米诺环素的敏感率较高。

PU-3390

多重耐药肺炎克雷伯菌酶型鉴定及治疗新策略

曹伟良、史莉
襄阳市第一人民医院

由于抗生素的大量使用，多重耐药肺炎克雷伯菌（CR—KPN）检出数量不断增加，酶型鉴定技术可以检出 CR-KPN 产生金属 β-内酰胺酶或丝氨酸酶，方便临床合理用药。

试验方法 将细菌用生理盐水稀释成 0.5 麦氏浊度后，用医用棉签均匀涂布在 MH 平板上；取亚胺培南纸片 4 片均匀贴到 MH 平板上，平板中间贴一片头孢他啶-阿维巴坦纸片；将四片纸片分别标记为 A、B、C、D；在 B 纸片上滴加 EDTA 溶液 10μL，在 C 纸片上滴加硼酸溶液 10μL，在 D 纸片上滴加 EDTA 溶液和硼酸溶液各 10μL，放 36℃培养箱孵育 24 小时观察结果。

结果 当 A 纸片抑菌圈直径<=16mm 时，说明细菌具有多重耐药性；当 B 纸片抑菌圈直径比 C 纸片抑菌圈直径大 5mm 以上时，细菌产生金属 β-内酰胺酶；当 B 纸片抑菌圈直径比 C 纸片抑菌圈直径小 5mm 以上时，细菌产生丝氨酸酶；无论产生金属酶还是丝氨酸酶，D 纸片的抑菌圈都有较大抑菌圈，其抑菌圈直径>=B 纸片抑菌圈直径和 C 纸片抑菌圈直径。头孢他啶-阿维巴坦敏感时抑菌圈>=22mm。

结论 酶型鉴定技术可以快速检测出多重耐药性肺炎克雷伯菌的酶型，帮助临床医生选择合理的抗生素。当 CR-KPN 产金属 β-内酰胺酶，而且头孢他啶-阿维巴坦敏感时可以选用此药物。

PU-3391

陕西 1712 例泌尿生殖道标本支原体培养结果分析

杨冰
西安金域医学检验所有限公司

目的 分析陕西某单位就诊患者泌尿生殖道标本支原体培养结果，为临床合理使用抗菌药物提供依据。

方法 使用支原体培养鉴定计数药敏试剂盒对陕西某单位 2020 年 1 月 1 日—2020 年 12 月 31 日就诊的 1712 例泌尿生殖道感染患者标本进行支原体培养及药敏试验。

结果 1712 例泌尿生殖道标本支原体感染者 691 例(40.36%)，其中单纯 Uu 感染 397 例(57.45%)，单纯 Mh 感染 89 例(12.88%)，Uu + Mh 混合感染 205 例(29.67%)。女性感染 683 例，男性感染 8 例，女性泌尿生殖道支原体感染率(98.84%) 高于男性(1.16%)，支原体感染患者在＜ 20 岁、 21 -30 岁、 31 -40 岁、 41 -50 岁、＞ 50 岁五个年龄段的感染率分别为 2.17%、31.26%、36.61%、23.30%、5.93%，以 31 -40 岁这个年龄段的感染为主。

结论 陕西某单位泌尿生殖道支原体感染以单纯 Uu 感染为主，女性感染率高于男性。通过支原体培养及药敏试验，可明确生殖道感染的病原体及指导临床的合理用药。

PU-3392

2014～2019 年某三甲医院血液分离病原菌耐药性变迁分析

李军、邹明祥
中南大学湘雅医院

目的 了解某三甲医院临床血液标本分离主要病原菌的分布及耐药性变迁，以指导临床合理使用抗菌药物。

方法 回顾性分析 2014 年 1 月～2019 年 12 月临床血液标本分离病原菌的药物敏感性，MALDI-TOF MS 质谱仪对其进行鉴定，VITEK 2 Compact 全自动细菌鉴定及药敏分析系统检测其药物敏感性，采用 WHONET5.6 软件进行数据分析。
结果 共分离到 5771 株各类病原菌，其中革兰阳性菌 3209 株，占 55.6%。2014～2019 年居前五的病原菌稍有变化，肺炎克雷伯菌和金黄色葡萄球菌的检出率有上升趋势。非发酵革兰阴性杆菌中鲍曼不动杆菌所占比例最高（4.4%，254/5771），但检出率有下降趋势。大肠埃希菌对亚胺培南和厄他培南的耐药率分别在 0～4.7%和 0～7.3%。近三年肺炎克雷伯菌对亚胺培南的耐药率有下降趋势。鲍曼不动杆菌对碳青霉烯类的耐药率约 80.0%，2018 年亚胺培南和美罗培南的耐药率甚至高达 90.7%。葡萄球菌属中，耐甲氧西林金黄色葡萄球菌（Methicillin-resistant Staphylococcus aureus，MRSA）有下降趋势，未发现对万古霉素和替加环素耐药的葡萄球菌属，金黄色葡萄球菌和凝固酶阴性葡萄球菌对利奈唑胺的耐药率分别为 0 和 0.3～1.3%。
结论 本院血液标本分离病原菌主要以革兰阳性菌为主，肺炎克雷伯菌和金黄色葡萄球菌的检出率有上升趋势。碳青霉烯类耐药肺炎克雷伯菌检出率虽有下降趋势，但是检出率仍较高，MRSA 的检出率有下降趋势。应加强临床血液分离病原菌耐药性监测，以合理使用抗菌药物。

PU-3393

Isolation and Characterization of Nocardia Species from Pulmonary Nocardiosis in a tertiary hospital in China

Jun Li、Mingxiang Zou
Department of Clinical Laboratory, Xiangya Hospital, Central South University

The aim of this study was to determine the clinical features, distribution and antimicrobial susceptibility of Nocardia species isolated from pulmonary nocardiosis cases in tertiary hospital in China. The species were collected from January 1, 2018 to May 31, 2019 and identified using MALDI-TOF MS or PCR. Antimicrobial susceptibility testing was performed using the broth microdilution method. Within the 44 Nocardia species, N. farcinica was the most frequently identified species (n = 36), followed by N. nova (n = 5), N. otitidiscaviarum (n = 1), N. cyriacigeorgica (n = 1), and N. transvalensis (n = 1). The top three predisposing factors of pulmonary nocardiosis were chronic obstructive pulmonary disease (45.45%), hypertension (34.09%), and tuberculosis (31.82%). All 44 Nocardia strains were susceptible to amikacin, trimethoprim / sulfamethoxazole, and linezolid. The resistance rates of Nocardia to amoxicillin-clavulanic acid, ciprofloxacin, clarithromycin, ceftriaxone, tobramycin, and imipenem were 4.5%, 9.1%, 79.5%, 72.7%, 63.6%, and 38.6%, respectively. Two Nocardia strains had decreased sensitivity to trimethoprim / sulfamethoxazole. In conclusion, N. farcinica was the most frequently isolated Nocardia species in our hospital. All isolated clinical Nocardia strains showed susceptible to amikacin, trimethoprim / sulfamethoxazole, and linezolid, suggesting that these drugs can be primary therapeutic choices for treating Nocardia infections.

PU-3394

Emergence of blaOXA-23 gene carried by Tn2006 on chromosome in hypervirulent Acinetobacter baumannii strain

Jun Li[2]、Mingxiang Zou[1]
1. Xiangya Hospital, Central South University
2. Xiangya Hospital, Central South University

Background Acinetobacter baumannii is notorious for its extensive drug resistance but has traditionally been considered an opportunistic pathogen with low virulence.
Objectives Here, to the best of our knowledge, we describe the first detection and characterization of blaOXA-23 gene carried by Tn2006 on chromosome in hypervirulent A. baumannii strain (hvAB).
Methods Characterization of XYAB2018 isolate was performed using MALDI-TOF MS, automated microdilution and MLST. The virulence experiments was carried out using a Galleria mellonella infection model. The genetic characterization of XYAB2018 was performed by Whole-genome sequencing (WGS).
Results XYAB2018 was more virulent in G. mellonella than that of A. baumannii ATCC 19606 with the 5 days survival rate of 10%. The isolate expressed ST457 was resistant to the most of antimicrobial agents detected, except for tigecycline and colistin. The genome of XYAB2018 strain included chromosome gene (3,909,403 bp) with blaOXA-23 gene and two plasmids with no drug resistance gene identified. The blaOXA-23 gene was downstream of ISAba1 and carried by transposon Tn2006. Phylogenetic analysis revealed that the closest related strains was VMKE01 with 91 SNPs difference, which was a hospital environment ST457 A. baumannii strain.
Conclusions The first detection (to the best of our knowledge) of blaOXA-23 gene carried by Tn2006 on chromosome in hvAB. It might derived from hospital environment, so we should strengthen the monitoring of these strains in the future.

PU-3395

Emergence of hypervirulent Klebsiella pneumoniae isolated from urine specimens in community adults in China

Jun Li[1]、Mingxiang ZOU [2]
1. Department of Clinical Laboratory, Xiangya Hospital, Central South University
2. Xiangya Hospital

The strain of Klebsiella pneumoniae known as hypervirulent K. pneumoniae (hvKP) is becoming more common as a source of nosocomial and healthcare-associated infections. Tracking its epidemiology and progression is critical to develop successful prevention and treatment strategies. K. pneumoniae isolates were collected from community adults between October and December 2020, and the antimicrobial susceptibility, virulence-associated genes and biofilm formation for isolates were examined. HvKP was defined by the presence of one or a combination of biomarkers (prmpA, prmpA2, iroB, peg344, and iucA) and the Galleria mellonella infection model. Whole-genome sequencing of hvKP strains was performed. A total of 61 K. pneumoniae isolates were collected from 7530 urine samples. The strains were highly sensitive to the antimicrobial agents tested, and a polymyxin resistant strain was found. Four hvKP strains with lower biofilm forming ability than KP (0.2625 ± 0.0579 vs. 0.6686 ± 0.0661, P = 0.0333) were identified as belonging to K2-ST65, K2-ST86, K57-ST592, and K2-ST5559 (a new ST type). Analysis with BacWGSTdb 2.0 showed that KPNY31 (ST5559) shared

a close genetic relationship with KPNY42 (ST86) and other ST86 isolates, which have been detected in both nosocomial and community-acquired infections. In conclusion, hvKP with relatively weak biofilm formation was detected for the first time in urine specimens from community adults. A novel sequence type (ST5559) hvKP derived from ST86 was found. Therefore, hvKP should be monitored in community adults.

PU-3396

MALDI-TOF MS 在微生物方面的应用

温金
山东大学第二医院

目的 MALDI-TOF MS 技术检测分析应用于病原微生物检测，是因为其所具有的特异性肽类和蛋白质,这些肽类和蛋白质主要取决于病原微生物自身的遗传因素，较少受到体外培养等外界因素的影响，通过采用 MALDI-TOF MS 技术准确、高效、快速、高通量和低成本鉴定微生物。
方法 1.MALDI-TOF MS 直接鉴定血培养阳性病原体；2.通过研究金黄色葡萄球菌的质谱图，发现甲氧西林敏感金黄色葡萄球菌（MRSA）与耐甲氧西林金黄色葡萄球菌(MSSA)的峰图之间有很大差异，通过在数据库中对 MRSA 和 MSSA 的质谱图进行聚类分析，分析质谱图之间的差异，选取有统计学意义的蛋白峰建立分类模型。
结果 1.在血培养中检测病原体方面，革兰阳性菌、真菌的细胞壁较革兰阴性菌厚，细胞壁更难被破坏，MALDI-TOF MS 对革兰阴性菌的准确鉴定概率，远高于革兰阳性菌和真菌，以及革兰阳性菌被污染的概率明显高于革兰阴性菌；2.在筛查 MRSA 方面，聚类分析的准确性较低，同源性菌株的质谱图较为相似，对其的鉴别率较低。
结论 1. MALDI-TOF MS 与传统仪器鉴定相比，优势突出，在血培养阳性标本直接检测方面，具有简便、快速、准确的优势。2.质谱图分析可以筛查区分 MRSA 和 MRRA，可以在临床中使用。综上所述， MALDI-TOF MS 可作为一种简单且快速的方法用于病原体微生物的检测，但在细菌同源性检验、体液等直接检测方面待深入研究，以期早日应用于临床。

PU-3397

Rare Mycoplasma hominis postoperative infection and rapid identification of MALDI-TOF MS

Peng Tang[2]、Pan Feng[1]、Weiwei Huang[1]、Tao Tang [1]、Liqun Zhang[1]、Fei Liu[1]
1. Department of Clinical Laboratory, The Second Clinical Hospital of Army Medical University, Chongqing 400037, China
2. Department of Clinical Laboratory, The Second Clinical Hospital of Army Medical University

Objectives To explore the application of matrix assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS) in rapid and accurate identification of Mycoplasma hominis infection in surgical incision, and analyze the drug sensitivity of M. hominis, so as to provide basis for clinical diagnosis and treatment.
Methods The clinical data, microbiological test Methods and drug sensitivity data of postoperative infection caused by M. hominis in our hospital from January 2019 to December 2020 were reviewed.
Results There were 8 cases of postoperative infection of M. hominis, including 4 cases of spinal surgery, 1 case of brain tumor resection, 1 case of lower abdominal incision herniorrhaphy, 1 case of bladder cancer operation and 1 case of caesarean section. Suspicious bacteria were isolated from the infection site of surgical incision, and identified as M. hominis by 16S rRNA gene sequencing analysis and MALDI-TOF MS self-built database analysis technology. M.

hominis is more sensitive to doxycycline, minocycline, josamycin, spectinomycin and gatifloxacin, but less sensitive to other macrocyclic lipids and quinolones.
Conclusions The MALDI-TOF MS analysis technology can quickly and accurately identify the M. hominis isolated from the incision infection site after operation, and can guide the clinical diagnosis and targeted treatment.

PU-3398

37 例 ESBLs 阳性大肠埃希致尿路感染及其耐药性分析

杨珊珊
新疆医科大学第五附属医院

目的 分析 37 例产超广谱 β-内酰胺酶（ESBLs）大肠埃希菌尿路感染的临床特征、耐药性及治疗转归，为临床合理使用抗菌药物提供参考。
方法 收集 2019 年 1-12 月临床送检患者中段尿标本，采用 VITEK2-Compact 全自动细菌鉴定及药敏分析仪对大肠埃希菌进行分离及鉴定。
结果 经培养、鉴定共获得 126 株病原菌，其中大肠埃希菌为 66 株，占 52.38%；37 例为产 ESBLs 大肠埃希菌，经药敏试验结果表明产 ESBLs 大肠埃希菌对广谱青霉素类抗菌药物哌拉西林、氨苄西林的耐药率高达 90％以上；对第 3 代头孢菌素类抗菌药物头孢他啶的耐药率达 56.76％，头孢曲松、头孢噻肟、头孢哌酮的耐药率均高达 80.0％以上；喹诺酮类抗菌药物的耐药率在 70.0％以上；氨基糖苷类抗菌药物的耐药率高达 60％以上；仅出现 1 株耐亚胺培南的菌株；含 β-内酰胺酶抑制剂的抗菌药物哌拉西林／他唑巴坦的耐药率低于 3.0％；对头孢哌酮／舒巴坦的耐药率低于 22.0％。
结论 产 ESBLs 大肠埃希菌尿路感染临床表现无明显特异性，结合病人临床主要表现：不同程度的发热、尿路刺激征、腰背部酸痛、下肢水肿，恶心呕吐和肾区叩击痛等。其中老年女性患者居多，且多有基础疾病及易感因素；其发生与患者基础疾病和危险因素等有关，对疑有尿路感染且伴有基础疾病及危险因素者应尽早做尿培养，经验选择使用覆盖 ESBLs 菌感染的药物，慎用氟喹诺酮类、氨基糖苷类及头孢菌素类抗菌药物治疗产 ESBLs 细菌尿路感染。

PU-3399

An Outbreak of Carbapenem-Resistant Klebsiella pneumoniae in an Intensive Care Unit of a Major Teaching Hospital in Chongqing, China

Lingyi Zeng[1]、Chengru Yang[1]、Jisheng Zhang[1]、Kewang Hu[1]、Jingbo Zou[2]、Jie Li[1]、Jianmin Wang[1]
1. Yongchuan Hospital of Chongqing Medical University
2. 重庆市永川区疾病预防控制中心

Background Due to the critical condition and poor immunity of patients, the intensive care unit (ICU) has always been the main hospital source of multidrug-resistant bacteria. In recent years, with the large-scale use of antibiotics, the detection rate and mortality of carbapenem-resistant Klebsiella pneumoniae (CRKP) have gradually increased. This study explores the molecular characteristics and prevalence of CRKP isolated from the ICU ward of a tertiary hospital in China.
Methods A total of 51 non-duplicated CRKP samples isolated from the ICU were collected from July 2018–July 2020. The enzyme production of the strains was preliminarily screened by carbapenemase phenotypic test, and drug-resistant and virulence genes were detected by PCR. The transferability of plasmid was verified by conjugation test. The minimal inhibitory

concentration (MIC) was determined by microbroth dilution method and genetic diversity was detected by multilocus sequence typing and pulsed-field gel electrophoresis.
Results blaKPC-2 was the only carbapenemase detected. The major virulence genes were uge (100%), mrkD (94.1%), kpn (94.1%), and fim-H (72.5%), while wcag, ironB, alls and magA genes were not detected. Only four out of 51 CRKP isolates (7.8%) exhibited the hypermucoviscous phenotype during the string test, the rest were negative. Two sequence types (STs) were identified among all isolates, with 50 (98.0%) belonging to ST11, and one (2.0%) being an isolate of ST1373.One sequence type ST1373 strain, hypervirulent K. pneumoniae (hvKP), was detected. CRKP strains were highly resistant to quinolones, cephalosporins, aminoglycosides, and polymyxin, but susceptive to tigecycline and ceftazidime–avibactam. The success rate of conjugation was 12.2%, indicating the horizontal transfer of blaKPC-2. Compared with the original donor, the MIC value of the transconjugants for carbapenems (IMP, MEM) was significantly decreased (4–64 times), similarly, LEV and PB were also decreased. On the contrary, AK, TIG, and CAZ-AVI did not show obvious changes, except for CRKPJ55, which had a change in CAZ-AVI. Homology analysis showed that there was a clonal transmission of ST11 CRKP in the ICU of our hospital.
Conclusion The present study showed the outbreak and dissemination in ICU were caused by ST11 CRKP, which were KPC-2 producers, and simultaneously, also carried some virulence genes. ST11 CRKP persisted in the ward for a long time and spread among different areas. Due to the widespread dispersal of the transferable blaKPC-2 plasmid, the hospital should promptly adopt effective surveillance and strict infection control strategies to prevent the further spread of CRKP. Ceftazidime–avibactam showed high effectiveness against CRKP and could be used for the treatment of ICU infections. Although this study did not conduct long-term and systematic sampling of all potentially contaminated areas in the ICU, there is a need for understanding the dynamic distribution and spread of CRKP, a major threat to clinical treatment that cannot be ignored. Timely and effective infection control measures are essential to contain and mitigate the risk of nosocomial transmission and outbreaks in hospitals. According to the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) guidelines, the implementation of hand hygiene education programs, contact precautions, and use of alert codes to promptly identify patients with CRKP infections should be applied and infected patients should be isolated. In addition, a program of active screening culture, and implementation of an antimicrobial stewardship program, should be implemented to reduce transmission of multidrug-resistant Gram-negative bacteria in hospital patients, especially in ICUs.

PU-3400

呼吸道感染病原体 IgM 抗体检测在呼吸道感染中的诊断价值

张谨
空军总医院

目的 呼吸道感染（RTI）是全球常见感染性疾病之一，有较高的感染率和死亡率，其病原学组成复杂。探讨所在区域呼吸道病原体的分布以及流行特征，进一步了解本地区 RTI 情况以及多方面的流行因素，为呼吸道感染的诊治和预防提供相关资料。
方法 采用间接免疫荧光法（IFA）对 967 例就诊于北京民航总医院的呼吸道感染患者血清中 Q 热立克次体（COX）、肺炎支原体（MP）、嗜肺军团菌（LP）、肺炎衣原体（CP）、副流感病毒（PIV）、呼吸道合胞病毒（RSV）、腺病毒（ADV）、甲型流感病毒（FluA）、乙型流感病毒（FluB）进行检测。采用荧光显微镜观察结果，计算各年龄段和季节的阳性率，并用统计学方法进行比较。
结果 9 种病原体 IgM 总阳性率为 28.23%（273/967），其中单一感染占 25.65%（248/967），MP 阳性率最高，为 21.61%（209/967），其余为 FluB3.21%（31/967），ADV0.31%（3/967），PIV0.21%（2/967），CP0.21%（2/967），RSV0.1%（1/967），未检出 FluA、COX、LP。混合感染阳性率为 2.59%（25/967），以 MP 合并 FluB 感染阳性率最高，为 1.96%（19/967）。

MP 和 FluB 感染阳性率在儿童组最高，分别为 51.40%（147/286）、7.69%（22/286），各年龄段的 MP 阳性率有统计学差异（P<0.05），但 FluB 结果相反。秋冬季多为 MP 感染，其与春夏之间差异有统计学意义（P<0.05）。而 FluB 感染多见于春冬季，但仅春夏之间有显著差异（P<0.05）。

结论 年龄、季节和地域差异可影响病原体分布。IFA 有较高的灵敏度和特异度，少量血清便可检测 9 种呼吸道病原体，解决了儿童痰培养取样困难、细菌培养时间较长以及阳性率较低的问题。而且 IgM 可表示近期感染，因此通过该方法检测 9 种呼吸道病原体，对临床早期诊断、指导用药以及防治 RTI 有重大意义。

PU-3401

省级三甲医院菌血症及 PCT 指标现状调查分析

张莉滟、赵越、叶龙、凌勇、欧阳峰
广东省人民医院

目的 对省级三甲医院菌血症及 PCT 指标现状进行调查分析，为临床工作提供合理指导。

方法 收集某省级三甲医院近几年菌血症确诊病例 401 例为试验组，并随机选取相同时期血培养阴性病例 100 例作为对照组，并观察血清 PCT 在两组中的表达情况。

结果 试验组中，革兰阴性菌（264 例，65.84％）、革兰阳性菌（99 例，24.68％）、真菌（35 例，8.73％）菌血症患者血清 PCT 浓度（ng/ml）的中位数与百分位数（P_{25}，P_{75}）分别为 1.20（0.23，8.58）、0.97（0.20，4.64）和 2.66（0.48，15.19），三类病原体菌血症患者组间血清 PCT 浓度无统计学差异（P＞0.05）。试验组与对照组相比，血清 PCT 浓度（ng/ml）的中位数与百分位数（P_{25}，P_{75}）分别为 1.21（0.23，7.66）和 0.24（0.06，0.74），其浓度差异具有统计学意义（P＜0.05）；试验组内科（289 例，72.07%）、ICU（81 例，20.20%）、外科（31 例，7.73%）血清 PCT 浓度（ng/ml）的中位数与百分位数（P_{25}，P_{75}）分别为 0.77（0.18，4.73)、4.32（1.00，19.96)和 3.60（0.56，18.99)，即不同科室间菌血症患者血清 PCT 浓度差异具有统计学意义（P＜0.05）。菌血症患者病原体大多为临床常见菌株，如大肠埃希菌、肺炎克雷伯菌、金黄色葡萄球菌、铜绿假单胞菌、肺炎链球菌、白念珠菌、近平滑念珠菌、热带念珠菌等，羊布鲁菌、戈登链球菌、产单核细胞李斯特菌等少见菌所致菌血症也时有发生。

结论 临床应结合 PCT 指标关注菌血症常见病原体的种类及科室分布，以做到精准施策。

PU-3402

血小板计数评估肺炎克雷伯菌血流感染患者预后价值研究

曹慧军、冯舒婷、杨蕾
贵州医科大学附属医院

目的 研究血小板计数对肺炎克雷伯菌血流感染患者预后的预测价值。

方法 收集 2019 年 1 月—2020 年 12 月期间入住贵州医科大学附属医院确诊为肺炎克雷伯菌血流感染患者的临床基本资料及血小板计数（PLT）的检测数据。根据患者的预后情况分为预后好及预后不良两组，按患者血小板减少差异分为血小板无减少组、血小板轻度减少组、血小板中度减少组和血小板重度减少组。采用 χ^2检验分析血小板减少不同程度组患者的预后。

结果 共收集患者 180 例，血小板无减少组共 114 例，血小板轻度减少组共 36 例，血小板中度减少组共 19 例，血小板重度减少组共 11 例。四组患者预后不良患者的百分率分别为 31.6%、61.10%、73.70%、90.9%。采用 χ^2检验分析血小板减少不同程度组患者的预后，与血小板无减少组相比较，血小板轻度减少组、血小板中度减少组、血小板重度减少组预后较差，且血小板越低，患者的预后不良比例越高，差异均有统计学意义（P<0.05）。

结论 PLT 减少是肺炎克雷伯菌血流感染患者预后差的危险因素，PLT 计数可作为评估患者预后情况的重要指标，用于预测患者病情的转归。

PU-3403

血培养阳性报警时间对血流感染患者的预后价值以及患者转归情况分析

曹啟新
内蒙古自治区内蒙古人民医院

目的 探讨血培养阳性报警时间（TTP）对血流感染患者预后的预测价值
方法 收集 2017-2020 年内蒙古自治区人民医院 435 例血流感染患者的临床资料和 TTP 值，采用 Logistic 回归分析影响患者预后的各项危险因素，ROC 曲线分析 TTP 值对患者预后的预测价值。
结果 分析 435 例血流感染患者 TTP 值，将其分为低 TTP 组（TTP≦0.68d）和高 TTP 组（TTP>0.68d）,二者之间比较发现低 TTP 组患者比高 TTP 组更易发生泌尿感染、严重脓毒血症及休克和住院期间死亡，且二者差异有统计学意义(P<0.05)；ROC 曲线分析 TTP 值预测住院期间病死率和脓毒血症及休克的最佳切点分别为 TTP≦0.67d 和 TTP≦0.78d，曲线面积分别为 0.56 和 0.57；Logistic 回归分析 TTP≦0.68d、脓毒血症及休克和入住 ICU 是患者预后的三个独立危险因素。各科血流感染患者转归情况：按药敏结果用药,发现经验用药与药敏结果的一致率为 55.8%。在 ICU、普外科、肾内科和干部保健所的患者死亡率明显低于经验用药患者的死亡率 (P<0.05)。
结论 血流感染患者病情复杂，实验室根据 TTP 值大小结合临床相关资料可以早期为临床预后提示预警信息，可以通过患者的转归情况为患者选择最合理有效的用药方案，提高患者的治愈率。

PU-3404

2017-2020 年内蒙古自治区人民医院血培养阳性报警时间（TTP）的临床分析

赵亚楠、曹啟新
内蒙古自治区内蒙古人民医院

目的 通过采集内蒙古自治区人民医院的血培养阳性报警时间（TTP），研究 TTP 值在初步鉴别微生物种类和区分病原菌与污染菌的意义，为临床早期提示预警以及合理用药提供依据。
方法 回顾性分析 2017-2020 年本院所有血流感染阳性菌株，剔除同一患者相同部位的重复菌株，共 534 株。结合临床资料进行综合分析。采用 SPSS 22.0 软件进行数据分析，TTP 值比较采用 t 检验或秩和检验。
结果 534 株血培养分离菌中，TTP≦1d 检出细菌 323 株（60.5%），TTP≦2d 检出 454 株（85.0%），TTP≦3d 检出 513 株（96.0%），不同微生物血培养阳性报警中位时间不同，从最快到最慢依次为肠杆菌科（0.57d）<链球菌属（0.68d）<非发酵菌属（0.71d）<肠球菌属（0.72d）<葡萄球菌属（1.36d）<酵母样真菌（1.98d）<马耳他布鲁杆菌（2.75d）。肠杆菌科细菌 TTP 除与非发酵菌属和链球菌属比较差异无统计学意义（P>0.05）外，与其他细菌比较差异均有统计学意义（P<0.05）。534 株血培养分离菌检出 99 株污染菌，污染率占 18.5%，污染菌在 1d 内检出率为 15.2%，1-2d 检出率为 46.5%，2-3d 检出率为 26.2%，>3d 检出率为 12.1%；报阳时间≧1d 的可疑污染菌占 84.8%。污染菌以凝固酶阴性葡萄球菌（CNS）及革兰阳性杆菌为主，其中 CNS

占 59.6%，革兰阳性杆菌占 9.1%，将病原菌与污染菌的报阳时间进行比较，发现二者均有统计学差异（P<0.05）。
结论 血流感染患者病原菌及其分布复杂，实验室可以根据 TTP 值的大小初步预测微生物的菌株类别，区分病原菌与污染菌，指导临床合理用药。

PU-3405

Outbreak of KPC-2–Producing Klebsiella pneumoniae ST76 Isolates in an Intensive Care Unit and Neurosurgery Unit

Shanshan Su
Yongchuan Hospital of Chongqing Medical University

Background The aim of this study was to investigate the characteristics of carbapenem-resistant Klebsiella pneumoniae (CRKP) ST76 isolates collected during an outbreak in a hospital's intensive care unit and neurosurgery unit. Whole-genome sequencing of ST76 CRKP was carried out to provide evidence to guide clinical anti-infective treatment and control of drug-resistant bacterial transmission.
Methods Seventeen separate clinical isolates of CRKP were collected from patients from March 2016 to February 2017. Bacterial isolates were identified, and antimicrobial susceptibility testing was conducted using the VITEK-2 compact system. Isolates containing antibiotic resistance genes were characterized by polymerase chain reaction and DNA sequencing. Clonal relatedness was assessed by multilocus sequence typing and pulsed-field gel electrophoresis. Conjugation experiments were performed to determine the transferability of plasmids with antibiotic resistance. The genomic features and mobile genetic elements of ST76 CRKP were detected by whole genome sequencing.
Results The 17 CRKP isolates were identified in a diverse population of ICU and neurosurgery unit patients from March 2016 to February 2017. Among these, 70.6% of patients had surgery, 76.5% had tracheotomy and mechanical ventilation, and all patients received antibiotic treatment, catheterization, and arteriovenous catheterization. Hospital admissions were typically long, and the average admission time was 25.9 days. The mortality rate was 35.3%. All isolates were resistant to ampicillin–sulbactam, piperacillin/tazobactam, cefazolin, ceftriaxone, aztreonam, and imipenem, and all were susceptible to amikacin. MLST analysis of 7 housekeeping genes of K. pneumoniae showed that 17 CRKP isolates belonged to the ST76 strain. According to a cutoff of 85% genetic similarity, all 17 CRKP isolates, of which 8 were obtained from the ICU and 9 were from neurosurgery unit, belonged to ST76 and shared the same PFGE pattern, suggesting that they were clonally related.ST76 KPC-2–producing CRKP prevailed in our hospital, causing an outbreak. The strains also carried blaSHV-1,blaCTX-M-15,blaTEM-1, qnrB, and acc(6')Ib-cr resistance genes. Plasmids from 17.7% of the isolated strains bearing these resistance genes could be transferred into the recipient Escherichia coli J53 through conjugation. Sequencing results showed that the KP4 genome mainly consisted of a circular chromosome and three antibiotic resistance plasmids. The plasmid carrying the blaKPC-2 gene was located on a 437kb IncFIB(pQil) plasmid with Tn1721-blaKPC-2-DT3 gene structure. Genes conferring resistance against aminoglycosides, quinolones, fluoroquinolones, beta-lactamase, phenicols, sulfonamides, and trimethoprims and the presence of virulence-associated genes related to iron acquisition or adhesins were determined.
Conclusion From March 2016 to February 2017, a total of 17 CRKP isolates were detected from the ICU and neurosurgery unit of our hospital, and all of them were ST76. PFGE showed homology between all isolates, indicating an outbreak and spread between the two departments. These strains were different from ST11, which is the main epidemic strain in China; cases of ST76 have been rarely reported. This is the first report of the whole genome sequence of the Klebsiella pneumoniae ST76 isolate that produced KPC-2, and the first report of Tn1721 in ST76 Klebsiella pneumoniae,suggesting that the transfer of mobile elements carrying the blaKPC gene

could cause more strains of K. pneumoniae to become resistant to carbapenem. The blaKPC gene copy number, the insertion or deletion of an upstream sequence to alter the structure of the promoter region, and loss of outer membrane porins are all factors that could affect the expression of the blaKPC gene, resulting in a change in the MIC value of the horizontally transmitted strain. This work provides a basis for understanding antibiotic resistance and resistant plasmid transmission. Relevant departments should implement infection control and prevention measures to reduce the incidence of nosocomial infections.

PU-3406

抗菌药物使用与多重耐药菌检出率的相关性分析

李绍红[1]、王晓茜[2]、武广晔[1]、温学红[1]
1. 天津中医药大学第二附属医院
2. 天津医科大学

目的 分析抗菌药物使用与多重耐药菌检出率的关系，关注病原菌的多重耐药现象，提示临床合理用药。
方法 1.使用世界卫生组织细菌耐药性监测网 WHONET 软件统计 2018 年-2020 年全院的病原菌检出总株数及三种耐碳青霉烯类药物多重耐药菌株数，包括：耐碳青霉烯类药物鲍曼不动杆菌（CR-Ab）、耐碳青霉烯类药物铜绿假单胞菌（CR-PS）、耐碳青霉烯类药物肺炎克雷伯菌（CR-KP），分析各季度上述多重耐药菌的检出率。2.回顾性分析 2018-2020 年本院抗菌药物的使用率和使用强度。3.分析本院多重耐药菌检出率、耐碳青霉烯类药物多重耐药菌占比、CR-Ab、CR-PS 和 CR-KP 的检出率以及抗菌药物使用率、抗菌药物使用强度与多重耐药菌（包括 CR-Ab、CR-PS、CR-KP）检出率的相关性。
结果 本院 2018-2020 年多重耐药菌检出率分别为 18.72%、19.03%和 24.05%；耐碳青霉烯类药物多重耐药菌占比分别为 16.23%、32.00%和 42.56%；CR-Ab 的检出率分别为 23.53%、38.12%和 26.19%；CR-PS 的检出率分别为 13.74%、17.85%和 17.85%；CR-KP 的检出率分别为 1.34%、6.28%和 22.52%；CR-Ab 科室分布前五名中 ICU 占比由 2018 年的 62.50%降为 2020 年的 15.91%；CR-Ab、CR-PS 和 CR-KP 抗菌药物使用强度与本院患者 CR-Ab、CR-PS 和 CR-KP 检出率的 r 值分别为 0.682、0.766 和 0.787，三者均 $P<0.05$，均有统计学意义。抗菌药物使用强度与 CR-Ab、CR-PS 和 CR-KP 检出率均呈正相关。
结论 本院 2018-2020 年期间多重耐药菌检出率呈上升趋势且耐碳青霉烯类药物多重耐药菌占比增加；本院 2018-2020 年期间 CR-Ab 有向非重症科室扩散的现象；2018-2020 年各季度的抗菌药物使用强度与 CR-Ab、CR-PS 和 CR-KP 的检出率有相关性且呈显著正相关，因此要多注意抗菌药物的合理使用，对于减少 MDRO 的产生有积极的意义。

PU-3407

某院 132 例替加环素用药合理性分析

李丽华
西安国际医学中心医院

目的 分析替加环素使用情况，评估替加环素用药合理性，为临床合理使用替加环素提供参考。
方法 本研究采取回顾性分析，收集医院 2020 年 5 月~2021 年 1 月使用过替加环素的出院患者病历 132 份，对病原学送检情况、替加环素使用情况、联合用药和不良反应监测情况进行分析。
结果 132 例出院患者中病原学送检 131 例（99.24%），92 例（69.70%）按照替加环素说明书要求用药。革兰阴性多重耐药菌感染均与其他抗菌药物联合使用，不良反应监测对肝功能、凝血功能、钙浓度均有监测，但对淀粉酶监测仅有 23 例（17.42%）。

结论 我院替加环素临床应用基本合理，但替加环素用法、用量和不良反应监测方面仍有待改善，以减少由于经验性用药引起多重耐药的发生。

PU-3408

2010-2020 年某三甲医院血培养分离菌的分布及耐药性分析

赵亚楠、曹啓新、赵建平
内蒙古自治区内蒙古人民医院

目的 研究内蒙古自治区人民医院 10 年间血培养分离菌的分布及耐药性
方法 回顾性分析我院 2010-2020 年所收集的 3754 株血培养分离菌，采用 WHONET 5.6 软件进行数据统计，率的比较采用 SPSS 22.0 进行统计比较。
结果 3754 株血培养分离菌前十位依次为凝固酶阴性葡萄球菌（CNS）（32.7%）、大肠埃希菌（29.3%）、肺炎克雷伯菌（10.1%）、金黄色葡萄球菌（6.2%）、屎肠球菌（4.4%）、铜绿假单胞菌（2.5%）、鲍曼不动杆菌（2.5%）、阴沟肠杆菌（2.4%）、粪肠球菌（2.0%）、奇异变形杆菌（0.8%）；对各类菌的检出率进行前五年与近五年的比较，发现 CNS、大肠埃希菌、肺炎克雷伯菌、鲍曼不动杆菌、阴沟肠杆菌及粪肠球菌近五年检出率明显升高，差异有统计学意义（P<0.05）；血培养分离菌科室主要分布在 ICU；药敏结果显示，MRSA 和 MRCNS 的检出率为 33.8%和 56.7%，未发现对万古霉素、利奈唑胺耐药的葡萄球菌和肠球菌，链球菌属对红霉素、复方新诺明的耐药率均较高，对其他抗菌药物的耐药率均较低；肠杆菌科以大肠埃希菌和肺炎克雷伯菌为主，耐碳青霉烯类的肺炎克雷伯菌（CRKP）检出率为 24.2% ，耐碳青霉烯类的大肠埃希菌（CRCE）检出率为 5.6%，CRKP 对多种抗菌药耐药率较高；铜绿假单胞菌对哌拉西林、氨曲南、亚胺培南、美罗培南、阿米卡星、庆大霉素、妥布霉素、环丙沙星以及左旋氧氟沙星耐药率低（<15%），鲍曼不动杆菌表现为多重耐药，但对阿米卡星耐药率低（20%）。
结论 血培养分离菌构成复杂，耐药率高，应加强细菌耐药性监测，指导临床合理用药

PU-3409

大肠埃希菌的感染分布与耐药性分析

侯向萍、王莉、岳帆、韩凯云、周志芳
新疆生产建设兵团第一师阿拉尔医院

目的 探讨 2016—2020 年阿拉尔医院大肠埃希菌的临床分布和耐药率变迁情况,为临床合理用药提供参考。
方法收集 2016—2020 年本院不同标本分离的大肠埃希菌 980 株,使用全自动细菌鉴定和药敏分析仪及纸片扩散法进行体外药敏试验。根据细菌鉴定和药敏试验结果,分析各年度大肠埃希菌科室分布、不同标本来源的细菌分布和细菌对常见抗菌药物的耐药。
结果 共检出大肠埃希菌非重复菌株 980 株, 2016 年-2020 年病区来源分布,其中来源呼吸内科有 103 株（10.51%）,门诊有 77 株（7.86%）,普外科有 104 株（10.61%）,泌尿外科有 260 株（26.53%）,肾病内科有 135 株（13.78%），内分泌内科有 86 株（8.78%）其他科室 215 株（21.93%）。980 菌株的标本来源分布,其中来源为呼吸道有 145 株（14.80%）,尿液有 440 株（44.90%）,血液有 300 株（30.61%）,分泌物有 95 株（9.70%）。标本来源和科室分布以尿液和泌尿外科为主,分别占 44.90%和 26.53%。大肠埃希菌的产超广谱 β-内酰胺酶（ESBL）整体检出率为 49.3%,对头孢菌素类和喹诺酮类的耐药性非常严峻,其中哌拉西林的耐药率为 78.6%，头孢呋辛的耐药率为 65.2%,环丙沙星的耐药率为 53.8%,左氧氟沙星的耐药率为 41.0%。其中亚胺培南的耐药率为 2.0%，美罗培南的敏感率为 5.5%,哌拉西林/他唑巴坦为 4.2%,阿米卡星敏感率为 6.8%.

结论 本院大肠埃希菌检出率高的是尿液标本，2016 年-2021 年对喹诺酮类抗菌药物和头孢菌素的耐药率总体仍然处于较高水平,而碳青霉烯类的美罗培南和亚胺培南的耐药率非常低,哌拉西林/他唑巴坦和阿米卡星也具有非常高的敏感性,与全国细菌耐药监测报告基本一致。近几年医院也制定各项措施降低细菌的耐药率，在《2021 年国家医疗质量安全改进目标说明》中提出提高抗菌药物治疗前病原学送检率，有效提高抗菌药物使用的科学性和规范性，对遏制细菌耐药、提升治疗效果和保障人民群众健康权益具有重要意义。通过国家政策及本院的相关制度，期待大肠埃希菌对头孢类及喹诺酮类的较高耐药现象能够得到缓解。

PU-3410

2018-2020 年流感抗原检测结果分析及人群分布特征

邓杰伦
四川大学华西医院

目的 调查我院近三年流感病毒抗原检测结果及分布特征并分析新冠病毒防控措施对流感病毒流行的影响。
方法 回顾性分析 2018-2020 年于我院就诊并检测流感病毒抗原的 23888 例患者，统计甲型、乙型流感病毒抗原检测阳性率及阳性患者的人群特征。
结果 23888 例患者中，流感抗原检出率为 11.97%（2860/23888），其中甲流抗原阳性率为 8.25%（1971/23888），乙流抗原阳性率为 3.80%（913/23888）。2018 年-2020 年甲流抗原阳性率分别为 8.99%（396/4403）、10.59%（1448/13667）和 1.50%（87/5818）；乙流抗原阳性率分别为 2.91%（128/4403）、5.22%（713/13667）、1.24%（72/5818）。2020 年甲流、乙流抗原阳性率明显低于 2018 年和 2019 年。甲流，乙流均以冬，春季节流行为主，甲流流行率更高。除 2019 年 4 月份乙流抗原阳性率高峰外，甲流、乙流抗原检测均在 1 月份阳性率达到峰值；甲流，乙流抗原阳性检出率女性均稍高于男性，差异无统计学意义（P=0.317）； 中年人群（25-64 岁）阳性检出率最高，儿童（<=14 岁）阳性检出率最低。
结论 我院 2018-2020 年流感流行以甲型流感为主，流行季节为冬春季，流行后期乙流感染人群增多，人群普遍易感。2020 年 1 月末开始实施新冠疫情防控之后甲流和乙流阳性检出率明显降低，说明加强个人防护和减少人群聚集等防控措施，大大减少了非新冠肺炎呼吸道疾病(甲流，乙流)的感染率

PU-3411

基质辅助激光解吸电离飞行时间质谱检测大肠埃希菌

张敏、杨丽英、刘明珠、李雨艳
吉林金域医学检验所有限公司

目的 通过对不同类型送检标本和年龄进行研究，了解大肠埃希菌的患病人群和比率，为临床提供参考依据。
方法 选取 2021 年 1 月至 2021 年 5 月送检吉林金域医学检验所有限公司的细菌培养+药敏检测项目的分泌物、咽拭子、浓汁等体液样本 1244 例，对单个纯菌落进行基质辅助激光解吸电离飞行时间质谱检测。
结果 1、质谱图谱，特征峰的相对丰度和质荷比符合对比标准谱库找到特征峰组高峰值特征峰集中在 4000 m/z ～9000 m/z 区；2、1244 例样本中标本类型数量为分泌物 125 例，浓汁 156 例，咽拭子 963 例，其中 125 例分泌物样本中 14 例检出大肠埃希菌，阳性率为 11.2%，其中 2 例同时检出无乳链球菌和奇异变形杆菌；156 例浓汁样本中 17 例检出大肠埃希菌，阳性率为 10.9%，其中 1 例同时检出凯斯特丛毛单胞菌；963 例咽拭子样本中 8 例检出大肠埃希菌，阳性率为 0.83%。3、

不同标本类型送检年龄分析：14 例分泌物样本中大肠埃希菌阳性患者年龄均为 25 岁以上，且 60 岁以上患者仅为 14%，17 例浓汁样本中大肠埃希菌阳性患者年龄均为 35 岁以上，且 60 岁以上患者仅为 17%，8 例咽拭子样本中大肠埃希菌阳性患者年龄均为 1 岁以下。4、大肠埃希菌阳性结果，经 VITEK 2 COMPACT 全自动鉴定及药敏分析系统鉴定符合。
结论 应用基质辅助激光解吸电离飞行时间质谱检测，结果准确率高、操作简便、重现性好、节省培养时间，可为临床快速提供结果，争取治疗时间。

PU-3412

脑脊液培养病原菌分布及耐药性分析

张楠
南京大学医学院附属鼓楼医院

目的 探讨临床送检脑脊液培养病原菌分布及耐药情况,为临床合理使用抗生素提供依据.
方法 采用 whonet 软件对临床送检的脑脊液培养阳性病原菌分布及耐药性资料进行回顾性分析.
结果 共分离出病原菌 110 株,其中革兰阳性(G+)球菌 40 株(36.4％),革兰阴性(G-)杆菌 53 株(48.2％),真菌 15 株(13.6％),G-球菌 2 株(1.8％).主要病原菌分布为:鲍曼不动杆菌 21 株(19.1％)、表皮葡萄球菌 11 株(10％)、金黄色葡萄球菌 8 株(7.3％)和铜绿假单胞菌 7 株(6.4％).药敏结果显示,G+球菌对万古霉素、利奈唑胺和替考拉宁敏感率最高;G-杆菌中,鲍曼不动杆菌耐药较严重,其药物敏感性均＜30％,其中阿米卡星敏感率为 23.5％,铜绿假单胞菌和肺炎克雷伯菌的药物敏感性均较好.
结论 临床送检脑脊液培养样本中以 G-杆菌的分离率较高,耐药情况不明显,可为中枢神经系统感染的用药提供建议和参考.

PU-3413

支原体感染与阴道微生态环境相关性回顾性研究

王青
西安医学院第一附属医院

目的 探讨和分析支原体感染患者阴道微生态的相关状况，为临床治疗提供有效参考。
方法 选取 2018 年 4 月至 2020 年 12 月这段时间内，我院妇科支原体阳性的 182 例患者同时统计该患者阴道微生态情况，分析支原体与阴道微生态环境改变的相关性。
结果 182 例支原体阳性的患者中单独解脲脲原体（Uu）132 例，占比 72.53%，单独人型支原体（Mh）2 例，占比 1.11%，混合感染 Uu＋Mh48 例，占比 26.37%，而单独解脲脲原体（Uu）的患者更易出现阴道微生态功能下降，人型支原体（Mh）+解脲脲原体感染（Uu）的患者更易出现阴道微生态菌群失调，患细菌性阴道病（P<0.05）,差异具有统计学意义。
结论 支原体感染的患者更易出现阴道微生态环境的改变，对于女性患者患者来说，支原体感染是重要的病原体，在临床诊疗的过程中应当予以高度重视，因此可将支原体衣原体感染与阴道微生态的检查作为患者的常规检验科目，对于降低阴道炎复发具有较大的应用价值，促进广大女性朋友的健康发展。

PU-3414

肺炎克雷伯菌阳性检出率情况及耐药分析

德非凡、杨丽英
吉林金域医学检验所有限公司

目的 肺炎克雷伯菌作为院感中常见菌类之一，可引起伤口创面、呼吸道、泌尿道感染及败血症、甚至脑膜炎等。本文分析送检样本中肺炎克雷伯菌的阳性率和药敏表型，并分析其临床意义，为临床合理化防治提供参考依据。
方法 回顾 2020 年 1 月至 2020 年 12 月送检我公司微生物室所有样本，进行数据统计分析。统计出肺炎克雷伯菌在所有样本类型中的检出率及耐药率。
结果 在 2987 例样本中，有 425 例分离出肺炎克雷伯菌，总阳性率为 14.2%。其中呼吸道样本中分离出 269 例，阳性率为 23.8%；尿液样本中分离出 48 例，阳性率为 8.9%；血液样本中分离出 10 例，阳性率为 7.6%；脓样本中分离出 23 例，阳性率为 8.9%；分泌物样本中分离出 14 例，阳性率为 7.8%。对氨苄西林、哌拉西林耐药率 70%；一、二代头孢耐药率 40.9%；三四代头孢耐药率 38.4%；碳青霉烯类基本敏感。
结论 肺炎克雷伯菌多在患者呼吸道及体表脓汁、分泌物样本中被分离出来。肺炎克雷伯菌作为人体正常菌群，为条件致病菌，当人体免疫力低下时，便会侵入机体造成疾病。肺炎克雷伯菌在院感菌类中也占相当大的一部分比例，上述数据中可以看到呼吸道样本中分离出肺炎克雷伯菌的例数最多，呼吸道也是肺炎克雷伯菌感染的主要途径。预防院感菌类需要从病原菌的内源感染途径和外源感染途径入手，需要医护人员和患者的共同配合，合理使用抗生素，避免耐药菌的产生。

PU-3415

肺炎克雷伯菌阳性检出率及耐药分析

杨丽英
吉林金域检验医学检验所有限公司

目的 肺炎克雷伯菌作为院感中常见菌类之一，可引起伤口创面、呼吸道、泌尿道感染及败血症、甚至脑膜炎等。本文分析送检样本中肺炎克雷伯菌的阳性率和药敏表型，并分析其临床意义，为临床合理化防治提供参考依据。
方法 回顾 2020 年 1 月至 2020 年 12 月送检我公司微生物室所有样本，进行数据统计分析。统计出肺炎克雷伯菌在所有样本类型中的检出率及耐药率。
结果 在 2987 例样本中，有 425 例分离出肺炎克雷伯菌，总阳性率为 14.2%。其中呼吸道样本中分离出 269 例，阳性率为 23.8%；尿液样本中分离出 48 例，阳性率为 8.9%；血液样本中分离出 10 例，阳性率为 7.6%；脓样本中分离出 23 例，阳性率为 8.9%；分泌物样本中分离出 14 例，阳性率为 7.8%。对氨苄西林、哌拉西林耐药率 70%；一、二代头孢耐药率 40.9%；三四代头孢耐药率 38.4%；碳青霉烯类基本敏感。
结论 肺炎克雷伯菌多在患者呼吸道及体表脓汁、分泌物样本中被分离出来。肺炎克雷伯菌作为人体正常菌群，为条件致病菌，当人体免疫力低下时，便会侵入机体造成疾病。肺炎克雷伯菌在院感菌类中也占相当大的一部分比例，上述数据中可以看到呼吸道样本中分离出肺炎克雷伯菌的例数最多，呼吸道也是肺炎克雷伯菌感染的主要途径。预防院感菌类需要从病原菌的内源感染途径和外源感染途径入手，需要医护人员和患者的共同配合，合理使用抗生素，避免耐药菌的产生。

PU-3416

过敏性鼻炎患者鼻腔微生物失调

苗平、李敏
上海交通大学医学院附属仁济医院

目的 过敏性鼻炎(allergic rhinitis，AR)是指特应性个体接触变应原后由 IgE 介导的释放炎性介质、有免疫活性细胞以及细胞因子、炎性介质等参与的鼻部变态反应性疾病。AR 发病机制复杂，影响因素众多，微生物和过敏原均能刺激鼻粘膜，导致 AR 的发生。本研究旨在探讨过敏性鼻炎患者鼻腔微生物群的改变，进而为 AR 的诊断和治疗提供新思路。
方法 收集健康人及 AR 患者鼻腔拭子各 100 例，提取细菌基因组 DNA，通过对 16S 核糖体 RNAV3-V4 区测序的方法，获得基因信息，之后运用生物信息学、医学统计学分析了 AR 患者鼻腔微生物群落的系统发育组成，并与健康人进行比较。
结果 两类患者在门水平的相对丰度上存在显著差异。在所有微生物中，厚壁菌门占的比重最大（两组均超过 50%）。与健康对照组相比，在 AR 患者组，厚壁菌门的比例明显升高，拟杆菌门、放线菌门、变形菌门、梭杆菌门、软皮菌门的比例均一定程度的下降，并且差异都具有显著统计学意义。有意思的是，在 AR 组厚壁菌门与拟杆菌门存在显著的负相关。
结论 过敏性鼻炎患者与健康人鼻腔微生物的组成存在明显的差异，可进一步深入研究 AR 患者鼻腔微生物的改变与 AR 发病机制的关联性，进而为 AR 患者的临床诊断和治疗提供新的思路。

PU-3417

同一种细菌菌落为何存在不同形态

陈璐
上海市第一人民医院嘉定分院

目的 不同细菌于琼脂平板上的菌落生长形态不同，因此我们可以通过菌落形态大致判断不同细菌的种属。但是，对于培养的结果，不仅仅是不同细菌菌落形态的差异，对于同一种细菌的也存在菌落形态的差异，那么是什么原因使这种现象出现，就很值得我们来进行探讨一番。比如：培养的环境（温度、湿度、明暗程度、二氧化碳浓度），接种平板的质量差异及培养时间等。
方法 针对不同的影响因素，保证只有求证的影响因素作为唯一变量。
培养环境
1、选取两块质量完全一样的血琼脂平板，接种已知菌种的细菌（如金黄色葡萄球菌：用标准且光滑接种环挑取一个完整单个菌落的一半，两块平板各接种一半，四区划线法进行接种，保证操作过程流畅且一致。）
2、按第一步准备的两块平板为一套实验标本，一共准备四套，分别置于不同温度、湿度、明暗程度、二氧化碳浓度的环境下进行培养 48 小时，保证唯一变量。（如温度不同时，湿度、明暗程度和二氧化碳浓度保持一致）
接种琼脂平板的质量
1、随机选取 2~4 块血琼脂平板，接种已知菌种的细菌（如金黄色葡萄球菌：用标准且光滑接种环挑取一个完整单个菌落的一半，两块平板各接种一半，四区划线法进行接种，保证操作过程流畅且一致。）
2、将接种好的平板置于相同的培养环境（相同温度、湿度、明暗程度和二氧化碳浓度）进行培养 48 小时。
培养时间
1、选取两块质量完全一样的血琼脂平板，接种已知菌种的细菌（如金黄色葡萄球菌：用标准且光滑接种环挑取一个完整单个菌落的一半，两块平板各接种一半，四区划线法进行接种，保证操作过程流畅且一致。）

2、将接种好的平板置于相同的培养环境（相同温度、湿度、明暗程度和二氧化碳浓度）进行分别培养，于 24 小时、36 小时、48 小时和 72 小时进行菌落形态观察并记录。
结果 1、对于培养环境，不同的温度、湿度、和二氧化碳浓度对于同一菌种的菌落形态会有少许的差别，大致形态特征是保持一致的。
2、接种琼脂平板平板质量的差异对于菌落的形态存在偶然的差异性，但整体来说，菌落大致形态特征是具有一致性的。
3、培养时间的对于菌落形态有较大影响，24 小时的菌落普遍较小和稚嫩，典型特征（如溶血环）没有完全显现；36 小时的菌落处于过渡期，典型特征逐渐显现；48 小时菌落处于形态特征最具明显，最容易分辨；72 小时的生长的菌落已经逐渐老化，特征形态渐渐失去不易辨别。
结论 培养的环境（温度、湿度、明暗程度、二氧化碳浓度），接种平板的质量差异对于同一种细菌菌落形态存在一定程度的影响，但是大致形态和特征可以辨别，培养时间长短对于菌落形态影响较大，对于菌落形态观察的最适宜。

PU-3418

上海瑞金医院 2019-2021 年临床艰难梭菌感染的流行病学研究

陈炜[1,2]、彭奕冰[1]
1. 上海交通大学医学院附属瑞金医院
2. 上海交通大学医学院检验系

艰难梭菌（*Clostridium difficile*，CD)是一种革兰阳性厌氧芽孢杆菌，过去十年来，艰难梭菌感染（*Clostridium difficile* infection，CDI)在全球的发病率和死亡率急剧升高，已经成为最常见的医院获得性感染。
目的 本研究旨在通过分子生物学检测、流行病学调查等研究方法，明确我院临床艰难梭菌感染现状、分子流行病学特点及其耐药情况，为临床 CDI 的预防性管理和治疗提供依据。
方法 收集本院 2019 年 12 月至 2021 年 3 月临床进行艰难梭菌毒素检测的粪便标本，经过微生物分离培养、鉴定获得分离株，通过聚合酶链式反应（Polymerase Chain Reaction,PCR）检测毒素基因并确定临床 CDI 病例，同时进行多位点序列分型（Multilocus sequence typing, MLST）区分其基因型。根据 CLSI 指南，采用琼脂稀释法进行药物敏感性试验，分析菌株对 9 种常用抗菌药物的耐药情况，包括克林霉素、四环素、头孢噻肟、莫西沙星、甲硝唑、万古霉素、利福平、非达霉素、氨苄西林。最后查阅病史，分析 CDI 患者人群特征，根据不同分型分组并进行多项临床指标的统计假设检验。
结果 在分离所得 51 株艰难梭菌中，毒素 A、B 均阳性（A^+B^+）有 22 例（43.1%），毒素 A 阴性，毒素 B 阳性（A^-B^+）有 22 例（43.1%），毒素 A、B 均为阴性（A^-B^-）有 7 例（13.8%），主要分离自急诊 ICU（31.25%）、消化（20.83%）、儿科（20.83%）等病区。MLST 分型方法产生 16 种基因型，其中 ST81 型为主要流行克隆，占 39.2%。所有菌株对甲硝唑、万古霉素、利福平、非达霉素、氨苄西林均敏感；对克林霉素、四环素、头孢噻肟、莫西沙星的耐药率分别为 73.47%、48.98%、89.80%、44.90%，多重耐药菌比例达 53.06%，且 ST81 型菌株的整体耐药水平显著高于非 ST81 菌株（$p<0.001$）。CDI 患者共有 41 例，其中高龄患者占 26.83%，超过半数患者（51.22%）有外科手术史，绝大部分患者（85.37%）近三个月有抗生素接触史。显著性检验结果显示不同毒素型患者在性别、年龄、原发疾病、白细胞、肌酐等方面无统计学差异，而 A^-B^+型 CDI 患者的白蛋白和血红蛋白值则显著低于 A^+B^+型 CDI（$p<0.01$）。
结论 我院 A^-B^+型艰难梭菌感染比例明显上升。与国内其他地区报道不同，ST81 型艰难梭菌为本院近两年的主要流行株，其耐药性明显强于其他型别艰难梭菌，需要进行持续严格的监测。

PU-3419

Detection of virulence genes and analysis of drug resistance of pseudomonas aeruginosa TTSS

Chengbin Lei、Wen Zhang
Zibo Central Hospital

Objective To detect the presence of virulence genes related to Pseudomonas aeruginosa (Pa) in 51 cases of Pseudomonas aeruginosa isolated from zibo region, and analyze their drug resistance.
Methods ATB system was used to identify Pa. Two virulence genes, exoU and exoS, were detected by PCR.
Results among the 51 cases of clinical pseudomonas aeruginosa, 12 cases were positive for exoU gene (23.5%) and 39 cases were positive for exoS gene (76.5%).There was no significant difference in the positive rate of the two virulence genes between mucous and non-mucous Pa strains (P >0.05).The drug resistance rate of Pa strain carrying exoU was higher than that of exoS strain, and there were significant differences in drug resistance rate of imipenem, levofloxacin and piperacillin/tazobactam (P <0.05).The clinical characteristics of exoU group and exoS group were analyzed retrospectively. The clinical characteristics of the exoU group were that most patients had endotracheal intubation history, ICU hospitalization history and anti-infection treatment were mostly treated with combined medication.
Conclusion exoU and exoS genes are mutually exclusive in isolated strains.The proportion of Pa strain carrying exoU was low in the isolated strain, but the drug resistance rate was higher than that of Pa strain carrying exoS.Patients in exoU group were mostly infected with pseudomonas aeruginosa, while those in exoS group were mostly colonized with pseudomonas aeruginosa.

PU-3420

一种基于抗菌肽的细菌快速鉴别方法的建立及初步评价

许伟[1]、范小波[2]、吴国球[1]
1. 东南大学附属中大医院
2. 东南大学

目的 基于抗菌肽与各种细菌的结合能力不同建立一种细菌快速鉴定方法并对其进行初步评价。
方法 抗菌肽 Ib 因其与各种细菌结合及裂解膜的特性具有抗菌的生物活性，在低浓度情况下，其裂解细菌的活性较弱，仅表现为与细菌结合的活性，而且其结合能力受离子影响而减弱。因此，根据其与各种细菌有不同结合能力的特性可开发一种细菌快速鉴别的方法。首先合成绿色荧光蛋白标记的抗菌肽 Ib-GFP，使用生物工程方法表达蛋白并进行提纯。探索 Ib-GFP 与细菌的结合能力并得出最适宜的反应条件。将细菌洗涤以除去盐分，然后将细菌与 Ib-GFP 共孵育 15 分钟。反复洗涤四次后分别使用 5%葡萄糖溶液以及 0.01M PBS 缓冲液重悬细菌。使用流式细胞仪检测两组菌液的绿色荧光。以葡萄糖组结果为横坐标，PBS 组为纵坐标，标记每种细菌的荧光强度在坐标轴范围，即可得到每种细菌对应的特异性荧光结果。使用该方法对 18 种常见临床致病菌进行检测（其中革兰氏阴性菌 10 例，阳性菌 8 例），评价该方法的检验效果。
结果 成功表达并纯化 Ib-GFP。使用该方法检测 18 株分离菌并成功地鉴别出 15 株细菌，占实验样本的 83%。无法分辨的另外三株均为革兰氏阴性菌，分别为肺炎克雷伯菌、阴沟肠杆菌、以及臭鼻克雷伯氏菌，其荧光结果在二维平面上有部分重叠而无法判断。
结论 本实验成功建立了一种新型快速的细菌鉴定方法，可用于细菌的快速鉴定诊断。其可用于多数的临床常见致病菌的快速鉴别，但是仍然有极大的优化空间。

PU-3421

血液病患者肠道定植 CRE 后感染的危险因素分析

晏群、陈霞
中南大学湘雅医院

目的 耐碳青霉烯类肠杆菌科细菌（carbapenem-resistant Enterobacteriaceae,CRE）检出率日渐上升，已引起广泛的国际关注，并对全球公共卫生安全带来严峻挑战。目前针对血液病患者肠道定植 CRE 后发生感染的相关研究在国内国外均较少。本研究旨在探究血液病患者肠道定植 CRE 与后续发生感染的相关性及其危险因素。
方法 筛选出 2017 年 1 月 1 日至 2021 年 4 月 26 日送检至中南大学湘雅医院检验科微生物室的耐碳青霉烯肠杆菌筛查标本中的 2304 例，其中肠道定植 CRE 的 146 例。去除同一患者重复送检的标本后，送检的血液病患者标本共 599 例，筛查出肠道定植 CRE 的 75 例。以其中检测出肠道定植 CRE 的患者为实验观察对象（共 75 例），以 17 例检出 CRE 定植后发生由同种菌属细菌引起感染的病例为实验组，58 例检出 CRE 定植后未发生由同种菌属引起感染的病例为对照组，回顾性比较两组病例在临床数据上的差异，以卡方检验进行单因素分析，以 logistic 回归分析分析危险因素。并比较不同类型血液病的定植率和各类病原菌的定植率。
结果 血液科患者定植率为 12.52%（75/599）。各类血液病中淋巴瘤定植率最高（16/62，25.81%），其次是急性髓细胞性白血病（29/197，14.72%），而后依次是骨髓增生异常综合征（5/35，14.29%）、急性淋巴细胞性白血病（13/143，9.09%）、红细胞相关疾病（7/93，7.53%），最后是其他类型血液病（5/69，7.52%）；在各类定植的 CRE 中，最常见的是肺炎克雷伯菌（34/75，45.3%），其次是大肠埃希菌（19/75，25.3%），而后依次是阴沟肠杆菌（7/75，9.3%）、枸橼酸杆菌（2/75，2.6%）、产气克雷伯菌（2/75，2.6%）、产酸克雷伯菌（1/75，1.3%）、克氏枸橼酸杆菌（1/75，1.3%），其他未分类的肠杆菌科细菌占 12%；单因素分析结果显示，血液病患者肠道定植 CRE 后发生感染与肝脏疾病、腹泻和休克有关（P<0.05）；多因素分析结果显示是否患有肝脏疾病、入院期间是否发生腹泻和休克是血液病患者肠道定植 CRE 后发生感染的独立危险因素（P<0.05）。
结论 血液病患者中淋巴瘤患者定植率最高，肝病、腹泻和休克是血液病患者肠道定植 CRE 后发生感染的独立危险因素，应对上述患者加强关注，采取合理有效的临床干预措施，减小感染发生的可能。

PU-3422

ICU 患者发生耐碳青霉烯类革兰阴性杆菌血流感染的危险因素分析

简子娟、李艳明、李虹玲、陈霞、晏群、刘文恩
中南大学湘雅医院

目的 分析 ICU 患者发生耐碳青霉烯类革兰阴性杆菌血流感染的危险因素，为临床制定防治策略提供参考依据。
方法 收集回顾性分析某大型三甲综合性教学医院 2018 年 1 月至 2020 年 12 月 ICU 血流感染患者分离的革兰阴性杆菌及相应临床资料，根据是否对碳青霉烯类抗菌药物耐药，分为耐碳青霉烯类革兰阴性杆菌（CR-GNB）组和碳青霉烯敏感革兰阴性杆菌（CS-GNB）组，采用 Logistic 回归分析患者耐碳青霉烯类革兰阴性杆菌感染发生 CR-GNB 血流感染的危险因素。
结果 405 例革兰阴性杆菌血流感染中，270 例为 CR-GNB，数量占比排在前三位的菌种为肺炎克雷伯菌、铜绿假单胞菌和大肠埃希菌。通过单因素分析，发现合并多器官功能障碍（MODS）（P=0.003）、患有呼吸系统疾病（P=0.021）、PBS 评分（0.001）、使用三代头孢菌素类抗菌

药物（P=0.020）以及使用三种或三种以上抗菌药物（P=0.015）是发生 CR-GNB 血流感染的危险因素，进一步多因素回归分析表明使用三种及三种以上抗菌药物（OR=3.503，95%CI 为 0.270-0.937，P=0.03）与患有呼吸系统疾病（OR=3.572，95%CI 值为 0.336-0.972，P=0.039）为 ICU 患者发生 CR-GNB 血流感染的独立危险因素。

结论 患有呼吸系统疾病及使用三种及三种以上抗菌药物为 ICU 患者发生 CR-GNB 血流感染的独立危险因素。临床应加强感控措施，合理使用抗菌药物，尽可能减少 CR-GNB 血流感染的发生。

PU-3423

假体周围关节感染的危险因素分析以及最佳诊断标志物筛选

陈霞、晏群
中南大学湘雅医院

目的 分析假体周围关节感染（periprosthetic joint infection，PJI）的危险因素、探索患者凝血相关指标对于 PJI 的诊断效能，并评估凝血相关指标结合常用感染相关血液标志物对 PJI 的诊断能力，尤其是区分培养阴性的 PJI 患者和无菌性松动患者的能力。

方法 对于 2014 年 1 月至 2020 年 12 月间在湘雅医院行翻修关节置换术的共 198 例患者进行回顾性分析。根据美国感染协会 2013 年指南提出的诊断标准定义 PJI。采用单因素卡方检验及多因素 Logistic 二元回归分析 PJI 的相关危险因素。绘制受试者工作曲线（ROC），计算 PJI 组与无菌组以及培养阴性 PJI 组与无菌组之间的各诊断指标的敏感度、特异度、阳性预测值和阴性预测值，并根据曲线下面积（AUC）判断诊断价值。

结果 本次研究中 PJI 患者与无菌组患者在性别、年龄或位置方面无显著的组间差异（P>0.05）。患有骨关节炎、骨折病史、糖尿病、高血压或冠心病等其他基础疾病并不会增加患 PJI 的概率（P>0.05）。多因素 Logistic 二元回归分析显示患者关节出现红肿、以及有吸烟史是 PJI 的独立危险因素（P<0.05）。PJI 患者 WBC、N%、NRL、PLT、PLT/MPV、FDP、CRP、ESR、IL-6、PCT 的水平显著高于无菌组患者（P<0.05）。CRP、ESR、FDP 三项指标能较好得鉴别培养阴性的 PJI 患者与无菌组患者（P 值均小于 0.05）。经分析 CRP+FDP 联合诊断时的诊断能力最佳，AUC 为 0.892，联合诊断性能大于单独时，诊断指标的临界值时的灵敏度、特异度分别为 96.4%、72.3%。

结论 关节红肿与有吸烟史是 PJI 患病的独立危险因素。凝血相关指标 PLT，PLT/MPV 和 FDP 对 PJI 的诊断有统计学意义。FDP 对于培养阴性的 PJI 具有良好的诊断性能，CRP 与 FDP 联合诊断的诊断性能最优。

PU-3424

江苏地区患儿分离产 NDM-5 酶大肠埃希菌的传播机制研究

孔子艳
江苏省连云港市第一人民医院

目的 分析江苏地区儿童分离的携带 bla_{NDM-5} 基因碳青霉烯类耐药大肠埃希菌（CRECO）传播机制，为临床抗感染治疗及制定相应的防控措施提供依据。

方法 收集江苏省南京市儿童医院 2018 年 6 月至 2019 年 6 月非重复 CRECO 菌株。采用微量肉汤法测定菌株对常见抗菌药物的敏感性。PCR 法以及 Sanger 测序检测碳青霉烯类耐药基因、超广谱 β-内酰胺酶耐药基因及头孢菌素酶耐药基因。脉冲场凝胶电泳（PFGE）及多位点序列分析（MLST）分析耐药菌株同源性。通过接合试验，质粒复制子分型，S1-PFGE，Southern blotting 以及全基因组测序对质粒进行特征分析。

结果 本研究共收集 25 株 CRECO 菌株，药敏结果显示均为多重耐药菌，对碳青霉烯类、头孢类，酶抑制剂类均显示耐药。PCR 检测 *bla*$_{NDM-5}$ 基因的阳性率为 100.0%（25/25）。同源性分析发现菌株可分为 5 个 ST 型，以 ST410 为主（64.0%，16/25），进一步的 PFGE 结果显示院内存在 ST410, ST167 以及 ST349 耐药菌株的克隆播散。质粒特征分析结果表明 CRECO 菌株接合成功，且接合子对碳青霉烯类药物耐药，说明携带 *bla*$_{NDM-5}$ 基因的质粒具有高度的自主转移性，并且 52.0%（13/25）的耐药质粒为 IncX3 型，另外 blaNDM-5 基因位于约 33~100kb 大小的质粒，其中以 47kb 的质粒最常见。本研究挑选了一株代表性的菌株进行全基因组测序，发现质粒 pNDM-XZA88 与经典型质粒 pNDM-MGR194 序列相比，blaNDM-5 基因的遗传背景中 ΔISAba125 部分拷贝缺失。
结论 携带 blaNDM-5 基因大肠埃希菌在儿童群体中广泛流行, 其中 IncX3 型质粒可介导 blaNDM-5 在不同的菌株进行水平转移，该型质粒是传播 *bla*$_{NDM-5}$ 基因的重要载体，质粒遗传背景在传播中也逐渐进化。

PU-3425

某三甲医院碳青霉烯耐药肺炎克雷伯菌下呼吸道医院感染流行病学分析

康海全、马萍
徐州医科大学附属医院

目的 分析碳青霉烯类肺炎克雷伯菌（carbapenemase resistant K. pneumoniae， CRKP）引起的医院内下呼吸道感染的流行病学特征，为 CRKP 医院内感染提供理论依据。
方法 收集 2018 年 1 月至 12 月在某三级甲等教学医院医院内下呼吸道感染 CRKP，并进行流行病学调查分析。研究对象为下呼吸道医院感染患者痰液、肺泡灌洗液培养 CRKP 的病例。通过 PCR 和 DNA 测序检测耐药基因。通过多基因座序列分型（Multilocus sequence typing，MLST）分析 CRKP 菌株的细菌克隆相关性。试验结果使用 WHONET 5.6 和 SPSS 18.0 进行汇总分析。
结果 2018 年医院 CRKP 感染年发病率为 5.71/10,000 出院人数（104 / 182,243 * 10,000）， 每 10 万患者住院日为 5.53（104/ 1,879,650 * 100,000）。104 名研究对象中，65 岁以上占 46.16%（48/104）， 既往史中高血压 42.83％（44/ 104）， ICU 入住史 27.89％（29 / 104）， 抗菌药物暴露史为 88.46％（92/104）。 最常见的 MLST 分型为 ST11（79/104，76.0%）， 其次是 ST48（9/104， 8.65%）。 KPC-2（101/104，97.12%）是主要的碳青霉烯酶，AmpC-酶和超广谱 b-内酰胺酶分别以 DHA-1、CTX-M-65 为主。
结论 医院内下呼吸道感染的 CRKP 菌以中产生 KPC-2 的 ST11 肺炎克雷伯菌最为常见。长期的、系统的检测以及严格的控制措施是遏制此类细菌传播的重要措施。

PU-3426

127 例金黄色葡萄球菌血流感染临床流行病学分析

康海全、马萍
徐州医科大学附属医院

目的 探究金黄色葡萄球菌（金葡菌）血流感染的临床特征，分析预后不良的危险因素，为金葡菌血流感染的诊治提供依据。
方法 回顾分析 2018 年 9 月-2020 年 8 月徐州医科大学附属医院 127 例金葡菌血流感染病例，收集临床特征和实验室数据，运用单因素和多因素 logistic 回归，分析转归相关的危险因素。
结果 logistic 多因素回归分析显示预后不良的独立危险因素为脑卒中、ICU、中心静脉插管、PCT 升高（OR 值为 12.123、4.906、3.315、15.879）。对金葡菌进行 MRSA 和 MSSA 分组，通过比

值比分析，中心静脉插管、ICU、PCT 升高三个独立危险因素存在时感染 MRSA 的可能性较大（OR 值为 4.048、4.141、3.231，且 95%CI 不包括 1），差异有统计学意义。
结论 脑卒中、中心静脉插管、ICU、PCT 升高在金葡菌血流感染患者预后不良中起到重要作用，控制好 MRSA 感染有利于改善患者预后。

PU-3427

肺炎链球菌小片段自溶素蛋白 LytA′的体外抗菌活性探讨

谢兴凤
绵阳市中心医院

目的 构建肺炎链球菌（ATCC49619）小片段自溶素基因 lytA′的原核表达载体，通过大肠埃希菌表达系统进行原核表达获得一种新型肺炎链球菌小片段自溶素重组蛋白 LytA′，初步探讨该蛋白的体外抗菌活性，并与青霉素 G 同时进行比较。
方法 设计 lytA 基因的特异性引物，并通过 PCR 方法从肺炎链球菌（ATCC49619）中扩增 lytA 基因，并将其插入原核表达载体 PGM-T 中，构建 PGM-T /lytA 重组质粒，使用限制性核酸内切酶 BamHI 和 HindIII 消化 PGM-T / lytA 获得小片段自溶素基因 lytA′。再构建表达质粒 pET-32a（+）/lytA′ 并转化到感受态细胞大肠埃希菌 BL21（DE3）中，经 IPTG 诱导表达目的蛋白，使用透析袋等电点洗脱技术纯化回收目的蛋白 LytA′；采用微量肉汤稀释法分别测定 LytA′和青霉素 G 对肺炎链球菌（ATCC49619）的最小抑菌浓度（MIC），并将其作用于青霉素 G 敏感菌株肺炎链球菌（ATCC49619），初步探讨小片段自溶素蛋白 LytA′的体外抗菌活性。
结果 成功构建重组质粒 PGM-T / lytA 和 pET-32a（+）/ lytA′。小片段自溶素重组蛋白表达良好，并显示出预期的抗菌活性。与生长对照组相比，LytA′和青霉素 G 在 3h 时显示出明显的抗菌活性在（P <0.05），抑菌效应持续至 7h（P<0.05），抑菌效应逐渐增强。此外，在 7h 时，LytA′ 的抑菌活性明显强于青霉素 G（P<0.05）。
结论 小片段自溶素重组蛋白 LytA′对青霉素 G 敏感肺炎链球菌显示出一定的体外抑菌活性，且持续时间久，有成为抗肺炎链球菌感染治疗药物的可能性。

PU-3428

无菌体液中耐碳青霉烯类肠杆菌科细菌的临床分布及耐药性分析

张鸿娟
昆明医科大学第一附属医院

目的 分析某院无菌体液中分离出的耐碳青霉烯类肠杆菌科细菌（CRE）的检出情况和耐药性。
方法 回顾性分析 2020 年 1 月-2021 年 2 月昆明医科大学第一附属医院医学检验科临床微生物实验室无菌体液中分离出的耐亚胺培南或美罗培南的肠杆菌科细菌，对表型确定的 CRE 菌株进行测序分析，确定基因型，同时统计无菌体液中 CRE 对常用抗菌药物的耐药情况。
结果 无菌体液中共分离出 46 株 CRE，其中肺炎克雷伯菌 43 株，大肠埃希菌 1 株，产气克雷伯菌 1 株，阴沟肠杆菌 1 株。其中 KPC 型 32 株，OXA-48 型 9 株，IMP 型 1 株，NDM1 株，同时存在 KPC、OXA-48 耐药基因的有 2 株，不产酶 1 株。 46 株无菌体液中的 CRE 除对碳青霉烯酶类抗生素（亚胺培南或美罗培南）绝对耐药外，对 β-内酰胺酶、氨基糖甙类、大环内酯类、磷霉素等耐药，对替加环素的普遍敏感，对复方新诺明部分敏感，对四环素部分敏感。
结论 无菌体液中的 CRE 以肺炎克雷伯菌为主，基因型以 KPC 为主，有多种耐药基因同时存在的情况。对常用抗菌药物普遍耐药，临床治疗建议采取的抗感染措施为碳青霉烯类、替加环素及其他抗菌药物两药或三药联合为首选用药方案。

PU-3429

腹腔积液标本的病原菌分布情况

郭媛媛
云南大学附属医院

目的 了解腹腔积液的病原菌构成情况。
方法 回顾性分析我院 2015 年 1 月-2019 年 12 月收集的腹腔积液标本分离的病原菌培养结果。
结果 共分离出腹腔积液非重复病原菌 687 株（54.78%），其中主要是以大肠埃希菌和肺炎克雷伯菌为主的革兰阴性菌（60.84%），其次是以屎肠球菌和表皮葡萄球菌为主的革兰阳性菌（28.97%）；真菌占 10.19%，最多见的是白色念珠菌。革兰阴性菌检出率由 2016 年的 79.82%下降至 2019 年的 53.21%，呈现明显下降趋势（X2= 17.800，P＜0.05），革兰阳性菌检出率由 2016 年的 20.18%上升至 2019 年的 46.79%，呈现明显上升趋势（X2= 17.800，P＜0.05）。
结论 我院腹腔积液分离病原菌中以革兰阴性菌为主，革兰阴性菌检出率逐渐下降，而革兰阳性菌检出率呈现明显上升趋势。

PU-3430

本院耐碳青霉烯类肠杆菌科细菌（CRE)主动筛查结果分析

邵靖懿[1]、陈永寿[2]、金秀秀[1]、李卫滨[2,3]、张胜行[2,3]
1. 联勤保障部队第九〇〇医院检验科
2. 福建医科大学福总临床医学院检验科
3. 联勤保障部队第九〇〇医院福建省适配体技术重点实验室

目的 通过主动筛查分析联勤保障部队第九〇〇医院 CRE 高流行科室内 CRE 流行特征，探究其与临床常规病原微生物检测结果的一致性，以期通过主动筛查指导临床医师合理化、规范化使用抗菌药物，控制院内 CRE 的流行与传播。
方法 以 2020 年 10 月 10 日-2021 年 4 月 21 日本院 CRE 高流行科室内住院患者为研究对象，采集住院患者的痰液、肺泡灌洗液（BALF）、中段尿、分泌物等标本进行病原微生物检测，同时采集 518 名住院患者的粪便常规标本进行主动筛查，对已分离的 CRE 菌株进行表型鉴定、菌种统计以及耐药性分析。
结果 ①临床常规病原微生物检出情况：362 份临床标本共分离 27 株 CRE 菌株，其中肺炎克雷伯菌的检出率最高，占 55.6% （15/27），分离菌株中产 A 类碳青霉烯酶的 CRE 菌株最多，占 66.7%；②CRE 高流行科室主动筛查检出情况：580 份粪便标本共分离 8 株 CRE 菌株，其中肺炎克雷伯菌的检出率最高，占 62.5% （5/8）,分离菌株中产 A 类碳青霉烯酶的 CRE 菌株最多，占 75.0%；③主动筛查检出的 1 株 CRE 菌株早于临床检出，有 3 株 CRE 菌株在实验期间临床尚未检出，其余 4 株 CRE 菌株均晚于临床检出。④有 3 例住院患者先后在其体内检出不同的 CRE 菌株。
结论 本院 CRE 高流行科室内住院患者 CRE 定植与感染的主要致病菌为肺炎克雷伯菌，对临床常用抗菌药物具有较高的耐药性；碳青霉烯酶耐药基因可能会在肠道内不同种属细菌中传播，造成耐药基因的扩散；主动筛查具有早于临床常规病原微生物检验发现 CRE 的可能性；利用主动筛查早期发现 CRE 定植或感染者，可能为临床医师针对性实施个体化治疗方案及预防控制措施提供参考依据，有利于控制 CRE 定植或感染者引起的院内感染。

PU-3431

30 株碳青霉烯类耐药肺炎克雷伯菌（CRKP）耐药表型、基因型及联合药敏分析

张震、甘宇必
重庆市人民医院

目的 本研究拟对从不同类型的临床标本中分离出 30 株 CRKP（Carbapenem-resistant Klebsiella pneumoniae,CRKP）耐药表型、耐药基因型和联合药敏情况进行分析，以期待获得本医疗机构 CRKP 的相关数据后，指导临床对 CRKP 感染进行更精准的治疗，为临床合理联合抗生素治疗 CRKP、提高 CRKP 感染救治成功率提供坚实的理论基础。
方法 本研究通过碳青霉烯酶抑制剂增强实验测试 30 株 CRKP 产碳青霉烯酶的表型；利用细菌免疫显色试剂盒测试 30 株 CRKP 的碳青霉烯酶基因型；采用 K-B 法测试对临床常见抗菌药物的敏感性，并利用微量肉汤稀释法和 E-test 法复核菌株对多黏菌素和替加环素的敏感性；用 K-B 法测试不同药物联合方式下的药敏情况。
结果 30 株 CRKP 中产 KPC 型酶的菌株有 29 株，产 NDM 型仅有 1 株，未发现产其他酶型的菌株；受试菌株已对美罗培南（MEM）、磷霉素（FOT）、复方新诺明（SXT）等耐药程度较高，但未发现对多粘菌素（PB）、替加环素（TGC）耐药的菌株；所有联合方式中仅 FOT+TGC、FOT+PB 表现出明显协同作用。
结论 本院分离 CRKP 中流行的碳青霉烯酶型仍以 KPC 和 NDM 为主，与国内流行情况一致，且 FOT 与 TGC 或 PB 联合均有明显协同作用，提示临床可结合这两个情况对本院 CRKP 感染进行更为精准的治疗。同时，我们的实验结果也显替加环素和多粘菌素联合阿米卡星和利福平均未显示出协同抗菌作用。

PU-3432

天津地区感染性心内膜炎临床特征及病原学分析

翟志楠、贺靖冬、侯敏
天津市胸科医院检验科

目的 通过对我院 2018 -2020 年近 3 年间 92 例感染性心内膜炎（Infective Endocarditis，IE）确诊病例的临床资料进行描述性分析，以了解天津地区 IE 患者的临床特征、检验指标、致病菌的分布、治疗及预后等，获得本地区 IE 变化趋势，为提高 IE 的临床诊疗结果提供参考。
方法 采用回顾性研究的方法，对 IE 患者的临床资料进行描述性分析及影响预后的因素进行研究，包括患者的一般情况、临床表现、实验室检查、病原菌分布、治疗方式及预后等。
结果 （1）IE 患者以男性为主，发病比例大致为 2.17：1。IE 患者以 50-70 岁为主。（2）IE 患者中有心脏基础病的患者最多，为 95.7%，其中非风湿性心脏病患者占 65.9%；风湿性心脏病为 1.1%；先天性心脏病为 11.4%；心脏外科术后为 21.6%。（3）IE 患者的临床症状中发热最常见，约有 75%。（4）80.8% IE 患者 CRP 升高；89.9% IE 患者 BNP 升高；80.6% IE 患者血沉升高。（5）35.9% IE 患者血培养阳性，其中链球菌最多，占 73.9%；凝固酶阴性葡萄球菌占 17.4%，革兰阴性杆菌占 4.3%，其他革兰阳性球菌占 4.3%。（6）预后不良组的肌酐、BNP 高于预后良好组且具有统计学差异（P＜0.05）。
结论 （1）IE 患者的发病以中老年人为主，而且男性多发于女性。（2）非风湿性心脏病是 IE 患者主要的基础心脏病类型。（3）IE 患者的临床症状中，发热为最常见的症状。（4）多数 IE 患者会出现不同程度的贫血、BNP 升高，超敏 CRP 升高，红细胞沉降率升高，CRP 升高。（5）IE 患者的病原菌以链球菌为主。（6）IE 患者的治疗以外科手术为主，而且在同样符合手术体征情况下，

外科手术治疗比内科保守治疗治愈率高，死亡率低。（7）预后不良组的肌酐、BNP 比预后良好组高且具有统计学意义。

PU-3433

高原地区 MS 与基因测序对诺卡菌鉴定评价 及病例分析研究

巢世兰、阿祥仁
青海省人民医院

以基因测序（16s rDNA、rpoB）为金标准，评价飞行时间质谱（MALDI-TOF MS）对高原地区诺卡菌临床分离株的准确性研究及病例分析。

方法 回顾性调查我院 2015.1-2019.12 月，5 年临床标本中分离的 16 株诺卡菌，对比 MS 与测序的鉴定结果，将质谱法鉴定与基因测序法结果不一致的菌株维护进质谱数据库；剔除病例缺如者，共收集完整诺卡菌感染临床病例 13 例，对其临床特点及耐药性进行分析。

结论 高原地区分离的 13 株诺卡菌中，肺部依然是主要感染部位,而且不同诺卡菌的药敏谱存在差异，因此菌种的鉴定和药敏试验至关重要。

PU-3434

免疫层析技术在耐碳青霉烯肠杆菌科细菌耐药基因检测的临床应用

赵雅[1]、白倩[2]
1. 西安市第一医院
2. 陕西中医药大学

目的 探讨胶体金免疫层析技术在检测耐碳青霉烯酶肠杆菌科细菌耐药基因上的临床应用效果。

方法 收集 2020 年 1 月—12 月西安市第一医院分离的 24 株耐碳青霉烯肠杆菌，采用胶体金免疫层析法检测碳青霉烯酶基因。

结果 24 株临床分离菌株中，肺炎克雷伯菌 23 株，产酸克雷伯菌 1 株。其中 21 株检出产 KPC 酶，3 株检出产 NDM 酶，无产双酶菌株检出。

结论 采用胶体金免疫层析技术可以快速地检测产碳青霉烯酶肠杆菌的产酶类型，且操作简单、方便，在临床具有较高的应用前景。

PU-3435

金黄色葡萄球菌的耐药与临床治疗研究进展

任莉[1]、陆嘉敏[2]
1. 西安市第一医院
2. 海南医学院

院内感染是人类共同关注的公共卫生健康问题。其中金黄色葡萄球菌(SAU)是目前临床常见的感染性革兰阳性致病菌，可导致患者皮肤软组织感染，引起肺炎、败血症、菌血症等严重疾病。本文通过查找相关文献，归纳汇总金黄色葡萄球菌的耐药情况及治疗方法进展，为金黄色葡萄球菌的耐药研究和临床治疗提供参考依据。

PU-3436

NICU 极低出生体重儿真菌血流感染的危险因素及预后分析

姜波、朱敏
昆明医科大学第一附属医院

目的 探讨 NICU 极低出生体重儿真菌血流感染的危险因素及对患儿预后的影响。
方法 回顾性采集 2014 年 1 月至 2020 年 12 月入住昆明医科大学第一附属医院 NICU 的极低出生体重儿近平滑假丝酵母菌血流感染患儿 43 例，其中单独近平滑假丝酵母菌感染者 17 例（40%），合并一种或两种革兰阴性菌感染者 26 例（60%）进行血流感染的危险因素分析。
结果 17 例单独感染近平滑假丝酵母菌和 26 例混合感染患儿两组中进行单因素分析，分析表明合并凝血功能障碍、血小板减低和复查血培养阳性三个因素的差异具有统计学意义（P<0.05）。真菌感染使用抗生素导致菌群失调继而合并感染革兰阴性菌是影响患儿真菌血流感染预后的独立危险因素。
结论 合并凝血功能障碍、血小板减低和复查血培养阳性是 NICU 极低出生体重儿真菌血液感染的独立危险因素；而抗生素的使用导致菌群失调继而合并感染革兰阴性菌是影响患儿真菌血流感染预后的独立危险因素，应引起重视以改善预后。

PU-3437

金黄色葡萄球菌分子分型技术研究进展

谢跃
西安市第一医院

金黄色葡萄球菌（Staphylococcus aureus）是人类的一种重要病原菌，可引起多种严重感染，被认为是导致食物中毒、皮肤和组织感染、甚至菌血症和心内膜炎的主要人类病原体之一,如今MRSA(耐甲氧西林金黄色葡萄球菌)已成为全球院内感染的首要致病菌。研究报道表明，金黄色葡萄球菌特别是 MRSA 治疗的复杂性和困难性已引起医疗保健预算不断增加，造成了许多国家严重的医疗和经济问题，故减少金黄色葡萄球菌尤其是 MRSA 感染成为临床医学的一大挑战。快速准确的金黄色葡萄球菌分型方法，对于获得包括菌株来源、进化规律及流行病学在内的后续信息尤为重要,故就近年来金黄色葡萄球菌的分子生物学检测方法研究及发展趋势作一综述。

PU-3438

从慢性鼻窦炎患者分离多杀巴斯德菌与鉴定

王淑玲、颜 令、徐兰兰、张震 、廖璞
重庆市人民医院

目的 分析首次从慢性鼻窦炎患者分离的多杀巴斯德菌的鉴定、药敏和临床。
方法 采用生化反应鉴定和飞行时间质谱方法对此菌株进行鉴定，纸片法进行药敏试验，并对患者临床病史进行回顾。
结果 两种方法鉴定为杀巴斯德菌，对测试抗菌药物敏感，患者有宠物猫接触史。
结论 多杀巴斯德菌可以引起慢性鼻窦炎，实验室人员加强该菌的检测能力，医生应对动物源性的多杀巴斯德菌感染提高警惕，饲养宠物者应注意卫生。

PU-3439

布洛芬可促进肺上皮细胞对铜绿假单胞菌的抑制作用

俞娟、向雅婷、曹静
南通大学附属医院

目的 铜绿假单胞菌的耐药性严重，而耐药性与其 QS 系统密切相关。本研究旨在探索非抗生素布洛芬促进肺上皮细胞对铜绿假单胞菌的抑制作用。
方法 建立铜绿假单胞菌 PAO1 感染肺上皮细胞 A549，用 qRT-PCR 和 WB 技术分别检测感染前后 A549 中 PPARγ 和 PON-2 的表达，向感染了 PAO1 的 A549 细胞中加入布洛芬，分别检测加药前后 A549 中 PPARγ 和 PON-2 的表达。比较加入布洛芬前后 PAO1 对 A549 细胞的粘附数及粘附后布洛芬对 A549 细胞中细菌数的影响。
结果 肺上皮细胞 PPARγ、PON-2 的表达被铜绿假单胞菌抑制，且表达下降趋势趋于一致；在感染铜绿假单胞菌的肺上皮细胞中加入布洛芬后，PPARγ 和 PON-2 的表达明显升高；PON-2 随 PPARγ 的表达而增加，随 PPARγ 的表达而减少；加入布洛芬后，铜绿假单胞菌对肺上皮细胞的黏附数及共培养后细菌数较未加药下降；将 siPPARγ 处理后的肺上皮细胞感染铜绿假单胞菌，与未处理肺上皮细胞相比，siPPARγ 处理后的肺上皮细胞中铜绿假单胞菌数量明显增加。肺上皮通过表达 PPARγ 激活 PON-2 抑制铜绿假单胞菌，加入 siPPARγ 后，PON-2 的表达明显降低，对铜绿假单胞菌的抑制作用下降。当将布洛芬加入到 siPPARγ 处理后的肺上皮细胞时，铜绿假单胞菌的数量下降。
结论 布洛芬可促进 PPARγ 和 PON-2 在感染铜绿假单胞菌的肺上皮细胞中的表达；在肺上皮细胞中，PON-2 的表达受 PPARγ 调控；布洛芬可激活 siPPARγ 从而激活 PON-2 表达，促进肺上皮细胞抑制铜绿假单胞菌。

PU-3440

A potential control for blaKPC plasmid—blaCTX-M-15 plasmid

Weiwen Wang
Huashan Hospital, Fudan University

Purpose The KPC-producing Klebsiella pneumoniae has formed a long-term, large-scale, and high-positive rate spread around the world. Almost all blaKPC plasmids selectively invade the CG258 Klebsiella pneumoniae strains, but relevant mechanism is still unclear. The study aims to explore the molecular epidemiological characteristics of blaCTX-M-15 plasmid, which determines whether blaCTX-M-15 plasmid could be used as a good reference plasmid for studying blaKPC plasmid.
Methods The complete genome sequences of blaCTX-M-15(+) Klebsiella pneumoniae were obtained from Genbank database. Meanwhile, we collected blaCTX-M-15 positive clinical strains (including eight provinces and cities) and analyzed the molecular epidemiological characteristics of blaCTX-M-15 plasmids, including drug susceptibility and MSLT typing. And representative clinical strains were selected for whole-genome sequencing, and corresponding transposon structures and Inc typings were analyzed.
Results Our studies found that blaCTX-M-15 plasmid was randomly distributed in the CG258 and Non-CG258 isolates, and the genome analysis showed that blaCTX-M-15 plasmids were the IncF plasmid carrying the FII replicon (IncFII plasmid), which was consistent with blaKPC plasmid. And almost blaCTX-M-15 plasmids carry Tn3 type transposons. The previous study found that transposons of domestic blaKPC plasmid are of type Tn1721, which belongs to Tn3 family. The above results all confirm that blaCTX-M-15 and blaKPC plasmids are highly similar, but their distribution is significantly different.

Conclusion To clarify the blaKPC-CG258 dissemination is the key to studying the mechanism of large-scale spread of carbapenem-resistant Klebsiella pneumoniae. Our study found that the genetic Background of blaCTX-M-15 and blaKPC plasmids are similar, but their distribution types of strains are different. Based on the above results, blaCTX-M-15 plasmid may be a good control plasmid for studying the selective invasion of blaKPC plasmid into the CG258 strains, providing a new direction for in-depth exploration of the blaKPC-CG258 epidemic.

PU-3441

白血病患者皮肤软组织感染分析

许青霞
河南省肿瘤医院

目的 探讨革兰氏阴性杆菌引起致命性皮肤软组织感染的有效治疗方法。
方法 报道 2 例革兰氏阴性杆菌引起致命性皮肤软组织感染，复习文献，并探讨其发病机制。
结果 1 例患者为嗜水气单胞菌，1 例为嗜麦芽窄食单胞菌革兰氏阴性杆菌引起的皮肤软组织感染，出现皮肤红肿、大疱，大疱液恶臭难闻，进展迅速，最终抢救无效死亡。
结论 无创伤时出现皮肤软组织嗜水气单胞菌感染罕见，碳青霉烯类暴露是嗜麦芽窄食单胞菌多重耐药的风险因子。革兰氏阴性杆菌引起皮肤软组织感染罕见，且进展迅速，治疗效果不佳，应及早发现，寻找病原菌，合理应用敏感抗生素，延长生存时间。

PU-3442

两种基质辅助激光解吸电离飞行时间质谱系统对常见微生物鉴定结果的比较

伊贝拜汗买卖提
新疆生产建设兵团总医院

目的 比较进口质谱 A 和国产质谱 B 两种商业化基质辅助激光解析电离飞行时间质谱系统对常见微生物的鉴定一致性。
方法 收集 2019 年 9 月至 2020 年 1 月本实验室临床常规分离菌株共 762 株，采用扩展直接涂抹法平行使用两种质谱系统进行鉴定，鉴定结果不一致者采用 16S rDNA 基因测序予以确证。采用 SPSS18.0 软件对数据进行统计分析。
结果 762 株菌株质中革兰阴性杆菌(G-b)430 株，革兰阳性球菌(G+c)200 株，革兰阳性杆菌 52 株，革兰阴性球菌 17 株，真菌 63 株。762 株菌株质谱鉴定在种水平置信度得分和可信任得分水平中，进口质谱 A 和国产质谱 B 准确鉴定率分别为 89.6%(683/762)、79.7%(607/762)，在属水平鉴定中，准确鉴定率分别为 98.7%(752/762)、90.9%(693/762)。63 株真菌进口质谱 A 和国产质谱 B 在真菌属水平鉴定率分别为 98.4%(62/64)、76.2%(48/64)，在种水平鉴定率分别为 76.2%(48/64)、52.4%(33/64)。430 株 G-b 中进口质谱 A 和国产质谱 B 在属水平鉴定率分别为 97.9%(422/430)、92.3%(398/430)，200 株 G+c 中进口质谱 A 和国产质谱 B 在属水平鉴定率分别为 100%(200/200)、180%(180/200)
结论 两种质谱系统对常见微生物鉴定有很好的一致性。依据质谱系统的鉴定分值评判原则，进口质谱 A 在种可信水平上的准确鉴定率较高。

PU-3443

甲型和乙型副伤寒沙门菌同时暴发流行事件的临床特征及菌株药物敏感性分析

伊贝拜汗买卖提
新疆生产建设兵团总医院

目的 对一起甲型和乙型副伤寒沙门菌同时暴发流行事件中的患者临床特征及菌株药物敏感性进行分析，为不同型别副伤寒同时暴发流行的防治提供参考。
方法 收集 2018 年 9 月到 11 月间新疆生产建设兵团医院副伤寒确诊病例及疑似病例临床资料进行回顾性分析，并对副伤寒沙门菌分离株进行药物敏感性分析。
结果 研究纳入副伤寒确诊病例 31 例和疑似病例 35 例，所有病例均为乌鲁木齐市某中学高中年级学生，其中 22 例男性、44 例女性，平均年龄为 16.22±0.57 岁。患者首发症状均为发热，部分患者伴有全身中毒症状及消化道症状，一般实验室检查以 PCT、CRP 异常升高为主。31 例确诊病例共分离 32 株副伤寒沙门菌，血清学分型为甲型 19 株、乙型 13 株。所有菌株对环丙沙星的中介率为 100%，对氨苄西林、复方新诺明、头孢他啶、头孢曲松、氯霉素的敏感率均为 100%。
结论 甲型和乙型副伤寒沙门菌同时传播具有临床表现典型及环丙沙星药物敏感性差的特点，应引起实验室及临床的高度关注。

PU-3444

维持性血液透析患者病原菌感染特点及耐药性分析

伊贝拜汗买卖提、王海叶
新疆生产建设兵团总医院

目的 通过回顾性分析 2016~2018 年维持性血液透析（MHD）患者的临床资料，分析 MHD 患者发生感染的相关因素及病原菌感染特点，为降低患者的感染发生率提供一定的理论依据。
方法 采用自动化仪器对临床分离菌株进行鉴定及药物敏感性试验，采用 CLSI M100-S27 标准判断药敏结果及 WHONET 5.6 软件进行数据分析。
结果 MHD 患者感染以血流感染为主占 39.8%，其次为泌尿系统和呼吸系统感染，分别占 26.1%和 18.8%；共分离 178 株病原菌，革兰阴性菌 85 株（47.8%），革兰阳性菌 79 株（44.4%），真菌 14 株（7.8%）；肺炎克雷伯菌和大肠埃希菌对头孢 1 代～3 代耐药率高于 68%，对亚胺培南、美罗培南、哌拉西林/他唑巴坦耐药率为 0，金黄色葡萄菌及表皮葡萄球菌对苯唑西林耐药率分别为 23%和 81%，革兰阳性菌对替考拉宁、万古霉素、利奈唑胺、替加环素耐药率为 0。
结论 MHD 患者病原菌以革兰阴性菌为主，病原菌耐药性较为严重，应根据药敏结果及时选用有效抗菌药物进行治疗，以减少感染的发生。

PU-3445

临床流行鲍曼不动杆菌基因型演变的研究

袁晨燕
东南大学附属中大医院

目的 临床上鲍曼不动杆菌检出率逐年上升，其中超过一半都是碳青霉烯耐药的菌株（CRAB），近年来，临床观察发现，不同于之前的认识，高致病的鲍曼不动杆菌逐渐出现。由于鲍曼不动杆菌可以耐药医院环境，耐药菌株对多数抗生素都不敏感，可以导致大规模的院内感染，高毒力菌株的出

现和流行将严重威胁患者生命对，研究十年来本院鲍曼不动杆菌流行的基因型可以为感染监控以及流行病学调查提供有力的支持。
方法 使用十年来临床分离的鲍曼不动杆菌菌株共 98 株，时间跨度为 10 年，使用 MLST 分型的方法对所有菌株进行分型，并利用 GeoBurst 软件分型菌株亲缘关系，利用 MAGA 软件绘制菌种进化图。
结果 十年前流行的鲍曼不动杆菌基因型与现在流行的型别有很大的差异，亲缘关系和进化关系显示，目前流行的鲍曼不动杆菌由之前的型别进化而来。
结论 鲍曼不动杆菌基因组出现进化趋势，可能已经获得毒力基因。

PU-3446

2020 年丹东市第一医院临床检出前 5 位病原菌的细菌耐药性分析

刘国强
丹东市第一医院

目的 对 2020 年丹东市第一医院临床送检标本分离出阳性菌株进行统计分析，检出前 5 位菌，按照全国细菌监测网主要监测的耐药机制和耐药指标进行分析。为全国细菌耐药网提供准确数据的同时，也为临床发布耐药分析，合理指导临床抗生素合理应用和控制。
方法 临床检出阳性标本的 1230 株菌进行分析和计算，使用贝克曼半自动微生物鉴定仪 MicroScan AutoScan-4.鉴定试剂采用 NCU61 和 PC33 以及迈瑞天地人公司微生物鉴定仪 TDR-200C 和配套检测试剂 TDR STAPH-96 和 TDR NF-96、TDR ONE-96。
结果 检出大肠埃希菌 297 株，占 24.1%；检出肺炎克雷伯菌 172 株，占 14%；检出铜绿假单胞菌 134 株，占 10.9%；检出鲍曼不动杆菌 99 株，占 8%；检出金黄色葡萄球菌 63 株，占 5.1%；其中大肠埃希菌中：碳青霉烯类耐药(CRECO)11 株，占 54.4%；三代头孢耐药 129 株，占 47.4%；产 ESBLs 菌株 148 株，占 54.4%。肺炎克雷伯菌中：碳青霉烯类耐药(CRKPN)7 株，占 4.4%；三代头孢耐药肺炎克雷伯菌 43 株，占 27.2%；产 ESBLs 菌株 41 株，占 25.9%.
铜绿假单胞菌：碳青霉烯类耐药铜绿假单胞菌（CRPAE）26 株，占 20.6%。鲍曼不动杆菌：碳青霉烯类耐药不动杆菌（CRAB）68 株，占 77.3%；金黄色葡萄球菌：耐甲氧西林金黄的葡萄球菌（MRSA）14 株，占 22.2%。
结论 随着广谱抗菌药物的广泛应用，抗菌药物的耐药性也在逐年增加，抗菌药物已越来越难以应对感染病原体。过度使用抗菌药物和临床无指征的预防用药及治疗用药；尤其是医师对用药指征掌握不必然导致细菌耐药性的产生和耐药率的增加。因此为有效地治疗感染性疾病并减少耐药菌株在院内的流行与传播。临床用药需要依据微生物学检验结果和药敏情况选择用药。

PU-3447

铜绿假单胞菌细菌生物膜形成及对抗生素敏感性的影响

袁晨燕
东南大学附属中大医院

目的 比较临床上使用的两种硅胶生物材料形成生物膜的难易程度，研究细菌生物膜形成对耐药性的影响，以指导临床合理使用材料和用药选择。
方法 经细菌孵育两种硅胶生物材料（硅胶眼科植入物环扎带，硅胶导尿管）制备生物膜模型，通过银染法直接观察生物膜形成情况并用扫描电镜观察生物膜的形态。测定游离细菌的 MIC 值及 MBC 值与形成 bbf 后的 MEBC 值，二者比较。

结果 两种不同硅胶材料的生物膜经银染后观察，导尿管上更易形成 BBF，又进一步经扫描电镜证实，硅胶导尿管材料制备的生物膜表面可观察到大块 BBF。游离细菌 MIC 与 BBF 的 MEBC 间比较，差异有统计学意义。
结论 硅胶眼科植入物环扎带较硅胶导尿管不容易形成 BBF；形成 BBF 后，细菌的耐药性增加。

PU-3448

梅毒螺旋体假定蛋白 Tp0259 促炎活性初步研究

谢亚锋
南华大学附属第二医院

目的 探讨梅毒螺旋体(Treponema pallidum,Tp)假定蛋白 Tp0259 的促炎活性并初步分析其可能机制。
方法 去除重组蛋白 Tp0259(rTp0259)中的内毒素，然后以其刺激 THP-1 细胞，ELISA 检测促炎细胞因子 IL-1β、IL-6 和 IL-8 的表达水平。ERK1/2、JNK、p38 和 NF-κB 特异性抑制剂分别预处理 THP-1 细胞 30min 后以 rTp0259 刺激 THP-1 细胞，ELISA 检测 IL-1β、IL-6 和 IL-8 的表达水平。
结果 rTp0259 在一定范围内以时间和剂量依赖方式刺激 THP-1 细胞表达 IL-1β、IL-6 和 IL-8，3.0μg/mL 刺激 24h 时各细胞因子表达水平最高。rTp0259 刺激经 ERK1/2、JNK、p38 和 NF-κB 特异性抑制剂预处理后的 THP-1 细胞，IL-1β、IL-6 与 IL-8 表达水平均明显下降 (P＜0.01))。
结论 rTp0259 可能通过 MAPK 和 NF-κB 通路诱导 THP-1 细胞表达促炎细胞因子 IL-1β、IL-6 和 IL-8，可能是 Tp 新的致病因子。

PU-3449

回顾性分析鲍曼不动杆菌血流感染的临床特征和结局

张肃川
自贡市第一人民医院

目的 探究血流感染鲍曼不动杆菌患者的临床特征、临床结局、危险因素及抗生素治疗。
方法 纳入自贡市第一人民医院 2015 年至 2019 年符合纳入与排除标准的患者 40 例，收集人口学资料、临床特征、基础疾病、抗菌药物治疗方案。根据 30 天预后分为死亡组（16 例）和存活组（24 例）和是否耐碳青酶烯类分为耐碳青酶烯类组（28 例）和非耐碳青酶烯类组（12 例），通过 COX 回归和 logistics 回归探究危险因素，K-M 法绘制生存曲线，对数秩检验比较生存率差异。
结果 鲍曼不动杆菌血流感染死亡率 40%。单因素分析发现糖皮质激素使用（HR=3.3, P=0.02）、PBS（HR=1.4, P=0.002）、脓毒性休克（HR=86.0, P=0.03）、不恰当经验性治疗（HR=8.9, P=0.04）是 30 天死亡的危险因素；多因素分析发现：PBS（HR=1.6, P＜0.01）是 30 天死亡的独立危险因素。对 CRAB 组和非 CRAB 组单因素分析显示：侵入性操作（OR=19.3, P=0.01）、入住 ICU（OR=25, P＜0.01）、入住 ICU 时间（OR=1.1, P=0.04）、抗生素暴露（OR=65, P＜0.01）、PBS（OR=2.1, P＜0.01）是感染 CRAB 的危险因素，多因素分析发现：抗生素暴露是感染 CRAB 的独立危险因素（OR=28.1, P＜0.01）。生存分析显示：与 CRAB 组和非 CRAB 组存在明显差异（P＜0.01），对治疗方案进行分析发现：包含替加环素方案与无替加环素方案死亡率没有明显差异（75% vs 50%，P=0.4）。
结论 鲍曼不动杆菌血流血流感染病死率高，感染前糖皮质激素使用、感染时 PBS 高、合并脓毒性休克、不恰当经验性治疗提示不良预后，侵入性操作、入住 ICU、入住 ICU 时间长、抗生素暴露、PBS 与发生碳青酶烯类耐药相关。以替加环素为基础的方案没有明显增加死亡率。

PU-3450

Serotype, antimicrobial resistance patterns and virulence genes of salmonella isolated from the intestinal tract

yue wang
Joint Logistics Support Unit 903 hospital

Salmonella (Salmonella. spp) is a zoonotic gram-negative pathogen in the Enterobacteriaceae family. It is mainly infected by the mouth after contaminating food and water sources, causing salmonellosis in humans and animals. Its clinical manifestations are gastroenteritis, food Poisoning, bacteremia, typhoid fever and paratyphoid fever, enteric fever, etc. According to reports, diseases caused by isolated Salmonella infection outside the intestine, such as bacteremia, gastrointestinal bleeding, intestinal perforation, and typhoid encephalopathy, etc., even if given appropriate antibacterial treatment, the mortality rate cannot be ignored [1]. In recent years, due to the abuse of antimicrobial drugs, the drug resistance of Salmonella has become more and more serious, and there are different degrees of resistance to one or more antimicrobial drugs, especially fluoroquinolones (the first choice) drug resistance, which brings clinical treatment Difficulty [2]. The pathogenicity of salmonella is related to its virulence factors. The pathogenicity of salmonella involves multiple virulence factors encoded by different genes, including virulence island genes (hilA, ssrB, marT, siiD, sopB, pagN, vexA), Virulence plasmid gene (icmF, spvB), pili operon virulence gene (pefA), and Cytotoxin (cdtB). These virulence factors help Salmonella to invade, multiply, exert virulence, and spread in a complex environment [3]. A variety of virulence genes are involved in the expression, and the higher the virulence gene carrying rate, the stronger the potential pathogenicity of Salmonella [4]. This study conducted a study on extra-intestinal Salmonella clinically isolated from the 903th Hospital of the Joint Logistics Support Force of the People's Liberation Army from 2016 to 2018, clarified its serotype distribution, antimicrobial resistance, and virulence gene distribution, and formulated preventive measures which provide a scientific basis for guiding the rational use of drugs in clinical practice.

PU-3451

田鼠巴贝虫颈部蛋白 2 的克隆、表达及蛋白特性分析

杨春利
中国人民解放军 903 医院

目的 为了获得田鼠巴贝虫颈部蛋白 2（RON-2），并对该蛋白特征进行分析。
方法 根据 PubMed 中田鼠巴贝虫颈部蛋白基因 1 已知序列，设计相应的引物，构建田鼠巴贝虫的动物模型，提取巴贝虫总 RNA，反转录，PCR 扩增该蛋白基因，构建重组质粒 pET30a-RON-2，异丙基-β-D-硫代半乳糖苷（IPTG）诱导表达。用 Ni+离子亲和层析柱纯化其重组蛋白，十二烷基磺酸钠-聚丙烯酰胺凝胶电泳（SDS-PAGE）鉴定其表达效果。
结果 成功确定田鼠巴贝虫棒状体蛋白基因，该基因该基因全长为 4443bp，只有 1 个开放阅读框架，可编码 1 480 个氨基酸。编码蛋白分子质量为 165.307 KDa，为分泌蛋白，含一个信号肽，4 个跨膜区，并含有较多抗原表位，并构建了重组质粒 pET30a-RON-2，SDS-PAGE 结果表明该蛋白基因在 Ecoli DHa 中获得良好的表达，经亲和层析纯化后，表达产物分质量约为 32.7KD 和 29.1KD。
结论 克隆表达了田鼠巴贝虫颈部蛋白，经纯化后获得较高纯度的重组蛋白，并对三级结构进行分析，为进一步研究该蛋白的结构和功能奠定了理论基础。

PU-3452

The Emergence of Multidrug-Resistant Candida duobushaemolnii : Using Whole-Genome Sequencing to Describe the Population Structure of Candida duobushaemolnii

Xinfei Chen、Meng Xiao、Xinmiao Jia、Xin Hou、Yingchun Xu
Peking Union Medical College Hospital

Background The emergence of a multidrug-resistant yeast, *Candida auris*, has drawn attention to the closely related species from the *Candida haemulonii* complex includeing *C. haemulonii*, *C. duobushaemulonii*, *C. pseudohaemulonii*, and *C. haemulonii var. vulnera*. The goal of this study was to investigate the genetic relationships and drug-resistance profiles among isolates of the *C. haemulonii* from different cities and to examine possible evidence of transmission if it existed.
Materials/Methods The12 *C. duobushaemulonii* isolates causing invasive fungal diseases were collected from nine tertiary hospitals through CHIF-NET. We used antifungal susceptibility testing and whole-genome sequencing (WGS) to investigate drug resistance and genetic diversity among isolates of *C. duobushaemulonii* from different geographic areas of China.
Results Between 2010 and 2017, 12 isolates of *C. duobushaemulonii* from China; In the China, 41.7% of *C. duobushaemulonii* was isolated from blood, and other invasive sites (Table 1). Phylogenetic analysis using SNPs called against the *C. duobushaemulonii* reference strain B09383. Genetic relationships among *C. duobushaemulonii* isolates are shown in (Figure 1). The average pairwise difference between the isolates was 691 SNPs (range 15–1273), and there was distinct phylogeographic population structure.
Three isolates, F4444, F4464 were different from each other by fewer than 15 SNPs. These two isolates were recovered from the same patients. In addition, two isolates, F4490, F4560, differed by fewer than 90 SNPs recovered from difference hospital. We observed high levels of susceptibility to amphotericin B among 12 tested Candida duobushaemulonii isolates: all had elevated MICs from 4μg/mL to >8μg/ ml. All isolates had elevated MICs of fluconazole ranging from 64 to 256μg/ml (Table 2). Interesting, these isolates don't have the known mutation in ERG11, only with synonymous mutation.
Conclusions Our results indicate that, although we are not observing the widespread of the *C. duobushaemulonii*, at least these isolates had elevated MICs of fluconazole. We need to investigated the antifungal-resistance mechanism.

PU-3453

下呼吸道感染常见病原菌耐药性分析

严纪梅
滨州医学院烟台附属医院

目的 收集所在医院 2019 年下呼吸道感染标本，分析主要病原菌构成和耐药特点,为本地下呼吸道感染的治疗和抗菌药物的应用提供参考。
方法 收集本医院 2019 年 1 月-2019 年 12 月下呼吸道感染病人的 8634 份痰标本,分离得到致病菌的数量是 2379,使用自动化仪器对病原菌实现鉴定和耐药检测（MIC 法）,并对病原菌分布和耐药率的数据进行分析处理。
结果 2379 株病原菌中，数量最多的细菌为肺炎克雷伯菌（K. pneumonia）、铜绿假单胞菌（P. aeruginosa）、鲍曼不动杆菌（E. cloacae）、白假丝酵母菌（C. albicans）、金黄色葡萄球菌（S. aureus）。G+菌共 216 株，占比为 9%，金葡菌共 156 株，占所有菌株数量的 7%,其次是肺炎链球菌、棒状杆菌、诺卡氏菌、溶血葡萄球菌。G-细菌共 1664 株,占总菌株 70%,真菌共 499 株,

占所有病原菌数量的 21.0%,在 2379 株病菌中，白假丝酵母菌共 259 株，占 11.0%。细菌耐药检测结果显示,糖肽类抗菌药物对和 SPN 的效果较好，没有发现耐药菌。除去鲍曼不动杆菌，对 G-菌效果较好的药物有阿米卡星（Amikacin，AMK）、碳青霉烯类（Carbapenems, CPMS）和头孢唑酮-舒巴坦（CSL）等。

结论 2019 年本院患者下呼吸道感染的病原菌以 G-为杆菌主，鲍曼不动杆菌对多种药物都表现出较高的耐药率，产超广谱内酰胺酶 ESBLs 细菌和 MRAS 值得注意。应对下呼吸道感染致病菌进行检测和耐药分析，及时发现问题并应用于临床和医院感染管理。

PU-3454

2019 年烟台地区小儿肺炎痰培养病原菌分布及耐药分析

李文文
滨州医学院烟台附属医院

目的 研究 2019 年本院小儿肺炎患者病原菌的分布及药物敏感性。

方法 对本院 410 例小儿肺炎患者进行痰培养以及药敏分析。

结果 410 例痰标本中检出细菌 109 株，阳性率 26.59%；革兰阴性杆菌 77 株（70.64%），革兰阳性杆菌 32 株（29.36%），检出的细菌依次为肺炎链球菌 30 株（27.52%）、卡它莫拉菌 45 株（41.28%）、流感嗜血杆菌 31 株（28.44%）、金黄色葡萄球菌 2 株（1.84%）、大肠埃希菌 1 株（0.92%）。以上细菌对常用的头孢类、亚胺培南、美罗培南敏感性较高，对青霉素、氨苄西林类药物耐药。革兰阴性菌对头孢类、红霉素、亚胺培南敏感性较高，对氨苄西林敏感性较低。

结论 本院的小儿肺炎患者培养的致病菌以革兰阴性杆菌为主，不同病种对抗菌药物存在差异。

PU-3455

The Emergence of Multidrug-Resistant Candida auris : Using Whole-Genome Sequencing to Describe the Population Structure

Xinfei Chen、Meng Xiao、Xinmiao Jia 、Xin Hou、Yingchun Xu
Peking Union Medical College Hospital

Background The emergence of a multidrug-resistant yeast, *Candida auris*, has drawn attention to allover the world. The goal of this study was to investigate the genetic relationships and drug-resistance profiles among isolates of the *Candida asuris* from different counties and to examine possible evidence of transmission if it existed.

Materials/Methods The 6 *Candida auris* isolates causing invasive fungal diseases were collected from one tertiary hospitals through CHIF-NET. We used antifungal susceptibility testing and whole-genome sequencing (WGS) to investigate drug resistance and genetic diversity among isolates of *Candida auris* from different geographic areas of China.

Results Between 2017~2018, 6 isolates of *Candida auris* from China; 5 (83%) of *Candida auris* was isolated from blood (Table 1). Phylogenetic analysis using SNPs called against the *Candida auris* reference strain B8441. Genetic relationships among *Candida auris* isolates are shown in (Figure 1). The average pairwise difference between the isolates was 1200 SNPs, and there was distinct phylogeographic population structure. Five isolates, F6410, F6412, F6414, F6416, F6418, F6420, were different from each other by fewer than 40 SNPs. These isolates These isolates were recovered from difference patients. In addition, one isolates, F6410 recovered from difference hospital different from each other by fewer than 40 SNPs. We observed high levels of susceptibility to amphotericin B among 6 tested Candida auris isolates: all had elevated MICs

from 2μg/ml to 4μg/ ml. All isolates had elevated MICs of fluconazole ranging from 256 to >256μg/ml (Table 2).
Conclusions Our results indicate that, we are observing the widespread of the *Candida auris* and these isolates had elevated MICs of fluconazole. We need to investigated the antifungal-resistance mechanism.

PU-3456

结核病的诊断与治疗及其研究进展

邹燕萍
中国人民解放军第一一七医院

目的 结核病（TB）是由结核分枝杆菌（MTB）引起的空气传播疾病，通常会影响肺部，导致严重的咳嗽，发烧和胸闷等。结核病也是世界范围内传染病最常见的死亡原因之一。尽管近期一系列的研究为结核病的传播，诊断和治疗提供了宝贵的见识，但要有效降低结核病的发病率并最终根除结核病，还有许多工作要做。结核病给世界范围内的公共健康带来了极大的压力，其在造成高死亡率方面仅次于艾滋病毒/艾滋病，引起了公共卫生领域和社会界的广泛关注。本文将从结核病的历史，流行病学分析，发病机理以及结核病免疫应答，治疗和控制等方面对其进行综合阐述。
方法 对目前国内外结核分枝杆菌进行回顾性分析。
结论 人们对结核病的认识从 19 世纪不断发展。然而，为了开发更加有效的治疗结核病的药物和疫苗，我们需要更全面地了解结核病的病理性免疫应答及其与免疫系统的相互作用。有研究表明，可以通过测量个体的转录特征，对疾病进行更个体化的监测。从而帮助减少 MDR 病例的数量，更好的替代 DOTS 疗法。值得注意的是，结核病自 19 世纪被发现以来便对公众健康构成了严重的威胁，但人们在对其的治疗研究等方面的进展一直是徒劳和缓慢的。在这场结核病作斗争的竞赛中，我们有必要从宏观角度对结核病有一个明确的了解。只有在社会各界的合作努力下，才能不断推进人们对结核病有新的认识，减轻结核病给全球带来的负担。

PU-3457

滨医附院 2017-2019 年感染铜绿假单胞菌的临床分布和耐药性分析

马静哲
滨州医学院烟台附属医院

目的 分析滨医附院 2017-2019 年间铜绿假单胞菌的临床分布和耐药性情况，为医院内感染监控提供参考数据，指导临床的合理用药。
方法 收集滨医附院 2017-2019 年间各临床科室送检的细菌培养标本，用常规办法对细菌进行分离培养，采用 VITEK MS IVD3.0 质谱仪鉴定病原菌，以及 Vitek2-Compact 全自动细菌药敏系统对病原菌进行药敏分析，并进行数据统计分析。
结果 2017-2019 年该院共分离 1029 株铜绿假单胞菌非重复菌株，其中临床分离痰标本最多，占 67.4%（694 株），其次为脓液占 7.1%（73 株）和分泌物占 5.9%（61 株）；在临床分布的情况中可以发现分布最多的为呼吸内科（18.0%）其次是泌尿外科（13.3%）和老年医学科（12.9%）；铜绿假单胞菌耐药率最高的是氨曲南（25.2%），耐药率最低的为阿米卡星（3.6%），而且调查发现，铜绿假单胞菌对碳青霉烯类药物的耐药率在一直在升高以及多重耐药铜绿假单胞菌的检出率也越来越高。
结论 耐碳青霉烯类铜绿假单胞菌的检出率呈上升趋势，结合药敏试验的结果，可以选择氨基糖苷类的妥布霉素和氟喹诺酮类的左氧氟沙星对铜绿假单胞菌进行抗感染治疗。

PU-3458

130 株阴沟肠杆菌耐药分析

贺莎莎
滨州医学院烟台附属医院

目的 研究医院内临床分离阴沟肠杆菌(ecl)的耐药情况，以及科室分布情况，为临床合理应用抗菌药物提供依据。
方法 收集医院 2019 年各临床科室分离阴沟肠杆菌(ecl)，采用美国 BD PHOENIX-100 全自动细菌鉴定/药敏分析系统进行菌株鉴定及药敏试验；血液培养采用法国梅里埃 3D 血培养仪；采用 WHONET5.6 软件对数据进行分析。
结果 阴沟肠杆菌对氨苄青霉素（AMP）、头孢菌素 V(CFZ)、头孢呋肟(CXM)、头孢西丁（CFX）、氨苄西林（AMP）/舒巴坦天然耐药，其次是头孢他啶(CAZ)、头孢曲松(CRO)、头孢哌酮(CFP)耐药率分别为 79.0%、28.7%、6.5%，氨苄青霉素(AMP)，替卡西林(TIC)，哌拉西林(PRL)耐药率分别为 98.9%，45.6%，32.3%，对阿米卡星(AK)等氨基糖苷类耐药率 83.6%。
结论 医院分离的阴沟肠杆菌骨外科检出率最高。除天然耐药的抗菌药物外的常用抗菌药耐药率均低于 30%，临床医生可以根据药敏试验选择抗菌药物。

PU-3459

铜绿假单胞菌的临床分布和耐药性分析

王熠
滨州医学院烟台附属医院

目的 了解医院内铜绿假单胞菌的临床分布和耐药性，对医院临床合理用药进行指导，从而能够及时切断多重耐药菌株的传播。
方法 收集 2018 年 6 月-2020 年 5 月医院住院患者分离的 280 株不重复铜绿假单胞菌，然后分析该菌的临床分布和耐药性。
结果 分离的 280 株铜绿假单胞菌主要分布在 ICU、呼吸内科、神经内科、神经外科、感染科等。其中标本主要来自痰液。根据药敏结果显示，复方新诺明的耐药率是最高的，占 80.4%，其次是哌拉西林，占 57.1%，而亚胺培南和美罗培南的耐药率是最低的，分别是 6.1%、5.4%。
结论 铜绿假单胞菌作为院内感染的主要机会致病菌之一，并且它的耐药机制较为复杂，并还具有多重耐药的特性。因此，应加强铜绿假单胞菌临床耐药性的监测，在临床治疗中，及时考虑其药敏结果，合理使用抗菌药物。

PU-3460

某儿童医院 2017 年-2019 年金黄色葡萄球菌的分布与耐药性分析

逯思显
呼和浩特金域检验所有限公司

目的 通过对某儿童医院 2017-2019 年就诊儿童中感染的金黄色葡萄球菌进行统计分析，加强对金黄色葡萄球菌耐药性的监测，从而为儿科合理使用抗生素提供更好的依据。
方法 回顾性分析某儿童医院 2017-2019 年各类临床标本中分离得到的金黄色葡萄球菌共 6387 株，利用 WHONET 5.6 系统收集 VITEK-2 Compact 全自动细菌鉴定药敏仪得到的金黄色葡萄球菌的药敏实验结果。

结果 某儿童医院检验中心微生物室在 2017-2019 年共分离得到金黄色葡萄球菌 6387 株，其中耐甲氧西林金黄色葡萄球菌（MRSA）1530 株（24.3%），其主要标本来源为痰液及咽拭子，约占 50.9%。药敏结果显示，检出的金黄色葡萄球菌对青霉素 G 的耐药率最高，其次为红霉素、苯唑西林、克林霉素、四环素，耐药率依次为 92.5%、50.1%、24.5%、22%、19%，对庆大霉素、利福平、左旋氧氟沙星、莫西沙星、呋喃妥因、利奈唑胺、万古霉素、替加环素高度敏感，敏感率均大于 95%，且目前尚未检出有对利奈唑胺、替加环素中介或耐药的菌株。
结论 某儿童医院检出的金黄色葡萄球菌主要来源于痰液、咽拭子，提示该院金黄色葡萄球菌感染的患儿以呼吸道感染多见，检出主要以 MSSA 为主，但金黄色葡萄球菌及 MRSA 的检出率均呈现出逐年上升的趋势，且对苯唑西林、庆大霉素、环丙沙星、左旋氧氟沙星、莫西沙星的耐药性也有所上升，提示临床上应根据药敏试验结果合理使用抗生素，加强儿童感染金黄色葡萄球菌的耐药监测，以减缓耐药菌株的出现。

PU-3461

腹透相关性新型隐球菌腹膜炎 1 例报道

陈士颖、杨爽
上海交通大学医学院附属仁济医院(东院)

腹透相关性腹膜炎是腹膜透析最常见的并发症，也是导致腹膜透析技术失败和患者死亡的主要原因。导致腹膜炎的致病菌中，50%以上为革兰阳性细菌，最常见凝固酶阴性的葡萄球菌和金黄色葡萄球菌。真菌性腹膜炎只占 3%-6%，但由真菌导致的腹膜炎死亡率达 20-30%。成人真菌性腹膜炎最常见的致病菌为酵母菌，70%-90%为念珠菌属。由隐球菌引起的腹透相关性腹膜炎比较罕见。现报道一例由新型隐球菌感染致腹透相关性腹膜炎，最终发展为散播性隐球菌病的病例。

PU-3462

肠道菌群与动脉粥样硬化

王新铭
哈尔滨医科大学附属第一医院

肠道菌群平衡指的是在肠道中所存在的多种微生物之间所保持的比例的，动态的，相对的平衡。动脉粥样硬化的特点是受累动脉的病变从内膜开始，先后有脂质积聚、纤维组织增生和钙质沉着，并有动脉中层的逐渐退变和钙化，在此基础上继发斑块内出血、斑块破裂及局部血栓形成。近年来越来越多的研究表明肠道菌群与心血管疾病关系密切，肠道菌群失衡极有可能是引起冠状动脉粥样硬化性心脏病的高危因素。

PU-3463

血培养病原菌分布和药敏分析

王雅江
雅安市人民医院

目的 统计四川省雅安市地区三甲医院市人民医院从 2018 年 1 月到 2018 年 12 月共计一年时间内的所有住院病人和门诊病人血培养病原菌鉴定结果并根据病原菌的种类进行药敏试验，最终指导临床合理的经验用药。

方法 使用 BacT/ ALERT 3D240 全自动血培养仪对血培养瓶进行培养，仪器报阳后立即转种并做革兰染色涂片，用布鲁克质谱仪进行血培养病原菌的鉴定，用 VITEK2 COMPACT 进行药敏试验，采用 WHONET 5.6 软件进行药敏试验分析。
结果 在该次试验中，总计 12541 瓶培血培养瓶标本中有 985 瓶报阳，共计 498 人次阳性，革兰阳性菌有 149 人次，构成比约为 29.92%，主要为金黄色葡萄球菌。革兰阴性菌有 337 人次，构成比约为 67.67%，主要为大肠埃细菌和肺炎克雷伯菌。真菌 12 人次，构成比约为 2.41%，均为酵母菌属。金黄色葡萄球菌的敏感性主要体现在对万古霉素、利奈唑胺、替加环素 100%的敏感，对红霉素的耐药率达到 62.31%，对青霉素的耐药率更高为 94.51%。肺炎克雷伯菌和大肠埃希菌在抗菌药物的敏感性上高的多为阿米卡星和亚胺培南等，在耐药性的表现上则是复方新诺明和头孢曲松等耐药。
结论 该次血培养试验统计中病原菌种类复杂，主要病原菌为革兰阳性球菌和革兰阴性杆菌，真菌查出率很低，其中又以大肠埃希菌（44.58%）肺炎克雷伯菌（10.04%）以及金黄色葡萄球菌（4.22%）构成比最高，根据血培养阳性鉴定后病原菌的药敏试验结果，指导临床合理经验用药和避免抗菌药物滥用有重要临床意义。

PU-3464

围产期生殖道分泌物无乳链球菌分布状况及耐药分析

徐红云、刘春林、陈弟、马众仙、杨宝瑞、余林、袁文丽、吴广娟、赵珠、杨文波
云南大学附属医院/云南省第二人民医院

目的 探讨围产期孕妇阴道分泌物无乳链球菌（GBS）的分布状况及耐药性分析，为临床预防性治疗提供依据。
方法 回顾性分析 2016 年 1 月-2020 年 12 月围产期孕妇送检的 7218 例阴道分泌物进行 GBS 筛查及体外药敏试验的结果。
结果 7218 例围产期孕妇阴道分泌物，共分离到 472 株 GBS，检出率为 6.54%，GBS 对青霉素、氨苄西林及万古霉素 100%敏感，对克林霉素、红霉素的耐药率在 60 %以上。
结论 围产期孕妇 GBS 的筛查对围产期孕妇感染诊断中具有重要的意义，GBS 的筛查对于临床医师及时进行干预，对于预防产妇和新生儿并发症的发生，减少婴儿及产妇的感染有非常重要的意义。针对携带无乳链球菌的围产期孕妇预防用药，可以首选青霉素，对于青霉素过敏者及其他细菌感染可根据药敏结果选用合适抗菌药物。

PU-3465

2019 年到 2020 年肺炎克雷伯菌的耐药性和应对方法

罗雅文
雅安市人民医院

目的 根据 2019 年到 2020 年一整年雅安市人民医院微生物室培养出肺炎克雷伯菌耐药的耐药分析研究，并探讨其战略，以提供临床依据。
方法 将痰液标本接种在琼脂培养基上并进行分离培养、 鉴定和药敏试验。
结果 检出肺炎克雷伯菌 535 例，敏感率在百分之九十以上的药物有：阿米卡星、哌拉西林/他唑巴坦、环丙沙星、头孢他啶、庆大霉素、头孢替坦、氨曲南、厄他培南、亚胺培南、妥布霉素、左旋氧氟沙星。其中耐药率最高的药物是氨苄西林，耐药率达到了 69.7%，其次为呋喃妥因，耐药率为 33.6%。对氨苄西林/舒巴坦、头孢唑林、头孢曲松、复方新诺明的耐药率为 14%-20%。
结论 肺炎克雷伯菌在临床上的耐药趋势越来越严重，我们应对其耐药趋势进行监测，及时控制耐药菌的流行传播。

PU-3466

不同痰液标本结核杆菌染色结果比较

杨名宇
雅安市人民医院检验科

目的 了解不同时间段,不同性状痰标本结核杆菌抗酸阳性率的大小，能更好的选择痰标本进行抗酸染色,节约成本。
方法 采用抗酸染色对 3756 例痰液标本进行染色镜检，痰液标本按时间和性状的不同分别分类，比较不同时间，不同性状痰液阳性率高低。
结果 对 3756 份标本进行镜检，其中 437 份培养为阳性，阳性率为 11.0%。按照咳痰时间进行分类，痰染色阳性率由高到低排序结果为：晨痰（16.0%）大于夜间痰（11.0%）大于即时痰（7.0%），三者比较有显著差异。按痰液性状进行分类，痰染色阳性率由高到低排序结果为：干酪痰阳性率（21.9%）大于粘液痰阳性率（15.0%）大于血痰阳性率（12.1%）大于唾痰阳性率（9.6%），四者相比同样有明显差异。
结论 痰涂片染色从时间上最佳选择是晨痰，性状上最佳选择是干酪痰。

PU-3467

新生儿无菌体液感染的细菌耐药性及危险因素分析

向丹[1]、张秀瑜[2]、何霞[1]
1. 雅安市人民医院检验科
2. 重庆医科大学附属第二医院检验科

目的 探讨新生儿无菌体液感染的细菌耐药性及危险因素，为临床合理用药、科学诊治提供依据。
方法 选取 2017 年 1 月-2020 年 1 月雅安市人民医院收治的 114 例无菌体液感染的新生儿作为研究对象，回顾性分析其病原学特点、临床特征及危险因素。
结果 114 例新生儿无菌体液感染以凝固酶阴性葡萄球菌最常见，低出生体重儿、羊水污染、入住暖箱、联合使用抗菌药物较非无菌体液感染患儿多见（P＜0.05），无菌体液感染患儿住院时长、抗生素使用时间较非无菌体液患儿长（P＜0.05）；单因素分析显示性别、羊水污染、入住暖箱、使用激素、联合使用抗菌药物、留置胃管、气管插管、抗菌药物使用时间（＞14 天）、住院时长（＞7 天）是新生儿无菌体液感染的危险因素（P＜0.05）；多因素分析提示使用激素、安置胃管、气管插管为新生儿无菌体液感染的独立危险因素（P＜0.05）。
结论 新生儿无菌体液感染以凝固酶阴性球菌为主，对常用抗菌药物敏感性较高；使用激素、安置胃管、气管插管为新生儿无菌体液感染的独立危险因素。

PU-3468

临床分离大肠杆菌的广泛耐药性及其 β-内酰胺类基因对其表型的作用

张旭华
山东大学第二医院

从山东大学第二附属医院的一名患者的尿液样本中分离出了一株广泛耐药（XDR）的大肠杆菌 W60。药敏实验研究了其 XDR 表型的遗传基础；全基因组测序以鉴定大肠杆菌 W60 中的遗传结构；进一步的克隆分析以鉴定 β-内酰胺/BLI 组合抗性的决定因素。大肠杆菌 W60 对几乎所有测试的抗生素都有抗性，包括所有常用的 β-内酰胺/BLI 组合。基因组结构分析表明，两个新的可转移质粒是

耐药表型的原因。进一步的遗传分析表明，blaNDM-5 导致对 β-内酰胺/BLI 组合的高抗性，这可通过共表达 bleMBL 来增强。pECW602 带有一个截短的 blaTEM，由于 N 端信号肽编码区的缺失而无法正常工作。这项研究得出了几个重要的结论大肠杆菌 W60 的 XDR 表型可归因于可转移的多药耐药质粒的存在。NDM-5 对 β-内酰胺/BLI 组合具有很高的抵抗力；bleMBL 的共表达增强了 NDM-5 引起的耐药性；TEM 型 β-内酰胺酶的信号肽对其分泌和功能至关重要。这项工作的发现表明了可转移的多重耐药性质粒和金属 β-内酰胺酶的危险性，在多重耐药菌的分析和治疗中应引起重视。

PU-3469

某院老年患者感染肺炎克雷伯菌的临床分布及耐药性分析

钟杰
中国人民解放军联勤保障部队第九二一医院

目的 探讨某院老年患者感染肺炎克雷伯菌的临床分布及耐药性情况，为临床用药和控制老年患者该菌的感染提供依据。
方法 采用回顾性分析，选取 2018 年 1 月至 2020 年 12 月本院≥65 岁的老年患者分离的 222 株肺炎克雷伯菌作为研究对象,对肺炎克雷伯菌进行科室分布、耐药性等分析。
结果 2015 年-2017 年共检出肺炎克雷伯菌 222 株，科室分布中呼吸内科(19.36%)、心血管内科(16.67%)、ICU(13.51%)居临床科室的前三位。送检标本中痰液标本的检出率最高，为 80.63%，其次是中段尿标本，检出率为 10.36%。药敏结果显示，老年患者分离的肺炎克雷伯菌对碳青霉烯类抗生素的耐药率最低，喹诺酮类药物耐药率在 16%左右，氨基糖苷类药物耐药率为 0.45%~11.26%，硝基呋喃类中的呋喃妥因耐药率高达 65.32%。
结论 从本院老年患者上分离得到的肺炎克雷伯菌主要侵袭上呼吸道和泌尿道，其主要分离自该院的呼吸内科，每年的耐药率无明显变化趋势且低于全国水平，在临床治疗上美洛培南可作为该院老年患者严重感染肺炎克雷伯菌时的首选药物。

PU-3470

肺部曲霉菌感染采取微生物检验的诊断效果

高伟
雅安市人民医院检验科

曲霉菌是导致肺部感染比较常见的病原菌，可根据其致使正常人患病的能力有致病性与条件致病性之分，临床上肺部曲霉菌感染多数继发于肺部疾病基础上，患者多表现为咳嗽、发热、呼吸困难等，可分为三大类型：过敏性支气管肺曲霉病、菌球型肺曲菌病、侵袭性肺曲霉菌病[1]。该疾病根据患者临床表现有不同的治疗方式，因此为了使患者采取最佳的治疗方案，疾病的诊断是至关重要的，本次实验对象选取 2018 年 6 月至 2020 年 6 月期间本院肺部曲霉菌感染患者，参与人数 46 例，针对肺部曲霉菌感染患者实行微生物检验，分析该方法诊断效果

PU-3471

慢性乙型肝炎免疫清除期患者血清 HBV RNA 与其它血清病毒学指标相关性分析

高玉华
郑州大学第一附属医院

目的 探索慢性乙型肝炎免疫清除期患者血清 HBV RNA 与 HBV DNA、表面抗原（HBsAg）、e 抗原（HBeAg）和 ALT 等指标相关性。
方法 收集 25 例慢性乙型肝炎免疫清除期患者血清样本，定量检测患者血清 HBV RNA、HBV DNA、HBsAg、HBeAg 和 ALT 等指标，分析血清 HBV RNA 与其它指标的相关性。
结果 25 例免疫清除期患者血清 HBV DNA 均值为 7.63 log IU/ml，而血清 HBV RNA 均值也高达 5.32 log IU/ml，血清 HBsAg 和 HBeAg 分别为 4.01 log IU/ml 和 2.38 log S/CO。相关性分析表明，血清 HBV RNA 与血清 HBsAg、HBeAg 和 HBV DNA 均有较强的相关性，r 值分别为 0.729、0.650 和 0.709，P 均<0.001，而血清 HBV RNA 与 ALT 之间无相关性（r=-0.113，P=0.591）。
结论 免疫清除期患者 HBV 病毒复制、转录和表达均处于活跃状态，血清 HBV RNA 与血清 HBsAg、HBeAg 和 HBV DNA 均有较强的相关性。

PU-3472

2451 例儿童支气管肺泡灌洗液分离细菌的特点及耐药性分析

甄杨
首都医科大学附属北京儿童医院

目的 研究儿童支气管肺泡灌洗分离细菌分布及耐药情况，指导临床合理用药。
方法 回顾性分析 2016 年 1 月-2016 年 12 月，临床送检 2451 例支气管肺泡灌洗液培养出细菌种类及耐药情况。
结果 共分离出病原菌 623 株，革兰阴性菌 386 株，占 62.0% ，革兰阳性菌 237 株，占 38.0%。分离革兰阴性杆菌排名依次为流感嗜血杆菌、铜绿假单胞菌、鲍曼不动杆菌、肺炎克雷伯菌、卡它莫拉菌、大肠埃希菌、阴沟肠杆菌；分离革兰阳性杆菌排名依次为肺炎链球菌、金黄色葡萄球菌。未发现金黄色葡萄球菌对万古霉素和利奈唑胺的耐药菌株，耐甲氧西林金黄色葡萄球菌（MRSA）24 株，占 30.8％。青霉素中介的肺炎链球菌（PISP）和青霉素敏感肺炎链球菌（PSSP）比例分别 52.8％为和 40.2％。流感嗜血杆菌 β-内酰胺酶阳性率为 62.1% 。肺炎克雷伯菌中 25 株细菌对碳青霉烯类耐药（CR-KPN）占 47.2％，并检测有 81.1％的菌株产 ESBLs。铜绿假单胞菌对亚胺培南和美罗培南耐药率分别为 46.7％和 42.2％.鲍曼不动杆菌对头孢哌拉、美罗培南和庆大霉素的耐药率较高，分别为 73.8％、73.8％、72.5％，对其他抗菌药物的耐药率在 70%以下。
结论 支气管肺泡灌洗液主要病原菌的特点主要是革兰阴性杆菌，多重耐药现象严重，合理用药是控制感染的关键。

PU-3473

梅毒螺旋体如何逃避宿主的免疫反应

唐云、刘双全
南华大学附属第一医院

梅毒是由梅毒螺旋体苍白亚种（Treponema pallidum；TP）引起的慢性感染性疾病。由于其生长缓慢，感染具有较长的潜伏期，因此具有明显的早期和晚期特征。在没有干预的情况下，有机

体通过血液和中枢神经系统广泛传播，随后产生不同的感染临床表现，因此其临床表现、治疗措施都因自然感染史而异。梅毒是一个重大的全球健康问题。在一些低收入的国家，梅毒是一个较为普遍的问题；而在一些高收入国家，梅毒似乎呈现一种周期性的特性。梅毒周期性复发的模式发生在10-15 年的时间内，其原因要么是未能努力维持控制措施，增加风险行为（such as crack-cocaine use，男男性行为者），要么是部分宿主对感染的保护性免疫增强和减弱。免疫力的存在对传染病的动力学有重要影响。尽管梅毒螺旋体在感染者中可以引发了强烈的免疫反应，早期梅毒患者的血液和其他体液中通常都有致病性的梅毒螺旋体，这表明 TP 发展了免疫逃逸策略。多年来，梅毒螺旋体对特异性抗体结合的固有抵抗力引起了梅毒研究人员的注意，因为这一体外现象与体内梅毒螺旋体的免疫逃避直接相关。其他人已经提出了几种机制来解释梅毒螺旋体的持久性，包括细胞内位置，停留在免疫特权部位，局部免疫反应过早下调，以及不能结合固定或中和抗体，可能是由于缺乏表面暴露的抗原。本文主要就梅毒螺旋体在体内形成的免疫反应以及如何逃避机体的免疫反应作出论述。

PU-3474

嗜水气单胞菌致眼内感染

郭建壮
山东第一医科大学第一附属医院（山东省千佛山医院）

嗜水气单孢菌是一种新的能够导致肠道疾病的细菌，目前已被纳入了腹泻病原菌的常规检测中，其中食品卫生检验部门也对此菌进行感染检测，同时也是导致院内感染的细菌。此菌是一种能够导致人-畜-鱼共患病的病原菌，具有多种不同的致病基因，同时具有相当的毒力和广泛的宿主感染能力[1]。

嗜水气单孢菌在人类感染中以胃肠感染最为常见，多为急性肠胃炎，其发病可能与食物中毒或引用被污染的水有关；发病多以爆发或流行为常见形式[2]。外伤感染的几率和败血症的几率远低于胃肠感染。帮助临床详细了解嗜水气单胞菌的生活习性及发病原因、药物敏感性协助临床对该菌所致感染的治疗及预防。

PU-3475

Distribution of type VI secretion system (T6SS) in clinical Klebsiella pneumoniae strains and its potential relationship with virulence and drug resistance

Yang Liu 、si chen
First Affiliated Hospital of Nanchang University

The type VI secretion system (T6SS) in K. pneumoniae strains isolated from the bloodstream, intestinal, the pyogenic liver abscess has been reported. Here we aimed to characterize T6SS in clinical K.pneumoniae isolates with all kinds of specimens and to investigate the potential association of T6SS with virulence and drug resistance. The frequency of T6SS genes among the clinical K. pneumoniae isolates was 72.2%. The hcp-positive isolates displayed higher resistance to piperacillin-tazobactam, ciprofloxacin, levofloxacin, meropenem than the hcp-negative isolates(P<0.05). The hcp-positive isolates formed significantly more biofilm mass than the hcp-negative isolates(mean±standard deviation [SD], 0.3±0.09 vs.0.16±0.06; P< 0.01). Compared to the hcp-negative isolates, the hcp-positive isolates had a higher frequency of virulence genes(rmpA, fimH, entB, kfu, ybtS) and the pLVPK-like plasmid(P<0.05). In conclusion, the prevalence of the type VI secretion system is high in clinical K.pneumoniae isolates in a Chinese

teaching hospital. T6SS-positive strains show higher biofilm-forming activity with highly drug resistance and exhibit higher virulence.

PU-3476

结核γ—干扰素酶联免疫法释放试验结果及影响相关因素分析

徐宁
云南省第一人民医院

目的 目前结核病诊断方法中，细菌学检查是诊断结核的金标准，但是阳性率较低，结核菌培养耗时长，对肺外结核的诊断阳性率更低，影像学、TST、抗体检测、分子诊断方法等在敏感性和特异性方面均都存在一定的局限性，近年来以 T 细胞免疫为基础的 γ 干扰素释放试验（IGRA）被证实在结核分枝杆菌感染检测中具有较好的敏感性和特异性，本研究针对 γ-干扰素酶联免疫法释放试验结果及影响因素进行探讨。
方法 纳入 2019 年 1 月至 2019 年 12 月云南省第一人民医院门诊及住院患者，且经相关病理及细菌学检查和临床转归而最终证实的结核感染患者 516 例为阳性组，而阴性组则是疑似结核，最终通过其他检查排除结核患者 444 例，探讨 γ-干扰素释放试验(IGRA)临床应用的准确性和特异性，以及实验的影响因素。
结果 干扰素试验结果和最终病理确诊结果之间比较 p 值<0.001 为差异有统计学意义，在年龄、干扰素释放量、淋巴细胞、CRP、单核细胞等方面差异有统计学意义（p<0.05）。
结论 γ-干扰素与病理结果有很高的一致性，可作为临床传统影像及病理判断结核方法的有力补充，年龄、干扰素释放量、淋巴细胞、CRP、单核细胞等都是实验结果的影响因素。

PU-3477

Current status of laundry management in 4,379 healthcare centers in Guangdong province, Southern China

Dianrong Zhou
Guangdong general hospital

Objectives Healthcare textile (HCT) associated infections are common, and many developed countries have implemented complete laundry outsourcing standard procedures. However, few data about healthcare textile management are available from the developing world. Study design: we conducted a census to determine the state of healthcare textile management in Guangdong province, China.
Methods The Guangdong Health Committee (GDHC; formerly the Guangdong Ministry of Health) and the Guangdong General Hospital-associated Infection Quality Control Center (GDHICC) organized all of the City Hospital Infection Quality Control Centers to hold a census about the stage of HCT management through a real-name questionnaire survey.
Results A total of 4,374 healthcare centers from 21 cities in Guangdong participated in the survey. It consisted of 213 (4.87%) tertiary hospitals, 499 (11.41%) secondary hospitals, and 3,662 (83.72%) primary and lower healthcare centers. Out of the participants 3,674 (84%) mainly washed in healthcare centers, 507 (11.59%) subscribed to laundry outsourcing, and 193 (4.41%) used the two modes. Healthcare laundries were managed and supervised by different departments in different healthcare centers, and no department was specifically responsible for HCT management. This survey included 3,867 healthcare laundries and 700 commercial laundries. According to the Chinese national standards, commercial laundries were better than healthcare laundries in quality control.
Conclusions Our study showed that a small number of healthcare laundries were outsourced. However, the quality control of healthcare laundries was not complete, and no professional

institutions were in charge of supervision. Basic healthcare laundries should be reintegrated, and regional laundries should be established.

PU-3478

基于单细胞拉曼的尿路致病菌耐药表型与基因型测定方法

屈丽平[1]、朱鹏飞[2]、徐健[2]、周宏伟[1]
1. 南方医科大学珠江医院
2. 中国科学院青岛生物能源与过程研究所

抗生素敏感性由抗生素暴露的表型反应决定，是临床决策治疗多种尿路致病菌和鉴定耐药标志物的关键。传统的金标准培养法检测药敏均依赖于耗时的细菌分裂增殖过程，只能反映细菌的生长；而基于群体耐药基因检测等分子诊断技术仅能推断耐药可能性，无法准确反映耐药表型。单细胞拉曼光谱以免标记和非侵入性的方式、根据细胞特征的"生化指纹"图谱，来快速识别病原体，同时，因重水标记呈现的拉曼光谱中氘峰替换率与细胞代谢活性线性相关，可实现细菌耐药性快速检测及其细胞间异质性分析。然而，由于微生物多样性、临床样本基质复杂性以及低细菌负荷，直接从临床样本检测药敏仍然存在巨大挑战。同时，单细胞异质性耐药也一直未在临床样本中被证实。因此建立单细胞精度的耐药表型与基因型耦合的研究方法，对于探究原位临床样品中耐药产生原因及其传播机制至关重要。本研究以全球首台"临床单细胞拉曼药敏快检仪"（CAST-R）在尿路感染致病菌中的应用为切入点，结合卷积神经网络建立了 13 种常见模式菌分类模型及方法，平均分类准确率为 94.7%。基于重水标记拉曼技术，结合重水延迟效应及相对代谢活性指标建立了大肠杆菌针对左氧氟沙星的快速药敏快检方案及评价阈值，进一步在 3h 内实现了临床尿液样本原位药敏快检。基于 D_2O-RAGE-Seq 策略可同时揭示目的单细胞的耐药表型和基因型，发现左氧氟沙星耐药程度与突变位点数目相关，且单细胞间基因型存在异质性，从而在单细胞层面揭示了临床样品中原位基因型的多态性。这种快速、精确和完整的解决方案为个体定制抗生素治疗和改进抗菌管理奠定了基础。

PU-3479

2017-2020 年南京医科大学第一附属医院血培养病原菌分布及耐药性分析

范坤、刘成成
江苏省人民医院（南京医科大学第一附属医院）

目的 分析 2017-2020 年南京医科大学第一附属医院血培养样本病原菌分布情况及耐药特点，为临床抗感染治疗经验性用药提供依据。
方法 采用 VITEK-2 Compact 全自动微生物分析系统对血培养样本中分离的病原菌进行鉴定及药敏试验，分析其分布特点和耐药情况。
结果 2017-2020 年血培养共分离出病原菌 3799 株，检出病原菌革兰阴性杆菌占 58.75%（2232/3799），革兰阳性球菌占 35.96%(1366/3799)，真菌占 4.61%(175/3799)，其余细菌占 0.68%（26/3799）；排名前 3 位的病原菌依次为大肠埃希菌、肺炎克雷伯菌和金黄色葡萄球菌。大肠埃希菌对亚胺培南和美罗培南耐药率较低，分别是 2.1%和 1.9%，对氨苄西林，头孢唑林和头孢呋辛耐药率较高，分别是 92.5%、73.5%和 72%；肺炎克雷伯菌对头孢替坦和阿米卡星耐药率较低，分别是 32.8%和 22%，对氨苄西林、头孢唑啉和氨苄西林/舒巴坦耐药率较高，分别是 91.1%、58.7%和 58.5%；金黄色葡萄球菌对利奈唑胺和万古霉素敏感性较高，未发现耐利奈唑胺和万古霉素的金黄色葡萄球菌，对红霉素，克林霉素和青霉素的耐药率较高，分别是 53.8%，49.8%和 39.1%。

结论 医院血培养样本中分离病原菌种类多样，且对常用抗菌药物耐药较为严重，临床应加强血流感染病原菌的耐药监测，合理使用抗菌药物。

PU-3480

诺卡菌所致肺炎并文献分析

马建萍
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 通过对诺卡菌所致肺炎患者的情况分析为临床对诺卡菌肺炎的治疗提供理论支持。
方法 通过实验介绍及文献回顾分析，对诺卡菌进行描述及药敏实验结果分析；阐述诺卡菌的生活习性及药敏特点。
结果 诺卡菌属于条件性致病菌，在环境中广泛存在，易对免疫力低下患者造成感染，诺卡菌肺炎是最常见表现。对复方新诺明、碳青霉烯类抗生素敏感，治疗时间较长。
结论 鼻吸入诺卡菌是最常见的进入体内方式，大多数感染累及肺部其严重程度不一，肺诺卡菌病临床常见，极少会发展为重症肺炎。

PU-3481

泛耐药鲍曼不动杆菌肺部感染的风险因素与抗菌药物治疗方案分析

周典蓉
广东省人民医院

背景 泛耐药的鲍曼不动杆菌是院内感染重要的病原菌，而肺部是鲍曼不动杆菌最常见的分离部位，严重威胁了住院病人的疾病预后。
目的 本次研究针对主要就泛耐鲍曼不动杆菌肺部感染的临床分布特征及危险因素相关问题进行分析研究。同时，调查泛耐鲍曼不动杆菌的药敏结果、临床治疗用药及患者预后情况，为有效防控医院感染和临床诊治提供参考依据。
方法 收集我院 2018 年 2019-2020 年所有住院患者病例下呼吸道标本分离出泛耐鲍曼不动杆菌的病例，剔除重复例数及定植菌株，采用病例回顾性分析的研究方法,系统阅读病例资料并进行研究。
结果 临床科室分布主要集中于危重病监护室，有 108 例（51.4%）；药敏试验结果 PDRAB 对大多数常用抗菌药物呈现高水平耐药，其中对碳青霉烯类、哌拉西林、头孢曲松等抗菌药物的耐药率均达到 100%。感染 PDRAB 的患者存在多种危险因素，包括长时间住院、基础疾病、侵袭性操作、入住危重病监护室、糖皮质激素的使用、抗菌药物的使用、三种以上多药联用及长期使用抗菌药物等等。其中呼吸道疾病、碳青霉烯类、喹诺酮类、β-内酰胺抑制剂、三种以上多药联用、留置引流管是感染 PDRAB 的独立危险因素。临床治疗感染 PDRAB 的患者使用最多的抗菌药物是替加环素联合舒巴坦合剂，有 27 例，好转率为 63.0%。感染 PDRAB 的临床治疗好转率为 50%，死亡率 27.6%。
结论 由 PDRAB 菌株标本分离情况可看出，主要来自呼吸道标本，分离自危重病监护室的比例最高，呼吸道疾病、碳青霉烯类、β-内酰胺抑制剂、喹诺酮类、三种以上多药联用、留置引流管是感染 PDRAB 的独立危险因素，通过分析 PDRAB 的药敏数据可得出，PDRAB 对碳青霉烯类、哌拉西林、头孢曲松等抗菌药物的耐药率达到 100%，替加环素联合舒巴坦合剂是临床治疗感染 PDRAB 使用最多的抗菌药物，感染 PDRAB 的死亡率较高，预后差。

PU-3482

新疆塔城地区肠杆菌科细菌对 β-内酰胺类药物的耐药状况分析

杨文婧
中国医科大学

目的 分析新疆塔城地区肠杆菌科细菌对 β-内酰胺类药物的耐药状况，了解常规药敏实验结果与特殊表型检测实验之间的差异。
研究方法 使用自动化仪器法进行药敏试验，使用纸片扩散法对特殊耐药机制表型进行检测。
结果 本研究收集了 2019-2020 年新疆塔城地区人民医院各类标本中分离出的肠杆菌科细菌共 750 株，产 ESBLs 的大肠杆菌有 132 株，占大肠杆菌总数的 41.3%，肺炎克雷伯菌为 61 株，占 25.5%
结论 塔城地区大肠埃希菌产 ESBLs 菌株检出率高于肺炎克雷伯菌，肠杆菌属细菌对头孢噻肟、头孢西丁耐药率高于 90%，应引起临床重视

PU-3483

高尿酸血症人群的肠道菌群特征

王展强、周宏伟
南方医科大学珠江医院

目的 探究高尿酸血症人群的肠道菌群的紊乱特征。
方法 采用多阶段整群随机抽样的方法(PPS)在广东省 14 个监测点按照人口规模抽取一定数量的志愿者进行调查，现场采集所有志愿者的新鲜粪便标本和通过问卷调查收集所有志愿者的相关信息，采用 illumina 高通量测序平台对志愿者的粪便进行 16S rRNA 测序，用 qiime 1.9.1 和 R 语言分析高尿酸血症人群的肠道菌群紊乱特征。
结果 与健康人群相比，高尿酸血症人群中肠道菌群 α 多样性降低，两者的 β 多样性存在差异，且肠道菌群结构上的差异不受性别的影响；LEfSe 分析和 MaAsLin 分析提示与健康人群相比，高尿酸血症人群的肠道菌群中 *Enterobacteriaceae*、*Oxalobacteraceae* 等细菌的相对丰度升高，而 *Ruminococcaceae*、*Bacteroides*、*Prevotella* 等细菌的相对丰度下降。
结论 高尿酸血症人群的肠道菌群结构与非高尿酸血症人群存在差异，在高尿酸血症人群的肠道菌群中机会致病菌的相对丰度升高，而常见定植菌的相对丰度下降。

PU-3484

2015-2020 年山东省某三甲综合医院临床分离肺炎链球菌的分布和耐药性变迁

张志军、赵书平
泰安市中心医院

目的 了解医院临床分离肺炎链球菌(Streptococcus Pneumonia，SP)的分布情况及耐药性变迁，为临床合理使用抗生素提供实验室依据。
方法 回顾分析山东省泰安市中心医院 2015-2020 年临床分离的肺炎链球菌的分布情况，纸片扩散法进行药物敏感性试验（青霉素、美罗培南、头孢噻肟、头孢曲松和头孢吡肟采用 E-test 试验法），应用 WHONET 5.6 软件对结果进行统计和分析。
结果 六年间，临床标本中共分离出 SP 菌株 2095 例；标本类型最主要来源于呼吸道，所占比例为 88.74%，其次为血液（2.24%）；以冬季分离出菌株为主，所占比例为 39.24%；年龄分布方面，以 0-14 周岁的儿童分离出为主，比例为 63.10%；同时科室分布主要为儿内科病房（60.76%）；

药敏结果显示：近六年，未发现对万古霉素、利奈唑胺耐药的 SP 菌株，对利福平、头孢吡肟、头孢噻肟、头孢曲松、美罗培南、莫西沙星以及青霉素耐药率均低于 1%。但对红霉素、克林霉素一直处于高耐药水平。
结论 我院肺炎链球菌主要引起儿童患者的呼吸道感染，对常用抗菌药物的敏感情况良好，临床医生应根据药敏试验结果选择合理的抗生素。

PU-3485

双侧双瓶血培养报阳时间分析

刘成成、范坤、刘根焰
江苏省人民医院（南京医科大学第一附属医院）

目的 分析双侧双瓶血培养阳性报警时间（TTP），为双侧双瓶血培养报阳后处理流程的改进提供参考。
方法 回顾性分析 2020 年 1 月至 2020 年 12 月南京医科大学第一附属医院微生物室有报阳瓶的外周血双侧双瓶血培养的报阳时间。
结果 2020 年 1 月至 2020 年 12 月共检测到有阳性报警的双侧双瓶血培养 756 套。其中，4 瓶全部报阳 255 套，3 瓶报阳 68 套，2 瓶报阳 174 套，1 瓶报阳 259 套，分别占 33.7%、9.0%、23.0%和 34.3%。以每套双侧双瓶中第 1 瓶报阳时间为基点，第 2、3、4 阳性瓶的报阳时间的中位数分别为 1、3 和 4 小时。88.7%（927/1045）阳性瓶在第 1 瓶报阳后的 12 小时内报警。
结论 仅 1/3 双侧双瓶血培养能够在培养期间全部报警。双侧双瓶血培养第 1 瓶报阳后，后续阳性瓶报警大部发生在 12 小时以内。目前的双侧双瓶血培养报阳后的处理流程尚存在一定优化的空间。

PU-3486

Gene X-pert MTB/RIF 检测在尘肺病人中的应用

彭艳华、刘艳芝、伏刚
湖南省职业病防治院

目的 探讨 Gene X-pert MTB/RIF 技术在尘肺病人中的使用价值。
方法 对湖南省职业病防治院 2020 年 4 月-8 月尘肺住院病人的痰标本进行抗酸染色，并运用 Gene X-pert MTB/RIF 技术检测结核分枝杆菌及利福平耐药基因。
结果 242 例尘肺病人痰抗酸染色阳性率为 7.0%，Gene X-pert MTB/RIF 检测结核分枝杆菌阳性率为 11.2%，其中利福平耐药的病人占 12.0%。**结论** Gene X-pert MTB/RIF 技术能够提高尘肺病人合并肺结核的检出率，并且能够检测结核分枝杆菌利福平耐药基因，为尘肺合并肺结核患者的诊断和治疗提供帮助。

PU-3487

多重耐药鲍曼不动杆菌 bla-oxa 酶型检测及分析研究

张峰领[1]、秦瑶[2]
1. 重庆医科大学附属第三医院
2. 重庆医科大学检验学院

目的 对临床分离的多重耐药鲍曼不动杆菌（MDR-AB）耐药性和产 bla-oxa 酶情况进行检测及分析。
方法 收集重庆医科大学附属第三医院 2020 年 1 月至 2020 年 12 月分离的 48 株多重耐药鲍曼不动

杆菌，通过微量肉汤稀释法和纸片扩散法进行抗菌药物敏感试验，同时采用 PCR 进行 OXA 酶基因检测分析。
结果 多重耐药鲍曼不动杆菌对替加环素敏感度高达 100.00%，庆大霉素和米诺环素药物敏感率分别为 10.42%和 8.33%。48 株多重耐药鲍曼不动杆菌均检测出 bla-oxa 酶基因。其中 48 株（100.00％）检出 blaoxa-51 基因阳性，45 株（93.75%）检出 blaoxa-23 基因阳性，30 株（62.50%）检出 blaoxa-58 基因阳性，11 株（22.92%）检出 blaoxa-24 基因阳性。
结论 我院临床分离的 MDR-AB 菌株耐药性较高，仅对替加环素敏感性较好，尚未分离出对替加环素耐药的菌株。分离菌株以携带 blaoxa-51 酶及 blaoxa-23 酶型为主，分离菌株未发现明显同源聚集现象。通过本研究可指导临床应合理使用抗生素防止 MDR-AB 的产生和传播。

PU-3488

2016-2020 年山东省某三级综合医院肺炎克雷伯杆菌的分布与耐药性变迁

张志军
泰安市中心医院

目的 分析院内近五年临床分离肺炎克雷伯杆菌的分布与耐药性变迁，为临床合理使用抗菌药物提供理论依据与数据支持。
方法 对 2016 年 01 月-2020 年 12 月间临床标本中分离的肺炎克雷伯杆菌，采用 WalkAway 96 PLUS 型全自动细菌分析仪进行鉴定和药敏试验，部分药物试验采用纸片扩散法进行补充，应用 WHONET 5.6 软件对结果进行统计和分析。
结果 五年间，我院临床标本中共分离出 4264 株目标菌株，药敏结果显示：肺炎克雷伯杆菌对头孢菌素的耐药率分布在 20.5%-52.2%，耐药率逐年下降，差异具有统计学意义（P<0.05）；对头孢哌酮/舒巴坦的耐药率呈上升趋势，差异具有统计学意义（P<0.05）；对哌拉西林/他唑巴坦的耐药率一直比较低（<11.5%）；对阿米卡星的耐药率为 4.8%-9.5%；对左氧氟沙星与环丙沙星的耐药率分别为 22.6%-27.2%与 28.3%-33.7%；对碳青霉烯类药物耐药率 7.3%-11%。科室分布主要为神经外科病房，重症医学科病房以及儿内科病房等，所占比例分别为 14.66%、13.51%、7.86%；检出率最高的标本为痰液（60.44%），其次是尿液（18.08%）与血液（7.86%）。
结论 肺炎克雷伯杆菌对临床常用的抗生素耐药差异比较大，是引起神经外科，重症医学科与儿内科患者呼吸道感染的重要病原菌之一。临床医生应根据药敏结果选择并及时调整合理的抗菌药物。

PU-3489

肠球菌血流感染危险因素及预后分析

吴婷婷
溧阳市人民医院

目的 进行肠球菌血流感染的流行病学调查，危险因素及预后分析。
方法 回顾性收集 2019 年 1 月至 2020 年 12 月江苏省人民医院肠球菌血流感染病例 164 例的临床资料，按照种类将病例分成粪肠球菌血流感染组（48 例），屎肠球菌血流感染组（95 例）和其它肠球菌血流感染组（21 例），用 WHONET 软件分析菌株构成及各组耐药情况，用 SPSS 分析粪肠球菌 42 例和屎肠球菌 84 例两组的危险因素差异。用 SPSS 对生存组 125 例和死亡组 22 例进行预后分析。
结果 164 例肠球菌中屎肠球菌 95 例（58%），粪肠球菌 48 例（29%），铅黄肠球菌 8 例（5%），鹑鸡肠球菌 7 例（4%），鸟肠球菌 3 例（2%），棉子糖肠球菌 2 例（1%），耐久肠球菌 1 例（1%）。164 例中，3 例对万古霉素耐药，对青霉素耐药率在 12.5%-90.4%之间。多因素分析结

果显示，留置导尿管是肠球菌血流感染的危险因素。 有无手术和有无感染性休克是影响肠球菌血流感染预后的危险因素。
结论 留置导尿管是肠球菌血流感染的危险因素。有无手术和有无感染性休克是影响肠球菌血流感染预后的危险因素。应加强关注并重视这些因素以改善预后。

PU-3490

产单核李斯特菌侵袭性感染的临床特征分析

刘素玲、周典蓉、高红林、张妮、赵云虎、顾兵
广东省人民医院

目的 分析成人非孕妇感染产单核李斯特菌的特点，为该病的诊治提供依据。
方法 纳入 2010 年 1 月至 2020 年 6 月广东省人民医院收治的产单核李斯特菌感染成人非孕妇患者 15 例。回顾性分析患者的年龄、症状、基础疾病和预后等临床资料,以及白细胞(WBC)、中性粒细胞与淋巴细胞比值(NLR)、降钙素原(PCT)、白细胞介素-6(IL-6)和 C 反应蛋白(CRP)等实验室结果，分析其临床感染和预后特点。
结果 15 例患者年龄 15～93 岁,60 岁以上占 26.6%(4/15)。季节分布以夏季发病最高(66.6%,10/15)。9 例合并基础疾病;13 例发生脓毒症,2 例脑膜炎。李斯特菌病确诊时间为(5.1±2.9)d,确诊后调整以碳青霉烯类(20%,3/15)、青霉素类(33.3%,5/15)为主的目标性治疗。住院治疗的 15 例患者治疗后的 WBC、NLR 和 CRP 水平明显低于治疗前(P 均<0.05)。12 例患者根据指南治疗后,10 例好转,1 例预后不佳,1 例死亡。
结论 成人非孕妇产单核李斯特菌感染的主要风险因素为其基础疾病,特别是自身免疫性疾病和肺部疾病。青霉素类可作为经验治疗首选药物,碳青霉烯类、红霉素等可联合足疗程治疗。

PU-3491

Performance of Resin or haemolysin-Containing Blood Culture Media in Detection of Bloodstream Infections：Clinical Comparison of the BacT/Alert VIRTUO and Bactec FX Systems

suling liu、yunhu zhao、dianrong zhou、xinqiang zhang、weisha wang、bin gu、tieying hou
Guangdong Provincial People's Hospital

Objective To evaluate the clinical performances of BacT/Alert VIRTUO media linein Detection of Bloodstream Infections.
Methods We compared the clinical performances of the BacT/Alert VIRTUO (bioMérieux) and Bactec FX (Becton Dickinson) aerobic and anaerobic blood culture (BC) media with Resin or haemolysin-Containing Blood Culture Media. Patients >16 years old with suspected bloodstream infections (BSIs) were enrolled in 6 ICU departments and 3 general departments of Guangdong Provincial People's Hospital from June 2020 to May 2021.Each patient collected 2 sites of blood samples, one site was inoculated into BacT/Alert VIRTUO (FA Plus & FN Plus) cultures and anotherwas inoculated into Bactec FX (Resin Aerobic & Hemolysin Anaerobic) cultures, each set consisting of one aerobic and one anaerobic bottle. Cultures were incubated <5 days in the BacT/Alert VIRTUO and Bactec FX instruments, respectively.
Results A total of 1772 unique BSI episodes were identified based on the recovery of clinically significant growth in 275 aerobic cultures (144 BacT/Alert VIRTUO and 131 Bactec FX) and 148 anaerobic cultures (91 BacT/Alert VIRTUO and 57 Bactec FX).The positive recovery rate of BACT/Alert Virtuo system was higher than that of BACTEC FX400 system (9.7% and 7.7%,

respectively). The positive recovery rate of BACT/Alert Virtuo system was significantly higher than that of FX system (9.4% vs. 1.9%) during the initial stage of 0-8h of culture.
Conclusion The BacT/Alert VIRTUO media line appears to be a reliable, time-saving tool for routine detection of BSIs in the population we studied。

PU-3492

豚鼠气单胞致肝内感染病例分析及文献回顾

郭亮亮
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 通过对豚鼠气单胞菌介绍及药敏实验对临床的诊断及治疗提供理论依据。
方法 利用文献回顾及对豚鼠气单胞菌的流行病学及生存特性进行阐述，并通过临床常规药敏实验对该菌进行体外药敏实验。
结果 豚鼠气单胞菌是一种环境中存在的条件致病菌，在水产养殖中常见；其临床感染常和水质污染相关。该菌对 β-内酰胺类抗生素耐药，对氨基糖苷类、碳青霉烯类抗生素敏感。
结论 豚鼠气单胞菌是一种条件致病菌，其在水污染后可对免疫力低下患者造成感染。其常对氨基糖苷类及碳青霉烯类抗生素敏感。

PU-3493

阴道五联检联合镜检对阴道分泌物清洁度、阴道疾病诊断的临床价值

湛文博、熊文娟、解晨曦、郑倩、李大伟
新疆医科大学第五附属医院

目的 探讨阴道五联检联合镜检对阴道分泌物清洁度、阴道疾病诊断的临床价值。
方法 选取 2019 年 12 月至 2020 年 12 月在新疆医科大学第五附属医院进行体检的 300 例女性，通过阴道分泌物五联检、常规镜检联合检测阴道分泌物的清洁度、诊断阴道疾病。
结果 与镜检法相比，阴道五联检方法对清洁度Ⅲ度和Ⅳ度阴道分泌物的检出率较高，P＜0.05；阴道五联检方法对阴道分泌物中念珠菌、滴虫的阳性检出率更显著，P＜0.05。
结论 阴道分泌物检测联合五联检与显微镜可提高检出率，准确反映阴道清洁度、病原菌分布，为治疗提供有价值的依据。

PU-3494

被纳米银杀死的细菌的二次杀菌活性特征研究

邓中华、熊艺灿、谭超超、陈杰、王璐、曹友德
湖南省人民医院（湖南师范大学附属第一医院）

目的 探讨被纳米银杀死的细菌的二次杀菌活性特征。
方法 以金黄色葡萄球菌(Staphylococcus aureus, S. aureus)标准菌株，耐甲氧西林金黄色葡萄球菌(Methicillin-resistant Staphylococcus aureus，MRSA)菌株，大肠埃希菌(Escherichia coli,E.coli)标准菌株，产超广谱 β 内酰胺酶(Extended-spectrum β-lactamase-producing，ESBLs)大肠埃希菌菌株四中菌为代表。用纳米银溶液直接杀死四种试验菌株，洗涤获得被纳米银杀死的各死菌悬液。以四种死菌悬液作为杀菌物质，与四种实验菌株新鲜活菌混合，探讨纳米银杀死的死菌悬液的二次杀

菌作用，比较二次杀菌作用在革兰氏阴阳性菌之间、耐药菌和敏感菌之间的差异，分析被纳米银溶液杀死的细菌的二次杀菌活性特征。
结果 金黄色葡萄球菌标准株和 MRSA 株的同菌株纳米银二次杀菌率分别为(59±9.1)%和(55±9.9)%，分别低于大肠埃希菌标准菌株同菌株二次杀菌率(75±9.3)%和产 ESBLs 菌株同菌株二次杀菌率(71±9.0)%，差异有统计学意义(P<0.05)。金黄色葡萄球菌和大肠埃希菌标准菌株的同菌株纳米银二次杀菌率与各耐药菌株之间经卡方检验无统计学差异(P>0.05)。纳米银杀死的大肠埃希菌标准菌株作用于大肠埃希菌标准菌株的二次杀菌率为(75±9.3)%，高于作用于金黄色葡萄球菌标准菌株的二次杀菌率(57±6.6)%，差异有统计学意义(P<0.05)。
结论 被纳米银杀死的细菌的二次杀菌活性对革兰氏阴性菌的杀伤作用更大，且对敏感株和耐药菌株有同等杀伤力。纳米银的二次杀菌能力在不同菌种之间也有杀菌功能。

PU-3495

健康妇女生殖道内格氏乳杆菌的分离鉴定与安全性评价

邱峰[1]、苏炳森[2]
1. 南方医科大学第七附属医院
2. 广东省中山市火炬开发区医院

目的 为了建设人体微生态样本库，对健康妇女生殖道内分离得到的格氏乳杆菌进行鉴定及安全性评价。
方法 通过对分离得到细菌的 16S rDNA 基因序列进行测定和分析，确定细菌种类并构建系统发育树。安全性评价包括微生物菌种溶血实验、药物敏感性实验和小鼠毒性实验。
结果 分离得到的格氏乳杆菌（LGV03）可发酵蔗糖、麦芽三糖、D-葡萄糖、熊果甙、D-纤维二糖、D-甘露糖、D-麦芽糖和 5-溴-4-氯-3-吲哚-β-D-葡萄糖苷。丙氨酸-苯丙氨酸-脯氨酸芳氨酶、亮氨酸芳氨酶、L-吡咯烷酮芳氨酶和苯丙氨酸芳氨酶实验为阳性，且能水解七叶苷。溶血反应阴性,小鼠毒性实验结果显示分离菌株无毒性。
结论 成功分离得到的格氏乳杆菌，并进行了鉴定及安全性评价。

PU-3496

黏液型细菌导致感染的临床特征及危险因素分析

张妮、刘伟江
广东省人民医院

目的 通过分析临床分离的黏液型细菌，了解黏液型细菌引起感染的临床分布特点和危险因素，提高临床对黏液型细菌的认知和干预。
方法 收集广东省人民医院 2018 年 1 月——2018 年 12 月临床分离出的黏液型细菌 51 例；采用病例-对照组回顾性分析，分析黏液型细菌导致感染的临床特征，通过 SPSS 多因素分析统计学方法，分析导致黏液型细菌形成的危险因素。
结果 51 例黏液型细菌主要是铜绿假单胞菌（18 例，占 35.29%）、大肠埃希菌（16 例，占 31.37%）、肺炎克雷伯菌（9 例，占 17，65%）；黏液型铜绿假单胞菌主要来自呼吸道，占 77.7%；黏液型大肠埃希菌主要来自泌尿道，占 100%，黏液型肺炎克雷伯菌主要来源于创面与无菌部位。检出病原菌患者的科室主要分布在泌尿外科（19.60%）、呼吸科（17.65%）和重症监护病房（15.69%）。单因素分析发现糖尿病、气管插管、手术史、感染前抗菌药物的使用以及头孢菌素类抗菌药物的使用是黏液型细菌引起感染的危险因素，多因素分析发现，糖尿病和手术史是黏液型细菌引起感染的独立危险因素。

结论 黏液型细菌更易形成生物膜，导致临床治疗困难。长期慢性呼吸道和泌尿道疾病患者、重症患者是黏液型细菌感染的易感人群，临床应予以重视，加强控制和干预，以达最佳治疗效果。

PU-3497

2011-2020 年感染性心内膜炎病原菌分布及耐药性分析

张鑫强[1]、陈文妍[2]、李正康[1]、凌勇[1]、刘素玲[1]
1. 广东省人民医院
2. 中山大学南方学院

目的 分析我院近 10 年来，感染性心内膜炎确诊患者病原菌分布及耐药性的差异，为临床提供准确的检测结果，提高感染性心内膜炎的诊疗效果。
方法 采用回顾性分析我院 2011-2020 年感染性心内膜炎患者作为研究的对象。药敏试验采用最低抑菌浓度和纸片扩散法进行测定。病原菌的分布及药敏结果均采用 WHONET5.6 软件分析。
结果 收集我院 2011-2020 年感染性心内膜炎患者分离病原菌 774 株。（1）病原菌分布：革兰阳性菌占有 661 例（占 85.40%），革兰阴性杆菌 61 例（占 7.88%），真菌 52 例（占 6.72%），分离率占前三的病原菌为草绿色链球菌群，金黄色葡萄球菌，粪肠球菌。（2）药敏试验:链球菌对万古霉素和利奈唑胺的耐药率为 0,对四环素的耐药率为 35.34%,对红霉素的耐药率为 36%，，对头孢噻肟，头孢吡肟，氯霉素及青霉素 G 的耐药率均<2%。
结论 近 10 年来我院链球菌药敏耐药率较低，仅红霉素和四环素耐药率有增高趋势。

PU-3498

降钙素原（PCT）诊断血流感染的应用研究

张妮、刘伟江、叶龙、刘素玲、陈晓丽
广东省人民医院

目的 探讨血清降钙素原（PCT）定量检测在血流感染中的应用价值。
方法 回顾性分析 2019 年 1 月至 12 月就诊于广东省人民医院同时送检血培养和 PCT 的住院患者的临床资料及检测结果记录，应用 ROC 曲线分析不同 PCT 界值对血流感染的敏感性、特异性、阳性预测值（PPV%）、阴性预测值（NPV%），分析不同 PCT 界值与血流感染病原菌种类的关系。
结果 4923 例血培养中，血培养阴性共 4423 例，该组 PCT 的平均值、中位数分别为 2.75ng/ml、0.23ng/ml；血培养阳性 500 例，该组 PCT 的平均值、中位数分别为 17.86ng/ml、2.01ng/ml，PCT 阳性率 68.6%，血培养阳性组 PCT 水平明显高于血培养阴性组（P＜0.001＝；建立 ROC 曲线分析不同 PCT 分界值对血培养结果时 ROC 曲线下面积为 0.729，当 PCT 为值为 0.05ng/ml 时，灵敏度达 94.4%，阴性预测值高达 100%；当 PCT 为 0.5ng/ml 时对血培养的敏感性、特异性、阳性预测值、阴性预测值分别为 68.6%、64.5%、18%和 94.8%，患者局部感染未导致血源播散或非感染因素诱导的 PCT 升高是导致 PCT 对血培养阳性预测值偏低的主要原因；革兰阴性细菌感染组、革兰阳性菌感染组、真菌感染组 PCT 平均值分别为 23.55ng/ml 、 7.04ng/ml、8.60ng/ml，PCT 值组间两两比较存在差异（P＜0.05＝，但不建议根据 PCT 水平确定感染的病原菌类型，PCT 水平在真菌感染患者中血清值绝大部分在 0.1-5.5ng/ml。
结论 血清 PCT 定量检测对血流感染患者早期诊断具有重要的指导意义，可以用于排除血流感染，不建议根据 PCT 水平确定感染的病原菌类型。PCT 水平必须结合临床情况进行判读，并应考虑假阳性和假阴性的可能性。

PU-3499

碳青霉烯酶耐药肺炎克雷伯菌耐药基因分布及与表型相关性分析

谢强
安徽省滁州市第一人民医院

目的 通过全基因组测序技术（Whole genome sequencing, WGS）分析某三甲医院耐碳青霉烯肺炎克雷伯菌（CRKP）的耐药基因分布及与耐药表型的关系，为临床治疗和防控提供参考。
方法 收集并鉴定临床分离非重复 CRKP 28 株。采用 VITEK-2 compact 全自动微生物鉴定药敏分析仪鉴定和药敏试验，使用全基因组测序技术进行测序。
结果 共检出 47 种耐药基因。其中碳青霉烯类耐药基因 3 种，主要为 blaKPC-2 基因（25 株，89.29%），其次为 blaNDM-5 基因（2 株，7.14%）和 blaOXA-48 基因（1 株，3.57%）；超广谱 β 内酰胺酶（Exterded spectrumβ-lactamases, ESBLs）耐药基因 8 种，主要为 blaTEM-1、blaSHV-28、blaCTX-M-15 和 blaOXA-33，检出率分别为 89.29%、75.00%、75.00%和 67.86%；氨基糖苷类耐药基因 10 种，以 AAC(6')-Ib-cr 和 AAC(3)-IIa 为主，检出率分别为 71.43%和 67.86%；喹诺酮类耐药基因 4 种，主要为 oqxA 和 AAC(6')-Ib-cr，检出率分别为 85.71%和 71.43%，其中 20 株 CRKP 同时携带 oqxA 和 AAC(6')-Ib-cr；磷霉素耐药基因 1 种，为 FosA6，检出率为 100%；磺胺类耐药基因 3 种，主要为 sul2 和 sul1，检出率分别为 21.43%和 17.86%。28 株 CRKP 的药敏结果显示，对碳青霉烯类抗菌药物、头孢菌素类、喹诺酮类和 β-内酰胺类/β-内酰胺酶抑制剂合剂的耐药率均为 100%；对阿米卡星的耐药率为 14.29%，未检出替加环素耐药株。28 株 CRKP 的耐药表型与耐药基因型在所测 β 内酰胺类抗菌药物完全一致。
结论 该院分离的 CRKP 同时携带多种抗菌药物的耐药基因，呈现泛耐药表型，其耐药表型和耐药基因型有很高的一致性。

PU-3500

碳青霉烯耐药肺炎克雷伯菌耐药机制及分子流行病学研究

谢强
安徽省滁州市第一人民医院

目的 分析本院耐碳青霉烯肺炎克雷伯菌（CRKP）的耐药情况及耐药基因，为临床治疗提供依据。
方法 收集并鉴定临床分离非重复 CRKP27 株，采用 Vitek2 compact 全自动微生物鉴定药敏分析仪鉴定和药敏试验，碳青霉烯酶抑制剂增强试验检测 A 类丝氨酸碳青霉烯酶和 B 类金属 β 内酰胺酶，聚合酶链反应(PCR)法和基因测序技术检测常见的耐药基因。使用肠杆菌目基因间重复一致序列 PCR(ERIC-PCR)对菌株进行同源性分析。
结果 27 株肺炎克雷伯菌对碳青霉烯类、头孢菌素类、喹诺酮类等抗菌药物的耐药率均大于 96%。碳青霉烯酶抑制剂增强试验显示 26 株 A 类丝氨酸碳青霉烯酶阳性，1 株 B 类金属 β 内酰胺酶阳性。PCR 和基因测序结果显示，26 株 CRKP 携带 KPC-2 基因，1 株携带 NDM-1 基因。ERIC-PCR 将 27 株 CRKP 分为 9 型，以Ⅳ型和Ⅴ型为主，集中于重症监护病房和神经外科。
结论 分离的 CRKP 对临床常用抗菌药物表现出高水平耐药；其耐药机制主要是该类细菌产 KPC-2 型碳青霉烯酶。

PU-3501

社区获得性血流感染病原菌分布及死亡相关危险因素分析

许雨乔
江苏省人民医院（南京医科大学第一附属医院）

目的 分析社区获得性血流感染（Community-acquired Bloodstream Infection，CABSI）的病原菌分布、耐药情况及死亡相关危险因素，为临床医师诊断及治疗提供依据。
方法 收集 2017 年 1 月至 2019 年 12 月 CABSI 患者分离的病原菌及临床资料，并按治疗 28d 转归分为死亡组和存活组。用 χ2 检验进行单因素分析，与死亡相关的变量采用 Logistic 二元回归进行多因素分析。
结果 本研究共从 292 例患者中分离病原菌 323 株，其中革兰阴性菌 192 株，革兰阳性菌 118 株，真菌 9 株，厌氧菌 4 株。革兰阴性菌对头霉素类、碳青霉烯类和氨基糖苷类抗菌药物耐药率均在 10%以下，金黄色葡萄球菌对庆大霉素和莫西沙星的耐药率小于 20%，链球菌属对青霉素类耐药率为 6.7%。292 例患者中 55 例死亡，死亡率为 19.0%。单因素分析显示脑梗塞、感染性休克、肺炎克雷伯菌感染、降钙素原（Procalcitonin，PCT）升高与患者死亡有关，死亡组 PCT 值显著高于存活组（P<0.05）。脑梗塞、感染性休克和较高 PCT 值是 CABSI 患者死亡相关的独立危险因素（P<0.05）。
结论 CABSI 病原菌对临床常用抗菌药物耐药率低于住院患者。脑梗塞、感染性休克和 PCT 升高能显著增加患者死亡率，临床医师应及时采取相应防治措施。

PU-3502

2044 例尿路感染病原学及耐药性分析

刘婕
山东大学第二医院

目的 探究尿路感染的细菌病原学及其耐药性，为尿路感染病原菌的精准诊断和抗生素合理应用提供依据。
方法 选取 2016 年 1 月-2020 年 8 月山东大学第二医院收治的 2044 例尿路感染患者为研究对象，用德国西门子公司 Micro ScanWalkaway 96 Plus 微生物全自动细菌鉴定和药敏分析仪进行病原菌鉴定及药敏试验，数据采用 WHONET 5.6 进行统计分析对其细菌分布及其耐药性进行分析。
结果 2044 例尿路感染患者检出中细菌中，革兰阴性菌 1428 株占 69.9%，革兰阳性菌 616 株占 30.1%，检出率最高的前 5 位病原菌依次为大肠埃希菌、屎肠球菌、肺炎克雷伯菌、粪肠球菌、奇异变形杆菌。主要革兰阳性菌对万古霉素的耐药率为 2.5%，对利奈唑胺的耐药率为 0%；主要革兰阴性菌中 ESBL 比例为 52.6%；对碳青霉素类耐药率为 1.1％。
结论 2044 例尿路感染病例中，病原菌以革兰阴性菌为主，不同病原菌的耐药性存在显著性差异，且多重耐药菌的比例呈增长趋势，提示临床诊疗中应依据病原菌药敏结果进行抗生素的合理应用。

PU-3503

肠道微生物与阿尔茨海默症

谭志霞
长沙市精神病医院

肠道微生物群由一个庞大而多样的微生态系统组成，科学家认为，肠道微生物群甚至可以称为“第二大脑”。肠道微生物和中枢神经系统（CNS）通过双向的神经、内分泌和免疫通讯形成“微生物

-肠-脑轴”。最近的临床前和临床试验表明，肠道微生物群在肠道与大脑相互作用中起着重要作用，肠道微生物组成的改变影响着中枢神经系统疾病，其中包括阿尔茨海默症（AD）。AD 是最常见的痴呆类型，是一种神经退行性疾病，主要可能机制有淀粉样蛋白 β（Aβ）沉积、高磷酸化 tau 蛋白的神经纤维缠结、神经元丢失和神经炎症等。有实验表明，肠道微生物群在宿主认知或 AD 相关的发病机制中起重要作用。肠道微生物菌群失调及其代谢产物等引起肠道和血脑屏障通透性增加，通过肠脑轴诱发神经炎症，可能介导 AD 和其他神经退行性疾病。本文主要介绍肠道微生物群在 AD 发病中的作用，充分的了解其发病机制，寻找新的有价值的治疗靶点，为更好的预防和治疗 AD 提供切实可行的方案。

PU-3504

耐甲氧西林金黄色葡萄球菌菌血症患者临床特征及预后危险因素分析

许雨乔
江苏省人民医院（南京医科大学第一附属医院）

目的 分析耐甲氧西林金黄色葡萄球菌(Methicillin- resistant Staphylococcus aureus，MRSA)菌血症患者临床特征及预后危险因素，为控制和预防 MRSA 血流感染提供依据。
方法 回顾性分析 2015-2020 年南京医科大学第一附属医院门诊及住院患者血液中分离的 MRSA 对常用抗菌药物敏感性，以及患者临床特征和预后危险因素。
结果 共收集 142 株 MRSA，其对青霉素、氨苄西林均耐药，对喹诺酮类抗菌药物耐药率在 50%以上。死亡组血清 PCT 值显著高于存活组，ROC 曲线下面积为 0.723，以 1.075mg/L 为诊断界值时，PCT 区分患者预后的敏感度 73.3%，特异度 66.2%。合并感染性休克和呼吸系统 MRSA 感染是患者死亡独立危险因素。
结论 血清 PCT 值与 MRSA 菌血症患者预后密切相关，合并感染性休克和呼吸系统 MRSA 感染是患者预后的独立危险因素，临床医师应早预防早治疗。

PU-3505

HO-1 mediates the anti-inflammatory actions of Sulforaphane in monocytes stimulated with a mycoplasmal lipopeptide

Haodang Luo[1,2]、lianmei qin[1]、Jun He[2]、Xiaoxing You[1]
1. 南华大学衡阳医学院病原生物学研究所
2. 南华大学附属南华医院检验科

Exposure to Mycoplasma pneumoniae leads to lung inflammation through a host defense pathway. Increasing evidence has indicated that the mycoplasma-derived membrane lipoprotein, or its analogue macrophage-activating lipopeptide-2 (MALP-2), excretes LPS as an immune system-stimulating substance and plays a crucial role in pathological injury during M. pneumoniae infection. It has been established that Sulforaphane confers anti-inflammatory properties. However, the underlying mechanism responsible for the inhibitory actions of Sulforaphane in the context of mycoplasmal pneumoniae are poorly understood. Here, we report that Sulforaphane is an inducer of heme oxygenase (HO)-1, a cytoprotective enzyme that catalyzes the degradation of heme through signaling pathways in human monocytes. Sulforaphane stimulated NF-E2-related factor 2 (Nrf2) translocation from the cytosol to the nucleus, and small interfering RNA-mediated knock-down of Nrf2 significantly inhibited Sulforaphane-induced HO-1 expression. Additionally, PI3K/Akt and ROS were also involved in Sulforaphane-induced Nrf2 activation and HO-1

expression, as revealed by the pharmacological inhibitors LY294002 and NAC. Moreover, Sulforaphane treatment inhibited MALP-2-induced pro-inflammatory cytokine secretion and pulmonary inflammation in mice, as well as MALP-2-triggered NF-κB activation. Furthermore, SnPP, a selective inhibitor of HO-1, reversed the inhibitory actions of Sulforaphane, while a carbon monoxidereleasing molecule, CORM-2, caused a significant decrease in MALP-2-induced cytokine secretion. Collectively, these results suggest that Sulforaphane functions as a suppressor of the MALP-2-induced inflammatory response, not only by inhibiting the expression of cytokines and the induction of HO-1 but also by diminishing NF-κB activation in cultured monocytes and the lungs of mice.

PU-3506

基于鹦鹉热衣原体质粒蛋白 CPSIT_p6 多表位融合抗原抗感染免疫保护作用研究

李育萌、陈恩、谢小平、刘双全
南华大学附属第一医院

目的 探究鹦鹉热衣原体（Chlamydia psittaci，Cps）质粒蛋白 CPSIT_p6 多表位融合抗原的抗感染免疫保护效果，为研制预防和治疗抗 Cps 感染的多肽疫苗奠定基础。
方法 生物信息学软件预测质粒蛋白 CPSIT_p6 的优势抗原表位，制备重组多表位肽段 P-P。重组肽段 P-P 经腹腔途径免疫雌性 BALB/c 小鼠，末次免疫 2w 后处死小鼠取血清检测血清抗体水平，取小鼠脾细胞上清细胞因子水平；末次免疫 2w 后呼吸道鼻滴接 Cps 6BC，评价重组肽段 P-P 抗 Cps 感染的保护效果，并通过免疫过继转移探讨 CD4+ T、CD8+ T 细胞在 P-P 诱导产生免疫保护中的作用。
结果 经腹腔免疫 3 次后，小鼠血清 IgG, IgA, IgM 以及 IgG 亚类水平均显著高于对照组；免疫小鼠脾细胞产生的 IFN-γ、IL-2 水平也明显高于对照组。P-P 免疫组小鼠经 Cps 6BC 呼吸道感染后，取肺组织进行培养，包涵体数量明显低于对照组（P＜0.01）；ELISA 法检测肺组织匀浆上清中细胞因子水平，实验组比对照组具有显著低的 IFN-γ 以及 IL-6 水平（P＜0.001）；肺组织经 H&E 染色和 S-P 免疫组织化学染色，对照组肺组织弥漫性炎性细胞大量浸润，重组肽段 P-P 免疫组肺组织病理改变明显轻于对照组，并能清晰识别肺泡结构，炎症清除明显；脾细胞过继转移实验结果显示，消耗 CD8+ T 细胞的脾细胞经过继转移后，实验组小鼠肺组织中的衣原体包涵体数量显著低于对照组，而消耗 CD4+ T 细胞的脾细胞经过继转移后，各组间的衣原体数量没有明显差异。
结论 多表位融合抗原 P-P 可诱导特异性体液免疫及 Th1 型细胞免疫应答，提示多表位融合抗原 P-P 是一种潜在的候选肽疫苗，对于衣原体疫苗研究与开发具有重要的价值。

PU-3507

Chlamydia trachomatis glycogen synthase promotes MAPKmediated proinflammatory cytokine production via TLR2/TLR4 in THP-1 cells

Yumeng Li[1]、zhenjie sun[2]、chunxue lu[2]、shuangquan liu[1]、en chen[1]
1. The First Affiliated Hospital of University of South China
2. University of South China

Aims To investigate the roles and mechanisms of C. trachomatis glycogen synthase (GlgA) in regulating the inflammatory response in THP-1 cells.
Main Methods In this work, after THP-1 cells were stimulated with GlgA, transcript and protein expression levels were measured by qRT-PCR and ELISA, respectively. Western blotting and

immunofluorescence were used to determine the signaling pathway involved in the inflammatory mechanism.
Key findings GlgA elicited the expression of interleukin-8 (IL-8), interleukin-1beta (IL-1β) and tumor necrosis factor alpha (TNF-α) in THP-1 cells, and the blockade of TLR2 and TLR4 signaling abrogated the induction of IL-8, TNF-α and IL-1β expression. Similarly, IL-8, IL-1β and TNF-α secretion was reduced by transfection with adominant negative plasmid (pDeNyhMyD88). Moreover, Western blotting and immunofluorescence experiments further validated that MAPKs and NF-κB signaling are involved in the transcription and translation of these cytokines. Treatment of the cells with ERK and JNK inhibitors dramatically attenuated the induction of IL-8, IL-1β and TNF-α.
Significance These results suggest that GlgA contributes to inflammation during C. trachomatis infection via the TLR2, TLR4 and MAPK/NF-κB pathways, which may enhance our understanding of the pathogenesis of C. trachomatis.

PU-3508

Emerging resistance mechanisms for 4 types of common anti-MRSA antibiotics in Staphylococcus aureus: a comprehensive review

刘婉婷
南方医科大学珠江医院

Staphylococcus aureus is one of the leading hospital-associated and community associated pathogens,which has caused a global public heath concern.The emergence of methicillin-resistant S.aureus(MRSA)along with the wide spread use of different classes of antibiotics has become a significant therapeutic challenge. Antibiotic resistance is a disturbing problem that poses a threat to humans.Treatment options for S.aureus resistanttoβ-lactam antibiotics include glycopeptide antibiotic,cyclic lipopeptide antibiotic,cephalosporins andoxazolidinone antibiotic.The most representative types of the se antibiotics are vancomycin,daptomycin,ceftaroline and linezolid.

PU-3509

Chlamydia psittaci plasmid-encoded CPSIT_P7 elicits inflammatory cytokines response in human monocytes via TLR4 and TLR6 signaling pathways

Yumeng Li[1]、qian chen[1]、shuanquan liu[1]、jian xiao[2]、yimou wu[3]
1. The First Affiliated Hospital of University of South China
2. Affiliated Nanhua Hospital
3. University of South China

The chlamydial plasmid, an important virulence factor, encodes plasmid proteins that play important roles in chlamydial infection and the corresponding immune response. However, the virulence factors and the molecular mechanisms of Chlamydia psittaci are not well understood. In the present study, we investigated the roles and mechanisms of plasmid-encoded protein CPSIT_P7 of C. psittaci in regulating the inflammatory response in THP-1 cells (human monocytic leukemia cell line). Based on cytokine arrays, THP-1 cells were stimulated by CPSIT_P7 can induce the expressions of interleukin-6 (IL-6), interleukin-8 (IL-8), and monocyte chemoattractant protein-1 (MCP-1). Moreover, the expressions of IL-6, IL-8, and MCP-1 stimulated by CPSIT_P7 were declined after the silencing of the Toll-like receptor 4 (TLR4) gene

by using small interfering RNA and transfection of dominant negative plasmid encoding TLR6 (pZERO-hTLR6), respectively. We further demonstrated that transfection with the dominant negative plasmid encoding MyD88 (pDeNy-hMyD88) and the dominant negative plasmid encoding Mal (pDeNy-hMal) could also abrogate them. Immunofluorescence assays showed that CPSIT_P7 could activate nuclear factor κB (NF-κB) signaling pathways. Altogether, our results indicate that CPSIT_P7 induces TLR4-Mal-MyD88-NF-κB and TLR6-Mal-MyD88-NF-κB signaling axis, and therefore contributing to inflammatory cytokines response.

PU-3510

TLR2 mediates autophagy through ERK signaling pathway in Chlamydia psittaci plasmid-encoded protein CPSIT_p7-stimulated RAW264.7 cells

Yumeng Li[3]、Ying Luo[2]、en chen[1]、xiaoping xie[1]、shuangquan liu[1]
1. The First Affiliated Hospital of University of South China
2. Qingyuan People's Hospital
3. The First Affiliated Hospital of University of South China

Chlamydia psittaci is a zoonotic pathogen in avian birds and humans. Macrophages as a major share of the innate immune defenses can fight infections by eradicating chlamydial infection and triggering an adaptive immune response. However, the molecular mechanisms of macrophages against C. psittaci infection are not well understood. In our current study, we investigated the roles and mechanisms of plasmid-encoded protein CPSIT_P7 of C. psittaci in regulating the autophagy in RAW264.7 cells (mouse macrophage cell line). The results demonstrated that stimulation of RAW264.7 with C. psittaci plasmid protein CPSIT_p7 induced the expressions of the autophagy signaling primal regulators LC3 and Beclin1, which could also significantly induced the phosphorylation levels of ERK, JNK, p38 and Akt. Next, siRNA knockdown of TLR2 resulted in a significant down-regulation of CPSIT_p7-triggered autophagy in RAW264.7 cells. Moreover, extracellular regulated protein kinase (ERK) inhibitor PD98059 could also markedly reduced the level of autophagy in CPSIT_p7-stimulated macrophages. In summary, these results indicate that TLR2 may play anessential role in induction of autophagy through ERK signaling pathway in CPSIT_p7-stimulated RAW264.7 cells.

PU-3511

5691 例住院儿童呼吸道合胞病毒感染检测分析

程相信、张宇培
柳州市妇幼保健院

目的 研究柳州地区住院患儿呼吸道合胞病毒感染现状，掌握柳州地区导致儿童急性呼吸道感染的呼吸道合胞病毒流行特征，为临床及社区防治提供依据。
方法 收集 2020 年 4 月至 2021 年 3 月在柳州地区某院住院的呼吸道感染患儿共 5691 例，取其鼻咽拭子，采用直接免疫荧光法，利用抗病毒特异性单克隆抗体快速对患儿鼻咽部分泌物进行呼吸道合胞病毒、腺病毒、流感病毒 A、B 型、副流感病毒Ⅰ、Ⅱ、Ⅲ型 7 种病毒抗原检测，对儿童急性呼吸道感染的病原体分布进行整体分析，统计出呼吸道合胞病毒的阳性率并分析其阳性率随不同季节及不同年龄段的变化规律。
结果 5691 例标本中 7 种呼吸道病原体阳性总数为 1038 例，总阳性率为 18.24%；其中呼吸道合胞病毒阳性为 797 例，阳性率 14.0%，占 7 种呼吸道病毒阳性病例中的 76.73%；其中以 1-6 月年龄组检出率最高，达阳性患儿的 43.54%，明显高于其他年龄段，其差异具有统计学意义（P＜

0.05），大于 1 岁的患儿呼吸道合胞病毒检出率随年龄的增加呈下降趋势；呼吸道合胞病毒检出率高峰在冬春季，明显高于夏秋季；混合感染参与率最高的是呼吸道合胞病毒，混合感染的患儿中，最常见的类型为 RSV+ADV 。

结论 呼吸道合胞病毒是柳州地区住院患儿呼吸道感染的重要病原体，好发于 1 岁以内的儿童，以 1-6 月龄为多，冬春季高发，近两年呼吸道感染合胞病毒感染率呈现上升趋势，提示临床及相关社区注意防治及避免交叉感染。

PU-3512

急性胰腺炎继发感染菌群分布及耐药性分析

谭超超
湖南省人民医院

目的 分析急性胰腺炎继发感染菌群分布及耐药性，为临床使用抗菌药物进行预防及控制感染提供依据。

方法 采取回顾性分析方法，统计某院三年内急性胰腺炎患者发生继发感染的病例，收集患者的基本信息以及继发感染的细菌培养和药敏分析结果，分析其菌群感染特点及耐药情况。

结果 2969 例急性胰腺炎患者中存在继发感染且微生物培养为阳性的有 138 例患者，总共分离出 216 例菌株，G-菌占 54.6%，G+菌占 36.1%，真菌 9.2%。其中大肠埃希菌占 25.9%，对头孢唑啉和氨苄西林耐药率高于 78%，具有多重耐药特点；肠球菌分离出 36 例，占 16.7%，粪肠球菌和屎肠球菌对四环素类抗生素均有较高的耐药性，屎肠球菌对青霉素、氨苄西林、高水平庆大霉素、环丙沙星、左氧氟沙星、莫西沙星、红霉素的耐药率均高于粪肠球菌；葡萄球菌 36（16.7%）例，头孢西丁筛选阳性率高于 78%，对多种抗生素具有较高的耐药率；真菌对常见抗真菌药物未见耐药情况。

结论 急性胰腺炎继发感染主要以肠道杆菌为主，其次为葡萄球菌及肠球菌，其耐药性大多呈现多重耐药。

PU-3513

鱼腥草素钠对 48 株多重耐药铜绿假单胞菌抑菌效果的研究

金秀秀、庄婉珍
中国人民解放军联勤保障部队第九〇〇医院

目的 分析多重耐药铜绿假单胞菌的临床分布特点和抗生素耐药情况，充分了解抗多重耐药铜绿假单胞菌的重要性，并通过体外药敏试验研究鱼腥草素钠对多重耐药铜绿假单胞菌体外抗菌作用，旨于为临床治疗提供思路和参考依据。

方法 对中国人民解放军联勤保障部队第 900 医院患者标本中的病原菌进行培养、分离，采用质谱仪和药敏系统及纸片扩散法鉴定出多重耐药铜绿假单胞菌并分析其临床分布特点和常用抗生素耐药情况。用琼脂打孔法确认鱼腥草素钠的抗多重耐药铜绿假单胞菌活性。

结果 共分离出中国人民解放军联勤保障部队第 900 医院的 48 株多重耐药铜绿假单胞菌中有 39 株对鱼腥草素钠敏感，其中属于高度敏感多重耐药铜绿假单胞菌有 30 株（61.22%），中度敏感有 9 株（18.75%）。39 株均出现不同大小的抑菌圈（79.59%），剩余 9 株未出现明显抑菌圈，占比 18.75%。鱼腥草素钠对质控菌株 ATCC 27853 的抑菌圈直径为 27mm，属于高度敏感。提示鱼腥草素钠对多重耐药铜绿假单胞菌有不同程度的抑制作用。

结论 本次研究在基于多重耐药铜绿假单胞菌的临床分布特点及抗生素耐药情况的基础上，进行琼脂打孔法形成鱼腥草素钠的抑菌圈，反映体外分离的多重耐药铜绿假单胞菌对鱼腥草素钠的敏感程

度。结果表明，鱼腥草素钠对多重耐药铜绿假单胞菌的生长有抑制作用，有成为临床上抗多重耐药菌的辅助药物的可能。

PU-3514

粘液型与非粘液型假单胞菌的院感分布及耐药性分析

肖启国、汤美华、郑康
衡阳市中心医院

目的 分析该院 2019 年 1 月-2020 年 12 月临床分离的粘液型与非粘液型铜绿假单胞菌（pseudomonas aeruginosa,PA）的分布情况及耐药性，指导临床合理用药，控制铜绿假单胞菌的医院感染。
方法 对临床分离出来的 486 株铜绿假单胞菌进行标本，科室分布的统计及耐药性分析，并对抗菌药物联合治疗前后的粘液型铜绿假单胞菌进行药敏分析。
结果 486 株铜绿假单胞菌中粘液型占 15.2%（74/486），非粘液型占 84.8%（412/486），标本主要来自痰液，占 63.2%（307/486），其次为伤口分泌物及穿刺液，分别占 21%（102/486），10%（49/486）；主要分布于 ICU，呼吸内科，分别占 36%（175/486），24.1%（117/486）;黏液型和非黏液型 PA 对常用 14 种抗菌药物的耐药率比较结果为：非黏液型 PA 对庆大霉素、头孢噻肟、氨曲南、头孢吡肟、环丙沙星和左氧氟沙星的耐药率显著高于黏液型 PA（P<0.05），而对亚胺培南、美罗培南、哌拉西林/他唑巴坦、阿米卡星、头孢他啶和头孢哌酮/舒巴坦的耐药率，两者差异无统计学意义（P>0.05）。抗菌药物联合治疗黏液型 PA 感染前后，对亚胺培南和美罗培南的耐药率一致；对阿米卡星、头孢噻肟的耐药性，治疗后明显高于治疗前（P<0.05）；其他抗菌药物的耐药率也出现不同程度的增高。
结论 该院 PA 主要分离自痰标本，以 ICU 感染最为严重，其次为呼吸内科，非粘液型 PA 的耐药率普遍较粘液型 PA 高，黏液型 PA 体外药敏试验虽耐药性较低，但体内用药治疗效果不佳，因此临床应使用体外药敏敏感的药物结合能抑制细菌表面生物膜作用的药物联合使用，方能达到较好的治疗效果。以便控制医院的感染。

PU-3515

无乳链球菌感染性疾病的体外药物敏感性及其临床分布研究

郭 昊
滨州医学院烟台附属医院

目的 了解无乳链球菌感染性疾病的临床分布并对其分离株进行药物敏感性分析，为临床合理使用抗菌药物提供依据。
方法 收集 2018 年 1 月－2019 年 12 月门诊及住院患者无乳链球菌阳性分离株，采用纸片扩散法(K-B 法)对抗菌药物进行敏感性分析，克林霉素和红霉素双纸片协同试验（D 试验）来确定其耐药表型.
结果 分离的 122 株无乳链球菌主要来自于妇产科，占 39.3％（48 株），标本的主要来源为阴道分泌物，占 40.9％（50 株）；克林霉素和红霉素的耐药率最高，分别为 58.1％ 和 55.7％，其中结构性耐药（红霉素耐药，克林霉素耐药）是其主要的耐药表型；其次为左氧氟沙星，耐药率为 20.4％；2018 年左氧氟沙星耐药率为 27.4％,高于 2017 年的 13.3％；未发现对头孢曲松、青霉素、万古霉素、头孢噻肟耐药的菌株。
结论 选择红霉素和克林霉素来作为治疗以及预防无乳链球菌感染的药物应用价值应重新评估；喹诺酮类抗菌药物的耐药率有所增加，应予以重视，青霉素类可作为无乳链球菌感染性疾病治疗的首选药物。

PU-3516

烟台地区 2016-2019 年大肠埃希菌耐药性分析

张允艺
滨州医学院烟台附属医院

目的 对烟台地区 2016-2019 年大肠埃希菌耐药性进行分析，为临床上快速合理有效的用药提供参考依据。
方法 使用 Excel 对 2016-2019 年大肠埃希菌的抗药性实验数据进行统计分析。而每年的结果是用全自动微生物分析系统 Vitek2 C60 进行初步药敏试验，再用纸片扩散法近一步验证结果。
结果 大肠埃希菌在烟台地区 2016-2019 年的检出率基本上保持在第二位。大肠杆菌对头霉素类、喹诺酮类部分药物具有稍微强的抗药性；对于氨基糖苷类等一些药物抗药率偏低。
结论 大肠埃希菌的耐药性变化明显，但治疗大肠杆菌药物选择多。感染后应及时治疗；平时也应养成良好的卫生习惯。

PU-3517

荧光定量 PCR 检测妊娠晚期妇女 B 族链球菌的情况

张娜
滨州医学院烟台附属医院

目的 分析荧光定量 PCR 法检测妊娠晚期妇女感染 B 族链球菌（GBS）的高危因素。
方法 随机选取 2018 年 6 月到 2019 年 6 月在威海市立医院就诊的妊娠晚期孕妇作为研究对象，取孕妇阴道分泌物和直肠标本后用实时荧光定量 PCR 的方法统计孕妇 B 族链球菌的带菌率，然后分别统计孕妇的年龄、是否多次妊娠、妊娠期糖尿病和瘢痕子宫对孕妇感染 B 族链球菌的影响。
结果 妊娠晚期孕妇感染 B 族链球菌受妊娠期糖尿病的影响（$P<0.05$），而与孕妇的年龄、妊娠次数以及是否瘢痕子宫等因素无关。
结论 妊娠期糖尿病会增加妊娠晚期孕妇感染 B 族链球菌的概率，是孕妇感染 GBS 的重要因素。

PU-3518

群体感应在鲍曼不动杆菌生物膜形成中的作用

张康见
山东大学第二医院

通过对浮游和生物膜状态鲍曼不动杆菌标准菌株 ATCC 17978 进行 RNA-seq 测序，并借助于生物信息学技术，研究其生物膜形成与群体感应之间的关系，进而寻找抑制鲍曼不动杆菌生物膜形成的靶点，为临床治疗生物膜相关感染提供新的启发。通过对浮游和生物膜状态下的鲍曼不动杆菌进行链特异性测序，获得差异表达基因，经生物信息学技术分析候选差异表达基因可能参与调控的细菌细胞组分、参与的代谢过程和具备的生物学功能。QRT-PCR 技术验证测序结果。建立生物膜模型，检测群体感应分子 C12-HSL 对生物膜形成的影响。以微孔板法定量，结晶紫染色和扫描电镜定性检测其生物膜的形成能力。用双硫仑和牛磺酸干预鲍曼不动杆菌生物膜的形成，以紫外分光光度法检测生物膜状细菌乙醇脱氢酶活性的变化。最后以一定量的临床鲍曼不动杆菌分离株验证双硫仑对生物膜的抑制作用。转录组测序共获得 504 个差异表达基因，264 个下调，240 个上调。QRT-PCR 验证结果与测序数据一致。C12-HSL 的加入使生物膜的形成能力增强，细菌运动性增强。双硫仑处理后，生物膜内细菌乙醇脱氢酶的活性减弱，群体感应相关基因的表达下调，生物膜形成能力下降。双硫仑对鲍曼不动杆菌生物膜形成的抑制作用在临床分离株中同样有效。鲍曼不动杆菌

生物膜的形成与群体感应系统相关。群体感应增强，生物膜形成能力和细菌运动性增强。双硫仑处理后鲍曼不动杆菌乙醇脱氢酶活性减弱，同时群体感应基因表达下调，生物膜形成能力下降。

PU-3519

一例肠炎沙门氏菌引起的血流感染

徐艳
江苏省人民医院（南京医科大学第一附属医院）

2021 年 5 月 26 日，我院于血培养结果中发现一例肠炎沙门氏菌引起的血流感染。患者约 5 月 12 日前后，因发热（体温 40℃）及后背下腹部疼痛于当地医院就诊，医生开具头孢他啶进行抗感染治疗。患者体温降至正常四天后，于 5 月 20 日再次发热（体温 38~39℃），后背下腹部疼痛未减轻。患者于 5 月 24 日于我院就诊，5 月 26 日血培养结果发布为肠炎沙门菌感染。感染科医生暂用比阿培南对患者进行抗感染治疗。明确后背部疼痛病因后，于 5 月 27 日转入 ICU 进行手术治疗，此时药敏结果已发布。值得一提的是，该菌对于氨基糖苷类抗生素、第一代和第二代头孢菌素和头霉素体内治疗无显著效果，对于左氧氟沙星无 MIC 折点。故改用 KB 法对左氧氟沙星重新进行药敏测试，结果显示为中介。随后临床抗生素用药更新为美罗培南、左氧氟沙星及利奈唑胺联合抗感染。目前病人情况已好转。

PU-3520

泰安市儿童流感嗜血杆菌感染耐药性分析

高雪
泰安市中心医院

目的 分析泰安市儿童流感嗜血杆菌感染药物敏感情况及病例分布，为临床诊疗提供依据。
方法 收集 2019-2020 年儿童患者呼吸道流感嗜血杆菌，采用头孢硝噻吩纸片法检测 β-内酰胺酶，纸片扩散法检测常用 13 种常用抗生素的耐药情况，进行分析统计。
结果 共收集 352 株流感嗜血杆菌，结果显示，流感嗜血杆菌对氨苄西林和复方新诺明耐药率为 84.5%、77.5%；对阿莫沙星/克拉维酸、氨苄西林/舒巴坦、头孢呋辛耐药率为 23.5%、31.5%、40.5%；对氯霉素、四环素耐药率为 3.8%、8.6%；对头孢噻肟、亚胺培南、美洛培南、环丙沙星、左氧氟沙星、阿奇霉素敏感性为 100%。
结论 流感嗜血杆菌是引起儿童呼吸道感染的重要致病菌，临床医生应熟悉流感嗜血杆菌对常用抗生素的药物敏感状况，提高用药准确率。

PU-3521

血流感染艰难梭菌病例分享

程芳
山东第一医科大学第一附属医院

患者老年男性，因“突发意识不清 3 月余”入院。因肺部感染长期使用抗菌药物，导致在治疗过程中出现顽固性腹泻，并不明原因的发热，为更进一步治疗，送检血培养，培养结果是艰难梭菌，告知临床，给与相应治疗患者体温恢复正常。

PU-3522

Construction of an autophagy interaction network based on competitive endogenous RNA reveals the key pathways and central genes of SARS-CoV-2 infection in vivo

Haifang Zhang、Hong Du
Department of Clinical Laboratory, The Second Affiliated Hospital of Soochow University, Suzhou, Jiangsu, 215004, China.

As of April 1, 2021, more than 2.8 million people have died of SARS-CoV-2 infection. In addition, the mutation of virus strains that have accompanied the pandemic has brought more severe challenges to epidemic control. Host microRNAs (miRNAs) are widely involved in a variety of biological processes of coronavirus infection, including autophagy in SARS-CoV-2 infection. However, the mechanisms underlying miRNAs involved in autophagy in SARS-CoV-2 infection have not been fully elucidated. In this study, the miRNA and messenger RNA (mRNA) expression profiles of patients with SARS-CoV-2 infection were investigated based on raw data from Gene Expression Omnibus (GEO) datasets, and potential novel biomarkers of autophagy were revealed by bioinformatics analyses. We identified 32 differentially expressed miRNAs and 332 differentially expressed mRNAs in patients with SARS-CoV-2 infection. Cytokine receptor related pathways were the most enriched pathways for differentially expressed miRNAs identified by pathway analysis. Most importantly, an autophagy interaction network, which was associated with the pathological processes of SARS-CoV-2 infection, especially with the cytokine storm, was constructed. In this network, hsa-miR-340-3p, hsa-miR-652-3p, hsa-miR-4772-5p, hsa-miR-192-5p, TP53INP2, and CCR2 may be biomarkers that predict changes in mild SARS-CoV-2 infection. Some molecules, including hsa-miR-1291 and CXCR4, were considered potential targets to predict the emergence of severe symptoms in SARS-CoV-2 infection. To our knowledge, this study provided the first profile analysis of an autophagy interaction network in SARS-CoV-2 infection and revealed several novel autophagy-related biomarkers for understanding the pathogenesis of SARS-CoV-2 infection in vivo.

PU-3523

降钙素原、C 反应蛋白在鉴别不同细菌血流感染中的应用价值

袁勇、姚瑶、孔凡斌、谢享园
昆明市延安医院

目的 探讨血清降钙素原（PCT）和 C 反应蛋白（CRP）在鉴别革兰阳性菌和革兰阴性菌所致的血流感染中的应用价值，为临床医生早期诊断和治疗提供依据。
方法 选取 2019 年 1 月-2020 年 12 月在昆明市延安医院同时进行血培养、PCT 和 CRP 检测的住院患者为研究对象，收集患者血培养、PCT 和 CRP 的结果，应用统计学软件 SPSS25.0 比较血培养阳性组和阴性组 PCT 和 CRP 检测水平之间的关系
结果 共收集到同时测定血培养、PCT 和 CRP 的病例 334 例。血培养阳性病例为 153 例，PCT 水平为 1.26（0.27，22.62）ug/L，CRP 水平为 100.68（25.00，178.69）mg/L；血培养阴性为 181 例，PCT 水平为 0.27（0.11，1.15）ug/L，CRP 水平为 33.98（2.15，128.91）mg/L。采用 Mann-Whitney U 检验比较血培养阳性组和血培养阴性组 PCT 及 CRP 水平均有显著的统计学差异（P<0.001）。血培养阳性组中革兰阳性菌感染病例 60 例，PCT 和 CRP 的水平分别为 0.33(0.13,1.21)ug/L、52.37(10.43,129.83)mg/L；革兰阴性菌感染病例 93 例，PCT 和 CRP 的水平分别为 8.57(0.61,43.23)ug/L、128.21(43.38,194.09)mg/L。Mann-Whitney U 检验比较革兰阳性菌组与革兰阴性菌组间 PCT 和 CRP 水平的差异有统计学意义（P<0.05）。分别对革兰阳性菌组和革兰阴性菌组做 ROC 曲线，曲线下面积分别为 0.527、0.583；在革兰阴性菌组的曲线下面积分

别为 0.79、0.69，PCT 和 CRP 在鉴别革兰阴性菌感染时有更高的价值，且 PCT 比 CRP 有更高的价值。
结论 PCT 和 CRP 对鉴别革兰阳性菌与革兰阴性菌血流感染有一定的临床应用价值。

PU-3524

肺炎克雷伯菌中新型毒素-抗毒素系统的鉴定

张小团、曾童、刘罗根、刘卓然
南华大学附属第二医院

目的 鉴定肺炎克雷伯菌毒力质粒中一对特殊结构基因序列的表达产物是否具有毒素-抗毒素系统的生物活性。
方法 采用细菌重基因组测序和纳米孔测序组装肺炎克雷伯菌的完成图，对全基因组序列进行注释和生物信息学分析，采用同源重组的方法构建基因表达载体并转入到大肠杆菌 DH5α 中，分别使用 IPTG 和阿拉伯糖诱导蛋白的表达，OD600 检测细菌的生长状态，平板菌落形成试验观察细菌的生长情况。
结果 通过对 13 株肺炎克雷伯菌进行全基因组测序发现，在毒力质粒中存在一对特殊结构的基因序列，它们之间共用 4 个碱基，基因注释为一对假定蛋白（本课题组暂命名为 KipTA），其中 KipT 以 ATG 为启动子，KipA 以 GTG 为启动子。标签蛋白 WB 提示成功构建 KipT-pBAD33 和 KipA-pQE-80L 表达载体。通过 IPTG 诱导 KipT 表达发现，KipT 可以对细菌生长产生显著的毒杀作用，但是诱导 KipA 表达却可以拮抗 KipT 对细菌的毒素作用。
结论 KipTA 为一对新型的毒素-抗毒素复合蛋白，其中 KipT 为毒素蛋白，KipA 为抗毒素蛋白。

PU-3525

柳州地区住院患儿肺炎链球菌临床分布及耐药性分析

张宇培、程相信
柳州市妇幼保健院

目的 评价柳州地区儿童肺炎链球菌临床分离株的临床分布及耐药情况，为儿童肺炎链球菌感染相关性疾病的治疗与防控提供参考依据。
方法 收集柳州市妇幼保健院 2020 年 4 月－2021 年 3 月间的儿科住院患者临床分离的肺炎链球菌 412 株，分析其来源标本、分离季节及来源患者年龄分布特征，及其临床常用抗菌药物敏感性试验情况。
结果 共分离到肺炎链球菌 412 株，占检出细菌总数的 14.91%。肺炎链球菌来源构成比中，前 3 位标本依次为痰液 398 例（96.60%）、肺泡灌洗液 8 例(1.94%)和分泌物 3 例(0．73%)，血液标本仅 1 例（0．24%）；412 株肺炎链球菌临床分离菌株中，冬季分离株数所占比例高于其他季节，差异具有统计学意义（P＜0.05），春、夏、秋季间比较差异无统计学意义（P＞0.05）；在各年龄段患儿中，以 3 岁以下患儿检出为主（83.64%）；药敏结果显示肺炎链球菌对青霉素、厄他培南、左氧氟沙星、泰利霉素、利奈唑胺、万古霉素、氯霉素、头孢噻肟较敏感（89.1%~100%），对红霉素、四环素和复方新诺明耐药率较高（88.9%~97.6%）。
结论 在寒冷冬季，应加强预防 3 岁以下儿童肺炎链球菌感染，引起重症感染时治疗应首选青霉素和头孢噻肟等三代头孢菌素，经验性治疗可选用左氧氟沙星、万古霉素，从分析可见肺炎链球菌对常用抗菌药物特别是大环内酯类耐药日趋严重，故临床上应避免选用红霉素、复方新诺明及四环素等抗菌药物，重视药敏检验结果，加强临床沟通，进行科学合理的规范治疗，尽量减少细菌耐药的发生。

PU-3526

血培养阳性标本质谱快速鉴定联合直接快速药敏试验的应用评估

陆燕飞、文怡
江苏省人民医院（南京医科大学第一附属医院）

目的 评估血培养阳性标本质谱快速鉴定联合直接快速药敏试验的可行性，为临床血流感染及时用药提供依据。
方法 收集 2020 年 4 月-2020 年 7 月南京医科大学第一附属医院血培养阳性标本，利用基质辅助激光解析电离飞行时间质谱直接鉴定，根据欧洲药敏试验委员会（EUCAST）颁布的阳性血培养液直接快速药敏（rapid antimicrobial susceptibility testing, RAST）指南进行快速药敏，将 4h、6h 和 8h 判读的药敏结果与常规药敏结果比较。
结果 本研究共纳入血培养阳性菌株 118 株，包括肺炎克雷伯菌 50 株、大肠埃希菌 40 株、金黄色葡萄球菌 16 株、肠球菌属 12 株。肠杆菌目细菌在 4h、6h、8h 判读药敏结果时与常规结果的符合率分别为 76.8%、92.6%、94.2%；金黄色葡萄球菌分别为 56.3%、100%、100%；肠球菌属分别为 41.7%、74.8%、94.5%。6h 判读肠杆菌目细菌药敏符合率优于 4h（P<0.05），与 8h 无差异（P>0.05）；耐碳青霉烯类肠杆菌科细菌（Carbapenem resistant Enterobacteriaceae bacteria，CRE） 在 4h、6h、8h 的检出率及药敏符合率无统计学差异（P>0.05）；肠球菌属在 8h 判读的药敏符合率高于 4h 和 6h（P<0.001）。
结论 阳性血培养液 RAST 4h 即可判断是否存在 CRE 感染并推测其整体抗菌谱，6h 判读 MRSA 及肠杆菌目细菌整体抗菌谱在时间和准确性上具有优势，8h 可作为肠球菌药敏结果判读的最佳时间。血培养阳性标本 MALDI-TOF MS 快速鉴定联合 EUCAST 直接快速药敏试验方法简单、速度快、易于标准化，常规试验室可开展。

PU-3527

院内混合血流感染患者临床特征及预后危险因素分析

陆燕飞、倪芳
江苏省人民医院（南京医科大学第一附属医院）

目的 分析院内混合血流感染（nosocomial polymicrobial bloodstream infection nPBSI）患者的临床特征及预后危险因素，为 nPBSI 患者治疗及预后判断提供依据。
方法 回顾性分析 2017-2020 年南京医科大学第一附属医院 nPBSI 患者的临床资料及病原菌分布情况，采用 Logistic 回归分析患者的死亡危险因素。
结果 共 159 例患者纳入研究，其中男性占 68.6%（109/159），患者平均年龄 60.1±15.5 岁，主要来自 ICU（51/159，32.1%）和肝胆胰外科（33/159，20.8%），消化系统疾病（106/159，66.7%）是最常见的基础疾病，患者多有外科手术史（127/159，79.9%），死亡率为 34%（54/159）；共分离病原菌 345 株，排名前三位的病原菌分别为肺炎克雷伯菌、大肠埃希菌、屎肠球菌，以两种病原菌混合感染为主（134/159，84.3%），最常见的细菌组合为大肠埃希菌+肠球菌属（16/159，10.1%）；多重耐药鲍曼不动杆菌（MDRAB）nPBSI、机械辅助通气、连续性血液净化、合并肺部感染、感染性休克是混合血流感染患者死亡的独立危险因素。
结论 nPBSI 患者多发生于存在消化道疾病的老年男性；临床用药应考虑到不同病原菌组合模式；患者存在 MDRAB nPBSI、机械辅助通气、感染性休克、肺部感染、连续性血液净化时死亡风险增加。

PU-3528

生殖支原体感染的临床分布和耐药性分析

曾丽洪、张小团、刘卓然
南华大学附属第二医院

生殖支原体的感染在临床上非常常见，其耐药率也受到广泛的关注。本文回顾性分析了 502 例临床疑似生殖支原体感染患者的临床资料和培养结果。共检出生殖支原体阳性 334 例，阳性率 66.53%，年龄中位数为 34 岁，其中女性阳性率显著高于男性，比例为 17.6:1。生殖支原体的临床分布中以解脲脲原体为主，检出率为 87.72%，男女性别构成比无明显差异。生殖支原体对喹诺酮类和大环内酯类的耐药性较高，对克林霉素的耐药率最高，达到 53.5%。其中解脲脲原体对加替沙星、左氧氟沙星、阿奇霉素、克拉霉素和红霉素的耐药率均低于 10%。而人型支原体或人型支原体与解脲脲原体的混合药敏却表现相反，对阿奇霉素、克拉霉素、红霉素和罗红霉素表现为高度耐药，耐药率均大于 60%。因此，临床应更加关注支原体培养及药敏结果，合理使用抗生素，延缓抗生素耐药。

PU-3529

827 例血流感染患者的临床分布及病原谱分析

张小团、刘卓然
南华大学附属第二医院

血流感染（Bloodstream infection，BSI）是一种严重感染性疾病，研究 BSI 的临床分布及病原菌流行特征，可为经验性治疗提供用药参考。分析某院 2016—2018 年发生 BSI 患者的临床资料及病原菌的耐药数据。827 例 BSI 患者共检出病原菌 863 株，其中革兰阴性菌 600 株，占 69.5%，以大肠埃希菌和肺炎克雷伯菌为主；革兰阳性菌 218 株，占 25.3%，以金黄色葡萄球菌为主；深部真菌 45 株，占比 5.2%。科室分布主要以消化内科、ICU、泌尿外科和儿科为主。儿童中 0-1 岁患儿 BSI 的发生率最高，成人中>60 岁患者 BSI 的发生率达到了 51.4%。大肠埃希菌和肺炎克雷伯菌对头孢曲松的耐药性较高，分别为 53.6%和 38.3%，对 β-内酰胺/酶抑制剂和碳青霉烯类的耐药性较低。未检出耐万古霉素金黄色葡萄球菌，但 MRSA 检出率 12.5%。因此，本院 BSI 患者病原菌分布以革兰阴性菌为主，常见细菌耐药性较为严重，年龄和科室分布存在较大差异，临床应进行分层诊疗，合理选用抗生素。

PU-3530

2016—2018 年某医院肺炎克雷伯菌的临床分布及耐药性分析

张小团、李蓓、徐畅、王露、刘卓然
南华大学附属第二医院

目的 分析某院肺炎克雷伯菌（Klebsiella pneumoniae, KPN）的临床分布，产超广谱 β-内酰胺酶（ESBLs）的情况以及综合耐药特点，为临床经验性选用抗生素提供参考。
方法 回顾性分析某院 2016—2018 年临床分离培养的 KPN 的耐药数据及临床资料，所有菌株均采用全自动分析仪进行菌种鉴定和药敏分析。
结果 3 年间共检出非重复 KPN2 211 株，主要样本类型为痰液（57.35%）和尿液标样本（14.97%），科室分布前三的依次为 ICU 病房（12.39%）、泌尿外科（11.80%）和儿科（11.22%）。2211 株 KPN 共检出 ESBLs 阳性 708 株，检出率为 32.02%。KPN 对复方新诺明、一、二代头孢和三代头孢曲松的耐药率已经超过 40%；但对酶抑制合剂哌拉西林他唑巴坦、头孢

哌酮舒巴坦的耐药率较低，分别为 9.60%和 10.09%。对阿米卡星、亚胺培南、美罗培南保持高度的敏感性，耐药率分别为 5.21%，5.20%，5.88%。然而，比较尿液、胆汁、血液和痰液样本中 KPN 的耐药性发现，尿液分离株的耐药性普遍较高（P <0.05）。
结论 KPN 样本来源以痰和尿液为主，主要分布在 ICU 病房、泌尿外科和儿科。ESBLs 检出率较高，耐药情况较为严峻，并且不同样本来源菌株的耐药性较大差异，以尿液分离株的耐药性更为严重。医院需加强对重点科室，不同样本中 KPN 的耐药性监测，合理使用抗菌药物。

PU-3531

海绵附生放线菌抗结核分枝杆菌 活性物质的筛选及分离

冯鹭
山东大学第二医院

目的 从海绵共附生的放线菌代谢物质中筛选出具有抗结核分枝杆菌活性的新型物质。
方法 采用平板稀释法从南海海域采集的海绵中分离共附生放线菌菌株，使用微孔板稀释法评估放线菌代谢物抗结核分枝杆菌 H37Rv 能力。根据分子量和极性，使用高效液相色谱(HPLC)对初筛具有较高抑菌活性的菌株培养上清进行分离，并分别从分离各组分中进一步筛选、鉴定具有抑制结核杆菌生长作用的活性物质。提取该菌株的基因组 DNA，采用通用引物对其 16SrRNA 行 PCR 扩增，并对扩增产物进行测序比对。
结果 分离出的 416 株放线菌中，6 株具有抗结核分枝杆菌功能，其中编号为 NH128 菌株的培养上清中含有抑制 H37Rv 生长的活性物质且作用较为明显;对其进行分离后的组分 F3 具有较高的抑菌活性;进一步通过 HPLC 和微孔板稀释法鉴定出，F3 的亚组分 S3 含有高抑菌活性的物质，其 MIC50 约为 3μg/mL。对 NH12816SrRNA 序列比对结果显示，其与 Aclinomycetales(R03AY94262)同源性为 9%。
结论 南海海域海绵附生放线菌能够产生较高的抗结核分枝杆菌活性物质;NH128 菌株可能为放线菌菌属 Aclinomycetales(R03AY94262)的变种。

PU-3532

1218 例泌尿生殖道支原体培养及药敏结果分析

何天娇
西安医学院第一附属医院

目的 研究我院支原体阳性率及 12 种抗生素药敏结果情况。
方法 回顾性分析本院 2018 年 5 月-2019 年 12 月在本院就诊的疑似泌尿生殖道支原体感染 1218 例患者的临床资料。
结果 所有患者中支原体阳性为 435 例（35.71%），女性支原体检出阳性率 56.09%高于男性 43.91%，差异显著，P<0.05；其中 Uu 阳性 322 例（74.02%）,Mh 阳性 11 例（2.53%）,Mh 混合型为 102 例（23.45%）。药敏试验显示药敏试验显示 Uu、Uu 十 Mh、Mh 耐药性存在一定差异。单纯 Uu 感染者对杭生素的敏感性明显高于混合感染者，美满霉素、强力霉素与新型大环内酯类抗生素交沙霉素对支原体敏感性最高。
结论 本院 Uu 是引起泌尿生殖道感染的主要支原体,女性患者感染率高于男性,对疑似支原体感染的患者需要进行支原体的分离培养鉴定和药敏检测，临床应根据感染类型和抗生素敏感性的不同选择合适的药物进行治疗。

PU-3533

某三级医院儿童下呼吸道感染细菌的流行特征及耐药性分析

张小团、徐畅、王露、李蓓、刘卓然
南华大学附属第二医院

目的 了解儿童呼吸道感染细菌的流行特征及耐药性，为临床经验性诊治提供参考。
方法 回顾性分析我院近三年儿童呼吸道感染细菌（除外肺炎支原体）的检出情况、不同季节的变化规律、年龄的分布和重点细菌的耐药性分析。
结果 共检出细菌 2267 株，其中革兰阳性菌 1133 例，占比 50.0%，革兰阴性菌 1114 例，占比 49.1%，真菌 20 株，占比 0.9%。检出率排名前五的细菌依次是肺炎链球菌 759 株，流感嗜血杆菌 450 株，金黄色葡萄球菌 352 株，卡他莫拉菌 232 株，肺炎克雷伯菌 136 株。这些细菌以冬、春季节为主要流行，且主要好发于婴幼儿期。细菌耐药性监测显示，肺炎链球菌青霉素的耐药率为 0.4%，甲氧西林耐药金黄色葡萄球菌的为 20.9%，产超广谱 β-内酰胺酶的肺炎克雷伯菌为 36.0%，β-内酰胺酶阳性的流感嗜血杆菌和卡他莫拉菌分别为 59.8%和 97.8%。
结论 儿童下呼吸道病原菌的耐药性较为严峻，其细菌感染以肺炎链球菌和流感嗜血杆菌为主，冬、春季为高发期，0-3 岁为高发人群，家庭护理和临床诊疗应尤其注意上述特征。

PU-3534

儿童感染铜绿假单胞菌的流行趋势及耐药变迁

杜琴
江西省儿童医院

目的 了解铜绿假单胞菌儿童分离株的临床分布特点及对临床常用抗菌药物耐药的耐药特征，以便指导临床合理用药。
方法 常规方法进行菌株分离，全自动微生物分析仪进行菌株鉴定及药敏试验，依据当年度美国临床实验室标准化委员会（CLSI）标准判断抗菌药物的敏感性，WHONET 5.5 软件进行统计分析。
结果 2015－2018 年共分离获得铜绿假单胞菌 319 株，药物耐药率较 2000-2001 年相比，头孢他啶耐药率下降达 47.25%，阿米卡星、环丙沙星、庆大霉素耐药率变化在 10%左右。2015-2018 四年间对亚胺培南的耐药率为 13.8%。
结论 近年来我院 MRPA 检出率明显下降;哌拉西林、哌拉西林他唑巴坦、头孢他啶可作为临床治疗铜绿假单胞菌感染的一线药物。

PU-3535

结核分枝杆菌抗原检测（胶体金法）的实验室诊断应用评价

夏文颖、刘根焰
南京医科大学第一附属医院（江苏省人民医院）

目的 评估结核分枝杆菌抗原检测（胶体金法）在结核分枝杆菌培养中的临床应用价值。
方法 收集南京医科大学第一附属医院（江苏省人民医院）2018 年 6 月至 2020 年 6 月的结核培养标本 875 例，BACTEC MGIT 320 仪器培养，仪器培养阳性后，培养液分别进行抗酸染色、结核分枝杆菌核酸检测（PCR 方法）和结核分枝杆菌抗原检测（胶体金法），以 PCR 方法作为金标准。
结果 875 例结核培养标本经仪器培养后，145 例标本培养阳性，抗酸涂片阳性为 101 例，结核分枝杆菌抗原检测阳性 62 例， PCR 检测阳性 64 例，以 PCR 方法为金标准，结核分枝杆菌胶体金

法的敏感性和特异性分别为 97.0%和 100%，阳性预测值和阴性预测值分别为 100%和 97.7%，与 PCR 方法结果一致性检验 Kappa 值为 0.972（P<0.01）。
结论 结核分枝杆菌抗原（胶体金法）检测方法在结核培养检测中具有很好的临床诊断应用价值。

PU-3536

耐碳青霉烯类肠杆菌科细菌血流感染临床特征和危险因素分析

夏文颖、倪芳
南京医科大学第一附属医院（江苏省人民医院）

目的 探讨医院耐碳青霉烯类肠杆菌科细菌(carbapenem-resistant Enterobacteriaceae，CRE)血流感染(bloodstream infection，BSI)患者的临床特征及危险因素分析，为临床耐碳青霉烯类肠杆菌科细菌血流感染防治提供依据。
方法 回顾性分析 2014 年 1 月至 2020 年 12 月江苏省人民医院诊断为耐碳青霉烯类肠杆菌科细菌血流感染的 228 例患者的临床资料，分析 CRE-BSI 患者临床特征，应用 Logistic 回归分析 CRE-BSI 的危险因素。
结果 175 例为男性患者，53 例为女性患者。其中，158 例（69.3%）患者合并有一种或一种以上基础疾病，130 例（57%）患者感染前有外科手术经历，220 例（96.5%）患者治疗过程中有一种或一种以上侵入性操作，患者中 132 例（57.9%）年龄在 60 岁及以上。肺炎克雷伯菌为临床最常见 CRE-BSI 感染病原菌，120 例（52.6%）患者预后不良。Logistic 回归显示年龄、机械通气血液透析是 CRE-BSI 的危险因素。
结论 本研究表明耐碳青霉烯类肠杆菌科细菌血流感染患者存在高龄化、高死亡率；年龄、机械通气和血液透析是耐碳青霉烯类肠杆菌科细菌血流感染预后不良的危险因素，临床应规避侵入操作的感染可能、尽早根据药敏结果合理用药干预以降低死亡风险。

PU-3537

2014-2019 年鲍曼不动杆菌的临床分布及耐药性分析

袁文丽、邓德耀、沈彦均、郭媛媛、顾津伊、徐红云、马众仙、陈弟、余林
云南大学附属医院

目的 探讨鲍曼不动杆菌的临床分布情况及耐药性变迁，为临床合理使用抗菌药物提供参考。
方法 回顾性分析某院 2014 年 1 月至 2019 年 12 月临床分离 2089 株鲍曼不动杆菌的患者临床资料和药敏结果。
结果 2089 株鲍曼不动杆菌中重症监护室(38.1%)和外科(20.8%)是分离鲍曼不动杆菌的主要科室；大于 60 岁男性患者的临床样本中鲍曼不动杆菌分离率较高；鲍曼不动杆菌对哌拉西林，哌拉西林/他唑巴坦，亚胺培南、美罗培南，阿米卡星耐药率逐年上升，对左旋氧氟沙星耐药率逐年下降；多重耐药的鲍曼不动杆菌分离率逐年上升；耐亚胺培南的鲍曼不动杆菌对哌拉西林等 12 种抗菌药物耐药率显著高于亚胺培南敏感株。
结论 重症监护室和外科的患者是鲍曼不动杆菌的易感人群；男性患者较女性更易分离出鲍曼不动杆菌；鲍曼不动杆菌对大部分抗菌药物耐药率总体呈逐年上升趋势，应加强对鲍曼不动杆菌耐药性的监测并合理使用抗菌药物。

PU-3538

优化万古霉素、利奈唑胺、替考拉宁和达托霉素在对葡萄球菌属血流感染患者中的给药方案：基于全国血流感染耐药监测联盟（BRICS）的蒙特卡洛模拟研究

金丹婷
连云港市第一人民医院

目的 借助全国血流感染细菌耐药监测联盟（BRICS）平台收集 2018-2019 年血培养中分离的葡萄球菌属，通过蒙特卡洛模拟预测和评价万古霉素、利奈唑胺、替考拉宁和达托霉素对葡萄球菌属的抗菌效果，进而优化临床给药方案。
方法 万古霉素、利奈唑胺和达托霉素采用肉汤稀释法，替考拉宁采用琼脂稀释法分别对 1847 株血培养中分离的葡萄球菌属进行最低抑菌浓度（minimuminhibitoryconcentration，MIC）的测定。通过蒙特卡洛模拟计算四种药物不同给药方案的的达标概率 (probability of target attainment，PTA) 和累计反应分数（cumulative fraction of response，CFR）。
结果 万古霉素给药剂量 500mg q6h、1000mg q12h、1500mg q12h、2000mg q12h 对葡萄球菌属的 CFR 分别为 51%、51%、80%和 83%。利奈唑胺给药剂量 800mg qd、 500mg q12h、600mg q12h、600mg q8h 对葡萄球菌属的 CFR 分别为 74%、84%、89%和 95%。替考拉宁给药剂量 400mg q12h、600mg q12h、800mg q12h、1000mg q12h 对葡萄球菌属的 CFR 分别为 89%、93%、94%、94%。达托霉素 4mg/kg/day、6mg/kg/day、8mg/kg/day、10mg/kg/day、12mg/kg/day 对葡萄球菌属的 CFR 分别为 97.429%、99.242%、99.936%、100%和 100%。
结论 针对葡萄球菌属引起的血流感染，利奈唑胺的 600mgq8h、替考拉宁的 600mgq12h、800mgq12h 和 1000mgq12h、达托霉素的 4mg/kg/day 给药方案即可达到较好的抗菌效果。

PU-3539

广东地区妊娠期糖尿病孕妇尿路感染的临床特点与危险因素分析

凌勇、刘洁、周典蓉、梁雪冰、周艳
广东省人民医院

目的 探讨广东地区妊娠期糖尿病（Gestational diabetes mellitus，GDM）孕妇尿路感染的临床特点与相关危险因素，为降低感染及临床治疗提供参考依据。
方法 收集 2016 年 1 月至 2020 年 12 月在广东省人民医院确诊为 GDM289 例患者，回顾性分析 GDM 孕妇尿路感染的发生率、病原菌分布及耐药情况，采用多因素 Logistic 回归分析 GDM 孕妇尿路感染的可能相关危险因素。
结果 289 例 GDM 孕妇中有 32 例发生尿路感染，发生率为 11.07%。中段尿培养共检出 32 株病原菌，其中以大肠埃希菌（53.13%，17/32）为主。大肠埃希菌对氨苄西林的耐药率较高，对碳青霉烯类、β-内酰胺酶抑制剂合剂、阿米卡星等抗菌药物的耐药率较低。多因素 Logistic 回归分析显示，甘油三酯（OR：1.276、95%CI：1.066-1.526、P＜0.05）是 GDM 孕妇尿路感染的独立危险因素。
结论 甘油三酯与 GDM 孕妇尿路感染的发生有关，临床上可采取相应措施，降低尿路感染的发生率，并根据患者病情合理选择抗菌药物。

PU-3540

云南省部分地区 HIV 共感染丙型肝炎病毒 NS5 基因的遗传进化及 C316N 耐药位点分析

王佳丽
云南省传染病医院

目的 探讨云南省 HIV 共感染丙型肝炎病毒（HCV）基因分型及分布和 NS5B C316N 抗病毒耐药位点变异，为当地共感染 HCV 患者抗病毒治疗提供科学依据。
方法 2018 年-2019 年在云南省传染病医院采集 HIV 共感染 HCV 患者血清及信息，经 RNA 提取、cDNA 合成，采用 HCV NS5 基因特异引物进行 PCR 扩增，阳性产物测序，采用 DNAstar、GeneDoc、MEGA-X 等生物信息学软件对基因序列进行遗传进化和耐药位点分析。
结果 共收集到 197 例丙型肝炎患者血清，67 例扩增阳性。序列分析结果显示普洱、西双版纳和德宏的 4 例（5.8 %）与 1a 型病毒核苷酸同源性最高在 92.7%-93.5%，表明这 4 例病毒为基因 1a 型；丽江、昆明、曲靖、玉溪、楚雄、普洱、红河的 13 例（18.8 %）与 1b 型 HCV 核苷酸同源性最高在 86.5%-91.5%，表明这 13 例病毒为基因 1b 型；普洱、曲靖、大理、玉溪、昆明、红河的 12 例(17.4 %)与 3a 型病毒核苷酸同源性最高在 88.1%-97.1%之间，表明 12 例 HCV 为基因 3a 型；版纳、昆明、保山、昭通、楚雄、红河、曲靖、临沧、大理、玉溪的 30 例(44.8 %)与 3b 型 HCV 核苷酸同源性最高在 85.6%-98.5%之间，表明 30 例 HCV 为基因 3b 型；临沧、怒江、版纳、德宏、昆明的 8 例（11.9%）与 6n 型 HCV 核苷酸同源性最高在 92.8%-96.5%，表明这 8 例 HCV 为基因 6n 型。耐药位点分析结果显示 1b 型病毒存在 dasabuvir 耐药位点 C316N 变异，而其它基因型或基因亚型未发现该耐药位点变异。
结论 云南省存在 HCV 1a、1b、3a、3b、6n 型等 3 个基因型 5 基因亚型流行，但以基因 3 型病毒为主要流行基因型，不同基因型型或亚型具有明显地域性，并在云南省流行的 1b 型 HCV NS5B 316 位上发生了 dasabuvir 耐药位点突变。

PU-3541

MALDI-TOF MS 技术快速鉴定在儿童血流感染诊治中的应用

周艳
江西省儿童医院

目的 应用基质辅助激光解吸电离飞行时间质谱（MALDI-TOF MS）技术快速鉴定儿童血培养阳性标本中的病原菌，分析 MALDI-TOF MS 快速鉴定法的符合率，探讨其是否适合直接快速鉴定儿童常见血流感染病原菌的鉴定。
方法 运用细胞裂解-分离胶管法以及分离胶法富集儿童阳性血培养瓶中的病原菌，应用 MALDI-TOF MS 对经前处理的血培养阳性标本进行直接鉴定，鉴定结果与传统培养 24 小时菌落 MALDI-TOF MS 鉴定结果以及传统的 Phoenix 100 全自动鉴定药敏分析仪鉴定结果进行比较。
结果 在实验的 160 株儿童阳性血培养标本中，革兰阴性菌的鉴定符合率达 94.3%；革兰阳性菌鉴定符合率达 96%。两种及两种以上细菌混合感染的阳性标本直接鉴定还存在一定困难，其直接鉴定方式还需进一步探讨。血培养假阳性标本直接鉴定均未鉴定出病原菌。
结论 MALDI-TOF MS 直接快速鉴定阳性儿童血培养标本中的病原菌，对血流感染中主要病原菌的鉴定符合率较高，可将细菌快速地鉴定到菌种，能够显著缩短阳性报警后血培养的最终报告时间，并且可提高临床抗菌药物初始化治疗的准确性，是适合在临床实验室推广的一种快速、准确、灵敏、特异的直接快速鉴定儿童血流感染病原菌的方法。

PU-3542

老药新用：五氟利多对金黄色葡萄球菌、持留菌及其生物膜的抗菌作用研究

刘亚倩、佘鹏飞、徐兰兰、陈丽华、李懿敏、刘莎莎、李泽浩、 Hussain Zubair 、伍勇
中南大学湘雅三医院

目的 探讨抗抑郁症药物五氟利多（PF）对金黄色葡萄球菌、持留菌及其生物膜的抗菌作用研究。
方法 采用微量肉汤稀释法检测 PF 对金黄色葡萄球菌的最低抑菌浓度（MIC）及最低杀菌浓度（MBC),应用时间-杀菌曲线评价其杀菌效果。采用棋盘稀释法检测 PF 与常规抗生素的联合抗菌作用。利用微孔板法构建生物膜，结晶紫染色和生物膜内活菌计数法检测 PF 对金黄色葡萄球菌生物膜的抑制和分散作用以及对膜内菌的杀灭作用，并在激光共聚焦显微镜下观察细菌生物膜的形态变化。通过诱导形成持留菌，检测 PF 对持留菌及生物膜内持留菌的杀灭效果。通过膜通透性试验、膜去极化实验、ATP 释放试验、RNA 测序和扫描及透射电子显微镜研究 PF 对细菌细胞膜完整性的影响，探讨其作用机制。人红细胞溶血试验和细胞活性试验用于检测 PF 的细胞毒性。利用一步和连续诱导耐药法检测 PF 对金黄色葡萄球菌的耐药突变选择。采用药代动力学模型研究 PF 在小鼠体内吸收和代谢的规律。构建小鼠 MRSA 感染的皮肤脓肿、伤口感染、急性腹膜炎模型，评估 PF 的体内抗菌效果。
结果 PF 对金黄色葡萄球菌的 MIC 在 4-8 μg/mL 之间，MBC 在 16-32 μg/mL 之间，2×MIC 和 4×MIC 的 PF 分别在 8h 和 2h 内迅速杀死所有的细菌细胞。棋盘法显示 PF 与四环素和 PMBN 具有协同抗菌作用。PF 可以抑制金黄色葡萄球菌生物膜形成，并以剂量依赖性方式分散 24h 成熟生物膜。PF 对持留菌及生物膜内持留菌具有显著清除作用。抗菌机制研究表明 PF 可通过提高细菌细胞膜通透性，破坏细胞膜完整性从而导致细菌难以存活而死亡。PF 的细胞毒性低，不易对金黄色葡萄球菌产生耐药，并且具有合理的药代动力学特性。在小鼠皮肤脓肿，伤口感染以及急性腹膜炎模型中，均展现出有效的抗菌作用。
结论 PF 在体内和体外对金黄色葡萄球菌均具有良好的抗菌效果，有潜力作为新型抗菌药物治疗金黄色葡萄球引起的相关感染。

PU-3543

Genetic and phenotypic characterization of the novel metallo- β-lactamase NDM-29 from Escherichia coli

Ying Zhu、Xinmiao Jia、Peiyao Jia、Li Xue、Qiwen Yang
Peking Union Medical College Hospital

Objectives The blaNDM can hydrolyze almost all clinically-available β-lactam antibiotics and has widely spread all over the world. An NDM-29-encoding Escherichia coli strain, 19NC225, isolated from a patient with biliary tract infection, was discovered in 2019 in China.
Methods PacBio Sequel and Illumina sequencing, conjugation, transformation, cloning test and fitness cost were performed to analyze the genetic and phenotypic characterization of the newly-discovered blaNDM-29 from plasmid and strain level.
Results The strain, 19NC225, containing two plasmids (pNC225-TEM1B and pNC225-NDM-29), belongs to ST1485 and O83:H42. blaNDM-29, carrying a G388A (D130N) mutation compared with blaNDM-1, is located on a 60 Kb plasmid, pNC225-NDM-29, which exhibited 99% identity with six blaNDM-1-carrying plasmids and showed responsibility for the MDR phenotype. The transferability and phenotypic function of the plasmid pNC225-NDM-29 and the blaNDM-29 gene was verified by conjugation/ transformation and cloning test. Furthermore, fitness cost test confirmed that the presence of NDM-29 exerts no survival pressure on bacteria, which strongly supports the transmission capacity of blaNDM-29-bearing plasmid.

Conclusions Our study provides a comprehensive view of the whole genome sequence of an NDM-29-encoding Escherichia coli strain and the novel NDM variant blaNDM-29 which mediates carbapenem resistance and has the capacity of transmission. Further epidemiological concerns should be warranted on NDM-29-producing isolates which has the potential capacity of spread.

PU-3544

感染性心内膜诊治的研究进展

张晓慧、倪芳、夏文颖
江苏省人民医院（南京医科大学第一附属医院）

感染性心内膜炎（Infective Endocarditis，IE）为心内膜或者心脏瓣膜受到细菌、真菌或其他微生物（如立克次体、螺旋体、衣原体等）感染，伴赘生物形成，是一种严重致死的感染性疾病。IE 的病因复杂，临床表现及并发症多样，对其诊断和治疗带来巨大困难。近年随着人口的老龄化，人工瓣膜置换、留置心脏装置、血液透析及各种血管内治疗技术的应用，IE 的发病率不断增加，同时其临床特征、致病菌的分布及耐药性均发生了显著变化。目前国内大部分地区引起 IE 的病原菌仍以链球菌为主。耐药菌株的不断涌现给临床治疗带来极大的困难。国内对 IE 的报道多为单中心研究，受地域、地区经济及气候条件限制，具有一定的局限性。本文旨在对近年 IE 诊断、病原菌分布及治疗等相关文献进行复习总结，为 IE 的诊治提供有利依据。

PU-3545

Evaluation of the clinical systems for polymyxin susceptibility testing of clinical gram-negative bacteria in China

Ying Zhu、Peiyao Jia、Menglan Zhou、Jingjia Zhang、Ge Zhang、Wei Kang、Simeng Duan、Tong Wang、Yingchun Xu、Qiwen Yang
Peking Union Medical College Hospital

Objectives The performance of mainstream commercial antimicrobial susceptibility testing systems on polymyxins have not been well evaluated in China. In this study, three antimicrobial susceptibility testing systems were evaluated for polymyxin B and colistin.
Methods The MICs of 257 Gram-negative strains collected from clinical cases and livestock were determined and analyzed. Using Broth Microdilution as the gold standard, the performance of VITEK 2® COMPACT, Phoenix™ M50 and Bio-kont AST System were evaluated. Essential agreement (EA), category agreement (CA), very major error (VME) and major error (ME) were calculated for comparison. The results of mcr-1 positive strains were separately discussed.
Results The EA, CA, VME and ME to polymyxin B for Bio-kont were 83.5%, 95.6%, 13.1% and 0.6%, respectively. The EAs, CAs, VMEs and MEs to colistin were as follows: Bio-kont, 86.7%/96.5%/7.2%/1.7%; Vitek 2, 64.2%/86.8%/41.0%/0% and Phoenix M50, 92.9%/92.9%/21.7%/0%. The performance of Bio-kont to polymyxin B and colistin for Pseudomonas spp. (EA, CA <90%, VME >1.5%, ME=5.6%/10%) and Enterobacter spp. (EA, CA <90%, VME >1.5% and ME= 0%), Vitek to colistin for most genera and Phoenix to colistin for Enterobacter spp. (EA, CA <90%, VME >1.5%, ME=0%) were unsatisfactory compared with other genera. The performance of Bio-kont to polymyxins for Escherichia spp. and Phoenix to colistin for Citrobacter spp., Escherichia spp. and Klebsiella spp., which all met the CLSI standard, were satisfactory. When the susceptibility of mcr-1 positive E. coli was tested, Bio-kont and Phoenix M50 presented excellent performance with no category errors, while Vitek 2 performed a high VME (25.5%).

Conclusions With relatively more accurate results for polymyxin B and colistin and lower VME, Bio-kont has its advantage for polymyxin antimicrobial susceptibility testing, especially for Escherichia spp., Klebsiella spp., Citrobacter spp. and Acinetobacter spp..

PU-3546

感染性心内膜炎患者病原菌分布及药物敏感性分析

张晓慧、夏文颖、倪芳
江苏省人民医院（南京医科大学第一附属医院）

目的 分析感染性心内膜炎（Infective endocarditis, IE）患者血培养的病原菌分布及其药物敏感性分析，为临床合理选用抗菌药物及择期手术提供理论依据。
方法 选取 2016 年 1 月至 2019 年 12 月我院血培养阳性的 IE 患者 104 例，回顾性分析其致病菌的类型及药物敏感性情况。
结果 2016 年至 2019 年我院共收治 IE 患者 249 例，其中血培养阳性 104 例，阳性率为 41.8%。104 例 IE 患者通过血培养共检出 108 株菌，其中革兰阳性菌 92 株（占 85.2%），主要以链球菌（50.9%）和葡萄球菌（26.9 %）为主；分离出革兰阴性菌共 13 株、真菌 2 株、厌氧菌 1 株。药敏试验结果显示，链球菌属对 β-内酰胺类、喹诺酮类药物敏感性较好（均>80%），但对红霉素、克林霉素耐药率较高。金黄色葡萄球菌对青霉素 G 的敏感性（11.1%）较低，红霉素（35.3%）、克林霉素（38.9%）次之，对庆大霉素（94.4%）和喹诺酮类药物（>80%）的敏感性较高，其中有 5 株为耐甲氧西林金黄色葡萄球菌。对苯唑西林耐药的凝固酶阴性葡萄球菌占 66.7%。两种菌属均未见对万古霉素或利奈唑胺耐药的菌株。
结论 链球菌仍是 IE 最常见的致病菌，其次是葡萄球菌。近年 IE 的病原菌分布呈现出多样化、复杂化趋势，临床需密切关注并根据药敏结果及时调整抗感染方案，以确保诊疗的有效性，提高患者的生存率。

PU-3547

Repurposing FDA-approved drugs against biofilm and persister cells of Pseudomonas aeruginosa

Pengfei She、Shijia Li、Linying Zhou、Wu Yong
The Third Xiangya Hospital of Central South University

Pseudomonas aeruginosa is a ubiquitous bacterium found in hospitals and the surrounding environment. The ability of P. aeruginosa to form biofilms confers high-level resistance to antibiotics, and the persister cells formed in the presence of high antibacterial drug concentrations make P. aeruginosa-related infections more refractory. Further, there rarely is an effective antimicrobial alternative when biofilm- and persister cell-targeting treatment fails. Using a high-throughput screening assay, we previously identified fluoroquinolones sitafloxacin, prulifloxacin, and tosufloxacin as well as aminoglycoside sisomicin as FDA-approved drugs with significant time- and dose-dependent P. aeruginosa biofilm eradication effects. These agents also exhibited bactericidal efficacy against antibiotic- or CCCP-induced P. aeruginosa persister cells. In addition, we confirmed the in vivo anti-biofilm efficacy of identified antibiotics in a subcutaneous implantation biofilm-related infection model. Taken together, our results indicate that sitafloxacin, prulifloxacin, tosufloxacin, and sisomicin have great potential as alternatives for the treatment of refractory infections caused by P. aeruginosa biofilms and persister cells.

PU-3548

湖南地区耐碳青霉烯肺炎克雷伯菌的耐药情况及耐药机制研究

唐云、罗椿意、刘双全
南华大学附属第一医院

目的 本研究收集湖南省多家医院的 CRKP 临床分离株，对其进行鉴定、药敏分析和耐药基因筛查，了解湖南省 CRKP 流行的耐药基因型及其对常见抗菌药物的耐药情况，为临床医师合理使用抗菌药物及控制院内感染提供理论依据。
方法 1. 收集 2019 年 5 月-2020 年 11 月期间来自湖南省衡阳、长沙、湘潭和怀化地区的 CRKP 菌株共 96 株，对其科室、性别、年龄分布等情况进行统计分析。
2. 利用拉丝实验筛检 CRKP 菌株中的高黏液型 CRKP 菌株，并使用微生物分析系统进行药敏分析、菌种鉴定。肉汤稀释法确定常见抗菌药物的最低抑菌浓度。
3. 通过 mCIM 联合 eCIM 试验检测 CRKP 菌株的碳青霉烯酶表型。使用 PCR 分子学方法检测 CRKP 菌株的相关耐药基因，同时测序鉴定检出的耐药基因。
结果 1. 96 株 CRKP 菌株主要分离自痰液标本 55.21%并主要分布于 ICU 40.63%；男性分离率 67.71%高于女性 32.29%；以 61-70 岁分离率最高，为 21.88%。
2.筛检高黏液表型 CRKP 菌株的阳性率为 14.43%。CRKP 菌株对碳青霉烯类抗生素耐药率均为 100%，对 26 种抗菌药物的耐药率均在 50%以上。
3. mCIM 试验单独阳性率为 79.17%，mCIM 和 eCIM 试验均阳性率为 16.67%。测得碳青霉烯类耐药基因 KPC 基因率最高，为 98.96%；多粘菌素 B 耐药基因 MCR-1 基因率为 35.42%；外膜孔蛋白基因 Ompk35 基因率为 100%，同时检测到 Ompk36 基因率为 94.79%，所有检出基因经基因测序验证为目的基因。
结论 1. 湖南省多家医院收集的 96 株 CRKP 菌株主要来源于痰液标本并主要集中分布于 ICU，男性较女性的分离率高。
2. 本次收集的 CRKP 菌株以产丝氨酸酶为主，且对多种常用的抗菌药物耐药，耐药机制主要以产生 KPC 耐药基因为主，同时存在 Ompk36 基因缺失，多粘菌素 B 耐药 MCR-1 基因阳性率亦较高。

PU-3549

内质网应激与感染性疾病研究进展

唐云、罗椿意、刘双全
南华大学附属第一医院

内质网(endoplasmic reticulum，ER)是一类膜细胞器，包含粗糙型和光滑型两种类型，其生物学功能多样化，同时也是脂质合成、蛋白质发挥功能和钙离子代谢的主要场所。但是当细胞受到刺激时，内质网会发生紊乱，内环境稳态发生改变可干扰内质网功能则引起内质网应激(Endoplasmic reticulum stress，ERS)，为保证机体的稳定性，大量异常堆积的错误/未折叠蛋白质所引发的未折叠蛋白反应(unfolded protein response，UPR)会恢复内质网稳态来减少 ERS 带来的不良反应。ERS 是一种机体自适应性机制，有着双重作用。一方面能诱导 GRP78 等分子伴侣的表达而产生保护作用，在一定程度上能够维持细胞和机体稳态；另一方面，若细胞中存在高强度的 ERS，又能诱导细胞自噬或凋亡，从而导致疾病的发生。细胞中存在几种维持内质网稳态的机制，其中 UPR 是最为主要的。近期，越来越多的文献报道指出 ERS 相关信号通路与炎症、自噬或凋亡存在显著关联性，其参与多种疾病(如病毒性肝炎、心血管、代谢性疾病和神经退行性疾病等)的病程进展。由于 ERS 相关信号通路在这些疾病中的复杂性，我们需要进一步加强对内质网作用机制的研究，从而更深入、更全面的掌握其与感染性疾病的发生发展中的潜在机制，有望为这一类疾病的诊治提供新方法、新思路。因此，本文主要针对内质网应激与几种感染性疾病的相关研究进展作简要的阐述，为探明感染性疾病的发病机制及其防控措施给予理论指导。

PU-3550

Fluconazole-Induced Microevolution of Candida parapsilosis harbouring novel mutation G490R in Tac1p: a new site responsible for the high MIC value

Yating Ning[2]、Tianshu Sun[1]、Li Zhang[1]
1. Peking Union Medical College Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College
2. Peking Union Medical College Hospital, Chinese Academy of Medical Sciences & Peking Union Medical College

Candida species are a major cause of life-threatening invasive infections worldwide. Even though Candida albicans is responsible for the vast majority of infections, the clinical relevance of other Candida species has also emerged over the last twenty years, especially Candida parapsilosis, which ranks second in total isolation rate of Candida species and first in bloodstream infections in China. Besides, azole-resistant C. parapsilosis strains are frequently isolated in the hospital setting. The mechanism for resistance to azoles is well-known in C. albicans and C. glabrata, where it is mediated by amino acid substitutions at defined locations of Erg11p, Mdr1p, Cdr1p and their upstream regulator Tac1p and Mrr1p. However, less is known about acquired substitutions in C. parapsilosis. In this study, we applied fluconazole to induce directed evolution experiments to generate C. parapsilosis strains with acquired resistance to azole. Then, SNPs were analyzed based on whole-genome sequencing results, and the role of SNPs was verified by CRISPR gene editing. The evolved strains gained cross-resistance to fluconazole, voriconazole, posaconazole and itraconzole. In particular, MIC value of fluconazole had the highest increase, from 2 mg/L (F0, ACTT22019) to 32 mg/L (F50). Sequencing of related drug resistance genes showed that the evolved strain harbored base substitution G1585A in TAC1 (L986P). Introduction of the mutation G1585A into fluconazole-susceptible isolate F0 using CRISPR-Cas9 was confirmed to increase fluconazole resistance by 16-fold, and the correction of the same mutation in the fluconazole-resistant isolate F50, decreased fluconazole MIC by 16-fold. In addition, we found virulence and biofilm formation ability of F50 were attenuated in vivo after fluconazole adaptation. Altogether, our results demonstrate fluconazole adaptation can result in azole cross-resistance and virulence attenuation in C. parapsilosis, and L986P mutation in Tac1p significantly contributes to fluconazole resistance.

PU-3551

临床微生物快速检测新技术发展的现状与前景

宁雅婷、徐英春
中国医学科学院北京协和医院

感染性疾病起病急、进展快，早期精准识别和监测病原体耐药性，对患者预后和遏制耐药至关重要。临床微生物常规技术已无法满足快速诊疗的需求，因此快速检测技术成为检验关注的焦点。本文论述了快速鉴定与药敏检测的最新技术的研究现状、问题及未来发展要点，为临床微生物实验室未来的引入新技术提供参考。

PU-3552

临床病原菌分布和耐药性分析

李晓凤
山东省千佛山医院

多重耐药菌感染的预防需要采取多层面的方法，包括一般的感染预防、准确及时的诊断和治疗、谨慎使用抗菌药物、有效且严格的院感防控措施，微生物室应定期通报医院病原菌的检出情况及耐药率，及时向临床报告多重耐药菌预警，为预防和控制多重耐药菌的传播提供重要的依据。

PU-3553

生艾叶对人肺炎支原体体外抑菌实验研究

杨川琪、柴琳
昆明市中医医院

目的 探讨生艾叶提取物对人肺炎支原体（MP）流行株、耐药株体外抑菌和杀菌的效果。
方法 将生艾叶中药原液倍比稀释成三个浓度，依次为：250 g/L,62.50 g/L,15.625 g/L；通过体外对三个浓度在 0 小时，12 小时，24 小时三个与 MP 作用时间段计数菌落数，筛选出生艾叶提取物对本地人肺炎支原体流行株 ATCC15531、ATCC29342 和耐药株 MP19 直接抑菌杀菌作用最佳的药物浓度和时间。
结果 生艾叶粗提药液浓度 250 g/L 对人肺炎支原体（MP）流行株、耐药株体外在 0 小时、12 小时、24 小时三个时间段均有杀菌作用，灭菌率在 83%~100%。生艾叶粗提药液浓度 62.5 g/L 在 24 小时对肺炎支原体流行株 ATCC15531 灭菌率为 92%，对 ATCC29342 灭菌率为 87%，对耐药株 MP19 灭菌率为 94%。
结论 浓度为 62.5 g/L 的生艾叶提取物对人肺炎支原体 MIC90 值在 65g/L-30g/L，与肺炎支原体作用 24 小时是最佳抑菌杀菌浓度和时间。

PU-3554

TPPA 和 TRUST 两种检查方法在梅毒血清抵抗检查应用及中医辨证施治观察

唐亚娟
昆明市中医医院

目的 探究明胶颗粒凝聚试验（TPPA）、甲苯胺红不加热血清试验（TRUST）两种检查方法在梅毒血清抵抗检查应用及中医辨证施治观察。
方法 收集笔者单位皮肤科收治梅毒血清抵抗患者为探查对象，病例筛查时间 2017 年 7 月到 2020 年 7 月，共计 52 例，依据患者入院序号划分小组，试验 1 组 26 例予以 TPPA 检查，试验 2 组 26 例予以 TRUST 检查，比对诊断结果，予以受查患者中医辨证治疗，观察疗效。
结果 试验 1 组特异性及敏感性高于试验 2 组（P<0.05）；所选患者均成功完成治疗，医学随访治疗后 3 个月、6 个月，转阴率 73.08%、98.15%，复发率 1.92%。
结论 TPPA、TRUST 检查方法均可检出梅毒血清抵抗情况，各具优缺点，可联合诊断，以便开展早期中医辨证治疗，确保预后转阴。

PU-3555

浅谈呼吸道九联检检测对儿童呼吸道感染的检测意义及分析

罗癸敏
昆明市中医医院

目的 通过间接荧光免疫技术对常见儿童呼吸道感染检测血清中发病率最高的 IgM 抗体九类病原体做临床意义分析。
方法 采用间接免疫荧光法(IFA)对昆明市中医医院儿科门诊的 435 例呼吸道感染疾病的儿童患者，其中男性患儿 237 例，女性患儿 198 例，年龄 0～6 岁同时检查嗜肺军团菌(LP)、肺炎支原体(MP)、Q 热立克次体(COX)、肺炎衣原体(CP)、腺病毒(ADV)、呼吸道合胞病毒(RSV)、甲型流感病毒(IFA)、乙型流感病毒(IFB)和副流感病毒九种病原体在小儿呼吸道感染患者中的检出阳性率，其中主要以肺炎支原体最为常见，占阳性例数的 53.73%，其次为合胞病毒 4.477%，混合感染占感染比例的 27.62%。
结论 呼吸道九联检的检测方法在儿童呼吸道感染检测中检出的阳性率高，能够同时检测九种病原体，及时发现感染的病原体，对临床呼吸道感染疾病的诊断及鉴别诊断，提供合理的支持依据，并对合理用药具有一定的指导意义,有助于避免抗菌药物的盲目使用及滥用。

PU-3556

两种 G 试验检测系统结果的比对分析

李晓丽
昆明市中医医院

目的 目前有关 G 试验不同检测系统检测结果的比对分析报道并不多，本文旨在探讨 MB-80 微生物快速动态检测系统（北京金山川科技有限公司）和 LGL200 系列动态检测系统（天津喜诺生物有限公司），两种 G 试验检测系统的检测结果之间是否具有可比性。
方法 参照 NCCLS 文件 EP9-A2 指南，对两种 G 试验检测系统进行重复性试验，计算 CV 值。收集符合要求的临床标本，在 5 个工作日内对 40 份标本进行测定，分别对两组数据进行统计分析，评价两系统检测结果的相关性。
结果 MB-80 微生物快速动态检测系统和 LGL200 系列动态检测系统的变异系数分别为 7.49%和 6.45%。线性回归计算得回归方程（R^2=0.969）。
结论 两系统在试验期间有较好的重复性，变异系数均≤10%，两系统检测结果相关性较好。

PU-3557

基于海胆状金纳米的细菌 ECL 广谱分析方法研究

韩道宾[1]、丁世家[2]
1. 山东大学第二医院
2. 重庆医科大学

本研究创新性地利用银纳米（Ag nanoparticle, AgNPs）的 LSPR 作用增强过硫酸系统的电化学发光强度。同时，海胆状金纳米（Sea urchin like gold nanoparticles, SAuNPs）不仅可以利用自身的物理结构穿刺细菌，而且可以在一定程度上发挥 LSPR 作用促进过硫酸系统的电化学发光。SAuNPs 和 AgNPs 的电化学发光双重增强作用使电化学发光强度显著提高。当细菌加入后，快速被 SAuNPs 表面的棘刺状结构刺破并牢固结合，细菌在电极表面的聚集会阻挡电子在电极表面的转移，从而猝灭电化学发光。本方法简单快速，30 min 内可实现细菌的广谱检测，对 S.aureus 和

大肠杆菌（Escherichia coli, E.coli）均可以实现快速灵敏检测，在 102-108 CFU/mL 内实现了良好的线性检测，最低检测限达到 52 CFU/mL。此外构建的生物传感方法实现了在血浆中细菌的快速检测。该生物传感器设计简单、检测灵敏，为细菌的广谱高效检测提供了实验依据。

PU-3558

基于二硫化钼-铂纳米-万古霉素的金黄色葡萄球菌 ECL 分析方法研究

韩道宾[1]、丁世家[2]
1. 山东大学第二医院
2. 重庆医科大学

基于金纳米（gold nanoparticle, AuNPs）和氯化高铁血红素（hemin）作为 S2O82−/O2 ECL 系统的可再生增强底物，利用二硫化钼-铂纳米（Molybdenum disulfide-Platinum nanoparticles, MoS2-PtNPs）作为猝灭剂，构建了一种“开关”式高灵敏 ECL 适体传感器用于金黄色葡萄球菌（Staphylococcus aureus, S.aureus）检测。在本研究中，AuNPs 不仅可以增强电极导电，而且可以通过局域表面等离子体共振效应（Localized SPR， LSPR）增强 S2O82−/O2 ECL 系统的发光强度。而且，hemin 也可以通过自身的氧化还原反应增强 S2O82−/O2 ECL 系统的发光强度，增强效应促使传感器达到“开”的状态。二硫化钼-铂纳米-万古霉素（MoS2-PtNPs-Vancomycin, MoS2-Pt-Van）通过结合青霉素结合蛋白进而结合到 S.aureus 的表面，MoS2 则通过消耗中间产物 OOHž 发挥猝灭作用。ECL 强度与 S.aureus 浓度对数在 1.5×102 - 1.5×108 CFU/mL 范围内的呈线性关系，检测限为 28 CFU/mL。此外，本方法可用于尿液样本中 S.aureus 的检测。因此，该方法可能成为医学研究和早期临床诊断中细菌检测的潜在应用工具。

PU-3559

2016-2020 年上海市某三甲医院骨科感染病原菌分布及药敏结果分析

权文强
上海市同济医院(同济大学附属同济医院)

目的 了解骨科住院患者感染的常见病原菌分布及其药物敏感实验（AST）结果情况，为临床医师合理应用抗菌药物提供科学依据。
方法 回顾性分析 2016 年 1 月 1 日至 2020 年 12 月 31 日上海市某三甲医院骨科住院患者术后感染的临床现状，采用 WHONET 5.6 软件对临床分离病原菌进行统计，利用 VITEK2 Compact 自动微生物鉴定药敏仪进行耐药性鉴定和分析。
结果 近 5 年该院骨科住院术后感染患者送检的各类标本中共分离出病原菌 698 株，其中革兰阴性菌 362 株（51.9%），革兰阳性菌 323 株（46.3%），假丝酵母菌属 13 株（1.9%）。革兰阳性菌中金黄色葡萄球菌（23.9%）、无乳链球菌（6.2%）和表皮葡萄球菌（2.6%）较多；革兰阴性菌中大肠埃希菌（13.8%）、肺炎克雷伯菌（11.2%）、铜绿假单胞菌（8.5%）较多。药敏试验结果显示，革兰阳性菌中金黄色葡萄球菌耐对青霉素、氨苄西林、红霉素、克林霉素等抗菌药物具有较高的抗药性（均>50%）；无乳链球菌耐药率较高的抗菌药物分别为四环素、头孢唑林和环丙沙星。革兰阴性菌中的大肠埃希菌和肺炎克雷伯菌的超广谱 B-内酰胺酶检出率分别为 33.3%和 25.8%。大肠埃希菌耐药率较高的抗菌药物分别为氨苄西林、环丙沙星和左氧氟沙星；肺炎克雷伯菌耐药率较高的抗菌药物分别为氨苄西林、头孢唑林和呋喃妥因；铜绿假单胞菌对多种抗菌药物明显耐药，其中对氨苄西林、头孢唑林、头孢曲松和呋喃妥因耐药率均为 100％。耐甲氧西林金黄色葡萄球菌

（MRSA）检出率为 45.5%，MRSA 组各种抗生素药物耐药性均高于 MSSA 组，且比较差异均有统计学意义（P＜0.05）。

结论 该院骨科感染的病原菌分布广泛，以金黄色葡萄球菌为主，致病菌呈现出广泛、多重耐药等特点。临床应合理使用抗菌药物，积极通过耐药监测预防控制感染，尽量避免骨科患者术后出现多重耐药菌感染。

PU-3560

179 株无乳链球菌的标本分布及耐药性分析

林宇岚、杨 滨
福建医科大学附属第一医院

目的 分析临床分离无乳链球菌的标本分布和对常用抗菌药物的耐药性。

方法 收集不同来源标本，在 VITEKⅡ微生物分析仪上采用 GPI 卡和 GP67 卡进行菌种鉴定和药敏实验，红霉素、美罗培南的药敏实验及 D-试验采用 K-B 纸片法检测。

结果 共收集无乳链球菌 179 株，标本的主要来源为中段尿（63.1%）、生殖道（7.8%）和伤口分泌物（6.7%）。来源患者年龄大于 50 岁的 110 例（61.5%），女性患者 113 例（63.1%），孕妇 12 例（6.7%），母婴垂直感染 3 例（1.7%），肿瘤、手术、放化疗、糖尿病、 结核等患者 82 例（45.8%）。无乳链球菌对青霉素的耐药率除 2008 年之外均小于 10%，对四环素的耐药率均大于 80%，对红 霉素的耐药率为 42.9%～93.3%，对克林霉素的耐药率为 41.9%～80.0%，D 实验阳性率为 4.1%。未发现对万古霉素、美罗培南 的耐药株，偶见喹奴普丁 / 达福普丁耐药株。

结论 成年人感染无乳链球菌中最常见的是泌尿生殖系统感染和软组织感染，女性患者比例高于男性；青霉素和其他 β－内酰胺类药物仍可作为无乳链球菌感染经验用药的首选药物；四环素、红霉素、克林霉素的抗 菌作用是有限的，必须有实验室药敏实验结果作为使用依据。

PU-3561

MALDI-TOF MS 与实时 FQ-PCR 检测淋病奈瑟菌比较分析

赵立红
泰安市中心医院

目的 评价基质辅助激光解析电离飞行时间质谱（matrix-assisted laser desorption ionization–time of flight mass spectrometry，MALDI-TOF MS)和实时实时荧光定量聚合酶链反应（Fluorescence Quantitative Polymerase Chain Reaction，FQ-PCR）两种方法检测淋病奈瑟菌（Neisseria gonorrhoeae，NG）的诊断敏感度和诊断特异度。

方法 选取 2018 年 1 月～2019 年 12 月泌尿外科、妇科、生殖科及性病科就诊患者泌尿生殖道标本，进行 NG 培养，然后采用 ATB Expression 全自动细菌鉴定仪进行 NG 生化反应鉴定。采用 MALDI-TOF MS 和实时 FQ-PCR 两种方法同时直接检测临床标本中 NG 和检测细菌培养后菌落中 NG。以细菌培养-生化反应鉴定作为 NG 检测的金标准，分别对 MALDI-TOF MS 和实时 FQ-PCR 两种方法检测 NG 的诊断敏感度和诊断特异度进行比较分析。

结果 细菌培养后，采用质谱鉴定法进行鉴定，临床敏感度、临床特异度、阳性预期值和阴性预期值均为 100%。采用质谱法直接检测临床标本中 NG，临床敏感度、临床特异度、阳性预期值和阴性预期值分别为 39.09%、100%、100%和 61.54%。细菌培养后，采用实时 FQ-PCR 法进行检测，临床敏感度为 100%，临床特异度为 97.92%，阳性预期值为 98.01%、阴性预期值均为 100%。采用实时 FQ-PCR 直接检测临床标本，临床敏感度为 95.94%，临床特异度为 97.92%、阳性预期值为 97.93%、阴性预期值均为 95.92%。

结论 采用细菌培养-质谱法检测 NG 的临床敏感度、临床特异度、阳性预期值和阴性预期值最优，优于实时 FQ-PCR 方法，为目前最好的 NG 检测方法。

PU-3562

Molecular epidemiology of invasive Klebsiella pneumonia at a children's medical center in east China

Yang Li、Qiwen Ju、Yunzhong Wang、Yunzhen Tao、Xuejun Shao
Children's Hospital of Soochow University

Objective Invasive infection caused by *Klebsiella pneumoniae* (*K. pneumoniae*) is a common disease in children, which is associated with high morbidity and mortality. The purpose of this study was to investigate the virulence and drug resistance of invasive *K. pneumoniae* clinical isolates at a children's medical center in east China and provide guidance for clinical anti-infection treatment.
Methods A total of 94 invasive *K. pneumoniae* strains were isolated from children between January 2016 and December 2020 in Children's Hospital of Soochow University. Mass spectrometry was used for the identification of *K. pneumoniae*, The Kirby-Bauer method and VITEK 2 Compact system were used to analyse antimicrobial susceptibility. Polymerase chain reaction (PCR) was performed to detect the capsular serotypes, virulence-associated genes and β-lactam antibiotic resistance genes.
Results The PCR results showed that 87 strains (92.55%) of invasive *K. pneumonia* carried hypervirulent capsular serotypes and the dominant capsular serotype was K57 (62.77%). The remaining serotypes were K2 (11.70%), K1 (7.45%), K54 (6.38%), K5 (4.26%) and others (7.45%). All invasive *K. pneumonia* strains carried virulence-associated genes. Among them, 84 strains (89.36%) carried hypervirulent genes, which were *iroB* (86.17%), *peg-344* (34.04%), *prmpA* (30.85%), *iucA* (13.83%), $_{c}$rmpA (6.38%) and *prmpA2* (2.13%). The other virulence genes, namely *wabG* (100.00%), *mrkD* (98.94%), *ycfM* (96.81%), *fimH* (95.74%) and *Uge* (88.30%), were detected in most of the strains. Antimicrobial susceptibility showed that the rates of resistance to antimicrobial drugs were low. The PCR results also showed that all invasive *K. pneumonia* strains carried β-lactam antibiotic resistance genes. The carbapenemase genes were *NDM-1* (19.15%), *VIM-1*(13.83%), *KPC-2* (10.64%) and *OXA-1* (5.32%). The extended-spectrum β-lactamase genes were *SHV-11* (86.17%), *CTX-M-14* (48.94%), *TEM-1* (19.15%) and *VEB-1* (6.38%). The AmpC cephalosporinase genes were *FOX-1* (86.17%), *ACT-1* (70.21%) and*DHA-1* (31.91%). Of note, 12 invasive *K. pneumonia* isolates were identified as carbapenem-resistant *Klebsiella pneumonia* (CRKP). Moreover, they all carried hypervirulent genes, indicating that they were carbapenem-resistant and hypervirulent *K. pneumonia* (CR-HVKP).
Conclusions All invasive *K. pneumonia* strains isolated from children carried virulence-associated genes, including hypervirulent genes, and a high proportion of β-lactam antibiotic resistance genes. 12 CR-HVKP strains were identified, which should be of concern to clinicians.

PU-3563

三种结核分枝杆菌检测方法的比较

王敏、曹璇
苏州大学附属第二医院

目的 本研究旨在对抗酸杆菌涂片法、Xpert MTB/RIF 检测和 NGS 测序这三种临床常用的结核分枝杆菌检测方法进行阳性率比较及结果一致性分析，为临床诊断结核分枝杆菌感染提供数据参考。

方法 本研究选取苏州大学附属第二医院 2020 年 9 月至 12 月收集的 134 例住院的疑似为肺结核患者的痰液、支气管肺泡灌洗液及胸水等标本作为研究对象，进行 Xpert MTB/RIF 检测及抗酸杆菌涂片镜检，并统计结果。同时查询病例信息，收集外送标本进行 NGS 检测的结果。对这三种检测方法的检测结果进行阳性率比较及结果一致性分析。
结果 我们的研究结果显示，在总共 134 例的病例中，涂片抗酸染色法的阳性率是三种方法中最低的，Xpert MTB/RIF 技术和 NGS 测序的阳性率较高，NGS 测序略高于 Xpert 法。涂片抗酸染色法的结果与 Xpert 法较为一致，但 Xpert 法与 NGS 检测存在 4 例结果不一致的现象。
结论 分子诊断技术耗时短、检出率高，具有极好的发展前景。在实际的临床工作中，应将涂片抗酸染色法这样的传统诊断技术与 Xpert MTB/RIF 检测、NGS 检测这样的分子诊断技术结合起来，从而提高结核分枝杆菌的检出率，促进结核病的快速诊断，减少结核病的传播。

PU-3564

南京地区儿童肠道沙门菌的流行病学特点及耐药性分析

成祥君、马金霞
江苏省人民医院（南京医科大学第一附属医院）

目的 了解南京地区儿童粪便分离沙门菌的流行病学特征及其对抗菌药物的敏感性，为疾病防治和临床选用抗菌药物提供依据。
方法 从 2017 年 1 月-2020 年 12 月江苏省人民医院妇幼医院 578 例儿童送检粪便标本中分离沙门菌 40 株，分析检出沙门菌儿童的年龄及检出时间的分布特点、用沙门菌诊断血清检测其血清型分布，并用药敏纸片法检测其药物敏感性。
结果 粪便检出沙门菌的儿童男女比例为 1.67（25/15），年龄分布为 2 月-8 岁，年龄主要集中在 0 ～ 3 岁（67.5%），＜ 1 岁最多(35%)， 3～4 岁其次（27.5%）。检出时间集中在 5～8 月（65%），5 月最多（30%）。血清型主要为 O4 群。对左氧氟沙星和复方新诺明的敏感率分别为 47.5%和 72.5%，三代头孢菌素的敏感率为 80%，对氨苄西林及氯霉素的敏感性分别为 20%和 37.5%。
结论 本地区沙门菌对氨苄西林及氯霉素敏感性较低，对三代头孢菌素及复方新诺明敏感性较高。临床要根据药物敏感性结果和疗效进行调整用药。

PU-3565

肺炎克雷伯菌血流感染患者的 NK 细胞功能研究

鲁敏仪、郑佳佳
北京大学第三医院

目的 通过检测肺炎克雷伯菌血流感染患者外周血中自然杀伤细胞（NK 细胞）的表型和功能，探讨其在肺炎克雷伯菌血流感染（KPBSI）引起机体固有免疫功能中的可能作用机制。
方法 选择 2020 年 10 月至 2021 年 5 月在北京大学第三医院被诊断为肺炎克雷伯菌血流感染的 20 名患者，收集其血液样本，采用流式细胞术等方法检测 NK 细胞的表型和功能，以同时间段收集的 16 名健康对照者的血液样本作为对照组。
结果 KPBSI 患者表现出明显的细菌感染炎症反应；从 KPBSI 患者血液标本中分离出的菌株对大部分抗菌药物敏感，但也出现高耐药性的菌株；KPBSI 患者同健康对照者的检测结果相比较，NK 细胞表面抑制性受体 CD158e 的表达水平较低（*P*=0.005）；KPBSI 合并糖尿病患者的 NK 细胞穿孔素表达水平低于非糖尿病患者（*P*=0.010）；KPBSI 患者 NK 细胞活性测定项目结果与其部分实验室检测项目相关性分析结果显示：NK 细胞表面抑制性受体 NKG2A 与淋巴细胞绝对值（*P*=0.037）呈负相关、与降钙素原（*P*=0.026）呈正相关；NK 细胞表面活化性受体 NKp44 与降钙素原

（*P*=0.004）呈正相关；NK 细胞表面活化性受体 NKp46 与血清谷丙转氨酶（*P*=0.030）呈负相关；颗粒酶 B 与淋巴细胞百分数（*P*=0.047）呈正相关、与血清 γ-谷氨酰转肽酶（*P*=0.034）呈负相关。**结论** KPBSI 患者的 NK 细胞功能检测结果表明，KPBSI 患者存在一定的 NK 细胞功能异常，可能影响机体潜在的抗菌免疫应答。在感染过程中 NK 细胞可能被激活从而分泌细胞因子，与其他免疫细胞一起协同抗感染免疫，但由于纳入研究的样本量较少，具体激活机制还有待进一步研究。

PU-3566

新生儿科血培养病原菌分布及耐药性分析

张旭华
山东大学第二医院

目的 通过分析三年内（2016 年-2020 年）本院新生儿科血培养病原菌菌株种类分布、耐药率、多重耐药性等，了解新生儿科主要病原菌及其耐药性，为新生儿科抗感染治疗提供理论基础。
方法 按照标本采集规范要求收集临床标本进行培养，使用安图微生物质谱仪进行细菌鉴定，使用 BD M50 药敏仪和西门子 MicroScan Walkaway-96 Plus 全自动细菌鉴定及药敏分析仪进行药敏试验，收集其中新生儿科血培养菌株及药敏数据信息，使用 WHONET 5.6 软件统计，分析病原菌菌株种类分布、耐药率、多重耐药性等。
结果 2016 年-2020 年新生儿科血培养中共分离菌株 332 株，其中以凝固酶阴性葡萄球菌占绝大多数，为 167 株；其次，肺炎克雷伯菌 42 株，大肠埃希菌 26 株，屎肠球菌 20 株，阴沟肠杆菌 16 株，金黄色葡萄球菌 11 株、粘质沙雷菌 8 株，其他 42 株。凝固酶阴性葡萄球菌和金黄色葡萄球菌 β-内酰胺酶阳性率分别为 92.7%和 90.9%，苯唑西林耐药率分别为 77.0%和 36.4%，对万古霉素和利奈唑胺均敏感。肺炎克雷伯菌和大肠埃希菌 ESBLs 阳性率分别为 61.9%和 26.9%，对厄他培南、亚胺培南、美罗培南的耐药率分别为 9.5%、4.8%、4.8%和 0、3.8%、3.8%，对三代头孢菌素耐药率分别为 85.7-95.0%和 7.7-30.8%，对喹诺酮类耐药率分别为 9.5-38.1%和 32.0%。
结论 新生儿科血培养中以凝固酶阴性葡萄球菌为主，其中部分可能为污染菌，其次以肺炎克雷伯菌、大肠埃希菌和屎肠球菌为主。凝固酶阴性葡萄球菌 β-内酰胺酶阳性率和苯唑西林耐药率均高于金黄色葡萄球菌。肺炎克雷伯菌耐药性普遍高于大肠埃希菌，除外喹诺酮类，这与成人细菌耐药性相似。新生儿科由于患者年龄特殊性、用药限制性，可能导致可用药物耐药率上升且可能高于成人，给临床用药带来极大困难。

PU-3567

重症医学科血培养分离菌株及耐药性分析

张旭华
山东大学第二医院

目的 通过分析 2016 年-2020 年本院重症医学科血培养分离菌株种类、耐药性、多重耐药性，了解重症医学科血流感染细菌耐药情况，为科室抗感染治疗及院内感染防控提供理论依据。
方法 使用安图微生物质谱仪对血培养分离株进行鉴定，使用 BD M50 全自动药敏仪和西门子 MicroScan Walkaway-96 Plus 全自动药敏分析仪对相应菌株进行药敏试验，收集菌株及其药敏信息，使用 WHONET 5.6 软件进行统计，分析重症医学科血培养分离株细菌种类、耐药性及多重耐药率。
结果 2016 年-2020 年重症医学科血培养共分离非重复细菌菌株 144 株，其中凝固酶阴性葡萄球菌 32 株、肺炎克雷伯菌 29 株，大肠埃希菌 29 株，鲍曼不动杆菌 20 株，屎肠球菌 13 株，铜绿假单胞菌 4 株等。分离耐碳青霉烯的鲍曼不动杆菌 18 株、肺炎克雷伯菌 20 株、大肠埃希菌 1 株，碳青霉烯耐药率分别为鲍曼不动杆菌 90.0%、肺炎克雷伯菌 69.0%、大肠埃希菌 3.4%。

结论 重症医学科血培养分离株以凝固酶阴性葡萄球菌为主，可能与患者留置中心静脉导管有关。其他分离株主要为肺炎克雷伯菌、大肠埃希菌、鲍曼不动杆菌等。鲍曼不动杆菌、铜绿假单胞菌、肠杆菌科细菌对碳青霉烯类药物耐药率高，其中肺炎克雷伯菌对碳青霉烯耐药性尤为突出。各类细菌耐药率居于较高水平，可能与室患者基本情况、科室布局设置、抗菌药物使用情况息息相关，迫切需要规范临床用药、避免院内感染，从而改善科室患者治疗效果。

PU-3568

耐碳青霉烯肠杆菌科细菌分析

张旭华
山东大学第二医院

目的 通过分析近四年（2016 年-2019 年）本院耐碳青霉烯肠杆菌科细菌（CRE）的菌株分布、科室分布、分离比率趋势，为临床合理用药提供依据，避免滥用抗菌药物。
方法 根据临床标本采集部位，分离可能病原菌，使用安图微生物质谱仪进行细菌鉴定，使用 BD M50 全自动药敏仪和西门子 MicroScan Walkaway-96 Plus 全自动细菌鉴定及药敏分析仪进行药敏试验，收集菌株及药敏信息，使用 WHONET 5.6 软件统计，分析耐碳青霉烯肠杆菌科细菌的菌株分布、科室分布、分离比率趋势。
结果 近四年共分离 632 株 CRE 菌株，其中肺炎克雷伯菌 478 株，产气肠杆菌 60 株，大肠埃希菌 36 株，粘质沙雷菌 26 株，阴沟肠杆菌 18 株，雷氏普罗威登斯菌 6 株，潘尼变形杆菌 2 株，科泽氏枸橼酸杆菌、弗劳地枸橼酸杆菌、阿氏肠杆菌、产酸克雷伯菌、摩根摩根菌和奇异变形杆菌各 1 株。CRE 菌株分离率逐年增高，分别为 5.3%、6.7%、10.9%和 16.8%，其中以肺炎克雷伯菌分离率升高最为明显，分别为 10.7%、13.4%、21.5%和 36.8%。CRE 的科室来源主要为重症医学科、呼吸内科、老年病科、急诊科和神经内科。CRE 标本来源依次为痰液 388 株、尿液 117 株、血液 45 株、分泌物 22 株、引流液 14 株、其他共 46 株。
结论 CRE 分离菌株数和分离率均呈逐年增高趋势，且增高大幅上升，其中以肺炎克雷伯菌最为明显。CRE 菌株来源科室广泛，并且可导致呼吸道感染、泌尿道感染、血流感染等多部位感染，已成为临床最为惧怕的病原菌种类。CRE 菌株的出现且快速增多，不仅与细菌自身遗传变异性相关，而且更与临床不合理应用抗菌药物、院内感染有关，临床科室迫切需要规范使用抗菌药物、做好院内感染防范措施，遏制耐药形势进一步加剧。

PU-3569

产 ESBLs 肺炎克雷伯菌耐药性及预后死亡风险研究

姚华、杨静
重庆医科大学附属第三医院

目的 分析我院产超广谱 β-内酰胺酶（ESBLs）肺炎克雷伯菌的临床分布特征及其耐药性，探讨影响 ESBL 阳性肺炎克雷伯菌感染患者预后相关因素。
方法 对 2016 年 6 月至 2020 年 12 月重庆医科大学附属第三医院收治的 111 例感染产 ESBLs 肺炎克雷伯菌住院患者临床资料进行回顾性分析，对不同科室疾病分类、临床特征及治疗等进行单因素分析和多因素 Logistic 回归分析。
结果 1140 株肺炎克雷伯菌中产 ESBLs 菌株共 111 株，检出率 9.70%；产 ESBLs 肺炎克雷伯菌在神经疾病中心、泌尿疾病中心和 ICU 三个科室的分离率较高；产 ESBLs 肺炎克雷伯菌对氨苄西林/舒巴坦、头孢曲松、头孢他啶、氨曲南、环丙沙星、复方新诺明的耐药率均>60%，显著高于非产 ESBLs 组；111 例产 ESBLs 肺炎克雷伯菌感染患者中死亡 14 例，死亡率 12.6%；单因素分析表明，与产 ESBLs 肺炎克雷伯菌感染患者死亡相关的因素包括肿瘤(P=0.007)、慢性肝病(P=0.029)、

慢性肺部疾病(P=0.017)、使用引流管(P=0.021)、中央静脉插管(P=0.043)和动脉穿刺置管(P=0.003)；多因素 logistic 回归分析发现肿瘤(P=0.003)、慢性肺部疾病(P=0.031)与产 ESBLs 肺炎克雷伯菌感染患者死亡密切相关。

结论 与非产 ESBLs 肺炎克雷伯菌相比，产 ESBLs 菌株对青霉素、头孢菌素、喹诺酮类以及磺胺类抗生素的耐药率明显升高；肿瘤性疾病和慢性肺部疾病是产 ESBLs 肺炎克雷伯菌感染患者死亡的独立危险因素。本研究表面临床在诊治过程中需进一步规范使用抗生素，重点监测肿瘤和慢性肺部疾病患者，从而减少感染病死率。

PU-3570

2019 年本医院细菌耐药监测数据分析

冯小艳、杨莉莉
成都市第三人民医院

目的 了解本医院临床分离细菌的分布及耐药情况进行统计分析，为本院临床合理应用抗菌药物提供参考。

方法 收集本院 2019 年全年成都市第三人民医院分离的临床菌株，依据 CLSI2019 年标准采用 WHONET5.6 软件进行数据分析。

结果 2019 年共分离出 6654 株细菌，其中革兰氏阳性菌 1498 株，占 22.51%，革兰氏阴性菌 5023 株，占 75.49%，真菌 126 株，占 1.89%。分离菌中前 5 位的细菌分别是肺炎克雷伯菌 956 株（14.4%）、大肠埃希菌 810 株（12.2%）、鲍曼不动杆菌 717 株（10.8%）、铜绿假单胞菌株 663 株（9.96%）、金黄色葡萄球菌 472 株（7.09%）等，标本类型以痰和尿液为主，其中痰中以肺炎克雷伯菌和鲍曼不动杆菌为主，尿液中以大肠埃希菌和屎肠球菌。耐甲氧西林金黄色葡萄球菌、（MRSA）和耐甲氧西林凝固酶阴性葡萄球菌（MRCNS）的检出率分别为 24.15%和 83.28%，未发现万古霉素、利奈唑胺耐药的葡萄球菌。万古霉素耐药的粪肠球菌和屎肠球菌分别占 0%和 1.1%，非脑脊液中分离的肺炎链球菌对青霉素的耐药率为 0%.革兰氏阴性菌中肺炎克雷伯菌和大肠埃希菌对碳青霉烯类抗生素耐药率 33.8%和 5.3%，大肠埃希菌对喹诺酮类耐药率 在 53.6%，对三代头孢菌素中头孢曲松耐药率在 64.5%左右，肺炎克雷伯菌对三代头孢菌素中孢曲松耐药率在 46.5%左右，比大肠埃希菌耐药率稍低，鲍曼不动杆菌和铜绿假单胞菌株对碳青霉烯类抗生素耐药率 32.1%和 34.7%，对氨基糖苷类、哌拉西林/他唑巴坦、多粘菌素 B 仍保持较高的抗菌活性。

结论 本院分离菌以革兰氏阴性菌为主，不同标本类型分离的菌的差异较大，尤其是肠杆菌科细菌对碳青霉烯类耐药菌株，监测本院细菌耐药监测对临床合理用药和有效控制感染具有重要意义

PU-3571

尿培养病原菌分布及耐药性分析

常欢
宝鸡高新医院

目的 了解医院门急诊和住院患者尿液细菌培养中病原菌分布及耐药性 ，为临床治疗提供可靠的参考依据 。

方法 432 株病原菌分离自 2018 年 1 月 一 2018 年 12 月医院门急诊和住院患者的尿液标本 ，采用 VITEK2 compact 全 自动微生物鉴定和药敏分析系统进行细菌鉴定和药敏试验 ，采用 WHONET5．6 软件进行统计分析。

结果 共分离病原菌 432 株 ，检出排前 3 位依 次为大肠埃希菌、粪肠球菌 、凝固酶阴性葡萄球菌 ，分别占 38.89 、11．11、5．55 ；168 株大肠埃希菌中有 106 株产超广谱 β 一内酰胺酶 (ESBLs)，占 63.64 ；大肠埃希菌对阿米卡星、亚胺培南较为敏感 ，耐药率较低；粪肠球菌和屎肠球菌对万

古霉素和利奈唑胺的耐药率均较低 ；分离 的凝固酶阴性葡萄球菌(CNS)中，最常见的是表皮葡萄球菌占 50．9 ；24 株 CNS 中耐甲氧西林凝固酶阴性葡萄球菌 (MRCNS)的检出率为 48.08 ，CNS 对呋喃妥因、克林霉素、利奈唑胺、利福平、万古霉素较敏感 。
结论 临床应根据尿培养药敏结果合理应用抗菌药物 ，控制耐药率的上升 。

PU-3572

碳青霉烯类抗生素非敏感肠杆菌产碳青霉烯酶的基因型分析

崔兰英、王希、赵金英、柏利婧
哈尔滨医科大学附属第一医院

目的 分析我院临床标本分离的碳青霉烯类抗生素非敏感肠杆菌碳青霉烯酶的产生情况及其基因型分布情况,为更好地指导临床合理用药提供依据。
方法 回顾性分析我院 2021 年 1 月至 2021 年 3 月期间收集的 38 株非重复碳青霉烯类抗生素非敏感肠杆菌菌株，采用 VITEK 全自动微生物分析仪鉴定卡及 MALDI-TOF 质谱仪对待检测菌进行鉴定；采用 VITEK 全自动微生物分析仪药敏卡结合药敏纸片琼脂扩散法（K-B）对待测菌株药敏试验进行检测。采用 PCR 方法扩增碳青霉烯酶待测基因，并进行 DNA 测序分析。PCR 扩增的 5 种常见碳青霉烯酶基因,包括 KPC 型,IMP 型,VIM 型及 NDM-1 型以及 OXA-48 型。
结果 38 株碳青霉烯类抗生素非敏感肠杆菌包括 35 株肺炎克雷伯菌，2 株大肠埃希菌，1 株阴沟肠杆菌。38 株待测菌对 ß-内酰胺酶类抗生素均耐药，对氨基糖苷类抗生素耐药率为 92.1%，对喹诺酮类抗生素耐药率为 97.4%。对多粘菌素均敏感。共 33 株待测菌株检测到 blaKPC-2，占 86.8%（33/38），2 株检测到 blaIMP-8，占 5.3%（2/38），另有 3 株未检出待测基因。
结论 碳青霉烯类抗生素非敏感肠杆菌产碳青霉烯酶基因型以 KPC 型为主，说明产碳青霉烯酶是碳青霉烯类抗生素非敏感肠杆菌重要的耐药机制之一，临床及相关部门应关注此类肠杆菌的流行情况，加强防控。

PU-3573

耐碳青霉烯类肠杆菌科细菌的流行情况及耐药性分析

崔兰英、孙妍、宋熙嫄、刘文博
哈尔滨医科大学附属第一医院

目的 了解我院临床标本分离的耐碳青霉烯类肠杆菌科细菌（CRE）的分布及耐药情况，为指导临床合理应用抗生素，及时掌握 CRE 的流行情况提供依据。
方法 回顾性分析我院 2020 年 9 月-2021 年 3 月临床分离出的 83 株非重复 CRE，采用 VITEK 全自动微生物分析仪及 MALDI-TOF 质谱仪对待检测菌进行鉴定,采用 VITEK 全自动微生物分析仪药敏卡及纸片扩散法（K-B 法）对待检测菌进行药敏试验测定，按美国临床和实验室标准协会的标准判读药物敏感试验结果。
结果 83 株 CRE 表现为对亚胺培南，美罗培南，厄他培南耐药率为 100%（83/83），对头孢菌素类抗生素耐药率为 100%（83/83），对多粘菌素敏感率为 100%（83/83），对替加环素敏感率为 96.4%（80/83）。83 株 CRE 中肺炎克雷伯菌所占比例最高，为 85.5%（71/83），其次为大肠埃希菌，占 6.0%（5/83）。标本种类以痰液所占比例最大，占 54.2%（45/83），其次为血液标本，占 21.7%（18/83）。83 株 CRE 分布科室以重症监护室多见。
结论 近年来 CRE 临床分离株的检出率在该院呈上升趋势。CRE 中菌种类型以肺炎克雷伯菌所占比例最高，其对临床常用抗菌药物有较高的耐药率，多表现为多重耐药，给临床治疗带来一定困难，应联合多部门，加强对 CRE 的检测，控制 CRE 的产生和传播。

PU-3574

第三方医学检验中心 2020 年血培养分离病原菌种类及耐药性分析

杨柳、陈莎、李慧
杭州迪安医学检验中心有限公司

目的 了解血流感染病原菌分布特点及耐药情况，为临床合理使用抗菌药物提供依据。
方法 回顾分析 2020 年 1 月至 2020 年 12 月本中心检测的血液样本，对其检出病原菌情况及耐药性进行回顾分析。
结果 共分离病原菌 2153 株，包括革兰氏阴性菌 1127 株(52.35%)，革兰氏阳性菌 856 株（39.76%），及酵母样真菌 170 株(7.89%)，分离最多的为凝固酶阴性的葡萄球菌，共 618 株（28.70%），其次为大肠埃希菌，共 281 株（13.05%）、肺炎克雷伯菌共 222 株（10.31%），洋葱伯克霍尔德菌共 199 株（7.39%）、金黄色葡萄球菌 101 株（4.69%），肠球菌属 82 株（3.81%）；耐甲氧西林金黄色葡萄球菌检出率为 60 株（59.4%），耐甲氧西林的凝固酶阴性的葡萄球菌检出率为 497 株（80.4%），未发现万古霉素、利奈唑胺和替考拉宁耐药的葡萄球菌，粪肠球菌对万古霉素和替考拉宁耐药的数量为 0，屎肠球菌对万古霉素耐药的为 4 株（12.12%），对替考拉宁耐药的为 1 株（3.03%），大肠埃希菌 ESBL 检出数量为 139 株（49.47%），肺炎克雷伯菌 ESBL 检出数量为 33 株（14.86%），其对头孢唑林、头孢噻肟、头孢呋辛全部耐药，且耐药率显著高于相应产 ESBLs 阴性菌。非发酵菌中铜绿假单胞菌及鲍曼不动杆菌对碳青霉烯类药物耐药率分别为 48.72%和 66.67%。
结论 回顾分析可看出，2020 年全年血培养分离病原菌以革兰氏阴性菌为主，且凝固酶阴性葡萄球菌的检出率较高，耐药菌株检出率也较高，故应在合理用药的同时加强血培养标本的规范操作。

PU-3575

沙门菌属特征分析及耐药基因检测

陈东杰、胡辛兰、吴长生、李宁、吴少莲、陈发林
福建省立医院

目的 观察福建省立医院 2013 年至 2021 年经证实为沙门菌属的 70 个标本的来源分布以及耐药情况；分析收集到的沙门菌耐药基因的分布情况。
方法 收集福建省立医院微生物实验室从 2013 年至 2021 年经证实为沙门菌属的 70 个标本；对其进行复苏、过夜培养、设计引物，确定耐药基因分布情况，对扩增产物进行凝胶电泳实验；做药敏试验，对氨苄青霉素、复方新诺明、环丙沙星、氯霉素、部分第三代头孢类等耐药情况，并结合临床信息进行相关统计学分析。
结果 从标本来源上看，标本大多数来自血液和粪便，分别占比 45.7%（32/70）以及 38.6%（27/70），其余标本来自于腹水、引流液、尿液、组织、切口分泌物，共占 15.7%。从患者年龄分布上看，大多数患者年龄＞69 岁，占 54.3%（38/70），其次是 46-69 岁，占 22.9%（16/70），其余分别为 18-45 岁占 11.4%（8/70）、13-17 岁占 1.4%（1/70）、7-12 岁占 1.4%（1/70）、0-6 岁占 8.6%（6/70）。分析其药敏情况，氨苄青霉素、复方新诺明、氯霉素的耐药率相对较高，达到 30%以上，环丙沙星、头孢曲松、头孢噻肟、头孢他啶、左旋氧氟沙星的耐药率相对较低，均为 10%左右。分析 qPCR 扩增结果，其中选取年份较近的 50 株沙门菌做 qPCR 扩增，其中基因 blaTEM、blaCTX-M、sul1、blaOXA、floR 的阳性率均为 100%，基因 acc(6')-Ib 的阳性率为 66%。分析凝胶电泳结果，基因 blaTEM、blaCTX-M、sul1、blaOXA、acc(6')-Ib 长度在 300-400bp 之间，基因 floR 在 200-300bp 之间。6 个耐药基因的扩增产物可测得基因序列，进行 Blast 比对后显示扩增结果无误。

PU-3576

探讨全自动快速微生物检测系统在鉴定流感嗜血杆菌的应用

李想、蓝依依、张宇培、徐少林、丁燕玲
柳州市妇幼保健院

目的 探讨全自动快速微生物检测系统（VITEK MS）在鉴定流感嗜血杆菌的应用价值 。
方法 收集柳州市妇幼保健院 2021 年 3 月 1 日至 2021 年 5 月 1 日从痰液或耳分泌物标本中分离的流感嗜血杆菌共 95 株 ，用 16S rDNA 测序确证 。并且用 VITEK MS 质谱仪 ，VITEK2 COMPACT 鉴定仪与脑心磷脂琼脂平板上卫星试验需求性试验 3 种方法对上述菌株鉴定分析。
结果 在 95 株流感嗜血杆菌细菌中，VITEK MS 质谱仪与 VITEK2 COMPACT 鉴定仪差异无统计学意义（P>0.5），而 VITEK MS 质谱仪与脑心磷脂琼脂平板上卫星试验需求性试验差异有统计学意义（P<0.5）。 在本研究中，VITEK MS 质谱仪与 VITKE 2 COMPACT 鉴定仪对流感嗜血杆菌的鉴定率都比较高，均为 90%以上。而传统的卫星试验对于流感嗜血杆菌的鉴定率仅为 75%，漏检情况比较严重，且受培养环境、菌悬液浊度、涂板时间厚度、所用金黄色葡萄球菌生长情况等诸多因素影响。鉴定时间方面，在涂板优秀的情况下，VITEK MS 仪能在 5-10 分钟内完成对细菌的鉴定，且马上能给临床发布鉴定报告，VITEK 2 COMPACT 鉴定仪则需 5-8 小时，而脑心磷脂琼脂平板上卫星试验需要在培养箱内培养 18-24 小时才能观察到较为准确的结果。但 VITKE MS 仪器成本过高，VITKE 2 COMPACT 鉴定仪仪器及鉴定卡成本也不便宜，所以现如今基层医院大多仍然使用成本低廉的脑心磷脂琼脂平板上卫星试验。
结论 对于 VITKE 2 COMPACT 鉴定仪鉴定与脑心磷脂琼脂平板上卫星试验需求性试验 ，VITEK MS 质谱仪能快速、准确地鉴定流感嗜血杆菌，对临床诊治提供很大的帮助，有非常好的应用前景 。

PU-3577

耐碳青霉烯类肠杆菌科细菌（CRE）的分离情况及耐药性分析

吴长生、陈东杰、胡辛兰、李宁、陈发林
福建省立医院

目的 探究我院 CRE 的临床分离情况，以及其对常用抗菌药物的耐药特征。
方法 收集 2000 年~2020 年间检测出的 CRE 菌株信息，运用 WHONET 5.6 软件对信息进行统计分析。
结果 共分离出 CRE 1549 株，位列前三的是肺炎克雷伯菌 1044 株（67.40％），大肠埃希菌 185 株（11.94％），阴沟肠杆菌 167 株（10.78％）； ICU 分离数量占 44.67%，非 ICU 占 55.33%；2000 年 10 月首次分离出一株 CRE，为产气肠杆菌。CRE 数量的增长呈现三个不同平台期：2000-2012 年，CRE 检出数量少；2012~2016 年， CRE 检出数量是前一阶段的 3-5 倍左右，主要分布在 ICU；2017~2020 年，CRE 检出数量暴增，是第一阶段的 10 倍左右。CRE 菌株耐药率很高，对 CZO、AMP、ETP 全部耐药；对 CRO、SAM 的耐药率也一直在 90%以上；对其他大部分常用药物耐药率在 80%左右，且有不断升高趋势。CRKP 的分离率在 CRE 中占比接近 70%，CRE 两次数量的暴发性上升主要是 CRKP 的增长，其耐药性也比其他 CRE 更高。在 CRKP 中，对 17 种药物全部耐药的表型最常见，占所有表型的 46.5%。
结论 我院 CRE 感染形势十分严峻，临床分离菌株对常用的抗菌药物的耐药率都较高，仍然呈现逐渐增长的趋势，医院应加强感染防控措施和抗菌药物的临床应用管理措施。

PU-3578

德尔卑沙门菌致呼吸道感染病例分析并文献复习

邓飘
山东省千佛山医院

目的 通过对德尔卑沙门菌所致的呼吸道感染及治疗并回顾性查阅文献复习该菌的流行病学情况及相关研究为临床对该菌的诊治提供理论支持。
方法 通过文献分析及常规药敏检测对德尔卑沙门菌进行研究分析。
结果 德尔卑沙门菌是一种在环境中存在的可导致人类食源性疾病的一种条件致病菌，该病感染常有水源污染或患者免疫力低下。
结论 德尔卑沙门菌是一种条件致病菌，常导致人类腹泻或食物中毒，其具有多种致病质粒，对该菌的感染应当引起重视，可能会导致爆发性感染。

PU-3579

育龄女性社区获得性生殖道支原体感染及耐药分析

甘龙杰、杨滨
福建医科大学附属第一医院

目的 了解本地区育龄女性社区获得性生殖道支原体感染及耐药情况,为临床诊治提供依据。
方法 2016 年 11 月至 2017 年 10 月,采集门诊育龄女性患者生殖道分泌物标本共 2 836 份进行支原体培养、鉴定及药敏操作。育龄女性按每 10 岁年龄段进行分组并计算分析结果。
结果 育龄女性社区获得性生殖道支原体感染以 Uu 单纯感染为主（430/574,74.9%）,其次为 Mh 单纯感染（83/574,14.5%）,同时感染 Uu+Mh（61/574,10.6%）,不同年龄段以 25～34 岁为感染检出的数量最多。单纯 Uu 感染时仅对氟喹诺酮类药物的耐药率大于 10%,其余抗生素耐药率较低（<10%）;单纯 Mh 感染时,仅对氟喹诺酮类药物的耐药率大于 50%;混合感染 Uu+Mh 时耐药性明显高于单纯感染。
结论 育龄女性社区获得性生殖道支原体感染以 25～34 岁居多,Uu 感染为主,其次为 Mh 感染,除氟喹诺酮类药物外,其余抗生素均较为敏感。

PU-3580

一株罕见 Ihumii 放线菌的分离和鉴定

张维清、杨滨
福建医科大学附属第一医院

放线菌大多存在于健康人口腔,上呼吸道,胃肠道和泌尿生殖道等与外界相通的腔道,是寄居人体的一种正常菌群^[1-2].当机体免疫力减弱,口腔卫生不良,拔牙或外伤时,可侵入组织导致皮肤,皮下组织,肌肉,骨骼及中枢神经系统化脓性感染^[3].根据感染的途径和涉及的器官不同,临床上分为面颈部,胸部,腹部和中枢神经系统感染.其主要特征为慢性化脓性肉芽肿病变,以向周围组织扩展形成瘘管并排出带有硫磺样颗粒的脓液为特征.绝大多数放线菌易引起内源性感染,大量应用免疫抑制剂是一个重要的诱发因素.2015 年,法国科学家从一个 50 岁的 HIV 感染者粪便中首次分离出一株新的放线菌,并命名为 Ihumii 放线菌^[4].福建医科大学附属第一医院于 2016 年收治一例由 Ihumii 放线菌引起的膝关节化脓性感染,现报道如下。

PU-3581

我院 2019 年第一季度血培养污染情况分析

余罗莉
福建医科大学附属第一医院

目的 分析我院 2019 年第一季度血培养污染情况,以提高临床血培养的合格率,从而使临床更有效地进行血流感染诊疗。
方法 由实验室信息系统统计同时收集 2019 年 1～3 月每个月的血培养送检总瓶数（n=6459）、污染总瓶数（n=42）,依据数据计算出月污染率。统计和分析各个科室中的污染情况,找到出现污染率较高的问题,然后有针对性地提出措施,以降低污染率。
结果 1 月份的污染率为 0.69%,2 月份为 0.51%,3 月份为 0.71%。凝固酶阴性葡萄球菌是主要的污染细菌,该细菌占比最高,达 69.05%。污染率最高的是 ICU 病区,占 42.86%;内、外科总的污染率为 42.86%,与 ICU 的污染率相似。
结论 污染情况发生的原因有很多种,而血培养污染的情况不能被忽视,有效预防并减少污染的情况,对临床血液感染的诊疗以及药物的应用非常有益。定期统计医院各科室送检标本污染率,有助于指导临床治疗。

PU-3582

碳青霉烯类耐药肠杆菌科细菌无症状携带者主动筛查的研究进展

陈善建、杨滨
福建医科大学附属第一医院

碳青霉烯类耐药肠杆菌科细菌（carbapenem resistant Enterobacteriaceae,CRE）的感染与传播是危害人类健康的公共问题。采取有效措施预防 CRE 感染是应对这种威胁的关键。住院患者肠道是耐药菌的储存库,这些定植的耐药菌具有引发院内感染暴发流行的潜在风险。CRE 的定植常先于 CRE 的感染或与感染并存,对入院患者进行 CRE 的主动筛查并对阳性患者采取一定的措施是预防 CRE 感染与传播的有效途径。现在,越来越多的研究关注 CRE 的主动筛查。该文就 CRE 的流行现状、CRE 主动筛查的人群及样本、筛查的方法等作简要综述。

PU-3583

基质辅助激光解吸电离飞行时间质谱仪鉴定临床分离菌的应用评估

林宇岚、杨滨
福建医科大学附属第一医院

目的 使用布鲁克基质辅助激光解吸电离飞行时间质谱仪对临床分离的病原菌进行鉴定并评价其准确性。
方法 收集福建医科大学附属第一医院 2015 年 11 月至 2016 年 12 月分离得到的 21 270 株病原菌,分别以布鲁克质谱仪以及 VITEK-Ⅱ/API 表型鉴定系统进行鉴定,并以分子生物学结果为金标准,验证鉴定结果的准确性。
结果 对临床常见病原菌,质谱系统的检出率>95%、表型系统的检出率>90%,具有较高的一致性。对 43 株厌氧菌,质谱有 90. 7%能鉴定到种,97. 7%被鉴定到属。表型系统有 65. 1%被鉴定到种,69.8%被鉴定到属,差异有统计学意义（X2=6. 76,P<0.01）; 1 558 株真菌中,丝孢酵母和念珠菌的检出率

差异均无统计学意义（均 P> 0. 05）,质谱对 78 株丝状真菌鉴定的准确率为 76%;18 株放线菌、诺卡菌、分枝杆菌和军团菌都能被鉴定到属。
结论 蛋白质谱鉴定技术操作简单、灵敏度高,能够对临床分离的常见病原菌、厌氧菌、真菌等提供快速、准确的鉴定。

PU-3584

改良显色平板在筛查碳青霉烯类耐药肠杆菌科细菌中的性能评价

陈善建、杨滨
福建医科大学附属第一医院

目的 碳青霉烯类耐药肠杆菌科细菌（CRE）的感染是威胁人类健康的重要卫生问题。建立一种快速、准确的筛查方法是应对这种威胁的关键措施;本研究旨在制备快速检测 CRE 的改良显色平板并对其性能进行评价。
方法 以传统的 PCR 方法为参考方法,用临床标本分离出的 49 株 CRE 及 24 株非 CRE 对 3 种改良显色平板的敏感度和特异度进行评价;其中,21 株 CRE 用于三种改良平板的检测限评价。
结果 亚胺培南改良显色平板的敏感度为 83.7%（41/49）,特异度为 100%（24/24）。美罗培南改良显色平板的敏感度为 87.8%（43/49）,特异度为 100%（24/24）;厄他培南改良显色平板的敏感度为 93.9%（46/49）,特异度为 95.8%（23/24）。
结论 三种改良显色平板均具有较高的敏感度与特异度,且操作简便,无需昂贵的仪器,对人员技术要求低;厄他培南改良显色平板相对于美罗培南与亚胺培南改良显色平板,其还具有检测限低的特点,更适用于临床的推广应用。

PU-3585

川东北地区耐头孢哌酮/舒巴坦鲍曼不动杆菌同源性分析

刘亮华、赵明才、刘海波、林芳、胡娟
遂宁中心医院

利用 MALDI-TOF MS 技术对重点科室耐药菌和主要的耐药基因共表达型进行同源性分析，探究重点科室细菌流行特点及 MALDI-TOF MS 技术在同源性研究中的应用价值。
方法 收集 2018 年 1 月至 2019 年 6 月我院微生物室分离的 157 株对头孢哌酮/舒巴坦耐药的鲍曼不动杆菌，利用基质辅助激光解吸电离飞行时间质谱（MALDI-TOF MS）对神经外科和 ICU 部分耐药菌进行同源性分析，同时对耐药基因 OXA-51、TEM 和 OXA-23 共表达型进行聚类分析。
结果 随机选取 23 株神经外科耐药菌，MALDI-TOF MS 聚类程度大于 60%，聚类树状图分为两大簇（I 型 7 株，II 型 16 株），II 型又分为四小簇（IIa 型 5 株，IIb 型 4 株，IIc 型 2 株，IId 型 5 株）；随机选取 28 株 ICU 耐药菌，聚类程度大于 65%，聚类树状图呈散在分布，未见时间聚类现象；随机选取 14 株 OXA-51、TEM 和 OXA-23 共表达菌株，聚类分析成同一簇分布。
结论 MALDI-TOF MS 同源性分析神经外科耐头孢哌酮/舒巴坦鲍曼不动杆菌成簇聚集分布，感染模式为阶段性同型菌株播散，而 ICU 耐头孢哌酮/舒巴坦鲍曼不动杆菌呈散在分布，遗传亲缘关系较神经外科更近；MALDI-TOF MS 技术有望成为分子流行病学研究新型手段。

PU-3586

2020 年遂宁地区铜绿假单胞菌分布及耐药性分析

赵明才、黎昆、刘家瑞、刘亮华、刘海波、胡娟
遂宁市中心医院

目的 分析 2020 年遂宁地区某医院临床分离的铜绿假单胞菌的分布特点和耐药状况，为该菌所致感染性疾病的防控提供实验室依据。
方法 分析 2020 年 1 月-2020 年 12 月临床各科室送检标本中铜绿假单胞菌的检出率、分布特点和药敏试验。
结果 临床送检各类标本 33855 份，阳性检出率 13.30%（3376/33855），其中铜绿假单胞菌总的检出率为 0.96%（326/33855），排名第四位；主要分布在呼吸中心 31.90%（104/326），ICU 13.80%（45/326），老年病科 4.91%（16/326），神经中心 4.29 %（14/326）和感染科 3.68%（12/326）；65.64 %（214/326）来自痰标本，5.52%（18/326）来自灌洗液标本；碳青霉烯耐药菌株占 9.20 %（ 30/ 326 ），铜绿假单胞菌耐药率（除天然耐药外）高于 30%的仅有氨曲南（37.40%），其他常见抗生素耐药率均小于 30%。
结论 铜绿假单胞菌是临床常见致病菌，主要分布在呼吸中心和重症监护室，且耐药率不高，及时监测其耐药趋势对指导临床用药有重要意义。

PU-3587

2020 年遂宁地区鲍曼不动杆菌临床分布及耐药性分析

赵明才、黎昆、刘家瑞、刘亮华、刘海波、胡娟
遂宁市中心医院

目的 分析 2020 年遂宁地区某医院临床分离的鲍曼不动杆菌的临床分布特点和耐药状况，为该菌所致感染性疾病的防控提供实验室依据。
方法 分析 2020 年 1 月-2020 年 12 月临床各科室送检标本中鲍曼不动杆菌的检出率、分布特点和药敏试验。
结果 临床送检各类标本 33855 份，阳性检出率 13.30%（3376/33855），其中鲍曼不动杆菌总的检出率为 0.43%（146/33855），排名第五位；主要分布在呼吸中心 23.5%（35/146），ICU 12.3%（18/146），神经中心 11.0 %（16/146），心血管中心 6.9 %（10/146）和骨科 4.8%（7/146）；69.9%（102/146）来自痰标本，7.5%（11/146）来自尿液标本；碳青霉烯耐药菌株占 30.8 %（45/146）。
结论 鲍曼不动杆菌是临床常见致病菌，主要分布在呼吸中心和重症监护室，且耐药性较高，亚胺培南、左氧氟沙星和阿米卡星可以作为本院推荐用药。

PU-3588

NDM-5 肺炎克雷伯菌美罗培南和多粘菌素体外诱导株的分子特性及其相关性研究

鲍金凤[1,2]、麻雅婷[1]、王驰[1]、周愿[2]、顾兵[2,3]、王成彬[1]
1. 中国人民解放军总医院第一医学中心
2. 徐州医科大学
3. 广东省人民医院

目的 探讨体外诱导美罗培南和多黏菌素耐药 NDM-5 肺炎克雷伯菌的适合度代价，并分析诱导株的分子特性，为开发新的有效抗生素提供理论依据。
方法 对临床分离的 2 株 NDM-5 肺炎克雷伯菌进行美罗培南和多粘菌素的体外诱导，分别诱导成对美罗培南耐药性进一步增加及多黏菌素耐药株；微量肉汤稀释法检测诱导耐药前后菌株对临床常用抗菌药物的最低抑菌浓度(minimal inhibititory concentration，MIC)；对诱导耐药菌株及其对应敏感菌株进行生长曲线分析、体外竞争试验及生物膜形成能力检测，分析诱导耐药后菌株的适合度代价；质粒接合实验确认 NDM 基因的转移能力，TapMan RT-PCR 检测 NDM 基因的表达量变化；对诱导前后菌株进行全基因组测序，分析诱导前后突变基因位点及其功能。
结果 成功诱导两株菌对多粘菌素由敏感到耐药，对美罗培南耐药性进一步增加。诱导株与原始株相比，对临床其他常用抗生素的药敏未发生明显变化；24 h 生长速率降低；体外竞争能力降低；NDM 基因表达量增加；与生物膜形成相关的三个基因（bsmA、fimI、yjfN）在两种抗生素诱导后均发生突变。
结论 肺炎克雷伯菌经美罗培南及多黏菌素诱导后会出现一定的适合度改变。碳青霉烯耐药表型与 NDM 基因表达量呈正相关性。抗生素条件会影响细菌生物膜形成相关基因（bsmA、fimI、yjfN）的表达，进而改变细菌的耐药性。

PU-3589

2018-2020 年川中地区鲍曼不动杆菌临床分布及耐药变迁

赵明才、林芳、刘亮华、刘家瑞、黎昆、刘海波、胡娟
遂宁市中心医院

目的 分析川中地区临床分离鲍曼不动杆菌的分布特点和耐药变迁，为该菌所致感染性疾病的有效防治提供实验室依据。
方法 分析 2018 年 1 月至 2020 年 12 月临床各科室送检标本中鲍曼不动杆菌的检出情况、分布特点和药敏试验。
结果 近三年鲍曼不动杆菌分离率分别是 0.6%（213）、0.4%（160）和 0.4%（146）。519 株鲍曼不动杆菌主要分离自呼吸道痰标本(68.1%)，其次为脓液(7.2%)，其他标本检出率较低。鲍曼不动杆菌以呼吸中心检出率最高(23.6%)，其次为神经外科(14.2%)，内科的检出率高于外科。2018 年 1 月至 2020 年 12 月耐药率总体呈下降趋势，除氨曲南、头孢唑林、头孢替坦和头孢曲松天然耐药外，头孢哌酮 / 舒巴坦、亚胺培南、米诺环素有所下降。
结论 川中地区鲍曼不动杆菌分离率有下降趋势，但仍然是临床常见致病菌，科室分布广泛，耐药率虽有下降，临床治疗也应根据药敏结果选择合适的抗菌药物。

PU-3590

昆明地区部分铜绿假单胞菌对碳青霉烯类抗生素的耐药机制研究

姚瑶、高辉、黄云昆、王佳、丁家伟、朱雯梅
昆明市延安医院

目的 研究昆明地区铜绿假单胞菌对碳青霉烯类抗生素的耐药机制。
方法 收集 2018 年 11 月-2019 年 12 月昆明地区三所三甲医院的耐碳青霉烯类铜绿假单胞菌共 60 株，采用纸片扩散法进行药物敏感试验，使用 WHONET5.6 软件进行药敏数据统计分析；采用 PCR 方法进行膜孔蛋白 oprD2 基因检测，扩增阳性产物进行测序分析，并选取扩增阳性的部分菌株采用 RT-PCR 方法进行 oprD2 基因的 mRNA 表达水平检测；对金属酶筛查阳性菌株采用 PCR 方法进行 IMP,VIM,SIM,GIM1,SPM,NDM 金属酶基因检测，扩增阳性产物进行测序分析；对外排泵筛查阳性菌株采用 RT-PCR 方法进行 MexA,MexC,MexE,MexX 基因的 mRNA 表达水平检测。
结果 60 株 CRPA 菌株对亚胺培南和美罗培南的的耐药率分别为 98.3% 和 81.7%，对头孢他啶、头孢吡肟、头孢哌酮/舒巴坦、头孢他啶/阿维巴坦的耐药率分别为 58.3% 、58.3%、63.3%、56.7%，对哌拉西林、哌拉西林/他唑巴坦的耐药率分别为 61.7%、 60%，对氨曲南的耐药率为 61.7%，对左氧氟沙星的耐药率为 63.3%，对阿米卡星、妥布霉素的耐药率分别为 48.3%、 41.7%；oprD2 基因缺失率为 6.7%（4/60），oprD2 基因表达降低率为 54.5%（12/22）； 20 株检出 MBLs 基因，金属酶基因检出率为 33%（20/60），其中 IMP 基因检出 16 株，VIM 基因检出 4 株；9 株 CRPA 菌株检出外排泵基因高表达，外排泵高表达检出率为 15%。
结论 耐碳青霉烯类铜绿假单胞菌对常用抗生素呈现较高的耐药率，临床需合理选择抗生素，控制 CRPA 的传播；本地区铜绿假单胞菌对碳青霉烯类抗生素耐药的机制以外膜通透性下降为主，其次为产金属酶，金属酶基因以 IMP 型为主，外排泵高表达可能不是本地区铜绿假单胞菌对碳青霉烯类抗生素耐药的主要耐药机制。

PU-3591

Genetic diversity and evolution of the virulence plasmids encoding aerobactin and salmochelin in Klebsiella pneumoniae

Dongxing Tian、Xiaofei Jiang
Huashan Hospital, Shanghai Medical College, Fudan University

Virulence plasmids of hypervirulent Klebsiella pneumoniae (hvKp) have the potential to transfer to drug-resistant strains or integrate with other plasmids, facilitating the genome evolution of threatening pathogens. We conducted an in-depth analysis of the publicly available 156 complete genome sequences of hvKp together with a multi-region clinical cohort of 171 hvKp strains from China to provide evidence for the virulence plasmid evolution. Virulence plasmids were frequently detected in the ST23 and ST11 K. pneumoniae strains. Multidrug-resistant hvKp (MDR-hvKp) occupied a large proportion of hvKp, and the coexistence of virulence and resistance plasmids may be the major cause. Virulence plasmids commonly possessed multiple replicons, of which IncFIBK was the most prevalent (84.6%). We identified 49 IncFIBK alleles among 583 IncFIBK plasmids, and they could be divided into Clades I, II, and III. We further observed that conjugative and non-conjugative virulence plasmids could be distinguished by IncFIBK genetic diversity, and IncFIBK subtyping could also indirectly indicate a chimeric preference of conjugative virulence plasmids. On this basis, we developed an open-access web tool called KpVR for IncFIBK subtyping. In conclusion, the genetic diversity of IncFIBK virulence plasmids could be used for tracking the evolution of virulence plasmids, and further preventing the emergence of MDR-hvKp strains.

PU-3592

VITEK MS 全自动微生物质谱检测系统性能验证

蓝依依[1]、何友[2]、徐少林[1]、李想[1]、张宇培[1]
1. 柳州市妇幼保健院
2. 柳州市中医医院

目的 针对医院检验科临床微生物检验实验室所用的 VITEK MS 全自动微生物质谱检测系统在常规的临床微生物鉴定中的性能要求进行验证，以确保所用仪器检测系统及试剂性能正常，微生物鉴定符合率能够满足临床的需求和要求。
方法 选取覆盖革兰阳性和革兰阴性的非苛养菌、苛养菌、厌氧菌、念珠菌等。包括临床留样菌株和标准/质控菌株，每种类型应至少 1 株，总体不少于 20 株及 VITEK MS 质控菌株（ATCC8739），所有的菌株均经过 VITEK 2 COMPACT 全自动鉴定药敏分析仪分析验证。菌株在试验前经过合适的琼脂培养基上复苏和分纯，35℃孵育 24-72 小时后待用，根据检测系统推荐的方法，按照其标准操作流程制备标本并通过质谱检测系统进行鉴定。每株菌株进行 2 个平行试验,于 VITEK MS 准备工作站中录入标本编号，结果于 Myla 数据分析平台查看并记录分析。标准/质控菌株符合率应为 100%，临床留样菌株的符合率应在 90％以上。
结果 VITEK MS 全自动微生物质谱检测系统对标准/质控菌株符合率为 100%，对临床留样菌株的符合率也为 100%，每一株细菌的鉴定率皆为 99.9%。
结论 VITEK MS 全自动微生物质谱检测系统在革兰阳性和革兰阴性非苛养菌、苛养菌、厌氧菌、念珠菌等的临床留样菌株和标准/质控菌株鉴定符合率符合要求，验证通过。本文建立的全自动微生物质谱检测系统性能验证方案能够满足现阶段医院临床微生物检验实验室常规的鉴定需求及要求。

PU-3593

血液病原菌种类分布和耐药性分析

牛瑜
山东大学第二医院

目的 分析 2016 年-2020 年本院临床科室血培养标本中病原菌的种类分布和耐药情况，为临床治疗血流感染感染提供理论依据。
方法 按照标本采集规范要求采集血培养标本，在血培养仪报警阳性时取出血培养瓶并接种血平板和巧克力平板，使用安图微生物质谱仪对可疑病原菌进行鉴定，并使用 BD M50 全自动药敏仪和西门子 MicroScan Walkaway-96 Plus 全自动药敏仪进行药敏试验，然后使用 WHONET 5.6 软件统计，分析尿液中病原菌菌株种类分布和耐药情况等。
结果 自 2016 年至 2020 年本院血培养病原菌共计 1573 株，其中凝固酶阴性葡萄球菌 601 株、大肠埃希菌 325 株、肺炎克雷伯菌 177 株、屎肠球菌 66 株、金黄色葡萄球菌 58 株、鲍曼不动杆菌 43 株等。血培养中碳青霉烯耐药的鲍曼不动杆菌 27 株、铜绿假单胞菌 12 株、肺炎克雷伯菌 50 株、大肠埃希菌 5 株，对碳青霉烯的耐药率分别为 62.8%、44.4%、28.2%、1.5%。苯唑西林耐药的金黄色葡萄球菌 17 株，耐药率为 29.3%。
结论 血培养分离菌株以凝固酶阴性葡萄球菌为主（38.2%），其中大部分来源于儿童，可能与采血过程污染有关，其次为大肠埃希菌（20.7%）、肺炎克雷伯菌（11.3%）、屎肠球菌（4.2%）、金黄色葡萄球菌（3.7%）。鲍曼不动杆菌和肺炎克雷伯菌对碳青霉烯的耐药率较高，延长患者的病程并增加了患者的病死率，应足够重视。

PU-3594

Integrated Signaling System under Endoplasmic Reticulum Stress in eukaryotic microorganisms

Ting Cao、Shuangquan Liu
The First Affiliated Hospital of University of South China

The endoplasmic reticulum (ER) is a multifunctional organelle, which is crucial for correct folding and assembly of secretory and transmembrane proteins. Perturbations of ER function can cause ER stress. ER stress can activate the unfolded protein response (UPR) to cope with the accumulation of misfolded proteins and protein toxicity. UPR is a coordination system that regulates transcription and translation, leading to the recovery of ER homeostasis or cell death. However, cells have an integrated signaling system to cope with ER stress, which helps cells to restore and balance their ER function. The main components of this system are ER-associated degradation (ERAD), autophagy, hypoxia signaling and mitochondrial biogenesis. If the balance cannot be restored, the imbalance will lead to cell death or apoptosis, or even to a series of diseases. In this review, a series of activities to restore the homeostasis of cells during ER stress are discussed.

Summary and perspectives Under normal conditions, in order to protect the survival of cells and maintain the balance of the body, ER stress components coordinate and work together to cope with various adverse stimuli. When these components are out of balance and cannot maintain the homeostasis of cells, disease can be progressed. Understanding how ischemia, hypoxia, nutrient deficiency, Ca2+ imbalance, pathogen infection and inflammation activate ER stress is helpful for us to better understand the occurrence and development of diseases. When ER stress occurs, it will produce ER protective signals to reshape the cell homeostasis, and related integration signals include degradation of abnormal proteins accumulated in the ER lumen through the ERAD pathway, removal of damaged organelles and generation of new cell components and energy by autophagy, activation of transcription of downstream genes by conduction of the hypoxia signal to alleviate the damage of hypoxia to cells, and mutual regulation of cells to cope with various adverse injuries by interaction between ER and mitochondria.

Moreover, understanding how ERAD, autophagy, hypoxia signal transmission and mitochondrial biogenesis respond to the adverse effects of ER stress will help us better grasp the treatment and prognosis of diseases. Additionally, exploring the signaling pathways between ER stress and ERAD, autophagy, hypoxia and mitochondrial biogenesis will provide us new therapeutic drugs or strategies for the treatment of various diseases, such as inflammation, tumor, heart, and nervous system diseases.

In summary, ER is the site for many crucial activities such as the biosynthesis of proteins of the secretory pathway, which is the main cell Ca2+ store and regulates synthesis and distribution of phospholipids and sterols. Alterations in such functions induce ER stress and may have detrimental consequences for the cell. Therefore, cells evolved a number of processes (UPR, ERAD, autophagy etc.) to counteract ER stress that may result in recovering cell homeostasis, in-depth study of the signal integration system under ER stress can help us further understand the self-regulation mechanism of cell biology when diseases occur, and it is helpful for us to identify the therapeutic targets and take more effective measures to prevent disease progression.

PU-3595

内质网应激与病理性血管生成相关疾病

曹婷、蔡佳伦、刘双全
南华大学附属第一医院

血管生成是由已存在的血管在多种促血管生长因子的共同作用下产生新血管的过程，这是一个多阶段、多分子调控的复杂过程。生理性血管生成是细胞处于增殖和快速代谢条件下由低氧诱导因子（HIF-1α)上调内皮细胞血管内皮生长因子(EGF)的分泌产生的。病理性血管生成除受血管内皮生长因子调控外，还与许多炎症因子、黏附分子、基质金属蛋白酶等相关。病理性血管生成在肿瘤中不仅可为肿瘤细胞提供血供和养分，还可促进肿瘤细胞向远端组织和器官转移。内质网应激（ERS）是真核细胞对于细胞内环境改变所做出的应激反应，轻微的 ERS 可引导蛋白质的正确折叠，恢复细胞内环境的稳态，然而持续性或剧烈的应激反应则会导致一系列疾病发生。许多病理情况下的血管生成与 ERS 相关，如病毒感染，肿瘤侵袭和慢性炎症等，病理性的血管生成涉及的机制和通路非常复杂，主要通过 ERS 激活内质网上的三个效应器: X-box 结合蛋白 1S、激活转录因子 4 和剪切后的 ATF-6，这三种效应器可作用于下游促血管生成因子 VEGF、炎症因子(IL-1β、IL-6、TNF-α、IL-8)、PIGF、bFGF 等的释放来促进内皮细胞的增殖和迁移进而促进血管生成。在此过程中内质网应激与病理性血管生成密切相关，当发生 ERS 时 GRP78/BIP 会与下游跨膜感受器解离从而激活 PERK 和 IRE1-α，其中 PERK 激活会进一步磷酸化下游 eIF-2α；而 IRE1-α 的激活则可剪切下游 XBP-1u 为 XBP-1s，两者共同促进 JNK 的磷酸化来促进炎症因子 IL-6、IL-8 的分泌，此外 NF-κB 也可响应 PERK 感受器的激活进而促进 IL-6、IL-8 的分泌来促进血管的生成。因此深入探讨 ERS 与血管生成之间的关系对于病理性血管生成相关疾病的致病机制和防治研究具有非常重要的意义。本文将从 ERS 与病理性血管生成相关疾病的发生机制做一综述。

PU-3596

Coinfection pulmonary mucormycosis and aspergillosis with disseminated mucormycosis involving gastrointestinalin in an acute B-lymphoblastic leukemia patient

胡志敏[1]、王兰兰[2]、邹亮[2]
1. 武汉市第一医院
2. 武汉市

Pulmonary mucormycosis and aspergillosis with disseminated mucormycosis involving gastrointestinalin is a very rare but lethal infection leading to extreme mortality. Herein, we present a unique case of pulmonary coinfection with Cunninghamella bertholletiae and Aspergillus flavus, with disseminated mucormycosis involving the jejunum caused by C. bertholletiae in an acute B-lymphocytic leukemia (B-ALL) patient with familial diabetes. Early administration of active antifungal agents at optimal doses and complete resection of all infected tissues led to improved therapeutic outcomes.

PU-3597

脑膜炎败血性伊丽莎白菌感染的分布及耐药性分析

石晓红
山东省千佛山医院

目的 脑膜炎败血性伊丽莎白菌（Elizabethkingia meningoseptica）EM 的定义经过了一系列的分类学演变。EM 被认可的时间并不长，既往被认为是一种无害细菌，EM 暴发性感染报道的逐渐增多，并且该菌耐药性强，临床治疗比较困难。并且在鉴定方面极可能与氧化酶阳性的多抗性非发酵剂如假单胞菌 、伯克霍尔德菌 、鞘氨醇单胞菌等相混淆，具体的属或种的鉴定比较困难。因此，对近年来该菌的感染分布及耐药性进行分析和研究，以便临床引起足够重视。
方法 2010-2021 临床分离株，药敏试验用 MH 琼脂或 HTM 琼脂，为 OXOID 公司商品。抗菌药物纸片为 BBL、OXOID 或国产公司商品 。药敏试验采用纸片扩散法（Kirby-bauer）或自动化药敏系统。
结果 临床分离菌住来自各个科室，以 ICU 病区为主，该菌对所有 β-内酰胺类抗菌药物头孢吡肟、头孢曲松、头孢噻肟、头孢西丁、头孢呋辛钠及阿莫西林阿维酸，亚胺培南 、美罗培南 、氨曲南，氨基糖苷类抗菌药物和甲氧苄啶-磺胺甲恶唑均有耐药性；对万古霉素、哌拉西林/他唑巴坦、头孢哌酮舒巴坦等相对敏感。
结论 脑膜炎败血性伊丽莎白菌是多重耐药菌，该菌的高耐药率与高产酶率有关，耐药机制较为复杂。其临床上引起感染时，应根据病情，参照实验室药敏结果选用合适的抗菌药物。并且要切实做好院感防控，预防该菌院内感染的发生。

PU-3598

尿路感染无乳链球菌的耐药性及分子流行病学特征研究

林锦琼、林子
广州医科大学附属第一医院

目的 了解近 5 年内由无乳链球菌感染引起尿路感染的分布情况，及其耐药性、耐药基因、毒力因子的特征，为临床个体化治疗提供准确的实验室数据。
方法 收集 2015 年 1 月至 2019 年 12 月广州医科大学附属第一医院无乳链球菌菌株标本 315 株，删除重复标本及不合格标本，筛选出 107 株有效标本，经 Vitek2Compact 全自动细菌鉴定及药敏分析系统进行药敏试验分析，进行菌株毒力因子基因分析以及耐药基因分析，同时进行菌株毒力因子基因分析以及耐药基因分析。
结果 经研究的 107 株尿路感染性无乳链球菌菌株中，检出率最高的科室是泌尿外科 70.1%（75/107）和泌尿男性科 21.5%（23/107）；临床标本类型检出率以中段尿 76.6%（82/107）和拭子 11.2%（12/107）占比最高。药敏结果显示，107 株菌株中未出现对利奈唑胺、氨苄西林、达托霉素、替加环素、青霉素这五钟抗生素耐药的无乳链球菌菌株，对红霉素的耐药率最高（62.3%），左氧氟沙星次之（27.1%）；毒力因子基因 PCR 结果显示，毒力因子及比例分别为 scpB（50%）、Lmb 和 bsaB（42.1%）、Cyl（19.6%）、Bac（6.5%）、Hvga（5.6%）。在 67 株红霉素耐药的无乳链球菌株中，scpB 基因检出阳性率最高。结论无乳链球菌对四环素的耐药性与耐药基因 tetM 密切相关，mefA/E 基因与菌株红霉素的耐药性有关。
结论 虽然青霉素的耐药菌株呈日益增长的趋势，但无乳链球菌对青霉素敏感性仍然保持较高水平，青霉素仍是目前临床治疗的首选药物。

PU-3599

2012-2019 年某院肺炎克雷伯菌的临床分布及耐药性变迁

欧阳鹏文[1]、腾静[2]
1. 湖南省人民医院
2. 湖南师范大学

目的 分析 2012～2019 年湖南省人民医院肺炎克雷伯菌感染及其耐药性的分布情况，更合理地指导耐药细菌的临床监测和监督。
方法 采用回顾性分析法, 收集 2012～2019 年送检至湖南省人民医院细菌实验室的各种临床标本 58583 例, 以及连续分离得出的 6388 例肺炎克雷伯菌的病例和药敏数据,采用 spss26.0 软件对其进行了统计学分析。
结果 从 2012 年的 619 株增加到 2019 年 1289 株，并且表现出逐年增加的趋势。标本主要是来源于痰液,占比 39.6%；在胆汁、血液、分泌液以及尿液的检出量分别占 12.1%、9.7、9.3%、8.0%。肺炎克雷伯菌对各类临床常用抗生素如亚胺培南的耐药率从 2012 年的 4.8%升到 2019 年 22.3%，表现出逐年增加的趋势。其中对氨苄西林的平均耐药率高达 99.9%,对头孢唑啉的平均耐药率高达 43.8%。一、二代头孢菌素的耐药性均超过 30%，对亚胺培南的平均耐药率 14.9%，对氨基糖苷类的抗菌素阿米卡星的平均耐药率最低为 6.2%。
结论 湖南省人民医院肺炎克雷伯菌的检出率呈逐年增加的趋势，同时其对临床常用抗菌药物耐药性严重。对此需要我们加强对抗生素的管控，重视对细菌耐药性的监测。

PU-3600

Virulence and Genomic Features of a virulent Burkholderia thailandensis strain BPM in China

Jin Li
Daping Hospital, Army Medical University

Introduction Burkholderia thailandensis is frequently isolated from the environment, however only a few studies describe the isolation of this subspecies from invasive human infections, so it is still not clear about the virulence and genomic features of B. thailandensis. In the present study, we described a case of B. thailandensis infection in a person in China.
Aim The aim of this study was to analyze the genomic features of a virulent B. thailandensis strain BPM, and to investigate the virulence-specific genes of BPM.
Methodology The potential virulence of B. thailandensis BPM was determined by in vitro and in vivo Methods And the whole-genome sequencing technology, molecular biology, and bioinformatics analysis Methods were used to analyze the genomic features associated with the virulence of BPM.
Results The BPM strain exhibited typical features of B. thailandensis, showing hypermucoviscosity phenotype, similar to B. thailandensis E264 (BtE264). In contrast to BtE264, we got molecular explanations for previously known virulence differences, discovered potentially 18 virulence-related genes, and then found that the acquisition of a 251 bp prophage gene BPM00110 in BPM, which is likely to have occurred non-randomly via horizontal gene transfer. Through bioinformatics analysis, we found that the BPM00110 gene is also a T3SS effector protein of BPM, indicating that it may be related to the hypervirulent of B. thailandensis.
Conclusion In this study, we provide a basic information on the phenotypic and genomic features of BPM, a strain displaying relatively high level of virulence. These findings support the notion that the virulence-associated genes (clusters) are sufficient for the hypervirulence of B. thailandensis. Therefore, we should take genome-based profile together with experimental work in the future studies to explore the virulence of B. thailandensis. The detailed mechanism involving in the virulence of BPM remains to be further explored.

PU-3601

浙南地区感染性角膜炎病因与致病菌特征分析

邵姣
温州医科大学附属眼视光医院

目的 感染性角膜炎，是全球失明的第四大病因。它主要是由细菌、真菌、病毒等病原微生物引起的眼睛和辅助组织化脓性疾病。由于地理环境、卫生状况、当地诊疗水平、经济发展水平等不同，感染性角膜炎的菌种分布、人口特点、临床特征在不同地区存在很大差异。

本课题拟对浙江省温州医科大学附属眼视光医院 2016 年 1 月至 2020 年 12 月收治入院的感染性角膜炎患者的临床资料进行回顾性分析，以期为浙南地区感染性角膜炎的诊疗提供理论依据。

PU-3602

The Diagnostic Value and Performance Evaluation of Five Serological Tests for the Detection of Treponema pallidum

Can Liu、Bin Yang
The First Affiliated Hospital of Fujian Medical University

Background Syphilis is caused by the bacterium Treponema pallidum (TP). The aim of this study was to establish a clinical approach for serodiagnosis of syphilis by evaluating the performance and diagnostic value of five serological tests for the detection of TP.
Methods Five tests were used to test the serum from syphilis patients and control patients, namely rapid plasma reagin (RPR) test, toluidine red unheated serum test (TRUST), TP passive particle agglutination assay (TPPA), TP-specific enzyme-linked immunosorbent assay (TP-ELISA), and TP-specific chemiluminescent immunoassay (TP-CMIA).
Results The sensitivity and diagnostic efficiency of TPPA (96.25%/98.38%), TP-ELISA (100%/95.41%), and TP-CMIA (100%/94.86%) were significantly higher than that of RPR (73.13%/86.22%) and TRUST (73.75%/86.49%) ($P < 0.05$). The minimum detectable concentrations for the five tests were 30 mIU/ml, 20 mIU/ml, 15 mIU/ml, 150 mIU/ml, and 150 mIU/ml, respectively. According to receiver operating characteristic (ROC) curve, the optimal cut-off values for syphilis diagnosis by TP-CMIA and TP-ELISA were 2.2 and 2.0 S/CO (where S/CO = Sample/calibrator cut off), and the area under the ROC curve (AUC) were 0.998 for TP-CMIA and 0.999 for TP-ELISA. The titers/positive rates for RPR and TRUST dropped from 1:4 (100%) to 1:1 (23.3%) (both $P < 0.05$) after treatment. However, there were no significant differences when we compared the positive rate of syphilis patients before and after treatment by TPPA, TP-ELISA, and TP-CMIA.
Conclusions Treponemal tests, such as TPPA, TP-ELISA, and TP-CMIA, are recommended for clinical routine screening of syphilis. However, nontreponemal tests, for example, RPR and TRUST, perform better in therapy response assessment. Serological test should be tailored to respective facilities and clinical demands.

PU-3603

Gut microbiota dysbiosis in patients with hepatitis B virus-induced chronic liver disease covering chronic hepatitis, liver cirrhosis and hepatocellular carcinoma.

Yongbin Zeng 、Qishui Ou
The First Affiliated Hospital of Fujian Medical University

The information regarding the effect of hepatitis B virus (HBV) infection on gut microbiota and the relationship between gut microbiota dysbiosis and hepatitis B virus-induced chronic liver disease (HBVCLD) is limited. In this study, we aimed at characterizing the gut microbiota composition in the three different stages of hepatitis B virus-induced chronic liver disease patients and healthy individuals. Faecal samples and clinical data were collected from HBVCLD patients and healthy individuals. The 16S rDNA gene amplification products were sequenced. Bioinformatic analysis including alpha diversity and PICRUSt was performed. A total of 19 phyla, 43 classes, 72 orders, 126 families and 225 genera were detected. The beta-diversity showed a separate clustering of healthy controls and HBVCLD patients covering chronic hepatitis (CHB), liver cirrhosis (LC) and hepatocellular carcinoma (HCC); and gut microbiota of healthy controls was more consistent, whereas those of CHB, LC and HCC varied substantially. The abundance of Firmicutes was lower, and Bacteroidetes was higher in patients with CHB, LC and HCC than in healthy controls. Predicted metagenomics of microbial communities showed an increase in glycan biosynthesis and metabolism-related genes and lipid metabolism-related genes in HBVCLD than in healthy individuals. Our study suggested that HBVCLD is associated with gut dysbiosis, with characteristics including, a gain in potential bacteria and a loss in potential beneficial bacteria or genes. Further study of CHB, LC and HCC based on microbiota may provide a novel insight into the pathogenesis of HBVCLD as well as a novel treatment strategy.

PU-3604

基于表面活性剂的敷料在各类伤口上的应用

李婷婷、李招吟倩
西南医科大学附属第一医院

表面活性剂为一类化合物，是指加入少量能使其溶液体系的界面状态发生明显变化的物质，它们是同时具有亲水和疏水部分的两亲性分子，在包括减少环境污染甚至食品和饮料工业、农业、微生物提高石油采收率，生物医学科学、纳米技术和各种其他领域在内的各个细分市场中发挥着不同和重要的作用。近年来，表面活性剂在伤口愈合方面的能力逐渐挖掘出来，被证明具有可以通过调节血管生成、炎症反应和细胞迁移而加速伤口愈合过程的能力，并且在慢性伤口或合并多种阻碍愈合因素的情况下，仍具有促进伤口愈合的作用。现目前基于泊洛沙姆的伤口敷料作为最常见且方便的治疗手段，既能防止水分与体液的损失，覆盖及保护创面不受感染，又利于上皮组织和肉芽的正常生长，从而促进伤口愈合过程本身。因此，本文将综述表面活性剂在临床不同伤口上的作用，着重讨论基于泊洛沙姆的伤口敷料的应用。

PU-3605

囊泡调控疏水性分子的输送和功能

刘瑶、李敏
上海交通大学医学院附属仁济医院

目的 人体皮肤共生人葡萄球菌可以分泌疏水性分子微球菌素，杀伤绝大部分的革兰阳性病原菌。人葡萄球菌依赖于该微球菌素的产生，从而可以作为益生菌直接杀伤病原菌，但疏水性的微球菌素分子在体内和体外都具有极差的抗菌活性。因此该疏水性分子发挥抑菌作用的机制还有待阐明。
方法 超高速离心和密度梯度离心法分离人葡萄球菌分泌的囊泡；脂质、蛋白含量检测和纳米粒径追踪技术检测囊泡的个数和粒径；透射电子显微镜观察囊泡的形状；抑菌实验检测囊泡的抗菌活性；荧光定量 PCR 技术检测不同时间点人葡萄球菌中抗菌分子的表达情况；小鼠皮肤脓肿模型检测携带抗菌分子的囊泡的体内抑菌效果。
结果 （1）将人葡萄球菌的上清液分为<>50kDa 组分，只有>50kDa 的部分才具有抗菌活性，考虑到微球菌素的分子大小只有 1.14kDa，因此该共生人葡萄球菌分泌的微球菌素并不是以游离的形式发挥抗菌活性。（2）对人葡萄球菌 2-22h 分泌的囊泡进行探究，发现囊泡的粒径和数量在 6h-12h 都是不断增加的，并在其后的生长时间内维持相对稳定的状态。（3）在密度梯度分离液的不同组分中，囊泡的含量与微球菌素的含量呈正相关关系提示囊泡可以携带微球菌素。（4）在不同的生长时间点，囊泡的抑菌活性与人葡萄球菌上清液的抑菌活性一致，且只有>50kDa 的部分才具有抑菌活性，提示人葡萄球菌的抑菌活性是由囊泡介导的。进一步实验证明微球菌素并不存在于囊泡的表面还是被富集于囊泡的内部。（5）动物模型和抗菌实验证明囊泡可以增强微球菌素的抑菌活性。
结论 这种以囊泡运输疏水性抗菌分子的机制不仅适用于该人葡萄球菌，也存在于其他细菌运输疏水性分子的过程。囊泡并不是细菌随意脱落的产物，它们对细菌发挥一定的功能具有重要的意义。

PU-3606

A part of 2020 Global Fungal Surveillance Program: the evaluation of in Vitro antifungal activity of isavuconazole against filamentous fungi from a multicenter study in China

Ran Jing[1]、Ian Morrissey[2]、Tian-Shu Sun[1]、Ge Zhang[1]、Ying-Chun Xu[1]
1. Peking Union Medical College Hospital
2. International Health Management Associates, Inc. (IHMA)

Objectives Monitoring antifungal susceptibility patterns for new or established antifungal agents against filamentous fungi is necessary, because the increasing antifungal resistance frequently occurred in filamentous fungi which are able to lead to invasive mold infections (IMIs) in immunocompromised patients with high morbidity and mortality in China. However, the resource of effective antifungal agents used for IMIs treatment are still limited in China, bringing an enormous challenge in clinic.
Methods We evaluated the *in vitro* activity of isavuconazole and comparator antifungal agents (voriconazole and amphotericin B) against 131 clinical isolates of *Aspergillus* spp. and order *Mucorales* collected from 2017-2020 under China Hospital Invasive Fungal Surveillance Net–North China Program. Identification of these isolates was performed using conventional morphological Methods and MALDI-TOF MS, and *in vitro* antifungal susceptibility testing was determined using the standard broth microdilution method according to CLSI M38-A3 document.
Results A total of 105 isolates of *Aspergillus* species were evaluated, including *A. fumigatus* complexes (n=75), *A. niger* complexes (n=11), *A. flavus* complexes (n=10) and *A. terreus* complexes (n=9). There were also 25 isolates of the order *Mucorales*. Against all of these *Aspergillus* species, both azoles had an MIC50 of 1 μg/ml and MIC90 of 2 μg/ml. Amphotericin B was less active than the azoles against *Aspergillus* spp. with an MIC50 of 4 μg/ml

and MIC90 of 8 μg/ml overall and susceptible wild-type MICs for 10.7%, 60%, 63.6% and 88.9% of *A. fumigatus* complexes, *A. flavus* complexes, *A. niger* complexes, and *A. terreus* complexes, respectively. Of note, the azoles showed contrasting activity against the order *Mucorales*, with isavuconazole producing an MIC50 of 0.5 μg/ml and MIC90 of 1 μg/ml, and voriconazole producing an MIC50 of 8 μg/ml and MIC90 of >8 μg/ml. Besides, one *Mucor circinelloide* isolate was found with the resistant to isavuconazole (MIC>8 mg/L). Amphotericin B produced an MIC50 and MIC90 of 1 μg/ml.

Conclusions This was the first multicenter study in China to evaluate *in vitro* antifungal activities of isavuconazole. Our study confirmed the excellent activities of isavuconazole against *Aspergillus* spp. and the order *Mucorales*, providing an advantage over other currently available broad-spectrum azole antifungals and a clinically useful alternative to voriconazole for IMIs treatment. However, it should be highly alerted in clinic with *Mucor* spp. has been resistant to new azole antifungal drugs.

PU-3607

人类免疫缺陷病毒合并侵袭性曲霉菌病的研究进展

邓佳敏
西南医科大学附属医院

侵袭性曲霉菌病是临床上较为常见的侵袭性真菌感染，主要见于免疫功能低下人群。然而，在人类免疫缺陷病毒感染的免疫功能低下人群中，侵袭性曲霉菌病却并不多见，到目前为止，全世界仅有数篇关于人类免疫缺陷病毒并发侵袭性曲霉菌病的病例报道。由于该病的临床诊断较为困难，且病死率高，极易出现误诊或漏诊，这一疾病逐渐受到国内外的高度重视，预计将成为临床研究的一大热点。针对这一现象，此综述通过对国内外人类免疫缺陷病毒合并侵袭性曲霉菌病的病因、流行病学特点、高危因素、发病机制、临床特点、辅助检查及药物治疗进行系统性回顾总结，以提高医务人员对该病的认识，降低临床死亡率。该文章是国内外迄今为止第一篇系统性报道人类免疫缺陷病毒合并侵袭性曲霉菌病的综述，对今后免疫缺陷病毒合并侵袭性曲霉菌病的发展具有一定的参考价值。

PU-3608

应用不同前处理法联合质谱技术快速检测血培养病原菌

刘鑫、张杰、张凯、钟敏、黄湘宁、殷琳、喻华*
电子科技大学附属医院•四川省人民医院

目的 通过不同前处理方法对阳性血培养标本进行前处理，联合基质辅助激光解析电离飞行时间质谱（MALDI-TOF MS），对阳性血培养标本病原菌进行快速检测，分析探讨不同前处理方法结合质谱技术快速检测病原菌与传统方法（即过夜培养后鉴定药敏）优劣性比较，优化目前血培养检测流程。

方法 将 30 份阳性血培养标本采用分离胶促凝管法、血培养试剂盒法、短时间培养法 2.5h、短时间培养法 5.5h 进行前处理后，分离病原微生物通过质谱进行快速鉴定，将不同前处理方法与传统方法相比较，就准确性、时间效益、经济效益、临床满意度等方面进行统计分析。

结果 以传统过夜培养后鉴定为参考方法，分离胶促凝管法鉴定率为 86.7%（23/30），短时间培养法 2.5h 的鉴定率为 46.7%（14/30），短时间培养法 5.5h 的鉴定率为 80.0%（24/30），血培养试剂盒法的鉴定率为 86.7%（26/30）。

结论 短时间培养法 5.5h 和分离胶法结合质谱仪进行血培养标本病原菌鉴定可快速有效的明确病原菌，血培养试剂盒法更为高效和便捷，利用不同前处理法分离到的病原菌同时进行药敏试验，可显著缩短血培养报告周期，为患者及早得到合适的抗菌药物治疗争取宝贵时间。

PU-3609

外伤性表皮葡萄球菌性眼内炎的危险因素及耐药性分析

张碟
温州医科大学

目的 通过回顾分析外伤性表皮葡萄球性眼内炎患者的资料，总结患者的流行病学特点，菌株耐药情况等，分析影响患者预后视力的危险因素，预测患者视力结局，为临床诊疗提供建议和参考，改善患者预后视力。
方法 选取 2013 年 9 月至 2020 年 12 月就诊于温州医科大学附属眼视光医院，诊断为外伤性眼内炎，且病原学确定为表皮葡萄球菌的患者共 90 例。将患者预后视力≥0.1 定义为预后好，＜0.1 定义为预后差。对等级资料使用使用秩和检验，对计量资料使用 t 检验或 u 检验，对计数资料使用卡方检验或 Fisher's 确切概率法，筛选影响因素，进行多因素 Logistic 回归分析获得预后视力相关的危险因素。绘制 ROC 曲线，评价 WBC、NEUT#、NLR 预测患者预后视力结局的诊断效率。
结果 绘制 ROC 曲线，WBC、NEUT#、NLR 诊断患者预后视力差 AUC 分别是 0.628、0.637、0.624（P＜0.05）。眼内异物、前房积脓、眼部伤口大小≥5mm 是影响外伤性表皮葡萄球性眼内炎患者预后视力的危险因素。患者眼部培养标本玻璃体液培养阳性率最高（占 86.5%）。患者眼部表皮葡萄球菌分离株对万古霉素、妥布霉素、左氧氟沙星敏感率较高，分别为 100%、81.2%、72.7%。对青霉素、红霉素、苯唑西林耐药率较高，分别为 95.5%、64.4%、61.2%。90 例患者中 56.7%的患者预后视力差，22.3%患者预后视力为无光感，3 例患者接受了眼内容物剜除术。
结论 存在前房积脓、眼内异物、眼部伤口大小≥5mm 的患者视力预后差。WBC、NEUT#、NLR 对于临床医师在疾病早期判断患者预后视力结局有一定价值。PPV 治疗可以改善患者预后视力。玻璃体注药可以继续使用万古霉素，眼部局部用药可以使用妥布霉素滴眼液和左氧氟沙星滴眼液。外伤性表皮葡萄球性眼内炎患者接受有效的治疗后仍有一半的患者的预后视力难以达到有效视力。

PU-3610

沙门菌外膜囊泡对小鼠髓源树突状细胞免疫功能的影响

韦莉
蚌埠医学院

目的 本试验以沙门菌为对象，利用超滤浓缩法提取沙门菌 OMVs，通过检测其对 DC 超微结构及免疫功能的影响，探索细菌 OMVs 的生物学活性。
方法 无菌取小鼠骨髓细胞，体外经粒细胞/巨噬细胞集落刺激因子(rm GM-CSF)和白细胞介素-4(rmIL-4)联合诱导扩增 DC，培养至第 7 天，于倒置相差显微镜下观察悬浮细胞形态变化情况；吸管轻轻吹打培养板收获半悬浮及疏松贴壁细胞，用抗鼠 CD11c-FITC 染色后经流式细胞术鉴定 DC 纯度。超速离心分离获取沙门菌 OMVs，CCK-8 法测定 OMVs 对 DC 存活率的影响，确定后续试验 OMVs 刺激浓度。不同浓度 OMVs 负载后，透射电镜观察 DC 超微结构，流式细胞术检测 DC 细胞因子分泌、表面分子表达和吞噬能力的变化。
结果 离心收集细胞样本经流式细胞仪检测分析，扩增到的细胞中 CD11c 阳性的 DC 能达到 85%以上，透射电镜可见 DC 表面有大量丝状伪足。CCK-8 法测定 DC 存活率结果显示：低浓度 OMVs(1 μg/mL, 5 μg/mL, 10 μg/mL)对 DC 的细胞毒性作用不强，对细胞生存率影响小。选择 5 μg/mL, 10 μg/mL 作为沙门菌 OMVs 的刺激浓度。流式细胞术检测 DC 细胞因子分泌、表面分子表达和吞噬能力结果显示：不同浓度 OMVs 处理后，DC 吞噬能力明显下降(P<0.05)，成熟表型特征性分子表达显著上调(P<0.05)，TNF-a 和 IL-1β 明显升高(P<0.05)。
结论 沙门菌 OMVs 可诱导 DC 分泌 IL-1β 和 TNF-a，促进 DC 成熟和抗原提呈的能力。

PU-3611

人体皮肤及鼻腔共定植金黄色葡萄球菌的分子特征

赵娜、刘倩
上海交通大学医学院附属仁济医院

背景 金黄色葡萄球菌是一种重要的条件致病菌，可引起多种疾病。正常情况下，金黄色葡萄球菌可定植在人体皮肤、粘膜、胃肠道和阴道等，而这被认为是引起金葡菌内源性感染的重要危险因素之一。然而，对于定植于人体的金黄色葡萄球菌的分子特征的鉴定，特别是针对同一个体不同部位定植的金黄色葡萄球菌，目前还没有很好的研究。
方法 本研究中，我们从 526 名健康人分为三个年龄组(儿童、青年和老人)并从他们的皮肤和鼻腔拭子中分离并培养了所有可培养细菌。其中，对于同一个体皮肤及鼻腔共定植的金黄色葡萄球菌，我们通过 spA 分型和 MLST 分型比较、药敏试验、溶血试验、生物膜半定量试验、细胞粘附试验以及建立小鼠鼻腔和皮肤定殖模型等方法，对这些金黄色葡萄球菌的分子特征进行了系统性分析与比较。
结果 无论是在皮肤或鼻孔中，葡萄球菌都是优势种属，其中以凝固酶阴性葡萄球菌丰度最高；此外，金黄色葡萄球菌也可从皮肤及鼻腔中分离得到。我们在 7 个个体的皮肤和鼻腔中同时分离到 52 株金黄色葡萄球菌，进一步研究表明，从同一个体不同甚至相同器官分离的金黄色葡萄球菌的基因型并不完全相同，而且在生物膜形成和溶血活性等表型方面也存在显著差异。同时，在细胞粘附实验和小鼠定植模型中，我们发现，相较于鼻腔，从皮肤分离出的金葡菌对皮肤上皮细胞有更强的粘附力。
结论 综上所述，金黄色葡萄球菌在人体不同器官的分布并非完全同质的，其传播或内源性感染的来源是多种多样的；并且细菌在人体不同部位定植期间能够发生微进化以适应人体内环境。

PU-3612

探讨 VISAVRSA 相关耐药进化史及耐药进化的代价

夏启航
上海市临床检验中心

金黄色葡萄球菌是最常见的临床病原菌之一，对医疗卫生构成重大威胁。1980 年以来，万古霉素作为治疗 MRSA 引起的严重感染的一线药物，成为治疗严重金黄色葡萄球菌感染的有效保障。然而，随着越来越多的万古霉素敏感减弱的菌株在全球范围报道，研究人员和医生们开始担心 VISA/VRSA 是否有一天也会爆发。这篇综述，我们简单回顾了金黄色葡萄球菌耐药性的历史，并还归纳了相关 VISA/VRSA 进化模式和相应的进化改变，提出如何更好得优化临床治疗策略。

PU-3613

上海地区 CA-MRSA/OS-MRSA ST59 进化分析

李天铭、简颖、李敏
上海交通大学医学院附属仁济医院

目的 研究一家教学医院临床分离金黄色葡萄球菌（Staphylococcus aureus, S. aureus）中苯唑西林敏感、mecA 阳性的金黄色葡萄球菌（OS-MRSA ST59）以及 CA-MRSA ST59 的进化特点及耐药规律，以指导临床预防和治疗 S. aureus 感染。
方法 收集 2008 年到 2018 年上海华山医院分离的非重复金黄色葡萄球菌 CA-MRSA ST59 81 株，以及儿中心分离的 OS-MRSA ST59 9 株，经质谱仪鉴定及 VITEK2 全自动细菌药敏分析，表型分

析判定苯唑西林耐药金黄色葡萄球菌（MRSA）和苯唑西林敏感金黄色葡萄球菌（MSSA）菌株。抽提 DNA 进行全基因组测序，并进行进化分析，分析 mecA 基因及其启动子 SNP，mecA 调控基因 SNP 以及相关基因的覆盖度分析。
结果 经全基因组序列比对，81 株 CA-MRSA ST59、9 株 OS-MRSA ST59 与全球金黄色葡萄球菌 ST59 数据共分析，本课题研究的 ST59 主要为 TaiWan 来源。SNP 分析发现，与 N315 比对，mecA SNP 分为 5 种 Cluster，其中 8 株 OS-MRSA 为 Cluster1 型；mecA 启动子 SNP 分为 4 种 Cluster，其中有文献报道 mecA 启动子 SNP 与耐药性相关；本研究又对 mecA 调控基因 blaR1 进行 SNP 分析，发现有 5 株 OS-MRSA 属于一种 Cluster，均缺失一个碱基。
结论 2008-2018 年上海华山医院分离的 CA-MRSA ST59 与课题组前期分离的 OS-MRSA ST59 均为 Taiwan 来源。blaR1 基因中，5 株 OS-MRSA 属于一种 Cluster，均缺失一个碱基，可能导致 bla 蛋白的失活，引起耐药性的降低。

PU-3614

普外科无菌体液多重耐药菌特征及混合感染危险因素分析

杨晓燕[1]、邸师红[2]、韩鹏鹏[2]、王利新[2]
1. 宁夏医科大学总医院
2. 宁夏医科大学总医院心脑血管病医院

目的 分析我院普通外科无菌体液病原菌感染特征以及混合感染的危险因素和预后，为降低医院感染的发生率和院感防控提供依据。
方法 回顾性分析 2018 年 1 月至 2021 年 1 月在普通外科住院且无菌体液培养阳性患者的临床资料、病原学分布以及多重耐药菌特征，再根据分离出病原菌的数量将患者分为单一感染组和混合感染组，两组资料进行单因素卡方检验后，用多因素 Logistic 回归模型进行多元分析筛选混合感染的危险因素。
结果 共纳入 882 例患者，检出 1075 株病原菌，排前五位的病原菌主要为大肠埃希菌、肺炎克雷伯菌、金黄色葡萄球菌、肠球菌属以及念珠菌。单一感染 700 例（79.37%），混合感染 182 例（20.63%），混合感染主要以大肠埃希菌+肠球菌属以及大肠埃希菌+肺炎克雷伯菌组合感染模式为主。与单一感染组相比，混合感染组多重耐药菌（MDRO）、耐甲氧西林金黄色葡萄球菌（MRSA）、耐甲氧西林凝固酶阴性葡萄球菌（MRCNS）、耐万古霉素的肠球菌（CRE）、产 ESBLs 的大肠埃希菌（ESBL-produding E-coli）、产 ESBLs 的肺炎克雷伯菌（ESBL-produding kpn ）、耐碳青霉烯类抗生素的鲍曼不动杆菌（CR-AB ）检出率（46.5%,28.9%,59.5%,43.0%,50.1%,40.2%,86.5%）明显升高，且混合感染组患者住院时间（t=18.85，P=0.000)明显延长，病死率（χ2=18.95，P=0.000)明显升高。多因素结果筛选出：高龄、恶性肿瘤、多脏器功能衰竭、基础疾病≥2 种、侵入性治疗、近期住院超过 7 天以及多重耐药菌感染是无菌体液混合感染的独立影响因素（P＜0.05）。
结论 普通外科患者无菌体液分离的病原菌种类多，耐药形式严峻，影响普外科混合感染的因素较多，根据监测结果采取针对性干预措施，可降低混合感染发生率，缩短患者住院时间，降低病死率。

PU-3615

新冠疫情爆发前后儿童呼吸道合胞病毒感染流行特征分析

王莉莉[1]、刘志[2]、彭虹艳[1]、吴舒婷[1]、阳青兰[1]、李梨平[1]
1. 湖南省儿童医院儿科医学研究所
2. 湖南省计量检测研究院

目的 了解新冠疫情爆发前后，2019-2020 年湖南省儿童医院就诊病人呼吸道合胞病毒（RSV）感染及流行病学特征。
方法 2019 年 1 月-2020 年 12 月期间，采集湖南省儿童医院门诊和住院病人急性呼吸道感染儿童鼻咽拭子标本，采用直接免疫荧光法对 RSV 抗原进行检测，对病例信息进行统计学分析，同时采用 RT-PCR 对 76 例 RSV 阳性标本进行亚型检测。
结果 2019 年和 2020 年共检测病例 25094 例和 15219 例，阳性率分别为 8.89%和 14.92%，2020 年阳性检出率高于 2019 年（$\chi 2=347.41$, $P<0.001$）；阳性率存在明显的季节性，冬季最高；年龄越小，阳性率越高，阳性率无性别差异；RSV 阳性标本中，A 型 13 例（17.10%），B 型 63 例（83.9%），2020 年 RSV 流行亚型以 B 型为主。
结论 通过对 2019-2020 年湖南省儿童急性呼吸道感染 RSV 进行监测，为湖南地区及全国儿童长期呼吸道 RSV 病原学检测提供资料，有利于新冠后疫情时代 RSV 防控和临床诊断。

PU-3616

真菌 1,3-β-D 葡聚糖检测室间质评的建立和结果探讨

徐蓉
上海市临床检验中心

目的 建立真菌 1,3-β-D 葡聚糖检测的室间质评，对室间质评结果进行分析以提高临床真菌 1,3-β-D 葡聚糖检测质量。
方法 使用模拟血清的质控品进行真菌 1,3-β-D 葡聚糖检测项目的室间质评，评判结果以定性（阴性或阳性）为准。
结果 通过 2016-2020 年 5 年 950 家次实验室的共 4750 次检测的室间质评结果来看真菌 1,3-β-D 葡聚糖检测的室间质评活动运行正常，各临床实验室上报定性的结果均能符合设定值。
结论 真菌 1,3-β-D 葡聚糖检测的室间质评适用于临床真菌 1,3-β-D 葡聚糖的检测，该室间质评方法的成功建立使参与室间质评的各临床实验室在该检测项目的质量得到保障，同时室间质评的定量检测值的统计结果也有助于参评实验室能发现本实验室的结果是否存在偏离。

PU-3617

Analysis on microbial contamination of 25202 umbilical cord blood units of Shanghai in the past 6 years

Xuejie Liu
Shanghai Center For Clinical Laboratory

To investigate the contamination situation of microbial contamination during cord blood collection and treatment, and provide some reference for reducing cord blood pollution，a total of 25202 cord blood samples were collected from Shanghai cord blood hematopoietic stem cell bank from August 2014 to July 2020, of which 458 strains of bacteria were isolated, which the total pollution rate was 1.82%, and what will be identified to search the possible sources. The research finds that 210 strains of the bacteria are the aerobic bacteria, accounting for 45.85%,

and the others are the anaerobic bacteria, accounting for 54.15%, and from the perspective of delivery mode, the proportion of cesarean section is 5.02%, a total of 23 strains of contaminated bacteria, and the proportion of eutocia is 94.98%, a total of 435 strains of contaminated bacteria. And most of the contaminating bacteria are escherichia, bacteroides, lactobacillus, eubacterium. The conclusion is that there is little difference between aerobic bacteria and anaerobic bacteria in the distribution of pathogenic bacteria. and from the aspect of delivery mode, the anaerobic bacteria species of the eutocia are more than the cesarean section in the umbilical cord blood contamination; amd from the detected bacteria, the heliconia, bacteroides, lactobacillus and the eubacteria are the main contaminating bacteria, and what are also the normal flora of the human mouth, respiratory, intestinal and reproductive tract. So the strengthening of the technical training in cord blood collectors and the strictly implementing the aseptic operation system is necessary, which will reduce the pollution rate of cord blood.

PU-3618

BLAF 标本中半乳甘露聚糖检测在侵袭性肺曲霉病中的价值研究

李伟、孙恩华、张义
山东大学齐鲁医院

目的 评估支气管肺泡灌洗液（BALF）与血清中半乳甘露聚糖（GM 试验），以及 1,3-β-D 葡聚糖（G 试验）联合检测在非粒缺患者侵袭性肺曲霉病（IPA）中的诊断价值，探讨 IPA 实验室诊断的最佳组合。

方法 前瞻性收集考虑为 IPA 的住院患者数据资料（排除粒细胞缺乏症患者），检测血清和 BALF 中 GM 试验，同时检测血清 G 试验；利用 ROC 曲线分别分析血清 G 试验、血清 GM 实验、BALF-GM 试验的敏感度、特异度、阳性预测值、阴性预测值，并通过 logistic 回归将三者数值引入方程，构建 IPA 诊断模型，评估联合后的新指标对 IPA 敏感度和特异度。

结果 血清 G 试验的敏感度 88.9%，特异度 85.4%，阳性预测值 82%，阴性预测值 91.21%；血清 GM 试验的敏感度 77.4%，特异度 92.5%，阳性预测值 76.0%，阴性预测值 90.6%；BALF-GM 试验的敏感度 82.6%，特异度 93.2%，阳性预测值 76.0%，阴性预测值 95.1%。经逐步 logistic 回归分析，血清 GM 被剔除（P=0.178,选入变量的检验标准为 P<0.05，剔除变量为 P>0.1），筛选出有意义的变量为血清 G 试验和 BALF-GM，构建联合检测 IPA 的诊断模型：logit(Y)=0.36+0.03*G－5.90*BALF-GM，得到新变量 Y 诊断 IPA 的 AUC 为 0.92(95%CI=0.873~0.967)，高于血清 G 试验和 BALF-GM（P<0.05），敏感度为 94.1%，特异度为 80.2%。

结论 G 试验和 GM 试验是 IPA 的重要早期实验室指标，BALF-GM 对 IPA 的诊断效能高于血清 GM 和 G 实验，联合检测 BALF-GM 和血清 G 实验可进一步提高诊断效能，可为 IPA 的早期诊断和治疗提供有力的实验室证据。

PU-3619

A Capillary Electrophoresis Method for analyzing the diversity of Vaginal Microbiome

Li Lai
Fujian Provincial Hospital

Background16S ribosomal RNA (rRNA) gene sequences analysis is the common method to identify the bacteria in human vaginal flora.While specific DNA primers were designed to target 16S rRNA gene sequences,DNA fragments analysis using capillary electrophoresis can obtain more accurate qualitative and quantitative information on the microbiome.This study aimed

to assess the ability of capillary electrophoresis method to analyze the diversity of vaginal microbiomes,and provide a theoretical basis for the accurate gene detection of vaginal flora.
Methods We collected 75 vaginal secretion samples from female outpatient aged 25-50,who had underwent routine gynecologic examinations in Fujian provincial hospital from March 2021 to April 2021.Clinical diagnosis was based on the results of Gram staining microscopic examination and biochemical tests of bacteria(pH value,
Catalase,Leukocyte esterase,Sialidases,β-Glucuronidase and Acetylglucosaminidase).
Vaginal secretion samples were collected and then total bacterial DNA was extracted.We used six pairs of fluorescent dye tagged specific primers that were designed base on the 16S rRNA genes of four Lactobacillus species (L. iners, L. crispatus, L. jensenii and L. gasseri), G. vaginalis and A. vaginae. PCR products of six species of bacteria were detected and analyzed by a 3130 Genetic Analyzer.
Results 75 samples were divided into two groups according to the viginal microbiome evaluation,including 50 cases which had vaginal bacteria balance and 25 cases which had vaginal bacteria disorder. PCR amplification of 16S ribosomal RNA genes of L. iners, L. crispatus, L. jensenii, L. gasseri,G. vaginalis and A. vaginae was successfully performed on the DNA extracted from vaginal secretion samples.Four Lactobacillus species were detected in 4-33 cases of “Balance” group ,and G. vaginalis was detected in 23 cases of“Disorder”group ,simultaneously A. vaginae was detected in 20 cases .
Conclusion Based on the technique of DNA fragments analysis using capillary electrophoresis method,the most common vaginal bacteria in Chinese healthy women are L.iners and L.crispatus. G.vaginalis and A. vaginae are the most common pathogenic bacteria detected in the patients who had vaginal bacteria disorder.Using capillary electrophoresis method to detect the vaginal bacteria will be useful for accurate identification of vaginal microbiome.There will be a application value to find out the composition of the vaginal microbiome rapidly and detect specific gene markers to identify potential pathogenic bacteria when women was at risk of serious illness before they develop obvious symptoms.

PU-3620

一种进口呋喃妥因药敏纸片试验性能评价

张戈、黄晶晶、赵颖
中国医学科学院北京协和医院

目的 评估一种进口呋喃妥因药敏纸片产品的检测性能。
方法 收集北京地区一家三甲医院 2016 至 2017 年从临床标本中分离的 118 株病原菌，包括肠杆菌目细菌 61 株、葡萄球菌属 48 株、肠球菌属 9 株。依照美国临床和实验室标准协会（The Clinical and Laboratory Standards Institute, CLSI）文件 M100ED30，对国产和进口呋喃妥因药敏纸片采用纸片扩散法进行体外药物敏感性试验检测，并根据其临床折点进行结果判读，比较两种纸片判读结果的分类一致率（CA）。
结果 118 株病原菌中，有 73 株对呋喃妥因敏感，4 株中介，41 株耐药。进口与国产体外药敏实验纸片的分类一致率为 100%。
结论 该呋喃妥因进口药敏实验纸片，体外抗菌药物敏感性试验结果可靠，与国产体外药敏实验纸片一致性好。可以满足实验室需求，为临床感染性疾病诊疗提供用药参考。

PU-3621

天津市某三级医院 2015-2019 年尿路致病性大肠埃希菌的耐药变迁

魏寒松、王永宁、马春红
天津市宁河区医院

目的 回顾性分析某三级医院临床患者尿样本中分离的大肠埃希菌耐药情况，评估其耐药趋势变化，为尿路感染诊疗提供理论依据。
方法 收集 2015 年 1 月至 2019 年 12 月疑似尿路感染患者的尿样本进行尿培养和药敏试验。用 Vitek 2 Compact 进行细菌鉴定和药敏试验，将所有大肠埃希菌分离株的耐药数据纳入本研究。
结果 尿路致病性大肠埃希菌（UPEC）所致尿路感染人群以老年人为主，年龄段分布以 50-70 岁年龄段为主。UPEC 耐药率最高的抗菌药物分别为氨苄西林、环丙沙星、左氧氟沙星和复方新诺明，分别为 87.80%，71.40%，67.50%，64.70%。耐药率最低的抗菌药物是美罗培南、亚胺培南、哌拉西林/他唑巴坦。所检测的抗菌药物中，哌拉西林、头孢唑林、头孢呋辛、呋喃妥因五年间的耐药率变化有统计学差异。
结论 大肠埃希菌所致泌尿道感染以五十岁以上老年人为主。UPEC 对氟喹诺酮类抗菌药物耐药率较高，临床上在治疗尿路感染时应当参考药敏结果给予合适的药物。在经验性治疗时要慎重选择氟喹诺酮类药物。

PU-3622

2017~2020 年孕产妇阴道致病菌群分布及无乳链球菌检出率分析

刘栋宾、陈敏、谭继权、董沅君
湖南省妇幼保健院

目的 对 2017~2020 年的孕产妇阴道致病菌群分布及无乳链球菌检出率进行分析比较。
方法 选取 2017 年 1 月至 2020 年 9 月在湖南省妇幼保健院产检且阴道分泌物需氧培养为阳性的 11282 例孕产妇作为本次研究对象，将收集到的数据进行统计与整理，探讨分析孕产妇的阴道菌群分布特征，并比较 2017~2020 四年间无乳链球菌的检出率以及耐药率的变化。
结果 孕产妇阴道分泌物需氧菌培养的 11282 例阳性中，真菌 8960 例（79.79%），革兰阳性菌 1505 例（13.34%），革兰阴性菌 817 例（7.24%）。分离率最高的前五位病原菌分别为：白色念珠菌 4742 例（42.03%）、光滑念珠菌 3497 例（31.00%）、无乳链球菌 566 例（5.02%）、大肠埃希菌 544 例（4.82%）、克柔念珠菌 370 例（3.28%）。2017~2020 年无乳链球菌在需氧培养阳性菌中的占比分别为 3.27%（96/2934）、4.24%(135/3186)、5.83%(191/3275)、7.63%（144/1887），无乳链球菌对红霉素（70.83%、75.56%、78.01%、81.25%）、四环素（51.04%、60.00%、80.68%、78.47%）、克林霉素（50.00%、59.26%、66.49%、65.97%）的耐药率呈现逐年上升的趋势。
结论 临床应关注孕产妇在围产期时阴道的微生物菌群变化。无乳链球菌的检出率和耐药率呈逐年上升的趋势。孕产妇应在孕期做好产检，重视阴道分泌物的培养，针对致病菌及早干预并合理使用抗生素进行治疗，避免孕期的不良结局出现。

PU-3623

1 例拟气味类香味菌的实验室特点和耐药分析

樊冰、张彦鹏、罗勇、张鑫、聂勇波、周明、陈锐锋、顾大勇*
深圳市第二人民医院

目的 研究拟气味类香味菌患者的临床特点，并分析该菌的耐药情况，为临床提供诊疗依据。
方法 对 ICU 住院患者尿标本中分离的 1 株拟气味类香味菌用 BD 全自动微生物鉴定飞行时间质谱仪鉴定，用 VITEK2 Compact 系统中国定制卡 AST-N335 进行抗菌药物的敏感性测定，用 mCIM 法检测碳青霉烯酶，碳青霉烯酶抑制剂增强试验，检测 A 类丝氨酸碳青霉烯酶和 B 类金属 β 内酰胺酶。
结果 这 1 例拟气味类香味对哌拉西林/他唑巴坦、头孢哌酮/舒巴坦、头孢他啶、头孢吡肟、氨曲南、美罗培南、亚胺培南、阿米卡星、妥布霉素、左旋氧氟沙星、环丙沙星片、复方新诺明、粘菌素、多西环素、米诺环素、替加环素均为耐药；用 mCIM 法检测碳青霉烯酶，抑菌圈的直径为 6mm，表明这例菌株是产碳青霉烯酶阳性菌株；碳青霉烯酶抑制剂试验显示添加 EDTA 溶液的亚胺培南纸片抑菌圈直径与单药纸片相差 7mm。
结论 类香味菌是一种寄居环境的革兰阴性非发酵细菌，在临床标本检出率低，可以引起免疫缺陷患者的尿路感染、蜂窝织炎、败血症、肺炎、脑膜炎、筋膜炎及静脉炎等感染性疾病，以尿路感染最为多见。该例拟气味类香味菌是从本院 ICU 患者导管尿中培养出来的，有报道显示，留置导尿管可以作为类香菌感染的一个独立危险因素。本研究中该例拟气味类香味菌的药敏结果显示对 16 种抗菌药物均耐药，类香味菌属对临床常见的抗菌药物具有广泛的耐药性，有报道指出当培养的药敏结果均为耐药时，在联合治疗方案中加入碳青霉烯类药物仍然可以取得比较理想的疗效。本研究中利用碳青霉烯酶抑制剂试验，推断该例拟气味类香味菌可能是产 B 类金属 β 内酰胺酶，但是该试验是针对肠杆菌目的细菌，对于非发酵细菌没有足够的数据支持，还需要进一步的研究。

PU-3624

Population genomics study revealed recent population expansion of multi-azole-non-susceptible Candida albicans associated with invasive infections

Meng Xiao[1]、Jie Gong[2]、Jianzhong Zhang[2]、Yingchun Xu[1]
1. Peking Union Medical College Hospital
2. 中国疾病预防控制中心传染病预防控制所

Widely application of antimicrobials may influence population of microbes. Here we present genomic population structure of C. albicans and its association with antifungal non-susceptible phenotypes. From 33 cities in China, 370 C. albicans isolates causing invasive fungal diseases were collected, and 181 global C. albicans genomes were involved as comparators. It revealed that 15.4% of isolates, including 66.6% of azole non-susceptible strains belonged to C. albicans Clade 1. Of note, two sub-clades in Clade 1, namely Clade 1-R1 (n=44) and Clade 1-R2 (n=9) were identified, and loss-of-heterozygosity events indicated two recent population expansions. Clade 1-R1 isolates exhibited higher azole non-susceptible rate (75.0%), while all Clade 1-R2 isolates were pan-azole-non-susceptible and carried A114S and Y257H substitutions in Erg11p. Worldwide, Clade 1-R2 isolates were exclusively identified in China, but from a large span of geographic origins. Our study illustrated dissemination of antifungal non-susceptibility coupled with pathogens' population expansion in C. albicans.

PU-3625

Significance of serology testing to assist timely diagnosis of SARS-CoV-2 infections: implication from a family cluster

Meng Xiao、Yan Xu、Xinchao Liu、Yingchun Xu
Peking Union Medical College Hospital

Confirmative diagnosis of SARS-CoV-2 infections has been challenged due to unsatisfactory positive rate of molecular assays. Here we identified a family cluster of SARS-CoV-2 infections, with five of six family members were SARS-CoV-2-specific immunoglobin serology testing positive, while molecular assays only detected two of this five patients even repeated twice. We comprehensively analyzed this familial cluster of cases based on the clinical characteristics, chest CT images, SARS-CoV-2 molecular detection results, and serology testing Results At last, two patients were diagnosed with COVID-19, two were suspected of COVID-19, and two were considered close contacts. Our results emphasized the significance of serology testing to assist timely diagnosis of SARS-CoV-2 infections, especially for COVID-19 close contacts screening.

PU-3626

Analysis of common pathogenic bacteria and drug resistance of biliary tract infection in Nanjing area

Ruixia Yang
Jiangsu Province Hospital （The First Affiliated Hospital of Nanjing Medical University）

Background Analyze the distribution and drug resistance of pathogenic bacteria that causebiliary tract infections in Nanjing, and provide evidence for the rational useof antibacterial drugs in clinical practice.
Methods Clinical strains isolated from bile specimens ofpatients suspected of biliary infection in the First Affiliated Hospital ofNanjing Medical University in 2019 were collected, The drug susceptibilitycriteria are based on the standards published by the National StandardizationCommittee of the US Clinical Laboratories. WHONET 5.6 software was used toanalyze the distribution of pathogens and drug resistance.
Results A total of 693 strains of pathogenic bacteria wereisolated, including 448 Gram-negative bacteria(64.6%), 245 Gram-positivebacteria(35.4%). The top three pathogens were 210 strains of Escherichiacoli(30.3%), 87 strains of enterococcusfaecium (12.6%), 76 strains of klebsiella pneumoniae (11.0%), The resistancerates of Escherichia coli to ampicillin, cefuroxime, cefazolin, ceftriaxone,piperacillin and ampicillin / sulbactam were 80.1%, 69.4%, 67.3%, 64.1%, 63.6%and 62.8%, The resistance rates of Klebsiella pneumoniae to ampicillin /sulbactam, cefuroxime and cefazolin were 65.8%, 64.5% and 61.1%, The resistancerates of Enterobacter cloacae to ceftriaxone, ceftazidime and aztreonam were56.2%, 53.1% and 53.1%, The resistance rates ofEnterococcus faecium to moxifloxacin, clindamycin, erythromycin, penicillin G,ampicillin, ciprofloxacin and levofloxacin were 100%, 90%, 76%, 72.1%, 64.4%,64% and 62%.
Conclusions Pathogens ofbiliary tract infections are mainly Enterobacteriaceae such as Escherichia coliand Klebsiella pneumoniae, followed by Enterococcus faecium and Enterococcus faecalis.There were many drug-resistant bacteria, so we should pay attention to bilespecimen culture and drug sensitivity test.

PU-3627

The molecular characteristics, clinical manifestations, and risk factors of hypervirulent Klebsiella pneumoniae infections in a large teaching hospital in Southwest China

Zixuan Ding、Zhaoyinqian Li
Department of Laboratory Medicine, the Affiliated Hospital of Southwest Medical University, 25 Taiping street, Luzhou, 646000, Sichuan, P.R. China.

Hypervirulent Klebsiella pneumoniae (hvKp) has been globally disseminated recently, especially in Asia. The purpose of this study was to identify the molecular characteristics, clinical manifestations, and clinical risk factors of hvKp infections among patients in a large teaching hospital. A retrospective study was conducted in 123 patients infected with K. pneumoniae at the Affiliated Hospital of Southwest Medical University (Luzhou, China) from October 2016 to November 2018. An isolate that positive for both PCR amplification of aerobactin gene and Galleria mellonella infection model was defined as hvKp. Overall, 43.1% (53/123) of K. pneumoniae isolates were hvKp. String tests were performed on all isolates, and MLSTs of all hvKp were conducted. The K1 ST23 isolates were the dominant clone of hvKp (35.8%). Univariate analysis revealed the following risk factors for hvKp: hepatic abscess (OR=41.818 [95% CI, 5.379-335.086]), bacteremia (OR=19.94 [95% CI, 5.565-71.446]), metastatic spread (OR=19.938 [95% CI, 6.344-62.654]), CRP (OR=1.008 [95% CI, 1.001-1.015]), nitroimidazole treatment (OR=7.907 [95% CI, 1.652-37.843]), diabetes (OR=3.067 [95% CI, 1.38-6.817]), and admission to positive culture interval (OR=3.636 [95% CI, 1.524-8.678]). Moreover, Multivariate analysis implicated hepatic abscess (OR=74.332 [95% CI, 3.121-1769.588]), bacteremia (OR=28.388 [95% CI, 3.039-264.200]), and metastatic spread (OR=19.391 [95% CI, 3.633-103.498]) as independent risk factors for hvKp infections. Thirteen of twenty-one tested antibiotics were founded resistance to non-hvKp, which is significantly greater than hvKp. Importantly, the ESBL-hvKp and MDR-hvKp were responsible for 7.5% and 15.1% in the hvKp group, respectively.

PU-3628

川南地区侵袭性感染念珠菌流行病学特征及耐药性分析

徐灵玲、曾章锐
西南医科大学附属医院

目的 分析侵袭性感染念珠菌的菌种分布，样本类型和抗真菌药物的敏感性等数据，为临床诊治提供依据。
方法 回顾性分析本单位 2013 年 7 月至 2019 年 12 月临床诊断为侵袭性念珠菌感染的患者临床资料，对菌种分布、样本类型、科室分布和抗真菌药敏感性等进行分析。
结果 共收集非重复性侵袭性念珠菌感染患者 686 例，男性 373 例，占 54.37%，大于 60 岁患者占 53.35%；最主要念珠菌是白念珠菌 332 株（48.40%），其次是光滑念珠菌 244 株（35.57%）和热带念珠菌 74 株（10.79%）；样本类型以创口深部分泌物（247 例，36.01%）为主； 其次是清洁尿液（182 例，26.53%）和血液（124 例，17.64%），侵袭性念珠菌感染前 3 位科室是内科（270 例,39.36%），外科（237 例，34.55%），儿科（78 例,11.37%）；所有念珠菌对氟康唑、伊曲康唑和伏立康唑总耐药率分别为 18.82%、36.15%和 19.38%，对两性霉素 B 和 5－氟胞嘧啶的敏感性均为 100.00%。
结论 本地区侵袭性念珠菌感染以老年患者和白念珠菌为主，但非白念珠菌占主要地位，念珠菌对唑类抗真菌药物耐药率较高，但对两性霉素 B 和 5－氟胞嘧啶保持高度敏感性。

PU-3629

临床高毒力肺炎克雷伯菌分离株生物膜诱导的抗生素耐药性

李招吟倩[1]、丁子煊[2]
1. 西南医科大学附属医院
2. 西南医科大学

目的 为了了解生物膜形成在抗生素耐药性中的作用，共研究了 65 株临床肺炎克雷伯菌（hvKp）菌株的生物膜形成能力和与生物膜形成相关的基因。
方法 从西南医科大学附属医院共收集 65 株 hvKp 临床分离株，MicroScan Walk-Away 96 Plus 系统确定了对 18 种抗生素耐药性。通过结晶紫染色评估生物膜形成能力并通过共聚焦激光扫描显微镜观察。环丙沙星、美罗培南和头孢他啶的最低抑菌浓度（MIC）、最低细菌浓度（MBC）、最低生物膜抑制浓度（MBIC）和最低生物膜根除浓度（MBEC）通过肉汤微量稀释法对选定菌株进行测试。通过聚合酶链反应（PCR）检测生物膜相关基因。
结果 大约 21％的分离株具有多重耐药性（MDR），但没有菌株对替加环素和多粘菌素 B 具有抗性。我们发现 88.1％的测试菌株可以形成生物膜，其中 48％是强生物膜生产者。非 MDR 菌株相比 MDR 菌株能够形成更强的生物膜。环丙沙星、头孢他啶和美罗培南的 MBECs 和 MBICs 与所有测试菌株的 MICs 和 MBCs 相比明显增加。此外，生物膜形成相关基因 bamb 和 fabZ 的携带率与生物膜形成成正比。
结论 尽管目前 hvKp 的耐药性不是很高，但大多数菌株能够形成生物膜，使耐药性显著增加。解决生物膜特异性抗性的调节机制，需要在基因组和转录水平上进行彻底的研究。

PU-3630

A novel conjugative pK2044-like virulence plasmid with multiple conjugation-related genes in a bacteremic hypervirulent Klebsiella pneumoniae strain

Yang Liu 、wenjian liao、qisen huang
First Affiliated Hospital of Nanchang University

In the present study, we characterized a novel pK2044-like virulence plasmid in AP8555, an ST23 hvKP strain, which induced a metastatic infection and fatal septic shock in a critically ill patient. The serum killing assay, the quantitative biofilm formation assay, the G. mellonella infection model, and the mouse lethality assay demonstrated that AP8555 was almost as virulent as the hvKP strain NUTH-K2044. Whole-genome sequencing revealed that the genetic Background of the AP8555 chromosome is the same as that of NTUH-K2044. The plasmid pAP855 (357.8 kb in size) was almost structurally similar to the pK2044 plasmid apart from the addition of a 130-kb fragment from a conjugative InFII(K) plasmid with multiple conjugation-related genes of type IV secretion systems (T4SS) and plasmid-mediated ccdAB toxin-antitoxin systems (TAS). The results of conjugation and transformation experiments showed that the novel virulence plasmid could be efficiently transferred to the recipients, enhancing their virulence-associated phenotypes. In conclusion, unlike the non-conjugative pK2044 plasmid, pAP855 may promote rapid dissemination of virulence-encoding elements among clinical K. pneumoniae strains because of the inserted T4SS and ccdAB TAS. Therefore, continuous monitoring the prevalence of the novel conjugative pK2044-like virulence plasmids and simultaneously minimizing potential risks from the acquisition of pAP855-like virulence plasmids by classic Klebsiella pneumoniae strains, especially carbapenem-resistant K. pneumoniae strains, are essential.

PU-3631

高盐对肠道菌群改变的影响

董召刚、张义
山东大学齐鲁医院

目的 高盐饮食被认为参与某些慢性疾病的发生发展，最近研究显示慢性疾病与肠道菌群密切相关，然而，对于高盐饮食对肠道菌群构成的影响尚不清楚。本研究的目的是探讨 Wistar 大鼠摄取高盐后肠道菌群构成的改变。
方法 4 周龄雄性 Wistar 大鼠按标准流程喂养后分为高盐组和对照组。高盐组大鼠通过灌胃方式给予 1 ml 10％NaCl 溶液，每周 3 次，共 4 周。收集粪便，提取 DNA 后，利用靶向 V4 区的 16S rRNA 基因测序技术分析粪便菌群表达谱。利用贝叶斯分类器对 OTUs 进行了分类分析，观察菌群多样性。LEfSe 分析比较微生物种群的相对丰度，并利用 PCA 和 LDA 分析来寻找两个或多个组之间差异表达菌群。使用微生物群落的系统发育研究，通过 PICRUSt 生物信息学软件预测微生物基因组的功能。
结果 结果表明高盐组和对照组粪便微生物 α 多样性无显着差异，而主成分分析（PCA）表明两组之间的菌群结构不同。在门水平，高盐组含量最丰富的是 Bacteroidetes（58.4％），而对照组为 Firmicutes（48.0％）。根据 LDA≥4 的标准使用 LEfSe 进一步分析显示，高盐摄入后 wistar 大鼠粪便中 Lactobacillus 和 Prevotella NK3B31 显着降低，而 Alloprevotella 和 Prevotella 9 在高盐组大鼠中增加。但是两组间的体重、肠道形态变化和血压、生化指标等参数均无明显差异。
结论 作为一项探索研究，高盐摄入与肠道微生物菌群构成变化有关，本研究为提高微生物菌群在高盐相关疾病发病机制中作用的认识提供了理论基础。

PU-3632

Increasing Prevalence of Hypervirulent ST5 Methicillin Susceptible Staphylococcus aureus Subtype Poses a Serious Clinical Threat

Ying Jian、Min Li
Shanghai Jiao Tong University School of Medicine Affiliated Renji Hospital

Staphylococcus aureus (S. aureus) is a clinical pathogen of great significance causing metastatic or complicated infections. ST5 clonotype isolates have dominated *S. aureus* infections for more than 10 years in Shanghai, China. The proportion of methicillin-susceptible *S. aureus* (MSSA) has remarkably increased in the past decades, although the vast majority of isolates in ST5 linages are methicillin-resistant *S. aureus* (MRSA). By whole-genome sequencing (WGS) 121 ST5 clonotype *S. aureus* isolates using next-generation sequencing (NGS) platforms and characterizing the evolutionary dynamics of ST5 linages, we found that MSSA evolved independently, making it a subtype differed from other MRSA clones. Drug resistance gene analysis by usage of the NGS data demonstrated that ST5 clonotype MRSA might be more tolerant under the threat of antimicrobials, which was confirmed in further *in vitro* susceptibility tests. However, MSSA subtype isolates exhibited relatively high virulence upon the analysis of virulence factors using NGS data. Furthermore, MSSA subtype isolates displayed higher hemolysis capacity and higher ability to adhere to epithelial cells including A549 human alveolar epithelial cells and HaCaT human skin keratinocytes, caused more severe infections in murine abscess model. With its high virulence and enhanced magnitude in the past decades, the ST5 MSSA subtype poses a serious threat in clinical *S. aureus* infections, hence more attention should be paid in the prevention and control of methicillin susceptible isolates.

PU-3633

肺炎克雷伯菌 β -内酰胺酶耐药基因及毒力因子的流行和分布特征

朱梅、陆颖、朱志军、童红芳
安徽医科大学附属巢湖医院

Objective To investigate the frequency of antibiotic resistance profile and virulence factors of Klebsiella pneumoniae isolated from our hospital.
Methods The MIC of antibiotics was determined by broth microdilution method. The phenotype were identified by mCIM, MHT and string test. The antibiotic resistance gene, virulence gene and MLST were detected by PCR.
Results All of strains carried mrkD virulence gene, followed by fimH (88.9%), ybtS (51.9%). MLST results showed that 32 STs were found in 54 isolates, and ST11 (14.8%) was the dominant sequence type. Two new STs were assigned as ST5214 and ST5215.
Conclusion Klebsiella pneumoniae carried high frequency and diversity of β-lactamase genes and virulence genes.

PU-3634

肺癌患者下呼吸道病原菌分布特征与耐药性分析

孟红委、娄加陶
上海市胸科医院

目的 了解肺癌患者下呼吸道病原菌分布及耐药性，以指导临床经验治疗及合理使用抗菌药物。
方法 收集 2015 年至 2019 年上海交通大学附属胸科医院肺癌患者的痰培养资料，对病原菌进行鉴定和体外药物敏感性实验，并分析其分布特点和耐药情况。
结果 2015-2019 年共收集 4753 份痰培养，有 672 份痰培养检出病原菌 720 株，检出率为 14.1%，其中革兰阴性菌、革兰阳性菌、真菌分别占 71.5%、6.9%、21.5%。在所有病原菌中排名前 5 的分别是肺炎克雷伯菌（21.0%）、铜绿假单胞菌（16.8%）、白色念珠菌（16.5%）、鲍曼不动杆菌（11.0%）和金黄色葡萄球菌（5.0%）。肺炎克雷伯菌、铜绿假单胞菌、鲍曼不动杆菌对氨苄西林/舒巴坦、左旋氧氟沙星、环丙沙星、头孢他啶、妥布霉素、庆大霉素均较为敏感。白色念珠菌对常用的抗真菌药物两性霉素 B、氟康唑、伊曲康唑、伏立康唑、5-氟胞嘧啶均敏感。未发现对替加环素、万古霉素、利奈唑胺、奎奴普丁/达福普汀耐药的金黄色葡萄球菌。
结论 肺癌患者下呼吸道病原菌种类复杂，以革兰阴性菌为主。临床对于下呼吸道感染的肺癌患者可以根据耐药监测结果进行经验治疗，并根据具体药物敏感性试验结果进行针对性治疗。

PU-3635

金黄色葡萄球菌克隆株 ST398 进化分析

吕慧颖、何磊
上海交通大学医学院附属仁济医院

目的 对 2008-2018 年患者分离的 ST398 克隆株及动物分离的 ST398 克隆株通过全基因组测序进行遗传进化分析。
方法 本研究主要对 2015-2018 年收集的 52 株 ST398 MRSA 进行了二代全基因组测序。基于 52 个当前 MRSA ST398 和我们先前发表的 76 个 ST398(包括 7 个人类来源 MRSA（human-adapted MRSA，HO-MRSA）分离株、54 个人类来源 MSSA(human-adapted MSSA，分离株和 15 个动物

来源 MSSA（livestock-associated MSSA，LA-MSSA）分离株)的核心基因组的 SNP 数据，建立系统进化树，分析高致病性的 ST398 HO-MRSA 的进化特征。
结果 2015 年开始，高毒力 HO-MRSA ST398 逐渐流行，我们发现 50 株 ST398 HO-MRSA 分离株与我们先前研究的 4 株 ST398 HO-MRSA 分离株聚集在一起，使其成为区别于 MSSA 和其他 MRSA 克隆群的主要类群。证明了这一类群在近几年中成为优势谱系，促进了 ST398 在社区甚至医院的流行。我们也再一次证实，部分动物源性 MSSA 起源于人源 MSSA 的进化。基于 NGS 数据的耐药性和毒力基因分析表明，ST398 HO-MRSA 主克隆群中的所有分离株有相似的毒力和耐药基因模式。通过比对 SCCmec 分型检索，我们发现，ST398 HO-MRSA 主簇均含有 D 型的短 SCCmec V 移动元件，保持了极低的甲氧西林抗性。进一步的表型研究证实，流行的 HO-MRSA ST398 在保持高毒力时表现出增强的生物膜形成能力。在 HO-MRSA ST398 亚型中形成了毒力和生物膜形成能力的双重优势。
结论 高致病高生物膜形成能力的 HO-MRSA 克隆株 ST398 是社区和医院感染的严重威胁因素。

PU-3636

社区获得性金黄色葡萄球菌 ST398 ESS 分泌系统毒力蛋白 EsxA、EsxB 诱导宿主细胞死亡的机制研究

吕慧颖
上海交通大学医学院附属仁济医院

目的 研究 CA-SA 克隆株 ST398 中 EsxA、EsxB 毒力蛋白在上皮细胞中发挥毒力、诱导细胞死亡的通路。揭示 CA-SA 克隆株 ST398 金黄色葡萄球菌 EsxA/EsxB 蛋白在侵染宿主细胞过程中发挥作用的机制。
方法 选取代表性的 ST398 临床分离株作为野生株，构建 esxA、esxB 基因的突变株，并用质粒 pOS1 构建回补株。通过裸鼠皮肤脓肿模型、小鼠菌血症模型等研究该基因对金黄色葡萄球菌毒力和致病性的作用。构建毒力蛋白表达载体，获得携带 His 标签的 EsxA、EsxB 蛋白。并用该毒力蛋白与肾小管上皮细胞 293T 共孵育，通过检测细胞 LDH 释放，并用流式细胞仪 FITC-AnnexinV/PI 双染法，确定 EsxA、EsxB 蛋白诱导宿主细胞死亡的主要方式。并用程序性坏死通路的主要蛋白 RIPK1、RIPK3、MLKL 抑制剂及其缺陷细胞株验证该通路。
结果 CA-SA 克隆株 ST398 ESS 系统分泌蛋白 EsxA、EsxB 促进金黄色葡萄球菌的毒力，esxA、esxB 缺陷株感染小鼠及皮肤脓肿形成能力均下降。EsxA、EsxB 蛋白主要引起上皮细胞的程序性坏死而非凋亡。并且该蛋白诱导细胞程序性坏死主要依赖于 RIPK3-MLKL 通路磷酸化，不依赖于 RIPK1 蛋白。RIPK1、RIPK3、MLKL 抑制剂及其缺陷细胞株证实了该通路的存在。
结论 EsxA、EsxB 是社区获得性金黄色葡萄球菌 ST398 的重要毒力蛋白，其缺陷株的皮肤脓肿形成能力和菌血症形成能力较野生株，发生明显下降。在社区获得性金黄色葡萄球菌侵染宿主的过程中，毒力蛋白 EsxA、EsxB 通过 RIPK3-MLKL 的程序性坏死通路诱导细胞死亡。

PU-3637

MALDI TOF MS 技术检测病原微生物影响因素探究

陈蓉
上海市临床检验中心

上海地区综合性医院患者多、周转快，疑难杂症多，如何在繁忙的工作中既能满足临床对微生物检测快速的需求，同时又能保障检验结果的准确性一直是困扰临床检验的重要难题。MALDI-TOF MS 技术的出现给微生物实验室带来了革命性的飞跃，它改变了现有的微生物鉴定流程，工作效率得到显著提升，检验结果回报时间明显缩短，为临床提供更有利的诊治支持。我们对其鉴定的

影响因素、性能验证和对无菌体液标本直接检测的适用性进行了研究，发现在不同培养基的培养条件下，质谱的检测结果无明显差异；在不同培养时间的培养条件下，24 h 获得的检测分数值明显高于 72 h 的分数值，且分数值均≥2.300，可正确鉴定到种。三种前处理方法中，提取法比直接法的检测结果分数值偏高，尤其是在革兰阳性菌的检测结果中体现的更加明显。性能验证方面 MALDI-TOF 质谱仪在需氧菌、厌氧菌、真菌方面都有很好鉴定结果，能够满足临床微生物常规的细菌鉴定要求。重复性好，灵敏度可达到 104 cfu/mL。但是也存在一些局限性，如对于同一菌属中某些蛋白质图谱十分相近的菌种无法直接鉴定到种,一些罕见菌种或新型细菌由于蛋白指纹图谱收录不完善导致鉴定率低或无鉴定结果。在直接检测无菌体液时，由于样品中菌量偏低以及其他成分的干扰影响了该技术对病原菌的检出率。我们认为应该自建数据库，进一步完善同一菌属中相近菌种图谱库以及罕见菌种的图谱库，使这些细菌得到更好的鉴定。对临床标本的直接检测，进一步优化标本的前处理，获得富集细菌，提高检出率。

PU-3638

从乳腺炎分泌物中分离到结核硬脂酸棒状杆菌

宋皓月[1]、舒文[1]、刘庆中[2]
1. 上海市第一人民医院
2. 上海市中医医院

目的 对患者乳腺炎分泌物中分离得到的一株棒状杆菌进行细菌鉴定、药敏检测、耐药基因、毒力基因分析。
方法 收集 2018 年一例因乳腺炎就诊病人，在无菌条件下于乳腺脓肿处，抽取脓液标本，经培养后，采用镜检、理化、质谱等方法，对细菌进行初步鉴定，并通过全基因组测序进一步鉴定，对所得菌株进行药敏检测，并鉴定耐药基因。
结果 分离培养所得细菌，最终鉴定结果为结核硬脂酸棒状杆菌，药敏结果提示对万古霉素、碳青霉烯类药物敏感，对克林霉素、磷霉素、复方新诺明等耐药，其所携带耐药基因为 blaTEM 及 erm（X）。
结论 此病例最终证实为结合硬脂酸棒状杆菌引起的感染，此菌株携带耐药基因 blaTEM 及 erm（X），药敏结果提示尚对大部分药物敏感，治疗效果好。目前相关病原菌临床分离株数较少，应注意病原菌筛检，为临床提供更多的参考依据。

PU-3639

Identification and characterization of lncRNA AP000253 in occult hepatitis B virus infection

qingqin hao
Wuxi red cross blood center

Background Recent studies suggest that lncRNAs may play significant roles in the development of hepatitis B virus (HBV) infection. However, as a special stage of HBV infection, the lncRNA expression in occult HBV infection (OBI) remains unclear.
Methods The plasma level of 15 HBV infection-related lncRNAs was initially detected using qRT-PCR in 10 OBI and 10 healthy controls (HCs) in discovery phase. Significantly dysregulated lncRNAs were subsequently validated in another 64 OBI, 20HCs, 31 chronic hepatitis B (CHB) and 20 asymptomatic HBsAg carriers (ASC). Moreover, the AP000253 expression in liver tissues and its potential biological functions in HBV infection were further investigate with public transcriptomic data and HBV-expressing cell lines.
Results Among candidate lncRNAs, the plasma level of AP000253 decreased significantly in OBI, ASC and CHB patients compared to HCs, while no difference was found among OBI, ASC and

CHB patients. In liver tissues, similar AP000253 expression was also observed from the GSE83148 dataset, while that in HBV-expressing hepatoma cells was opposite. ROC curve analysis indicated that plasma AP000253 yielded an AUC of 0.73 with 60% sensitivity and 75% specificity when differentiating OBI from HCs, but it could not specifically separate the stage of chronic HBV infection. Furthermore, functional experiments suggested that AP000253 could promote HBV transcription and replication in hepatoma cell lines.
Conclusions AP000253 might be involved in HBV replication, and be served as a potential biomarker for HBV infection. In the setting of blood donations, plasma AP000253 would be more useful to moderately distinguish OBI in HBsAg-negative donors. However, the AP000253 expression in liver tissues and associated molecular mechanism of HBV infection deserve further study in future.

PU-3640

PCR、LAMP、PCT 在细菌性痢疾诊断中的应用价值及与免疫指标的相关性

姚杰、李昕、程娟、唐伟、周强
安徽医科大学第二附属医院

目的 探究聚合酶链反应（PCR）、环介导等温扩增法（LAMP）、降钙素原（PCT）在细菌性痢疾诊断中的应用价值及与免疫指标的相关性。
方法 收集 2019 年 5 月~2020 年 5 月我院收治的 110 例细菌性痢疾患者粪便标本为观察组，同时选择同期 50 例健康体检者为对照组，均使用 PCR、LAMP、PCT 进行联合检验，对 PCR、LAMP、PCT 三种技术的特异性、灵敏度进行评价，并检验两组的免疫指标水平。
结果 观察组与对照组使用 3 种检测志贺菌阳性差异有统计学意义（P<0. 05）；以临床诊断为标准，PCR、LAMP、PCT 的灵敏度分别为 62.56%、58.72%、60.26%，特异度分别为 71.67%、75.00%、74.17%，准确度分别为 59.11%、62.22%、59.44%。观察组 CD3+、CD4+、CD4+/CD8+水平均低于对照组，组间差异有统计学意义（P＜0. 05）。
结论 联合应用 PCR、LAMP、PCT 法检测细菌性痢疾可提高临床诊断准确性。免疫指标水平可对细菌性痢疾中志贺菌检测提供临床依据，可辅助上述检测方法进行检测。

PU-3641

尿路感染主要致病菌流行病学分析

郭敏、杜鸿
苏州大学附属第二医院

目前，临床尿路感染治疗主要存在致病菌多重耐药的难题。为此，本文拟围绕尿路感染主要病原菌分子流行病学展开研究，以期为临床合理用药、避免暴发流行提供理论依据。同时，评估由产碳青霉烯酶大肠埃希菌与肺炎克雷伯菌引起尿路感染的临床特征和结局。
方法 1、微生物鉴定与药敏。
2、耐药表型确证实验。
3、耐药基因的检测。
4、分子流行病学分析。
5、全基因组测序。
6、ST 分型、血清荚膜分型及毒力基因检测。
7、评估由产碳青霉烯酶大肠埃希菌与肺炎克雷伯菌引起尿路感染的临床特征和结局。

结果 1、尿液标本中头孢噻肟耐药大肠埃希菌(CTX-R-ECO)检出率 55.2%，略高于全国细菌耐药监测网(CARSS)监测数据，头孢噻肟耐药肺炎克雷伯菌(CTX-R-KPN)检出率 46.0%，略低于全国细菌耐药监测网监测数据。
2、本研究中，尿路感染分离到的产碳青霉烯酶大肠埃希菌、肺炎克雷伯菌，分别为 2 株、9 株。
3、从耐药基因来看，我院产碳青霉烯酶大肠埃希菌与肺炎克雷伯菌中，产碳青霉烯酶 NDM、KPC 是主要的耐药机制。产 ESBLs 大肠埃希菌与肺炎克雷伯菌，主要是以产 CTX、TEM、SHV 的菌株为主。
4、同源性分析中，PFGE 研究结果显示我院尿路感染大肠埃希菌为非克隆性传播。
5、全基因组测序显示：与耐药基因、ST 分型、毒力基因筛查结果相吻合。
6、ST 分型、血清荚膜分型和毒力相关基因检测结果显示：尿路感染肺炎克雷伯菌均为 ST11 型，血清荚膜分型大多数为 KL64 型，毒力相关基因检测显示多样化。
7、评估由产碳青霉烯酶大肠埃希菌与肺炎克雷伯菌引起尿路感染的临床特征和结局：由产生碳青霉烯酶和大肠埃希菌引起的大多数泌尿道感染患者恶化，放弃治疗并自动出院，只有 2 例敏感药物有效地改善了感染。
结论 非克隆性传播为尿路感染大肠埃希菌的主要传播方式。由产生碳青霉烯酶和大肠埃希菌引起的大多数泌尿道感染患者恶化。

PU-3642

Hospital sewage isolated lytic bacteriophages against epidemic carbapenem-resistantKlebsiella pneumoniae ST11 strains

Min Guo 、Hong Du
The Second Affiliated Hospital of Soochow University

Carbapenem-resistanceKlebsiella pneumoniae (CRKP) poses a significant clinical problem given the limited choices of effective antibiotics. Alternative anti-bacterial agents, such as bacteriophages, could be used as a valuable tool to treat the infections caused by these highly resistant bacteria. In this study, we isolated 54phages from medical and domestic sewage wastewater between July and Sepetember2019, and tested their activities against 54 clinical CRKP isolates collected from a tertiary hospital in Eastern China. These CRKP isolates were from 7sequence types (STs) and belonged to 9 capsular K locus types (KLs), harboring blaKPC-2 (n=49), blaNDM-1 (n=5), and blaIMP-4 (n=3). The 54 phages showed the host ranges from 7 to 52 CRKP strains, and were all active against some CRKP ST11 strains. The combination of various phages showed the capacity to cover all CRKP isolates. Among the 54 phages, phage P545has the widest host range (96.3%), which was classified as a member of Myoviridaes, order Caudovirales. Physiological characterization suggested that P545 had a short latent period of 20 min, a low burst size of 82 PFU/cell and was stably maintained at different pH values (4-10) and temperatures (up to 60 oC). In addition, plaque morphology analysis indicated that four phages, P507, P560, P569 and P551, may encode depolymerases with polysaccharide-degrading activity. Taken together, our study showed that phages isolated from local sewagewastewater had wide host range and excellent properties against clinical CRKP isolates, especially the epidemic CRKP ST11 strains, providing promising phage candidates for future phage therapy applications.

PU-3643

MALDI-TOF MS 结合 UF1000i、短期培养法在尿路感染微生物快速鉴定中的应用

郭敏、杜鸿
苏州大学附属第二医院

目的 拟研究 MALDI-TOF MS 结合 UF1000i、短期培养法对快速鉴定尿路感染微生物的应用价值。
方法 1、标本前处理-差速离心法浓集细菌。2、直接 MALDI-TOF MS 检测。3、短期培养后 MALDI-TOF MS 鉴定。4、ROC 曲线计数细菌阈值。
结果 1、质谱检测鉴定率：短期培养 5h 后，取菌膜质谱检测鉴定率为 87.2%，高于直接质谱检测鉴定率的 77.1%。2、标本菌落计数对应质谱检测鉴定率：标本的菌落计数越多，则直接质谱检测鉴定率及短期培养后质谱检测鉴定率越高。3、质谱鉴定分值：本实验可以发现：短期培养后质谱检测分值≥1.7（大肠埃希菌≥1.5）的菌株数，明显多于直接质谱检测分值≥1.7（大肠埃希菌≥1.5）的菌株数。4、混合感染：不论是直接质谱检测，还是短期培养后质谱检测，大部分情况下只能鉴定出所占比例较高的菌种，且可信度较高。5、ROC 曲线计数细菌阈值：当 UF1000i 检测细菌数值≥1100/μl 时，直接质谱检测容易成功鉴定出菌种。同样，当 UF1000i 检测细菌数值≥470/μl 时，短期培养后质谱检测容易成功鉴定出菌种。
结论 与传统的尿培养相比，本研究中对尿培养标本进行差速离心浓集细菌，通过 MALDI-TOF MS 结合 UF1000i、短期培养法在快速鉴定尿路感染微生物，具有简单快速、成本低、准确率高等优点，可极大提高 MALDI-TOF MS 技术快速鉴定尿路感染微生物的临床应用价值，对于明确尿路感染微生物、指导临床用药和及时控制尿路感染有着重要的临床意义。

PU-3644

MALDI-TOF MS 直接检测血流感染病原菌产碳青霉烯酶效果的评估

谢小芳、王敏、郑毅、朱雪明、杜鸿
核工业总医院（苏州大学附属第二医院）

目的 利用基质辅助激光解吸电离飞行时间质谱(Matrix Assisted Laser Desorption Ionization-Time Of Flight，MALDI-TOF MS)技术快速检测血培养瓶中肠杆菌科细菌是否产生碳青霉烯酶。
方法 收集本实验室保存的 67 株对碳青霉烯类耐药的肠杆菌科菌株，包含 33 株肺炎克雷伯菌、11 株阴沟肠杆菌、8 株产酸克雷伯菌、6 株大肠埃希菌、4 株产气肠杆菌、3 株弗劳地枸橼酸杆菌和 2 株粘质沙雷菌。将菌株配制为 0.5 麦氏浊度的菌悬液，稀释至 10cfu/ml 后与绵羊血一同注入需氧和厌氧瓶中建立血培养模型，置于 BD FX100 全自动血培养仪中培养。待血培养瓶阳性报警后，差速离心法富集细菌，取细菌沉淀与 0.1g/L 厄他培南溶液混匀孵育 2h 后再次离心取上清进行 MALDI-TOF MS 检测，通过菌株与药物反应后产生的药物特征性谱峰的存在与消失来快速判断菌株是否产碳青霉烯酶，并将其与 PCR 检测结果进行比较。
结果 PCR 检测结果表明 67 株肠杆菌科细菌均含有碳青霉烯酶基因。MALDI-TOF MS 快速检测结果显示该 67 株肠杆菌与厄他培南孵育后，需氧瓶中有 66 株与厄他培南孵育后将其水解，而厌氧瓶中有 64 株与厄他培南孵育后将其水解，质谱图显示水解后厄他培南有四个特征峰 335m/z、379m/z、422m/z、465m/z 明显消失，结果提示携带有 KPC、GES、NDM、IMP 基因的肠杆菌需氧与厌氧瓶检出率都为 100%，携带有 VIM 基因的肠杆菌需氧瓶和厌氧瓶检出率分别为 100%和 83.3%，携带有 GIM 基因的肠杆菌需氧瓶和厌氧瓶检出率分别为 100%和 75%，而 1 株携带有 SIM 基因的阴沟肠杆菌，需氧与厌氧瓶均未检测出。

结论 本研究利用 MALDI-TOF MS 技术快速检测血流感染中肠杆菌科细菌是否产碳青霉烯酶，为血流感染病原菌的临床治疗提供早期依据。

PU-3645

HAdV-B55 腺病毒 LAMP 检测方法的建立及评价

董磊、刘娟
空军特色医学中心(原空军总医院)

目的 HAdV-B55 为经呼吸道和消化道传播的 DNA 病毒，感染人体可引发急性腺病毒型肺炎、急性胃肠炎、眼角膜炎、乳糜泻和急性间质性肾炎等多种疾病。环介导等温扩增(loop-mediated isothermal amplification, LAMP)法是一种新型的核酸扩增技术，具有较高的灵敏度及特异性，可以通过颜色的变化判断结果，无需开盖，容易判读，且可以完全避免样本污染。本研究尝试建立了一种针对 HAdV-B55 病毒的 LAMP 检测方法，为临床快速诊断和监测 HAdV-B55 提供技术支持。
方法 采用在线 LAMP 引物设计工具设计获得针对 HAdV-B55 Hexon 基因序列的特异性引物，建立 HAdV-B55 腺病毒的 LAMP 扩增方法。将 HAdV-B55 病毒标准品进行梯度稀释，评估该检测方法的灵敏度；提取 HAdVB3、B5、B7、B55/Y16、B11、B14 及 H1N1、H5N1、H3N2 病毒 DNA，评估该检测方法的特异性。之后随机选取疑似临床腺病毒感染患者的咽拭子样本进行该方法的临床应用评价，同时以报道的腺病毒通用引物作为检测对照方法。
结果 获得了针对 HAdV-B55 的特异性引物，建立了特异检测 HAdV-B55 的 LAMP 检测方法，该方法特异性良好，选取的最终引物具有较好的种属特异性。该方法灵敏度较高，最低可检测到 4PFU/ml 的病毒 DNA，灵敏度可达 0.008PFU/反应。在临床样本评估中，与已公布的腺病毒通用 PCR 检测方法相比，LAMP 法在 65 份疑似腺病毒感染患者样本中检测到 19 份为阳性，且阳性及阴性对照成立，而已公布的腺病毒通用 PCR 检测方法仅检测到 13 份阳性样本，结果表明本研究建立的 LAMP 检测方法具备更高的灵敏度。
结论 该研究成功建立了针对我国 HAdV-B55 的特异性 LAMP 检测方法，具备良好的灵敏度及特异性，为我国 HAdV-B55 的快速检测及防控提供了有力的技术支持。

PU-3646

耐碳青霉烯类大肠埃希菌整合子的分子特征与耐药性研究

王育慧
潍坊市人民医院

回顾分析 2012.01 至 2019.12 潍坊市人民医院临床分离的 117 株耐碳青霉烯类大肠埃希菌（carbapenem-resistant escherichia coli ，CR-Eco）的临床分布及其对常用抗菌药物的敏感性变化，检测其 1、2、3 类整合子及基因盒的分布情况，探讨其耐药机制并追踪溯源其亲缘关系。117 株 CR-Eco 检测到底一类整合子阳性的菌株 92 株，其中 77 株检测到可变区，通过测序分析，共检测到 7 种基因盒组合 dfrA17-aadA5、aadA22、dfrA12-aadA2、dfrA12、dfrA17、dfrA27 和 aadA1，以 dfrA17-aadA5 最常见。药敏试验结果显示，IPM 和 MEM 均耐药组菌株对部分抗菌药物的耐药率高于 IPM 单一耐药组，包括 AMK、ATM、CAZ、CIP、FOX、LVX、SXT 和 TOB 等（P<0.05）；另 IPM 和 MEM 均耐药组菌株对部分抗菌药物的耐药率高于 MEM 单一耐药组，包括 CAZ、FEP、FOX 和 TZP 等（P<0.05）。第 1 类整合酶阳性菌株耐药性也高于阴性菌株，包括 ATM、CAZ、CIP、CRO、GEN、MEM 和 SXT 等药物（P<0.05）。运用 Eric-PCR 技术针对临床分离的 117 株耐碳青霉烯类大肠埃希菌分为 A、B、C、D、E、F 六个分型，其中 A 型 25 株、B 型 27 株、C 型 12 株、D 型 25 株、E 型 11 株、F 型 17 株。进行追踪溯源通过 Quantity one 软件作出基因树状图谱，发现 3 株细菌高度同源性，提示可能存在院内克隆传播。

PU-3647

霉烯高毒力肺炎克雷伯菌的临床特征及分子分析

黄韵
武汉大学人民医院

目的 分析耐碳青霉烯的高毒力肺炎克雷伯菌(CR-HvKP)的临床及分子特征,加强临床医生对该菌的认识。
方法 收集 2019 年 10 月至 2020 年 10 月分离自武汉大学人民医院的 CR-HvKP 菌株，碳青霉烯酶抑制剂增强试验对碳青霉烯酶进行表型确证，通过拉丝试验、毒力耐药基因检测、毒力相关荚膜抗原基因检测、多位点序列分型和患者临床表现分析该菌的临床及分子特征。
结果 共收集到 CR-HvKP 13 株，均为产 KPC-2 的 ST11 型，荚膜血清学分型均为 K64 型，表型确证试验也均显示产 A 类碳青霉烯酶。毒力基因以 rmpA+rmpA2+iucA+peg-344 4 种共同携带为主，占 69.2%（9/13），其中，3 株拉丝实验阳性。感染集中发生在重症医学科，患者大都患有多种严重的基础性疾病
结论 本院 CR-HvKP 菌株为同一型别，CR-HvKP 因其高耐药性和高毒力的结合可引起较为复杂和严重的感染,应加强院感监测，提高临床医生对该菌的认识，防止其暴发流行。

PU-3648

碳青霉烯酶抑制剂增强试验在肺炎克雷伯菌中检测碳青霉烯酶的应用

黄韵
武汉大学人民医院

目的 评价碳青霉烯酶抑制剂增强试验在产碳青霉烯酶肺炎克雷伯菌耐药表型检测中的应用效能。
方法 随机选取 105 株耐碳青霉烯肺炎克雷伯菌（CRKP），采用 PCR 法检测碳青霉烯酶基因(blaKPC、blaNDM、blaIMP、blaVIM、blaOXA-48)，采用碳青霉烯酶抑制剂增强试验检测产碳青霉烯酶肺炎克雷伯菌耐药表型。以碳青霉烯酶基因检测结果为金标准, 计算该试验检测产 A 类碳青霉烯酶,B 类碳青霉烯酶及共产 A 类与 B 类碳青霉烯酶菌株的敏感性和特异性。
结果 105 株 CRKP 中,104 株碳青霉烯酶基因检测阳性（99.0%，104/105）,其中 88 株仅 KPC 基因阳性菌株在碳青霉烯酶抑制剂增强试验中检测为产 A 类碳青霉烯酶, 即该试验检测产 A 类碳青霉烯酶菌株的敏感性为 100.0% (88/88) ,1 株碳青霉烯酶基因检测阴性菌株在该表型试验中呈阳性，特异性为 94.1%（16/17）。7 株基因检测仅携带金属-β 内酰胺酶（6 株 NDM 与 1 株 NDM+IMP）菌株在碳青霉烯酶抑制剂增强实验中也呈 B 类碳青霉烯酶(也称金属 β 内酰胺酶)阳性，即该试验检测 B 类碳青霉烯酶敏感性与特异性均为 100%。 9 株 KPC 与 NDM 基因阳性菌株在碳青霉烯酶抑制剂增强试验中检测为共同产 A 类与 B 类碳青霉烯酶，即该试验检测共同产 A 类与 B 类碳青霉烯酶敏感性与特异性均为 100%。
结论 碳青霉烯酶抑制剂增强试验检测产碳青霉烯酶肺炎克雷伯菌耐药表型的敏感性和特异性极高，且具有操作简单、结果容易阅读以及可检测单产或同时产不同类型碳青霉烯酶的特点，适合所有临床微生物实验室开展。

PU-3649

2179 例晚期妊娠妇女生殖道Ｂ族链球菌筛查及耐药性分析

熊劲芝
郴州市第一人民医院

目的 分析晚期妊娠妇女生殖道 B 族链球菌（GBS）感染状况及耐药性情况，为临床用药提供参考。
方法 收集 2018 年 1 月-2020 年 12 月就诊的妊娠 35 周及以上妇女生殖道分泌物标本 2179 份，孕妇年龄 25～49 岁。纳入标准：妊娠＞35 周、2 周内无抗生素使用史。排除标准：急性泌尿系统感染、2 周内有抗生素使用史、合并高血压、糖尿病等基础疾病。将采集的阴道分泌物标本接种于 5%羊血琼脂培养皿中，并培养 18～24 h，在血琼脂培养皿上挑显灰白色、圆形、β-溶血的可疑菌落借助质谱仪进行菌种鉴定。对 GBS 阳性标本取单个菌落溶于 3mL 无菌生理盐水中，调整 GBS 菌悬液浓度为 0.5 麦氏单位，使用全自动微生物分析仪和革兰阳性球菌药敏卡进行细菌的耐药性检测，检测药物包括:青霉素、氨苄青霉素、奎奴普汀/达福普汀、利奈唑胺、万古霉素、左氧氟沙星、克林霉素、红霉素、四环素。
结果 疑似菌株借助 VITEK MS 质谱仪鉴定为 GBS 139 例，阳性率为 6.38%(139/2179)。分离出的 139 株 GBS 标本全部上机进行药物敏感试验，抗生素的药物敏感性分析显示:139 株 GBS 对青霉素、氨苄青霉素、利奈唑胺、奎奴普丁/达福普汀、万古霉素高度敏感，无中介及耐药现象；对左氧氟沙星的耐药率为 29.50%、对克林霉素的耐药率为 90.65%、对红霉素的耐药率为 77.70%、对四环素的耐药率为 87.05%。
结论 应重视晚期妊娠妇女 GBS 筛查，根据药敏试验结果合理选用抗菌药物进行预防治疗。

PU-3650

Characteristic analysis on the minimal inhibitory concentration drift of vancomycin against methicillin-resistant staphylococcus aureus in Xuzhou area from 2015 to 2019

Shuai Zong
The Affiliated Hosipital of Xuzhou Medical University

OBJECTIVE To retrospective analysis the characteristic change of minimal inhibitory concentration(MIC) value change trend and drift features of vancomycin against methicillin-resistant Staphylococcus aureus(MRSA), and provide a scientific reference for clinical treatment of MRSA infection.
METHODS A total of 900 non repetitive strains of MRSA were collected from three general hospitals according to the standard of nosocomial infection in Xuzhou area during 2015-2019. The MIC values were collected, and then the mean value of MIC was calculated by statistical method, and their variation characteristics were analyzed.
RESULTS All the 900 strains of MRSA were sensitive to vancomycin. The mean value of MIC in recent five years was 1.058, 1.100, 1.108, 1.122 and 1.147, respectively, and there were statistically significant differences among groups (P<0.05)；The mean MIC of ICU departments was 1.159, 1.253, 1.320, 1.413 and 1.451, respectively(P<0.05), the mean MIC of non ICU departments was 0.995，1.005，1.005，1.016 and 1.006, respectively(P＞0.05), and the mean differences between ICU and non ICU departments in 2015-2019 were statistically significant (P<0.05). The ratio of MIC≥1.5μg/mL of vancomycin against MRSA had an increasing trend year by year.

CONCLUSIONS It turned out that no strains were resistant or intermediate to vancomycin in Xuzhou region during 2015-2019, but the drift had been discovered in MIC value of vancomycin against MRSA, which mainly came from ICU departments; MIC drift was not found in non ICU departments. The patients with MRSA infection, whose vancomycin MIC≥1.5μg/mL in ICU departments, should be given more intensive monitoring and active treatment.

PU-3651

ICU 老年患者血培养阳性细菌的分布及耐药情况分析

王莹
沈阳金域医学检验所有限公司

目的 分析 ICU 老年患者血培养阳性样本中的病原菌构成及耐药情况。
方法 搜集 2019-2020 沈阳金域医学检验所微生物室接收的 ICU 老年患者血培养阳性样本 196 例。使用质谱分析仪（AUTOF MS1000）对其进行鉴定试验，使用梅里埃全自动微生物鉴定和药敏分析系统（VITEK2 COPACT）对其进行药敏试验。并使用 WHONET 5.6 软件对数据进行统计分析。
结果 196 例病原菌中排名前五位的分别为肺炎克雷伯菌、大肠埃希菌、金黄色葡萄球菌、鲍曼不动杆菌、凝固酶阴性葡萄球菌。此外还分离出铜绿假单胞菌、嗜麦芽窄食单胞菌、肠球菌、其他非发酵革兰阴性杆菌等。其中肺炎克雷伯菌数量最多，碳青霉烯类耐药肺炎克雷伯菌和大肠埃希菌和检出率分别为 26.5％和 6.4％。金黄色葡萄球菌和凝固酶阴性葡萄球菌中甲氧西林耐药株(MRSA、MRCNS)的检出率分别为 38.6％和 31.4％。所有细菌对药物青霉素、头孢曲松、左氧氟沙星等药物均存在不同程度的耐药性。ICU 老年患者菌株耐药性明显高于青年人，差异具有统计学意义（P<0.05）。
结论 ICU 老年患者血培养样本中检出病原菌数量及种类较多，临床应根据病原菌对药物的耐药性差异选择合理的抗菌药物。

PU-3652

抗生素所致肠道菌群失衡的研究

赵妍
沈阳金域医学检验所有限公司

目的 探讨使用抗生素后肠道菌群紊乱与菌群代谢的关系,协助评估抗生素使用后的肠道菌群紊乱。
方法 实验组为 2021 年 1 月至 2021 年 5 月期间送检于本公司的 23 例有静脉使用抗生素治疗的患者,其中男 10 例,女 13 例,年龄在 18 岁 23 岁之间,平均年龄 21.5 岁,均符合以下入选标准:(1)年龄小于 23 周岁;(2)病原学检查确诊为细菌感染;(3)治疗经过均有静脉使用抗生素(如阿莫西林、头孢美唑、头孢呋辛、头孢地嗪、头孢曲松、头孢哌酮、阿奇霉素),使用时间 37 天;同时设有对照组。收集并处理其粪便标本后置于低聚糖培养基、棉籽糖(RAF)、低聚果糖(FOS)、低聚半乳糖(GOS)、低聚异麦芽糖(IMO)、低聚甘露醇(MOS)、低聚木糖(XOS)、菊粉(INU)、可溶性淀粉(STA)、甘露糖醇(MAI)、木糖醇(XYI)等)中恒温发酵,24h 后采用气相色谱法(GC)检测各培养基中的短链脂肪酸(SCFA)含量及产气量,最后应用 SPASS 19.0 对数据进行统计学分析。
结果 1.抗生素组患者粪便中总短链脂肪酸(SCFA)、丙酸、丁酸含量等明显低于正常对照组(P0.05),乙酸值无差异(P0.65)。2.抗生素组丙酸、丁酸含量明显低于正常对照组(P0.05)。3.抗生素组 24h 发酵后,各低聚糖培养基总 SCFA、丙酸、丁酸含量明显低于对照组(P0.05)。
结论 1.通过测定粪便发酵前总 SCFA 含量,以及丙酸和丁酸含量,可间接印证抗生素对肠道菌群有显著影响。2.抗生素导致肠道菌群代谢发生紊乱,还表现在乙酸:丙酸:丁酸三者百分比率明显失调。

PU-3653

女性生殖道微生态评价的临床价值研究

付莉
沈阳金域医学检验所有限公司

目的 研究女性生殖道微生态评价的临床价值。
方法 选取医院接收的体检的健康女性体检者及患有生殖道感染就诊患者作为本次研究的观察对象，采用问卷调查及辅助检查结合的方式对每一位体检者及就诊者进行统计分析,分析阴道分泌物结果,统计各类阴道炎症的构成比,对阴道微生态进行评价,分析阴道微生态失调检出率,并分析阴道微生态失调与阴道炎的关系。
结果 1800 例女性阴道微生态失调者为 954 例,占百分比为 53%,BV 的发生率最高,占比在 12%,接着是 VVC 占 8%,阴道微生态失调率与 BV 的感染率随年龄的增长不断攀升,VVC 的感染率随年龄的增加,不断下降,差异具有统计学意义（P <0.05）,阴道微生态失调和 BV、VVC 的感染率在不同季节感染率也是不尽相同的。数据差异具有统计学意义（P <0.05）。
结论 阴道微生态失调与各种阴道炎的发生具有一定的相关性。是阴道炎发生的重要影响因素。

PU-3654

全自动细菌鉴定仪法在快速检测耐甲氧西林金黄色葡萄球菌中的应用价值

张震
沈阳金域医学检验所有限公司

目的 全自动细菌鉴定仪法在快速检测耐甲氧西林金黄色葡萄球菌中的应用价值。
方法 金黄色葡萄球菌阳性标本作为研究对象,进行实时荧光聚合酶链反应（PCR）检测,将其检验结果作为金标准。分析全自动细菌鉴定仪法检测耐甲氧西林金黄色葡萄球菌的灵敏度及特异度。
结果 金黄色葡萄球菌阳性标本中,经实时荧光 PCR 法检测出耐甲氧西林金黄色葡萄球菌耐甲氧西林金黄色葡萄球菌。全自动细菌鉴定仪法检测耐甲氧西林金黄色葡萄球菌的灵敏度及特异度分别为 94.44%、100.00%。不同类型临床标本检出率由高到低为:痰液标本>咽拭子标本>伤口分泌物标本>血液标本。
结论 全自动细菌鉴定仪法检测耐甲氧西林金黄色葡萄球菌具有较高的灵敏度与特异度。

PU-3655

嗜麦芽窄食单胞菌鉴定及药敏分析

张寅卓
沈阳金域医学检验所有限公司

目的 探讨嗜麦芽窄食单胞菌简易鉴定方法和对抗菌药物的耐药情况，为临床医师能有效预防及合理使用抗生素提供可靠依据。
方法 对嗜麦芽窄食单胞菌菌落生长及部分理化特性进行简易鉴定,并采用全自动微生物鉴定药敏系统与其对照及药敏实验。
结果 采用简易鉴定方法检出的嗜麦芽窄食单胞菌与全自动微生物鉴定系统结果均一致。嗜麦芽窄食单胞菌对抗菌药物呈广泛耐药,仅对复方新诺明和左旋氧氟沙星、加替沙星保持较高的敏感性。
结论 药敏试验结果显示,对替卡西林/克拉维酸、左氧氟沙星、复方新诺明和米诺环素有较高的敏感性,对头孢他啶耐药率较高。 该简易鉴定方法可及早检出嗜麦芽窄食单胞菌的感染发生,临床治疗首

选复方新诺明和左旋氧氟沙星,靶向性治疗效果较好。临床需要根据药敏试验结果合理选用抗菌药物。

PU-3656

痰标本中分离鉴定金黄色葡萄球菌的临床实验研究

张震
沈阳金域医学检验所有限公司

目的分析从感染患者痰液中分离鉴定金黄色葡萄球菌（SAU）及耐药性的临床实验,为合理应用抗菌药物提供参考。
方法用全自动细菌培养鉴定仪对痰标本进行 SAU 分离鉴定,选择 15 种临床中常用抗菌药物对其耐药性进行药敏试验。替考拉宁、万古霉素和呋喃妥因对 SAU 的抗菌活性较好;青霉素、诺氟沙星、氨苄西林、克林霉素、庆大霉素、四环素、利福平和红霉素等对 SAU 抗菌活性差;其他抗菌药物对 SAU 耐药性一般。
结论 SAU 是化脓感染中最常见的病原菌,痰标本中检出率较高,且耐甲氧西林增强,万古霉素、替考拉宁和呋喃妥因等是目前杀灭 SAU 的理想药物,临床中应依据药敏试验合理选择抗菌药物。

PU-3657

Disseminated Trichosporon asahii infection presenting as eosinophilia in an immunocompetent patient

Fengzhen Yang
Yantai Yuhuangding Hospital

Trichosporon are naturally found in external environments and are a part of the normal flora of the human skin, respiratory tract, and gastrointestinal tract. Disseminated Trichosporon infection occurs sporadically in patients with immunodeficiency, and is mainly manifested as blood, urine, catheter, and thorax/peritoneum infections, rarely as lymphatic, liver and spleen infections. Elevated blood eosinophil granulocyte from Trichosporon infection have rarely been reported. Here,we report a rare case of eosinophilia associated with lymphatic, liver and spleen infections due to Trichosporon asahii in an immunocompetent patient. No reports of eosinophilia from Trichosporon infections other than lung, to our knowledge, have been published.

PU-3658

B 族链球菌检测在孕妇孕晚期的临床意义分析

蒋瑜采
柳州市妇幼保健院

目的 B 族链球菌是围生期女性泌尿生殖道感染和新生儿期重症肺炎、败血症和脑膜炎的常见病原菌。本研究针对孕晚期检测 B 族链球菌的临床意义进行探讨。
方法 选 2019 年 1 月～12 月来我院产前检查的 325 例孕妇作为研究对象。统计 325 例孕妇 B 族链球菌检测结果，观察 B 族链球菌阳性孕妇的孕周分布特征，同时对 325 例孕妇都进行随访，比较 B 族链球菌阳性组孕妇和阴性组孕妇的妊娠结局以及新生儿健康状况。
结果（1）325 例孕妇 B 族链球菌检测中，共 37 例结果阳性，阳性检出率为 11.4% ，28 例孕妇的孕周超过 34w，所占比例为 75.7%。其中 24～34+6w 占 9 例，构成比为 24.3%；35～37+6w 占

18 例，构成比为 48.6%，38w 及以上占 10 例，构成比为 27.1%，B 族链球菌阳性孕妇的孕周多为 35～37+6w，所占比例与其他孕周比较存在差异，具有统计学意义（P<0.05）；（2）对 325 例孕妇均进行有效的随访，经统计 B 族链球菌较阳性组孕妇的不良妊娠结局发生率为 24.3%，阴性组孕妇的不良妊娠结局发生率为 5.2%，两组组间比较存在的差异具有统计学意义(P<0.05) ；（3）B 族链球菌阳性组和阴性组新生儿的健康状况比较，经统计发现 B 族链球菌阳性组新生儿的阿氏评分较阴性组新生儿低，肺炎发生率较阴性组新生儿高，组间上述指标比较均存在明显差异(P<0.05)。
结论 孕晚期 35～37+6w 及以上孕妇 B 族链球菌检测阳性率比其他孕周数明显增高，B 族链球菌感染可增加孕妇的不良妊娠结局发生率，影响新生儿健康状况，建议将 B 族链球菌检测纳入常规产前检查项目，改善孕妇妊娠结局。

PU-3659

镜检法和核酸杂交法检测念珠菌性阴道炎的差异及评价

蒋瑜采
广西柳州市妇幼保健院

目的 念珠菌性阴道炎是临床中十分常见的一种妇科疾病，其有着较高的发病率.尤其是在近几年，我国女性群体因不良生活习惯以及饮食习惯的影响，使得念珠菌性阴道炎的发病率持续上升。本文研究镜检法与核酸杂交法，对念珠菌性阴道炎患者检测价值的影响，帮助念珠菌性阴道炎患者提高临床治疗效果。
方法 选 2020 年 1-12 月到我院诊治的 94 例念珠菌阴道炎患者纳入研究，取患者分泌物分别采用镜检法与核酸杂交法进行检测，计算两种方法学的检出率和方法学性能比。
结果 94 例念珠菌性阴道炎患者，镜检法念珠菌阳性检出率为（90.43%），核酸杂交法法念珠菌阳性检出率为（96.81%），P＞0.05。镜检法与核酸杂交法检查结果有着较高的一致性，符合率为（91.49%），特异度为（22.22%），灵敏度为（92.31%），P＞0.05。
结论 镜检法对念珠菌阴道炎阳性检出率为（90.43%），虽低于核酸杂交法对念珠菌阴道炎阳性检出率（96.81%），但二者比价无差异，（P＞0.05）。这说明了镜检法以及核酸杂交法对念珠菌阴道炎患者均有着积极的临床诊断价值，可提高临床诊断的准确性，可提高诊疗效果。同时镜检法与核酸杂交法对念珠菌性阴道炎患者的检查结果的一致性较高，其中符合率为为（91.49%），特异度为（22.22%），灵敏度为（92.31%），P＞0.05，这一研究结果再一次说明了镜检法与核酸杂交法的应用可靠性，在临床中应当灵活选择。

PU-3660

231 例胎盘拭子细菌培养阳性结果与产妇宫内感染临床情况分析

叶辉铭、陈玲、林雪燕、林雅茵、吴佳音
厦门市妇幼保健院（厦门大学附属妇女儿童医院）

目的 回顾分析产妇胎盘拭子细菌培养结果与其宫内感染的临床情况，了解产妇下生殖道细菌上行性感染的临床特点，为围产期母婴相关细菌感染性疾病提供实验室依据。
方法 整理我院 2016 年 1 月 1 日至 2018 年 12 月 31 日胎盘拭子细菌培养阳性结果、胎盘病理检查结果及临床特征，并进行回顾性分析。
结果 该院 2016 年 1 月 1 日至 2018 年 12 月 31 日期间胎盘拭子细菌培养的 231 例阳性标本，最终临床确诊为宫内感染的有 155 例（67.1%），其余的 76 例（32.9%）为未感染者，将两者分为感染组与未感染组比较发现，两组在侵入性操作和生产方式之间有统计学差异。且如产前有宫内侵入性操作史者确诊率可提高到 76.8%，特别是生产方式为剖宫产产妇胎盘分泌物拭子细菌培养阳性的宫内感染确诊率高达 95.2%。宫内细菌感染胎盘病理结果比较，细菌培养结果与病理阳性符合率为

49.0%，两组在孕周与宫腔内操作存在统计差异。宫内细菌感染胎盘拭子培养分离的病原菌以大肠埃希菌为主，所占比率高达 56.8%，其它分离较多的菌株依次为粪肠球菌、无乳链球菌、金黄色葡萄球菌、肺炎克雷伯菌，各占阳性标本比率为 18.7%、4.5%、3.9%、3.9%；革兰阴性杆菌对亚胺培南、美罗培南、哌拉西林/他唑巴坦敏感性最高；无乳链球菌青霉素敏感率 100%，未检出耐甲氧西林金黄色葡萄球菌（MRSA）和对万古霉素耐药的粪肠球菌（VRE）。

结论 行胎盘拭子细菌培养阳性样本可提高产时宫内感染的诊断率，并且分离得到的病原菌可通过细菌鉴定和抗菌药物药敏试验给临床提供诊疗依据，是一种可行、有效的检查方案。

PU-3661

糖尿病伴尿路感染患者中段尿标本细菌培养及其耐药分析

付莉
沈阳金域医学检验所有限公司

目的 探究糖尿病伴尿路感染患者清洁中段尿标本中致病菌的分布及其对抗菌药物的耐药性。

方法 选取糖尿病合并尿路感染患者 145 例,收集其清洁中段尿实施细菌分离培养与菌株鉴定,并实施药敏试验分析各菌种对各类抗菌药物耐药性。

结果 145 例糖尿病伴尿路感染患者尿液中,分离出病原菌 122 株,其中革兰阴性菌 88 株（65%）、革兰阳性菌 47 株（30%）和真菌 4 株（5%）;革兰阴性菌中以大肠埃希菌为主（79.55%）;革兰阳性菌中以肠球菌及凝固酶阴性葡萄球菌为主,凝固酶阴性葡萄球菌占 42.55%;其中粪肠球菌属对青霉素、环丙沙星耐药性较高,分别为 42.11%（16/38）、36.84%（14/38）,凝固酶阴性葡萄球菌对青霉素、红霉素耐药性较高,分别为 88.24%（15/17）、47.06%（8/17）;大肠埃希菌、肺炎克雷伯菌为主要革兰氏阴性杆菌,其中大肠埃希菌对磺胺甲恶唑甲氧苄啶、环丙沙星耐药性较高,分别为 63.16%（108/171）、50.88%（87/171）,肺炎克雷伯菌对磺胺甲恶唑甲氧苄啶、环丙沙星耐药性也较高,分别为 62.07%（18/29）、51.72%（15/29）;凝固酶阴性葡萄球菌中,MRS 检出率为 41.18%（7/17）,大肠埃希菌、肺炎克雷伯菌中,ESBLs 菌株检出率分别为 63.74%（109/171）、51.72%（15/29）。

结论 糖尿病伴尿路感染患者尿液中病原菌以革兰阴性菌居多,其中尤以大肠埃希菌为主,临床应根据病原菌检出情况及药敏试验结果合理选用抗菌药物,以提高糖尿病伴尿路感染的治愈率。

PU-3662

一例犬巴斯德菌的鉴定及药敏分析

任艳俏
沈阳金域医学检验所有限公司

目的 研究一例犬巴斯德菌的鉴定及药敏分析，掌握其生物学特性、鉴定及药敏试验。

方法 将伤口分泌样本接种哥伦比亚血琼脂平板及巧克力琼脂平板，置于 35±1℃,5%二氧化碳培养箱中培养 18-24 小时，挑取哥伦比亚血琼脂平板上灰白菌落，使用快速鉴定，取该菌落配置 0.5 麦氏浓度菌悬液，参考 WS/T639-2018《抗菌药物敏感性试验的技术要求》使用 K-B 药敏纸片法进行药敏试验。

结果 经全自动质谱检测系统 AUTOF MS1000 鉴定为犬巴斯德菌，药敏结果对氨苄西林、红霉素、青霉素、左氧氟沙星、头孢曲松均表现为敏感。

结论 犬巴斯德菌较为罕见，对于多种抗生素敏感。

PU-3663

疫情下病原微生物实验室生物危害及安全防护

王莹
沈阳金域医学检验所有限公司

目的 探讨病原微生物实验室可能产生的生物危害及采取的相应措施，保证病原微生物实验室安全有序运行。
方法 通过查阅相关资料，结合病原微生物实验室的工作特点，分析病原微生物实验室可能存在的安全隐患，制定相应的防护措施。
结果 临床实验室所面临的微生物危害主要为1、细菌、真菌、病毒等极易引起实验室安全事件的生物因素；2、实验室设计建造、安全设施的配置、个体防护装备等环境因素；3、工作人员生物安全意识的主观因素。采取的措施主要有：1、制定标准化的病原微生物实验室操作规程及安全管理的规章制度，所有工作人员必须在工作中严格遵守各项操作规程；2、合理设计，完善和配备相应的安全设施和防护设备装备；3、规范病原微生物实验室消毒措施及医疗废物处置；4、不断提升人员防护意识，并进行生物安全知识培训。
结论 充分了解病原微生物实验室生物危害，采用有效的生物安全防护措施提高病原微生物检验工作的效率和质量，减少职业卫生相关事件发生。

PU-3664

应用全自动质谱检测系统 AUTOF MS1000 快速鉴定临床酵母菌

任艳俏
沈阳金域医学检验所有限公司

目的 评价全自动质谱检测系统 AUTOF MS1000 快速鉴定应用于临床快速鉴定临床酵母菌感染的可行性。
方法 分别应用安图显色培养基和全自动质谱检测系统 AUTOF MS1000 系统鉴定 522 株临床酵母菌。对未能鉴定、鉴定结果不一致或质谱鉴定得分低于 1.7 的菌株通过基因测序进行确证。
结果 安图显色培养基和全自动质谱检测系统 AUTOF MS1000 种鉴定符合率分别为 72.2%和96.9%。
结论 基于全自动质谱检测系统 AUTOF MS1000 具有很好的准确性,并且其检测成本较低,实验准备时间很短,与安图显色培养基相比全自动质谱检测系统 AUTOF MS1000 更加适用于临床酵母菌感染的快速鉴定。

PU-3665

临床分离泌尿生殖道支原体的感染状况及药敏分析

张红艳[1]、郑良建[2]
1. 四川省医学科学院•四川省人民医院（东院）
2. 成都市第三人民医院

目的 探讨临床分离泌尿生殖道支原体的感染状况及对常用抗菌药物的敏感性，为掌握本地区支原体感染的流行病学资料和指导临床合理用药提供依据。
方法 采用商品化支原体培养及药敏试剂盒对 2019 年 3 月至 2021 年 1 月四川省医学科学院·四川省人民医院（东院）泌尿生殖道来源的标本进行支原体培养和药敏试验，数据采用 SPSS 软件进行统计学分析。

结果 送检的 5548 份样本中，共 3016 份检出了支原体，阳性率为 55.9%，以 20-35 岁居多。解脲脲原体单独感染、人型支原体单独感染、解脲脲原体和人型支原体混合感染的阳性率分别为 43.7%（2424/3016）、0.8%（44/3016）和 11.5%（638/3016）。女性支原体阳性率为 57.3%，高于男性的 41.9% (P<0. 01)。解脲脲原体对强力霉素、美满霉素和克拉霉素的敏感性较高（>89%），人型支原体对强力霉素、美满霉素和交沙霉素的敏感性较高（>88%），生殖道支原体对喹诺酮类药物的耐药性较严重。
结论 泌尿生殖道支原体以单独解脲脲原体感染多见，其次为解脲脲原体和人型支原体混合感染。四环素类药物如强力霉素和美满霉素可以作为临床治疗泌尿生殖道支原体感染的首选药物。

PU-3666

2015-2019 年江苏连云港市布鲁菌病的流行病学及临床特征分析

刘波
连云港市第一人民医院

目的 分析布鲁菌病患者的临床特点和实验室检查结果，以提高非疫区临床医生对布鲁菌病的认识，减少临床对该病的误诊和漏诊率。
方法 收集 2015 年 1 月到 2019 年 12 月连云港市第一人民医院收治并确诊的布鲁菌病患者 54 例，剔除 8 例门诊及复发患者，对 46 例患者的科室分布、人口学信息、临床特征、流行病学史、实验室检查及诊治等方面进行了回顾性分析。
结果 46 例布鲁菌病患者中，男性 33 例，女性 13 例，年龄从 4 岁到 78 岁，确诊的布病患者分布在医院多个科室。职业分布主要以农民为主，占比达到 63%（29/46）；有 10 例患者来自市区，其余 36 例均来自辖区内各县，其中 26 例来自于东海县。有明确牛、羊等接触史的患者 21 例。全年各个月份均有病例出现，以 2-6 月最多见，占到了 71.7%（33/46）。患者首发症状主要以发热为主，占比达到 91%（42/46）。所有患者的血培养均检出布鲁菌，且虎红凝集试验均为阳性。患者在明确病因前使用多种药物，确诊后均采用多西环素加利福平，必要时联合喹诺酮类或 ß 内酰胺类等药物。患者经规范治疗后，预后较好，4 例患者出现复发。
结论 布病的临床表现常无特异性，一半以上的患者自述无明确的接触史；非疫区医生对此病的接触较少或认识不足，导致一些患者常被误诊或漏诊。因此对于不明原因发热的病人，在常规抗感染治疗无效的情况下，应考虑本病的可能。

PU-3667

HPV16 E7 蛋白经 Daxx/JNK 通路拮抗 HeLa 细胞凋亡

谢小平[2]、唐双阳[1]、丁霜[1]、廖雅琪[1]
1. 南华大学病原生物学研究所
2. 南华大学附属第一医院检验医学中心

目的 研究人乳头瘤病毒（Human papilloma virus，HPV）16 型 E7 蛋白对 Daxx/JNK 通路以及宫颈癌细胞凋亡的影响，为进一步阐明 HPV16 E7 在 HPV 致病机制中的作用提供理论依据。
方法 pET30a/HPV16 E7 重组质粒经 IPTG 诱导重组蛋白表达，并经 Ni-NTA 树脂纯化重组蛋白，用多粘菌素去内毒素处理后刺激 HeLa 细胞；经 Western blot 分析 Daxx 和 Bax、Bcl2 以及 t-JNK、p-JNK 蛋白表达，并经 DAPI 染色及流式细胞术检测细胞凋亡情况。
结果 经 HPV16 E7 蛋白刺激的 HeLa 细胞表现出 Daxx、Bcl2 蛋白表达上调，Bax 蛋白下调，且 Bcl2/Bax 比值上调，同时凋亡率降低；t-JNK 与 p-JNK 蛋白表达下调；干扰 Daxx 表达或经茴香毒素预处理后 HPV16 E7 蛋白的抗细胞凋亡效应减弱。
结论 HPV16 E7 蛋白能经 Daxx/JNK 通路拮抗 HeLa 细胞凋亡。

PU-3668

PDCA 循环法优化临床微生物学检验流程

于桥爱
柳州市妇幼保健院

目的意义及主要用途：国家政策的要求:做好微生物检验,持续落实抗菌药物管理力度。实验室检测结果是临床医师为患者进行病情诊断、治疗的临床依据，要求检测结果要准确、及时。由于各种原因造成微生物检验结果回报不及时，可给临床工作带来不良影响，甚至失去最佳抢救患者时机。因此优化微生物室的检验流程，缩短实验室周转时间(TAT) ，是微生物工作人员赖以追求的目标，也是医院管理者关注的重点。

PDCA 循环法又称戴明循环，是由美国著名质量管理专家戴明于 1954 年首先提出的，是全面质量管理所应遵循的标准化、科学化循环体系。PDCA 包含 4 个阶段，即 P（plan）计划、D（do）执行、C（check）检查、A（action）行动、改进。应用 PDCA 循环对优化医院工作流程和加强医院管理起到了重要的作用，只有不断改进工作流程中不完善的地方，科学应用全面流程管理，及时找到影响相关工作的瓶颈，对其有针对性地提出改进意见并追踪评价， 确认其改进效果，才能达到提高检验质量、提升医患满意度的目的，才能实现检验质量的持续改进，更好地为临床和患者服务。

PU-3669

广州地区 1015 株淋球菌对阿奇霉素耐药性结果分析

曹文苓
广州市皮肤病防治所

目的 淋病是我国法定的乙类传染病，由于临床上滥用抗生素和不规则治疗，使淋球菌的耐药率逐年增加，为了解广州地区淋球菌对阿奇霉素的耐药状况而进行耐药监测。
方法 用琼脂稀释法测定阿奇霉素的最低抑菌浓度（MIC）。以 WHO　P 株标准菌株作为质控菌株。阿奇霉素折点参考 WHO 的标准，敏感：MIC≤0.5mg/L,耐药：MIC ≥1mg/L。
结果 1015 株淋球菌中检出阿奇霉素敏感株 873(86%)株，耐药株 142 株(14%)。
结论 阿奇霉素是一种半合成的新型大环内酯类抗生素，2001 年 WHO 在性传播疾病感染处理指南中将阿奇霉素纳入治疗淋病的一线药物，２０１０年美国ＣＤＣ在成人宫颈、尿道及直肠无并发症淋球菌感染推荐方案是头孢曲松注射联合阿奇霉素治疗，阿奇霉素在临床上不仅对淋球菌有杀菌作用，对衣原体、支原体、梅毒等性病病原体引起的感染都也有治疗作用，临床使用比较广泛。但是由于药物不规范使用或用药剂量的不合理， 阿奇霉素的耐药率达到 14%，应该引起临床重视，临床要规范合理应用抗生素，同时加强淋球菌耐药性的连续性监测十分重要。

PU-3670

黏液脓性宫颈炎微生物的培养及药敏测定分析

姑丽尼格尔库来西、李晓勤、蒋斓、李维艳、韩婷婷
新疆维吾尔自治区妇幼保健院

目的 分析黏液脓性宫颈炎微生物的培养及药敏测定。
方法 选取 2019 年 1 月-2020 年 12 月 280 例医院收治黏液脓性宫颈炎患者的临床资料进行回顾性分析，所有患者均采集阴道分泌物行微生物培养检查，观察培养结果并行药敏试验，对药物敏感情况进行统计观察。

结果 280 例患者经微生物培养检查共检出病原菌阳性 188 例（67.14%），其中单一细菌感染 19 例（6.79%），细菌合并支原体感染 126 例（45.00%），细菌合并假丝酵母菌感染 43 例（15.35%）。本次研究中 188 份阳性样本中有革兰阴性菌 49 株（26.06%）、革兰阳性菌 94 株（50.00%）、真菌 45 株（23.93%），其中以革兰阳性菌检出率明显高于革兰阴性菌和真菌（P＜0.05）。达托霉素、利奈唑胺、万古霉素等药物对革兰阳性菌均有较高的敏感性，美罗培南、亚胺培南、阿米卡星以及氨苄西林对革兰阴性菌具有较高的敏感性。
结论 黏液脓性宫颈炎患者中主要以细菌感染最为常见，且致病菌中以革兰阳性菌的检出率较高，达托霉素、利奈唑胺、万古霉素等药物对革兰阳性菌均有较高的敏感性；美罗培南、亚胺培南、阿米卡星以及氨苄西林对革兰阴性菌具有较高的敏感性。

PU-3671

乳酸杆菌对海洛因成瘾小鼠急性戒断综合征的影响

张宇航[1,2]、马岩团进[1,2]、钱源[1,2]
1. 昆明医科大学第一附属医院
2. 云南省检验医学重点实验室

目的 通过乳酸杆菌干预海洛因急性戒断期小鼠，改善小鼠的急性戒断综合征以及乳酸杆菌对海洛因急性戒断期大脑单胺类神经递质水平的影响。
方法 将 36 只 C57 小鼠随机分为 3 组（A： 空白组、B：海洛因成瘾组、C：海洛因成瘾组+乳酸杆菌组），每组 12 只，采取 CPP 成瘾方法建立海洛因成瘾模型，利用 FMT 给予小鼠乳酸杆菌，用 ELISA 检测小鼠大脑 GABA 神经递质水平。
结果 乳酸杆菌能够改善小鼠急性戒断综合征，并且能使小鼠大脑 GABA 神经递质水平接近正常水平。
结论 通过乳酸杆菌干预海洛因成瘾小鼠，能够有效改善急性戒断综合征以及大脑神经递质水平，希望本研究能够为临床进一步治疗海洛因吸毒人群急性戒断综合征提供帮助。

PU-3672

2328 例阴道微生态阳性率的汇总

杨冰
西安金域医学检验所有限公司

目的 统计 2328 例女性阴道微生态中各种诊断的阳性率，为临床预防和治疗各种阴道炎提供依据。
方法 对 2328 例女性阴道拭子进行涂片，固定，采用硕世诊断自动染色仪进行革兰染色，全自动显微镜在 100 倍油镜下进行采图，并结合硕世诊断阴道炎自动检测工作站的干化学结果进行分析。
结果 通过对 2328 例女性阴道微生态进行分析，共检出 BV（细菌性阴道炎）354 例，阳性率 15.21%，AV（需氧性阴道炎）73 例，阳性率 3.14%，VVC（念珠菌性阴道炎）164 例，阳性率 7.04%，TV（滴虫性阴道炎）32 例，阳性率 1.37%，BV+AV（细菌性阴道炎+需氧性阴道炎）110 例，阳性率 4.73%，BV+VVC（细菌性阴道炎+念珠菌性阴道炎）25 例，阳性率 1.07%，其他合并感染 20 例，阳性率 0.86%，菌群抑制 382 例，阳性率 16.41%。
结论 女性阴道炎是阴道粘膜及粘膜下结缔组织的炎症，是妇科门诊常见的疾病。正常健康妇女，由于解剖学及生物化学特点，阴道对病原体的侵入有自然防御功能，当阴道的自然防御功能遭到破坏，则病原体易于侵入，导致阴道炎症。本次研究阴道炎的阳性率为 33.42%，菌群抑制阳性率为 16.41%，所以女性阴道炎更应引起临床的高度重视。

PU-3673

腹腔结核的临床特征及诊断方法来自非结核病定点医院 5 年经验分享

金文婷、马玉燕、史庆丰、鲍容、郭玮、高晓东、潘珏、胡必杰
复旦大学附属中山医院

背景 腹腔结核是肺外结核的一种常见类型，但临床诊断存在困境。本研究旨在介绍非结核病定点医院感染病科收治的腹腔结核的临床特征及诊断方法。
方法 回顾性收集 2015 年 8 月至 2020 年 7 月复旦大学附属中山医院感染病科收治的腹腔结核患者 70 例，将腹腔结核分为腹膜结核、腹腔淋巴结结核、胃肠道结核、实质脏器结核和混合腹腔结核共 5 组。
结果 70 例患者中 18 例(25.7%)为腹膜结核,9 例(12.9%)为腹腔淋巴结结核，5 例(7.1%)为胃肠道结核，2 例(2.9%)为实质脏器结核，混合腹腔结核共 36 例（52.45%）。24 例(34.3%)患者未累及腹腔外其他部位，7 例(10.0%)合并肺结核，7 例(10.0%)合并肺结核，19 例(27.1%)合并至少 1 处其他部位结核，另外 20 例(28.6%)即合并肺结核又合并其他部位肺外结核。中位诊断时间为 60 天(30-120 天)。腹水(58.6%)、腹胀(48.6%)、体重减轻(44.3%)和发热(42.9%)为最常见的临床症状。总体微生物确诊率和组织学确诊率分别为 70.0%(49/70)和 38.6%(22/70).在非腹水标本微生物确诊率(63.6%,14/22)高于所有标本(40.8%, 20/49)。组织学确诊病例共 18 例，占 69.2%(18/26)。共有 45 例患者为临床诊断病例(64.3%, 45/70)。经有创性操作确诊的比例较高，如手术确诊率 85.7%(6/7)，经皮腹腔组织活检确诊率 100.0%(7/7)，腹腔淋巴结结核中内镜下淋巴结细针活检确诊率 80.0%(4/5)。
总结 腹腔结核的诊断需临床表现、实验室检查、影像学、微生物结果及病理才能获得更高诊断率。

PU-3674

上海市 101 所医院 2016-2019 年血标本送检调查分析

史庆丰、胡必杰、崔扬文、郭玮、孙伟、沈燕、孙翔、林佳冰、高晓东
复旦大学附属中山医院

目的 分析上海市 101 所医院 2016-2019 年血标本送检情况。
方法 上海市院内感染质控中心对市监测网 101 所医院每季度开展一次血标本送检率调查，对该季度最后一个月第 2 周的前三天发热≥38.5℃的住院患者信息及血标本送检情况进行收集和分析，数据采用 SPSS 20.0 软件进行录入和分析。
结果 2016-2019 年，上海市 101 所医院发热患者血标本总送检率分别为 56.7%，57.8%，58.3%，62.1%，呈逐年上升趋势（线性 $\chi 2=49.360$，$P<0.001$）；ICU 和普通病房发热患者前三日抗菌药物总使用率为 81.6%~92.7%。发热患者伴疑似肺部感染时血标本送检率为 67.5%~75%；伴留置深静脉导管＞5 天时血标本送检率为 64.7%~71.1%；送检痰标本同时送检血标本率为 76.5%~77.1%。未送检原因合理比例呈逐年上升趋势。
结论 上海市 101 所医院血标本送检率呈逐年上升，但送检前抗菌药物使用率较高，高危合并因素条件下送检率有待进一步提升。

PU-3675

热和呼吸困难患者九联检 IgM 抗体检测结果分析

杨耀永、唐满玲、蒋最明、何聪玲、吴莹
株洲市中心医院

目的 了解本地区发热和呼吸困难患儿的病原谱, 为临床抗感染及病原体检测提供依据。
方法 收集 1033 例临床症状表现为发热和呼吸困难患儿的血清标本, 采用间接免疫荧光法检测其中 9 种常见病原体的 IgM 抗体。
结果 1033 例患儿中肺炎支原体抗体阳性 495 例,春季、夏季和秋季都是肺炎支原体高发期。
结论 湖南株洲地区引起儿童发热和呼吸困难的主要病原体是肺炎支原体，并且春季、夏季和秋季感染率都很高。

PU-3676

2017-2019 年上海某教学医院 ICU 患者血流感染分离的耐碳青霉烯类肺炎克雷伯菌耐药机制和分子流行病学特征

周春妹、黄声雷、胡必杰、郭玮
复旦大学附属中山医院

目的 研究复旦大学附属中山医院 ICU 患者血流感染中分离的耐碳青霉烯类肺炎克雷伯菌血流感染(carbapenem resistant Klebsiella pneumoniae, CRKP)的耐药性、耐药基因与同源性，为临床用药与院感控制提供依据。
方法 收集复旦大学附属中山医院 2017 年 1 月—2019 年 5 月 ICU 患者血流感感染分离的 53 株 CRKP，检测其对 28 种抗菌药物的敏感性。PCR 法扩增碳青霉烯酶基因(blaKPC、blaIMP、blaVIM、blaOXA 和 blaNDM-1)并对扩增阳性产物进行测序，所得序列与 GenBank 数据库进行比对，确定耐药基因分型。采用 PFGE 和 MLST 法进行同源性分析。
结果 53 株 CRKP 对 19 种抗菌药物耐药率中，耐药率低于 50%的抗菌药物仅有替加环素 0%、黏菌素 7.1%。对复方磺胺甲噁唑的耐药率为 57.5%、四环素 63.8%、阿米卡星 64.2%。对碳青霉烯类、头孢菌素、氨曲南、含酶抑制剂、以及喹诺酮类、氨基糖苷类的耐药率为 80%~100%。53 株 CRKP 中，均检出碳青霉烯酶基因，其中 49 株(92.5%)blaKPC、3 株(5.7%)blaNDM 和 1 株（1.8%）同时产 blaKPC 和 blaNDM。53 株 CRKPMLST 分型均为 ST11 型，PFGE 分型显示 ICU 中以 K1 型 15 株（28.3%）为主，其次是 K2 型 5 株（9.4%）和 K3 型 4 株（7.5%）。
结论 CRKP 的耐药率高，主要耐药机制是产 KPC 型碳青霉烯酶。CRKP 存在不同 ICU 科室间、科室内的克隆传播，应加强对 CRKP 的监测和院感控制。

PU-3677

2018-2021 全球革兰阴性杆菌细菌对粘菌素类药物耐药性的 meta 分析

黄嘉仪、黄声雷、周春妹、郭玮
复旦大学附属中山医院

目的 了解近年来革兰阴性杆菌对粘菌素类药物的耐药情况，为临床提供精确的抗菌药物方案选择。
方法 从 PubMed 上收集发表于 2018-2021 年的关于粘菌素类药物耐药性研究性文献，提取内容包

括文献来源杂志、菌株收集时间、菌种来源地区、作者、文献标题、菌种、菌株总数、耐药菌株数，比较不同地区、不同时间段、不同菌种对粘菌素类药物敏感率或耐药率的差异。
结果 2018-2021 年发布文献中的粘菌素类药物在革兰阴性杆菌非天然耐药菌中总体耐药水平为 16.19%，与 2015 年的研究相比有所上升。粘菌素类药物主要对埃希氏菌属、铜绿假单胞菌、不动杆菌属、克雷伯氏菌属、肠杆菌属有较强抗菌活性，耐药率分别为 11.1%（95%CI 10.1%~12.0%）、12.7%（95%CI 12.1%~13.3%）、13.8%（95%CI 13.3%~14.3%）、21.5%（95%CI 20.4%~22.6%）、24.6%（95%CI 23.7%~25.5%）。其次为枸橼酸杆菌属（37.9%）和沙门氏菌属（46.8%）。此外对粘菌素天然耐药的沙雷氏菌属和嗜麦芽窄食单胞菌分别出现了敏感菌的报道。
结论 2018-2021 年全球的粘菌素类药物在革兰阴性杆菌中总体耐药水平较之前有所上升。建议定期进行耐药菌流行病学调查，监控各菌属对粘菌素类药物耐药性的改变，更加规范进行粘菌素类药物的使用管理。

PU-3678

肠杆菌目细菌产耐碳青霉烯酶的耐药基因分型检测方法新进展

曹锦楠、黄声雷、周春妹、胡必杰、郭玮
复旦大学附属中山医院

目的 介绍临床微生物实验室鉴定肠杆菌目细菌产碳青霉烯酶型别的检测方法及最新临床应用进展，为不同层次的实验室结合自身情况选择合适的检测方法提供依据。
方法 围绕微生物实验室鉴定碳青霉烯酶型别的检测方法的原理、结果判读、检测性能以及优缺点等方面作一综述。
结果 由于不同种类的抗菌药物对产生不同类型的碳青霉烯酶菌株体外抗菌活性不同，因此准确而快速地对 CRE 产生的碳青霉烯酶进行型别的鉴定，对于临床抗多重耐药菌感染的精准治疗和医院感染预防控制其传播流行具有重要的意义。目前实验室用于检测碳青霉烯酶的方法主要包括改良 Hodge 实验、Carba NP 试验、改良碳青霉烯灭活试验（mCIM 和 eCIM）、分光光度计法、碳青霉烯酶抑制增强试验、免疫层析方法、时间飞行质谱试验、耐药基因精准检测、二代测序、Xpert® Carba-P 和宏基因组测序。
结论 本文对比各试验的优缺点，推荐使用碳青霉烯酶抑制增强试验，因其操作简便、成本低、结果观察直观，所以适合绝大多数实验室常规开展。

PU-3679

168 株淋病奈瑟菌耐药监测结果分析

王有为、李红霞、李春花、杨阳、赵薇、陈媛玮
电子科技大学附属医院•四川省人民医院

目的 分析 2019-2020 年本院 168 株淋病奈瑟菌临床分离菌株对六种抗菌药物的敏感性，为淋病的社会防治提供参考。
方法 收集四川省人民医院皮肤性病门诊患者生殖道分泌物，T-M 淋球菌分离培养基分离培养，通过纸片酸度法测定产青霉素酶淋球菌，琼脂稀释法测定青霉素、环丙沙星、大观霉素、阿奇霉素、头孢曲松和头孢克肟的最小抑菌浓度(MIC) 。
结果 168 株淋球菌中，共检出 PPNG 67 株（39.88%）、TRNG 47 株（27.98%）。未发现头孢曲松、头孢克肟和大观霉素的耐药菌株。对环丙沙星、青霉素和阿奇霉素的耐药比例分别为 98.81%、77.97%和 13.09%。两年共发现 22 株对头孢曲松低敏的淋球菌、且比例有所增加。

结论 大观霉素和头孢曲松适合本地区作为治疗淋病的一线药物。持续开展淋球菌耐药监测对于淋病的防治具有重要的意义。

PU-3680

热休克蛋白 90α 对脓毒症的诊断及预后价值探究

赵卫东、李福兴、张玉琳、程明璟
大理大学第一附属医院

目的 探讨血清 HSP90α 在脓毒症诊断及预后中的价值。
方法 选取 2019 年 9 月-2020 年 9 月入住大理某三甲医院 ICU 的 150 例脓毒症患者作为研究对象，110 例非脓毒症患者作为同型病例对照，110 例体检中心健康人群作为健康对照。随后根据脓毒症患者预后分成生存组(n=94)及死亡组(n=56)，在医院信息系统收集所有研究对象的临床资料，用酶联免疫吸附实验(ELISA)法测定 HSP90α 水平，流式细胞术测定细胞因子(IL-1β，IL-18)和趋化因子(MIP-3α，ENA-78)的表达水平，并进行统计学比较，利用受试者工作特征(ROC)曲线比较各实验室指标对脓毒症患者预后判断的价值，以 28 天作为随访终点，用 Kaplan-Meier 生存分析评估不同组别脓毒症患者的存活时间，采用单变量 Logistic 回归分析脓毒症的危险因素，Pearson 相关性分析分析 HSP90α 与 SOFA 评分、PCT、IL-1β、IL-18、MIP-3α、ENA-78 的相关性。
结果 脓毒症组 HSP90α 水平显著高于病例对照组及健康组(P <0.05)，脓毒症死亡组 HSP90α 水平显著高于生存组(P <0.05)；ROC 曲线分析表明 HSP90α 对脓毒症的预后判断价值最佳，AUC 为 0.84［95%CI（0.77~0.90）］；生存分析表明 HSP90α 水平越高则脓毒症患者 28 天死亡率越高(P <0.05)；单变量 Logistic 回归分析提示 SOFA 评分、HSP90α、IL-18 是脓毒症的独立危险因素；相关性分析提示 HSP90α 水平与 SOFA、IL-1β、IL-18、MIP-3α 水平成明显正相关。
结论 HSP90α 对脓毒症具有较好的诊断及预后判断价值，其作用机制可能与细胞因子风暴相关。

PU-3681

陕西地区泌尿生殖系统感染患者 NG、CT 和 UU 感染状况分析

张强
西安金域医学检验所有限公司

目的 了解陕西地区泌尿生殖系统感染患者淋球菌(NG)、沙眼衣原体(CT)和解脲脲原体(UU)的感染情况，为性传播疾病的临床治疗和预防提供依据。
方法 选取从 2018 年 5 月到 2021 年 4 月在西安金域医学检验所进行 NG、CT、UU 检测的 1419 例患者标本，其中女性 1266 例，男性 153 例，使用实时荧光 PCR 法检测上述 3 种病原体。
结果 NG、CT、UU 的总阳性率分别为 1.76%(25/1419)、3.59%(51/1419)和 56.24%(798/1419)，女性和男性最常见的病原体均为 UU，但 NG 阳性率男性显著高于女性($\chi2=44.94$,$P<0.01$)，UU 阳性率女性显著高于男性($\chi2=65.87$,$P<0.01$)。在混合感染类型中，NG+CT 混合感染具有性别差异($\chi2=6.41$,$P<0.05$)，另外女性以 CT+UU 感染为主。男性和女性的主要感染人群集中在≤20 岁。
结论 NG、CT 和 UU 是泌尿生殖系统感染常见的 3 种病原体，陕西地区男性和女性均以 UU 感染为主，并部分伴有混合感染，≤20 岁的年轻男性和女性为易感人群。在临床诊断和治疗中，应同时检测多种病原体，并加强青年人群的早期筛查和检测，普及性传播疾病预防知识的宣传教育。

PU-3682

山东地区诺卡菌属的鉴定、临床特点及药物敏感性分析

谢莲[1]、陆书华[2]
1. 胜利油田中心医院
2. 济宁医学院附属医院

诺卡菌是引起多种临床感染的病原体。本研究旨在调查中国两所三级综合医院 3 年多来诺卡菌的种类分布、临床特点及药物敏感性。自 2017 年 1 月至 2019 年 12 月，本回顾性研究共从 27 个患者中分离出 27 株诺卡菌。从病历中收集临床资料，并通过质谱和 16S rRNA 测序鉴定诺卡菌属。采用标准发酵液微量稀释法测定药敏性。27 例诺卡菌感染患者（男 12 例，女 15 例）平均年龄为 60.11 岁。27 株诺卡菌分离株中共鉴定出 7 个诺卡菌种，其中最常见的为豚鼠耳炎诺卡菌(otitidiscaviarum，40.7%)。不同诺卡菌种的抗菌敏感性差异较大。所有诺卡菌分离株都对利奈唑胺敏感。诺卡菌分离株主要来自呼吸内科(55.56%)和痰标本(44.44%)。肺区受累最多(70.37%)，其次是皮肤(7.4%)和胸腔(7.4%)。大多数诺卡菌感染患者需要联合抗生素治疗。在治疗期间 2 例患者死亡，24 例患者在抗生素治疗后得到改善。诺卡氏菌感染的临床表现和药敏特征随种类的不同而不同。因此，菌株的准确识别对诊断和选择抗生素治疗至关重要。

PU-3683

老年性阴道炎患者阴道微生态变化分析

罗雪
柳州市妇幼保健院

目的 分析老年性阴道炎患者与正常体检老年女性的阴道微生态构成及微生态失调的病原分布，为老年女性阴道感染性疾病的病原学诊断及治疗提供实验室依据。
方法 选取 2018 年 3 月～2019 年 6 月在某市妇幼保健院就诊的 938 例老年性阴道炎患者为病例组，病例组所有诊断符合人卫出版社第 9 版《妇产科学》中阴道炎诊断标准，另选取同期正常体检的 441 例老年女性为对照组，两组人群年龄比较差异无统计学意义（P>0.05）。采集所有研究对象的阴道分泌物进行阴道微生态综合检测，比较两组阴道清洁度、乳酸杆菌含量、病原分布以及酶学指标等情况。
结果 病例组阴道微生态失衡率为 96.2%、清洁度Ⅲ～Ⅳ度占比为 52.7%，均高于对照组的 93.4%、38.1%，但两组乳酸杆菌含量无或少量占比比较，差异无统计学意义，分别为 77.8%、73.9%。病例组各种阴道炎总患病率（54.8%，514/938）高于对照组各种阴道炎总患病率（38.8%，171/441），其中病例组中混合感染占比最高，为 18.3%（172/938）；其次 AV（需氧菌性阴道病），为 17.2%（161/938）；然后 VVC（外阴阴道假丝酵母菌病），为 10.7%（100/938）；观察组中 BV（细菌性阴道病）占比最高，为 13.8%（61/441）；其次 AV，为 11.6%（51/441）。病例组的 AV、VVC 及混合感染发生率高于对照组（P<0.05），BV 发生率低于对照组（P<0.01）。两组间 PH＞4.5 占比、H2O2 阳性率及唾液酸苷酶阳性率比较差异无统计学意义（P>0.05），但病例组白细胞酯酶阳性率显著高于对照组（P<0.01）。
结论 老年女性阴道微生态失衡率高，应重视混合感染和 AV 的防治工作。

PU-3684

骨科患者伤口感染菌的分布及耐药性分析

杨雅琼[1]、丁倩倩[2]
1. 天津市天津医院
2. 天津医科大学 临床医学院

目的 分析骨科伤口感染菌的分布以及病原菌对常用抗菌药物的耐药情况为临床合理应用抗菌药物提供合理的科学依据。
方法 收集天津医院骨科创伤患者 2020 年 1 月至 12 月伤口分泌物及脓液标本，对分离出的病原菌及耐药性情况进行回顾性分析、分组，资料的统计分析及药敏实验应用 VITEK2-compact 全自动细菌分析系统。
结果 2020 年 1 月-12 月骨科患者伤口分泌物中共分离出致病菌 1541 株，其中革兰阳性菌 733 株（47.57％），革兰阴性菌 792 株（51.40％）。革兰阳性菌以金黄色葡萄球菌（20.57％），粪肠球菌（9.15％），表皮葡萄球菌（7.14％）为主。革兰阴性菌中以铜绿假单胞菌（10.06％），大肠埃希菌（8.63％），鲍曼不动杆菌（7.07％），肺炎克雷伯菌肺炎亚种（6.23％），阴沟肠杆菌阴沟亚种（5.71％）为主。革兰阳性优势菌为金黄色葡萄球菌和粪肠球菌，针对金黄色葡萄球菌耐药率较高的抗菌药物为阿莫西林、青霉素、克林霉素、红霉素、阿奇霉素;针对粪肠球菌耐药率较高的抗菌药物为四环素、红霉素、环丙沙星。革兰阴性优势菌为铜绿假单胞菌和大肠埃希菌，针对铜绿假单胞菌耐药率较高的抗菌药物为呋喃妥因、头孢泊肟、莫西沙星、萘啶酸；针对大肠埃希菌耐药率较高的抗菌药物为青霉素类抗菌药物、一二代头孢菌素、环丙沙星、左氧氟沙星。
结论 金黄色葡萄球菌、铜绿假单胞菌、粪肠球菌、大肠埃希菌是骨科患者伤口感染的主要病原菌。了解骨科伤口感染主要病原菌和它们的耐药情况，对于制定有效的用药治疗方案和避免术后感染有着重要意义。

PU-3685

B 族链球菌液固双相显色培养基的临床应用研究

瞿颖、童郁、林建萍、江俊华
温州市人民医院

目的 通过与荧光 PCR 法结果进行比对来，并评价 B 族链球菌液固双相显色培养基临床应用价值。
方法 采集孕晚期孕妇的阴道及肛门样本共 1026 例，通过液固双相显色培养基和 PCR 方法进行检测，结果不一致时使用质谱仪进行验证。
结果 PCR 方法检出阳性 82 例，阳性率为 7.99%（82/1 026）。液固双相显色培养基检测阳性 76 例，阳性率为 7.41%（76/1026）。液固双相显色培养基与 PCR 方法检测 GBS 阳性率差异无统计学意义（P>0.05），液固双相显色培养基与 PCR 方法检测 GBS 特异性差异有统计学意义（P<0.05）。
结论 B 族链球菌液固双相显色培养基检测 GBS 的性能能在临床比对试验中得到验证。由于 B 族链球菌液固双相显色培养法技术难度低，特异性优，成本低，对比 PCR 方法不需要大型仪器，可作为 GBS 筛查方法在基层医院推广应用。

PU-3686

不同年龄段女性生殖道支原体感染及耐药性分析

王超慧
吉林金域检验

目的 了解不同年龄段女性生殖道支原体感染情况的分布及其耐药情况，为临床治疗不同年龄女性支原体感染提供依据。
方法 选取我公司 2020 年 1 月 1 日至 2020 年 12 月 31 日送检的 820 例女性生殖道分泌物标本进行布支原体培养鉴定。实验前将冷藏保存的试剂和生殖道分泌物标本平衡至室温，接种标本于基础液中，加盖混匀；将混匀之后含有样本的基础液按每孔 100 微升加入到含有药物的微孔中；在所有微孔上滴加 1 滴矿物油，以防止基础液蒸发；将药敏实验板置于培养箱中，35-37℃培养 24 小时，观察结果。
结果 820 例标本中，20-30 岁女性生殖道分泌物支原体感染阳性率为 15.4%，其中单纯解脲支原体（U urealyticum,Uu）感染阳性率为 40.5%；30-40 岁女性生殖道分泌物支原体感染阳性率为 49.1%，其中单纯 UU 感染阳性率为 36.5%；40-50 岁女性生殖道分泌物支原体感染阳性率为 35.5%，其中单纯 UU 感染阳性率为 39.2%。药敏结果显示左氧氟沙星（89.0%）、美满霉素（83.1%）、强力霉素（80.0%）对所有年龄段患者敏感性均高于其他抗生素,阿奇霉素对年龄≤30 岁的患者敏感性高于其他年龄段患者。
结论 30-40 岁女性由于受到婚后阴道酸碱度改变以及生产后机体免疫力下降等多种因素的影响，女性支原体感染和单纯解脲支原体感染阳性率较大，感染风险较高。治疗支原体感染所引起的妇科疾病应首选左氧氟沙星、美满霉素、强力霉素。由支原体引起的女性阴道炎、宫颈炎等妇科疾病日渐增多，通过对不同年龄女性生殖道分必物标本进行常规的支原体检测及药敏分析，对指导临床合理治疗及用药具有重要意义。

PU-3687

基于自增强鲁米诺复合物功能化 CuMn-CeO2 纳米球的无酶电化学发光生物传感器用于无乳链球菌的超灵敏检测

凌佳继
四川大学华西第二医院

目的 无乳链球菌（GBS），是一种重要的致病菌，全球成年人感染率高，尤其是孕产妇。新生儿早发感染通常是由母亲无症状携带的 GBS 引起的，并在分娩时垂直传播给婴儿，由于新生儿免疫力低下，感染后可引起新生儿败血症甚至死亡，由此可见，早期筛查 GBS 至关重要。因此本文致力于建立一种灵敏高效的方法用于 GBS 早期监测，以此提高孕产妇和新生儿 GBS 的检出率。
方法 本研究将自增强的聚乙烯亚胺-鲁米诺复合物（PEI-luminol）功能化的 CuMn-CeO2 (CuMn-CeO2-PEI-luminol)与多组分核酸酶（MNAzyme）介导的目标物循环扩增相结合，建立了一种新型实用的电化学发光（ECL）生物传感方法，对 GBS 进行超灵敏特异性检测。首先将共反应物（PEI）与鲁米诺（luminol）合成高效自增强的 PEI-luminol 发光集团，缩短电子转移距离，增强了 ECL 信号。利用 CuMn-CeO2 负载大量的 PEI-luminol，通过对 H2O2 氧化的高催化活性，增强了鲁米诺的发光效率。然后，利用目标物驱动的 MNAzyme 系统实现了 GBS 核酸序列的循环，生产丰富的触发链，在电极表面实现核酸杂交反应，将信号分子引入电极表面，输出 ECL 信号。
结果 本研究设计的无酶 ECL 生物传感器对目标 DNA 检测具有超强灵敏性，检测限分别为 68 aM （合成 DNA） 和 5×102 CFU mL-1 （GBS 菌株基因组 DNA）。更重要的是，该生物传感器成功地应用于临床阴道/肛门拭子中提取的 GBS 基因组 DNA 的检测，检测结果低至 320 拷贝数。

结论 本文提出的基于 CuMn-CeO2 的新型自增强鲁米诺复合物功能化 ECL 生物传感策略，不仅可以实现对靶 DNA 的高灵敏、高效检测，而且为临床样品中 GBS 的超灵敏检测提供了一个新的实用平台，为核酸分析和临床诊断提供了一种潜在的通用工具。

PU-3688

支原体培养加药敏试验在生殖道分泌物检测中的应用价值

杨丽英、齐春林、王超慧
吉林金域检验医学检验所有限公司

目的 分析生殖道分泌物检测中支原体培养+药敏的结果情况，为临床合理用药选择提供一定参考依据。
方法 收集 2020.01.01-2020.12.31 期间送检我司的生殖道分泌物检测样本 994 例，均进行支原体培养及药敏试验，统计分析支原体培养及药敏耐药结果。
结果 2020.01.01-2020.12.31 期间送检我司支原体培养+药敏共 994 例样本，其中单独解脲脲原体阳性 369 例，单独人型支原体阳性 11 例，两者均阳性有 73 例，解脲脲原体总体阳性率：44.47%，人型支原体总体阳性率：8.45%。送检样本中女性为 973 例，男性为 11 例。女性送检比例大大超过男性。其中单独生长解脲脲原体的患者对美满霉素、强力霉素、红霉素、阿奇霉素、交沙霉素普遍较敏感，而单独人型支原体和联合感染的患者对美满霉素、强力霉素、交沙霉素普遍较敏感。
结论 生殖道分泌物中支原体感染包括解脲脲原体和人型支原体感染，男女均可引起感染。通过药敏试验可分析支原体耐药性，对支原体感染患者可选择美满霉素、强力霉素、交沙霉素抗生素进行治疗，对临床用药有一定指导作用。

PU-3689

奴卡菌感染的临床特点、分子分型和药敏结果分析

潘少敏、黄东红
福建医科大学附属第二医院

目的 为了提高临床医生对诺卡菌病的认识以及早期作出诊断，并指导临床医生合理使用抗生素。
方法 收集 2019 年 1 月到 2020 年 12 月诺卡菌感染患者菌株，用质谱仪和 16S rRNA 序列分析鉴定到种，用微量肉汤稀释法检测诺卡菌药敏。
结果 10 株诺卡菌来源于 10 个不同的病人，包括 2 名女性和 8 名男性，平均年龄 58 岁。共检出 7 种不同的诺卡菌，不同种诺卡菌对抗生素的敏感性不同。所有的菌株对复方新诺明，阿米卡星，利奈唑胺均敏感，妥布霉素敏感率 90%，米诺环素敏感率 80%，亚胺培南和头孢曲松敏感率 60%,阿莫西林/克拉维酸敏感率 50%,克拉霉素敏感率 40%，环丙沙星敏感率 20%。
结论 诺卡菌感染的临床表现和抗菌敏感性随诺卡菌种类的不同而不同。 因此，准确鉴定诺卡菌对于诊断和选择抗生素治疗至关重要。复方新诺明仍然是治疗奴卡菌病的首选药物。

PU-3690

Mechanisms and biological characteristics of acquisition of daptomycin resistance by Enterococcus faecium strains

Weiliang Zeng[2]、tao chen[2]、qing wu[2]、ye xu[2]、kaihang yu[1]、ying zhang[1]、shixing liu[2]、jianming cao[1]、tieli zhou[2]
1. Department of Medical Lab Science, School of Laboratory Medicine and Life Science, Wenzhou Medical University, Wenzhou, Zhejiang Province, China.
2. 温州医科大学附属第一医院

Objective Daptomycin-resistant (DAP-R) Enterococcus faecium (E. faecium) strains are well documented, but have not been reported yet in China. It is great important to investigate the resistance mechanism of daptomycin (DAP) and its effect on biological characteristics to prevent the occurrence of DAP-R E. faecium.
Methods Six daptomycin-susceptible (DAP-S) E. faecium clinical isolates were exposed to DAP in vitro to induce DAP-R mutants. Then the resistance mechanisms of DAP and bacterial biological characteristics, such phenotype changes and fitness costs, were investigated among these mutants.
Results In vitro, a total of twenty-one DAP-R mutants were obtained, which carried more than one mutation of liaFSR or yycFG. More positive charges were detected among highly DAP-R mutants than parent isolates, and the cell walls of SC1174-D and SC1762-D mutants were remarkly thicker than those of the parent isolates, these phenotypic changes which were compatible with significant differences in dltABCD and tagGH genes expression of parent strains versus mutant strains. Fitness costs were also observed among highly DAP-R mutants. The growth, competition ability and virulence were significantly reduced except biofilm formation capacity.
Conclusion E. faecium isolates acquire DAP resistance easily in vitro through different dynamic resistance mechanisms, which often accompany by significant phenotypic changes and fitness costs. It is necessary to take preventive and control measures to deal with DAP-R E. faecium that may appear in China in the future.

PU-3691

Identification and antifungal susceptibility analysis of Stephanoascus ciferrii complex species isolated from patients with chronic suppurative otitis media

Yuting He、Penghao Guo、Zhongwen Wu、Pingjuan Liu、Yili Chen、Kang Liao、Yaqin Peng
The First Affiliated Hospital, Sun Yat-sen University

Backgroud Stephanoascus ciferrii is a heterothallic ascomycetous yeast-like fungus. Recently, the concept of microbial complexes is applied. Microbial complex refers to a group of pathogens which are phenotypically indistinguishable but different at the genetic level, such as Acinetobacter calcoaceticus-baumannii complex and Candida parapsilosis complex. By sequencing of the 18S rRNA gene, Kumiko Ueda-Nishimura and Kozaburo Mikata divided S.ciferrii into three groups and proposed the S.ciferrii complex, which consists of S.ciferrii, Candida allociferrii and Candida mucifera. Usually, the widely used VITEK 2 yeast identification system (bioMérieux, France) just identified the microorganism as S.ciferrii complex and it doesn't identify the complex at species level. However, as for a rare kind of opportunistic pathogenic fungus, identifying S.ciferrii complex at species level is of great importance in epidemiological studies and the management of empirical antifungal therapy. We aimed to identify 32 strains of S.ciferrii complex isolated from patients with chronic suppurative otitis media at the species level and analyze the morphology and antifungal susceptibility profiles of the three species.

Method The sequencing of ITS region and MALDI-TOF MS were used to identify S.ciferrii complex species. The SARAMIS software was used for cluster analysis of the mass spectra. All the strains were cultured on SDA and CHROM plate for 7 days. Meantime, colonies of the 32 strains went through Gram staining. The Sensititre YeastOne YO10 colorimetric panel was used for the antifungal susceptibility analysis.
Results There were 10 strains of C.allociferrii (31.25%), 6 strains of C.mucifera (18.75%) and 16 strains of S.ciferrii (50%) in the 32 strains of S.ciferrii complex according to the sequencing of ITS region. MALDI-TOF MS could identify S.ciferrii but showed no results for C.allociferrii and C.mucifera. The cluster analysis of the mass spectra by SARAMIS indicated the MALDI-TOF MS could distinguish the three species. For MALDI-TOF MS, the limitation lies in its inability to identify non-clinically validated species or species not included in MALDI-TOF database. The three species of S.ciferrii complex had their own special peaks in the mass spectra, making it possible to identify them using MALDI-TOF MS by constructing reference databases at species level. The morphology characteristics of the three species were similar. The colonies embedded to the agar and the texture became hard after 72 hours. A week later, creamy or slightly yellowish colonies could be seen and the center of the colonies was gyri-like or cauliflower-like. The three species all had low MICs for echinocandins, making this kind of antifungal a good choice to treat S.ciferrii complex infection. The MICs for posaconazole, voriconazole and itraconazole were relatively small and there were no differences among the antifungal susceptibility of the three species for them. However, for fluconazole, all the strains had high MICs. Besides, S.ciferrii and C.mucifera tended to have high fluconazole MICs compared with C.allociferrii. Moreover, C.mucifera and C.allociferrii had relatively low flucytosine MICs while the S.ciferrii owned high flucytosine MICs. Besides, C.mucifera tended to have higher MIC value than S.ciferrii for amphotericin B and C.allociferrii for anidulafungin, micafungin, caspofungin.
Conclusion The morphology observation, antifungal susceptibility analysis and the mass spectra from MALDI-TOF MS of the 32 strains of S.ciferrii complex could provide experimental evidence and clinical experience for the diagnosis and treatment of the rare fungi at species level. Actually, the macroscopic and microscopic characteristics of the three species were similar, making it hard to distinguish them based on morphology. The antifungal susceptibility profiles of the three species of S.ciferrii complex had their own characteristics. Besides, more mass spectra of C.allociferrii and C.mucifera are needed to construct the reference database for Stephanoascus ciferrii complex species, enabling MALDI-TOF MS to identify S.ciferrii complex at species level.

PU-3692

临床分离大肠埃希菌第一类整合子的分布及其对耐药作用研究

李万翔
潍坊市人民医院

目的 筛查临床分离大肠埃希菌中第一类整合子的分布，研究其对大肠埃希菌耐药性的影响，为临床治疗和控制院内感染播撒提供理论依据。
方法 收集 2018 年 9 月至 10 月潍坊市人民医院就诊患者临床标本中分离的非重复 138 株大肠埃希菌。应用 Vitek 2 Compact 进行鉴定和药敏；应用 PCR 方法筛查第一类整合子基因，确定整合子在大肠埃希菌中分布。应用 SPSS 软件对整合子阳性株和整合子阴性株药敏分析以确定整合子对大肠埃希菌的药敏影响。
结果 第一类整合子阳性率为 67.39%（93/138）；临床常用药物耐药率最高的药物为氨苄西林 89.86%（124/138），其次为环丙沙星 73.91%（102/138），氨基糖苷类、碳青霉烯类耐药性最低；临床常用药物中庆大霉素、妥布霉素、复方新诺明、环丙沙星耐药率为整合子阳性菌株显著高于整合子阴性菌株，其他药物均无统计学差异。
结论 本次实验大肠埃希菌主要来源于泌尿外科、肾内科等科室的尿液标本。对 β-内酰胺类及氟喹诺酮类药物耐药率最高，而氨基糖苷类及碳青霉烯类耐药性处于较低水平。I 类整合子阳性率处于

较高水平，因整合子有明显耐药改变的药物主要为传统药物如复方新诺明、氨基糖苷类。这些药物恰恰是本实验相对敏感的一些药物，整合子的表达将加速菌株对这些药物的耐药进程。整合子对大肠埃希菌耐药起到关键作用，应当引起足够的重视。

PU-3693

2015～2019 年我院金黄色葡萄球菌分布及耐药变化分析

盛以泉
中国人民解放军陆军第 72 集团军医院

目的 分析我院 2015～2019 年金黄色葡萄球（SAU）分布及耐药性，为抗菌药物合理选用提供参考。
方法 收集本院临床分离的 SAU，并使用 MicroScan WalkAway96 plus 全自动微生物分析仪进行鉴定及药敏，采用ＷＨＯＮＥＴ5.5 软件对我院 2015 年-2019 年临床标本分离 SAU 病原体资料进行回顾性分析。
结果 期间共分离 SAU 1154 株，其中耐甲氧西林金黄色葡萄球菌(MRSA)438 株，检出率为 37.95％。MRSA 的检出率从 2015 年的 45.64％降至 2019 年的 35.80％，下降趋势明显。SAU 主要分布于骨科(421 株，36.48％)、外科(288 株，24.96％)、烧伤科(141 株，12.22％)和 ICU(53 株，4.59％)。各类临床标本中，分泌物标本中分离的 SAU 最多(631 株，54.68％)，其次痰标本(343 株，29.72％)。 MRSA 对常用的抗菌药物均有较高的耐药率，但对庆大霉素、左氧氟沙星呈下降趋势，对复方新诺明、环丙沙星呈明显下降趋势。而甲氧西林敏感金黄色葡萄球菌(MSSAU)对常用的抗菌药物耐药率较低，除青霉素 G 、氨苄西林、红霉素、克林霉素外，其耐药率均呈下降趋势且低于 18.8%。应注意的是每年均检出利奈唑胺耐药菌株，未检出万古霉素耐药株。
结论 SAU 的临床分离率呈上升再下降趋势，应时刻加强对其耐药性监测，以便临床合理用药并有效防控 SAU，特别加强 MRSA 的院内感染防控。

PU-3694

2020 年包头市细菌耐药性监测

李静
内蒙古科技大学包头医学院第一附属医院

目的 分析内蒙古包头市临床分离菌对常用抗菌药物的耐药情况。
方法 收集包头市 11 所参加全国细菌耐药监测网的三级医院 2020 年临床分离菌数据，利用 WHONET 5.6 及 SPSS 22.0 统计软件对所收集到的数据进行统计分析。
结果 2020 年包头市 11 所医院共检出 8094 株非重复菌株，其中革兰阴性菌 5950 株（73.5%），革兰阳性菌 2144 株（26.5%）。耐甲氧西林金黄色葡萄球菌(MRSA)和耐甲氧西林凝固酶阴性葡萄球菌(MRCNS)的检出率分别为 12.4%和 68.0%，未检出利奈唑胺、万古霉素和替考拉宁耐药菌株。屎肠球菌（EFM）对大多数抗菌药物的耐药率显著高于粪肠球菌（EFA），EFA 中发现有 1 株利奈唑胺和 1 株万古霉素耐药菌株。大肠埃希菌（ECO）、克雷伯菌属细菌和奇异变形杆菌中 ESBLs 阳性率分别为 46.2%、16.7%和 26.8%。产 ESBLs 菌株对所测抗菌药物的耐药率高于非产 ESBLs 菌株。耐碳青霉烯类的克雷伯菌属(CRKL)细菌检出率为 2.3%，耐碳青霉烯类的大肠埃希菌（CREC）检出率为 0.6%。铜绿假单胞菌(PAE)对亚胺培南和美罗培南的耐药率为 12.9%和 10.4%。鲍曼不动杆菌(ABA)对亚胺培南和美罗培南的耐药率为 19.1%和 21%。
结论 包头地区大肠埃希菌对喹诺酮类抗菌药物的耐药率和耐碳青霉烯类克雷伯菌属的检出率有所增长，其余细菌耐药情况低于全国平均水平，需要继续加强抗菌药物的合理使用和科学管理。

PU-3695

抗菌肽 lycosin-Ⅰ抗黏液型铜绿假单胞菌活性研究

程优、牛文彦
天津医科大学朱宪彝纪念医院

目的 通过体外实验探讨 lycosin-I 对黏液型铜绿假单胞菌浮游以及成膜状态的抗菌活性。
方法 收集临床中的黏液型以及普通型铜绿假单胞菌标本，应用微量肉汤稀释法检测 lycosin-I 的体外参数；微量平板法构建上述菌株的体外生物膜模型，结晶紫染色法检测 lycosin-I 对细菌生物膜形成的抑制和破坏作用。
结果 L-及 D-lycosin-I 在体外条件下对两种铜绿假单胞菌均有良好的抗菌效果，其中对普通型更为敏感；两种 lycosin-I 体外抗菌活性差异不明显，均在较低浓度下即有抗菌活性；L-或 D-lycosin-I 在 40min 时即能杀灭 50%左右的铜绿假单胞菌；体外培养二十四小时可见在 MIC 以下浓度抗菌肽干预下普通型铜绿假单胞菌于 6-16 小时快速生长，18 小时后其生长速度趋于平缓；黏液型铜绿假单胞菌于 6-16 小时快速生长，20 小时后其生长速度趋于平缓；在 MIC 及以上浓度抗菌肽干预下，细菌均难以生长；钙离子或镁离子可以提高 lycosin-I 针对上述实验菌的 MIC 值，减弱抗菌肽的体外抗菌活性，钙离子较镁离子具有更强的减弱效果。但是当抗菌肽处于高浓度状态时，钙、镁离子作用会被削弱。L-或 D-lycosin-I 能够抑制 30%~60%黏液型或者 20%~50%普通型铜绿假单胞菌的生物膜的形成；L-或 D-lycosin-I 能够消除 10%~40%的黏液型或者 10%~20%的普通型铜绿假单胞菌的成熟生物膜。 两种 lycosin-I 的抗生物膜活性、抑制和消除效果差异不明显。
结论 L-及 D-lycosin-I 在体外条件下可以有效对抗黏液型以及普通型铜绿假单胞菌浮游菌的生长，具有起效快、效果彻底和一定的盐耐受的特点，同时在体外均可以表现出一定的抗生物膜活性，极有可能成为一种新的药物被开发利用。

PU-3696

细菌对喹诺酮类抗生素耐药机制的研究

张钊冠、柴剑男
吉林大学第一医院

近年来，多重耐药菌尤呼吸系统多重耐药菌在临床的检出率呈逐年增多趋势[1]，氟喹诺酮类药物是近年来治疗下呼吸道感染的重要药物，多用于治疗院内呼吸道感染及重症监护室中的感染[2]。但由于其广泛和过度使用，具有喹诺酮类抗生素抗性的菌株自从 20 世纪 90 年代起就开始稳定增长[3]。细菌对其耐药性产生包括受体介导，质粒介导和染色体介导三种主要机制，前者通过突变改变促旋酶和拓扑异构酶 IV 与喹诺酮类药物的相互作用，后两种变化则减少细胞内喹诺酮类药物的浓度。

本文讨论了喹诺酮类药物如何与促旋酶和拓扑异构酶 IV 相互作用，以及这些酶中的突变怎样导致喹诺酮类药物的耐药性的最近进展，可为设计新药物来增强其对耐药菌株的作用活性提供可能的依据。

PU-3697

基于液相色谱-串联质谱技术骨关节结核血清代谢组学的初步研究

陈汐濛、温新宇、王成彬
中国人民解放军总医院第一医学中心

目的 骨关节结核是结核分枝杆菌感染骨关节组织或由活动性肺结核迁延至骨关节组织所引起的一种常见的肺外结核病。该病早期临床表现特异性低，同时现有临床影像学和实验室检查对该病早期检出率低，极大地影响患者的治疗和预后。针对骨关节结核早期诊断较为困难的现状，本课题利用液相色谱-串联质谱 (LC-MS/MS) 检测骨关节结核患者血清中特异性表达的血清差异代谢物，从分子水平对骨关节结核可能的发病机制提供思路并探究代谢物作为诊断标志物的价值。
方法 收集临床上已确诊的骨关节结核、类风湿关节炎、强直性脊柱炎患者血清样本各 30 例，同时收集健康成人血清样本 30 例为对照，并据此设置相应的分组。应用 LC-MS/MS 对所收集血清样本的代谢物成分进行分析并生成代谢图谱，经 SIMCA 软件处理后进行正交偏最小二乘辨别分析（OPLS-DA），通过其模型的变量重要性投影值（阈值>1）并结合 t-test 的 p 值（ $p<0.05$）来归纳各组间差异性代谢物质，并对差异代谢物质进行生物信息学分析。
结果 经过 LC-MS/MS 分析， 共鉴定出在骨关节结核组中特异性表达的差异代谢物 34 种，包含表达上调 19 种和表达下调 15 种。上调代谢物主要有卵磷脂类、鞘磷脂类、神经酰胺类，下调代谢物主要有氨基酸类、脂肪酸类、神经酰胺类。对上述差异代谢物的信号通路进行了分析，主要与丙氨酸代谢、甘氨酸代谢、鞘磷脂代谢、甘油磷脂代谢、花生四烯酸代谢等氨基酸和脂类物质代谢有关，提示骨关节结核发病过程可能涉及上述相关机制。
结论 应用 LC-MS/MS 初步筛选出 34 种骨关节结核组中特异表达的差异代谢物，经信号通路分析有助于从分子水平认识和了解骨关节结核的发病机制。同时下一步的研究还可以挑选代表性较好的差异代谢物，经临床样本靶向代谢组学验证后，探讨其作为诊断标志物的可能性，为骨关节结核的早期诊断提供参考价值。

PU-3698

粘液型铜绿药敏试验方法探讨

俞晓晨[1]、孙妍[2]
1. 哈尔滨医科大学附属第一医院
2. 黑龙江省哈尔滨市医科大学附属第一医院

目的 探讨临床常见的粘液型铜绿假单胞菌（Pseudomonas aexuginosa, PA）药敏试验（K-B 法）操作和报告。
方法 对分离得出的 15 株粘液型 PA 进行体外药敏试验（K-B）法，分别选择 M-H 平板和血平板，且记录不同时间点（24h、48h、72h）的结果。并将结果进行对比。
结果 不同时间药敏环直径不同；血平板和 M-H 平板制作药敏结果有差异
结论 1 黏铜 MH 平板上 24h 报结果不可信，因为黏铜生长不良
2 原有研究体外药敏试验都表明黏铜的药敏耐药性要低于普通铜绿，但是体内的抗菌效果不佳，除了粘液的原因，是否读取药敏的时间过短是其中原因之一。
3 药敏结果黏铜偏敏感，可能和做药敏实验时挑起了大量的粘液，从而使实际的菌液浓度偏低所致。

PU-3699

布鲁菌的鉴别

俞晓晨[1]、孙妍[2]
1. 哈尔滨医科大学附属第一医院
2. 黑龙江省哈尔滨市医科大学附属第一医院

目的 目前我国布鲁菌疫情严重，疫区扩大。作为一种传染性极强的细菌，快速鉴别出布鲁菌，可以减少实验室感染。
方法 柯氏染色法可以利用实验室常用的染色试剂，快速的帮助鉴别布鲁菌。
结果 对于临床中常见的细菌，柯氏染色鉴别布鲁菌优势明显。染色结果特异，染色时间快速。
结论 对于临床革兰染色疑似布鲁菌的细菌均可开展柯氏染色。

PU-3700

碳青霉烯耐药高毒力肺炎克雷伯菌血流感染血清蛋白组学分析

鲍金凤
中国人民解放军总医院第一医学中心

目的 应用液相色谱-质谱仪（LC-MS）分析碳青霉烯耐药高毒力肺炎克雷伯菌（CR-hvKP）血流感染小鼠的血清蛋白变化，寻找差异表达蛋白，并进行相应的生物学功能分析。
方法 建立 ICR 小鼠 CR-hvKP 及经典的肺炎克雷伯菌（cKP）血流感染模型，收集感染 12h 的小鼠血清，进行 LC-MS 检测。采用 Maxquant 软件对 LC-MS 结果进行鉴定，并对差异蛋白进行相应的生物信息学分析。
结果 与正常对照组相比，CR-hvKP 分别有 24 和 20 个蛋白上调和下调（>1.5 Log2, p<0.05）。与 cKP 组相比，CR-hvKP 组有 107 个蛋白上调，无下调蛋白。134 个差异表达蛋白参与生物调控、细胞过程、发展过程、免疫过程、生物间相互作用、本地化、运动、代谢过程、对刺激的反应、信号转导、炎症反应、氧化应激、血管生成等过程；信号通路分析涉及补体和凝血级联、胆固醇代谢、细菌感染、血红素的清除、血浆脂蛋白的组装、重塑和清除等多条代谢相关通路。 我们重点分析了 SAA1、KLKB1、VNN3、HBB-b2、Serpina1b 这 5 个差异蛋白。其中 KLKB1 及 Serpina1b 与正常组相比下调但与 cKP 组相比上调。其余在 4 个蛋白与 cKP 组及正常组相比均上调。经功能分析及文献检索证实这 5 个蛋白与 CR-hvKP 血流感染相关。
结论 CR-hvKP 血流感染涉及多个蛋白的激活及作用，SAA1、VNN3、HBB-b2 升高或 KLKB1、Serpina1b 下降时或提示 CR-hvKP 血流感染。

PU-3701

乌鲁木齐地区产 ESBLs 肺炎克雷伯菌耐药基因的差异化分析

马晶[2]、杨丽[1]、王昌敏[2]、师东豪[1]、徐菲莉[1]
1. 新疆医科大学附属中医医院临床检验中心
2. 新疆维吾尔自治区人民医院临床检验中心

目的 探讨分析产超广谱 β-内酰胺酶(extended-spectrum β-Lactamase，ESBLs) 肺炎克雷伯菌的耐药基因型的种类和药物敏感性，探讨本地区分离的肺炎克雷伯菌的耐药机制，指导临床降低耐药率并能够有效使用抗生素。
方法 采用全自动快速微生物质谱检测系统对分离的肺炎克雷伯菌进行菌种鉴定，采用 VITEK-2 Compact 全自动微生物分析仪进行药敏试验，收集 2019 年 1 月至 2019 年 12 月临床标本中分离的产 ESBLs 和不产 ESBLs 肺炎克雷伯菌，按照常规标准纸片扩散法进行超广谱 ESBLs 表型筛选

和确认试验，分析产与不产 ESBLs 肺炎克雷伯菌的耐药性，采用聚合酶链式反应（PCR）及测序分析 ESBLs 的基因型。
结果 共分离 4918 株肺炎克雷伯菌，其中男性患者 3688 人（74.99%），女性患者 1230 人（25.01%），年龄为 28~89 岁。临床分离的产 ESBLs 的肺炎克雷伯菌共 2238 株，阳性检出率 45.50%。产 ESBLs 的肺炎克雷伯菌对哌拉西林、头孢唑啉、头孢曲松的耐药率较高，分别为 87.52%、84.32%、83.79%。对亚胺培南、美罗培南、米诺环素的耐药率相对较低，分别为 3.61%、2.45%、2.35%。除了头孢替坦外，大多数产超广谱 β-内酰胺酶的肺炎克雷伯菌比不产 ESBLs 的耐药率高，差异有统计学意义（P<0.05）。经过测序后发现，38 株产与不产 ESBLs 的肺炎克雷伯菌中均含耐药基因 TEM 、SHV 和 CTX-M 型。
结论 本地区产超广谱 β-内酰胺酶的肺炎克雷伯菌的耐药性比不产 ESBLs 的要高；产超广谱 β-内酰胺酶的肺炎克雷伯菌的基因型在本地主要是 TEM 型、SHV 型和 CTX-M 型，需要继续增强肺炎克雷伯菌的监测，从而更好的降低肺炎克雷伯菌的耐药率，有效阻止肺炎克雷伯菌的传播。

PU-3702

ICU 住院患者抗菌药物应用与耐药菌感染相关性研究

景丽萍、庄学伟
山东省立第三医院

目的 分析 ICU 住院患者抗菌药物应用与耐药菌感染的相关性，探讨发生耐药菌感染的相关危险因素，为临床合理应用抗菌药物，降低耐药菌感染提供科学依据。
方法 用整群抽样的方法选取 2016 年 1 月 1 日至 2016 年 12 月 31 日入住某三甲医院 ICU 的住院患者 454 例，用目标性监测方法，将病人资料填写到自行设计的《ICU 住院患者耐药菌感染目标性监测调查表》中，分析抗菌药物应用与耐药菌感染情况。
结果 应用抗菌药物的患者耐药菌感染率较未应用者高，为 30.44%；耐药菌感染的发生率随着抗菌药物应用时间的延长而增加；耐药菌感染率随着药物联用种类的增加而显著增加；入 ICU 前应用抗菌药物的患者耐药菌感染率较未应用者高，为 37.58%；死亡患者的耐药菌感染率高，为 62.96%。
结论 抗菌药物应用与耐药菌发生有一定相关性，临床应加强抗菌药物应用管理，合理使用抗菌药物，以降低耐药菌感染发生率。

PU-3703

YouTube™ as a source of information for Candida auris infection: a systematic review

Jiangqing Huang、Bin Li
Fujian Medical University Union Hospital

Background Candida auris is a novel Candida species, and has emerged globally as a multidrug-resistant health care-associated fungal pathogen. YouTube™ (http://www.youtube.com) as the largest free video-sharing website is increasingly used to search health information. Thus, the aim of this study was to evaluate the content, reliability and quality of YouTube™ videos regarding Candida auris infection, and to identify whether it is a useful resource for people.
Methods The YouTube™ was used to search systematically for videos using the keywords: "Candida auris infection" and "Candida auris". Strict inclusion and exclusion criteria were used to select the videos. The videos were reviewed and scored by two independent reviewers and recorded the "title", "length", "views", "comments", "dislike", "like", "posted days" and "category of videos". The videos were categorized as "poor", "good" and "excellent" by the score. The DISCERN tool was used to assess the reliability of the YouTube™ videos.

Results Seventy-six videos were included in final analysis in our study. Most videos (59.2%, 55/76) had better quality. There were no statistically significant differences between groups in respect of the number of likes, dislikes, views, comments, percentage positivity, likebility, view rate and viewers' interaction. Length and posted days were significantly associated with the classification. The videos were categorized as "educational video", "new report", "personal experience and blog entertainment" and "interview". Significant differences were found in the source of videos and the characteristics of the individuals appearing in a video between the groups.
Conclusion YouTube™ has striking potential to be an effective user-friendly learning interface for people to obtain information of Candida auris infection.

PU-3704

Hospital Wastewater as a Reservoir for Antibiotic Resistance Genes: A Meta-Analysis

shengcen zhang、Bin Li
Fujian Medical University Union Hospital

Background The emergence and dissemination of antibiotic resistance genes (ARGs) in the environment poses a huge global health hazard. Hospital wastewater (HWW), in which a high density of antibiotic residues and antibiotic-resistant bacteria are present, may be a reservoir of ARGs dissemination into the environment. Our meta-analysis comprehensively analyzes the prevalence of ARGs in HWW, as well as the influencing factors in ARGs distribution.
Methods Online databases were used to search for literature using the subject terms: "Drug Resistance" AND "Genes" AND "Hospitals" AND "Wastewater." Two reviewers independently applied predefined criteria to assess the literature and extract data including "relative abundance of ARGs," "title," "authors," "country," "location," "sampling year," and "sampling seasons." The median values and 95% confidence intervals of ARGs abundance were calculated by Wilcox.test function in R. Temporal trends, spatial differences, seasonal variations and removal efficiency of ARGs were analyzed by Pearson correlation analysis and Kruskal-Wallis H test.
Results Resistance genes to carbapenems, sulfonamides, tetracyclines and mobile genetic elements were found at high relative abundance (>10-4 gene copies/16S rRNA gene copies) in HWW. The abundance of resistance genes to extended-spectrum β-lactams, carbapenems, sulfonamides and glycopeptide significantly decreased, while tetracycline resistance genes abundance increased from 2014 to 2018. The abundance of ARGs was significantly different by country but not by season. ARGs could not be completely removed by on-site HWW treatments and the removal efficiency varies for different ARGs.
Conclusions HWW presents more types of ARGs, and their abundance is higher than those in most wastewater systems. HWW may be a reservoir of ARGs and play an important role in the dissemination of ARGs.

PU-3705

Characterization of Integrons and Antimicrobial Resistance in Escherichia coli Sequence Type 131 Isolates

Jiangqing Huang、Bin Li
Fujian Medical University Union Hospital

Background Escherichia coli sequence type 131 (ST131) is an important multidrug-resistant extraintestinal pathogen, which can cause many kinds of infections. Integrons may play a crucial

role in the dissemination of antibiotic resistance genes. The purpose of this study was to characterize the prevelance of integrons among E. coli ST131 strains in China.
Methods Eighty-three E. coli ST131 strains in China. E. coli ST131 strains in China.
Results Overall, 26.5% (22/83) of the E. coli ST131 strains in China. dfrA17-aadA5 and aac(6')-Ib-cr-cmlA5. Only one type of Pc promoter variant was detected among 22 integron-positive isolates (PcW). In vivo transfer of integron was successful for 9 of integron-positive E. coli ST131 strains in China. E. coli ST131 strains in China.
Conclusions Our study showed a low prevalence of integrons was detected in E. coli ST131. Continued surveillance of this mobile genetic element should be performed to study the evolution of antibiotic resistance among E. coli ST131.E. coli ST131 strains in China. E. coli ST131 strains in China.

PU-3706

Pathogenicity- and survivability-associated phenotypic characteristics reveal ST1193 superiority: a comparative study of fluoroquinolone-resistant Escherichia coli lineages

黄江庆、李彬
福建医科大学附属协和医院

Background The aim of this study was to compare the pathogenicity and survivability features of E. coli ST1193.
Methods E. coli ST1193 (n=15) and ST131 (n=15) were used in this study. Adhesion and invasion and serum resistance were quantified. Biofilm formation capacity was assessed by crystal violet assay. Macrocolony formation was detected. Anti-phagocytic function and hydrogen Peroxide resistance were assessed.
Results E. coli ST1193 could adhere and invade T24 cells. most E. coli ST1193 could form biofilms and 66.7% strains possessed no curli/no cellulose. E. coli ST1193 showed significant growth in serum and hydrogen peroxide.
Conclusion Our study provided more insights into pathogenicity and survivability features of E. coli ST1193.

PU-3707

耐碳青霉烯类肺炎克雷伯菌的耐药基因及毒力基因研究

谢屿平、曹颖平
福建医科大学附属协和医院

目的 分析福建医科大学附属协和医院 2014 年-2015 年收集的耐碳青霉烯类肺炎克雷伯菌（CR-KP）的临床分布、耐药基因、毒力基因。
方法 采用 PCR 及测序法检测 CR-KP 碳青霉烯酶基因，并进行多位点序列分型（MLST），并通过 PCR 扩增毒力基因，检测并分析 CR-KP 的毒力因子表型。
结果 对 101 株耐碳青霉烯类肺炎克雷伯菌进行碳青霉烯酶基因的检测发现，KPC-2 检出率最高，阳性率为 67.3%（68/101）；其次为 IMP-4 基因占 5.0%（5/101）；NDM-1 阳性率为 1.0%（1/101），其中有 1 株 CR-KP 同时携带 KPC-2 和 NDM-1 基因。101 株 CR-KP 中未发现 SME、GES、IMI、VIM、SIM、GIM、SPM 和 OXA-48。在 MLST 的检测结果中，68 株产 KPC-2 酶的肺炎克雷伯菌均为 ST11；在 5 株产 IMP-4 的肺炎克雷伯菌中，3 株为 ST26，2 株为 ST334。毒力相关基因中 urea(92.1%), fimH(91.1%), uge(81.2%), wabG(87.1%)的检出率高。

结论 本院临床分离的 CR-KP 耐药基因主要是 KPC-2 和 IMP-4 基因。毒力因子尤其是 ureA、fimH、uge、wabG 的高检出率使菌株具有更强的适应力与生存特性，需引起重视。

PU-3708

人感染猪链球菌致感染性心内膜炎一例

丛培珊、何宏、孙桂荣
青岛大学附属医院

猪链球菌是一种革兰阳性，圆形或卵圆形，单个、成对或短链状排列的兼性厌氧菌。可引起猪多部位感染，人通过直接接触病(死)猪，致病菌经破损皮肤或黏膜侵入人体而引发感染，是一种人畜共患病原菌。猪链球菌感染通常引起化脓性脑膜炎及菌血症，病情进展快，预后差，很多病例存在严重的后遗症。本文报道一例少见猪链球菌感染导致感染性心内膜炎患者，发现治疗及时，预后好，未出现严重并发症。患者，男，54 岁，厨师。因反复发作活动后胸闷、憋气、心慌 2 月，于 2020 年 10 月 14 日入住我院。患者 2 月前始出现活动后胸闷、憋气、心慌不适，休息后可缓解，平素无咳嗽、咳痰、咯血，可从事轻度体力活动，曾就诊于我院门诊，行心脏彩超检查，诊断为：二尖瓣脱垂并反流，为行手术治疗入住我院。入院查体：体温：37.3 ℃，脉搏：91 次/分，呼吸：32 次/分，辅助检查：白细胞计数 10.37×109/L，中性粒细胞计数 7.9×109 /L，C 反应蛋白 20.9 mg/L；考虑存在感染的可能，于是暂停手术查找病原，于 10 月 15 日采集患者双侧上肢静脉血做需氧+厌氧血培养。16 小时后，4 瓶血培养全部报阳，经鉴定为猪链球菌。药敏试验结果显示，对青霉素、头孢噻肟、红霉素、克林霉素、左旋氧氟沙星、氯霉素、奎奴普丁/达福普汀，利奈唑胺、万古霉素敏感，四环素耐药。明确诊断为猪链球菌感染性心内膜炎，遂用邦达抗感染治疗。11 月 5 日，患者无发热，一般情况可，全麻下行二尖瓣机械瓣膜置换术+主动脉瓣机械瓣置换。患者手术顺利，术后好转出院，未出现严重的后遗症。

PU-3709

全程高脂肪饮食对益生菌调节大鼠变应性进程的影响及机制研究

宋佳平、徐永成
大连市第三人民医院

背景与目的 变应性疾病，包括变应性皮炎，变应性鼻炎和变应性哮喘等。而变应性皮炎到变应性哮喘是一个逐渐发展的过程，称为变应性进程。在动物模型中，益生菌缓解变应性疾病效果明显，但在临床上作用却不明确。这可能与人类的饮食习惯不同相关。本研究探究全程高脂肪饮食对变应性疾病的发展及调节的影响，为变应性疾病的治疗以及益生菌的临床应用奠定基础。
方法 利用鸡卵清白蛋白建立大鼠变应性进程的模型，灌服益生菌治疗，全程用高脂肪饮食喂食。观察大鼠的喷嚏和抓鼻次数，进行 HE 组织学染色，利用 DGGE 分析对肠道菌群的影响， 检测血清、鼻腔和肺中各免疫因子的水平。
结果 1.临床表现：与模型组（M）比，益生菌组（NP）在滴鼻激发和雾化激发后 15min 内喷嚏和抓鼻数量均有下降趋势，鼻粘膜上皮完整，肺组织炎症浸润减少，全程高脂肪模型组（HM）喷嚏数量有增多趋势粘膜破坏更严重，全程高脂肪益生菌组（HP）的喷嚏和抓鼻数量均有上升趋势，鼻粘膜上皮破坏明显，肺组织炎症浸润增多。2.菌群变化：DGGE 实验结果显示，M 组的 DGGE 条带数明显减少（$p<0.01$），与 M 组相比，NP 组条带数增加明显（$p<0.05$），HM 组的条带数显著减少（$p<0.05$）；与 NP 组相比，HP 组的条带数明显减少（$p<0.01$）。3.免疫机制：与 M 组相比，NP 组在血清、鼻腔和肺 IL-4 的含量均有下降趋势，IFN-γ 均升高，其中在鼻腔中显著上升（$p<0.001$），HM 组的 IL-4 含量均上升，其中在血清中显著上升（$p<0.001$），IFN-γ 在血清和肺中有降低的趋势；与 NP 组相比，HP 组的 IL-4 含量有升高趋势，IFN-γ 有下降趋势。

结论 益生菌通过调节菌群和免疫失调，缓解变应性进程，高脂肪饮食会促进变应性疾病的严重程度，延缓益生菌的缓解作用。

PU-3710

铜绿假单胞菌药敏结果分析

赵楠楠、杨丽英
吉林金域医学检验所有限公司

目的 细菌培养周期长，结果发布较慢，对临床上的急重症患者用药起到一定的限制，通过分析我实验室痰培养+药敏结果，其中致病菌为铜绿假单胞菌的药物敏感性，了解其耐药性的分布，为临床经验用药提供参考依据，从而缩短患者的治疗周期、一定程度上减轻患者痛苦。
方法 分析我实验室 2020 年 1 月 1 日-2020 年 12 月 31 日全年铜绿假单胞菌阳性样本的药敏结果。
结果 我实验室 2020 年全年共接收痰液培养+药敏标本 2940 例，阳性样本 1244 例，阳性率 42.31%；其中致病菌为铜绿假单胞菌的有 241 例，阳性率 19.37%。通过对此 241 例标本药敏结果进行分析发现：阿米卡星- 敏感占比 93.78% 耐药占比 2.90%；妥布霉素- 敏感占比 88.38%、 耐药占比 6.22% ；对头孢他啶-敏感占比 81.74%、 耐药占比 13.27% ；美罗培南-敏感占比 80.50%、耐药占比 16.18%；庆大霉素-敏感占比 78.42%、 耐药占比 11.62%；哌拉西林舒巴坦- 敏感占比 76.35% 、耐药占比 6.22%；头孢吡肟-敏感占比 76.35% 、 耐药 10.79%； 亚胺培南- 敏感占比 74.69%、耐药占比 19.09%；哌拉西林-敏感占比 73.03%、耐药占比 13.28%；左氧氟沙星- 敏感占比 62.66%、 耐药占比 26.97%；环丙沙星-敏感占比 57.68%、 耐药占比 29.05。
结论 铜绿假单胞菌对阿米卡星、妥布霉素、头孢他啶、美罗培南等敏感性较强，在急重症患者治疗过程中，当确定感染菌为铜绿假单胞菌时，可优先提前使用以上药物；而对环丙沙星、左氧氟沙星出现耐药趋势。

PU-3711

口腔白念珠菌的毒力、耐药性及其相关性研究

孙康德、张家胜、陈旭
上海交通大学医学院附属第九人民医院

目的 了解口腔白念珠菌分泌型水解酶、生物膜和菌丝相形成等毒力因子的体外表达水平及其耐药性，以及两者的相关性。
方法 分别采用牛血清白蛋白平板、卵黄琼脂平板和三丁酸甘油脂平板检测口腔白念珠菌分泌型天冬氨酸蛋白酶（SAP）、磷脂酶（PL）和脂肪酶（Lip）的活性；使用结晶紫法检测其生物膜的形成；采用实时荧光 PCR 法检测菌丝壁蛋白 1 基因（HWP1）的表达；并用 ATB FUGUS 3 法检测白念珠菌对常用抗真菌药物的耐药性；且运用皮尔逊相关性分析和 T 检验进行数据分析。
结果 80%的菌株高产分泌型天冬氨酸蛋白酶，98%的菌株高产磷脂酶，然而 78%的菌株脂肪酶产量中等，且无菌株高产脂肪酶；50 株菌株均能形成生物膜，其中 30 株（60%）生物膜形成强；SAP 和 PL 的体外表达水平呈正相关（$P<0.05$），其他毒力因子之间均无相关性；耐药株与敏感株的毒力因子体外表达及 HWP1 表达之间没有显著性差异。
结论 大部分口腔白念珠菌高表达 SAP 和 PL，中等表达 Lip，生物膜形成能力强，SAP 和 PL 的体外表达水平呈正相关，口腔白念珠菌的毒力与耐药性之间没有显著相关性。

PU-3712

基于代谢组学分析结核分枝杆菌耐药机制的研究

朱彧[1]、吴敏[1]、张丽霞[1]、陈怀永[2]
1. 天津市海河医院检验科
2. 天津市海河医院基础研究中心

背景 据世界卫生组织估计，2019 年全球有 1000 万人患结核病。耐药结核病（DR-TB）是当今人类重大的公共卫生威胁，2019 年全球有接近 50 万的利福平耐药结核病（RR-TB）患者，其中 78%患者是耐多药结核病（MDR-TB）。我们通过代谢组学分析耐药结核分枝杆菌（MTB）上清液中的代谢物和代谢途径，进而探索结核病耐药机制的潜在标志物。
方法 收集药物敏感（DS）、耐多药（MDR）和泛耐药（XDR）结核分枝杆菌菌株的培养物上清液并以空白上清液作为阴性对照（NC）。采用 LC/MS 方法检测上清液中的代谢物质，分析代谢途径并预测代谢物相关的酶和基因。
结果 我们分析定量了 5478 种代谢产物。与 DS 组代谢物质相比，MDR 组和 XDR 组分别有 11 种和 23 种显著上调，6 种和 13 种显著下调。与 MDR 组相比，XDR 组有 3 种上调，3 种下调。生物信息学分析表明，涉及到结核分枝杆菌的细胞壁成分以及氧化还原过程的代谢途径包括果糖和甘露糖代谢、鞘磷脂和甘油磷脂代谢、半胱氨酸和蛋氨酸代谢以及烟酰胺和叶酸的代谢等。代谢物相关酶和基因预测显示外聚磷酸酶(PRUNE)、甲酰四氢叶酸脱氢酶(ALDH1L1/2)、鞘氨酰胺激酶(SPHK1/2)等是与上述代谢途径相关的酶和基因。
结论 细胞壁组成和氧化还原特性的改变可能在 MTB 耐药性中起重要作用，代谢产物可能是评估结核病耐药性发展的潜在生物标志物。

PU-3713

结核分枝杆菌耐药特异性代谢物鉴定研究

吴敏[1]、朱彧[1]、张丽霞[1]、陈怀永[2]
1. 天津市海河医院检验科
2. 天津市海河医院基础研究中心

目的 筛选结核分支杆菌(MTB)不同耐药性培养物上清液代谢标志物，研究 MTB 特异性代谢物化学结构和生物途径，发现新的结核耐药诊断标记物。
方法 收集空白对照组(NTC)、敏感结核菌(ALS)、耐多药结核菌(MDR)、泛耐药结核菌(XDR)培养物上清液，样品经预处理、代谢物提取，LC-MS 技术检测样本中的代谢物质，结合代谢组学数据处理软件 Progenesis QI v2.3，对原始数据进行定性及相对定量分析，采用多维分析和单维分析相结合的办法筛选组间差异代谢产物。筛选的标准为 OPLS-DA 模型第一主成分的 VIP 值>1，T 检验的 P<0.05，FC>1.2 或 FC<1/1.2。基于 KEGG 数据库对差异代谢物进行代谢通路富集分析，探讨差异样品中代谢途径变化机制。利用软件 Legend 分析筛选结核代谢预测基因反应酶。
结果 富集通路差异代谢物分析得出，与 ALS 组相比，MDR 组检测出 17 种差异代谢物，其中上调 11 种、下调 6 种。同 ALS 组相比，XDR 组检测出 36 种差异性代谢物，其中 23 种上调、13 种下调。与 MDR 组相比，XDR 组检测出 6 种差异代谢物，其中上调 3 种，下调 3 种。利用多元统计分析、t 检验筛选差异代谢物；分析结果表明，不同处理组的代谢物有明显的差异。
结论 差异性代谢物可能是指示结核多耐药的潜在标志物，联合分子标志物来评估结核耐药的发生发展，可以增强诊断的灵敏度和特异性，具有一定的临床应用前景。

PU-3714

沙门氏菌现行国内外标准中基于选择性增菌的等效性研究和评估

刘玥[1,2]、胡屹[2,3]、刘弘[1]、顾其芳[1]、陈敏[1]、崔琳[4]、许学斌[1]
1. 上海市疾病预防控制中心
2. 复旦大学公共卫生学院
3. 复旦大学公共卫生安全教育部重点实验室
4. 上海市临床检验中心

目的 评估现行国内与国际食品沙门氏菌标准中基于前增菌步骤的等效性。
方法 构建现行标准中基于沙门氏菌选择性增菌液对接两种沙门氏菌选择性分离平板的检测流程，使用 5 种参比菌株测试对沙门氏菌选择性增菌液的回收效果，对 5 种常用沙门氏菌选择性平板的沙门氏菌典型菌落特征进行评估；通过实样比较不同沙门氏菌增菌流程的分离敏感性、相对真值（Relative Trueness, RT）和可接受限值（Acceptability Limit, AL）。
结果 纯菌液和模拟样回收罗伯特增菌液（Rappaport Vassiliadis broth, RV）、四硫磺酸钠煌绿增菌液（Tetrathionate Broth, TTB）、亚硒酸盐煌绿增菌液（selenite brilliant green enrichment broth, SBG）、穆勒-考夫曼四硫酸盐新生霉素增菌液（Muller-Kauffmann tetrathionate-novobiocin, MKTTn ）和亚硒酸盐胱氨酸增菌液（Selenite Cystine broth, SC）的稀释度相差 1~2 个梯度，前 4 种增菌液适合非伤寒沙门氏菌增殖，SC 仅适用伤寒沙门氏菌、副伤寒沙门氏菌的增殖；84 件肉制品和水产品样品经 5 种选择性增菌组合方法处理后分离、筛选和确认，结果发现 25 件阳性样品（29.76%），共检出 42 株沙门氏菌。5 种组合方法的沙门氏菌分离敏感性分别为 84.00%、100.00%、88.00%、88.00%和 92.00%；RT 分别为 95.24%、100.00%、96.43%、96.43%和 96.72%。方法 1 的 AL 超出 ISO16140 释义的一类样本可接受限值，其他方法的 AL 均在可接受范围内。
结论 我国现行的国标方法基于 SC 增菌液的无效检验将导致结果偏倚，其他 4 种选择性增菌液的随机组合均可避免负偏差结果产生。

PU-3715

A predictive nomogram for mortality of cancer patients with invasive candidiasis: a 10-year study in a cancer center of North China

Ding Li
Tianjin medical university cancer institute and hospital

Background Invasive candidiasis is the most common fungal disease among hospitalized patients and continues to be a major cause of mortality. Risk factors for mortality have been studied previously but rarely developed into a predictive nomogram, especially for cancer patients. We constructed a nomogram for mortality prediction based on a retrospective review of 10 years of data for cancer patients with invasive candidiasis.
Methods Clinical data for cancer patients with invasive candidiasis during the period of 2010-2019 were studied; the cases were randomly divided into training and validation cohorts. Variables in the training cohort were subjected to a predictive nomogram based on multivariate logistic regression analysis and a stepwise algorithm. We assessed the performance of the nomogram through the area under the receiver operating characteristic (ROC) curve (AUC) and decision curve analysis (DCA) in both the training and validation cohorts.
Results A total of 207 cases of invasive candidiasis were examined, and the crude 30-day mortality was 28.0%. Candida albicans (48.3%) was the predominant species responsible for infection, followed by the Candida glabrata complex (24.2%) and Candida tropicalis (10.1%). The training and validation cohorts contained 147 and 60 cases, respectively. The predictive

nomogram consisted of bloodstream infections, intensive care unit (ICU) admitted > 3 days, no prior surgery, metastasis and no source control. The AUCs of the training and validation cohorts were 0.895 (95% confidence interval [CI], 0.846-0.945) and 0.862 (95% CI, 0.770-0.955), respectively. The net benefit of the model performed better than “treatment for all” in DCA and was also better for opting low-risk patients out of treatment than “treatment for none” in opt-out DCA.
Conclusion Cancer patients with invasive candidiasis exhibit high crude mortality. The predictive nomogram established in this study can provide a probability of mortality for a given patient, which will be beneficial for therapeutic strategies and outcome improvement.

PU-3716

临床 VAP 患者下呼吸道分离 CRKP 菌株临床特征、基因分型及毒力因子研究

刘周、储雯雯、李昕、汪雅婷、周强
安徽医科大学第二附属医院

目的 分析呼吸相关性肺炎（VAP）患者下呼吸标本分离碳青霉烯耐药肺炎克雷伯菌（CRKP）菌株临床特征、基因型及主要毒力因子携带情况。
方法 收集 2019 年 1 月至 12 月期间，临床 VAP 患者合格下呼吸道标本分离非重复肺炎克雷伯菌（KP），药敏试验筛选 CRKP 并检测其碳青霉烯耐药基因。将碳青霉烯非耐药 KP（CnRKP）作为对照组，分析 CRKP 组患者临床感染特征。应用 PCR 联合测序技术检测 KP 菌株多位点序列分型、荚膜 wzi 分型及毒力因子。应用脉冲场凝胶电泳（PFGE）分析 CRKP 菌株同源性。
结果 共收集 56 株 KP，60.7%为 CRKP（34 株），CRKP 主要携带 blaKPC-2（97.1%），对除替加环素以外的抗菌药物耐药率高。CRKP 组患者死亡比例显著高于 CnRKP 组（P＜0.05）。82.4%的 CRKP 属于 ST11 型，K64（50.0%）为主要荚膜型。CRKP 携带多种毒力因子，pLVPK-like 质粒介导的毒力因子 rmpA2、iucA 及 iroN 主要由 K64-ST11 型 CRKP 携带，且 PFGE 显示 K64-ST11 型 CRKP 存在克隆传播。
结论 VAP 患者下呼吸分离 CRKP 菌株呈现多重耐药，K64-ST11 型为其主要分子型别。K64-ST11 型 CRKP 携带多种质粒介导的毒力因子并存在克隆播撒，应密切监控该基因型 CRKP 菌株临床流行趋势。

PU-3717

2013—2020 年某医院耐碳青霉烯类铜绿假单胞菌的临床分布、耐药性及金属 β-内酰胺酶基因检测

李进
重庆医科大学

目的 回顾性分析 2013—2020 年重庆某医院耐碳青霉烯类铜绿假单胞菌的临床分布、耐药性及金属 β-内酰胺酶常见基因分布情况，为指导临床抗感染治疗提供可靠的依据。
方法 收集重庆某医院 2013 年 1 月至 2020 年 12 月临床分离的非重复 CRPA 菌株 482 株，利用 DL-96 全自动细菌测定系统进行菌株鉴定和药敏实验，参照 2020 版 CLSI-M100 文件标准判断结果，并通过 WHONET 5.6 软件对菌株的临床分布和耐药特征进行统计分析，同时采用亚胺培南-EDTA 双纸片协同法筛选金属酶表型阳性的菌株，再利用 PCR 法检测铜绿假单胞菌 MBL 基因的分布情况。
结果 2013 年 1 月至 2020 年 12 月我院住院患者送检的临床标本共检出 CRPA 菌株 482 株，其中，2013 年 78 株、2014 年 24 株、2015 年 55 株、2016 年 32 株、2017 年 78 株、2018 年 90 株、

2019 年 82 株、2020 年 43 株。从标本类型来看，482 株 CRPA 菌株中痰液占 83.6%，肺泡灌洗液占 7.5%，分泌物占 2.1%，尿液占 3.1%，血液占 1.0%，其它占 2.7%；从年龄分布来看，CRPA 菌株中，61-70 岁的患者人数最多，共 152 例，其次为 71-80 岁的患者，共 107 例，20 岁及以下无患者；482 株 CRPA 菌株主要分布的科室为呼吸内科、重症医学科和神经外科。药敏结果显示 482 株 CRPA 菌株对临床常见抗菌药物的敏感率相对稳定。PCR 检测结果显示，MBL 基因阳性 98 株，其中 IMP 型 42 株，VIM 型 36 株，SPM 型 20 株，未检测出其他基因型。
结论 2013—2020 年分离出来的 482 株 CRPA 菌株临床分布广泛，对临床上常用的抗菌药物耐药率普遍较低，产 MBL 是引起铜绿假单胞菌对亚胺培南耐药的主要原因，临床应加强对产金属酶铜绿假单胞菌的检测和监控，制定合理有效的感染控制措施，合理使用广谱抗菌药物，最大限度阻止 CRPA 菌株的播散。

PU-3718

东北地区 1233 例布鲁菌抗体三项样本的结果分析

杨丽英、齐春林
吉林金域检验医学检验所有限公司

目的 分析 2020.09-05-2020.12.31 期间送检我司布鲁菌抗体三项样本 1233 例样本的结果情况，给流行病学资料调查提供一定参考依据。
方法 收集 2020.09-05-2020.12.31 期间送检我司布鲁菌抗体三项样本 1233 例样本结果数据进行分析。
结果 2020.09-05-2020.12.31 期间送检我司布鲁菌抗体三项样本 1233 例样本，其中布鲁菌 IGG 抗体检测阳性 351 例，阳性率为 28.47%；布鲁菌病虎红平板凝集试验阳性 263 例，阳性率为：21.33%；布鲁菌病试管凝集试验阳性 222 例，阳性率为：18.00%。其中 1233 例样本中三项全阳患者为 167 例，1233 例样本中两项全阳（含布鲁菌病试管凝集）患者为 38 例。由于无法逐一溯源患者的流行病史和临床表现，结合中华人民共和国卫生行业标准《WS 269-2019 布鲁氏菌病诊断》Diagnosis for brucellosis 标准，可以判断有 205 例患者感染布鲁氏菌。
结论 2020.09-05-2020.12.31 期间送检我司布鲁菌抗体三项样本 1233 例样本，感染布鲁菌的患者有 205 例，患者综合感染率为 16.63%， 需引起相关行业及医务人员的关注。

PU-3719

Bloodstream infection in hospitalized COVID-19 patients: a retrospective cohort study

Kewen Tang[2]、Congrong Li[1]
1. Renmin Hospital of Wuhan University
2. Renmin Hospital of Wuhan University

Background Bacteraemia is a global healthcare issue and continues to be the leading cause of death from infection. There is little information about the clinical characteristics of COVID-19 patients with bloodstream infections.
Objectives To describe the incidence of bloodstream infection (BSI) in hospitalized patients with COVID-19 and the clinical characteristics of these patients with BSI.
Methods In this retrospective study, one hundred and twenty-one COVID-19 patients who underwent blood culture tests in Renmin Hospital of Wuhan University from January 1st to June 30th, 2020 were included. We collected the clinical electronic medical records of these patients, and the data of demography, clinical symptoms, microbiology and clinical outcomes were compared and analysed.

Results The incidence of bacteraemia in patients diagnosed with COVID-19 was very low (1.23%). A total of 23 types of pathogenic bacteria were detected in patients with BSI, including 9 bacteria and 2 fungi. Compared with patients who without BSI, patients with BSI have significantly increased hospitalization time and mortality.
Conclusions Secondary bloodstream infection is not common in the diagnosis of COVID-19. These results may be crucial for determining the role of empirical antibacterial therapy or antibiotic management strategies, and suggest that we strictly abide by standard surveillance management practices and infection control protocols.

PU-3720

一例血培养胎儿弯曲菌引起的思考

王秀菊、单星星、赵水娣
南京金域医学检验所有限公司

目的 通过对一例送检三瓶血培养，在 120h 内仅有一瓶仪器报阳并鉴定出胎儿弯曲菌、另外两瓶“阴性瓶”经转种后均有胎儿弯曲菌生长的案例进行分析，思考怎样提高实验室关于血培养检出少见菌及疑难菌的能力。
方法 通过革兰染色涂片镜检及郑州安图质谱鉴定仪和法国梅里埃质谱鉴定仪认识胎儿弯曲菌，了解其生长特性，同时关注血培养仪检测原理及细菌生长曲线，对疑似“阴性瓶”进行验证。
结果 检出的细菌经过染色及质谱鉴定确认为胎儿弯曲菌，“阴性瓶”中生长的细菌经过确认与报阳瓶中结果一致，这是一例由胎儿弯曲菌感染所引起的菌血症。
结论 少见菌引起的血流感染常常由于细菌生长缓慢导致结果“假阴性”，实验室应当认真慎重对待每一个报阳血瓶及生长曲线，并关注感染病原体，发放出最值得有参考意义的检测报告单。

PU-3721

人型支原体对四环素、左氧氟沙星敏感性方法研究

王秀菊、单星星
南京金域医学检验所有限公司

目的 比较 CLSI-M43-A 琼脂稀释法（固体法）与支原体液体培养基法（液体法）测定人型支原体对四环素和左氧氟沙星的敏感性差异。
方法 选取从泌尿道中段尿、生殖道分泌物培养标本中分离的 20 株人型支原体菌株经质谱仪鉴定后，用固体法测定左氧氟沙星、四环素对这些人型支原体的最低抑菌浓度（MIC），并与液体法得出的结果进行比较。
结果 固体法显示四环素 MIC 值范围 0.125－1ug/mL，左氧氟沙星 1－32ug/mL。液体法显示 20 株人型支原体对四环素（TE）均敏感（S）；左氧氟沙星(LEV)6 例中介(I)14 例耐(R)。两种方法检测泌尿道和生殖道标本人型支原体对 TE、LEV 敏感性结果无明显差异。
结论 四环素对人型支原体仍保持较好的抗菌活性，左氧氟沙星的耐药性较高。固体法与液体法检测人型支原体对四环素、左氧氟沙星敏感性结果一致性较好，可以用液体培养基作为尿液标本中人型支原体的药敏检测方法。

PU-3722

Molecular epidemiology of Candida tropicalis isolated from urogenital tract infections

Qianyu Wang
Renmin Hospital of Wuhan University

Candida tropicalis is a common human pathogenic yeast, and its molecular typing is important for studying the population structure and epidemiology of this opportunistic yeast, such as epidemic genotype, population dynamics, nosocomial infection, and drug resistance surveillance. In this study, the antifungal susceptibility test and multilocus sequence typing (MLST) analysis were carried out on C. tropicalis from central China. Among 64 urogenital isolates, 45 diploid sequence types (DST) were found, of which 20 DSTs (44.4%) were new to the central database. The goeBURST analysis showed that CC1 (clonal complex) was the only azole-resistant (100%, 10/10) cluster in Wuhan, which was composed of DST546, DST225, DST376, and DST506, and most of the strains (90%, 9/10) were isolated from the urinary tract. Potential nosocomial infections were mainly caused by CC1 strains. The azole resistance rate of urinary isolates (50.0%, 21/42) was higher than that of vaginal isolates (27.3%, 6/22). The genotype diversity and novelty of vaginal isolates were higher than those of urinary isolates. C. tropicalis population in Wuhan was genetically diverse and divergent from that seen in other countries. In this study, there were significant differences in genotype and azole susceptibility between urine and vaginal strains. The azole-resistant cluster (CC1) found in urine is of great significance for the clinical treatment and prevention of nosocomial infection. The newly discovered DSTs will contribute to further study the similarity, genetic relationship, and molecular epidemiology of C. tropicalis worldwide.

PU-3723

血液中检出脓肿奴卡菌 1 例

杜赛君、单星星
南京金域医学检验所有限公司

目的 探讨基质辅助激光解吸电离飞行时间质谱（MALDI-TOF MS）对于奴卡菌属的快速鉴定，并分析奴卡菌的药敏结果，为临床诊疗提供依据。

方法 取阳性需氧血培养瓶中血液转种哥伦比亚血琼脂培养基和巧克力培养基后置于 35℃ CO2 环境进行培养。对培养后的细菌经涂片染色一系列试验后判断疑似为奴卡菌，再使用 MALDI-TOF MS 方法对于临床分离的疑似奴卡菌进行快速鉴定。

结果 本次我们报告一例乳腺癌术后合并脓肿奴卡菌血源性感染，鉴定为脓肿奴卡菌，置信度 9.195。药敏结果显示莫西沙星 2μg/ml，阿米沙星≤4μg/ml，利福平≤0.5 μg/ml，乙胺丁醇≥512μg/ml 左氟氧沙星 4μg/ml，克拉霉素 256μg/ml，异烟肼≥128μg/ml。选择敏感抗生素进行抗菌治疗后，感染症状得到有效控制。

结论 应用 MALDI-TOF MS 技术可快速鉴定临床分离疑似奴卡菌，指导实验室正确选择药敏试验，为临床提供感染诊断及药物治疗依据。

PU-3724

住院患者血流感染大肠埃希菌的实验室与临床分析

曹敬荣、王岩、陈典典、李文军、谢威、刘云屹、闵嵘、王培昌
首都医科大学宣武医院

了解住院患者大肠埃希菌血流感染的临床特点及实验室结果，为临床诊疗提供实验室依据。
方法 回顾性分析本院 2015 年 1 月至 2019 年 1 月大肠埃希菌血流感染患者的临床分布、耐药情况和实验室检查结果，并与同期血培养阴性患者实验室检查结果对比；比较感染产超广谱 β-内酰胺酶（ESBLs）大肠埃希菌组和非产 ESBLs 组）患者的耐药性及临床特征。
结果 四年间共收集 255 例大肠埃希菌引起血流感染患者，男 107 例（41.96%），女 148 例（58.04%），年龄 16-95 岁（平均 62.79±17.92 岁），≥60 岁占 63.14%（161/255）；产 ESBLs 大肠埃希菌占 57.14%，对呋喃妥因、阿米卡星和碳青霉烯类药物耐药率较低（＜10%）；患者总病死率为 5.49%（14/255），其中 ESBLs 组死亡率为 8.28%（12/145）远高于非产 ESBLs 组的死亡率 1.82%（2/110），差异有统计学意义（p＜0.05）；是否合并肾功能不全、机械通气、入住 ICU 是患者产 ESBLs 的危险因素（p＜0.05）。成对血培养阳性报警比率（56.79%）显著高于单需氧瓶（16.08%）和单厌氧瓶（20.39%）；成对报阳瓶中厌氧瓶先报阳的比率（64.81%）明显高于需氧先报阳（35.19%），差异有统计学意义（p＜0.05）；TTP≤24h 者占 95.29%（243/255），≤12h 者占 71.76%（183/255）。实验室检查白细胞、C 反应蛋白和降钙素原升高者分别占 44.31%、63.53%和 78.04%，高于同期血培养阴性者（p＜0.05）。
结论 大肠埃希菌血流感染分布广泛，血培养成套送检有助于提高阳性检出率，碳青霉烯类耐药菌的出现应引起重视。

PU-3725

SARS-COV2 神经系统相关症状研究进展

曹敬荣、凌佳意
首都医科大学宣武医院

新型冠状病毒肺炎目前已成为全球性重大的公共卫生事件，为结束当前疫情和获取未来防疫经验，深入了解 COVID-19 和 SARS-CoV-2 以成为当务之急。COVID-19 为急性呼吸道传染病，以发热、干咳、乏力为主要表现，除典型的呼吸系统症状，很多 COVID-19 患者表现出嗅觉、味觉减退、颅内出血等症状。本文探讨 SARS-CoV-2 对于神经系统的影响以及神经系统症状发生机制，SARS-CoV-2 具有神经侵袭性，可以至少通过神经途径和血行途径造成各种神经病变；SARS-CoV-2 诱导“细胞因子风暴”即对于 CNS 病毒感染的免疫反应，免疫应答水平的差异可能与 CNS 症状产生有关；小胶质细胞被认为是脑损伤和神经炎症事件的标志物，ENS 胶质细胞起到包括免疫调节和抗原呈递的作用，这些细胞的感染可能会产生合适的免疫反应，转而可能导致全身疾病的播散或者或细胞因子风暴。帕金森病，多发性硬化和发作性睡眠病等神经系统疾病的发病机制与神经系统症状产生机制存在关系。神经影像一般改变以及免疫抑制等情况对诊断用药产生了影响。

PU-3726

中枢神经系统感染主要病原菌的构成及药物治疗研究进展

曹敬荣、杨蕾
首都医科大学宣武医院

各种病原菌侵犯中枢神经系统可引起脑膜炎、脑炎、脓肿等各种感染性疾病，引起中枢系统功能障碍，严重威胁人类健康。严重者可出现菌血症、脓毒症等全身炎性反应症状，危及生命。因此对于发现是中枢神经系统感染的患者，应根据具体情况，及时进行抗感染治疗，保护中枢神经系统功能和避免全身炎症反应。本文主要讨论导致中枢神经系统感染的病原菌的构成和抗感染药物选择的研究进展。

PU-3727

碳青霉烯耐药高毒力肺炎克雷伯菌的耐药性与毒力研究进展

陈典典、曹敬荣
首都医科大学宣武医院

肺炎克雷伯菌是引起多种感染的常见致病菌，可通过获得耐药基因或毒力基因两种方式形成泛耐药高毒力肺炎克雷伯菌（extensively drug-resistant hypervirulent Klebsiella pneumoniae, XDR-hvKP）。相比于经典肺炎克雷伯菌，高毒力肺炎克雷伯菌（hypervirulent Klebsiella pneumoniae, hvKP）的感染程度更加严重。而随着碳青霉烯耐药肺炎克雷伯菌（Carbpenem resistant Klebsiella pneumoniae，CRKP）引起感染的增加，新出现的碳青霉烯耐药高毒力肺炎克雷伯菌（CR-hvKP）由于其高致病性和高耐药性，成为临床面临的一种新的“超级细菌”，CR-hvKP 感染病例的报道已出现并有逐渐增加趋势，位于可移动元件上的耐药基因与毒力基因在肺炎克雷伯菌中的传播会造成 CR-hvKP 在医院内或社区的流行，其危害和后果将更加严重，给临床治疗带来严峻挑战。本文从感染现状与危险因素、流行病学特征、耐药机制、毒力特点等方面对碳青霉烯耐药高毒力肺炎克雷伯菌进行综述，以期对临床防治该类细菌感染提供有用信息，使临床对其有更清楚的认识和根据其进化规律采取有效的预防手段。

PU-3728

成人和儿童中枢神经感染的差异研究进展

曹敬荣、宋妍
首都医科大学宣武医院

目的 研究中枢神经系统感染相关疾病中成人和儿童的差异，为临床诊治提供帮助。
方法 通过阅读大量文献，分析整理在中枢神经系统感染相关疾病中，成人和儿童在危险因素、流行病学等方面的差异之处。
结果 中枢神经系统感染相关疾病中，成人和儿童存在差异。危险因素方面，主要体现在感染方式的不同以及免疫因素对疾病的影响；流行病学方面，在细菌性脑膜炎患者中，可以看到明显的随年龄分布的病原体差异；结核性脑膜炎多见于 4 岁以下的儿童和老人，在成年人中主要是免疫抑制患者；病毒性感染，真菌性感染也各有其分布特征；临床表现方面，不同类型的中枢神经感染疾病在不同年龄患者中表现各异，缺乏特异性表现；检查手段方面，腰椎穿刺是目前中枢神经感染相关疾病鉴别病因方面的重要手段，病原学检查，影像学检查，特殊标记物等也发挥着不同的作用；诊疗过程方面，由于存在儿童和成人在上述的差异，在诊断流程自然方面存在着差异，更由于儿童的特

殊性，治疗往往也有所差异；在预后方面，成人中枢神经感染疾病相较儿童往往并发症更多，更严重，预后较为不良。而儿童主要应该考虑并发症对其未来生长发育和生活的影响。
结论 在中枢神经系统感染相关疾病中，成人和儿童在危险因素、流行病学、临床表现、检查手段、诊疗过程以及预后方面存在着差异，临床医生面对不同年龄的患者，应该结合病情，综合考虑。

PU-3729

Susceptibility Testing of Aspergillus against Mold-Active Antifungal Drugs Using the broth microdilution Methods of the Clinical and Laboratory Standards Institute and the European Committee on Antimicrobial Susceptibility Testing

Ying Li、Jingrong Cao、Rong Min、Peichang Wang
Department of Clinical Laboratory, Xuanwu Hospital, Capital Medical University, Beijing, China

Background Aspergillus is an important opportunistic pathogen with high morbidity and mortality among immuno-compromised patients. Antifungal susceptibility testing (AFST) based on broth microdilution method is recommended to detect the resistant isolates and provide informative message for the clinicians to choose the optimal treatment drugs.
Materials/Methods We compared three broth microdilution AFST methods, namely the two reference Methods of EUCAST E.DEF 9.3.1 and CLSI M38-A2 and the commercial method of Sensititre YeatOne for 289 isoaltes of clinically important Aspergillus species including A. fumigatus (n=141), A. flavus (n=83), A. niger (n=26), A. terreus (n=10), A. nidulans (n=15) and other 7 rare species (n=14) against amphotericin B, itraconazole, voriconazole, posaconazole, caspofungin and micafungin. The MIC50/MIC90 or MEC50/MEC90 were calculated for each species - antifungal agent combination. Differences in MICs or MECs of within ±1/±2 dilutions between the each two Methods were calculated to assess the agreement percent.
Results The MIC50/MIC90 values of the 289 isolates against the six drugs among the three AFST Methods in this study were quietly being close of ≤ 2 mg/L. The total agreement within ±1/±2 dilutions were 78.2%/93.7% between the CLSI and EUCAST Methods and 66.8%/91.1% between the CLSI and YeastOne Methods and 67.9%/82.6% between the EUCAST and YeastOne Methods The agreements on susceptibility classification of the tested isolates were 98.0% between the CLSI and EUCAST methods, 95.5% between the CLSI and YeastOne methods, and 94.1% between the EUCAST and YeastOne Methods In details, most of the categorical discrepancy concentrated on A. flavus - amphotericin B combination which YeastOne method mainly got MICs >2 mg/L for this group and categorized as being resistant according to the YeastOne's instruction while the other two Methods just got lower values of <2 mg/L as being susceptible.
Conclusions the agreements between the three AFST Methods are quiet good for Aspergillus especially on the triazoles susceptibility testing. However, extra notice should be paid when Sensititre YeastOne system was used to detect the susceptibility of amphotericin B for A. flavus, which may give higher MIC values than the two reference Methods

PU-3730

真菌性中枢神经系统感染的实验室检测进展

曹敬荣、葛小铭
首都医科大学宣武医院

中枢神经系统真菌感染在免疫力低下的人群中易感，发病率有逐年上升的趋势，常见的病原菌有新型隐球菌、念珠菌、曲霉菌、毛霉菌等。其病程长，复发率和死亡率高，早期病原体诊断对临床治疗具有重要指导作用。因大多数患者的临床症状不典型，传统病原体检测方法特异性有限，临床诊断和治疗较为困难。随着分子生物学的不断发展，基因测序、扩增等技术的逐渐成熟，聚合酶链反应、基因芯片等技术已经逐步运用到真菌性中枢神经系统感染的检测中。本文主要介绍了真菌性中枢神经系统感染的流行病学、实验室检测进展及这些检测方法的优缺点，并对未来真菌检测新技术的发展进行了展望。

PU-3731

Phosphorylcholine esterase plays a critical role in Dolichos biflorus agglutinin and Helix pomatia agglutinin binding to pneumococci

Menglan Zhou、Yingchun Xu
Peking Union Medical College Hospital

Background Streptococcus pneumoniae (pneumococcus) has lipoteichoic acid (LTA) and cell wall teichoic acid (WTA) expressing the Forssman antigen (FA), which is created when phosphorylcholine esterase (Pce) removes phosphorylcholine from GalNAcα1→3GalNAcβ1 at the non-reducing end of LTA/WTA. Dolichos biflorus agglutinin (DBA) and Helix pomatia agglutinin (HPA) are two lectins targeting FA, and may be useful in identifying pneumococcus.
Methods To investigate the usefulness of DBA for pneumococcal identification, 15 pneumococcal strains, including one non-encapsulated strain, were studied for DBA binding with flow cytometry and fluorescence microscopy.
Results Twelve strains were positive for DBA binding while three were negative. Structured illumination microscopy showed that DBA stained only the subcapsular area of pneumococci. The three DBA non-binders showed no Pce activity in vitro while the 10 DBA binders displayed Pce activity (the remaining two strains were DBA binders with no Pce activity in vitro). The pce gene sequence for 10 representative strains revealed two functional pce alleles, the previously recognized “allele A” and a newly discovered “allele B” (with 12 additional nucleotides). Isolates with allele B showed no Pce activity in vitro but did bind to DBA, indicating allele B Pce is functional in vivo. Genetic transfer experiments confirmed that either allele is sufficient (and necessary) for DBA binding. The three DBA non-binders had various mutations that affected Pce function. Observations with HPA were identical to those with DBA.
Conclusion We show that DBA and HPA fail to identify some pneumococcal isolates and that they bind only to the LTA/WTA of pneumococcal isolates with functional Pce.

PU-3732

Rapid identification of Streptococcus pneumoniae serotypes by cpsB gene-based sequetyping combined with multiplex PCR

Menglan Zhou、Xu Yingchun
Peking Union Medical College Hospital

Background/purpose Streptococcus pneumoniae is an important human pathogen that causes invasive infections in adults and children. Accurate serotyping is important to study its epidemiological distribution and to assess vaccine efficacy.
Methods Invasive S. pneumoniae isolates (n = 300) from 27 teaching hospitals in China were studied. The Quellung reaction was used as the gold standard to identify the S. pneumoniae serotypes. Subsequently, multiplex PCR and cpsB gene-based sequetyping Methods were used to identify the serotypes.Methods Based on the Quellung reaction, 299 S. pneumoniae isolates were accurately identified to the serotype level and 40 different serotypes were detected. Only one strain was non-typeable, and five most common serotypes were identified: 23F (43, 14.3%), 19A (41, 13.7%), 19F (41, 13.7%), 3 (31, 10.3%), and 14 (27, 9.0%). Overall, the multiplex PCR method identified 73.3 and 20.7% of the isolates to the serotype and cluster levels, respectively, with 1.7% of the isolates misidentified. In contrast, the cpsB sequetyping method identified 59.0 and 30.3% of the isolates to the serotype and cluster levels, respectively, and 7% were misidentified.
Conclusions The cpsB gene sequetyping method combined with multiplex PCR and the Quellung reaction can greatly improve the accuracy and efficiency of serotyping, besides reducing the associated costs.

PU-3733

Early Predictors of Severe COVID-19 Among Hospitalised Patients

Youhua Yuan、Wenjuan Yan、Qi Zhang、Baoya Wang
Henan Provincial People's Hospital

This study aimed to develop a reliable early prediction model for identifying who will develop severe illness from COVID-19 at hospital admission to ensure appropriate treatment delivery and optimal use of resources. In total, 52 and 64 severe and mild cases of COVID-19, respectively, were enrolled in this retrospective, multicentre, cohort study from January to March 2020. Least Absolute Shrinkage and Selection Operator (LASSO) and logistic regression were used to construct a predictive risk score. A prediction model was then developed and verified, using data from four hospitals in central China. Of the 50 variables assessed, 8 were identified as independent predictors and risk scores for severe COVID-19, including age (OR = 14.01, 95% CI 2.1–22.7), number of comorbidities (OR = 7.8, 95% CI 1.4–15.5), abnormal bilateral chest computed tomography images (OR = 8.5, 95% CI 4.5–10), lactate dehydrogenase (OR = 4.6, 95% CI 1.2–19.2), C-reaction protein OR = 16.7, 95% CI 2.9–18.9), neutrophil cell count (OR = 10.1, 95% CI 1.88–21.1), haemoglobin (OR = 16.8, 95% CI 2.4–19.1), and D-dimer (OR = 5.2, 95% CI 1.2–23.1). The model was effective, with an area under the receiver-operating characteristic curve of 0.944 (95% CI 0.89–0.99, $p < 0.001$) in the derived cohort and 0.8152 (95% CI 0.803–0.97; $p < 0.001$) in the validation cohort. The score has been translated into a nomogram risk calculator card that is freely available to the clinician. In **Conclusions** Predictors based on the characteristics of COVID-19 patients at the time of hospital admission may help in the early prediction of risk of developing critical illness later.

PU-3734

一种快速检测耶氏肺孢子菌的荧光定量 PCR 方法

许婉怡、杨洋、张磊、陈敬贤
广州金域医学检验中心

耶氏肺孢子菌是一种酵母样真菌，分布广泛。血清学研究表明 3-4 岁以上儿童大多已经受到暴露。耶氏肺孢子菌在正常健康人呼吸道中定植或引起无症状感染并不罕见，而在长期住院的病房里颇为常见。耶氏肺孢子菌通常在免疫受损病人中引起肺孢子菌肺炎，临床表现包括呼吸困难、发热、干咳等，胸部影像可见异常。肺孢子菌目前还未能体外培养，主要的实验诊断方法包括组织学检查（六胺银染色可见菌体包囊外壁）、免疫荧光染色、PCR 扩增病原体的核酸以及微生物宏基因组测序等。

为了能够快速地检出病人下呼吸道样品中是否存在耶氏肺孢子菌，并提高敏感性，我们建立了基于荧光探针的实时定量 PCR 法。该方法在 103～108 拷贝/微升范围有良好的线性范围，其最低检出量为 2000 拷贝/反应。干扰实验表明，B 族链球菌、肺炎链球菌、化脓链球菌、卡他链球菌、表皮葡萄球菌、金葡、肺炎克雷伯菌、铜绿假单胞菌、百日咳杆菌、D 群沙门氏菌、白念、光滑念、近平滑念、结核杆菌、烟曲霉、黄曲霉、黑曲霉、土曲霉，以及腺病毒、鼻病毒、副流感病毒、呼吸道合胞病毒对肺孢子菌实时定量 PCR 都没有干扰。

用本方法共分析了 190 例病人的肺泡灌洗液、深咳痰液或血液样品，其中 186 例同时做了六胺银染色。与六胺银染色的阳性率 4.3%相比，荧光 PCR 为 20.96%。PCR 阳性的标本包括 18 份肺泡灌洗液和 21 份深咳痰，没有在外周血标本中检出（仅 3 份样品）。总之，我们建立的耶氏肺孢子菌分子检测法特异性和敏感性高，能够从临床病人的样品中快速地诊断是否含耶氏肺孢子菌的 DNA。

PU-3735

MALDI-TOF MS 技术在侵袭性丝状真菌快速鉴定中的应用

宗来斌[1]、吕火烊[2]
1. 浙江大学医学院附属第四医院
2. 浙江省人民医院

目的 探索不同培养基、不同培养时间和不同蛋白质提取方法对侵袭性丝状真菌质谱鉴定准确率的影响，旨在提高 MALDI-TOF MS 技术鉴定侵袭性丝状真菌的准确率。

方法 采用分子生物学方法为金标准，同时运用 MALDI-TOF MS 技术对所收集临床丝状真菌进行鉴定。根据分子生物学的鉴定结果，去除 VITEK-MS V3.0 数据库中没有的菌株，其余菌株接种在三种不同的培养基中（SDA、PDA 和 CA），采用两种不同的蛋白质提取方法(甲酸乙腈法和磁珠法)，获得了不同培养时间点（2、3、5、7 和 9 天）的特异性质谱指纹图谱。

结果 不同丝状真菌蛋白质提取方法进行比较，甲酸乙腈法总鉴定准确率为 79.8%，磁珠法总鉴定准确率为 77.5%，两种丝状真菌蛋白质提取方法的质谱鉴定准确率无显著性差异（$\chi2 = 1.040$，$P = 0.308$）。不同培养基进行比较，SDA 培养基总鉴定准确率为 90.7%，PDA 培养基总鉴定准确率为 81.4%， CA 培养基总鉴定准确率为 67.4%，三种不同培养基的丝状真菌质谱鉴定准确率有显著性差异（$\chi2 = 36.609$，$P = 0.000$），其中使用 SDA 培养基鉴定准确率最高，使用 CA 培养基鉴定准确率最低。不同培养时间进行比较，丝状真菌培养 2 天、3 天、5 天、7 天和 9 天后的质谱总鉴定准确率分别为 64.3%、88.4%、89.1%、79.1%和 78.3%，不同培养天数的质谱鉴定准确率有显著性差异（$\chi2 = 32.274$，$P = 0.000$）。培养 3 天和培养 5 天的质谱鉴定准确率优于培养 7 天和培养 9 天的质谱鉴定准确率，培养 2 天的质谱鉴定准确率明显低于其它天数。

结论 侵袭性丝状真菌使用 SDA 培养基培养 3 天，运用甲酸乙腈法提取蛋白质进行质谱鉴定最理想。

PU-3736

杭州地区 2015-2019 年 356 例耐碳青霉烯类肠杆菌科细菌的分布特点和耐药性分析

翁远珍[1]、王欢[2]、单宇[2]、刘军权[1,2]
1. 杭州市下城区中西医结合医院
2. 杭州金域医检验所有限公司

目的 了解我院 2015-2019 年检出的 356 例耐碳青霉烯类肠杆菌科细菌（carbapenem-resistant Enterobacteriaceae，CRE）的分布特点和耐药性，以期为临床的抗感染与治疗提供依据。
方法 收集我院 2015-2019 年临床分离的 356 例碳青霉烯类肠杆菌科细菌及患者临床资料，对检出的 CRE 菌属分布、标本来源、检出病区、检出患者年龄分布和耐药性情况进行统计分析。
结果 2015-2019 年，我院共检出 CRE 菌株 356 例，总检出率为 5.62%，各年度 CRE 菌株检出率分别为 2.15%、3.97%、5.19%、6.95%、8.30%，呈逐年上升趋势。在检出的 356 株 CRE 菌株中，主要是肺炎克雷伯菌（66.6%）、大肠埃希菌（19.1%）两种菌株；标本主要来源是痰液（51.7%）、尿液（22.2%）、脓液及分泌物（6.4%）、血（6.4%）、胆汁（4.5%）；检出病区主要是重症监护室（43.8%）、儿科（18.0%）、泌尿外科（12.1%）、脑病科（10.4%）、呼吸内科（7.3%）；新生儿（9.06%）、老年人（6.05%）的 CRE 菌株检出率高于儿童（4.97%）和青少年人群（5.05%）；两种主要 CRE 菌株对阿米卡星、妥布霉素、庆大霉素较为敏感，对青霉素类、头孢类、氟喹诺酮类抗菌药物耐药率较高。
结论 耐碳青霉烯类肠杆菌科细菌检出率逐年升高，且对临床常见抗菌药耐药率普遍较高，临床中应加强耐药菌株的监测，合理选择使用抗菌药物，避免 CRE 的大规模传播。

PU-3737

杭州地区老年病医院 2017-2019 年 2097 例耐碳青霉烯类肠杆菌科细菌的分布特点和耐药性分析

单宇[1,2]、翁远珍[2]、刘军权[1]
1. 杭州金域医学检验所有限公司
2. 杭州下城区中西医结合医院

目的 探究杭州地区老年患者耐碳青霉烯类肠杆菌科细菌(carbapenem-resistant Enterobacteriaceae, CRE)的分布特点和耐药性状况，以期指导临床合理用药。
方法 收集 2017-2019 年杭州地区 60 余家老年病医院送检标本分离菌株，并采用 VITEK-2 Compact 全自动微生物分析系统和 K-B 法药敏纸片补充完善药敏结果，并分析耐碳青霉烯类肠杆菌科细菌的分布特点和耐药性。
结果 2017-2019 年，共检出肠杆菌科细菌 12819 株，含耐碳青霉烯类肠杆菌科细菌 2097 株，总检出率为 16.36%，且 CRE 检出率逐年上升；主要菌属为肺炎克雷伯菌(64.09%)和大肠埃希菌(18.74%)，各年中各菌属类型分布占比没有明显变化。产酸克雷伯菌、肺炎克雷伯菌、粘质沙雷菌、摩氏摩根菌 2017-2019 年总计耐药率均超过了 10%，肺炎克雷伯菌、大肠埃希菌、产酸克雷伯菌、摩氏摩根菌的耐碳青霉烯类药物耐药检出率日益增高。检出 CRE 菌株的标本类型主要是痰液(56.60%)和尿液(28.04%)，其次是咽拭子(6.15%)、全血(3.24%)、导管(2.72%)、脓液及分泌物(1.86%)。2097 株 CRE 对阿米卡星、庆大霉素、妥布霉素、环丙沙星、左旋氧氟沙星、复方新诺明、四环素等相对敏感，敏感率在 42.7~75.3%。
结论 杭州地区老年患者耐碳青霉烯类肠杆菌科细菌检出率呈逐年上升趋势，对多数临床常用抗菌药物敏感性呈逐年下降趋势，临床应加大对老年患者用药的重视程度并采取相应措施。

PU-3738

Enhancement in serum (1–3)-β-D-glucan level by cutaneous alternariosis: A case report and literature review

zongyao chen、yayun jiang、dengchao wang、mao zheng、xiao liu、chengliang yuan
People's Hospital of Deyang City

Objective Report a case of cutaneous alternariosis, to provide reference for the diagnosis and treatment of cutaneous alternariosis.
Methods Retrospective analysis of the diagnosis and treatment process of this case, this diagnosis was based on microscopic examination and mycological culturing of patient's vesicular lesions, with the use of 5 molecular markers (namely, ITS, ATPase, Actin, rpb2, and tef1) for strain identification. serum (1–3)-β-D-glucan (BG)assay was performed using a kit (Dynamiker Biotechnology [Tianjin] Co., Ltd.) based on spectrophotometry for the quantitative detection of BG in the human serum.
Results Microscopic examination of the blister fluid showed hyphae with light green, obtusely round at the top and slender at the end, the blister fluid was cultured on SDA at 28◦C for 3 days, we got the colony appeared round, grayish-green, margin regular, and fluffy. The strain was identified by sequencing for 5 phylogenetic markers, and the results from this 5 phylogenetic markers blast sequence alignment revealed that our strain highly matched A. alternata. The value of BG assay of the patient was >600 pg/mL. Repeated mycological culturing and BG assay were conducted 2 days later and obtained the same Results After pathogen identification, methylprednisolone therapy was discontinued and voriconazole
therapy was initiated. After 5 days, the blisters subsided, and the patient was discharged with improved symptoms; but he was continued on the oral voriconazole therapy. After 2 weeks, no recurrence of the skin infection of the limbs was noted.
Conclusion Alternaria often causes infection in immunocompromised people. In addition to histopathological examination and microbial culturing, the serum BG level detection can be used as a potential auxiliary diagnostic, albeit further research is required to validate and confirm its significance.

PU-3739

乙型副伤寒沙门菌致颈深部脓肿一例报道并文献复习

肖华亮
德阳市人民医院检验科

目的 促进检验科与临床科室之间的沟通，提高广大医务工作者对乙型副伤寒沙门菌导致颈部脓肿的认识。
方法 通过质谱鉴定技术和沙门菌特异性血清鉴定法对患者颈部脓肿所分离出测沙门菌进行分型，运用法国梅里埃 VITEK 2 Compact GN13 卡及纸片扩散法双复核的方式进行药敏试验，结合患者的病史及临床症状进行病例讨论，并对相关发病机制和文献进行复习。
结果 经过鉴定该患者颈深部脓肿分离出的是一株耐环丙沙星的乙型副伤寒沙门菌，由该患者病史推测患者可能进食被乙型副伤寒沙门菌污染的食物后，乙型副伤寒沙门菌侵入肠腔深部，通过淋巴管或血液向颈部等远处播散，同时也不排除通过患者口咽部间隙直接感染并扩散到颈部淋巴结，从而形成颈深部巨大脓肿。积极给予哌拉西林他唑巴坦联合奥硝唑抗感染治疗，患者治愈出院。同时查阅相关文献可知 2017 年我国西部地区沙门菌耐喹诺酮类药物的耐药率为 16.2%，高于同期全国水平。
结论 对于患有糖尿病的老年患者，存在沙门菌感染的高危因素，即使没有消化道症状也要考虑到沙门菌感染的可能，通过积极控制血糖、根据需氧或厌氧菌的鉴定及药敏结果调整抗菌药物、及时

清创引流等有效的诊治方法可明显降低患者的病死率。对于临床工作者，抗菌药物的选择要根据本地区或本单位的细菌耐药监测数据和患者感染的具体情况并结合相关指南综合考虑。对于检验工作者，更要积极的进入到临床疾病的诊治中，结合病史资料、临床症状等共同判断，不断提高微生物鉴定水平，用及时准确的药敏和鉴定技术为患者服务。

PU-3740

肺部念珠菌感染与定植--荧光 PCR 结合多种检测方法及患者转归前瞻性研究

欧阳津、龙军
南方医科大学珠江医院

目的 念珠菌广泛定植于呼吸道表面，但对于肺念珠菌感染与定植的界限，尚缺乏依据。
方法 采用念珠菌荧光 PCR 法，结合基因测序、荧光镜检（检测孢子和菌丝）、真菌培养、革兰氏染色、G 试验及临床抗真菌治疗效果，旨在研究肺部念珠菌感染与定植的关系，探寻检测肺部念珠菌感染的有效方法。纳入住院疑似肺部真菌感染重症患者 47 例，主要来源于 ICU 和呼吸内科，男 36 例，女 11 例；收集痰 13 例、纤支镜抽吸痰 22 例及肺泡灌洗液 12 例。
结果 念珠菌荧光 PCR 有 31 例阳性，其中强阳性 14 例（29.79%），中阳性 9 例（19.15%），弱阳性 8 例（17.02%），阴性 16 例（34.04%）。在念珠菌荧光 PCR 强阳性的 14 例中，有 13 例荧光镜检阳性，阳性符合率 92.86%。总阳性率为荧光 PCR（65.96%）>基因测序（57.45%）>荧光镜检（51.06%）>>革兰氏染色（19.15%）>培养（14.89%）>G 实验（14.29%）。治疗效果，弱阳性组和中阳性组缓解率分别为 62.50%和 77.78%，死亡率均为零；强阳性组缓解率为 50.00%，恶化及死亡率为 50.00%。荧光 PCR 阳性程度与念珠菌菌丝的发生呈正相关关系，与治疗缓解率呈负相关关系。
结论 念珠菌荧光 PCR 弱阳性和中阳性基本为念珠菌定植，强阳性肺部可能存在念珠菌感染，其感染率为 19.15%。应用荧光 PCR 法结合荧光镜检可以鉴别肺部念珠菌感染和定植，为临床抗真菌治疗提供依据。

PU-3741

建立基于流式细胞仪检测碳青霉烯类耐药菌的新方法

盛华芳、凌嘉慧、陈定强、周宏伟
南方医科大学珠江医院

目的 建立基于流式细胞仪检测碳青霉烯类耐药菌的新方法，为临床耐药菌的检测提供新的思路。
方法 基于 SYTO9 能够通过所有的细胞膜而 PI 仅能通过受损的细胞膜，故在两种染料的共同作用下，活菌仅能被 SYTO9 染上在激光激发下呈现绿色而 PI 则呈现红色的特性，通过流式细胞仪进行死活比分析。①选取肠道的常见菌群进行不同比例死活菌混合后染色分析；②选取敏感株及耐药株给予抗生素干预后染色分析。
结果 ①利用不同比例的死活菌混合染色分析后，对其进行曲线绘制，横坐标为混合的比例，纵坐标为流式细胞仪检测的比例，可以看见其基本接近，我们进一步对其进行了线性分析，其 R2 均大于 0.97，呈明显的线性关系。故可得出利用染色后流式细胞仪的信号分析能准确反应死活菌的比例。②在敏感株及耐药株的抗生素干预实验中，敏感株可见明显的总菌量减少及死菌增多，而耐药株则无明显变化，且随着浓度的增加，此趋势更加明显。故可知流式可区分碳青霉烯耐药菌及敏感菌。

结论 染色后流式细胞仪的信号分析能够帮助我们获取单菌株甚至菌群的活性分析，在此基础上还可以对耐药菌及敏感菌在流式上呈明显的区分，为传统的药敏实验提供新的思路。

PU-3742

利用阿拉伯糖甘露糖脂检测结核分枝杆菌的 meta 分析

周妍冰、吕梦媛、王义莉、应斌武
四川大学华西医院

目的 采用 Meta 分析的方法综合评价阿拉伯糖甘露糖（lipoarabinomannan，LAM）在结核病中诊断价值。LAM 是一种结核分枝杆菌（mycobacterium tuberculosis，MTB）包膜上的糖脂成分，LAM 的检测可直接提示结核分枝杆菌的活跃感染。因此本研究通过 Meta 分析探究 LAM 在结核感染中的诊断性能。
方法 通过检索 3 个数据库中的文献（PubMed，OVID 和 Web of Science），制定文献的纳入排除标准。提取纳入研究的特征信息，并对纳入文献使用 QADAS-2 进行质量评估。使用 Review Manager Version 5.3 和 STATA Version 15 对提取的纳入文献特征进行分析。并评估发表偏倚，检验研究间的异质性，Meta 回归用来分析异质性的来源。
结果 检索了相关文献 1,830 篇，最终纳入了 159 个研究。将纳入研究根据检测 LAM 的方法不同分为 5 个亚组。其中 80 个研究使用了胶体金的方法检测 LAM，特异性为 0.89，敏感性为 0.43，71 个研究使用了 ELISA 的方法，特异性为 0.92，敏感性为 0.52。其他 27 个研究使用包括电化学发光等方法。Meta 回归探究显示，LFA 检测 LAM 的异质性主要来源于纳入患者的的 CD4 计数中位数不同，样本类型不同等，种族也影响了研究的异质性。ELISA 检测 LAM 的异质性主要来源于 ELISA 商品化试剂盒的厂家以及种族和样本类型。
结论 使用 ELISA 检测 LAM 的方法特异性很高，尤其是在血清标本中，并且不同的生产厂家 ELISA 的检测性能也有一定的差距。LFA 虽然灵敏度和特异性稍差，但其操作简便，适用于尿液标本，可以实现床旁检测。因其具有操作简便及较好的诊断性能，因此 LAM 检测是结核患者的有效辅助诊断手段。

PU-3743

应用脉冲场凝胶电泳方法和 MALDI-TOF RUO 模式对临床分离的肺炎克雷伯菌进行同源性分析和方法比较及耐药表型研究

傅俊方
南方医科大学珠江医院

目的 脉冲场凝胶电泳（Pulse-field gel electrophoresis, PFGE）方法是微生物分型的金标准。本研究希望利用 MALDI-TOF RUO 模式来对想要进行流行病学相关研究的细菌进行初筛，通过聚类分析，筛出认为可能有研究意义的菌株，再利用其他的方法做进一步的验证。
方法 收集 2013 年 4 月至 2013 年 10 月分离的肺炎克雷伯菌 29 株，进行脉冲场凝胶电泳分析其同源性。同时，再利用 MALDI-TOF RUO 模式进行质谱检测，得到的结果进行聚类分析，得到聚类分析图。此外，采用 VITEK-2 微生物鉴定系统测定其对 18 种抗生素最低抑菌浓度。
结果 29 株肺炎克雷伯菌实验菌株种，经过 PFGE 指纹图谱分析，分为 21 个基因型。其中 11 株 PFGE 图谱分为 A 型（5 株）、B 型（4 株）、C 型（2 株）。其中的 11 株肺炎克雷伯菌虽然并非全部为 ESBLs 株，但其对青霉素类、头孢菌素类以及单环内酰胺类耐药率为 100%，对碳青霉烯类耐药率为 27.3%，对环丙沙星耐药率为 27.3%，对左氧氟沙星保持敏感，对丁胺卡那霉素、庆大霉素、妥布霉素耐药率分别为 45.5%、54.5%、90.9。MALDI-TOF RUO 模式得到的聚类分析图显示的分类结果与 PFGE 方法得到的结果没有明显的统一性，利用 PFGE 分为同一型的菌株，在

MALDI-TOF RUO 模式下未能分到同一类，可能的原因为两者在原理上的差异，以及 MALDI-TOF RUO 模式的数据分析软件需进一步更新完善。但 MALDI-TOF RUO 模式下得到的聚类分析结果具有初步的参考意义。
结论 脉冲场凝胶电泳方法是分型的金标准，MALDI-TOF RUO 模式对研究细菌分型具有一定的意义。

PU-3744

环介导恒温扩增芯片法在 AECOPD 伴感染患者可疑病原体检测中的应用价值

陶建霞
四川大学华西医院

目的 探讨环介导恒温扩增芯片法（LAMP）在慢性阻塞性肺疾病急性加重（AECOPD）伴感染患者可疑病原体检测中的应用价值。
方法 收集我院 2019 年 2 月至 2020 年 5 月收治的 159 例 AECOPD 伴感染患者的下呼吸道合格标本，同时进行 LAMP 检测和病原体分离培养，分析两种方法呼吸道病原体检出情况并比较。
结果 159 例标本中，LAMP 检测出呼吸道病原体的阳性标本 58 例，总阳性率 34.3%，其中单一病原体 46 例（77.6%），混合病原体 13 例（22.4%）；共检出 10 种呼吸道病原体，鲍曼不动杆菌检出率最高（13.8%），其次为铜绿假单胞菌（9.4%）；检出结核分枝杆菌复合群 6 例。159 例标本同时进行病原体分离培养，培养阳性 48 例，阳性率 30.2%，其中鲍曼不动杆菌 18 例（11.3%），铜绿假单胞菌 12 例（7.5%）。对两种方法检出呼吸道病原体的检出率进行比较，除大肠埃希菌外，其他细菌的检出率均有差异，差异具有统计学意义。
结论 对于 AECOPD 伴感染患者可疑病原体检测，呼吸道病原体 LAMP 十三联检操作简便快捷，常见病原体检出率高于分离培养法。

PU-3745

CD248 抗体干预小鼠肾纤维化形成的实验研究

刘婉婷
南方医科大学珠江医院

目的 本研究拟以小鼠肾纤维化模型为研究对象,输注 CD248 单克隆抗体,检测纤维化相关指标,探讨 CD248 在纤维化中的作用机制。
方法 1.建立叶酸肾纤维化小鼠模型:将 C57BL/6 小鼠随机分为正常对照组和叶酸(Folicacid, FA)组,分别予以腹腔注射 NaHC03 或者叶酸(剂量 250mg/kg)。在注射叶酸后第 3、14 和 28 天处死小鼠,检测血肌酐和尿素水平,免疫组化检测肾组织 a-SMA、Collagen Ⅰ、Fibronectin 以及 CD248 蛋白表达水平。
结果 1.与正常对照组比较,FA3 天、FA14 天和 FA28 天叶酸模型组血肌酐和尿素水平显著升高（P<0.05）,肾纤维化程度逐渐加重,肾组织 α-SMA、Collagen Ⅰ、Fibronectin 以及 CD248 蛋白表达均显著升高。
结论 1.成功建立叶酸肾纤维化小鼠模型。2.CD248 抗体干预能够改善纤维化程度,CD248 可能成为纤维化诊疗的重要靶点。

PU-3746

新型冠状病毒血清特异性抗体检测技术应用探讨

宁雅婷、徐英春、侯欣、陆旻雅、吴宪、李永哲
中国医学科学院北京协和医院

新型冠状病毒肺炎疫情发展迅速，早期诊断成为疫情防控的关键。2019 新型冠状病毒（2019 novel coronavirus，2019-nCoV）核酸检测阳性虽是疑似患者确诊的“金标准”，但其操作繁琐、耗时长，检测结果受抗本质量、病毒感染部位及表达量等众多因素影响，因而核酸单项检测不能满足疫情期间对疑似病例快速筛查的要求。血清特异性抗体是诊断病毒感染的另一关键证据，抗体检测可协同核酸检测用于辅助诊断和快速筛查。本文从抗体产生特点、检测方法及灵敏度/特异度、检测结果假阴性/假阳性及核酸与抗体联合检测等方面进行讨论，以期推动 2019-nCoV 血清抗体检测技术的建立与应用。

PU-3747

呼吸道感染儿童血清维生素 D 水平与体液免疫情况分析

范文廷
徐州医科大学附属医院

目的 研究维生素 D 对体液免疫及儿童呼吸道感染的影响，为临床治疗与预防儿童呼吸道感染提供实验依据和线索。
方法 收集呼吸道感染儿童（感染组）与正常体检儿童（对照组）的外周血及一般资料。检测分析感染组与对照组儿童血清维生素 D 水平，血清抗体 IgG、IgM 和 IgA 水平的差异。
结果 共收集了 961 例呼吸道感染儿童与 120 正常体检儿童的资料，两组在性别分布上无统计学差异。感染组儿童的血清维生素 D 水平（25.58±12.55）显著低于对照组儿童（36.23±8.92, t=9.01，P<0.05），儿童血清维生素 D 缺乏与不足与呼吸道感染存在一定的联系（）。感染组儿童血清 IgG 和 IgA 含量显著低于对照组儿童（t=3.706,P<0,05;t=4.687，P<0.05），而 IgM 两组儿童相比差异无显著性（t=1.587, P=0.11）。儿童血清维生素 D 水平与免疫球蛋白 IgG、IgA、IgM 含量呈正相关（）。
结论 儿童血清维生素 D 的缺乏与儿童呼吸道感染有相关性，可能是低维生素 D 儿童体内免疫球蛋白水平较低所致。

PU-3748

Aspartate aminotransferase and Lactate dehydrogenase predict the severity of COVID-19: lessons from a front-line primary hospital

Wenting Fan
Department of Laboratory Medicine, Affiliated Hospital of Xuzhou Medical University,

Objective Since December 2019, coronavirus disease 2019 (COVID-19) caused by a novel coronavirus emerged in Wuhan and rapidly spread around the world. The predictors of the severity of COVID-19 remain unclear.
Methods The aim of our study was to determine the biomarkers of severe COVID-19 in a front-line primary hospital. Clinical data from 109 COVID-19 patients admitted to the People’s Hospital of Gongan County, Hubei Province, China, from January 19, 2020, to March 5, 2020, were

collected. The general status, clinical manifestations, laboratory tests and radiologic findings of non-severe and severe patients were analyzed.
Results Decreased lymphocytes (LYM) and albumin (ALB), elevated alanine aminotransferase (ALT), aspartate aminotransferase (AST), lactate dehydrogenase (LDH), D-Dimer, fibrinogen (FIB), C-reactive protein (CRP) and erythrocyte sedimentation rate (ESR) were observed in severe COVID-19 patients. AST and LDH were main predictors related to the severity of COVID-19, and a positive correlation was observed between the two markers. The combined use of LDH and AST showed a sensitivity of 88.9% and specificity of 91.0%.
Conclusions Abnormal blood biochemical tests were more frequent in COVID-19 patients with severe pneumonia than patients with non-severe pneumonia. High levels of AST and LDH were positively related to the severity of COVID-19. Thus, AST and LDH may be used as considerable predictors of COVID-19 prognosis in primary hospitals.

PU-3749

Seroprevalence of Talaromyces marneffei Mp1p specific antibodies in HIV infected patients during 2004-2011 in Guangzhou, China.

Yanfang Wang[1]、Zhigang Han[2]、Caiyun Liang[2]、Huifang Xu[2]
1. 南方医科大学珠江医院
2. 广州市疾病预防控制中心

Seroprevalence of Talaromycosis marneffei infection by antibody response is not known in human immunodeficiency virus (HIV) infected patients. This retrospective study aimed to evaluate the seroprevalence of and risk factors for T.marneffei infection in HIV-infected patients during 2004-2011 in Guangzhou, China. We tested 8131 archived HIV-infected patient serum samples for T.marneffei-specific mannoprotein (Mp1p) antibody using double antigen sandwich ELISA we previously established. The CD4+T cell of 2686 cases was determined by flow cytometry. Logistic regression was used to assess predictors of Mp1p antibody. The overall seroprevalence of talaromycosis as detected by positive serum Mp1p antibody was 2.82% (229/8131). There was no significant difference among 8 years and months. Talaromycosis was strongly associated with AIDS related. (P<0.001), and slightly associated with sex(male) (OR 0.55, 95%CI 0.37-0.78，P=0.001), age (OR 1.01，95%CI 1.00-1.02，P<0.05) . For 2686 cases with known CD4 cell count, 5.09% (67/1315) of patients developed T.marneffei-specific antibody when CD4 count of <200 cell/μL. In conclusion, approximately 2.82% of the HIV-infected patients in our study developed T.marneffei-specific antibody. A joint application of Mp1p antigen and antibody test, a prevalence of 11.89% (967/8131) for talaromycosis in HIV-infected patients.

PU-3750

慢性粒单核细胞白血病伴马尔尼菲篮状菌合并新泻诺卡菌感染一例

赵燕、王艳芳
南方医科大学珠江医院

目的 马尔尼菲篮状菌是一种机会致病真菌，长期以来一直被认为是艾滋病患者的标志性感染，近年来，其在血液恶性肿瘤患者人群中的感染逐渐被重视。目前对马尔尼菲篮状菌病的诊断主要依赖于病原学诊断，由于病理活检是有创操作，培养阳性率不高且耗时较久，常造成患者治疗的延误而

影响预后。本研究报告一例慢性粒单核细胞白血病患者发生的马尔尼菲篮状菌感染，旨在通过报告此病例对马尔尼菲篮状菌感染的诊疗提出建议。
方法 报告一例慢性粒单核细胞白血病患者发生的马尔尼菲篮状菌血流感染。
结果 患者为一位 71 岁的老年男性，入院前 10 天出现了脚疼、乏力、纳差，患者 10 年前具有肺结核病史，入院时左足局部脓肿，胸片提示肺部感染，在下级医院抗细菌治疗效果不佳，因此在入院后即送检了真菌感染相关指标如半乳甘露聚糖检测、隐球菌荚膜抗原检测等，抽取了静脉血进行培养，同时穿刺取左足脓肿脓液进行涂片及培养。最终，患者艾滋病抗体检测结果是阴性的，骨髓穿刺明确了慢性粒单核细胞白血病的诊断。脓液涂片见革兰氏染色阳性的丝状杆菌，培养 3 天后被鉴定为新泻诺卡菌，静脉血培养提示了马尔尼菲篮状菌的生长。另外，该患者曲霉半乳甘露聚糖抗原检测结果为：GMI=0.463。住院期间应用了莫西沙星、卡泊芬净、泊沙康唑等抗菌药物，遗憾的是，患者最终放弃治疗。
结论 下级医院对真菌感染如马尔尼菲篮状菌感染的认识不够，马尔尼菲篮状菌和曲霉属真菌细胞壁均存在半乳甘露聚糖而可使 GM 试验呈现阳性，但本例中检测结果未升高，快速诊断试验存在一定的局限性，因此还是要联合培养、病理等对患者情况作出正确判断，针对马尔尼菲篮状菌的敏感而特异的快速诊断试验仍需要进一步的研究开发。

PU-3751

Colistin resistance due to site mutations of the mgrB gene in carbapenem-resistant Klebsiella pneumoniae of clinical origin: first report from Jiangsu province, China

Shulong Zhao
Laboratory Department of Affiliated Hospital of Xuzhou Medical University

Objectives To investigate the molecular mechanism of colistin resistance in clinically isolated carbapenem-resistant Enterobacteriaceae (CRE).
Methods Clinical isolates of Enterobacteriaceae with colistin resistance from May 1st, 2018 to July 31st, 2019 were collected from the Affiliated Hospital of Xuzhou Medical University. Minimum inhibitory concentrations (MICs) of all isolated strains were determined by using the broth microdilution method. The existence and mutations of mgrB and mcr-1 genes were then detected by gene sequencing.
Results A total of 10 colistin resistant strains were collected, five of which were Escherichia coli and contained the mcr-1 gene, and the other five strains were Klebsiella pneumoniae, in which point mutations of mgrB gene were identified by comparison with sensitive strains.
Conclusion Point mutations in mgrB gene lead to the inactivation of mgrB, which plays an important role in the molecular mechanism of polymyxin resistance of Klebsiella pneumoniae.

PU-3752

耐碳青霉烯类革兰氏阴性杆菌分布及耐药机制研究

曹希武
南方医科大学珠江医院

目的 碳青霉烯类是菌 β-内酰胺类抗生素，由产生超广谱 β-内酰胺酶（ESBL）的细菌 引起的在严重感染中具有良好的功效。 例如亚胺培南，美罗培南，多利培南，厄他培南， 帕尼培南和比阿培南，然而，全球范围内肠杆菌科细菌对头孢菌素类抗生素的耐药性逐渐 上升。细菌通过水解碳青霉烯类抗生素，产生了新的耐 β-内酰胺酶的机制，使抗生素治疗 的选择越来越少。

方法 碳青霉烯耐药性是全球范围内一个持续存在的公共卫生问题。 它主要发生在革 兰氏阴性杆菌中，如肺炎克雷伯菌，铜绿假单胞菌和鲍曼不动杆菌等，可能是由固有的或 可转移的碳青霉烯酶编码介导基因。 这种抗性基因已经在世界某些地区广泛传播，特别是 欧洲，亚洲和南美，而其他地区（如撒哈拉以南非洲）的情况目前并不清楚。 在本文中， 我们将提供对碳青霉烯类药物耐药性有关的最新信息。
结果 细菌耐药对公共健康的威胁越来越大，其中包括耐碳青霉烯酶的肠杆菌科细菌 （CRE）在社区中的迅速传播。多重耐药的革兰氏阴性细菌，例如不动杆菌和假单胞菌属， 是造成医院感染的主要病原菌。 这些微生物也有可能将对细菌的抗性传播到社区。 尽管 要控制碳青霉烯的耐药性，但解决该问题的方法仍在积极探索中。
结论 碳青霉烯酶编码基因已经在世界某些地区广泛传播，特别是，欧洲，亚洲和南 美，而其他地区（如撒哈拉以南的非洲）的情况却并不明确，需要监测碳青霉烯酶编码基 因来控制细菌耐药性的传播。

PU-3753

安图 ms 1000 与梅里埃 VITEK MS 质谱仪鉴定准确性对比研究

王淋荆
南方医科大学珠江医院

目的 对比安图 ms 1000 全自动微生物质谱检测系统与梅里埃 VITEK MS 全自动快速微生物质谱检测系对于临床微生物菌株鉴定的准确性。
方法 本研究采用 334 株临床菌株和 17 株标准菌株分别用安图 ms 1000 全自动微生物质谱检测系统与梅里埃 VITEK MS 全自动快速微生物质谱检测系统做鉴定，以梅里埃 VITEK MS 结果为参考，两者鉴定不一致的菌株采用 16SRNA 测序定鉴定，将测序结果在 NCBI blast 数据库做比对，以得分率最高的菌株未参考标准，评价两种质谱仪的鉴定准确性。
结果 准确性试验共采用 351 株（涵盖革兰氏阴性杆菌阳、阳性杆菌、阳性球菌、阴性球菌、酵母样真菌），其中标准菌株 17 株,临床菌株 334 株，17 株标准中菌株安图质谱 Autof ms1000 属水平鉴定一致性为 100%，种水平鉴定一致性为 100%，334 株临床菌株中安图质谱 Autof ms1000 属水平鉴定一致性为 99.40%，种水平鉴定一致性为 97.31%。而安图 ms 1000 全自动微生物质谱检测系统重复性、样本新鲜度的测定结果准确性均为 100%。
结论 安图质谱 Autof ms 鉴定准确性优于 1000 梅里埃 VITEK MS

PU-3754

肺诺卡菌病 5 例实验室检查分析

蒋苏苏
南方医科大学珠江医院

目的 提高对肺诺卡菌病的认识以及诊疗水平。
方法 收集南方医科大学珠江医院 2018-2020 年确诊的诺卡菌肺部感染病例 5 例，回顾性分析患者的临床资料， 包括人口统计学、临床表现、影像学检查、实验室检查、治疗方法及预后。
结果 5 例患者中男性患者有 3 例，女性患者 2 例，年龄在 31~63 岁不等；基础疾病分别为支气管扩张症 3 例，非霍奇金淋巴瘤异基因造血干细胞移植术后 1 例，慢性阻塞性肺病 1 例；患者的常见临床表现依次为咳嗽、咳痰、发热、咯血、呼吸困难以及乏力，2 例外周血白细胞和中性粒细胞升高，3 例外周血白细胞和中性粒细胞正常； 3 例抗酸染色弱阳性，另 2 例未查；2 例弱抗酸染色阳性，3 例未查； 4 例痰培养诺卡菌阳性，1 例肺泡灌洗液培养阳性；鉴定结果为烯蓓诺卡菌 1 例，

乔治教堂诺卡菌 2 例，未分型诺卡菌 2 例；患者均单独或联合使用头孢哌酮/他唑巴坦或哌拉西林/他唑巴坦和复方磺胺甲噁唑抗感染；5 例患者均经治疗后病情好转。
结论 肺诺卡菌病的临床表现和影像学表现均为非特异性表现，临床很难依靠这些表现准确诊断肺诺卡菌病，目前主要依靠实验室检出诺卡菌来明确诊断。

PU-3755

Clinical Characteristics and Virulence Gene Analysis of Pseudomonas aeruginosa in Bloodstream Infections

Xin Li
The Second Hospital of Anhui Medical University

Introduction We aimed to explore the clinical characteristics and isolate, type III secretion system (T3SS) genotypes of patients with bloodstream infection due to community-acquired Pseudomonas aeruginosa (CA-PA) or hospital-acquired P. aeruginosa (HA-PA), and to analyse the differences in risk factors between them.
Methodology Clinical data were collected from 2015-2019. We designated two groups: CA-PA and HA-PA. The clinical characteristics, drug sensitivity data, and T3SS genotypes were compared. The χ2 test and χ2 trend tests were used to analyse the data, and logistic regression was used to analyse the independent risk factors of the two groups.
Results P. aeruginosa was collected from 89 patients, including 43 patients with CA-PA and 46 patients with HA-PA. Most patients with CA-PA were ≥ 60 years old, accompanied by diabetes mellitus and kidney disease, and susceptible to catheter-associated infection. Hospital stay ≥ 15 days, mechanical respiration, and prior antibiotic treatment readily led to HA-PA bloodstream infection. HA-PA bloodstream infection was often complicated with other bacterial infections. Most P. aeruginosa isolates were drug sensitive, and the CA-PA resistance rate to imipenem was lower than that of HA-PA (P = 0.038). CA-PA carried mainly exoS and HA-PA and multidrug-resistant P. aeruginosa (MDR-PA) carried mainly exoU.
Conclusions The CA-PA and HA-PA risk factors and imipenem resistance rates differed. The T3SS virulence genes in the two groups also differed. Further research is needed to elucidate the relationship between the T3SS and disease.

PU-3756

金黄色葡萄球菌临床检测方法的研究

黄婉婷
吉林金域医学检验所有限公司

目的 本文对目前金黄色葡萄球菌的检测方法进行综述，目的是对金黄色葡萄球菌进行快速有效的检测和精准的鉴定，为临床实验室检验提供参考和指导。
方法 通过查阅大量文献及对实验室日常检测方法进行分析，总结出金黄色葡糖球菌的临床检测方法。
结果 1.常规检测方法包含直接涂片染色法和细菌培养与鉴定 。
2.快速检测法包含免疫学方法和分子生物学方法。其中免疫学方法包含乳胶凝集法，酶联免疫吸附法，化学发光酶联免疫检测法。分子生物学方法则包含多重 PCR 技术，实时荧光定量 PCR，环介导等温扩增技术，基因芯片技术检测 。
3.其他快速检测方法则有显色培养基，快速测试片，生物传感器技术，计算机视觉技术。
结论 该菌常规培养鉴定法检测成本较低，是临床最为常用普遍方法。但这种方法操作时间长，已经不能适应当代临床实验室快速检测的大环境。免疫学方法使用将抗原和抗体相结合的方式，但存

在假阳性或假阴性结果。PCR 检验结果准确，从分子水平定性，实验时间缩短 50%以上，明显节约了成本，但容易出现外源 DNA 的污染。LAMP 易于操作，提高了金黄色葡萄球菌的检测灵敏性，具有良好的前景。该细菌在未来临床检验的发展趋势是准确，方便和快速。以常规检测方法为基础，结合快速检测方法对细菌进行有效检测，特别是分子生物学方法，在基因的角度，提供了新的检测手段，极大推动了对该细菌的检测手段，现如今计算机视觉技术以及生物传感器检测等方法也逐步走向成熟。

PU-3757

Two rapid protein extraction Methods using focused-ultrasonication and zirconia-silica beads for filamentous fungi identification by MALDI-TOF MS

Yating Ning[1,2]、Wenhang Yang[1,2]、Li Zhang[2]、Yingchun Xu[2]
1. Graduate School, Peking Union Medical College, Chinese Academy of Medical Sciences, Beijing 100730, P. R. China
2. Beijing Key Laboratory for Mechanisms Research and Precision Diagnosis of Invasive Fungal Diseases, Beijing, China.

Filamentous fungi identification by Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) has been challenging due to the lack of simple and rapid protein extraction Methods and insufficient species coverage in the database. In this study, we created two rapid protein extraction Methods for filamentous fungi: an one-step zirconia-silica beads (ZSB) method without using a homogenizer and a focused-ultrasonication method (FUS). The two rapid sample processing Methods were evaluated with the VITEK MALDI-TOF MS (bioMérieux, Marcy-l'Étoile, France) and compared to the routine method. The more efficient method was applied as a means to build a filamentous fungi in-house spectra library for the M-Discover 100 MALDI-TOF MS (Zhuhai Meihua Medical Technology Co., Ltd., China). The routine method was then performed in parallel to verify the accuracy and commonality of the in-house library. Two rapid Methods were evaluated using 123 filamentous fungi isolates belonging to 13 genera and 29 species by VITEK MS with the commercial database v3.2 and compared to the routine method. Both ZSB and FUS Methods identified isolates from most mold types equal to or better than the routine method, and the total correct identification rate using VITEK MS was 79.67%, 76.42%, and 76.42%, respectively. An in-house library of M-Discover MS was built with 135 isolates from 42 species belonging to 18 genera using the ZSB method. Analysis of 467 isolates resulted in 97.22% correctly identified isolates to the species level by the ZSB method versus 95.50% by the routine method. Using the two optimized methods, the dedicated operating time before MALDI-TOF MS analysis was reduced from 30 min (routine method) to 7 (ZSB) or 5 (FUS) min per sample, with only a few seconds added for each additional strain. The two novel Methods are time- and cost-effective and allow efficient identification of filamentous fungi while providing a simplified procedure to build an in-house library. Thus, more clinical laboratories may consider adopting MALDI-TOF for filamentous fungi identification in the future.

PU-3758

自身抗体对甲苯胺红不加热血清试验检测结果的影响分析

黄学东[1]、杨翠丽[2]、侯晓芹[3]、李冬冬[1]、胡静[1]、牛倩[1]
1. 四川大学华西医院
2. 新疆医科大学第一附属医院昌吉分院
3. 四川省老年病医院·四川省第五人民医院

目的 探讨不同类型的自身抗体对甲苯胺红不加热血清试验（TRUST）检测结果的影响，为梅毒相关临床诊疗实践提供参考依据。
方法 纳入 2020 年 3 月至 7 月于我院进行抗核抗体（Antinuclear antibody，ANA)、抗心磷脂抗体（anti-cardiolipin antibody，ACA）、抗可溶性抗原可提取性核抗原（extractable nuclear antigen，ENA）抗体、狼疮抗凝物（lupus anticoagulant，LA）检测且具有阳性结果的患者 140 例，以及性别、年龄匹配且上述自身抗体检测阴性的健康对照者 107 例，收集血清样本进行 TRUST 和梅毒螺旋体颗粒凝集试验（TPPA）检测，当 TRUST 阳性而 TPPA 阴性时认为 TRUST 为假阳性结果，分析不同类型自身抗体导致 TRUST 假阳性的情况。
结果 病例组中 TRUST 阳性患者有 17 例（12.14%），阳性率明显高于健康对照组（0.00%）（P＜0.05）。17 例 TRUST 阳性患者的 ANA 均为阳性，其中，ANA 单阳性者 5 例、ANA+ENA 双阳性者 8 例、ANA+ENA+ACA+LA 均阳性者 4 例。17 例患者中 1 例经 TPPA 和临床确诊为梅毒患者，其 TRUST 滴度为 1:8；其余 16 例患者经 TPPA 验证均为 TRUST 假阳性，其 TRUST 滴度分别为 1:1 阳性 15 例和 1:2 阳性 1 例。
结论 自身抗体如 ANA 的存在可导致 TRUST 试验出现低滴度（≤1:2）假阳性，因此，在诊断梅毒相关疾病时应结合流行病学、临床表现及其他血清学检测结果，降低误诊率，提高诊断水平。

PU-3759

Complete genome comparative analysis of CV-A6 causing Hand, foot and mouth disease and Herpangina in Yunnan province

Hongchao Jiang、Jiaollian Tang、Xiaolin Zhang
KUNMING CHILDREN'S HOSPITAL

Objective to understand the genome characteristics of CV-A6（Coxsackie virus A6） strains causing Herpangina (HA) and Hand，foot and mouth disease(HFMD), so as to explore the possible reasons for the difference of clinical symptoms between HA and HFMD.
Methods 9 strains of CV-A6 causing HFMD and 8 strains of CV-A6 causing HA from Kunming children’s Hospital in Yunnan Province were selected for genome-wide characterization.Positive samples were screened for sequencing using enterovirus group A universal primers, samples that were CV-A6 after alignment by NCBI, and 17 CV-A6 strains that caused HA and HFMD were randomly selected for sequence amplification using whole genome primers, and sequencing was spliced to generate whole genome analysis using BioEdit, MEGA7.0, SimPlot, Heml1.0 and Phyre2 were used for analysis of genome characteristics.
Results The results showed that CV-A6（Coxsackie virus A6） causing HA and HFMD were both belong to type IV branches in the phylogenetic tree based on the whole genome sequence，and there might be small fragment recombination in VP1, VP3, and 2C regions between HA321 and HFMD 275 strains. Meanwhile, nucleotide differences were observed between HA and HFMD isolates at S597T, Q705Land Q663L of VP1.

Conclusion CV-A6（Coxsackie virus A6） strains that cause HA and HFMD have high homology. Mutations of amino acid in P1 region of CV-A6（Coxsackie virus A6） may lead to different clinical symptoms.

PU-3760

patients: a comparative cohort study during 2014-19

Yijun Shi
Department of Clinical Diagnosis Laboratory of Beijing Tiantan Hospital, Capital Medical University

Purpose Our study is a retrospective observational study conducted in one of the largest clinical centers of neurosurgery in China. We aimed to investigate the antimicrobial susceptibility patterns of the Enterobacteriaceae isolates responsible for nosocomial meningitis/encephalitis in post-neurosurgical patients. Meanwhile, we tried to evaluate the risk factors for mortality following Enterobacteriaceae meningitis/encephalitis.
Patients and Methods Medical data on clinical characteristics, antibiotic susceptibilities, and mortality were reviewed until patients discharge or death in the hospital. Data for a total of 164 cerebrospinal fluid (CSF) infection cases due to Enterobacteriaceae after neurosurgery were collected between January 2014 and November 2019 in order to identify risk factors affecting the outcome. Kaplan–Meier survival analysis and multivariable Cox proportional hazard models were applied.
Results In this study, a total of 2416 neurosurgical meningitis/encephalitis cases were reported between 2014 and 2019, Enterobacteriaceae accounted for 7.3% (176/2416) of all the bacterial infections. Of them, 164 Enterobacteriaceae isolates were available to divide into two groups according to the final outcome of whether the patient died or survived. In total, 38 patients died (23.2%) and 126 patients survived (76.8%). The most frequent infecting species was Klebsiella pneumoniae (47.0%, 77/164). Fourteen-day and 30-day mortality rates were 7.9% (13/164) and 15.2% (25/164). Kaplan–Meier survival analysis revealed that the risk factors of Enterobacteriaceae meningitis/encephalitis that resulted in poor outcomes included comorbidities, Glasgow Coma Scale (GCS) score, sepsis, Intensive Care Unit (ICU) admission, Extended-Spectrum Beta-Lactamase (ESBLs) producing Enterobacteriaceae, and ventilation. A GCS score of less than or equal to 8 (P=0.04, HR 2.562) was identified to be a significant risk factor for mortality according to the multivariable Cox proportional hazards model.
Conclusion In-hospital mortality caused by Enterobacteriaceae meningitis/encephalitis in neurosurgery was high. A GCS score of ≤8 was an independent risk factor for mortality Enterobacteriaceae meningitis/encephalitis in post-neurosurgical patients.

PU-3761

Metagenomic Next-generation Sequencing of Cerebrospinal Fluid for the Diagnosis of External Ventricular and Lumbar Drainage-associated Ventriculitis and Meningitis

Lingye Qian
NO. 119 Nansihuan West road, Fengtai district Beijing

Metagenomic next-generation sequencing (mNGS) has become a widely-used technology that can accurately detect individual pathogens. This prospective study was performed between February 2019 and September 2019 in one of the largest clinical neurosurgery centers in China. The study aimed to evaluate the performance of mNGS on cerebrospinal fluid (CSF) from

neurosurgical patients for the diagnosis of external ventricular and lumbar drainage (EVD/LD)-associated ventriculitis and meningitis (VM). We collected CSF specimens from neurosurgical patients with EVD/LD for more than 24 hours to perform conventional microbiological studies and mNGS analyses in a pairwise manner. We also investigated the usefulness of mNGS of CSF for the diagnosis of EVD/LD-associated VM. In total, 102 patients were enrolled in this study and divided into three groups, including confirmed VM (cVM) (39), suspected VM (sVM) (49), and non-VM (nVM) (14) groups. Of all the patients, mNGS detected 21 Gram-positive bacteria, 20 Gram-negative bacteria, and five fungi. The three primary bacteria detected were Staphylococcus epidermidis (9), Acinetobacter baumannii (5) and Staphylococcus aureus (3). The mNGS-positive coincidence rate of confirmed EVD/LD-associated VM was 61.54% (24/39), and the negative coincidence rate of the nVM group was 100% (14/14). Of 15 VM pathogens not identified by mNGS in the cVM group, eight were negative with mNGS and seven were inconsistent with the conventional microbiological identification Results In addition, mNGS identified pathogens in 22 cases that were negative using conventional methods; of them, 10 patients received a favorable clinical treatment; thus, showing the benefit of mNGS-guided therapy.

PU-3762

多重耐药肠杆菌致医院获得性脑膜炎的分子流行病学及生存分析

郑光辉
首都医科大学附属北京天坛医院

背景 探讨多重耐药肠杆菌 (multi-drug resistance Enterobacteriaceae, MDRE) 所致的医院获得性脑膜炎 (nosocomial meningitis, NM) 的死亡危险因素。同时分析了 MDRE 的分子流行病学特征。
方法 研究者来自于 2014-2019 年间 2 个中国神经外科中心 MDRE NM 患者。对每种 MDRE 进行分子微生物学流行病学调查，建立 Kaplan-Meier 生存分析，并用 Cox 风险模型进行多变量分析。
结果 90 例 MDRE-NM 患者被纳入本研究。肺炎克雷伯菌所占比例最高 (51.11%，46/90) ，其中有 44 例 (44.44%) 对美罗培南耐药。blaKPC (67.50%，27/40) 是碳青霉烯类抗生素的主要耐药基因。多因素 Cox 分析显示，室外引流 (EVD，危险比 (HR) 2.524，95%可信区间 (CI) 1.101-5.787，P=0.029) 和格拉斯哥昏迷评分 (GCS) ≤8 (HR 4.033，95%可信区间 (CI) 1.526-10.645，P=0.005) 是 MDRE NM 的死亡危险因素。
结论 MDRE 引起的 NM 是神经外科手术失败的重要因素，MDRE 具有多种耐药基因型，EVD 和 GCS≤8 是 MDRE-NM 的独立死亡危险因素，这值得微生物学家和神经外科临床医生引起重视。

PU-3763

徐州地区 2015-2019 年万古霉素对 MRSA 最低抑菌浓度值的特征分析

纵帅
徐州医科大学附属医院

目的 回顾性分析万古霉素对耐甲氧西林金黄色葡萄球菌（MRSA）最低抑菌浓度（MIC）值的特征性变化，为临床使用万古霉素治疗 MRSA 感染提供参考。
方法 按医院院内感染标准纳入 2015-2019 年徐州地区三家三级甲等综合性医院临床标本分离的非重复 MRSA 共 540 株，收集其 MIC 值，采用统计学方法计算 MIC 几何均值，MIC50 和 MIC90 等，并分析其特征。
结果 540 株 MRSA 全部对万古霉素敏感；近五年万古霉素对 MRSA 的 MIC 几何均值分别为 1.058，1.100，1.108，1.122 和 1.147，组间整体差异有统计学意义（P＜0.05）；ICU 科室的 MIC 均值

分别为 1.155，1.252，1.309，1.399 和 1.445，非 ICU 科室 MIC 均值分别为 0.996，1.003，0.979，0.944 和 0.956，其中 2016-2019 年四年间 ICU 和非 ICU 科室同年份均值差异有统计学意义（P＜0.05）；万古霉素对 MRSA 的 MIC≥1.5μg/mL 的比例逐年增加（P＜0.05）。
结论 2015-2019 年间徐州地区未发现耐万古霉素的 MRSA 株；万古霉素 MIC 值存在漂移，漂移主要来自 ICU 科室；对 ICU 科室万古霉素 MIC≥1.5μg/mL 的 MRSA 菌株和患者应重点监控，积极治疗，防止感染暴发。

PU-3764

房水中分离嗜水气单胞菌 1 例并文献复习

郭建壮
山东省千佛山医院

嗜水气单孢菌是一种新的能够导致肠道疾病的细菌，目前已被纳入了腹泻病原菌的常规检测中，其中食品卫生检验部门也对此菌进行感染检测，同时也是导致院内感染的细菌。此菌是一种能够导致人-畜-鱼共患病的病原菌，具有多种不同的致病基因，同时具有相当的毒力和广泛的宿主感染能力[1]。

嗜水气单孢菌在人类感染中以胃肠感染最为常见，多为急性肠胃炎，其发病可能与食物中毒或引用被污染的水有关；发病多以爆发或流行为常见形式[2]。外伤感染的几率和败血症的几率远低于胃肠感染。帮助临床详细了解嗜水气单胞菌的生活习性及发病原因、药物敏感性协助临床对该菌所致感染的治疗及预防。

PU-3765

老年性阴道炎患者阴道微生态状况分析

罗雪
柳州市妇幼保健院

近年随着阴道微生态理念的兴起，老年性阴道炎的阴道微生态研究也逐渐成为热点，但报道多为治疗方法的探讨，对患者阴道微生态整体状况分析则较少，本研究通过分析老年性阴道炎患者与正常体检老年女性的阴道微生态构成及微生态失调的病原分布，以期为老年女性阴道感染性疾病的病原学诊断及治疗提供实验室依据。

PU-3766

新型 BacT/ALert FA/FN PLUS 聚合物吸附珠血培养瓶对模拟菌血分析性能的研究

谢宁、郭斌
川北医学院附属医院

目的 探索新型 BacT/Alert FA/FN Plus 聚合物吸附珠血培养瓶对菌血症的检验分析性能。
方法 选择菌血症患者常见细菌病原体和常用抗菌药物，将预制的菌液、抗菌药物和血液注入血培养瓶，采集 5 天内各培养瓶报阳率和报阳时间，比较具有不同抗菌药物吸附剂的血培养瓶对不同细菌的分析性能。

结果 新一代 Bio-FA/FN Plus 培养瓶对大肠埃希菌、金黄色葡萄球菌、白色念珠菌或热带念珠菌检出时间明显快于其他培养瓶；但铜绿假单胞菌-哌拉西林/他唑巴坦组 BacT/Alert FA/FN Plus 和 BACTEC PLUS 培养瓶 TTD 差异不显著；对厌氧菌无抗菌药物时 BD-L 厌氧瓶检出时间最快。
结论 BacT/Alert FA/FN Plus 聚合物吸附珠血培养瓶对临床常用抗菌药物均具有强吸附能力，能提高血培养阳性率，有利于更快速、高效检出病原菌。

PU-3767

近 5 年我院耐碳青霉烯类鲍曼不动杆菌的分布 及耐药分析

幸运
陆军特色医学中心（大坪医院）

目的 通过对近 5 年我院耐碳青霉烯类鲍曼不动杆菌（Carbapenem-resistant Acinetobacter baumannii，CRAB）和碳青霉烯类敏感鲍曼不动杆菌（Carbapenems-sensitive Acinetobacter baumannii，CSAB）的分布及耐药性分析，指导临床合理用药。
方法 采用 WHONET 5.6 软件对 2016 年 1 月至 2020 年 12 月本院住院患者送检的临床标本中分离的鲍曼不动杆菌(Acinetobacter baumannii， AB）进行回顾性分析。
结果 2016 年 1 月至 2020 年 12 月本院住院患者送检的临床标本共检出细菌 24259 株，其中 AB 2211 株（占 9.1%）；AB 包含 CRAB 和 CSAB，分别检出 1482 株（占 6.1%）和 729 株（占 3.0%）。CRAB 和 CSAB 主要分离自痰、肺泡灌洗液标本，五年共计检出 1665 株(占 75.3%)，其次是尿液 142 株(占 6.4%)及分泌物 123 株(占 5.6%)。CRAB 和 CSAB 科室分布以重症监护室（ICU）为主，五年共计 782 株（占 52.8%），其次是呼吸科 302 株（占 20.4%）。CRAB 和 CSAB 感染患者中，51-80 岁的患者人数最多，五年共计 1249 例(占 56.5%)，明显多于其他年龄段。CRAB 对 14 种常用抗菌药物的耐药性普遍较高，其中对米诺环素耐药率最低，五年平均耐药率 44.5% ；CSAB 对 14 种常用抗菌药物的耐药性普遍较低，其中对氨苄西林/舒巴坦耐药率最低，五年平均耐药率 10.2%。
结论 鲍曼不动杆菌临床分布广泛，耐药率高，特别是对 CRAB，实验室和医院应重视对该菌的耐药性监测,应制定合理有效的措施，抑止耐药菌株传播。

PU-3768

云南省昆明市 HIV-1 流行株 pol 基因序列特征分析

李健健
云南省传染病医院

目的 了解云南省昆明市人类免疫缺陷病毒 1 型（HIV-1）的亚型分布特征及其 pol 结构基因的变异特征。
方法 随机抽取 2015-2019 年昆明市抗病毒治疗半年以上的样本 390 例，收集其流行病学信息，血浆提纯 HIV-1RNA，采用巢式聚合酶链式反应扩增 HIV-1pol 基因，应用 Genotyping Tool、BLAST 在线分型工具及 MEGA 6.06 软件进行基因分型，运用 MEGA Distance 程序计算基因距离，Entropy 程序分析氨基酸多态性，进而对 HIV-1 流行株的 pol 基因序列特征进行分析。
结果 成功扩增获得 pol 基因序列 318 例，亚型分析结果显示：B 亚型 10 例（3.1%）、C 亚型 14 例（4.4%）、CRF01_AE 83 例（26.1%）、CRF07_BC 65 例（20.4%）、CRF08_BC 136 例（42.8%）以及其他亚型 10 例（3.1%），各个亚型在性别、年龄及感染途径的构成上均有差别（P<0.001）。CRF01_AE、CRF07_BC、CRF08_BC 的基因距离分别为 0.018±0.008、0.015±0.006、0.006±0.004，差异有统计学意义（P<0.01）。CRF01_AE 亚型中静脉药瘾感染者与性接触感染者的氨基酸序列存在差异，共有 45 个位点的氨基酸差异存在统计学意义（P<0.05）。

结论 昆明市 HIV-1 亚型分布复杂多样，以 CRF08_BC 为主，传播途径以异性性传播为主，CRF01_AE 亚型为昆明地区变异程度较高的流行株，不同感染途径毒株的氨基酸突变位点存在差异，应密切监视其变化。

PU-3769

新型冠状病毒肺炎病例治疗进程中不同类型样本核酸检测 CT 值与结果分析

李健健
云南省传染病医院

目的 分析 2019 新型冠状病毒(2019 Novel Coronairus,2019-nCoV)感染患者住院治疗进程中不同类型样本中的核酸检测 CT 值及结果，为疫情的防控和疾病治疗提供参考建议。
方法 收集 2020 年 1 月至 2020 年 4 月在云南省某医院住院治疗的 24 例新型冠状病毒肺炎(COVID-19)确诊病例资料，采用荧光定量逆转录聚合酶链反应(real-time fluorescence reverse transcriptase polymerase chain reaction, RT-PCR)方法检测患者口咽拭子、鼻咽拭子和痰液中的 2019-nCoV 核酸，分析不同治疗阶段 CT 值和阳性率变化情况。
结果 24 例 COVID-19 确诊病例中男性 14 人，女性 12 人，集中分布在 18-44 年龄段，其中轻型 9 例，普通型 10 例，重型/危重型 5 例；在不同的治疗进程中各部位标本的阳性率不同，治疗后期痰液的阳性率最高为 83.3%，鼻咽拭子 41.7%，口咽拭子最低；口咽拭子的 Ct 值均值在治疗进程中呈上升的趋势，在治疗后的 20 天 Ct 值均值为 38.5,鼻咽拭子的 Ct 值均值在治疗进程中波动明显，在治疗后 5 天最低为 20，而在治疗后的 11-20 天 Ct 值均值高于痰液；各临床分型患者的口咽拭子的 Ct 值均值在治疗进程中都呈上升的趋势，鼻咽拭子的重型/危重型标本的 Ct 值均值随治疗的进程波动较为明显。
结论 COVID-19 患者在治疗后期痰标本的阳性率最高，阳性持续时间最长；鼻咽拭子的 Ct 值受疾病进程影响较为明显，研究提示在开展新型冠状病毒实验室核酸检测中，监测各种类型标本的 Ct 尤为重要。

PU-3770

重度子痫前期患者与正常孕妇凝血功能差异比较

王 璐
滨州医学院烟台附属医院

目的 同时观察重度子痫前期患者和同期正常孕妇的凝血功能指标和血小板参数，并根据两者之间的差异得出结论。
方法 将我院住院的 300 例重度子痫患者作为实验组，同期 300 例来院检查的正常孕妇作为对照组。两组分别测定凝血酶原时间（PT）、凝血酶原时间国际标准化比值（INR）、部分凝血活酶时间（APTT）、凝血酶时间（TT）、纤维蛋白原（Fib）、血小板（PLT）、平均血小板体积（MPV），接着进行实验组和对照组的比较分析，得出相应结论。
结果 得出结论，实验组中，PT、INR、Fib 低于对照组，TT 高于对照组，差异具有统计学意义（$P<0.05$）。APTT、PLT、MPV 的差异无统计学意义（$P>0.05$）。
结论 通过对重度子痫前期患者的凝血状态进行观察，可以发现重度子痫前期患者孕期和分娩期出血的危险性增加，凝血功能指标的检测可以对此做出一定的解读，方便做出判断。

PU-3771

降钙素原、超敏 C-反应蛋白、白细胞计数及中性粒细胞淋巴细胞计数比值对住院患者血流感染的早期诊断研究

白珊珊
雅安市人民医院

目的 探讨降钙素原（PCT）、超敏 C-反应蛋白(CRP)、白细胞计数(WBC)及中性粒细胞/淋巴细胞计数比值(NLR)对住院患者血流感染的早期诊效能，为临床早期诊断提供参考依据。
方法 回顾性分析研究 2018 年 12 月-2019 年 12 月我院疑似血流感染者(873 例)，以临床诊断为准，分为血流感染组与非血流感染组，基于 Logistic 回归的受试者工作特征(ROC)曲线分析 PCT、CRP、WBC、NLR 单独与联合检测对病原菌血流感染的诊断价值，数据采用 SPSS19.0 软件进行统计分析。
结果 873 例疑似血流感染患者中，血流感染组有 228 例（26.117%），其中血培养阳性 102 例（11.684%），非血流感染组 645 例（73.883%），其中血培养阴性 618 例（70.790%），其灵敏度为 44.74%，特异度为 95.81%，诊断符合率为 82.47%；分析两组 WBC、PCT、CRP、NLR 指标，差异均有统计学意义（P<0.05）；当 PCT cut-off 值为 1.245 ng/ml 时，AUC 面积最大为 0.843，诊断效能最高，灵敏度、特异度分别为 75.44%及 80.78%；当 CRP cut-off 值为 82.63 mg/l 时，AUC 面积最大为 0.643，其灵敏度、特异度分别为 61.4%及 64.5%，仅次于 PCT；WBC、NLR 在 cut-off 值为 12.21 x109/L、16.85 时，特异性较高分别为 72.87%及 79.85%，但灵敏度均较低（<50%）；双指标组合中，PCT/CRP 组合的 ROC 曲线下面积最高为 0.843，且与 PCT 单项检测比较差异没有统计学意义（P>0.05）； PCT 以 1.245 为 cut-off 值，从血流感染组中选取 PCT 及血培养同时阳性患者，分为革兰阴性菌组（57 例），革兰阳性菌组（12 例），两组间 PCT 值无统计学差异。

PU-3772

隐血粪便检测方法

李梅、董莉芹
哈尔滨医科大学附属第一医院

目的 隐血干扰因素多，灵敏性和特异性较差，而近年来发展的单克隆抗体法检测粪便隐血不受饮食限制，快速、简便、准确，方便临床。
方法 用单克隆抗体法对 5 种浓度的人和动物的血红蛋白液进行检测，结果单克隆抗体法隐血试验，可测出样本中微量的血红蛋白(0.2μg/ml)，这使得单克隆法对人体无症状的消化道微量出血更敏感。结果从试验结果也可看出，单克隆抗体法仅特异性地针对人血红蛋白，其他动物肉类对此试验无干扰作用。含过氧化物酶的新鲜蔬菜，铁剂、维生素 C 及对化学法有干扰作用的某些药物对此法的结果均无影响。此法比愈创木酯法(化学方法)的灵敏度也要高很多结论它可以检测出 0.2μg/ml 的血红蛋白(0.03mgHb/g 粪便)，也就是说，它可检测出粪便中微量的血红蛋白，如前所述，这对胃肠道出血性疾病的早期诊断是非常重要的。

PU-3773

AVE-562 粪便分析仪性能验证结果评价及临床应用评估

何亚琼
东南大学附属中大医院

目的 对 AVE-562 全自动粪便分析仪进行性能评价，探讨其在临床粪便检验中的应用价值.
方法 采用新鲜大便标本对 AVE-562 全自动粪便分析仪检测标本的颜色、性状、准确性、重复性、携带污染率等指标进行验证。
结果 选取的临床粪便标本（含正常和异常），仪器检测与人工目测结果比较，颜色 85%符合、性状 90%符合。AVE-562 粪便分析仪检测的红细胞、白细胞、虫卵、脂肪球、真菌等指标与人工显微镜结果的符合率均为 100%；重复性：仪器检测的红细胞（低值、高值）、白细胞（低值、高值）的变异系数分别为：8%、4%、3%、1.45%；回收率分别为：96%、92%、101.45%、103%。隐血实验结果与手工检测结果的符合率为 100%、回收率 100%；携带污染实验，隐血阴性组标本结果均为阴性，且镜检细胞结果均为 0 个/ul。
结论 经验证，AVE-562 粪便分析仪在人工修正的情况下，其颜色性状识别能力、准确性、重复性、携带污染率等性能参数均符合临床实验要求，在实际工作中需定期进行仪器各种性能检查,以保证仪器更高速准确得检测结果。
关键词 AVE-562 全自动粪便分析仪；粪便；红细胞；白细胞；隐血

PU-3774

临床检验血细胞的注意点

李梅、董莉芹
哈尔滨医科大学附属第一医院

目的 抗凝剂对血细胞形态影响很小，因此适用于血细胞计数，特别是血小板计数。
方法 血液标本在室温中必须 6 h 内上机检测，上机前一定要将血液标本颠倒混匀至少 8 次，如需制备血涂片，应在采血后 3 h 内涂制。无论多先进的血液分析仪，只能当作一种过筛手段，不能完全替代目视法显微镜镜检,因为仪器还不能准确区分幼稚细胞、异常淋巴细胞、有核红细胞等。结果一般医院显微镜档次偏低，分辨率低，维修和正确使用欠缺，提高显微镜档次更好发挥光镜的观察效应；但要做到准确分类 结论目前还存在不少困难，个别细胞的分类标准至今尚未全国统一。

PU-3775

353 例住院患者红细胞制剂输注疗效回顾性分析

华诗
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 探讨临床患者红细胞悬液输注的疗效并分析其影响因素，为临床医生合理、有效用血提供依据。
方法 通过检验科及输血科 LIS 和 HIS 系统分析四川省人民医院 2018 年 9 月至 2018 年 10 月 353 例部分临床患者红细胞悬液输注疗效及其与年龄、性别、输血前血红蛋白(Hb)浓度、输血量和基础疾病的关系。
结果 353 例贫血患者总输血量为 1259U；“有效”输血 194 例(54.96%)，输血量为 520.5U；“无效”输血 159 例(45.14%)，输血量为 738.5U。对资料进行 x^2检验分析得到：不同基础疾病患者、输血

前血红蛋白浓度、输血量、性别,红细胞疗效各组组内因素比较 P<0.05，差异有统计学意义；不同年龄段患者红细胞输注疗效组内因素比较 P>0.05，差异无统计学意义。
结论 临床患者的无效输注与其性别、输血前 Hb 浓度、输血量和基础疾病有关。输血量越多则无效输注的发生率越高，可能与免疫因素有关。临床患者红细胞输注效果的发生机制尚需进一步研究，有必要针对相关影响因素制定独立、安全、有效的个体化输血策略，以帮助临床医生更加合理用血，并达到最佳输血效果。

PU-3776

肾综合征出血热

张怡婷
江苏省人民医院（南京医科大学第一附属医院）

目的 通过实验室常规检查助力临床肾综合征出血热诊断
方法 采集患者 EDTA 抗凝静脉血 2ml，采用 Sysmex XN-1000 全自动血液分析仪进行检测，同时用 Sysmex XN 流水线 SP-10 推片机推片，瑞氏染色，用全自动细胞形态学分析仪 DI60 进行分析
结果 散点图淋巴细胞和单核细胞灰区，幼稚粒区面积大，仪器报警提示：白细胞异常散点图，幼稚粒细胞存在，异型淋巴细胞？左移？外周血涂片可见核左移，浆样淋多，细胞核浆变化大，有大血小板。治疗过程中的变化：可见散点图趋于正常，白细胞降低，血红蛋白降低，血小板升高。
结论 看似最基本的血常规，通过分析血常规结果、散点图特点以及外周血涂片特点，我们依旧可以给临床诊断指引方向，更好地服务于临床。

PU-3777

不同剂量的铁剂对缺铁性贫血的治疗效果

翟贺
吉林金域医学

目的 缺铁性贫血是由于体内铁缺乏引起的，骨髓象表现为小细胞低色素性贫血，诊断为缺铁性贫血后，应采取有效的方法铁剂治疗。本文分析了小剂量铁剂与常规剂量铁剂对缺铁性患者的补铁治疗效果。
方法 选取 100 例缺铁性患者作为研究对象，运用生物对比试验方法将其随机分为实验组与对照组，实验组服用正常剂量铁剂，对照组服用小剂量铁剂，分别测得每个患者的网织红细胞，红细胞，血红蛋白，平均红细胞体积，平均红细胞血红蛋白量，平均红细胞血红蛋白浓度，铁蛋白，通过对以上指标测量分析评估疗效。一个月内，对两组进行铁剂补充后，选取血细胞比容，铁蛋白，血红蛋白浓度其中三项较为灵敏的指标进行测量。
结果 实验组治疗前的三项指标为 26.34%,6.1μg/L,42g/L,对照组治疗前的三项指标为 24.79%，7.5μg/L,46g/L。铁剂补充后，实验组的三项指标为 33.96%,8.7μg/L,97g/L，对照组的三项指标为 35.29%,10.5μg/L,104g/L。实验组的血细胞比容升高了 7.62%，铁蛋白升高了 2.6μg/L，血红蛋白浓度升高了 55g/L，而对照组血细胞比容升高了 10.5%，铁蛋白升高了 3μg/L，血红蛋白浓度升高了 58g/L。
结论 铁剂补充后，实验组与对照组的指标均升高，但升高程度不一，对照组指标升高幅度大一些，通过指标分析治疗效果，对照组优于实验组。对缺铁性患者治疗，应采取小剂量铁剂补充，铁是人体所必须的微量元素，大剂量补充可能会产生不耐受，也会造成胃肠道紊乱，使其补铁效果不佳，然而小剂量铁更利于患者机体吸收，治疗效果较好。

PU-3778

浓缩尿与非离心尿非定量有形成分沉渣定量计数板换算关系初探

李焱鑫
四川省医学科学院·四川省人民医院

目的 探讨浓缩尿与非离心尿非定量有形成分沉渣定量计数板换算。
方法 取含草酸钙结晶的新鲜尿液使用尿沉渣计数板定量对非离心尿和离心尿草酸钙结晶计数。
结果 两方法的相关系数为 0.978，线形方程为 Y 离心法=28.243X 非离心法+125.897；获得近似的定量结果与等级值结果的对应关系。
结论 草酸钙结晶适用于尿沉渣计数板的评价；可保证所报告结果与现行国家报告标准的一致性和可读性，提高样本检测效率。

PU-3779

不典型慢性髓系白血病一例及其实验室诊断体会

陈涛[1]、杨旭旭[2]、黄滔[1]、高伟[1]、唐明霞[1]
1. 雅安市人民医院检验科
2. 雅安市人民医院输血科

不典型慢性髓系白血病，BCR-ABL1 阴性（aCML）是一种同时具有骨髓增生异常与骨髓增值特点的白血病，特点是具有发育异常的幼稚和成熟中性粒细胞增多，但白血病细胞无 Ph 染色体或 BCR-ABL1 融合基因。患者多为老年人，男女比例为（1-2.5）:1。多数患者有与贫血或血小板减少有关的临床表现，其他主要是与脾大相关的症状[1]。不典型慢性髓系白血病的实验室诊断主要依靠外周血计数、骨髓细胞形态检查，相关遗传学检查，但目前暂未发现其特征性的遗传学改变，所以 aCML 的诊断更多的是排除性诊断，骨髓涂片检查则显得尤为重要。现将我院诊治的一例以皮肤症状为首发表现到院就诊的 aCML 报道如下。

PU-3780

血浆 D-二聚体在类风湿性关节炎诊断中的应用研究

尹智平、施雄飞、詹倩
云南省中医医院（云南中医药大学第一附属医院）

目的 探讨血浆 D-二聚体及类风湿因子（RF）、血沉（ESR）、C-反应蛋白（CRP）检测在类风湿性关节炎（RA）诊断中的应用价值。
方法 选取云南省中医医院 2017 年 3 月～2018 年 5 月期间收治的 80 名 RA 患者为研究对象，另取 60 名正常人群为对照组，免疫比浊法测定血浆 D-D、 透射比浊法测定 RF、全自动动态血沉仪测定 ESR、免疫荧光分析仪测定 CRP，并对结果采用方差分析、独立 t 检验进行统计分析。
结果 RA 患者组的 D-D、ESR、CRP 水平明显高于对照组（P<0.05），[d1] 两组比较差异有统计学意义。
结论 D-D、RF、ESR、和 CRP 水平与 RA 患者的病情活动有关，对 RA 患者病情的早期诊断、用药及预后判断有重要的临床参考意义。

PU-3781

NLR，SAA 与 CRP 联合检测在儿童感染性疾病早期诊断中的价值

宋子阳[2]、杨双[1]
1. 湖南师范大学第一附属医院
2. 湖南师范大学医学院

目的 探究中性粒细胞淋巴比值（NLR）、血清淀粉样蛋白 A（SAA）、C 反应蛋白（CRP）对儿童感染性疾病初期的诊断价值。
方法 采用回顾性分析方法，选取 2018 年 1 月至 2021 年 3 月来院就诊儿童 100 例为研究对象，其中病毒感染病例为 50 例，细菌感染病例为 50 例。并以来院就诊为健康的儿童 50 例为对照，检测所以实验对象外周血 NLR 以及 SAA、CRP 数值，运用受试者工作曲线（ROC）分析各检测项目及其联合检测对儿童感染性疾病的诊断价值。**结果** 细菌感染和病毒感染组的 NLR、SAA 和 CRP 数值都明显比健康组要高(P<0.05)，细菌感染组的 SAA 和 CRP 数值明显比病毒感染组要高(P＜0.05)，NLR 数值略高于病毒感染组(P<0.05)。对于单独诊断儿童早期细菌感染时，CRP 在三项指标中的 ROC 曲线下面积(AUC)和灵敏度均最高或最大，而 SAA 特异度在这三项中最高；对于单独诊断儿童早期病毒感染时，SAA 在三项指标中的 AUC 和灵敏度均较大，NLR 的特异度为最高;与各项指标单独诊断相比较，NLR、SAA 和 CRP 三者的联合诊断儿童早期细菌感染与病毒感染的 AUC 和灵敏度均有增大或增高，联合诊断病毒感染的特异度亦有所增大，但在联合诊断细菌感染时特异度相较 SAA 单独诊断时有所下降。
结论 NLR、SAA 和 CRP 三者的联合诊断对儿童开始感染的初期的感染类型的鉴别具有重要的临床参考价值，且这三种检测指标进行相结合对病毒感染的诊断的特异度要好于细菌感染的特异度。

PU-3782

评估血清 AMH 检测预测多囊卵巢综合征卵巢反应的应用价值

赵军
厦门大学附属第一医院

目的 评估多囊卵巢综合征卵巢反应利用血清 AMH 检测预测的应用价值。
方法 研究对象纳入我院 2018 年 2 月至 2019 年 8 月收治的 IUI 多卵巢综合征患者 48 例作为研究组，选取同期我院收治的 IUI 普通产妇 48 例，并作为对照组。借助微粒子化学发光免疫法进行两组患者 LH 水平检测、利用 ELISA 测定两组患者血清 AMH 水平，分析比对患者卵泡数。
结果 两组患者 AMH 水平比对，研究组明显高于对照组，P<0.05；两组患者黄体生成素比对，研究组明显高于对照组，P<0.05；两组患者卵泡数比对，研究组明显高于对照组，P<0.05。
结论 对多囊卵巢综合征患者利用血清 AMH 检测预测，其卵巢反应准确，并且卵泡数会随着 AMH 水平的提高而增多，具有较高临床应用价值。

PU-3783

导致血小板假性减少的因素及处理办法

文思雨
大理大学第一附属医院（云南省第四人民医院）

目的 分析影响血小板计数导致血小板假性减少的因素，为检验工作中能够及时分辨血小板是假性减少还是真性减少提供经验,为临床诊治提供可靠的诊断依据。

方法 选择红河州第三人民医院检验科 2020 年 8 月份到 2021 年 2 月份六个月里收集的经血细胞分析仪检测血小板假性减少的 15 例标本为实验对象，对十五例血小板假性减少的标本进行回顾性分析，总结导致血小板出现假性减少的原因。
结果 15 例患者由于乙二胺四乙酸二钾依赖性凝集而使血小板假性减少 7 例，采血过程不顺利而使血小板假性减少 6 例，存在较多大血小板而使血小板假性减少 2 例。
结论 掌握导致血小板假性减少的影响因素, 实施相应的纠正处理方法,得出准确的检验结果,为临床提供正确的诊治依据,以避免血小板假性异常造成临床误诊

PU-3784

Procoagulant platelet: generation, characteristics and therapeutic target

Yaxin Chu、Rui Qiao
Peking University Third Hospital

Platelets play a pivotal role in thrombosis and hemostasis. It is recognised platelets respond differently to activation. In response to agonist(thrombin and/or collagen), activated platelets are heterogeneous, some of them belong to the procoagulant subgroup, basically involved in promoting formation of thrombin and fibrin, and others are aggregatory, mainly involved in the platelets aggregation, connection with damaged vessel wall and clot restraction. Different populations of platelets play different roles in the process of thrombus formation. Procoagulant platelet with PS externalization binds tenase and prothrombinase complexes, promoting thrombin and stable fibrin clot formation at the wound site. Therefore, procoagulant platelet can be seen as the connector between the primary and the secondary hemostasis. In this review, We discuss the primary generation mechanisms of procoagulant platelet, pivotal characteristics of it and its potential as a clinical biomarker and therapeutic target.

PU-3785

血凝仪 TOP750 与 TOP300 结果比对

马瑜婷
西安医学院第一附属医院

目的 探讨同一实验室同一厂家不同型号的全自动血凝分析仪检测凝血酶原时间（ PT),部分凝血酶原时间（ APTT),凝血酶时间（ TT),纤维蛋白原（ FIB), 纤维蛋白原降解产物（ FDP)与 D-二聚体（ DD)结果的可比性和一致性。
方法 参加室间质评且成绩优秀的血凝仪为参比仪器，随机采取 50 份患者新鲜血浆，在 ACL TOP700 与 ACL TOP300 上检测并进行结果比对。
结果 俩台血凝仪 6 项检测项目的结果变异系数（ CV)均小于 5%,相关系数（ r）值均大于 0.975，结果具有良好的相关性。
结论 两台血凝仪的可比性与一致性较好，可满足临床需要。

PU-3786

1685 例血液病患者骨髓染色体核型分析

杨冰
西安金域医学检验所有限公司

目的 通过对血液病患者进行骨髓染色体核型分析，为血液系统疾病的诊断、治疗、病情监测及预后判断提供细胞遗传学数据。
方法 采集陕西 1685 例各种恶性血液系统疾病患者的骨髓样本，骨髓细胞经过短期培养及秋水仙素处理，使其停止在分裂中期，经 G 显带法进行染色体核型分析。
结果 在 1685 例骨髓染色体核型分析中共检出异常核型 560 例，检出率为 33.23% 。其中＞70 岁的异常核型 107 例占比 19.11%，51-70 岁的异常核型 247 例占比 44.11%，31-50 岁的异常核型 151 例占比 26.96%，＜30 岁的异常核型 36 例占比 6.43%。
结论 骨髓染色体核型分析为血液系统疾病明确诊断、指导治疗、病情监测及预后判断等提供了必不可少的依据。

PU-3787

肝素在凝血障碍患者治疗中的作用

刘阔
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 研究手术患者自体输血与非自体输血对凝血结果的影响。
方法 收集自体输血手术患者与常规输血手术患者，在手术期间运用肝素抗凝后对凝血结果的影响。用 t 检验及卡方检验进行统计学分析。
结果 围手术期药物如阿司匹林可诱发血小板功能障碍。自体输血具有成本效益，是避免或减少同源输血的最安全方法。鼓励术前，术中抢救和术后抢救。促红细胞生成素可能有助于增加先天性红细胞的数量。
结论 凝血障碍是由多种因素引起的，例如肝素，血小板功能障碍和纤溶。必须合理使用血液成分疗法和药物，例如肝素，鱼精蛋白和去氨加压素。自体输血在减少或避免使用同种输血中非常有用。

PU-3788

孕早中晚期尿碘/尿肌酐比值与甲状腺功能的关系

肖建波
绵阳市中心医院

目的 了解当地妊娠妇女不同孕期的甲状腺功能与尿碘/尿肌酐比值情况，并探讨尿碘尿肌酐比值与甲状腺功能的关系。
方法 纳入从某年月某日至某年某月某日某某市妊娠 12 周前来某某医院接受产前护理的单胎妊娠妇女 158 例。分别于研究对象的妊娠早期、中期、晚期采集清晨尿样和血清标本，测定尿碘和肌酐浓度，计算尿碘尿肌酐比值，检测甲状腺功能指标 TSH 和 FT4，探讨不同孕期不同尿碘尿肌酐比值范围的妊娠妇女甲状腺功能异常情况。
结果 妊娠早、中、晚期 TSH（mIU/L）中位数及四分位数间距分别为 1.33（0.72,2.17），2.00（1.28,2.71），2.06（1.44,2.88），中位数随着妊娠的进展升高；TSH 异常率分别为 6.96%，10.76%，1.90%，妊娠中期异常率最高。FT4（ng/dl）妊娠早、中、晚期中位数及四分位数间距分别为 0.83（0.77,0.92），0.62（0.55,0.67），0.61（0.55,0.66），随着妊娠的进展，FT4 中位数

降低。孕早期尿碘尿肌酐比值中位数为 116.47ug/g；孕中期尿碘尿肌酐比值中位数为 175.43ug/g；孕晚期尿碘尿肌酐比值中位数为 233.40ug/g，尿碘尿肌酐比值中位数随着妊娠的进展而升高。妊娠早期，＜150 ug/g 组 TSH 异常率（8.04%）高于≥150 ug/g 组异常率（4.35%）；妊娠中期，＜150 ug/g 组 TSH 异常率（12.31%）高于≥150 ug/g 组异常率（为 9.68%），差异均有统计学意义。

结论 当地的妊娠妇女在妊娠早中期，应高度重视碘营养状况，按时检测甲状腺功能及尿碘尿肌酐比值，当尿碘尿肌酐比值低于 150 ug/g 时，应适当食用富碘食品，当甲状腺功能出现异常时，及时治疗，降低不良妊娠结局的发生。

PU-3789

Aptio-CS5100 流水线自动审核系统的建立及应用

赵太强
电子科技大学附属医院•四川省人民医院

目的 建立 Aptio-CS5100 凝血分析流水线自动审核规则，有效收集分析前、中、后数据并综合判读，以提高检验报告 TAT 并保证检测结果的准确性。

方法 参照国家卫健委卫生行业标准 WS/T 616-2018、美国 CLSI AUTO-10A 指南以及 ISO15189:2012 认可准则要求，制定自动审核规则，通过自动化流水线中间体软件 Centralink 、实验室信息系统(LIS) 和智能化连接的 CS5100 凝血分析仪与西门子 Aptio 流水线轨道，搭建凝血分析自动审核系统。经初步摸索，共设定标本状态判断规则(SS)、质控判断规则(QS)、仪器状态判断规则(IS)、结果范围判断规则(NS)、历史结果判断规则(DS)、逻辑判断规则(LS)六类审核规则，数据要素全面涵盖分析前、中、后整个检验过程，并通过 2019 年 9 月至 2019 年 12 月约 5 万份凝血分析结果验证自动审核规则。多次调整、改进并最终确定暂行规则后，比较 2020 年 1 月至 2020 年 5 月试运行期间 31835 份凝血分析结果与 2019 年全人工审核同期检验单，对自动审核系统的实施效果进行评价。

结果 经多轮调整改进，最终确立 SS、QS、IS、NS、DS 和 LS 六类共计 42 条规则，用于凝血酶原时间(PT)、活化部分凝血活酶时间(APTT)、凝血酶时间(TT)、纤维蛋白原浓度(FIB)、D 二聚体(D-Dimer)、纤维蛋白(原)降解产物(P-FDP)和抗凝血酶Ⅲ活性(AT3)七项凝血常规分析结果的自动审核。2020 年 1 月至 2020 年 5 月 5 个月的验证期间 31835 份凝血分析结果，自动审核通过率为 76.1%，通过结果与人工审核符合率为 100%，即假阴性率为 0%。未通过自动审核触发的规则及比例分别为 SS 12.1%、QS 1.2%、IS 8.7%、NS 50.4%、DS 21.3%和 LS 6.3%；其中 NS 和 DS 占较高比例是因为我院信息系统未标准化临床诊断信息和同步用药情况，故自动审核规则设置趋严谨，留待调阅病例资料后人工审核。2020 年 1 月至 2020 年 5 月与 2019 同期相比，TAT 中位数从 115min 降为 72min，缩短 37.3%；同时脂血、溶血和血浆凝固等异常标本识别和处理比例大幅增加，员工满意度亦有所提高。

结论 借助自动审核系统，真正实现了凝血流水线的智能化、自动化管理，提高检测效率，降低分析前误差，缩短 TAT，保证检测结果准确性，保证患者生命安全，降低医疗风险。

PU-3790

79 例血小板减少症病因及临床分析

朱云波
芷江侗族自治县人民医院

目的 探讨血小板减少症的病因,提高此类疾病的临床分析能力，尽早明确诊断。

方法 对 2019 年 1 月-2020 年 12 月，在本院住院的 79 例外周血血小板减少查因的患者，对其实验室血小板计数、外周血血涂片、骨髓细胞形态检查结果及临床资料进行回顾性分析。
结果 1、病因构成：79 例患者，特发性血小板减少性紫殿 23 例，再生障碍性贫血 4 例，急性白血病 5 例，慢性肝病 10 例、脾功能亢进 6 例、巨幼细胞性贫血 5 例、妊娠合并血小板减少症 2 例，药物性血小板减少 3 例、重症感染 5 例、骨髓增生异常综合征 4 例、弥漫性血管内凝血（DIC）1 例、艾滋病 2 例、甲状腺功能亢进 1 例、不明原因 8 例。2、急性白血病外周血，伴有血红蛋白下降、白细胞增高、骨髓增生极度活跃、肝脾肿大。巨幼细胞性贫血外周血血小板减少，伴有血细胞巨幼变。
结论 1.血小板减少症病因复杂多样、见于血液系统疾病、非血液系统疾病及不明原因血小板减少。血小板减少往往以一些伴发症状及并发症症状表现，不是单纯的以某种疾病存在。非血液系统疾病及不明原因血小板减少，临床并不少见，应予以重视鉴别诊断，以免延误治疗时间。2.实验室血小板计数、外周血血涂片、骨髓细胞形态检查联合诊断、与临床全面分析、可进一步明确血小板减少的病因、提高诊断率。

PU-3791

非淋巴细胞/淋巴细胞比值在系统性红斑狼疮患者中的临床意义

张琳琳
四川省医学科学院·四川省人民医院

目的 探讨系统性红斑狼疮（SLE）患者中性粒细胞（NLR），单核细胞（MLR），嗜酸性粒细胞（ELR）和嗜碱性粒细胞（BLR）与淋巴细胞的比值及临床意义。
方法 收集本院 350 例 SLE 患者和 200 例健康体检者血常规检验和临床信息。非参检验分析 NLR、MLR、ELR 和 BLR 在各组的表达差异，Spearman 相关性分析其与年龄、血沉、C 反应蛋白和免疫球蛋白的相关性。ROC 曲线分析 NLR、MLR、ELR 和 BLR 对 SLE 的诊断价值。
结果 SLE 患者 NLR[3.05（1.88-5.53）]，明显高于对照组[1.72（1.33-2.34）]；MLR[0.32（0.24--0.46）]明显高于对照组[0.21（0.18-0.25）]；ELR[0.027（0.008-0.056）]明显低于对照组[0.045（0.029-0.081）]；BLR[0.011（0-0.025）]明显低于对照组[0.021（0.01-0.026）]，差异有统计学意义（P 均<0.05）。NLR 与 CRP 明显正相关（r=0.2, P<0.001）,与 IgG、IgM 明显负相关（r=-0.131,-0.158,P=0.019，0.005）；MLR 与 CRP 明显正相关（r=0.162, P=0.003）,与 IgM 明显负相关（r=-0.134,P=0.017）；ELR 与 IgG、IgA 明显正相关（r=0.118、0.114, P=0.035,0.042）；BLR 与 CRP 明显正相关（r=0.113, P=0.041）。 ROC 曲线分析示 NLR 诊断 SLE 的曲线下面积（AUC）为 0.627（0.591-0.663），MLR 诊断 SLE 的 AUC 为 0.643（0.608-0.678），ELR 诊断 SLE 的 AUC 为 0.691（0.656-0.725）（P 均<0.01）；BLR 诊断 SLE 的 AUC 为 0.505（0.466-0.544）（P=0.794）。
结论 SLE 患者 NLR,MLR 明显升高，而 ELR,BLR 明显降低；NLR,MLR,BLR 可能反映 SLE 患者炎症状态；NLR,MLR 和 ELR 对 SLE 有较好的诊断价值。

PU-3792

NLS-RARα 在 APL 中的研究进展

叶娇
德阳市人民医院

急性早幼粒细胞性白血病（APL）属于急性髓系白血病，其特征是 15 号染色体与 17 号染色体分别断裂并易位形成了 PML-RARα 融合蛋白，血液学特征是粒细胞阻滞于早幼粒细胞阶段。APL 发病迅速，由于全身性弥漫性血管内凝血（DIC）等严重并发症导致早期死亡。ATRA 是 20 世纪

80 年代后期最具革命性的，被认为是近来用于白血病细胞分化治疗的最合适和最有效的药物之一。遗憾的是，ATRA 对于所有髓系白血病类型并不是非常有效，寻找新的诊断和治疗靶点已经刻不容缓。

PU-3793

强效血浆置换术治疗血栓性血小板减少性紫癜的临床指标观察

李艳红[1,3,4]、武坤[2,3,4]
1. 昆明医科大学第一附属医院
2. 昆明医科大学第一附属医院医学检验科
3. 云南省检验医学重点实验室
4. 云南省实验诊断研究所

目的 观察血栓性血小板减少性紫癜（TTP）患者经强效血浆置换术治疗后的临床检验指标，分析疗效和生存状况，探讨该治疗方法的临床意义。
方法 2017 年 2 月至 3 月，对我院血液科收治的 1 例血栓性血小板减少性紫癜患者行强效血浆置换术，并结合免疫抑制及营养支持进行综合治疗。
结果 本例 TTP 患者经过连续 11 次的血浆置换，结合其他相关治疗，最终痊愈出院。出院一年后，复查血常规检查、生化及凝血功能检查等指标，均接近或处于正常水平，随访至 2021 年 05 月未复发。
结论 TTP 患者病情危重，一旦确诊或高度怀疑，应尽早行强效血浆置换治疗，对降低死亡率，提高患者生存质量至关重要。关键词：强效血浆置换；血栓性血小板减少性紫癜；临床检验

PU-3794

应血栓弹力图分析慢性肾脏病患者高凝状态的危险因素

吴思弦、袁浩、周毅峰、龙贞义、彭亚梦、彭芳
湖南省人民医院

目的 应用血栓弹力图(TEG)分析慢性肾脏病(chronic kidney disease, CKD)患者凝血变化特征，及影响 CKD 患者高凝状态的危险因素。
方法 选取 2018 年 8 月~2019 年 5 月湖南省人民医院收治的 CKD 患者 128 例，比较不同阶段 CKD 患者和对照组（n = 21）的常规凝血试验和血栓弹力图(TEG)指标。根据 TEG 最大振幅(MA)将 CKD 患者分为高凝组（maximum amplitude (MA) > 68 mm，n = 66）和非高凝组（MA ≤ 68 mm，n = 62），比较两组间实验室指标，分析 CKD 患者高凝状态影响因素及相关性。
结果 （1）与对照组相比，CKD 不同阶段患者纤维蛋白原 (Fib)、D-二聚体水平明显增高，CKD 3-4 期、CKD 5 期未透析及 CKD 5 期透析患者反应时间(R)、K-时间降低，而 MA、α-角和凝血指数均升高。（2）高凝组与非高凝组在估算的肾小球滤过率（eGFR）、糖尿病比例、脑卒中史、中性粒细胞百分比、中性粒细胞淋巴细胞比值、红细胞计数、血红蛋白（Hb）、血小板计数（PLT）、血清肌酐、血清胱抑素-C、血清白蛋白、脂蛋白（a）等方面均存在显著差异（P<0.05）。其中 eGFR、PLT、和 Hb 水平是 CKD 患者高凝状态的独立影响因素。
结论 CKD 患者相对正常对照处于高凝状态。eGFR，PLT 和 Hb 可能是 CKD 患者高凝状态的危险因素。

PU-3795

The role of NLRP3 inflammasome in lymphoma

Kun Wu 、Mingxia Shi
First Affiliated Hospital of Kunming Medical University

The role of chronic inflammation in tumor progression has been demonstrated in previous studies. The activation of inflammasomes is mediated by the assembled signal of multi-protein complexes and the activation of inflammation-related caspase and maturation of inflammatory factors such as Interleukin-1 and Interleukin-18. Nucleotide binding oligomerization domain-like receptor family 3 (NLRP3) is the most well-studied type of inflammasome, which is closely related to the occurrence and development of many diseases such as inflammation and tumors. In recent years, several studies have explored the potential role of NLRP3 in lymphoma. In this review, we summarize current knowledge of NLRP3 in lymphoma and discuss its feasibility as a novel target.

PU-3796

贫血样本用于自动推片与手工推片在数字化细胞形态阅片仪上的评价分析

黄小天
电子科技大学附属医院.四川省人民医院医学检验中心

目的 探讨和分析贫血样本的自动推片和手工推片的质量控制，分别对外周血白细胞分类相关性分析。
方法 选取我院贫血样本 45 例，分别进行自动推片和手工推片，并采用数字化细胞形态阅片仪的外周血推片质量分析软件 SmearChecker 检测其单细胞层长度，采用数字化细胞形态阅片仪采集的红细胞概览图计数单层红细胞层不重叠的红细胞数量，并对数字化细胞形态阅片仪白细胞形态分析预分类后再经人工分类审核后的结果，分别于自动血细胞分析仪和人工显微镜镜检结果作比较进行线性回归分析。
结果 自动推片法制备的样本，相对于手工推片制备的样本，其单细胞层长度更长且合格率更高、红细胞概览图不重叠数量更多，数字化细胞形态分析仪白细胞分类结果与自动血细胞分析仪和人工显微镜镜检结果相关性更高。
结论 贫血样本在自动推片法制备的外周血推片质量和稳定性更高，有效的保证数字化细胞形态分析仪白细胞分类结果与自动血细胞分析仪和人工显微镜镜检结果相关性。

PU-3797

一例强效血浆置换术治疗血栓性血小板减少性紫癜的临床指标观察

李艳红
昆明医科大学第一附属医院

目的 观察血栓性血小板减少性紫癜（TTP）患者经强效血浆置换术治疗后的临床检验指标，分析疗效和生存状况，探讨该治疗方法的临床意义。
方法 2017 年 2 月至 3 月，对我院血液科收治的 1 例血栓性血小板减少性紫癜患者行强效血浆置换术，并结合免疫抑制及营养支持进行综合治疗。

结果 本例 TTP 患者经过连续 11 次的血浆置换，结合其他相关治疗，最终痊愈出院。出院一年后，复查血常规检查、生化及凝血功能检查等指标，均接近或处于正常水平，随访至 2018 年 11 月未复发。
结论 TTP 患者病情危重，一旦确诊或高度怀疑，应尽早行强效血浆置换治疗，对降低死亡率，提高患者生存质量至关重要。

PU-3798

未成熟血小板比率对评估造血干细胞移植效果的分析

丁爽
徐州医科大学附属医院

目的 探讨采用未成熟血小板比率(IPF)监测造血干细胞移植(HSCT)患者造血功能恢复的临床价值。
方法 采用 Sysmex XN-1000 全自动血细胞分析仪检测 120 例白血病患者 HSCT 后的 WBC、PLT、中性粒细胞绝对计数(ANC)、网织红细胞百分比 (RET%)及 IPF，并对结果进行对比分析。
结果 80 例患者移植后 IRF、ANC、RET%、WBC、PLT 分别在 16.2、19 .0、18 .6、20.4、25 .0 d 达到恢复指标。有 95.0%（76 /80）的患者 IRF 最早达到造血功能恢复的指标。IPF 达到造血功能恢复指标的时间要早于 WBC、PLT、ANC 及 RET%（P<0.05）。ANC 及 RET%达到造血功能恢复指标的天数要早于 WBC 及 PLT（P <0.05）。ANC 与 RET%间比较差异无统计学意义（P>0.05）。
结论 IRF 是 HSCT 后造血功能恢复较敏感的指标，可用于 HSCT 后造血功能恢复的监测、病情观察及指导临床治疗。

PU-3799

妊娠期易栓症患者经抗凝治疗后对凝血功能指标的调节作用

庄文玉
潍坊市中医院

目的 研究妊娠期易栓症患者经抗凝治疗后对凝血功能指数的调节作用。
方法 本次 54 例研究对象均来自 2019 年 1 月—12 月在我院接受治疗的妊娠期易栓症患者，均进行抗凝治疗。对比患者治疗前与治疗后凝血功能指数。
结果 治疗后 PT 和 APTT 指数比治疗前低，差异具有统计学意义（P＜0.05）。
结论 妊娠期易栓症患者经抗凝治疗后，凝血功能有明显的改善。

PU-3800

D-D，FDP 结果倒置原因分析

邢丽丽
西安医学院第一附属医院

目的 分析日常凝血检验中 D-D，FDP 结果倒置产生的原因和解决方案。
方法 选取我院凝血标本 4000 例中 38 例 D-D，FDP 结果倒置标本，按结果异常程度的不同进行分类分析。
结果 D-D，FDP 倒置产生主要集中在 FDP 结果低值时，另外类风湿因子的存在，标本溶血脂血也可导致 D-D，FDP 倒置。

1.分析为什么会出现这种情况，我们首先要从 D-D、FDP 来源说起。FDP 为纤维蛋白原及纤维蛋白在纤溶酶作用下的降解产物。纤维蛋白原在纤溶酶的作用下产生三个球形的产物 D、E、D 和 Bβ1-42。Aα 链上的极性附属物（含 A、B、C、H 片段）。统称为纤维蛋白原降解产物。交联纤维蛋白在纤溶酶的作用下，形成有极性的附属物的多聚体、D 二聚体、r-r 二聚体，或有些成分的片段以及 XYDE 片段。理论上 D 二聚体应该是 FDP 众多片段的一种。
》我科室 DD 的检测方法采用的是微粒凝集定量检测方法（免疫比浊法）。其原理是利用鼠抗人单克隆抗体、（8D3）共价包被的聚乙烯颗粒凝集。D 二聚体交联的区域具有立体对称的结构，即单克隆抗体作用的抗原表位出现两次。因此，一个抗体有足够能力触发凝集反应，从而浊度的升高可以用比浊法检测。FDP 检测方法也是免疫比浊法，其原理是利用鼠抗人 FDP 单克隆抗体胶乳颗粒发生抗原抗体反应，产生凝集以致浊度上升。通过测定浊度的变化量求出 FDP 的浓度。FDP 是一个混合物，那么其试剂中的单克隆抗体也是混合物，并非单一的抗体（具体抗原表位不详），由于设计的不同抗体的亲和力不相同，导致了在检测时两者并不完全具有可比性，在临床上仅作为参考。
2．我科室 FDP 定标采用多点定标，校准品含有不同浓度的人源性纤维蛋白和纤维蛋白原降解产物，采用因子稀释液做为校准品 0。包括 0，7.5，15.2，31，62，124 五种浓度，0 浓度到 7.5 浓度之间有较大的浓度空白区间。FDP 低浓度超过线性范围，结果准确性偏低。因此，在 FDP 低浓度时会产生 D-D，FDP 倒置现象。
3.病人体内存在较高浓度的 IgG，如类风湿因子等可能干扰检测。因为测定 D-D 采用免疫比浊法，将 D-D 的抗体包被在乳胶颗粒上，类风湿因子是一种变性的 IgG，它与形成的免疫复合物发生聚集，使结果偏高。FDP 因其检测片段较多，特异性不强，干扰物质对 FDP 的影响不是很大。因此，较高浓度的干扰物质会产生 D-D，FDP 倒置现象。
结论 D-D，FDP 倒置是由于方法学的缺陷及干扰因素导致的，但也有一定的临床价值。出现这种情况时，怀疑干扰导致时，可采用连续稀释方式排除干扰影响，同时结合 FDP 项目来辨别是否为真的增高。

PU-3801

17 例 CD 患儿的临床分析

鄂建飞、赵铭、杨浩、詹璐、郑茂
德阳市人民医院

目的 通过分析 17 例乳糜泻患儿临床特征以及血清特异性抗体 EMA、DGP 检出情况，提高临床对 CD 诊治的认识。
方法 选取 2018 年 1 月至 2020 年 10 月 CD 患儿 17 例作为观察组，选取健康儿童 30 例作为对照组，回顾性分析患者临床资料。
结果 17 例 CD 患儿腹泻次数平均每日 4 次。9 例（52.9%）患者表现为稀糊便，其中 5 例（29.4%）可见明显脂肪滴；5 例（29.4%）为糊状便，2 例（11.8%）为稀汁便。粪便苏丹Ⅲ染色阳性 7 例（41.2%）。伴随消化系统症状腹胀 12 例（70.6%）、纳差 11 例（64.7%）、腹痛 10 例（58.8%）。观察组 EMA-IgA 检测阳性 16 例（94.1%），EMA-IgG 检测阳性 14 例（82.4%），DGP-IgA 和 DGP-IgG 检测阳性 16 例（94.1%），均显著高于健康对照组，差异有统计学意义（P＜0.05）。DGP 检测效能指标最好，敏感性 94.1%，特异性 100%，阳性预期值 100%，阴性预期值 96.8%。
结论 乳糜泻导致的吸收不良主要表现为腹泻和腹胀。DGP 检测是血清特异性抗体检测的重要补充。

PU-3802

陕西地区 8724 例外周血染色体核型分析

杨冰
西安金域医学检验所有限公司

目的 探讨陕西地区遗传性疾病染色体异常的类型和发生率，旨在为临床染色体病的诊断及遗传咨询提供指导。
方法 选取陕西地区 8724 例遗传咨询者作为研究对象。抽取外周静脉血并通外周血淋巴细胞培养及秋水仙素处理，使其停止在分裂中期，经 G 显带后进行染色体核型分析，并统计异常核型的类型和发生率。
结果 在 8724 例外周血染色体核型分析中共检出异常核型 768 例，检出率为 8.80% 。其中染色体数目异常 259 例（33.72%），染色体结构异常 206 例（26.82%），染色体多态性变异 303 例（39.45%）。
结论 染色体核型异常是导致智力低下、发育迟缓、不孕不育、流产及胚胎停育、闭经等的重要原因之一。 临床上应重视对上述疾病的染色体核型检查，对寻找病因、指导优生优育、临床遗传咨询具有重要意义。

PU-3803

IgM 和 IgG 双克隆型华氏巨球蛋白血症一例报道并文献复习

李建新[1]、赖裕轶[2]、聂李平[1]、徐安平[1]、周宇[1]
1. 北京大学深圳医院
2. 南宁市第一人民医院

华氏巨球蛋白血症（Waldenstrom’s macroglobulinemia,WM）是由淋巴样浆细胞恶性增生，合成分泌大量单克隆巨球蛋白 IgM 所致的较为少见的疾病，在非霍奇金淋巴瘤中所占比例<2%。90%的患者检测出 MYD88 L265p 基因突变，可能为该疾病的致病原因。该病好发于老年人，临床表现为贫血、乏力、出血、脾肿大，淋巴结也可肿大，还可有感染、雷诺现象、高粘滞综合征，神经系统症状、视力下降、肾功能损害等。一般地，通常在患者血清中仅能检测到单克隆性 IgM 蛋白，IgM 和 IgG 双克隆 M 蛋白阳性病例极其罕见。本文报道一例 IgG-Kappa 和 IgM-Kappa 双克隆 M 蛋白同时表达的 WM 病例。

PU-3804

浅入探索肝功能不全与血小板减低的关系

孟双双、侯向萍
新疆生产建设兵团第一师阿拉尔医院

目的 通过对在医院就诊的肝功能不全患者的检查结果，进行统计分析，寻找肝功能不全患与血小板减低的关系。
方法 收集 2020 年 1 月至 2021 年 5 月肝功能不全患者病例，按年龄将其分为中青年组（18-45 岁）与中老年组（46-95 岁），将患者的常规生化检查数据（包括谷丙转氨酶、谷草转氨酶、碱性磷酸酶、GGT 等指标），与血小板结果做收集整理，应用 SPSS 统计分析软件对所得数据进行分析，看是否成线性关系，并于临床做进一步的追踪调查。
结果 收集 2020 年 1 月至 2021 年 5 月共 417 例肝功能不全患者，其中中青年组 106 例（25.42%，106/417），中老年组 311 例（74.58%，311/417），中青年组伴血小板减少 11 例（10.38%，

11/106），中老年组伴血小板减少 198 例（63.67%，198/311），分析检查数据得出：1.中老年组肝功能不全患者的严重程度与常规生化指标（包括谷丙转氨酶、谷草转氨酶、碱性磷酸酶、GGT 等）基本成正相关，肝功能不全越严重，生化指标越高。2.中老年组肝功能不全的患者比起中青年组肝功能不全的患者出现血小板减低的情况更为普遍，中老年组肝功能不全患者血小板比中青年组肝功能不全患者血小板明显减低，差异显著（P<0.05）。3.中老年组肝功能不全患者的严重程度与血小板减低的程度基本成线性关系，随着肝功能不全严重程度的增大，血小板减低的程度显著（P<0.05）。

结论 血小板减低的程度基本可以对中老年肝功能不全患者的严重程度起到提示作用，有助于临床对肝功能不全患者的预后治疗。

PU-3805

急性非心源性缺血性中风后复发中风的危险因素分析

张丽敏
首都医科大学附属北京天坛医院

背景 相当比例的急性非心源性缺血性脑卒中患者在标准治疗后经历复发性缺血事件。

目的 我们旨在早期识别复发性缺血事件预测的危险因素。

方法 纳入 286 例出现症状不到三天的非心源性缺血性脑卒中患者。

评估氯吡格雷治疗 7 天内和 1 一年内的出现任何复发事件患者的血管危险因素、入院时的常规实验室数据、血栓弹力图测试等指标。患者被分为病例组（出现临床不良事件的患者，包括缺血性中风、短暂性脑缺血发作、心肌梗塞和血管相关死亡率）和对照组（无事件患者）。缺血复发事件由受试者工作特征曲线和多变量逻辑回归分析确定。

结果 43 例患者（病例组）出现临床不良事件。入院时病例组患者的患者的平均血小板体积(MPV)、血小板/淋巴细胞比 (PLR)、淋巴细胞计数 (LY) 和纤维蛋白原 (Fib)和对照组相比，有明显升高(P<0.001)。氯吡格雷后治疗 7 天后，病例组 ADP 诱导的血小板聚集率（ADP%）水平较低，而病例组的最大振幅（MA）水平高于对照组（P<0.01）。LY、PLR、Fib、MA、ADP%和 MPV 的受试者工作特征（ROC）曲线下面积（AUC）分别为 0.602、0.614、0.629、0.770、0.800 和 0.808。逻辑回归分析表明，MPV、ADP% 和 MA 确实是预测因素。

结论 MPV、ADP%和 MA 是急性非心源性缺血性中风术后缺血事件复发的危险因素。应尽可能快的向这些患者提供紧急评估和个体化药物治疗

PU-3806

血浆病毒载量对 HIV，HBV 共感染患者肝脏影响的研究

赵苛岑
陆军军医大学第一附属医院（西南医院）

分析血浆病毒载量对 HIV、HBV 共感染患者肝脏的影响。

方法 选取 2018 年 5 月-2020 年 6 月我院收治的 HIV 感染合并乙型肝炎患者 80 例为研究组，A 组为 40 例患者一直服用抗病毒药物，B 组为 40 例较晚服用抗病毒药物，分析患者的血浆病毒载量，谷丙转氨酶(ALT)、谷草转氨酶(AST)、总胆红素(TBIL)、白蛋白(ALB)水平，分析血浆病毒载量与肝功能的相关性。

结果 A 组 ALB 水平高于 B 组，而 AST、HIV RNA 载量、ALT、TBIL 水平低于 B 组(P<0.05）；在 A 组患者中，一直注射抗病毒药物的患者 HBV DNA 载量、HIVRNA 载量及 ALT、AST、TBIL 水平最低，而 ALB 水平最高，随着注入抗病毒药物的增加， HBV DNA 载量、HIV RNA 载量及 ALT、AST、TBIL 水平逐渐下降，ALB 逐渐升高，差异均有统计学意义(P<0.05）；以 A 组患者资料为样

本，进行血浆 HIV 病毒载量与肝功能指标的 Pearson 相关检验分析：血浆 HIV 病毒载量与 ALT、AST、TBIL 呈正相关，与 ALB 呈负相关（P＜0.05）。
结论 血浆病毒载量对 HIV 感染的影响具有正相关性，对乙肝患者肝脏呈负相关性，HIV 病毒载量升高，HIV 感染加重，肝受损严重

PU-3807

A case of a severe FXI deficiency in a Chinese pregnancy woman

Yingyu Wang、Ping Ma
The Affiliated Hospital of Xuzhou Medical University

Congenital factor XI deficiency is a rare disorder characterized by low coagulant activity, associated with a variable injury-related bleeding diathesis. However, the severity of bleeding does not correlate with plasma FXI coagulant levels. This makes management of these patients difficult. Here, we present a case of 35-year-old pregnancy woman who was born from an consanguineous family. She was found to have a markedly prolonged activated partial thromboplastin time during antenatal examination. Further study reveled the activity and antigen levels of factor XI in the proband were 4 and 11%, respectively. Thus diagnosis of severe FXI deficiency (cross-reacting material negative, type I) can be made. she did not show any bleeding tendency in the past. Notablely, she gives birth to a daughter four weeks later, and no post-partum hemorrhage occurred also.

PU-3808

血栓弹力图在鉴别诊断血友病 A 和抗磷脂综合征中的作用

刘禹、许冠群、王学锋、武文漫
上海交通大学医学院附属瑞金医院

目的 分析探讨血栓弹力图(TEG)在鉴别诊断血友病 A(HA)和抗磷脂综合征(APS)中的作用。
方法 收集 2010 年 1 月至 2021 年 6 月上海交通大学医学院附属瑞金医院收治的 HA 患者 38 例（其中包括 23 例遗传性 HA 和 15 例获得性 HA）和狼疮抗凝物质阳性的 APS 患者 133 例。分别对 HA 患者进行凝血因子Ⅷ活性测定，对 APS 患者进行狼疮抗凝物质测定，同时对两组患者进行 TEG 检测。比较各组间和亚组间各指标的差异，并绘制 TEG R 时间的受试者工作特征曲线(ROC)。
结果 HA 和 APS 两组间 TEG R 时间的差异有统计学意义(Z=-7.181,p＜0.001)，曲线下面积(AUC)为 0.882(95%CI:0.816～0.948)，cut-off 值为 12.80min，其诊断灵敏度为 73.68%，特异性为 93.23%。遗传性 HA 与获得性 HA 两组间 TEG R 时间的差异有统计学意义(Z=-3.784,p＜0.001)，AUC 为 0.858(95%CI:0.734～0.982)，cut-off 值为 18.50min，其诊断灵敏度为 93.33%，特异性为 82.61%。
结论 TEG R 时间可用于 HA 和 APS 的鉴别诊断中。

PU-3809

微流控凝血分析仪自动化 APTT 纠正试验性能评估

宋鉴清
中国医科大学附属第一医院

目的 微流控凝血分析仪自动化 APTT 纠正试验在临床应用中的性能评估。
方法 比较普施康 MC500 仪器的自动化 APTT 纠正试验与用希森美康 CS-5100 进行的手工 APTT 纠正试验结果是否一致；分析判读结果与临床诊断是否相符。
结果 使用 SPSS23.0 软件进行统计学分析，用两种方法测定并计算的两组 RI-0h 值具有相关性（回归方程 Y=0.97X+7.05;相关系数 r=0.618）。仪器自动化 APTT 纠正试验和手工 APTT 纠正试验两种方法对凝血因子缺乏血浆样本判定结果的临床符合率分别为 62.5%和 37.5%，对狼疮阳性血浆样本判定结果的临床符合率分别为 17.2%和 65.6%，对凝血因子八抑制物阳性样本判定结果的临床符合率均为 100%。
结论 普施康 MC500APTT 自动化 APTT 纠正试验结果与利用希森美康 CS-5100 进行的手工 APTT 纠正试验操作结果具有一致性，但对狼疮阳性血浆样本结果判读的临床符合率低于手工 APTT 纠正试验。

PU-3810

因肝功能衰竭诱导血栓性血小板减少性紫癜案例分析 1 例

王妍[1]、赵慧茹[2]、邢丽丽[1]、马瑜婷[1]、袁博[1]
1. 西安医学院第一附属医院
2. 北京积水潭医院

目的 分析 1 例风湿性心脏病患者因肝功能衰竭导致血栓性血小板减少性紫癜发生，以提高对 TTP 的鉴别诊断。
方法 选取某医院收治的风湿性心脏病患者 1 例，该患者行冠脉搭桥+主动脉球囊反博植入术后，因血小板不明原因减少局部紫癜形成伴 D 二聚体升高 2 日等临床症状，对该病例进行完整鉴别分析，从而总结 TTP 的临床诊断要点。
结果 该病例进行了 DIC、HIT 等相关鉴别实验后，提示该病例是因患者心功能衰竭至肝脏灌注不足，血管性血友病因子裂解酶（ADAMTS13）分泌异常而至 TTP 发生。
结论 血管性血友病因子裂解酶对 TTP 的鉴别诊断具有临床意义，血浆置换可改善患者临床结局。

PU-3811

Establishment of the risk prediction model for significant bacteriuria in adult patients with automated urine analysis

jianmin li
Taian Central Hospital

Introduction Urinary Tract Infections (UTIs) have been proven to be the most encountered bacterial infection in humans. We hope to establish a prediction model for significant bacteriuria by comprehensively analyzing the relevant parameters of age, gender and urine automatic analysis data.
Methods A retrospective study was performed at Tai'an central Hospital. All samples included in the study were tested for urine culture and urine automatic analysis. Data analysis was conducted with the SPSS.

Results The binary logistic regression module is used to establish the forecast formula, which gender, age, leukocyte count, bacterial count, leukocyte esterase and nitrite were included. Receiver Operating Characteristic (ROC) curves showed that the area under ROC curve (AUC) of the prediction model was 0.878, bigger than the AUCs of the other six independent variables. The sensitivity and specificity of prediction model were 61.68% and 95.98% respectively. The positive predictive value and the negative predictive value of the predictive model is 87.13% and 85.02% respectively.
Conclusions The prediction formula obtained in our study can achieve good prediction effect for significant bacteriuria, which can effectively avoid the treatment delay or antibiotic abuse caused by the subjective judgment of doctors.

PU-3812

血浆凝固曲线波形分析临床应用的最新进展

旷永君、伍柏青
江西省人民医院

凝固曲线波形分析(Clot waveform analysis,CWA)是近年发展起来的一种基于凝血试验过程并对凝固曲线进行分析的新技术，其除了报告凝血时间之外，还能提供被测标本整体凝血状态的许多有用信息。关于血友病 A(Hemophilia A,HA)患者的诊断和治疗，以及弥漫性血管内凝血和脓毒症的早期诊断及预后，新型冠状病毒肺炎(Corona Virus Disease 2019,COVID-19)和狼疮抗凝物(Lupus anticoagulant,LA)的诊断等潜在临床应用方面，均有许多研究成果发表。大量研究展示了凝固曲线分析提高患者管理的能力，特别是这种工具价格低廉、能够快速分析，而且通过带有光学检测系统的凝血分析仪就可以获得。本文通过广泛回顾与 CWA 研究相关的文献，综述其潜在的临床应用，希望能对临床疾病的诊断、治疗提供帮助。

PU-3813

SAA 与 CRP 联合检测应用于早期感染预判及鉴别感染类型的临床效果评价

钱朵朵、陈燚琼、蔡玉婵
同济大学附属杨浦医院

目的 探讨 SAA(血清淀粉样蛋白 A)与 CRP(C-反应蛋白)在早期感染、不同感染类型、感染严重程度不同时，绘制两者升高曲线并判断 SAA 与 CRP 在早期感染与不同感染类型患者中的实际临床应用价值。
方法 同时选取白细胞总数正常但诊断为初发感染患者 9 例；白细胞总数大于医学参考范围的已知中期感染患者 12 例；已达白细胞总数危急值（>30*109/L）患者 7 例。使用 QuikRead go 仪器测定选取标本 CRP 值及 Genrui PA200 测定 SAA 值；判断两者测定值是否会伴随感染的程度增加而升高、升高速度、升高幅度是否一致，即灵敏度、敏感性、特异性指标方面的评价；升高曲线做图横坐标为 CRP 浓度，纵坐标为 SAA 浓度，并计算 SAA/CRP(SCR)来判断感染的类型。
结果 早期初发感染患者的 CRP 升高 3 例，未升高 6 例、SAA 均升高，升高幅度均大于 CRP；已知中期感染患者 CRP 升高 8 例，未升高 1 例、SAA 均升高，升高幅度已远大于 CRP；重度感染患者 SAA 与 CRP 均已升高，都有很大程度的升高。画图计算 SCR 发现，病毒感染患者 CRP 早期不升高或仅稍许升高；而 SAA 早期升高，且升高幅度大，并随病毒感染严重程度直线快速上升。细菌感染患者 CRP 与 SAA 均早期升高、但随着细菌感染的进展，SAA 值升高幅度将低于 CRP 升高幅度，出现较明显的背离现象（即 SCR 比值将不会一直增加），差异具有统计学意义（P<0.05）。

结论 SAA 对于反映早期感染及病毒感染的灵敏度、特异性优于 CRP（即 SAA 阴性可排除细菌和病毒的感染，而 CRP 阴性仅排除细菌感染）；SAA 同 CRP 一同适用于细菌早期感染的诊断，且两者比值 SCR 能更清楚地区分轻、中、重度细菌和病毒感染。大大提到了临床的正确诊断率，降低了临床的误诊与漏诊。

PU-3814

尿微量白蛋白测定在糖尿病早期肾损伤诊断中的价值

徐红燕[2]、杨晓平[1]
1. 中国人民解放军医院第九七O医院
2. 中国人民解放军医院第九七O医院

目的 这次研究的主要目的是为了解糖尿病早期肾损伤的诊断中尿微量白蛋白（mALB）的作用。
方法 收集 2019 年 6 月至 2019 年 10 月在中国人民解放军联勤保障部队第九七〇医院的糖尿病患者、糖尿病肾病患者及健康者的病例共 137 例，糖尿病患者 64 例，糖尿病肾病共 73 例，对取本院军人健康管理体检中心的 30 例健康者作为对照组，采用免疫投射比浊法检测尿微量白蛋白的水平，同时用胶乳免疫比浊法对血液中的胱抑素 C（Cys-C）和 β2-微球蛋白（β2-MG）的含量。根据近期来医院进行检查的糖尿病患者的检查结果进行统计学分析，判断早期肾损伤的指标。
结果 经非参数分析，三组数据之间均有显著差异（P<0.05），具有统计学意义。糖尿病肾病组、糖尿病组和正常对照组三组变量之间进行对比，有显著差异，糖尿病肾病组的三项检查结果均高于剩于两组。除正常对照组外，其他两组进行对比，有显著差异，且糖尿病肾病组明显。
结论 通过尿微量白蛋白、胱抑素 C 和 β2-微球蛋白联合检测，可得知尿微量白蛋白对检测糖尿病早期肾损伤具有重要价值。

PU-3815

迈瑞 BC-7500 全自动血液细胞分析仪的性能验证及评价

陶晓燕[1,2]、柳洁[1]、黄燚[1]、牟勇[1]、傅珺[1]
1. 电子科技大学附属医院·四川省人民医院
2. 中南大学湘雅医院

目的 验证迈瑞 BC-7500CRP 全自动血液细胞分析仪的分析性能。
方法 参照参照国际血液学标准委员会（ICSH）、WS/T 406-2012《临床血液学检验常规项目分析质量要求》及美国临床和实验室标准化委员会相关文件，对 BC-7500 CRP 全自动血液细胞分析仪的本底计数、携带污染、精密度、正确度、准确度、线性范围和实验室内的结果可比性等指标进行性能验证。
结果 迈瑞 BC-7500 CRP 全自动血液细胞分析仪的本底计数和携带污染均符合标准；仪器的批内精密度和批间精密度良好；准确度、正确度均通过验证；线性范围宽，符合标准；实验室内不同仪器间的结果具有可比性。
结论 迈瑞 BC-7500 CRP 全自动血液细胞分析仪在本实验室能达到厂家声明的分析性能，检验结果的准确可靠，是一种较理想的全血细胞分析仪。

PU-3816

SYSMEX XN-350 血球仪在脑脊液和胸腹水白细胞计数中的可行性探讨

孟荣
西安医学院第一附属医院

目的 探讨 SYSMEX XN-350 血液分析仪(简称 SYSMEX XN-350)的体液模式在脑脊液和胸腹水白细胞计数中应用的可行性。
方法 分别采用手工显微镜镜检法和 SYSMEX XN-350 对 100 例脑脊液和胸腹水标本进行白细胞计数，结果 XN-350 检测体液中高、中和低值有核细胞的变异系数(CV) 均低于仪器设定标准，重复性好;与手工显微镜镜检法相比，SYSMEX XN-350 所测结果差异无统计学意义(P＞0.05); XN350 分析仪 WBC 和 RBC 测定结果与手工计数法有良好的相关性（ r ＞0.98），各项指标的验证结果均符合厂商的技术指标要
求。
结论 XN-350 体液检测模式精密度高，线性范围宽，与手工显微镜计数有较好的符合性，其操作简单易行，结果稳定可靠，适用于日常临床脑脊液标本的检测.但如果仪器进行样品检测时报警，应当手工镜检复核，以提高结果的准确性和可靠性。

PU-3817

用 RET 和 RDW-CV 可初步鉴别缺铁性贫血与地中海贫血

马丽菊[1]、尹艳[2]、邵文萍[1]、万秋涵[1]
1. 昆明医科大学第一附属医院
2. 昆明医科大学

目的 从自动血细胞分析仪一次检验结果中，寻找能快速初步鉴别缺铁性贫血与地中海贫血的外周血液学指标，为临床早期诊断治疗提供有价值的线索。
方法 回顾性分析昆明医科大学第一附属医院 2020 年 1 月至 2021 年 4 月门诊及住院病人缺铁性贫血 72 例、地中海贫血 52 例及健康体检 31 例，对血常规中红细胞平均体积(mean corpuscular volume，MCV)、红细胞平均血红蛋白量（mean corpuscular hemoglobin，MCH）、红细胞体积分布宽度（red cell volume distribution width，RDW-CV）、网织红细胞（reticulocyte count，RET）等各参数进行统计分析，探究三组间上述红细胞指标的差异与关系。
结果 本研究发现：（1）贫血程度方面，缺铁性贫血组共 72 例，其中轻度贫血 22 例（30.56%）、中度贫血 47 例（65.28%）、重度贫血 3 例（4.16%）；地中海贫血组共 52 例，其中轻度贫血 35 例（67.31%）、中度贫血 15 例（28.85%），重度贫血 2 例（3.84%）。缺铁性贫血组以中度贫血占优势，地中海贫血组以轻度贫血为主。（2）轻度贫血时， MCV、MCH 在两贫血组均明显低于对照组（P＜0.05），而缺铁贫组 MCV、MCH 大于地贫组（P＜0.05）； RDW-CV 在两贫血组明显大于对照组（P＜0.05），两贫血组 RDW-CV 无差异（P=0.221）；RET 在对照组、缺铁贫组明显小于地贫组（P＜0.05），但对照组与缺铁贫组无明显差异（P=0.308）。(3)中度贫血时，MCV、MCH 在两贫血组亦明显低于对照组（P＜0.05），但两贫血组间无明显差异（P =0.702，P=0.149）；RDW-CV 在两贫血组明显大于对照组（P＜0.05），缺铁贫组 RDW-CV 明显小于地贫组（P<0.05）；两贫血组 RET 均明显高于对照组，但两贫血组间无明显差异（P=0.079）。
结论（1）检测 MCV、MCH、RDW-CV、RET，能够协助诊断缺铁性贫血与地中海贫血。（2）小细胞低色素贫血时，在轻度贫血中，RET 明显高于参考范围、而 MCH、MCV 小幅升高时，地贫的可能性更大；中度贫血者，若 RDW-CV 明显增加，则地贫的可能性为大。（3）重度贫血时，缺铁贫的 MCH、MCV、RET、RDW-CV 均低于地贫。

PU-3818

含氯消毒剂（84）在泌尿系感染（革兰氏阴性双球菌感染）检验中的应用

洪国勇
贵州金域医学检验中心

目的 观察含氯消毒剂（84 消毒液）在泌尿系统感染（革兰氏阴性双球菌感染）检验中的应用及效果。
方法 对 137 例革兰氏阴性双球菌引起的感染患者尿标本进行分组观察，对患者尿标本对含氯消毒剂（84 消毒液）敏感性进行统计分析。
结果 含氯消毒剂（84 消毒液）在尿标本中反应水平与革兰氏阴性双球菌感染呈现正相关，随着感染程度增高，含氯消毒剂（84 消毒液）在尿标本中的反应越明显。

PU-3819

COVID-19 腹泻患者实验室指标分析及感染致结肠组织单细胞基因表达变化的研究

宋晓东[1,2]、夏欣一[2]
1. 连云港市第一人民医院
2. 中国人民解放军东部战区总医院

目的 通过回顾性研究，统计分析新冠相关腹泻患者与非腹泻患者的临床特点、检测指标、疾病病程、疾病结局等差异；通过分析尸检患者结肠组织单细胞基因表达变化探讨新冠患者腹泻的可能发病机制以及粪口传播途径的可能。
方法 收集 2019 年 12 月至 2020 年 4 月在武汉火神山医院住院期间伴随腹泻症状病例，剔除其他明显致病因素导致的腹泻病例，如消化道肿瘤、使用抗生素后导致的一过性腹泻后共 343 例，设置为腹泻组。通过倾向性匹配评分消除了年龄、性别、并发症等混杂因素设置了对照组。统计分析两组间病情严重程度、病程、治疗结局、检查指标差异。在腹泻组中，比较隐血阳性组与阴性组的疾病严重程度、病程，临床转归等差异。此外，对一份腹泻患者冷冻建库的尸检结肠组织做单细胞测序，结果与公共数据集作比较，找出存在的分子与基因表达差异。
结果 腹泻组患者性别分布无差异，年龄分布以中老年为主，相比对照组病危重度评分要高。腹泻组病人大便常规结果多为正常，粪便隐血阳性 83 例，临床转归比隐血阴性组要差，其余检查指标腹泻组相比非腹泻组无统计学差异（P>0.05）。新冠腹泻病人结肠尸检测序结果 ACE2、AQP1、AQP3、AQP8 等表达与公共数据集中结果有差异，ACE2 表达的差异表明了新冠病毒可以通过 ACE2 受体结合直接入侵肠上皮细胞，提示病毒粪口途径传播的可能性；而 AQP1、AQP3、AQP8 表达差异则验证了患者腹泻多为非水样性腹泻这一特点。
结论 新冠患者伴随腹泻症状的出现可能加重患者病情，影响病情转归。应当重视新冠相关腹泻症状的早期发现和大便隐血指标的检测，尽早进行临床干预同时警惕粪口途径的传播。

PU-3820

Bone marrow particle enrichment analysis for the laboratory diagnosis of multiple myeloma: A case study

Congming Zhang、Yanan Zhang
The Third Xiangya Hospital of Central South University

Background Bone marrow smear and biopsy are the main Methods for the diagnosis of multiple myeloma (MM), bone marrow infiltration, and metastasis in lymphoma and cancer. However, several factors, including the focal growth of tumor cells, inappropriate puncture sites, and hemodilution of bone marrow aspirates, lower the rate of target cell detection. To solve this problem, we developed a novel method—bone marrow particle enrichment analysis—and here, we describe this procedure and its use in the diagnosis of a rare case of MM.
Methods An 88-year-old man with primary gastric gamma delta T-cell lymphoma (γδTCL) was found to have anemia. As the cause of anemia could not be determined, hemodilution was suspected, warranting the re-examination of the bone marrow aspirate. Re-puncture could not be performed because of the patient's age and unwillingness to undergo this procedure. Hence, we used a novel approach to enrich bone marrow particles and isolate marrow cells, and subsequently performed morphological and flow cytometric analysis.
Results Examinations performed after bone marrow particle enrichment revealed the presence of myeloma cells, and the patient was diagnosed with primary gastric γδTCL accompanied by MM.
Conclusions Bone marrow particle enrichment analysis may be applied to overcome the problems caused by hemodilution of bone marrow aspirates and to improve the rate of tumor cell detection. The application of this method for the diagnosis of hematological disorders should be explored further.

PU-3821

Differential diagnosis of thalassemia and iron deficiency anemia using CellaVision Advanced Red Blood Cell software

Fei Wang
Peking Union Medical College Hospital

Background Morphological changes of red blood cells (RBCs) in patients with thalassemia and iron deficiency anemia (IDA) had different patterns, with potential value of differential diagnosis. However, quantitative analysis of RBC morphologic changes manually is time-consuming and subjective, which limits its use in differential diagnosis. The aim of this study is to evaluate the CellaVision Advanced RBC Software as a prescreening tool of differential diagnosis of thalassemia and IDA in routine screening of blood smears.
Methods Forty-seven thalassemia and Forty-six IDA cases were recruited. CellaVision DM96 Advanced RBC Software was used to analyze RBC morphology.
Results Specific patterns of quantitative changes of RBC shapes were found between thalassemia and IDA patients. Thalassemia patients had more target cells, teardrop cells and stomatocytes while IDA patients had more hypochromatic cells, ovalocytes and echinocytes. Target cells as a single parameter, was the best morphological cell type to distinguish thalassemia from IDA with area under the curve (AUC) of 0.79, following hypochromatic cells with AUC of 0.70. Combined target cells and hypochromatic cells together by T/H ratio (target cells %/hypochromic RBC %) showed better differential diagnosis ability than every single parameter with AUC of 0.88. Cut-off value of 1.755 for T/H ratio showed a sensitivity of 80.43 and a specificity of 81.48, respectively, for thalassemia vs IDA.

Conclusions Target cell/hypochromasia ratio by CellaVision Advanced RBC Software is a relatively simple and economic screening index that gives direction for further diagnostic testing of thalassemia and IDA.

PU-3822

甲状腺结节患者的凝血功能研究

陈俊丽、王佳宁
中国医科大学附属第一医院

目的 探讨凝血指标与甲状腺激素水平的相关性及他们在甲状腺结节患者病情进展中的变化规律，研究甲状腺结节患者凝血功能的特点及其相关机制。
方法 选取 2020 年 7 月至 2021 年 3 月中国医科大学附属第一医院收治的甲状腺结节患者 110 例设为患者组，其中包括甲状腺良性结节 55 例，甲状腺恶性结节 55 例。随机选取同期入院健康体检者 140 例设为对照组。通过测定各组血浆凝血酶原时间（PT）、活化部分凝血活酶时间（APTT）、凝血酶时间（TT）、纤维蛋白原（FIB）和 D-二聚体（D-D）水平，及血清促甲状腺激素（TSH）、游离甲状腺素（FT4）和游离三碘甲状腺原氨酸（FT3）水平，比较分析良恶性患者凝血功能状态及其与甲状腺功能的相关性。
结果 1. 凝血指标比较
患者组 PT 水平显著低于健康对照组（P＜0.01），且良恶性组之间 PT 水平无统计学差异；患者组 APTT 水平低于健康对照组（P＜0.05），且良恶性组之间 APTT 水平无统计学差异；患者组 FIB 水平显著高于健康对照组（P＜0.01），且良恶性组之间 FIB 水平无统计学差异；患者组 TT 水平变化与健康对照组之间无统计学差异（P＞0.05）；患者组 D-二聚体水平变化与健康对照组之间无统计学差异（P＞0.05）。
2. 相关性分析
甲状腺良性结节患者的凝血指标与甲状腺激素不存在相关性。甲状腺恶性结节患者的 FIB 与 FT4 存在弱负相关（P＜0.05）；PT 与 FT3 存在显著弱负相关（P＜0.01）；APTT 与 FT3 存在弱负相关（P＜0.05）。
结论 1. 与正常健康者相比，甲状腺结节患者普遍存在凝血功能的紊乱，血液处于高凝状态，有血栓形成倾向。
2. 甲状腺恶性结节患者血浆 PT、APTT、FIB 与甲状腺相关激素之间存在一定相关性，但相关性不强，提示甲状腺功能状态的异常能够对甲状腺恶性结节患者的凝血功能产生一定影响，但作用不大，可能还不需要进行临床特殊干预。

PU-3823

厦门地区育龄妇女常规优生血清学筛查结果分析

陈海明[1,2]、王涛[1,2]、黄宇[1,2]、王前明[1,2]
1. 厦门大学附属第一医院检验科
2. 厦门市基因检测重点实验室

目的 分析厦门地区育龄妇女常规优生血清筛查结果，为本地区的优生保健工作提供数据参考。
方法 采用多重微珠流式免疫荧光法对 2018 年 1 月－2020 年 12 月在厦门大学附属第一医院就诊的 3070 例育龄妇女进行 TORCH 血清特异性抗体检测，并对其结果进行回顾分析。
结果 TORCH-IgM 总阳性率为 11.04%（339/3070），单项病原体阳性率为 10.59%（325/3070），合并两种以上感染阳性率为 0.46%(14/3070),其中以 HSVⅡ-IgM 阳性率最高，为 6.5%，其次分别是 CMV-IgM（1.7%）、HSVⅠ-IgM（1.6%）、RV-IgM（0.8%），TOX-IgM 最低（0.5%）；

TORCH-IgG 中 HSVⅠ-IgG 、CMV-IgG、RV-IgG、HSVⅡ-IgG、TOX-IgG 阳性率分别为 86.4%、82.1%、65.6%、11.6%、0.7%。此外 TORCH 感染具有一定季节性，夏、秋两季为 HSVⅡ病毒感染的高发季节；RV 病毒夏季感染率较高，分别与春、冬季相比，差异有统计学意义（P＜0.05）。在不同年龄分组阳性率分布方面，TORCH-IgM 在各年龄组间无明显差异（P＞0.05）；高龄组 TOX-IgG、CMV-IgG、HSVⅠ-IgG 、HSVⅡ-IgG 阳性率及合并感染率均明显高于低龄组，组间差异有统计学意义（P＜0.05），而低龄组 RV-IgG 阳性率明显高于高龄组，组间差异有统计学意义（P＜0.05）。

结论 厦门地区育龄妇女人群中存在一定比例的 TORCH 感染，应加强孕前检测及成人风疹疫苗接种宣传教育力度，建议育龄妇女孕前及围产期都应进行 TORCH 筛查，以便尽早进行临床干预，以防不良妊娠，实现优生优育。

PU-3824

血栓弹力图应用于预测冠脉介入术后心血管不良事件的临床价值

陈卫红
湖北省中西医结合医院

目的 观察血栓弹力图应用于预测 ACS 患者 PCI 术后心血管不良事件的临床价值。

方法 以自 2015 年 1 月-2016 年 4 月于我院就诊并进行 PCI 的 320 例 ACS 患者为研究对象，包括急性心肌梗死患者 146 例，不稳定心绞痛患者 174 例，所有患者 PCI 术后进行 TEG 检测，统计分析不同组患者 R、K、Angle、MA 和 CI 等 TEG 参数指标水平差异情况，随访患者 PCI 术后 24 个月内冠脉再狭窄、支架内血栓、非致死性心肌梗死、再次血运重建、心源性死亡等 MACE 发生情况，分析 ACS 患者 TEG 参数指标与 PCI 术后 MACE 的相关性。

结果 在全部进行 PCI 的 320 例 ACS 患者中，随访 24 个月内 MACE 发生率为 21.88%（P<0.05），AMI 组患者 PCI 术后 MACE 发生率（24.66%）高于 UAP 组患者水平（19.54%），但不具有统计学意义（χ2=1.216，P=0.270>0.05）；AMI 组与 UAP 组患者 R、K、Angle、MA 和 CI 等 TEG 参数指标水平差异不具有统计学意义（P>0.05）；MACE 组患者 R 和 K 指标数值显著低于非 MACE 组患者水平，而 MACE 组患者 PCI 术后 Angle、MA 和 CI 指标数值显著高于非 MACE 组患者水平（P<0.05）；R 和 K 数值均与 ACS 患者 PCI 术后 MACE 的发生呈负相关性（P<0.05），而 Angle、MA 和 CI 数值均与 ACS 患者 PCI 术后 MACE 的发生呈正相关性（P<0.05）。

结论 TEG 参数指标水平与 ACS 患者 PCI 术后 MACE 的发生密切相关， TEG 对 ACS 患者 PCI 术后 MACE 具有一定的预测价值，可用于指导 PCI 术后治疗和不良反应的预防，临床应予以重视。

PU-3825

儿童 ADP 诱导的血小板最大聚集率与血栓弹力图 MA 值的对比分析

苗文佳、李刚
北京儿童医院

目的 比较 ADP 诱导血小板最大聚集率与血栓弹力图 MA 值检测儿童血小板聚集功能差异。

方法 收集 2019 年 1 月至 2020 年 8 月期间我院血液专业门诊就诊患儿 124 例，对二磷酸腺苷诱导 LTA 血小板最大聚集率与 TEG 的最大振幅 MA 值进行相关性分析，探讨两种方法差异产生原因。

结果 LTA 检测血小板聚集功能的阳性率 40.3%高于 TEG(22.6%)，差异有统计学意义（R<0.05）。ADP 诱导的血小板最大聚集率与 MA 值具有弱相关性（r=0.248，R<0.05）。

结论 LTA 与 TEG 存在一定的相关性，各有优势及自身局限性，相互之间不可替代。

PU-3826

载脂蛋白 A1 抗体作用于人精子后抑制其活力并影响小鼠体外受精

池秀平、孟美玲、王新颖、赵书平
泰安市中心医院

目的 载脂蛋白 A1 抗体对人精子活力和小鼠受精率的影响。
方法 基础研究 收集 2020 年 10 月份来泰安市中心医院健康查体的精液标本 20 例，经过密度梯度离心(40%/80%)留取高活力精子进行实验。设空白对照组、兔多克隆 IgG 组（40 μg/ml）、APOA1 抗体处理组即不同浓度 APOA1 抗体（10、20 和 40 μg/ml）处理高活力精子标本，37 ℃温箱孵育 1、2 和 4 h 后，通过计算机辅助系统(CASA)观察人精子前向运动变化。采用免疫荧光法检测 APOA1 蛋白在小鼠精子的表达。40 μg/ml 的 IgG 抗体和 APOA1 抗体孵育小鼠精子 1h 后，进行体外受精实验，观察受精率的差异。精子前向运动的变化采用独立样本 t 检验，小鼠体外受精率的差异采用卡方检验。
结果 APOA1 抗体作用于人高活力精子后，随着抗体浓度增加和孵育时间延长，精子前向运动逐渐下降。精子前向运动孵育 1h 后空白对照组（66.58±5.47）与 APOA1 抗体浓度 20 μg/ml 组（50.8±10.98）和 40 μg/ml 组（47.28±9.88）间差异具有显著统计学意义，t 值分别为 t=2.865，3.822，P 分别为 P <0.05， P <0.01。孵育 2 h 后空白对照组（72.14±9.01）与 APOA1 抗体浓度 10 μg/ml 组（58.16±9.46）、20 μg/ml 组（51.2±11.3）和 40 μg/ml 组（44.4±10.48）间具有统计学差异，t=2.393，3.240，4.482，P 分别为 P<0.05，P<0.05，P<0.01。孵育 4 h 后空白对照组（69.16±6.48）与 APOA1 抗体浓度 10 μg/ml 组（51.9±11.75）、20 μg/ml 组（41.2±13.9）和 APOA1 抗体浓度 40 μg/ml 组（34.9±13.72）间差异具有显著统计学意义，t=2.870，4.076，5.043，P 分别为 P<0.05，P<0.05，P<0.01。小鼠精子中 APOA1 蛋白位于精子头部，小鼠体外受精实验 IgG 组卵裂率为 81%，APOA1 抗体处理组为 35%，差异具有显著统计学意义，2=48.664，p<0.001。
结论 APOA1 蛋白在维持精子活力中有一定作用，其抗体作用于精子后会抑制体外受精率。

PU-3827

门诊患者阴道分泌物病原菌的检出率及其年龄、季节分布特征

杨双双
重庆医科大学附属第一医院

目的分析我院门诊患者阴道分泌物的病原菌分布以及其与年龄和季节的关系；
方法统计 2018 年 11 月～2020 年 11 月门诊患者阴道分泌物的革兰染色镜检结果，计算阴道加德纳菌、滴虫、假丝酵母菌（出芽孢子和/或假菌丝）三种病原菌的检出率及其混合检出率，进一步分析其检出率的年龄和季节分布特征；
结果研究期间共检测阴道分泌物 42327 例，检出假丝酵母菌 6941 例（16.40%），阴道加德纳菌 3283 例（7.76%）、阴道毛滴虫 309 例（0.73%）以及混合感染 529 例（1.25%）。三种病原菌的检出率表现出显著且不同的年龄分布特征，但仅假丝酵母菌具有显著的季节分布特征，以冬季检出率最高；
结论我院门诊患者阴道分泌物病原菌以假丝酵母菌为主，在<20 岁门诊患者和冬季最为常见。

PU-3828

基于机器学习的阿尔兹海默病诊断模型的建立研究

余抒、李如飞
重庆市重钢总医院

目的 通过机器学习算法提取特异性指标参数特征，拟合血清蛋白标志物、临床智能评分（MMSE）、影像学纹理值参数，采用随机森林建立阿尔兹海默病（Alzheimer's disease, AD）诊断模型，为 AD 的早期精准诊断提供实验依据。
方法 本研究从样本库中随机抽取 170 例 AD 及 170 例非 AD 样本进行队列研究，采用区域增长法得到 11 个 MRI 纹理值参数；同时，采用高效液相芯片技术检测 34 种血清蛋白表达，通过多元线性回归分析蛋白组间差异，将具有统计学差异（$p<0.05$）的蛋白纳入建模体系；拟合血清生物标志物、临床智能评分、影像学诊断多维参数，采用随机森林算法进行建模，将各标志物和因素按照重要性系数从高到低进行排序，采用迭代的方法依次将各标志物或者因素加入模型，并利用样本集训练模型的卡分阈值(Threshold, T)选取模型参数。采用 SPSS 17.0 统计学软件分析、比较模型的预测能力，选择受试者特征曲线(receiver operating characteristic curve，简称 ROC 曲线)下面积(AUC)最大为最优组合模型。
结果 研究得到以 8 个蛋白为基础的诊断模型，分别为 Leptin、IL13、IL1α、IP10、Resistin、IL3、PAL1、TNFα，来自细胞因子、代谢因子以及生长因子家族，具备不同的生物学特性和功能，通过差异表达分析，疾病组与对照组差异显著，具有统计学意义。随机森林的分类树经过 ROC test 分析后，发现含 MMSE 的模型之间没有显著差异（$p > 0.05$），其中 p 值最小的比较组合为 0.0622596，即模型 A（8 个指标+MMSE+MRI）和模型 B（MMSE+自然信息），模型 A 的错误率分析仅为 4.05%，已达到诊断建模中的错误率低限，特异性和敏感度分别达到 97.6%和 88.6%，ROC 曲线下面积为 0.9846(95%置信区间：0.95-0.99)，为最优组合。
结论 通过机器学习算法—随机森林，在高维复杂变量中分析模型的分类精度、泛化能力和稳定性，该研究从统计学分析、参数优化、模型效能多方面开展 AD 的诊断学模型研究，建立了随机森林算法的数学模型，同时发现 8 个关键血清蛋白质在判断是否有患病趋势的诊断中具有潜在价值。本研究提供了基于血清蛋白标志物在 AD 诊断中的应用前景，同时也首次将随机森林这样的数学算法应用到适合中国人群的大规模筛查中。

PU-3829

UF5000 尿液分析仪在肿瘤患者尿路感染中的应用价值探讨

翟丽[1]、张永瑞[1]、任苒[2]、高莉丽[1]
1. 云南省肿瘤医院
2. 昆明医科大学学生

目的 泌尿道感染（UTI）作为泌尿系统常见的疾病之一，本课题所研究的是应用受试者工作特征曲线（ROC）来探讨尿液分析仪 Sysmex-UF5000 的相关检测项目——白细胞（WBC）计数以及细菌（BACT）计数在肿瘤患者 UTI 中的应用价值。
方法 标本来自是 2020 年 10 月至 2021 年 3 月昆明医科大学第三附属医院门诊及住院疑似尿路感染的肿瘤患者的清洁、无终止中段尿，分别进行定量尿培养和 Sysmex-UF5000 检测 WBC 与 BACT 计数。
结果 1.127 例尿标本中细菌培养阳性 55 例，阳性率 43.31%，病原菌多为革兰氏阴性菌。 2.大肠埃希菌的直线回归方程为：$y = 0.969x - 0.295$，金黄色葡萄球菌的直线回归方程为：$y = 0.9754x + 0.0481$，即定量尿培养与 sysmex-UF5000BACT 计数两者检测所得结果之间的相关关系良好。 3.以定量尿培养作为金标准，与 sysmex-UF5000 检测 BACT 计数和 WBC 计数的测定值均取对数后进行 ROC 曲线的绘制，曲线下面积（AUC）分别为 0.87 和 0.71；选取最佳尤登指数处的 BACT

计数>=452.2/ul，WBC 计数>=124.95/ul 作为最优临界值。以该值作为临界值时，BACT 计数的敏感度(Sen)为 76.4%、特异度(Spe)为 97.2%、诊断准确度(Acc)为 88.19%、阴性似然比（NLR）为 0.24、阳性似然比（PLR）为 27.29、阴性预测值（NPV）为 84.34%、阳性预测值(PPV)为 95.45%；其 WBC 计数的敏感度(Sen)为 52.7%、特异度(Spe)为 81.7%、诊断准确度(Acc)为 69.29%、阴性似然比（NLR）为 0.58、阳性似然比（PLR）为 2.88、阴性预测值（NPV）为 69.41%、阳性预测值（PPV）为 69.05。
结论 Sysmex-UF5000 可用于尿液中各类细菌的计数，检测速度快，能够有效缩短报告时间。为临床提供了简单便捷、快速有效的诊断指标，可指导早期临床经验用药及合理应用抗生素，缩短诊疗时间。

PU-3830

不同地区 COVID-19 患者的临床特征

高骞
中南大学湘雅医院

目的 研究表明湖南与武汉地区 COVID-19 患者临床特征存在显著差异，了解不同地区 COVID-19 患者之间临床特征的差异有助于医生结合实际情况进行更有针对性的诊断与治疗。了解不同地区 COVID-19 患者之间临床特征的差异，比较在疾病发展过程中患者临床特征的变化。
方法 比较 320 例武汉地区患者与 794 例非武汉患者之间临床特征的差异；对所收集到的 21 例湖南省患者进行分类，分为重症患者组和非重症患者组，比较自就诊 30 天后患者各项指标之间变化趋势的差异。
结果 武汉与非武汉地区的临床特征总体来说具有显著的差异，其中武汉地区有更多的患者会出现疲劳与呼吸困难症状，实验室检查表现为淋巴细胞降低、中性粒细胞增加、凝血酶原时间和 D-二聚体异常、心肌酶异常；非武汉地区有更多的患者会出现咽痛与肌肉酸痛的症状、实验室检查表现为中性粒细胞减少；武汉地区表示肝肾功能的实验室指标、感染相关生物标志物、胸部 CT 的表现与非武汉地区没有显著差异。重症与非重症患者的大多数临床指标的变化趋势是具有显著差异性的。其中重症患者表现为更低的淋巴细胞分类计数水平；嗜酸性粒细胞增多在疾病好转时出现；重症患者具有更高的丙氨酸氨基转移酶、肌酸激酶、肌酐、D-二聚体水平。
结论 长沙与武汉地区 COVID-19 患者临床特征不同

PU-3831

全自动血细胞分析仪红细胞碎片参数检测性能评价

李轶勋、王丽英、夏春燕、陈睿、斯南卓玛
昆明医科大学第一 附属医院

目的 红细胞碎片（FRC）是全自动血液细胞分析仪提供的一项新参数，其与血栓性微血管病等密切相关。本文将对血液细胞分析仪红细胞碎片的检测性能进行评价。
方法 参考中华人民共和国卫生行业标准 WST 406-2012《临床血液学检验常规项目分析质量要求》，通过携带污染率、精密度、线性、正确度、灵敏度、特异度等指标，对 SYSMEX XN 系列全自动血液细胞分析仪红细胞碎片的检测性能进行评价。所有数据采用 Excel 软件进行分析整理。
结果 SYSMEX XN 系列全自动血细胞分析仪检测红细胞碎片的携带污染率为 0.11%；批内精密度：各实验浓度下其变异系数（CV）分别为 8.75%（FRC：42.15×109/L ）、6.38%（FRC：83.42×109/L ）、4.57%（FRC：228.74×109/L）、5.31%（FRC：796.89×109/L）；线性验证：线性回归方程为 Y =0.9939X +10.961，相关系数为 R2 =0.99；正确度验证：以人工镜检为金标准，仪器法与其比较，其相关系数为 R2 =0.82，灵敏度为 92%，特异度为 82%。

结论 SYSMEX XN 系列全自动血液细胞分析仪检测红细胞碎片快速、简便，携带污染率低，精密度尚佳，线性范围满足要求，与人工镜检法相比具有较好的相关性，特异度和敏感度也较高。血液细胞分析仪可作为外周血红细胞碎片的快速筛查手段，但其检测的精密度仍需进一步提高，且由于方法的局限性，阳性标本需要在显微镜下进行确认。

PU-3832

PLT-F 通道在 EDTA-K2 依赖性血小板聚集病例中的价值

施琦
同济大学附属杨浦医院

目的 血细胞分析仪是检验最常用的仪器之一，血小板技术检测则是其中一项重要检测指标，对多种临床疾病的诊断、治疗具有重要的意义。而在血小板检测中易受溶血、红细胞碎片、抗凝剂等诸多因素的影响，其中又以依赖 EDTA-K2 抗凝剂所引起的假性血小板减低更易被忽视。目前检验科最常用的血细胞分析仪为 SYSMEX 系列，分别有 PLT-I、PLT-O、PLT-F 三种通道计数血小板，本文探讨 SYSMEX XN9000 血细胞分析仪的 PLT-F（荧光血小板）通道在 EDTA-K2 依赖性血小板聚集病例中的价值。
方法 随机选取门诊及病房中出现 EDTA-K2 依赖性血小板聚集的抗凝血标本 10 份，须同时留取同一病人的枸橼酸钠抗凝血标本并进行推片染色。将各标本在相同情况、时间段内分别在 PLT-I 通道和 PLT-F 通道进行检测，同时显微镜下观察血小板聚集情况，进行手工计数校准。
结果 显微镜下血小板呈微聚集的标本 PLT-I 通道与 PLT-F 通道结果相差较大(差异具有统计学意义)，其中 PLT-F 通道结果更接近枸橼酸钠抗凝标本的结果；显微镜下血小板呈大片聚集的 EDTA-K2 标本两通道结果相差不大，且与枸橼酸钠抗凝标本结果差异较大。
结论 SYSMEX XN9000 血细胞分析仪的 PLT-F 通道可以排除由疾病或药物引起的微小、一过性 EDTA 依赖性血小板聚集的干扰，当出现血小板不明原因降低时，应采用 PLT-F 通道进行复查，并推片染色观察并采用手工计数法进行校准。

PU-3833

探讨血小板指标在 HBV 肝炎肝硬化进程中的变化

王海霞
重庆医科大学附属第一医院

目的 探讨 HBV 肝炎肝硬化进程中血小板数量（PLT）、平均血小板体积（MPV）、血小板分布宽度（PDW）、血小板最大聚集率的变化。
方法 根据《慢性乙型肝炎防治指南》的纳入排除标准，选择我院住院病人 226 例，其中慢性乙型肝炎非复制期组 27 例，慢性 HBV 携带者组 50 例，非活动性 HBV 携带者组 26 例，HBeAg（+）慢性乙型肝炎组 31 例，HBeAg（-）慢性乙型肝炎组 37 例，慢性乙型肝炎肝硬化代偿期组 21 例，慢性乙型肝炎肝硬化失代偿期组 34 例。采用 SPSS17.0 软件包对各组间 PLT、MPV、PDW 指标进行组间差异性分析，$P<0.05$ 具有统计学意义，并进行受试者工作曲线分析。另外，收集慢性乙型肝炎住院患者 66 例，其中 HBV 感染携带肝功正常组 36 例，慢性乙型肝炎组 18 例，慢性乙型肝炎肝硬化组 11 例。采用江苏英诺华公司 PL-12 血小板功能分析仪检测血小板聚集功能。
结果 1. PLT 在疾病进程中呈降低趋势，但肝功能正常（慢性乙型肝炎非复制期、慢性 HBV 携带者与非活动性 HBV 携带者）组间、慢性乙型肝炎（HBeAg+与 HBeAg-）组间、慢性乙型肝炎肝硬化（代偿期与失代偿期）组间均无显著性差异（$P>0.05$）；肝功正常组、慢性乙型肝炎组、慢性乙型肝炎肝硬化组间差异具有统计学意义（$P<0.05$）。

2. PLT 临界值在肝功正常组与慢性乙型肝炎组间为 181.5×109/L（AUC=0.634）（图 1A），慢性乙型肝炎肝硬化组与肝功正常组间为 126.5×109/L（AUC=0.951）
3.MPV、PDW 仅在慢性乙型肝炎肝硬化组增高，MPV 临界值为 11.25fl（AUC=0.596），PDW 临界值 13.35（AUC=0.63）。
4.ADP、AA 最大聚集率在 HBV 携带肝功能正常组与慢性乙型肝炎组组间差异较小（P<0.05），在慢性乙型肝炎肝硬化组最低（P<0.05）
结论 在 HBV 感染进程中，PLT 呈下降趋势；当发展为慢性乙型肝炎肝硬化时 MPV 和 PDW 增高，最大聚集率最低。

PU-3834

吉林地区 34466 例粪便筛查中肝吸虫感染情况分析

潘一娜
吉林大学第一医院

目的 分析吉林省肝吸虫主要分布情况，为肝吸虫筛查防治提供依据。
方法 对 2021 年 1 月至 2021 年 5 月，我院收治的 34466 例粪便常规检查中 65 例肝吸虫阳性的患者进行回顾性分析。在阳性患者中，分析肝吸虫感染城市间的感染率差异，比较长春市、白城市、松原市、白山市、吉林市、通化市及四平等市不同城市间阳性患者所占比率、不同性别所占比率、就诊科室人数、年龄所占比率进行分析。
结果 粪便筛查共 34466 例，肝吸虫阳性率为 0.19%（65/34466)。分析肝吸虫感染城市间的感染率差异，阳性患者中比较不同城市的所占比率。来自白城市阳性患者所占比率为 49.2%（32/65）,主要分布在大安市占 29.2%（19/65）,其次是镇赉县占 13.9%（9/65)；来自长春市阳性患者所占比率为 24.6%（16/65）,主要分布在长春市区（15.4%,10/65），其次九台市占 4.6%（3/65）；来自松原市阳性患者所占比率为 12.3%（8/65）;通化市 6.2%（4/65）;白山市 4.6%（3/65）;吉林市 0.2%（1/65）;四平市 0.2%（1/65）。按性别分男性的阳性率占比 80%（52/65）,女性阳性率占比 20%（13/65）,男性明显高于女。按就诊科室分布心血管中心 22 例、肝胆胰内科 5 例、肿瘤中心 8 例、神经内科 6 例、肾病科 6 例、内分泌、老年病、干部病房和呼吸科各 3 例，小儿消化、风湿科和胃肠内科各 2 例，小儿呼吸、ICU 和全科医学各 1 例。按年龄组分，小于<11 岁组 1.55%(1/65)、11-20 岁组 3.1%(2/65)、21-30 岁组 1.5%(1/65)、31-40 岁组 3.1%(1/65)、41-50 岁组 15.4%(1/65)、51-60 岁组 33.8%(22/66)、61-70 岁组 35.4%(23/67)、>70 岁组 6.2%(4/67)，整体随年龄增长呈增高趋势，尤其是 41 岁以后的年龄组升高幅度大。
结论 整体肝吸虫感染率虽低，但感染存在地域趋势，只是白城市感染率明显高于其他城市，几乎是省内其他城市的总和。感染人数分布在各个年龄段，已中老年感染人群为主，也不乏儿童感染，男性明显高于女性。通过统计，绝大多数患者并不是出现消化系统相应症状直接就诊于与消化系统有关的科室，而是因不同疾病前往相应科室就诊，通过粪便常规检查筛查出虫卵，只有少数几例是以消化系统问题甚至出现肝吸虫病继发病症急性发作前来就诊。注重肝吸虫虫卵的筛查，尤其是高发地域，高发年龄群的重点筛查，在面对不明诱因消化系统疾病时，更应关注粪便筛查的重要性，做到尽早发现尽早治疗。

PU-3835

免疫无标记型急性淋巴细胞白血病的临床特点

陈颖洁
山东大学第二医院

目的 了解免疫无标记型急性淋巴细胞白血病!"##$的临床特点。
方法 对 ++, 例形态学 上诊断为 "## 的病例，取其外周血或骨髓，分离出单个核细胞，应用 "3""3 法作免疫表型分析，对免疫 无标记型病例的临床特点、化疗疗效及预后进行了观察。
结果 +(例患者未表达任何系统性分化标记， 或仅表达 45*-、6#"758 或 45’ 等非系限性抗原。与分化型 "## 相比，免疫无标记型 "## 肝、脾、淋巴 结肿大及纵隔肿块发生率与白细胞数量均较高，化疗完全缓解率!48$较低!!9)&)2$，存活期较短!!9)&)%$。
结论 免疫无标记型 "## 有其临床上的特殊性，预后较差。

PU-3836

90 例急性髓系白血病患者免疫表型与 FAB 分型相关性分析

陈颖洁
山东大学第二医院

本研究通过分析急性髓系白血病(AML)患者免疫表型的特点,探讨急性髓系白血病免疫标记与 FAB 分型的关系，旨在建立准确完善的诊断体系。 90 例初诊患者均行骨髓穿刺，经细胞形态学诊断为急性髓系白血病，根据 FAB 分型分为 6 个亚型：2 例 M1、31 例 M2、13 例 M3、15 例 M4、28 例 M5、1 例 M6；同时采用四色流式细胞术检测 90 例 AML 患者相关抗原表达。结果显示，AML 患者最常见表达髓系抗原 MPO、CD117、CD33、CD13，同时伴有少量淋系抗原表达。流式细胞术将 90 例 AML 分为 2 例 M0、2 例 M1、25 例 M2，13 例 M3，15 例 M4，32 例 M5，1 例 M6；**结论** 急性髓系白血病诊断中 FAB 分型与免疫表型分析具有高度一致性，其在白血病 MICM 综合诊断体系中占有重要地位，综合细胞形态学、免疫表型分析及遗传学，对 AML 患者诊断、分型及预后评估具有重要意义。

PU-3837

国产与进口 vWF 抗原检测试剂盒的性能评价

何利娜、高爱民、蔡华雅、赵旭初
北京九强生物技术股份有限公司

目的 采用胶乳免疫比浊法对国产血管性血友病因子抗原（vWFAg）进行测定，以验证其性能是否满足厂家声明，以及是否能够达到或超越进口试剂盒的性能要求。
方法 对北京九强生物技术股份有限公司生产的 vWFAg 试剂盒的精密度、测量标物和线性进行验证评价，并分别与进口沃芬和 Stago 的 vWFAg 试剂盒对临床样本测值进行比较。
结果 九强公司生产的 vWFAg 试剂盒在 TOP ACL 750 仪器上检测 3 个不同水平的质控样本批内不精密度分别为 0.8%、0.9%和 0.9%，日间不精密度分别为 2.8%、3.6%和 3.2%，测量标物的平均结果为 103.0%，线性评价回归方程 y=328.12x-1.3657（R2=0.9976）；进口沃芬 vWFAg 试剂盒检测 3 个不同水平批内不精密度分别为 1.9%、1.7%和 2.2%，日间不精密度分别为 2.6%、3.4%和 3.9%；测量标物的平均结果为 94.6%；线性评价回归方程 y=273.94x+4.5157（R2=0.985）；九强 vWFAg 试剂盒在 TOP ACL 750 上检测临床样本的结果和沃芬进口试剂盒结果的相关性

y=0.9722x＋2.8806，R2=0.9857；在 Stago R MAX 仪器上，九强 vWFAg 试剂盒与 Stago 试剂盒的相关性 y=1.0373x-3.4503，R2=0.9827。

结论 北京九强生物技术股份有限公司生产的免疫比浊法 vWF 试剂盒与进口沃芬 vWF 试剂盒在 TOP ACL 750 全自动血凝分析仪上测量批内精密度更优，日间精密度结果相当，九强试剂盒和沃芬的比对相关性较好；线性优于进口沃芬试剂盒。此外，九强 vWFAg 试剂盒与进口 Stago 的测值相关性也较好。九强 vWFAg 试剂盒性能已经达到或超越了进口试剂盒。

PU-3838

LncRNA BC200/miR-150-5p/Myb 正反馈环促进骨髓增生异常综合征的恶性增殖

刘兆平[1,2]、袁顺玲[1]、王攀[3]、王妍妍[1]、曹鹏飞[4]、文锋[1]、荔辉[3]、朱林[3]、梁龙[3]、王梓[3]、胡彬[3]、刘静[3]、萧小鹃[3]、张济[2]

1. 南华大学附属第一医院
2. 深圳市中医院
3. 中南大学
4. 中南大学湘雅医院

Myelodysplastic syndrome (MDS) is a group of heterogeneous hematologic malignancies. Understanding the molecular mechanisms of the specific roles of long noncoding RNAs in MDS would create novel ways to identify diagnostic and therapeutic targets. Here, we found that BC200 was highly expressed in MDS patients compared with normal individuals. Knockdown of BC200 inhibited MDS cell proliferation, colony formation and cell cycle progression in vitro and suppressed the growth of MDS cells in vivo. Mechanistic investigations revealed that BC200 functioned as a miRNA sponge to positively regulate the expression of MYB through sponging miR-150-5p and subsequently promoted malignant proliferation of MDS cells. Conversely, we found that BC200 was a direct transcriptional target of MYB, and knockdown of MYB abolished the oncogenic effect of BC200/miR-150-5p. Taken together, our results revealed that the BC200/miR-150-5p/MYB positive feedback loop promoted the proliferation of MDS cells and is expected to be a potential biomarker and therapeutic target in MDS.

PU-3839

关于 XE–2100 血细胞分析仪淋巴细胞分类复检规则的验证

夏春燕、马晓波
昆明医科大学第一附属医院

目的 对本实验室淋巴细胞百分比的复检规则进行验证，探索适合本实验室关于淋巴细胞分类异常报警的人工镜检标准。

方法 选取本院 2016.3-2017.3 期间血常规标本 522 例，其中关于淋巴细胞百分比异常增高报警 230 例，无淋巴细胞百分比异常报警 292 例。从可靠性、真实性方面对两种结果进行分析。

结果 ①ROC 曲线下面积为 0.967。②仪器对淋巴细胞百分比异常报警的灵敏度为 97.39%、特异度为 96.92%、假阳性为 3.08%、假阴性为 2.61%、一致性为 97.13%、Kappa 值为 0.94。③参照 Rümke 表关于白细胞分类计数 95%可信区间，计算仪器检测与人工镜检分类结果的符合率。第一组（<50）:91.3%、第二组（50~59）:91.3%、第三组（60~69):92.7%、第四组（>70）:68.8%。

结论 本实验室制定的复片规则能很好的指导临床工作，在此基础上，当淋巴细胞百分比异常增高

在 50%-69%的范围内有较高的符合率，在排除异常报警（异型淋巴细胞、有核红细胞、原始细胞等）的情况下，在此范围内可涂片镜检，无需进行人工分类。

PU-3840

达肝素钠对进展期胃肠道恶性肿瘤患者凝血及纤溶系统功能的影响

陈卓诚[1]、杨伟[2]
1. 深圳市罗湖医院集团医学检验实验室
2. 深圳市罗湖医院集团罗湖区人民医院

目的 探讨达肝素钠注射液对进展期胃肠道恶性肿瘤患者凝血及纤溶系统功能的影响。
方法 选取 2018 年 09 月～2021 年 04 月在深圳市罗湖医院集团肿瘤内科治疗的进展期胃肠道恶性肿瘤患者 60 例，根据血栓预防治疗指南，Caprini 评分＞3 分者予达肝素钠注射液: 5000IU，1 次/d，常规皮下注射抗凝 10d。分别于达肝素钠治疗前 d0、治疗 d5、d10 后抽取外周静脉血，采用凝固法通过凝血测试仪检测凝血酶时间(TT)、凝血酶原时间(PT)、纤维蛋白原(FNG)、活化部分凝血酶时间(APTT)。采用免疫比浊法检测 D-二聚体(D-D)水平。通过化学发光仪器 HISCL-5000 检测血栓调节蛋白(TM)、凝血酶抗凝酶复合物(TAT)、组织型纤溶酶原激活抑制复合物(PIC)、纤溶酶-α2-抗纤溶酶复合物(t-PAIC)水平。
结果 治疗前 d0 与治疗 d5、d10 后不同时间点各检测指标比较，结果显示: D-二聚体(D-D) [(2.40±0.22) mg/L vs (1.64±0.15)、(1.70±0.15) mg/L]，血栓调节蛋白(TM) [(19.48±5.52) TU/ml vs (16.77±4.75)、(17.17±5.04) TU/ml]，凝血酶抗凝酶复合物(TAT) [(7.50±1.24) ng/ml vs (6.52±1.06)、(6.61±1.05) ng/ml]，组织型纤溶酶原激活抑制复合物（t-PAIC）[(14.31±3.98) ng/ml vs (13.18±3.88)、(13.14±3.81) ng/ml]水平均较治疗前 d0 均显著降低，差异具有统计学意义(P<0.01)。达肝素钠注射液预防使用 d10 比使用 d5 出现的不良事件增多，差异具有统计学意义(P<0.05)。
结论 监测凝血和纤溶标志物有助于早期发现患者血液高凝状态，达肝素钠注射液明显下调机体凝血和纤溶标志物分子水平。

PU-3841

Platelet to lymphocyte ratio is associated with in-hospital mortality in patients admitted to the emergency department

军 周
First affiliated Hospital of Nanjing Medical University / Jiangsu Provincial people's Hospital

Background The objective of this study was to test the hypothesis that an elevated platelet to lymphocyte ratio (PLR) at admission is associated with and increased risk of mortality in patients admitted to the emergency department (ED).
Methods We performed a retrospective analysis of patients admitted to the ED between January 2016 and February 2019. We included patients who were older than 60 years who visited the ED with medical problem. Baseline PLR values were measured at the time of admission. The primary outcome was all-cause in-hospital mortality.
Results A total of 500 patients were included in this study. The median age was 71 years (IQR 65–91), and 267 patients were male. The PLR value was higher innonsurvivors than in survivors. Multivariate showed that PLR was associated with all cause in-hospital mortality after adjusting for confounding factors.
Conclusions These results show that the PLR at admission is associated with in-hospital mortality among patients (>60 years) ED

PU-3842

探索人工智能阅片仪在血细胞形态教学中的应用

李庆、李轶勋
昆明医科大学第一附属医院

血液细胞形态识别是医学检验专业学生日后从事血液病诊断工作必须掌握的知识和技能，同时也是教学的重点和难点。如何提高学生对血液细胞形态学学习兴趣以及识别能力，成为教学的重点和难点。若采用传统的教学模式，老师对细胞形态进行讲解，学生应用显微镜对血液细胞形态进行观察学习，这种教学模式容易让学生难以理解和掌握。目前，人工智能阅片仪已广泛应用于各大教学医院，基于人工智能的新技术、新设备逐步在医学检验领域崭露头角。2019 年底，在新型冠状病毒肺炎疫情下，各学校将课程转移至线上教学，教师可以通过人工智能阅片仪收集典型图片，结合微信、QQ、APP 等移动教学平台进行教学，积极响应疫情防控要求。本文将在血液细胞形态学教学领域，探索运用人工智能阅片仪建立参考细胞图库、典型病例细胞图库等教学资源库，进行病例讨论式教学以及利用人工智能阅片仪的细胞分类软件进行学生实践能力考核，增强师生互动。教学研究结束后，与传统教学模式相比，客观上学生的理论知识成绩、细胞识别能力均得到提高，主观上学生对课程的满意度、自主学习的能力、临床思维的能力也得到了提升。

PU-3843

A simple model predicting in-hospital death in patients with type A acute aortic dissection

Ning Dong
Jiangsu People's Hospital

Background Type A actue aortic dissection (TAAAD) is a destructive cardiovascular disease, with high morbidity and mortality rates. Identifying the high-risk TAAAD patients at an early stage is an urgent need.
Methods A retrospective study of 160 patients was conducted. The admission data was retrospectively gathered. Logistic regression analysis and receiver operator characteristic curve (AUC) was utilized.
Results Compared with the survivor group, the nonsurvivor group was older, had higher D-dimer levels, red blood cell distribution width (RDW) levels and platelet distribution width (PDW) levels and lower fibrinogen levels, platelet levels and plateletcrit levels. Multivariate analysis displayed that four independent factors, age (hazard ratio (HR): 7.877, 95% confidence interval (CI) 2.740-22.641, P<0.001), D-dimer (HR: 3.791, 95% CI 1.520-9.452, P=0.004), RDW (HR: 3.300, 95% CI 1.109-9.825, P=0.032), PDW (HR: 3.755, 95% CI 1.436-9.815, P=0.007) were incorporated into the model. The predict accuracy of the model (AUC 0.857, 95% CI 0.852-0.863, P<0.001) was best.
Conclusions Age, D-dimer, RDW and PDW are independent markers of in-hospital death in TAAAD patients and the newly established model has better performance in predicting high-risk patients. This model can be used as a quick screening tool to assess the prognosis of patients in individualize.

PU-3844

新型尿液分析仪 UF5000 在疑似尿路感染病人中快速筛查应用研究

李江
湖南省人民医院

目的 评估新型自动化尿有形分析仪 UF-5000 在筛查疑似尿路感染患者尿培养阴性的分析性能，并研究新细菌革兰染色信息(Bact-info)用于评估尿路感染细菌革兰染色阴 / 阳性与尿培养结果的相关性。
方法 收集 1162 名疑似尿路感染的患者的晨起的第一次尿或随机尿或清洗后的中段尿，并在 2 小时内完成各项检测。将每个样本分成两份，一管用于尿培养，另一管用 UF-5000 尿有形成分仪分析。收集患者的检测结果数据资料，分析 UF-5000 在快速筛查疑似尿路感染病人的中的应用价值。
结果 在 1162 例尿培养标本中，239 例为阳性(20.6%)，923 例为阴性(79.4％)。在 1162 例相应的 UF-5000 分析的标本中，315 例为阳性（27.10%），847 例为阴性（72.90%）。在评估 UF-5000 尿有形成分分析仪快速筛查疑似尿路感染病人的性能方面，UF-5000 检测细菌的敏感度为 100%，特异度为 91.77%，阳性预测值为 75.87%，阴性预测值为 100%，诊断效率为 93.46%，阳性似然比为 12.15，阴性似然比 0。使用 UF-5000 的 BACT-info 信息正确识别了 72.7％(101/139)的病例，Cohen’S kappa 一致性为 0.781(x2=32.61，p<0.001)。UF-5000 细菌菌落计数结果与标准尿培养结果之间呈现较好的等级相关性。
结论 UF-5000 分析尿液有很高的敏感度和阴性预测值，且特异性和阳性预测值都不低，有望成为临床快速筛查疑似尿路感染病人的首选，可以减少不必要的抗生素使用，提高医院的诊断水平和患者的就医质量。

PU-3845

HNL、PCT、CRP、IL-6 在血流感染中的应用

朱益佳
南京大学医学院附属鼓楼医院

目的 探讨人中性粒细胞载脂蛋白（HNL）、降钙素原（PCT）、C 反应蛋白（CRP）、白介素-6（IL-6）在诊断血流感染中的应用价值。
方法 选取血培养阳性的患者（血流感染组）79 例和健康体检人群（健康对照组）92 例，检测所有患者的中性粒细胞载脂蛋白（HNL）、降钙素原（PCT）、C 反应蛋白（CRP）、白介素-6（IL-6）的水平。采用受试者工作曲线（ROC 曲线）评价各项指标诊断血流感染的效能。联合分析 HNL、PCT、CRP、IL-6 在血流感染中的应用价值。
结果 血流感染组 HNL、PCT、CRP、IL-6 水平显著高于健康对照组（P<0.000 1 ）。
结论 HNL、PCT、CRP、IL-6 联合应用在诊断血流感染患者中具有较好的价值。

PU-3846

临床医学检验中血液细胞检验质量控制要点分析

陈洁
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 探究在临床医学检验中，标本检测温度、存放时间对血液细胞检验质量产生的影响。

方法 将我院 2018 年 4 月～2019 年 3 月内的 70 例健康人群作为研究对象展开，对比不同放置时间（恒定温度 24～25 度）、不同检测温度下（恒定时间 30 min）的血液细胞结果。

结果 相对于 3 h，30 min 内检测结果是最准确，p<0.05;相对于 19-20℃，27-28℃，检测温度在 24-25℃时的结果最准确，P<0.05。

结论 标本检测温度以及存放时间等因素均会对血液细胞检测结果产生影响，所以要求我们必须做好各环节工作，将采集完成后的标本存放在适宜的环境内，在 30 min 内进行检验，并且要确保检测温度在 24～25 度左右，从而保证检验结果准确性。

PU-3847

应用四项新型凝血指标评估妇科肿瘤手术患者的凝血功能

罗玲清、陈燕
福建省肿瘤医院

目的 检测妇科肿瘤患者手术前、后凝血及纤溶分子标志物的变化及探讨其临床意义。

方法 以 55 例健康体检者为对照组，92 例妇科肿瘤患者为研究组（良性肿瘤组 38 例、恶性肿瘤 54 例）。研究组于术前、术后 1d、3 d、5 d、7 d 分别采血，采用高敏化学发光免疫分析方法检测上述标本中凝血酶-抗凝血酶复合物（TAT）、纤溶酶-α2-抗纤溶酶复合物（PIC）、组织型纤溶酶原激活剂及其抑制剂-1 复合物（tPAI·C）、血栓调节蛋白（TM）的表达水平。

结果 恶性肿瘤组术前的四项指标水平均较健康对照组及良性肿瘤组升高（P<0.05），良性肿瘤组术前仅 TAT 及 TM 水平高于健康对照组（P<0.05）；恶性肿瘤组术后 1d、3d、5d 的 PIC 及 TAT 水平均高于术前（P<0.05），tPAI·C 仅在术后第 1d 较术前高（P<0.05），但 TM 水平术前术后无差异（P>0.05），但均高于正常组；良性肿瘤组术后四项指标仅在术后第一天短暂性的升高，术后 3d 即恢复至术前水平或者正常水平。除了术后第一天的 TM，恶性肿瘤组 tPAI·C、TM、TAT、PIC 表达均明显高于同一时期的良性肿瘤组。

结论 妇科恶性肿瘤患者机体内存在着明显的凝血与纤溶系统功能的异常，TAT、PIC、tPAI·C、TM 等指标的动态检测和分析有利予血栓前状态的判断，对预警血栓形成具有重要意义。

PU-3848

P13K/mTOR 信号通路参与调控 KG1a 细胞 NKG2D 配体的表达

何川疆、许爱敏
喀什地区第一人民医院

目的 自然杀伤细胞活化性受体(NKG2D)配体的低表达是白血病干细胞(LSC)逃避免疫杀伤的关键因素，磷脂酰肌醇 3-激酶/雷帕霉素靶蛋白(PI3K/mTOR)信号通路在 LSC 中高度活化，探讨 PI3K/mTOR 信号通路是否参与调控 LSC 中 NKG2D 配体的表达。

方法 采用 PI3K/mTOR 信号通路抑制剂 NVP-BEZ235 对人急性骨髓白血病细胞 KG1a 细胞进行干预后，采用细胞技术试剂盒 CCK-8 检测 KG1a 细胞增殖，采用流式细胞术检测 KG1a 细胞周期及凋亡，采用实时荧光定量聚合酶链反应(RT-qPCR)及免疫印迹(Western blot)检测细胞中 NKG2D 配体 MICB、ULBP1、ULBP2 和 ULBP3 的表达。

结果 抑制剂 NVP-BEZ235 显著抑制 KG1a 细胞的增殖，并将 KG1a 细胞周期阻滞于细胞周期 G0/G1 期；NVP-BEZ235 抑制剂干预后，KG1a 细胞 NKG2D 配体 MICB 信使核糖核酸(mRNA)相对表达量显著升高，ULBP1、ULBP2、ULBP3、 mRNA 及蛋白表达量也显著升高。

结论 PI3K/mTOR 调控 LSC 的增殖及周期，且其能够调控 NKG2D 的表达，该结果为通过 PI3K/mTOR 抑制靶向治疗耐药的 LSC 提供了数据支持。

PU-3849

CA 15-3 和 KL-6 在 ILD、CTD 中的相关性和诊断价值比较

李伟[1,2]、石柯[1]
1. 中南大学湘雅医院老年医学科检验室
2. 兰州大学第二医院检验医学中心

目的 KL-6 和 CA 15-3 均属于 Mucin-样糖蛋白，两者在某些疾病中的表达具有相关性，KL-6 目前多用于间质性肺疾病（Interstitial lung disease，ILD）的辅助诊断，而 CA 15-3 目前在临床上广泛应用，检测技术成熟，结果相对可靠，且成本远远低于 KL-6。本研究旨在探讨 CA 15-3 在结缔组织病（Connective tissue disease，CTD）和 ILD 中与 KL-6 的相关性及对这两类疾病诊断效能的差异。
方法 收集 2020 年 11 月至 2021 年 4 月期间在我院首次诊断为 CTD 或 ILD 患者的血液标本作为实验组，其中 CTD 患者 176 例、ILD 患者 56 例，另收集同期 150 例非 CTD、非 ILD 和非肿瘤的体检人群血液标本作为对照组。分别利用化学发光法和免疫比浊法检测每例血液样本中 CA 15-3 和 KL-6 的含量，进行统计学分析，探讨两者在三组人群中的表达、相关性和诊断价值。
结果 ILD 组患者的血清 CA 15-3 和 KL-6 的浓度均显著高于 CTD 组（P<0.001）和体检组（P<0.001），且 CTD 组患者的血清 CA 15-3 和 KL-6 的浓度均显著高于体检组（P<0.001）；线性回归分析表明体检组、ILD 组和 CTD 组人群中血清 CA 15-3 和 KL-6 的浓度均呈正相关（P<0.001），R2 值分别为 0.165，0.770 和 0.708；ROC 分析表明，血清 KL-6 和 CA53 均能很好的区分 ILD 患者和体检人群，AUC 分别为 0.87（95% CI: 0.85-0.90, P <0.0001）和 0.85（95% CI: 0.84-0.88, P <0.0001），而对 CTD 诊断的 AUC 分别为 0.84（95% CI: 0.82-0.87, P <0.0001）和 0.83（95% CI: 0.80-0.86, P <0.0001）。
结论 CA 15-3 和 KL-6 浓度在 ILD 和 CTD 人群中具有强的相关性，且诊断效能接近，可以作为替代 KL-6 诊断 ILD 和 CTD 的潜在生物标志物。

PU-3850

卵巢癌患者血小板参数的变化情况分析

郭俊英、陈燕
福建省肿瘤医院

目的 探讨血小板七项参数 PLT、PDW、MPV、PCT、P-LCR、PNR 、PLR 在卵巢癌患者化疗前后的变化。
方法 收集在福建省肿瘤医院诊断为卵巢癌的患者、卵巢癌后进行化疗的患者以及体检人员的临床资料。通过各类检验方法回顾性分析各组间血小板七项参数的差异性。
结果 PLT、MPV、P-LCR 的临界值分别为 225.000、9.750、22.550 时，对卵巢癌的临床分期具有一定的预测价值。PLT、PCT、PLR 的临界值分别 312.500、0.265、179.935 时，对卵巢癌的诊断具有一定的预测价值。卵巢癌患者 PLT、PCT、PLR 较体检组的高，接受化疗后 PLT、PCT、PLR 显著低于化疗前。血小板参数受不同病理类型，肿瘤直径、不同年龄段等的影响并不大。
结论 血小板的各项参数(PLT、PCT、PLR)在卵巢癌的诊断以及分期，化疗效果等方面可以起到判断预测效果，各项差异有统计学意义。

PU-3851

红细胞冷凝集对血常规多项参数结果的影响分析

高嫣妮、陈燕
福建省肿瘤医院

目的 研究红细胞冷凝集对血细胞分析各项检测参数检测结果的影响及处理办法。
方法 选取本院 2017 年 12 月—2018 年 3 月冷凝集标本 83 例，用 SysmexXN-9000 全自动血细胞分析仪检测 37℃水浴前、后的红细胞计数（RBC）、血细胞比容（Hct）、红细胞平均容积（MCV）、红细胞平均血红蛋白含量（MCH）、血红蛋白浓度（Hb）、红细胞平均血红蛋白浓度（MCHC）、白细胞计数（WBC）、血小板计数（PLT）等参数，再进行结果比较。
结果 RBC、HCT、MCV、MCH、MCHC 的结果水浴前后对比差异有统计学意义（P＜0.05），而 Hb、WBC 和 PLT 水浴前后结果无统计学意义(P＜0.05)。
结论 冷凝集标本会引起血细胞分析过程中多项参数检测结果严重失真并出现直方图、散点图异常及仪器报警提示。因此，在血细胞分析检测时应保证实验室温度，检验人员应加强质量控制，仔细审核分析检验结果，及时发现冷凝集标本，立即进行 37℃水浴 30min 后，即刻上机检测。同时应注意运送过程中的保温，对标本及检验试剂和用具作适当的加温处理，有助于解除标本凝集，从而使血常规各参数的检测结果得到校正。

PU-3852

N6-methyladenosine RNA as a potential diagnostic biomarker for breast cancer in peripheral blood

Han Xiao
Zhongda Hospital Southest University

Objective Breast cancer (BC) is one of the most commonly diagnosed malignancies and is the second most common cause of cancer deaths in women. In general, early BC has a 5-year survival rate of >80% with a good prognosis during the early stages and with basic treatment. In the past few decades, several Methods have been used to clinically diagnose BC. These include breast ultrasonography, mammography, exfoliative cytology, and tumor markers that include carcinoembryonic antigen (CEA), cancer antigen 125 (CA125), and carbohydrate antigen 153 (CA153) . However, the sensitivity or specificity is not sufficient to screen for BC, or especially, for the early diagnosis of BC. Therefore, a simple, sensitive, and effective diagnostic method is needed to detect BC at an early stage and obtain a better prognosis. Functions of m6A change the expression of target genes and affect the corresponding physiological functions. However, whether the m6A modification in peripheral blood RNA can be a novel diagnostic biomarker for BC has not been investigated.
Methods In this study, peripheral blood samples from 62 female patients with BC (including 53 tumor resection and 9 without surgery), 41 female patients with BBD (benign fibroadenoma of breast or mastopathy), and 41 female NCs who sought a routine health check-up during the same period and who did not have any breast diseases or other cancerous diseases. All patients were recruited at the Zhongda Hospital of Southeast University. All samples were initially diagnosed and untreated (including surgery, chemotherapy, and radiotherapy). m6A in total RNA was measured using a colorimetric method with EpiQuik™ m6A RNA Methylation Quantification Kit. qRT-PCR was performed to quantify the expression levels of METTL14 and FTO.
Results The m6A in the peripheral blood RNA of patients with BC was significantly higher than that in the NCs ($p < 0.0001$) and patients with BBD ($p < 0.0001$). These results indicated that the upregulation of peripheral blood m6A in patients with BC can differentiate patients with BC from the patients with BBD or NCs. m6A in patients with BC with carcinoma in situ was significantly

different from that in stage I, II, and Ⅲ + Ⅳ in peripheral blood RNA. The area under the curve (AUC) for m6A was 0.887 (95% confidence interval; [CI]: 0.826 to 0.948; $p < 0.0001$) and the optimal cutoff value was 0.070 (sensitivity 91.94%, specificity 65.85%), as determined using the highest Youden index. ROC curve analysis of other clinical tumor indicators revealed an AUC of 0.599 (95% CI: 0.489 to 0.709) and 0.572 (95% CI: 0.461 to 0.683) for CEA and CA153, respectively. These results indicated that the diagnostic value of m6A alone was better than that of CEA or CA153. Additionally, the AUC for the combination of m6A, CEA, and CA153 improved to 0.914 (95% CI: 0.861 to 0.966; $p < 0.0001$) with a specificity of 89.2% specificity with compromised sensitivity 80.3% as the optimal cutoff value for 0.0992. We examined the mRNA expression of m6A methylases and demethylases. The upregulation of METTL14 and downregulation of FTO may be related to the increased dynamic m6A modification in peripheral blood RNA of patients with BC.
Conclusion In conclusion, m6A in peripheral blood can be a potential novel diagnostic biomarker for BC.

PU-3853

凝血五项指标在肝癌各期的临床意义

魏斯斯
西安金域医学检验所

目的 探讨凝血五项指标的变化与不同临床分期肝癌之间的关系
方法 对 120 例肝癌患者与 50 例对照人群的凝血指标进行检测，其中 PT、FIB、APTT 采用凝固法，D-D、FDP 采用免疫比浊法。
结果 在肝癌各期中，II 期与 I 期相比，PT、FDP、FIB 呈递增趋势，APTT、D-D 呈递减趋势，III 期与 II 期相比，PT、APTT、FIB、FDP、D-D 五项指标均呈上升趋势，IV 期与 III 期相比，FIB 仍呈递增趋势，而 PT、APTT、FDP、D-D 四项指标呈下降趋势。
结论 凝血五项指标在肝癌各期的变化大不相同，临床上可将凝血指标的变化作为评价肝癌不同分期的依据之一。

PU-3854

Systematic and comprehensive analysis of the expression of cytokines related to COVID-19 in testicular cells and the interaction network between cells

Haihong He、Fan Yu、Tingting Huang、Yiwen Zhou
Clinical Laboratory Medical Center, Shenzhen Hospital, Southern Medical University

COVID-19 has become a global pandemic, with more than 75 million people infected with SARS-Cov-2 and more than 1.6 million deaths. Some COVID-19 patients have symptoms of scrotal discomfort and orchitis. Inflammatory cytokine storm (CS) is widespread in COVID-19 patients. It has been confirmed that 13 cytokines are elevated in COVID-19 patients. CS can cause testicular cell damage and immune microenvironment disorders, thereby affecting male fertility Ability, but the expression of cytokines in testicular cells and their role in cell-to-cell communication are rarely related. We integrated 10 single-cell sequencing data of testicular cells, and annotated 20 cell clusters using marker genes combined with the Human Cell Landscape (HPL) database. Twelve types of testicular cells were identified, and we found that 4 types of cytokines (IL8, CCL2, CCL3, TNF) might play a role in the immune process of testicular cells. Next, the pseudo-chronological trajectory of the testicular cells was successfully constructed, and

it was found that IL8 and CCL3 may play an important role in the development of the testicular Macrophage and Endothelial cells, thereby affecting the immune microenvironment of the testicular cells. Furthermore, the functions of 8 key cytokines (IL1, IL2, IL4, IL6, CCL, CSF3, TNF, IFN-Ⅱ) in the interaction network between cells were then identified. Based on the network analysis of imported cytokines directly acting on testicular cells, IL2 is believed to act directly or indirectly on all testicular cells and play an important role in testicular cell communication.

PU-3855

吉林地区维生素 D 水平研究进展

王晶晶
吉林金域医学检验所有限公司

目的 维生素 D（VD）是脂溶性类胆固醇激素，与人类健康最为密切的是维生素 D2 和维生素 D3，维生素 D2 是来自于人工合成制剂或某些植物性食物的外源性维生素 D；维生素 D3 既可来自于奶、蛋、鱼、肉等动物性食物，也可来自于皮肤内源合成；在体内有活性作用的主要是 1，25-OHD。本文通过了解 480 位人群维生素 D（VD）含量水平状况及其影响因素，分析导致 VD 不足的原因，为后续研究和临床防治提供依据。
方法 选取 2020 年 6 月至 2020 年 12 月送检我公司，项目为维生素 D 的样本 480 例，采用蛋白沉淀及液液萃取等方法对样本进行前处理，运用高效液相色谱串联质谱仪，经过三重四极杆对其进行筛选，根据相应离子在检测器产生的信号强度及所绘制的标准曲线来定量待测物的浓度。
结果 在 480 例样本中，有 355 例表现为 VD 水平均为缺乏，缺乏率为 74%，其余 125 例孕妇、儿童的 VD 水平相对正常；同时，冬季的 VD 缺乏率高于夏季的 VD 缺乏率。
结论 维生素 D 为人体重要的微量元素，维持体内钙磷及骨代谢平衡，并参与某些蛋白质转录的调节，发挥激素样作用参与体内免疫调节，能够降低慢性疾病如糖尿病、心血管疾病的发病率，降低癌症风险等生理作用。目前，人们对维生素 D 的重视程度不足，所以导致 VD 的缺乏率高达 74%，同时，由于孕妇和儿童为特殊人群，可能会进行相关 VD 的补充，饮食方面也会进行相关注意，所以 VD 的水平多为正常。冬季室外温度较低，外出时间减少，日照时间变少，VD 水平也较为缺乏。平时应在饮食方面多多注意并增加一些户外活动，或者进行维生素补剂的补充以做到早发现、早预防、早治疗，保证身体健康。

PU-3856

FA280 全自动粪便分析仪临床应用价值分析

黄雪琴、林珊、陈卓诚、黄日雄、莫红梅
深圳市罗湖医院集团医学检验实验室

目的 为进一步缩短粪便常规检查项目实验室内 TAT，提高寄生虫检出率，采用全自动粪便分析仪。
方法 回顾性分析我院 2020 年 4 月-2021 年 5 月 17939 例门诊及住院患者粪便常规检测项目实验室内 30min、60minTAT 达标率及寄生虫检出率，与 2019 年 3 月至 2020 年 3 月未使用全自动粪便分析仪之前的 15086 例门诊及住院患者该项目实验室内 30min、60minTAT 达标率，寄生虫检出率比较，分析使用全自动粪便分析仪的价值。
结果 使用全自动粪便分析仪前门诊患者实验室内 30min TAT 达标率为 58.49%，使用后 83.33%，使用前住院患者实验室内 30min TAT33.52%，使用后 47.16%；60min 门诊患者从 88.68%到 100%，住院患者从 61.45%到 80.36%。寄生虫虫卵检出率从使用前 0.06%到 0.34%，包囊/滋养体检出率则是 0.05%和 0.06%。粪便常规检测项目实验室内 30min、60minTAT 达标率在使用全自动粪便分析仪后，均有明显提升，有效缩短了患者等候时间。使用前门诊患者实验室内 TAT 中位

数是 21min， 95 百分位数是 49min，住院患者实验室内 TAT 中位数是 25min，95 百分位数是 73min，使用后门诊患者实验室内 TAT 中位数是 18min，95 百分位数是 33min，住院患者实验室内 TAT 中位数是 23min，95 百分位数是 43min，实验室内 TAT 得到显著提升。检出虫卵的种类主要有肝吸虫卵、蛲虫卵、钩虫卵、蛔虫卵；检出包囊有蓝氏贾第鞭毛虫包囊、滋养体、肠道滴虫、结肠内阿米巴包囊。

结论 使用全自动粪便分析仪，在不增加人员岗位的前提下，极大提高了粪便常规检查项目门诊及住院患者的 30minTAT、60minTAT 达标率，并且显著提高了肠道寄生虫虫卵的检出率，对提高实验室的质量管理有重要价值。

PU-3857

外周血中性粒细胞与淋巴细胞比值（NLR）和血小板与淋巴细胞比值（PLR）联合鳞状细胞癌抗原（SCC）在早期宫颈鳞癌诊断中的价值探讨

王红旭
重庆医科大学附属第一医院

目的 通过对早期宫颈鳞癌患者和健康女性的血常规结果和鳞状细胞癌抗原检测结果进行分析,探究中性粒细胞-淋巴细胞比值(NLR)和血小板-淋巴细胞比值（PLR）以及鳞状细胞癌抗原（SCC）在早期宫颈鳞癌癌中的诊断价值。

方法 收集 2017 年至 2020 年重庆医科大学附属第一医院确诊的早期宫颈鳞癌患者 165 例（实验组）和同期健康体检女性 150 例（对照组）的病历资料。比较两组 NLR、PLR、SCC 水平，采用受试者工作特征曲线(ROC 曲线)分析各指标单独检测和联合检测对宫颈癌的诊断效能。

结果 早期宫颈鳞癌患者 NLR、PLR 和 SCC 水平明显高于对照组（$P<0.05$）； NLR 诊断早期宫颈鳞癌的截断值为 2.63 曲线下面积为 0.569，灵敏度为 28.3%，特异度为 86.4%；PLR 诊断早期宫颈鳞癌的截断值为 126.72，曲线下面积为 0.615，灵敏度为 56%，特异度为 63.9%；SCC 诊断早期宫颈鳞癌的截断值为 1.35，曲线下面积为 0.729，灵敏度为 42.8%特异度为 97.6%;NLR 与 SCC 联合诊断早期宫颈鳞癌的曲线下面积 0.755；PLR 与 SCC 联合诊断早期宫颈鳞癌的曲线下面积为 0.785；PLR，NLR 和 SCC 三者联合诊断的曲线下面积为 0.786.

结论 NLR、PLR 和 SCC 对早期宫颈癌具有一定的诊断价值，联合检测可有效提高诊断效能。

PU-3858

新冠康复者血浆用于两例危重患者治疗的血细胞参数变化分析

陈伟[1]、梁剑琦[1]、刘艳[2]、黄小晔[1]、彭丽[1]
1. 娄底市中心医院
2. 娄底市妇幼保健院

目的 探讨康复期血浆用于 SARS-CoV-2 感染危重患者治疗血常规参数的变化趋势。

方法 实验室确诊新冠肺炎并伴急性呼吸窘迫综合征(ARDS)危重患者病例 2 例，经抗病毒治疗后病情进展迅速、病毒载量持续高的重症肺炎，Pao2/Fio2 <300，机械通气。治疗方案：盐酸阿比朵尔(200mg，一天 3 次)、干扰素吸入(500 万 U，一天 2 次)、磷酸氯喹(500mg，一天 2 次)和其他支持治疗。2 例患者均接受新冠康复者血浆输血，血浆 SARS-CoV-2 特异性抗体(IgG)结合效价大于 1:200(酶联免疫吸附试验终点稀释效价)，中和效价大于 40(终点稀释效价)，患者自入院起每天上午 9 时采集患者血液标本监测血常规变化情况，在治疗方案无改变的前提下比较输血前后 6 天血常规的变化趋势。

结果 自 2020 年 2 月 19 日至 2020 年 2 月 24 日每天输入 200ML 康复者血浆，共 1200ML。病例 1 输血前后 WBC、淋巴细胞比率、NLR（中性粒细胞/淋巴细胞）、PLT 均值为：13.7 和 12.16、3.77 和 6.83、29.26 和 13.96、218 和 102。病例 1 输血前后 WBC、淋巴比率、NLR、PLT 均值为：10.8 和 10.7、2.48 和 3.73、40.28 和 26.44、114 和 62。两个病例在输血前后 WBC 总数无明显的变化趋势，而淋巴比率在接受康复血浆输注后明显上升，NLR 和 PLT 明显下降。
结论 康复血浆输注对新冠危重患者有一定的临床疗效，血常规常用参数淋巴细胞比率、PLT 及经过转换的 NLR 对新冠危重患者的动态监测及预后评估具有积极的临床意义。

PU-3859

结直肠癌血清 lncRNA 诊断公式的建立及对结直肠癌预后评估

段伟丽、王传新
山东大学第二医院

目的 筛选并验证结直肠癌（CRC）血清中差异表达的 lncRNAs，建立 CRC 血清 lncRNA 诊断模型，并探讨其在 CRC 预后监测中的意义。
方法 对 CRC 及癌旁正常组织进行基因芯片分析,并结合相关文献，选出候选 lncRNAs。采用 qRT-PCR 技术，在 80 对 CRC 及癌旁组织中检测候选 lncRNAs，将差异表达具有统计学意义的候选分子在 120 例 CRC 患者及 120 例对照者血清中进一步验证，最终确定在组织及血清中均存在显著差异表达的 lncRNAs。基于 logisitic 回归建立 CRC 血清 lncRNA 诊断模型，采用受试者工作曲线（ROC）分析结直肠癌血清 lncRNA 模型的诊断效能。通过 Kaplan-Meier 和 Cox 比例风险回归模型对 CRC 患者进行生存曲线分析和监测复发的独立预后因素分析。
结果 筛选出 18 个候选 lncRNAs，经 qRT-PCR 验证，4 个 lncRNAs（BANCR, NR_026817,NR_029373 和 NR_034119）在 CRC 组织及血清中均存在显著差异表达（均 $p < 0.001$），其中 BANCR 表达上调， NR_026817, NR_029373 和 NR_034119 表达下调。4 个 lncRNAs 的受试者工作曲线下面积（AUC）分别为 0.638, 0.708, 0.812 和 0.724。通过 Logistic 多元回归分析建立 4 个 lncRNAs 的结直肠癌血清 lncRNA 诊断模型（AUC 为 0.891）。Kaplan-Meier 分析显示， NR_029373 和 NR_034119 越低，结直肠癌患者生存率越低（$p = 0.013$ 和 0.044）。Cox 回归分析显示,NR_029373 和 NR_034119 可作为结直肠癌的独立预后指标 (p 分别为 0.013 和 0.038)。
结论 结直肠癌血清 lncRNA 诊断模型（BANCR, NR_026817, NR_029373 和 NR_034119）对结直肠癌早期诊断具有一定的临床意义。
NR_029373 和 NR_034119 可作为结直肠癌监测的独立预后指标。

PU-3860

稳定同位素代谢标记技术联合质谱多重反应监测技术在 5、7、55 型腺病毒鉴定中的应用

徐忠伟、朱文清、王天添、范开元
中国人民武装警察部队后勤学院

目的 利用质谱多重反应监测（Multiple Reaction Monitoring，MRM）技术实现对 5、7、55 型人腺病毒的准确鉴定。
方法 分别合成 5、7 和 55 型人腺病毒六邻体基因，将目的片段构建于 pGEX-4T-1 载体上，BL21 感受态感受质粒，利用细胞培养条件下稳定同位素代谢标记技术（stable isotope labeling by amino acids in cell culture, SILAC）培养细胞，分别采用轻度、中度和重度 SILAC 培养基培养大肠杆菌，培养基中赖氨酸和精氨酸的浓度分别为 0.798 和 0.398 mmol/L；轻度标记培养基含有赖

氨酸 $^{12}C_6{}^{14}N_2$-Lysine（Lys0）和精氨酸 $^{12}C_6{}^{14}N_2$-Arginine（Arg0）；中度标记培养基含有赖氨酸 4,4,5,5-D^4-Lysine（Lys4）和精氨酸 $^{13}C^6$-Arginine（Arg6）；重度标记培养基含有赖氨酸 $^{13}C_6{}^{15}N_2$-Lysine（Lys8）和精氨酸 $^{13}C_6{}^{15}N_4$-Arginine（Arg10）；培养至大肠杆菌生长至对数生长期，1 mmol/L IPTG 低温诱导蛋白表达，提取相应标记蛋白，通过 GST 表达纯化富集表达六连体蛋白。采用胶消化策略分别消化 3 种不同标记策略的纯化蛋白，消化产物等量混合脱盐后经毛细管色谱柱分离以 MRM 模式进行 LC-MS 方法检测。
结果 成功构建 pGEX-4T-1-hexon 载体，通过 SILAC 方法实现大肠杆菌的完整代谢标记，成功诱导表达腺病毒六邻体蛋白，通过 MRM 技术实现对轻、中、重度标记六邻体蛋白标志性肽段鉴定。
结论 成功实现三种 SILAC 条件下大肠杆菌中 5 型、7 型、55 型人腺病毒六邻体蛋白的完整标记，为 5 型、7 型、55 型人腺病毒感染的快速分型检测提供了新的鉴定策略。

PU-3861

尿红细胞位相的检测及临床应用

崔晓凤
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 使用超高倍显微镜系统人工对尿沉渣进行红细胞形态分析，提供给临床测量数据，以便临床对相应的病人进行病情监测。
方法 尿红细胞位相检查是利用超高倍显微镜系统在镜下利用形态学人工对尿液中的红细胞形态分析的一种方法。一般认为，正常人尿中有红细胞者约 4%，其中红细胞数 0.5---5.0×10^{12}/ml,多为正常红细胞。如尿中发现畸形红细胞（其大小、形态呈多形性，血红蛋白含量异常）占 75%以上，且红细胞数≥800ml 者，可诊断为肾小球性血尿，为提高超高倍显微镜鉴别血尿诊断价值的临床应用，我们对 50 例不同来源的血尿进行超高倍显微镜镜检分析。
结果 28 例肾小球性血尿中，多形性红细胞阳性率 80%（22/28），混合性阳性率 20%（6/28）；22 例非肾小球性血尿中均一性阳性率 85%（19/22），混合性阳性率 15%（3/22）。
结论 综上所述，尿红细胞位相检查可根据尿液中红细胞形态（均一性、非均一性、混哈性）判定血尿的来源，有助于某些疾病的鉴别诊断。一般均一性血尿病变部位在膀胱、尿道，非均一性血尿病变部位在肾脏，混合性血尿提示病变涉及整个泌尿生殖系统。

PU-3862

中国客家人群中 AML 患者血清乳酸脱氢酶水平与早期死亡之间的关联分析

肖作淼、陈先春、肖德俊、罗诗、陈昌坤
赣州市人民医院

目的 有证据说明了 LDH 水平与急性髓系白血病（AML）不良预后相关，但与 AML 患者的早期死亡之间的关系依旧不清楚。
方法 连续收集 2013 年至 2021 年期间所有收治的初诊急性髓系白血病（非 APL）病例。通过多元回归分析血清乳酸脱氢酶（LDH）（以 Log2 及 2 倍正常参考高值的形式来分析）与早期死亡的相关性，并将常规项目之白血胞、血红蛋白、血小板，血清标志物如肝、肾、心肌损伤标志物等参数进行逐步调整分析。
结果 有 368 例年龄大于 16 岁的初诊急性白血病患者入组。早期死亡率为 29.1%(107/368). 早期死亡率在正常参考值 2 倍上限值组(LDH≥570U/L)为 35.2% (44/125)，高于非正常参考值 2 倍上限值组的 25.9% (63/243)（LDH<570U/L），但现两者间没有统计学差异。在多参数回归分析中 OR 值

和 95%置信区间分别为 1.70(1.18,2.35) and 2.38 (1.21,4.69),交互作用分析显示所分析的参数对 LDH 与早期死亡影响无关性。
结论 中国客家 AML 人群中具有早期死亡高风险，LDH 之 Log2 及正常参考值 2 倍上限值组(LDH≥570U/L)有较高的相关性，需要更多试验进行验证。

PU-3863

血液分析仪在脂血状态下血小板计数准确性的临床性能评价

张伟红
广州市第一人民医院

目的 对希森美康 XE-5000 血液分析仪在脂血标本下进行血小板计数准确性的临床性能评价。
方法 选取无红细胞碎片，100fL>平均红细胞体积（MCV）>82fL,12.5fL>平均血小板容积（MPV）>9.4fL 的脂血标本 45 例及正常对照 90 例，分别用希森美康 XE-5000 和 XN-2000 血液分析仪进行电阻抗法（PLT-I），光学法（PLT-O），XN-2000 光散射法（PLT-F）测定血小板，并且进行血小板人工计数，然后将标本离心，2000rpm,5 分钟，吸取血浆，并在贝克曼库尔特 AU5800 全自动生化分析仪进行血清指数测定，确定脂血程度。血小板数值参照人工计数法所测定的血小板数将脂血组与对照组分成低（PLT<100×10^9/L）、中（100≤PLT×10^9/L≤300）、高（PLT＞300×10^9/L）三组，分别与人工计数测得值比较，以此来评价血小板三种测定方法的准确性。
结果 低值脂血标本组中，XE-5000 PLT-O 和 PLT-I 通道血小板计数中位数分别为 31 ×10^9/L、43×10^9/L，XN-2000 PLT-I、PLT-O 和 PLT-F 通道血小板计数中位数分别为 30 ×10^9/L、29×10^9/L、24×10^9/L，人工计数血小板中位数为 20×10^9/L。经 SPSS 秩和检验，低值脂血标本 XE-5000 仪器上的 PLT-O 中位数显著高于人工计数法（P<0.05），具有显著性差异。XE-5000 PLT-I、XN-2000（ PLT-O、PLT-I、PLT-F）方法检测血小板中位数与人工计数无显著性差异（P>0.05）。
结论 在低值脂血标本中，XE-5000 血液分析仪 PLT-O 通道检测结果与人工血小板计数具有显著性差异（P<0.05），具有统计学意义。其他检测方法与人工计数没有显著性差异（P>0.05），无统计学意义。在脂血标本检测低值血小板时，XE-5000 电阻抗法的准确性比光学法高，与人工计数相符，而 XE-5000 光化学法易引起血小板假性增高。

PU-3864

一例 Ph+CML 罕见型 BCRABL1 融合基因患者的诊断与治疗

程沈菊、李轶勋
昆明医科大学第一附属医院

目的 通过临床表现、细胞形态学、分子生物学及细胞遗传学对一例疑难病例进行诊断并观察其治疗效果。
方法 运用细胞形态学，分子生物学及细胞遗传学等检测方法与临床相结合进行诊断和疗效分析。
结果 确诊一例罕见型 e13a3（b2a3）和 e14a3（b3a3）双阳性慢性粒细胞白血病，经 TKIs（伊马替尼）治疗后有效。
结论 该病例为 Ph+e13a3（b2a3）和 e14a3（b3a3）融合基因双阳性的慢性粒细胞白血病，通过 TKI 治疗后使患者达到了较好的治疗效果，自行停药后复发并急变，且 T315I 突变耐药。

PU-3865

浆膜腔积液常规联合细胞学分析图文报告的应用价值研究

李晴[1]、刘俊平[2]
1. 西南医科大学附属医院
2. 重庆医科大学检验医学院

目的 建立、运行并不断优化本地区浆膜腔积液常规联合有形成分分析的质量体系，在常规检测的基础上 新增有形成分图文分析报告，并结合临床病理诊断结果，深入探讨该方法体系的临床应用价值。
方法 收集西南医科大学附属医院自 2019 年 1 月至 2020 年 4 月共计 622 例常规送检的浆膜腔积液标本，在完成传统常规检测后进行离心、有形成分沉淀物推片、瑞特-姬姆萨复合染色镜检，以临床诊断为金标准，分析常规细胞学检查结果，对于明显特征的肿瘤细胞给予异常细胞和异型细胞（计为阳性）以及核异质细胞等分级格式提示临床。
结果 1、 622 例浆膜腔积液中，病理诊断为恶性肿瘤 172 例，运用常规检测联合有形成分分析法检出阳性 142 例，真阳性 139 例，灵敏度(80.81%)、特异度(99.26%)、阳性预测值（97.88%）、阴性预测值（92.41%）、诊断符合率(93.76 %)。2、结核性浆膜腔积液淋巴细胞增生积分(2.70±0.754)明显高于肿瘤组(1.16±0.452)及非特异性炎症组(1.11±0.309), P <0.001。3、脓性积液 37 例，图文示含脓细胞、细菌、真菌、脂肪滴和胆色素结晶等。
结论 1、该类新报告体系模式可作为一种有效的恶性肿瘤的早期筛查方法，还能为结核和其他炎症性积液的液鉴别诊断提供一定的依据。2、该法与病理脱落细胞学互有优缺，优势互补。3、本体系对于转移量较少的肿瘤细胞，体积较小的低分化癌细胞、白血病细胞以及其他病理有形成分均有较好的识别和临床提示价值。

PU-3866

郴州市某医院 10728 例粪便寄生虫检测结果分析

彭玉凤
郴州市第一人民医院

目的 分析郴州市某医院粪便常规寄生虫检出率和感染特点，为临床肠道寄生虫病的防治工作提供帮助。
方法 采用生理盐水对郴州市某医院就诊患者粪便标本进行涂片镜检，统计分析粪便检出寄生虫种类及感染特点等。
结果 10728 例粪便有 173 例检出寄生虫，肠道寄生虫总感染率为 1.61%；共检出 7 种寄生虫，包括人芽囊原虫（166 例，1.55%）、蓝氏贾第鞭毛虫（5 例，0.05%）、脆弱类双核阿米巴（5 例，0.05%）、微小内延阿米巴（1 例，0.01%）、布氏嗜碘阿米巴（1 例，0.01%）、粪类圆线虫（1 例，0.01%）、肠道滴虫（1 例，0.01%），其中 3 例（0.03%）标本为混合感染。人芽囊原虫、蓝氏贾第鞭毛虫、脆弱类双核阿米巴构成了肠道寄生虫感染的主要虫种，占总感染人数的 97.73%（172 / 176）。肠道寄生虫感染率女性（2.14%）高于男性（1.24%），差异有统计学意义（χ2=17.00，P<0.01）。不同年龄组人群肠道寄生虫病表现为中间年龄感染率低、两端年龄感染率高，但各年龄组人群寄生虫感染率差异无统计学意义（χ2=12.45，P>0.05），感染率较高的年龄组为 20～岁组(2.99%)、>80 岁组(2.86%)、10～岁组(2.10%)、和 70～岁组(1.98%)。
结论 人类肠道寄生虫总感染率较低，感染人群存在性别差异；肠道寄生虫感染以人芽囊原虫、蓝氏贾第鞭毛虫、脆弱类双核阿米巴等食源性寄生虫或机会致病性原虫为主，为临床肠道寄生虫病的防治指明了方向。

PU-3867

全自动凝血仪特殊凝血项目的临床前性能验证与评价

邹梦雪、程云
南方医科大学珠江医院

目的 对全自动血凝分析仪的特殊凝血项目进行临床前的性能验证及评价，为临床血栓与止血相关疾病提供可靠的检验结果。
方法 根据《临床血液学检验常规项目分析质量要求》、《临床化学设备线性评价指南》和《临床实验室检验项目参考区间的制定》等标准，对本实验室 ACL TOP 700 全自动凝血分析仪测定 PC，PS，VWFAg,Ⅷ,IX,La，抗Ⅹa，AT 等特殊项目的精密度、准确度、携带污染率、线性以及正常参考范围进行性能验证。
结果 精密度、准确度、携带污染率、线性等均符合要求
结论 ACL TOP 700 全自动凝血分析仪对血栓与止血特殊项目检测的准确度、不精密度、携带污染率、线性范围及正常参考范围验证等性能验证评价效果良好，符合临床使用要求，可为临床血栓与止血相关疾病提供可靠的检验结果。

PU-3868

尿干化学法和尿沉渣镜检法检测红细胞的比较

史永胜、金英玉
哈尔滨医科大学附属第一医院

目的 对比研究尿干化学法和尿沉渣镜检法检测红细胞结果。
方法 随机收集 1000 份来自医院门诊以及住院患者的新鲜尿液标本，其中男性标本和女性标本各 500 例，其中，年龄上限为 85 岁，下限为 16 岁。将尿液标本充分混匀后先进行尿干化学分析，然后以 1500r/min，离心 5 分钟，取沉渣于载玻片上进行镜检。
结果 以显微镜镜检为准，两种方法检测红细胞结果符合率为 92.4％，尿干化学检查红细胞假阳性率为 18.63％，假阴性率为 3.66％。采用配对 2 检验统计分析。
结论 尿干化学法检测红细胞虽然方便快捷，敏感性高，但是会出现一定的假阳性和假阴性结果，所以临床检查时不能单独应用，必须结合尿沉渣镜检，以减少漏诊和误诊。

PU-3869

血浆 D-二聚体和 FDP 联合检测在诊断 DIC 中的应用价值

史永胜、金英玉
哈尔滨医科大学附属第一医院

目的 用于研究血浆 D-二聚体 (DD) 和纤维蛋白(原)降解产物 (FDP) 联合测定，在弥散性血管内凝血 (D1C) 诊疗中的临床意义。
方法 选取哈尔滨医科大学附属第一医院的健康体检人群 25 例，DIC 患者 23 例，分别作为健康对照组和 DIC 组。抽取受检者血浆，检测血浆中 DD 和 FDP 的水平。用 Sysmex CA-7000 血凝仪分别检测两组受检者血浆 DD 和 FDP 的水平，并进行统计学处理和分析。
结果 DIC 组的 DD 和 FDP 水平显著高于健康对照组，其差异具有统计学意义（P＜0.05）；随着治疗的进展，DIC 患者的 DD 和 FDP 水平呈现下降的趋势。
结论 检测血浆 DD 和 FDP 的水平有利于早期诊断 DIC、监测疾病进程，对 DIC 诊治与判断临床诊疗疗效具有重要临床意义。

PU-3870

全自动尿有形成分分析仪 UF-5000 联合相差显微镜对血尿来源的鉴别

王晨[1]、张鑫悦[2]
1. 中国医科大学附属第一医院
2. 中国医科大学

目的 探讨尿沉渣分析仪 UF-5000 对肾小球和非肾小球血尿来源鉴别诊断的应用价值。
方法 选取 2021 年 3 月—5 月在中国医大一院肾内科和泌尿外科住院患者共 117 例，使用 UF-5000 对获得的患者晨尿或随机尿进行尿沉渣检测。分别检测尿 70%红细胞前向散射光强度(RBC-P70Fsc)、尿红细胞前向散射光分布宽度(RBC-Fsc-DW)、未溶红细胞(NL RBC)、溶解红细胞(Lysed RBC)、大红细胞(Large RBC)、小红细胞(Small RBC)等红细胞信息，并使用相差显微镜检测红细胞形态，计算红细胞变形率。用临床诊断结果作为标椎，计算比较全自动尿有形成分分析仪 UF-5000 和相差显微镜之间的敏感度和特异度。采用受试者工作特征（ROC）曲线，分别计算尿液沉渣分析仪 UF-5000 红细胞信息（RBC-Info）、相差显微镜下红细胞变形率的曲线下面积（AUC）。使用 MedCalc 进行 ROC 曲线间的比较。
结果 与肾小球源性血尿组对比，RBC-P70Fsc（ch）、NL RBC 计数（/μL）以及 Large RBC 计数（/μL）在非肾小球源性血尿组显著增高（p<0.001），而相差显微镜镜下红细胞变形率显著降低（p<0.001）。用 UF-5000 尿沉渣分析仪 RBC-Info 非均一性判断为肾小球源性血尿，均一性判断为非肾小球源性血尿可以得出敏感度为 55%，特异度为 57.9%；将 RBC-Info 非均一性和混合性均判断为肾小球源性血尿可将敏感度提高到 96.7%。相差显微镜非均一性判断为肾小球源性血尿，均一性判断为非肾小球源性血尿可以得出敏感度为 75%，特异度为 63.2%。RBC-P70Fsc 的 AUC 为 0.938（p<0.05）、NL RBC 的 AUC 为 0.782（p<0.05）、Large RBC 的 AUC 为 0.892（p<0.05）、相差显微镜镜下红细胞变形率的 AUC 为 0.994（p<0.05）。UF-5000 的 RBC-Info 联合使用的 AUC 为 0.943（p<0.05）。根据 ROC 曲线可知使用相差显微镜的敏感度为 96.5%，特异度为 98.3%（p<0.05）；将仪器指标联合使用的敏感度为 86%，特异度为 93.3%（p<0.05）；两组间 UF-5000 与相差显微镜联合使用的敏感度为 98.2%，特异度为 98.3%（p<0.05）。经 ROC 曲线间的比较，仪器结果与单独使用相差显微镜对结果的判断有一定的差异，而两种方法的联合使用与单独使用相差显微镜的对结果的判断并没有显著性差异。
结论 UF-5000 尿沉渣分析仪和相差显微镜联合检测对临床诊断明确血尿来源定位有一定的价值。

PU-3871

粪钙卫蛋白、CRP、IL-6 水平变化与克罗恩病患者黏膜愈合状态的 关系及其应用价值

马继荣、沈薇、顾怡、沈文艳、周景艺
上海交通大学医学院附属仁济医院

目的 探讨粪钙卫蛋白（FC）、C 反应蛋白（CRP）、白介素 6（IL-6）在克罗恩病（CD）患者黏膜愈合状态中的水平变化及应用价值。
方法 选取 2019 年 6 月至 2020 年 6 月我院收治的 CD 患者 52 例，依据内镜结果分为黏膜愈合与黏膜未愈合组，检测 FC、CRP、IL-6 水平。建立单项检测的 ROC 曲线，确定各指标的最佳诊断临界值（cutoff 值），并通过二元 Logistic 回归评价多变量检测模型的诊断价值。
结果 黏膜未愈合 CD 患者 IL-6、CRP、FC 水平均显著高于黏膜愈合组 (P<0.05)。回归方程结果显示 FC 是判断 CD 肠道黏膜愈合与否的独立影响因素（P<0.05）。单项血清 IL-6、CRP 和 FC 检测判断肠道黏膜未愈合的 ROC 曲线下面积(AUC)分别为 0.71（95% CI 0.77~0.97）、0.88（95% CI

0.88~1.00）、0.85（95% CI 0.66~0.92）(p<0.01)。FC+CRP 和 FC+IL-6 双项检测时其 AUC 分别为 0.91（95% CI 0.83-0.99）和 0.84 (95% CI 0.73-0.94) (p<0.01)。FC+IL-6+CRP 三项联合检测时其 AUC 为 0.92（95% CI 0.85~1.00）(p<0.01)，大于单项检测和双项检测多项联合检测。三项联合检测预测值的 cut-off 值为 0.75 时其敏感度和特异性分别为 77%和 100%。
结论 FC+CRP+IL-6 三者联合检测能较好判断 CD 患者肠道黏膜愈合情况。

PU-3872

健康个体动脉血与静脉血血细胞分析之间存在的差异

付春燕、张婷
四川省人民医院

研究背景 在国内外 ICU 中均存在长期使用动脉置管采血后检测，其中的原因有 ICU 重症患者已留置动脉导管，且通过动脉导管抽取血标本更方便，同时可以减轻患者痛苦，减少感染机会，ICU 重症患者已经较难建立其它静脉通道。此前已有研究表明，与静脉血参数相比，动脉血参数如白细胞、红细胞和血红蛋白的测量间差异更大。获得可靠、准确的实验结果的前提是正确采集血标本，现在静脉采血法进行全血细胞计数分析在临床上比较常用。因此，我们要比较正常健康人动脉血与静脉血之间的血细胞计数参数结果是否存在差异。
材料与方法 本研究与 2021 年 2 月至 2021 年 3 月于四川省人民医院检验科采集正常健康人动脉血与静脉血血标本，采用 4ml 紫头管 EDTA-K2 7.2mg 抗凝的真空采血管，静脉血抽取肘部静脉，动脉血抽取桡动脉，利用 Sysmex XN1000/迈瑞 BC-6800 原装配套试剂进行检测。检测指标包括:红细胞计数（RBC）；血红蛋白（HGB）;白细胞计数（WBC）；红细胞平均容量（MCV）；红细胞平均血红蛋白浓度（MCHC）；红细胞压积（HCT）;血小板（PLT）。其后利用非参数检验，t 检验检测动脉血与静脉血之间存在的差异。P<0.05 有统计学意义。
结果 本研究中发现，红细胞计数（P>0.05）、血红蛋白（P>0.05）、白细胞计数（P>0.05）、红细胞平均容量（P<0.05）、红细胞平均血红蛋白浓度（P<0.05）、红细胞压积（P>0.05）、血小板（P>0.05）,红细胞平均容量、红细胞平均血红蛋白浓度 P<0.05 有统计学差异。
总结 在健康个体的动静脉血中，血细胞计数的检测结果显示，大多数参数如白细胞、红细胞、红细胞压积和血小板，在测量之间的差异比用静脉血测量的差异更大。从统计学上来说，静脉血中的血细胞计数比动脉血更有效。因此，必要时可建立动脉血血细胞计数参考区间。

PU-3873

血清外泌体 miR-377-3p 和 miR-381-3p 能够作为结直肠癌诊断标志物

王莉[1,2]、谢丽[1]、唐有勇[1,2]
1. 山东省肿瘤医院
2. 山东第一医科大学

血清外泌体 microRNAs(ExmiRNAs)为癌症诊断提供了一种理想的非侵入性方法。在这项研究中，我们评估了两种结直肠癌患者血清中的 ExmiRNAs 作为早期结直肠癌(CRC)的诊断工具。用 qNano、透射电子显微镜和 Western blot 对外泌体进行了表征鉴定。用 RT-qPCR 方法检测 CRC 患者(n=175)和健康献血员(n=172)血清中差异表达的 miRNAs。通过受试者工作特性(ROC)分析测定其诊断值。结果表明，在结直肠癌患者中，ExmiR-377-3p 和 ExmiR-381-3p 的表达均显著降低。ExmiR-377-3p 和 ExmiR-381-3p 的 ROC 曲线下面积分别为 0.798 和 0.792。当这两个 ExmiRNA 联合在一起时，AUC 值增加到 0.807。ExmiR-377-3p 和 ExmiR-381-3p 均可用于区分早期结直肠癌(I 期和 II 期)和健康对照。ROC 曲线显示 AUC 分别为 0.794 和 0.805。当它们联合时，AUC 值

增加到 0.814。另外，用癌胚抗原(CEA)或糖链抗原 19-9(CA19-9)检测结直肠癌进展时，发现 AUC 值分别为 0.739 和 0.707。综上所述，循环血清外泌体 miR-377-3p 和 miR-381-3p 可作为结直肠癌早期诊断的有效、无创性生物标志物，联合应用效果进一步提高。

PU-3874

红细胞九分图及红细胞新参数在辅助诊断小细胞性贫血中的价值初探

郭平、艾力
上海交通大学医学院附属瑞金医院

目的 探索血细胞分析仪红细胞九分图及红细胞新参数在辅助诊断小细胞性贫血中的应用价值。
方法 选取小细胞性贫血 273 例（缺铁性贫血 102 例、α 地中海贫血 63 例、β 地中海贫血 108 例）及健康对照 111 例为研究对象。使用 BC-6800 Plus 血细胞分析仪进行检测，收集仪器红细胞九分图及红系相关参数（共 68 项，此处略）。对红细胞九分图及红细胞参数进行 ROC 曲线分析以及 logistic 回归分析，比较各参数单独或联合诊断缺铁性贫血、α 地中海贫血、β 地中海贫血的价值。
结果 红细胞分布宽度、九分图区域五的红细胞分布宽度标准差与红细胞碎片绝对数分别鉴别缺铁性贫血与 α 地中海贫血、缺铁性贫血与 β 地中海贫血、α 地中海贫血与 β 地中海贫血时效能好。联合运用九分图区域四的红细胞体积、平均红细胞体积与九分图区域八的红细胞体积鉴别缺铁性贫血与 β 地中海贫血时，鉴别效率比传统的红细胞参数更高。对红细胞参数进行 logistic 回归模型分析得到鉴别的新公式 Mb＝－0.376×MCV＋0.444×(ERP4-RBC-Vol-P)＋0.577×(ERP8-RBC-Vol-P)－35.19 在鉴别缺铁性贫血与 β 地贫中的应用价值最高，其 AUC、截断值、敏感度、特异度分别为 0.98、0.45、0.96、0.98。
结论 联合应用红细胞新参数及新公式对不同小细胞性贫血具有较高的鉴别价值。

PU-3875

慢性粒细胞白血病的骨髓细胞形态和化学染色的个案分析

孙艳
新疆生产建设兵团第一师医院

探讨骨髓细胞形态学和化学染色在慢性粒细胞白血病诊断中的价值。
方法 综合观察我院二例比较特殊的诊断为慢性粒细胞白血病的住院病人，收集时间是 2020 年 1 月至 2021 年 6 月，方法比较这三类患者的血常规和骨髓细胞形态及化学染色与慢性粒细胞白血病诊断标准的差异，讨论慢性粒细胞白血病的形态学筛查，血常规白细胞不是明显增高，嗜碱性粒细胞稍高，骨髓象增生不是明显活跃，NAP 积分没有减低能不能排除慢性粒细胞白血病。
结论 血象白细胞不是明显增高，嗜碱性粒细胞稍高，骨髓象增生不是明显活跃，NAP 积分没有减低，能不能排除慢性粒细胞白血病，骨髓涂片中增生程度、粒系增生程度、原始细胞、幼粒细胞、嗜碱粒细胞、嗜酸粒细胞、单核细胞、幼红细胞、NAP 积分有差异, 可与外周血常规互相补充, 提高鉴别诊断的价值。

慢性粒细胞白血病患者大多数诊断于慢性期，20%~40%在诊断时无症状，bcr/abl 融合基因是诊断慢性粒细胞白血病的金标准，在一些偏远或者基层不能及时做染色体基因检测的医院，最开始的筛查血液形态学检查尤为重要，医生需要通过形态学检测做出初步筛查，再进一步选择染色体基因的检测。TKI 治疗时代已来，有研究显示 TKI 对 CML-CP 患者的疗效以及患者的生活质量都远高于 CML-AC 和 CML-BC 的患者。大部分慢性粒细胞白血病患者诊断于慢性期，但是仍然有小部分患者，在初始的慢性期漏诊了，在加速期、急变期临床症状出现，形态改变也更典型，才会考虑慢性粒细胞白血病的可能，再通过去查 bcr/abl 融合基因确诊。

PU-3876

MiR-150-5p 靶向抑制 Myb 调控 MDS 细胞增殖作用机制研究

袁顺玲
中山大学附属第五医院

研究背景 骨髓增生异常综合征（Myelodysplastic syndrome，MDS）是一种造血干细胞发生异质性克隆的血液系统肿瘤。它的主要特征是血细胞分化发育异常、骨髓无效造血并伴有向急性髓系白血病（acute myeloid leukemia, AML）转化的风险。MDS 的发生和进展是一个多基因、多步骤的病理过程，病因不明确，发病机制仍不清楚, MDS 的临床治疗效果仍不理想。因此，进一步深入研究 MDS 疾病的发生分子机制，寻找新的治疗靶标或研制新的药物是 MDS 的诊治紧迫任务。microRNA 是体内具有重要调控功能的非编码 RNA，研究发现 miR-150-5p 在多种癌症表达减低，且扮演抑癌基因角色。然而，miR-150-5p 在 MDS 细胞中的表达、临床意义以及作用仍不清楚。
研究方法 通过 GEO 数据库和 qRT-PCR 研究 miR-150-5p 在 MDS 患者和细胞系中的表达。体外培养人 MDS 细胞株 SKM-1 和 MDS-L，通过 CCK-8 和流式细胞术检测了 miR-150-5p 在 MDS 细胞增殖，细胞凋亡和周期中的作用。通过生信分析预测和荧光素酶报告基因实验检测 miR-150-5p 靶向调控 Myb。进一步使用上述方法研究 Myb 在 MDS 患者和细胞系中的表达，检测 Myb 在 MDS 细胞增殖，细胞凋亡和周期中的作用。最后，在 MDS 细胞中采用 CCK-8 检测了 Myb 对 miR-150-5p 调节细胞增殖的作用。
研究结果 我们发现与正常个体相比，miR-150-5p 在 MDS 患者和细胞系中低表达。过表达 miR-150-5p 能够抑制 MDS 细胞增殖，促进细胞凋亡和抑制细胞周期进程。机制研究表明，miR-150-5p 直接靶向抑制 Myb 的表达。而 Myb 在 MDS 患者和细胞系中高表达，敲低 Myb 能够抑制 MDS 细胞增殖，促进细胞凋亡和抑制细胞周期进程。同时，过表达 Myb 消除了 miR-150-5p 对 MDS 细胞增殖的抑制作用。
结论 我们的结果表明，miR-150-5p 在 MDS 中表达减低，使其对原癌基因 Myb 靶向抑制解除，高表达 Myb 导致 MDS 细胞恶性增殖。miR-150-5p/Myb 有望成为 MDS 基因治疗的潜在靶标。

PU-3877

血型鉴定室内比对及人员比对

徐娜
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 建立和实施血型鉴定的室内比对以及人员比对，以确保不同的检测仪器及试剂卡对于同一项目的检验结果具有可比性以及不同人员的操作之间的差异在可接受范围之内。
方法 仪器比对：由经验丰富的工作人员对已知血型为 A 型 RH(D)阳性、B 型 RH(D)阳性、O 型 RH(D)阳性、AB 型 RH(D)阳性、O 型 RH(D)阴性的 5 份标本分别在奥森多全自动血型仪和长春博讯试剂卡上面进行血型检测。
人员比对：由参与比对的 2 位工作人员对 A 型 RH(D)阳性、B 型 RH(D)阳性、O 型 RH(D)阳性、AB 型 RH(D)阳性、O 型 RH(D)阴性的 5 份标本分别进行奥森多全自动血型仪上机检测，长春博讯试剂卡检测和试管法的操作。
要求：ABO 正定型结果一致，ABO 反定型结果一致，RH(D)血型结果一致，符合率计算**方法** 符合率=检测结果符合样本数/总样本数。
结果 本实验的符合率均为 100%。人员比对：本实验室工作人员血型鉴定结果与实际的检测结果符合率均为 100％，ABO 血型及 RH（D）血型人员比对验证结果为“通过”。仪器比对： 5 份标本 2 种仪器试剂卡进行比对，与原始结果进行比较，合格率均为 100％，该项目仪器比对验证结果为“通过”。

结论 进行奥森多全自动血型仪和长春博讯试剂卡的比对，实验室工作人员 3 种方法之间的比对，实验室血型项目检测结果可靠，实验室人员操作符合要求，实验设备均符合相应要求，检测结果可用于临床供血标本的血型检测，保障临床用血安全。

PU-3878

杜氏利什曼原虫与组织胞浆菌、马内菲青霉菌形态学鉴别

朱爱民
娄底市中心医院

杜氏利什曼原虫、组织胞浆菌和马内菲青霉菌在骨髓涂片中病原体形态相似，易造成误诊，并常导致严重后果。现通过我院 3 个病例对这三种病原体的形态学鉴别进行简要阐述，给骨髓细胞形态室检验技师提供帮助。

杜氏利什曼原虫无鞭毛体与组织胞浆菌、马内菲青霉菌分别是黑热病、组织胞浆菌病、马内菲青霉菌病的病原体，这三种疾病均为少见的感染性疾病，不但临床症状极为相似，如发热、肝脾淋巴结肿大，全血细胞减少等。且在骨髓涂片中病原体形态也相似，容易混淆，导致误诊[1]。

近十年来，我院骨髓细胞形态室发现荚膜组织胞浆菌 6 例，马内菲青霉菌 3 例，杜氏利什曼原虫 1 例（后转省人民医院确诊），现找出其中 3 个病例与大家分享：

PU-3879

肺癌患者凝血指标变化及其临床意义

石琼、马萍
徐州医科大学附属医院

目的 探讨肺癌患者凝血功能指标的变化及其临床意义。
方法 选择我院 2016 年 1 月—2017 年 12 月均经病史、临床表现、CT 和病理检查确诊的肺癌患者 98 例作为研究对象，另选我院同期 60 例健康体检者作为健康对照组，检测凝血酶原时间（PT）、部分凝血酶原时间（APTT）、纤维蛋白原（FIB）、凝血酶时间（TT）、D-二聚体（D-D）和抗凝血酶-III（AT-III）的变化。
结果 与健康对照组相比，肺癌患者的 PT、APTT、TT 均明显延长，FIB、D-D 明显增高，而 AT-III 明显减低。
结论 PT、APTT、TT 结果延长，表明肺癌患者凝血功能紊乱；FIB、D-D 结果增高可致血栓形成和肺癌的转移，提示凝血功能指标的检测对于肺癌患者的治疗有一定的临床意义。

PU-3880

血常规散点图检出 3 例非霍奇金淋巴瘤病例讨论及分析

张楠[1]、郝云静[2]、刘翠清[2]、王金伟[2]、刘成[2]
1. 河北省中医院/河北中医学院附属医院
2. 河北省中医院

血常规是血液病筛查的最基础检查，血常规结果是否准确，一要看血常规个项目的数值，还有非常重要的一点就是要看血常规的散点图和直方图。血常规散点图包括 Diff 通道散点图，Baso 通道散点图，现在比较先进的机型还有 NRBC 通道散点图。其中，Diff 通道散点图与白细胞五分类密切相关，它通过测量细胞体积、内含物复杂程度、细胞核 DNA/RNA 含量，将白细胞分为淋巴细胞、单核细胞、中性粒细胞（含嗜碱性粒细胞）、嗜酸性粒细胞四大类。如果外周血出现异常细胞，因

其细胞体积、细胞质中内含物、细胞核 DNA/RNA 含量的变化，会分布在散点图的不同位置，因此在审阅血常规结果时一定要看散点图，笔者近几个月从血常规散点图初诊 3 例淋巴瘤患者，除此之外，笔者还发现一例浆细胞白血病患者有相似的散点图，Diff 散点图仅是通过细胞大小、细胞质内含物多少、细胞 DNA/RNA 含量的多少来判断是哪种细胞，因此不同的疾病可能会出现相似的散点图，同样笔者也观察了多例传染性单个核细胞增多症异型淋巴细胞比例明显增多的散点图、急性淋巴细胞白血病散点图、急性髓细胞白血病散点图，同样发现对于不同的疾病可能会出现相似的散点图，而同种类型的疾病也可能会出现不同的散点图，这就需要我们在显微镜下认真辨识细胞的形态。同样对于全自动血液分析仪的研发者来说提出一个新的挑战，今后的血液分析义是否可以标记不同细胞表面的某个细胞标志物，从而能更清楚的区分不同类型的细胞。

PU-3881

CRP、SAA 和 PCT 水平在慢性乙肝合并感染患者中的诊断价值

郑国娜
临沂市人民医院

目的 分析判断血清 C-反应蛋白（CRP）、血清淀粉样蛋白 A（SAA）和降钙素原（PCT）水平在慢性乙型肝炎合并感染患者中的临床诊断价值，为慢性乙型肝炎患者临床感染的控制提供科学依据。
方法 选取 2019 年 3 月—2021 年 3 月我院收治的 210 例慢性乙肝感染患者为研究对象，根据有无感染分为感染组和未感染组。 检测所有患者血清 CRP 、SAA 和 PCT 水平，绘制 ROC 曲线，评价其特异性和敏感性。
结果 感染组和未感染组慢性乙肝患者的血清 PCT、SAA、CRP 水平均高于正常参考值，与未感染组相比，感染组患者的 PCT 、SAA 和 CRP 水平显著增高（P <0.01）。使用 Logistic 回归方程计算 SAA、PCT、CRP 联合诊断的概率，再绘制 ROC 曲线，计算联合 AUC 值：CRP 联合 PCT 的 AUC 值为 0.878（P=0.000）， 敏感度：83.9%，特异度：84.5%；CRP 联合 SAA 的 AUC 值为 0.810（P=0.000），敏感度：69.8%，特异度：92.2%；PCT 联合 SAA 的 AUC 值为 0.814（P=0.000），敏感度：73.4%，特异度：92.1%；CRP、PCT、SAA 三者联合后的 AUC 值为 0.855（P=0.000），敏感度：70.1%，特异度：97.5%。与 CRP 相比，PCT 诊断细菌感染的特异性、敏感性均相对更高，SAA 对于病毒性感染比 CRP 更敏感，升高幅度更明显。
结论 血清 CRP、SAA 和 PCT 水平在慢性乙型肝炎合并感染患者中明显高于正常个体，与 CRP 比较，PCT 诊断细菌感染的临床效能更高,SAA 诊断病毒感染更敏感。联合检测有助于早期鉴别细菌和病毒感染，合理指导抗生素使用，并在治疗后，准确评估疗效。

PU-3882

尿细菌计数在尿路感染的快速诊断中的应用

侯利霞、汪春新
安徽医科大学附属阜阳医院

目的 探讨尿细菌计数在尿路感染快速诊断中的应用。
方法 收集 2018 年 3 月-2020 年 8 月住院患者 1081 例中段尿标本，采用 Sysmex UF4000 尿液分析仪计数尿中细菌数，并与尿培养结果比较，以评价尿细菌计数对排除尿培养阴性标本的意义及对提示细菌革兰染色信息的评价。
结果 1081 例标本中，尿培养阳性率为 10.0%（108/1081），当总标本中细菌计数的 cut-off 值为 57.4 个/μl 时，尿细菌计数对尿路感染快速诊断的敏感性为 96.3%，特异性为 73.2%，阴性预测值为 99.4%，阳性预测值为 28.6%，与尿培养的一致性为 75.6%，可以减少 66.0%的尿培养。去除

污染后，在 81 例培养阳性标本中，仪器提示的细菌革兰染色信息与尿培养的一致性为 61.7%（50/81），一致性系数为 0.716（X2=31.256，P<0.001）。
结论 尿细菌计数可用于快速排除尿路感染；而且对于尿路感染患者，能预测尿路感染的细菌革兰染色类型，帮助临床合理选择抗菌药物。

PU-3883

外周血白细胞群落数据与肾移植后急性排斥反应的相关性研究

殷睿映
郑州大学第一附属医院

目的 为了研究外周血白细胞的细胞群落数据与肾移植手术后急性排斥反应的相关性，并进一步挖掘对评估急性排斥反应的发生可能发挥作用的参数。
方法 根据肾移植手术后三个月内是否发生排斥反应为依据，将共 68 名患者作为研究对象分为两个组别，其中发生急性排斥组（ARE）32 例，非急性排斥组（non-ARE）36 例。收集移植手术后的外周血细胞分析数据、白细胞群落数据、肾脏功能相关的生化指标以及病历基本信息，使用 SPSS 软件统计分析两组患者之间白细胞群落数据的差异，以及其与急性排斥反应的发生之间的相关性。
结果 在 ARE 和 non-ARE 两组之间，外周血中性粒细胞、淋巴细胞和单核细胞的细胞群落数据参数均有显著的差异（包括 Ne-V-sd, Ne-UMS-sd, Ly-V, Ly-MS, Ly-UMS, Ly-LS and Mo-UMS）。其中，Ne-UMS-sd 和 Ly-UMS 对 ARE 的发生与否具有最强的区分作用。这些具有差异的参数中，Ly-UMS 的受试者曲线下面积（AUC）最大，为 0.756。同时，Ne-UMS-sd 联合 Ly-UMS 的受试者曲线下面积达到 0.823。在 ARE 组，Ne-UMS-sd 和 Ly-UMS 均呈现与估算肾小球滤过率（eGFR）的负线性相关性，其 r 值分别为-0.527（p=0.002）和-0.436（p=0.013）。
结论 外周血白细胞群落数据中的参数 Ne-UMS-sd 和 Ly-UMS 可能对于诊断肾移植后急性排斥的发生具有一定的参考意义。

PU-3884

一例 EDTA 依赖性血小板假性减低患者的结果分析

陈婕
西安医学院第一附属医院

血小板减少为临床常见症状,表现为由于各种原因导致的血小板计数结果低于参考值下限。当血小板减少时可出现一系列症状,如皮肤淤血、鼻出血、口腔黏膜出血等,严重者可出现内脏出血、脑出血甚至危及生命。乙二胺四乙酸二钾（EDTA-K2）为血液分析的常用抗凝剂,但有时会引起血小板聚集,使血小板计数假性减少,临床诊断为 EDTA 依赖性假性血小板减少症（EDTA-PTCP）。我院 2021 年 5 月收治 1 例血小板减少的患者,首次血常规检测所得血小板计数结果较低，仪器报警“血小板聚集”，触发我室复检规则，对血小板进行复检。显微镜下可见血小板呈小簇状聚集，于是联系临床给患者重新抽取枸橼酸钠管和 EDTA 管立即检测。结果发现 EDTA 管结果正常，且仪器未报警，之后 15 分钟，30 分钟，1 小时后再用 EDTA 管分别检测及显微镜复检，血小板数值呈明显下降趋势，镜下可见血小板聚集逐渐加重。所以 EDTA 依赖的血小板假性减低随着血液离体的时间延长，表现出聚集程度加重。

PU-3885

The morphological Characterization and mechanism exploration of EDTA-Dependent Extensive Platelet satellitism and Phagocytosis

Ping Guo
Department of Clinical Laboratory Medicine, Ruijin Hospital affiliated to Shanghai Jiaotong University School of Medicine

Platelet satellitism and phagocytosis by neutrophils are rare phenomena induced by the anticoagulant EDTA. In a 55-year-old female, the prominent platelet satellitism and extensive phagocytosis was revealed accidently in the absence of pseudothrombocytopenia usually presented by the subjects with both artificial laboratory phenomena. The extensive binding and phagocytosis of platelet by neutrophil were further confirmed by flow-cytometry. Following the dynamic of platelet satellitism formation and extent of platelet phagocytosis showed that the attachment of platelets with neutrophils and phagocytized by latter occurred simultaneously and the processes were closely associated. The mechanism underlying the platelet satellitism and phagocytosis in the presence of EDTA is still unclear and believed to be antiplatelet autoantibodies related. Consistently, mixing the platelet poor plasma isolated from the investigated subjects with blood cells collected from blood type matching healthy individuals elicited similar time dependent platelet satellitism and phagocytosis albeit at lower magnitude, indicating plasma components of the investigated subject mediating the processes. Although the anti-GP IIb/IIIa antibodies were detected at high titers in the subject investigated, the mixture experiments performed in similar fashion with plasma acquired from patients with Idiopathic thrombocytopenic purpura positive for anti-GP IIb/IIIa antibodies failed to reproduce neither platelet satellitism nor phagocytosis, suggesting that the apparent platelet satellitism and phagocytosis presented in the subject attributed to autoantibodies other than antibodies directed against platelet alone. Although no pathological conditions have been revealed to be associated with the platelet satellitism and phagocytosis induced by EDTA, the phenomena require concerted processes and warrant further studies to clarify.

PU-3886

凝血和纤溶指标与静脉血栓形成的相关性

姚嘉怡
复旦大学附属中山医院青浦分院

目的 静脉血栓栓塞（VTE）包括深静脉血栓形成（DVT）和肺血栓栓塞（PTE）。研究静脉血栓栓塞患者血清中凝血和纤溶相关指标的表达水平，探讨其对于 VTE 的诊断价值。
方法 2020 年 1 月至 2021 年 6 月，以我院 100 例发生静脉血栓栓塞的患者为 VTE 组（其中 50 例深静脉血栓形成患者为 DVT 组，50 例肺血栓栓塞患者为 PTE 组），以 50 例健康人为健康对照组。检测血清凝血和纤溶相关指标（APTT、PT、FIB、TT、DD、FDP）水平，分析其与 VTE 发生的关系。
结果 VTE 组血清 APTT、PT、FIB、DD、FDP 高于和健康对照组（P 均小于 0.05），其中 PTE 组血清 PT、APTT、DD、FDP 高于健康对照组（P 均小于 0.05），DVT 组血清 APTT、FIB、DD、FDP 高于健康对照组（P 均小于 0.05）；PTE 组与 DVT 组相比，各项凝血和纤溶指标无显著性差异（P 均大于 0.05）。
结论 静脉血栓栓塞患者 APTT、PT、FIB、DD、FDP 升高，早期监测凝血和纤溶标志物可预防血栓的发生。

PU-3887

UF5000 尿沉渣分析仪细菌参数对尿路感染的研究探讨

李东阳、吴雁
天津市泰达医院

目的 评价 UF5000 尿沉渣分析仪的细菌参数（BACT-INFO、细菌散点图）在筛查尿路感染中的作用。
方法 2021 年 3 月-4 月收集 100 例疑似尿路感染患者的中段尿尿液标本，采取尿培养、希森美康 UF5000 尿沉渣分析的方法，统计 UF5000WBC、BACT、BACT-Info、细菌散点图（CB_FLH_P×CB_FSC_P），并以尿培养为金标准。并统计比较 BACT-Info 与尿培养结果的一致性。
结果 相比之下 UF5000 的 BACT-Info、细菌散点图与中段尿细菌培养的结果表明，革兰阴性菌符合率为 94%，革兰阳性菌符合率为 87%，细菌总符合率为 75%。
UF5000 尿沉渣分析仪细菌分型（BACT-Info）和细菌散点图可以作为快速诊断尿路感染的辅助方法。
结论 UF5000 尿沉渣分析仪的细菌参数（包括：细菌分型（BACT-Info）和细菌散点图）作为早期诊断尿路感染的依据，符合率达到 75%，具有良好的诊断价值，可以减少一些不必要的尿培养成本，结合尿沉渣分析结果及细菌散点图可提前预判细菌分型，为患者临床用药提供早期指导。

PU-3888

肝素抗凝与 EDTA 抗凝在血小板计数中的比对

黄坚[1]、彭郑林[2]
1. 联勤保障部队第九 00 医院
2. 福建医科大学校医院

目的 血小板计数异常与正常的标本，在乙二胺四乙酸二钾（EDTA-K2 ）与肝素锂抗凝剂中的计数情况的比对。随机观察本院 69 例血常规检验的标本血小板计数在乙二胺四乙酸二钾、肝素锂抗凝管的计数情况，与金标准草酸铵手工法进行比较，探究血小板计数假性减低时的标本，能否可以直接用肝素锂抗凝管抽血进行检测，结果与金标准是否一致。
方法 随机选取 69 例标本，用乙二胺四乙酸二钾、肝素锂抗凝管采集静脉血，先用德国西门子 SIEMENS AVDIA 2120I 血细胞分析仪进行血常规检验，再用金标准手工计数法充池计数血小板，随后进行推片，用瑞氏-姬姆萨染液染色 8 分钟后镜检观察有无血小板聚集。
结果 在 69 例患者标本中，46 例患者采用肝素锂抗凝管抽血时镜下观察有血小板聚集的现象发生，占标本总数的 66.6%，乙二胺四乙酸二钾抗凝管抽血检测的有 1 例标本镜下观察有血小板聚集的现象，占标本总数的 1.5 %。其中急诊科 20 例肝素锂抗凝静脉血标本在 15 分钟内完成检测，有 4 例发生聚集；49 例肝素锂抗凝静脉血标本在 2 小时内检测，有 42 例标本发生聚集。
结论 在血小板计数中，乙二胺四乙酸二钾抗凝比肝素抗凝更接近手工计数结果，血常规检验血小板计数还是推荐用乙二胺四乙酸二钾抗凝剂抽血进行检验。如果在乙二胺四乙酸二钾抗凝出现血小板假性聚集，枸橼酸无法纠正假性聚集时，可以使用肝素锂纠正，检测时间在抽完血 15 分钟内完成。

PU-3889

一种使用数字显微镜(Morphogo)识别骨髓中异常淋巴细胞的机器学习工具

唐古生[1]、付鑫炎[2]、王贞[3]、陈明义[4]
1. 海军军医大学第一附属医院（上海长海医院）
2. 杭州智微信息技术有限公司医学部
3. 中南大学湘雅医院血液科
4. 德克萨斯大学西南医学中心血液科

目的 骨髓形态学分析是血液病诊断的重要步骤。人工计数骨髓涂片分析耗时，工作量大且存在观察者间的偏差。本研究旨在探讨基于数字病理方法与先进的机器学习相结合的 Morphogo 系统区分骨髓涂片中异常和正常淋巴细胞的可行性及其意义。
方法 本研究入组分析了 53 例经临床及实验室形态学、流式细胞术等综合检查确诊为淋巴系统肿瘤伴骨髓浸润患者的骨髓涂片的高分辨率图像。为了提高系统识别骨髓淋巴细胞的范围和精度，我们通过人工智能训练开发了一种结合淋巴细胞图像的细胞大小、细胞核/质颜色和纹理以及几何细胞学特征的算法，对淋巴细胞进行识别和分类。从 43 例训练组患者骨髓涂片显微镜下选择合适视野，由 Morphogo 系统采集了 4579 个淋巴细胞进行反复训练识别，其中形态学专家确认淋巴细胞/淋巴瘤细胞的有 4432 个。进一步对区分正常淋巴和异常淋巴细胞训练后，采用 10 例患者骨髓涂片作为测试集进行算法识别异常淋巴瘤细胞的性能确认。
结果 通过人工智能（AI）的识别系统对测试集 10 例患者的骨髓涂片采集的 3616 张细胞图像中的 5454 个细胞进行识别分类，共识别出 833 个异常淋巴细胞，4621 个非淋巴细胞。经细胞病理医生审核，确认 825 个为异常淋巴细胞，4551 个为非淋巴细胞。对异常淋巴瘤细胞识别的灵敏度，特异度，准确率分别是 92.18%，99.82%，98.57%，阳性预测值和阴性预测值为 99.04%和 98.49%。
结论 Morphogo 自动识别异常淋巴细胞为诊断骨髓淋巴瘤细胞提供了可行性。进一步训练和改进算法将有助于进一步细分特定谱系亚组病理学，从而提供一个强大的、更快的恶性疾病筛查诊断工具。骨髓细胞形态学有望实现 AI 阅片部分或全部替代骨髓人工形态学镜检。

PU-3890

Altered Peripheral B lymphocyte subsets in patients with hepatocellular carcinoma

jiaoxiang wu[1]、yue wang[2]、hanxiao sun[1]、jie shu[1]、yajie wang[1]、meiyu tan[1]、lida zhou[1]、biao huang[3]、qiuhui pan[4]、huiming sheng[1]
1. Tong Ren Hospital, Shanghai Jiaotong University School of Medicine
2. Shanghai 10th people's hospital affiliated to Tong Ji University school of medicine
3. Immunoassay laboratory, College of Life Sciences and Medicine, Zhejiang Sci-Tech University
4. Department of Clinical Laboratory Medicine, Shanghai Children’s Medical Center, School of Medicine, Shanghai Jiaotong University

Background Although B lymphocytes are widely known to participate in the immune response, the conclusive roles of B lymphocyte subsets in the antitumor immune response have not yet been determined.
Aims To investigate the association between altered B cell subsets and hepatocellular carcinoma (HCC).
Materials and Methods Single-cell data from GEO datasets were first analyzed, and then a B cell flow cytometry panel was used to analyze the peripheral blood of 83 HCC patients and 33 healthy controls recruited to participate in our research. We explored three B cell subsets in the peripheral blood of all subjects: interleukin-10-producing regulatory B cells (B10 cells), marginal zone B cells (MZB cells), and follicular B cells (FoB cells).

Results The B cell subsets in HCC patients were changed. In particular, patients with HCC had a higher frequency of B10 cells and a lower percentage of MZB cells than healthy controls. In addition, FoB cells were increased in patients who had stage III or IV disease compared with patients with stage I or II disease. Moreover, we explored the paired presurgery and postsurgery data of 15 patients who underwent tumor excision and found that the frequency of B10 cells decreased but the frequency of FoB cells increased after surgery.
Conclusions The results suggest that altered B cell subsets are associated with the development and prognosis of HCC. B cell subsets may have predictive value in HCC patients and could be potential targets for immunotherapy in HCC.

PU-3891

A Rare Cause of hypofibrinogenemia with high level anticyclic citrullinated peptide

Hanxiao Sun、Jiaoxiang Wu、Binbin Xuan、Jie Shu、Huiming Sheng
Department of Laboratory Medicine, Tongren Hospital, Shanghai Jiao Tong University School of Medicine

It was reported that patients with systemic amyloidosis tend to bleed with an activated coagulation system, and show significant fibrinolysis with a high or normal level of fibrinogen. Herein, we report our experience in managing an unusual case of amyloidosis with hypofibrinogenemia and a high level of serum anticyclic citrullinated peptide(Anti-CCP). A 74-year-old woman who presented with a ten-day history of lumbago and extreme weakness of lower limbs under no obvious inducement, was admitted to the Hematology ward with a diagnosis of coagulation disorders. Eight years ago she received radiotherapy for early-stage lung cancer. Global coagulation and a comprehensive coagulation factor screen were performed, while deranged hemostasis had been observed with a decrease fibrinogen concentration of 0.3g/L (reference interval, RI 2-4 g/L). High levels of serum albumin A (SAA, 161.955, 51.4-207.3 mg/L, RI 0-10 mg/L), Anti-CCP, and rheumatoid factor (RF) were detected. The amyloid deposit was detected in the bone marrow which suggested the possibility of amyloidosis. In order to rule out hereditary fibrinogen Aα-chain amyloidosis, Sanger sequencing was applied to analyze the fibrinogen Aalpha chain gene (c1600-1721) and no mutation was detected. The patient was given plasmapheresis and immunosuppressant intermittently in the following 3 months. However, fibrinogenopenia was not alleviated (≤1 g/L, medium: 0.7 g/L), along with a high level of serum anti-CCP（>500 U/ml). Next, we carried out liquid chromatography-mass spectrometry (LC-MS) analysis to measure the post-transcriptional modification of fibrinogen by Easy-nLC1200-Q-Exactive Plus instrument (ThermoFisher Scientific) and analyzed by Human_uniprot database (https://www.uniprot.org/, precursor mass tolerance: 10ppm, fragment ion mass tolerance: 0.02Da), because a rare subtype of amyloidosis was caused by deposition of misfolded fibrinogen resultant from fibrinogen citrullination, and thereby affects the hemostatic homeostasis. A total of 6 serum samples, 3 from Rheumatoid arthritis (RA) patients and 3 from healthy human beings (non-RA), were applied as controls and measured simultaneously with the sample from our patient mentioned above. According to the clustering analysis for the Area values of citrullinated protein, we found the type and number of citrullinated proteins in our patient serum were remarkably different from both RA and non-RA controls (by WocEA1.0). Two citrullination sites in fibrinogen Aα-chain were detected only in our patient, and one site (K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGF Cit RH) was only reported once in previous studies. Since the sequencing and immunofixation results had ruled out the hereditary fibrinogen Aα-chain amyloidosis and AL amyloidosis (light chain), systemic AA amyloidosis was diagnosed for this patient.

In conclusion, AA amyloidosis should be considered in patients with elevated plasma anti-cyclic citrullinated peptides, especially when the symptoms of coagulation disorders are presented. And great progress has been made in the treatment of systemic amyloidosis. Early diagnosis and correct classification of amyloidosis are imperative before specific therapy can be

implemented. Combined sequencing and LC-MS measurement could be a powerful tool for the accurate diagnosis of amyloid subtypes.

PU-3892

血清 ITGBL1 水平对乙型肝炎病毒相关原发性肝细胞癌的诊断价值分析

叶菲[1]、石峰椿[2]、张欣欣[2]、于德敏[2]
1. 瑞金医院传染科
2. 上海交通大学医学院附属瑞金医院

目的 既往研究表明整合素 β 样 1 蛋白（Integrinbeta-like1，ITGBL1)在乙型肝炎病毒（HBV）相关肝硬化或者肝癌组织表达明显升高，并且在肝癌的侵袭和转移以及 EMT 的发生有重要作用。本研究评估了血清中 ITGBL1 水平预测感染 HBV 相关 HCC 的诊断能力，旨在鉴定一种 HBV 相关 HCC 特异性血清生物标志物。

材料和方法 采用回顾性研究方式收集了自 2017 年至 2020 年 716 例受试者其中试验组共 299 例患者、验证组共 417 例患者。将所有患者分为 4 组：HBV 相关性肝细胞癌患者、HBV 相关肝硬化患者、慢性乙型肝炎患者、健康对照人群。采用酶联免疫吸附测定（ELISA）方法检测各组血清中 ITGBL1 的表达水平，采用二元 Logistic 回归分析，探究高危人群（包括慢乙肝患者和 HBV 相关肝硬化患者）发生 HBV-HCC 的高危独立影响因素，并在验证组中进行验证。同时结合研究对象的各项临床数据,使用灵敏度，特异性和受体工作特征曲线（AUC）下的面积评估 ITGBL1 的诊断性能，进一步分别以 400ng/mL（AFP400）、20ng/mL（AFP20）作为 AFP 的诊断临界值将血清中 ITGBL1 与 AFP 进行了诊断效能的比较。

结果 使用 ELISA 方法对血清样品检测和分析，HBV-HCC 患者的血清 ITGBL1 水平明显低于肝癌高危人群(CHB 和 HBV-LC)，CHB 患者与健康对照组之间无明显差异。通过对高危人群和 HBV-HCC 患者的临床参数进行单因素和多因素 logistic 回归分析，结果确定血清 ITGBL1 水平是高危人群发生肝癌的独立危险因素。鉴别高危人群与 HBV-HCC 时，血清 ITGBL1 的最佳诊断临界值为 54.30ng/mL(试验组：AUC 为 0.773，95%CI 为 0.716-0.823，敏感性 66.98%，特异性 71.62%；验证组：AUC 为 0.732，95%CI 为 0.682-0.778，敏感性 62.41%，特异性 74.07%)。进一步分析血清 ITGBL1 在鉴别早期 HBV-HCC 与高危人群(试验组：AUC 为 0.787，95%CI 为 0.723-0.842，敏感性 62.75%，特异性 79.73%；验证组：AUC 为 0.764，95%CI 为 0.710-0.813，敏感性 67.69%，特异性 74.07%)中的诊断准确率高于 AFP20(临界值 AFP=20ng/mL)(试验组：AUC 为 0.638，95%CI 为 0.567-0.704，敏感性 45.10%，特异性 82.43%；验证组：AUC 为 0.718，95%CI 为 0.662-0.770，敏感性 49.23%，特异性 94.44%)。尤其对于 AFP 阴性(<20ng/mL)的 HBV-HCC 患者，血清 ITGBL1 仍保持较高的诊断价值(试验组：AUC，0.756，95CI%，0.683-0.819，68.18%和 68.85%；验证组：AUC,0.744，95CI%，0.686-0.796，81.13%和 55.88%)。当血清 ITGBL1 联合 AFP20 时，无论是在诊断 HBVHCC 或者早期诊断 HBV-HCC 方面均获得优异的诊断价值。

结论 血清中 ITGBL1 可作为 CHB 患者发生肝癌风险潜在有效的非侵入性生物标志物，在与 AFP 联合后，即使对于 AFP 低水平的 HCC 也具有较好的诊断效能，表现出较好的临床应用前景。

PU-3893

INSMI 过表达可作为前列腺癌患者预后的重要标志物

唐丽娟
云南省第二人民医院

前列腺癌作为一种世界范围内的男性常见恶性肿瘤，我国的其癌症发病率逐年上升，其中 30%为临床局限型，而另外的 70%均为晚期或广泛转移的无法接受局部的根治性治疗患者，预后较差，这就对我国前列腺癌患者的早期诊断和治疗提出了更高的要求。本次研究综合了来自 GEO 的 10 个前列腺癌微阵列数据集及 TCGA 的前列腺癌数据集，数据显示前列腺患者中 INSMI 表达上调，INSMI 过表达与 COL17A1 相关，而 INSMI 过表达与 SCGB1A1 相关。然而，INSMI 上调对前列腺癌患者的总生存期(OS)有影响，表现为 OS 减低。本研究数据表明 INSMI 过表达可影响前列腺患者预后，然而 INSMI 通过何种机制调节患者预后有待后续分子体外及动物体内实验研究。

PU-3894

浆膜腔积液高荧光细胞比率联合血清 CA199、CA125、CA153 对恶性肿瘤的诊断价值

林花[2]、赵瑞[1]
1. 昆明医科大学第二附属医院检验科
2. 昆明医科大学第二附属医院检验科

目的 比较浆膜腔积液中的高荧光细胞比率、血清 CA199、CA125、CA153 在恶性肿瘤和良性病变中的浓度差异，探讨单项及联合检测诊断恶性肿瘤的价值。
方法 选取 2020 年 5 月至 2021 年 2 月于昆明医科大学第二附属医院住院治疗及门诊确诊的恶性肿瘤病人 68 例，良性病变病人 132 例，检测其浆膜腔积液高荧光细胞比率(HF-BF%)和血清 CA199、CA125、CA153 浓度，进行两组间比较并绘制 ROC 曲线，分析单项及联合检测对恶性肿瘤的诊断价值。
结果 1、恶性肿瘤组的 HF-BF%、CA199、CA153 浓度高于良性病变组，差异有统计学意义（$p<0.05$），CA125 在两组之间的差异无统计学意义（$p>0.05$）。2、单项的诊断效能较低，AUC 均小于 0.700，单项诊断恶性肿瘤的灵敏度依次为 CA125>HF-BF%>CA199>CA153，特异度依次为 CA153>CA199>HF-BF%>CA125。3、有三种两两联合检测方式的 AUC>0.700，分别是 HF-BF%+CA199、HF-BF%+CA153 及 CA199+CA153，其中 HF-BF%联合 CA153 的诊断效能最佳，其 AUC 为 0.730，灵敏度为 57.4%，特异度为 82.6%。4、三项联合检测对恶性肿瘤的诊断效能明显提高，其中 HF-BF%+CA199+CA153 的 AUC 为 0.749，灵敏度为 60.3%，特异度为 83.3%，但四项联合检测的 AUC 为 0.750，灵敏度可到 60.3%，特异度 84.1%，与 HF-BF%+CA199+CA153 相比无明显提升。
结论 单项指标检测时，HF-BF%、CA199、CA153 诊断效能均较差，单项 CA125 对恶性肿瘤的诊断无明显价值，但 HF-BF%+CA199+CA125+CA153 四项联合检测对恶性肿瘤的诊断有重要价值，因其灵敏度和特异性与 HF-BF%+CA199+CA153 三项联合无明显差异，从经济角度考虑，HF-BF%+CA199+CA153 三项联合检测是一种更优选择，探究更高效合理的联合检测组合有助于提高诊断的灵敏度及准确度。

PU-3895

Continuous changes in biological levels of complete blood count in a high altitude area of China

Xuan Luo 、Lei Feng、Xuejing Bai、Jiangxian Zhu、Guancheng Zhao、Mengna Wu、Zefeng Yan
Department of Laboratory, People's Hospital of Yuxi City （Department of Laboratory, The Sixth Affiliated Hospital of Kunming Medical University）

Objectives We aimed to establish a new reference interval of blood cell parameters by classifying and counting blood Cells of 16- to 85-year-old healthy volunteers and observing continuous changes with age.
Methods We analyzed the blood cell parameters of 42,678 cases (men, 24,406; women, 18,272), and compared the blood cell parameters of men and women in different age groups using an independent samples t-test. Using limits of 2.5%–97.5%, a 90% confidence interval was used to develop new reference intervals.
Results Counts of blood cell parameters, including white blood Cells, neutrophils, lymphocytes, monocytes, eosinophils, basophils, red blood Cells, hemoglobin, hematocrit, distribution width of red blood Cells and platelets, were found to differ between men and women in different age groups. These parameters were used to establish a new reference interval of blood Cells.
Conclusion The blood cell parameters of both men and women changed with increasing age. The reference interval that we established will provide more accurate basic evidence for clinical diagnosis and treatment of diseases.

PU-3896

急性髓系白血病患者血清腺苷脱氨酶测定的意义

韩静颖
山东第一医科大学附属省立医院

目的 探讨血清腺苷脱氨酶(ADA)在急性髓系白血病（AML）的变化规律及发生发展中的意义。
方法 收集 75 例急性髓系白血病（AML）患者、63 例治疗前急性髓系白血病（AML）患者、62 例治疗后急性髓系白血病（AML）患者和 86 例健康对照者外周血血清，利用 PNP-XTO-POD 偶联连续监测法测定血清腺苷脱氨酶(ADA)的值，利用速率法测定谷草转氨酶（AST）、谷丙转氨酶（ALT）和谷氨酰转肽酶（GGT）的值。检测正常组与 AML 组血清 ADA 水平，比较治疗前组和治疗后组 ADA 水平变化，利用受试者工作特征曲线(ROC 曲线)确定 ADA 最佳截点并将治疗前 AML 患者分为低 ADA 组（ADA<13.50U/L） 和高 ADA 组（ADA≥13.50U/L），分析两组间年龄、性别、AST、ALT 和 GGT 差异。
结果 AML 患者 ADA 数值增高；治疗前组显著高于治疗后组 ADA；采用 ROC 曲线，将治疗前患者分为高 ADA 组和低 ADA 组，与 ALT、AST 和 GGT 有显著差异（P<0.05）。
结论 AML 患者的 ADA 水平显著高于正常对照者，治疗后 ADA 显著低于治疗前，采用 ROC 曲线，高 ADA 组 ALT、AST、GGT 显著升高提示血清 ADA 在 AML 疾病辅助诊断中有重要意义。

PU-3897

红细胞分布宽度的变化在早期胃癌中的意义

韩静颖
山东第一医科大学附属省立医院

目的 探讨早期胃癌患者红细胞分布宽度（RDW）的变化及临床意义。
方法 选取 90 例早期胃癌患者术前抽血检测血常规、CA125、CA199 等相关指标，并选取 89 例体检健康志愿者（正常对照组），比较 2 组中 RDW 水平，并绘制受试者工作特征曲线（ROC 曲线），确定 RDW 最佳截点，根据早期胃癌患者 RDW 水平分为低 RDW 组（RDW<12.5）和高 RDW 组（RDW≥12,5）。分析 RDW 与年龄、性别、CA125、CA199 的关系。
结果 早期胃癌患者 RDW 水平高于正常对照组，差异有统计学意义（P<0.001）；绘制 ROC 曲线，将早期胃癌患者分为低 RDW 组和高 RDW 组，高 RDW 组与年龄有差异（P<0.05）；与性别、CA125、CA199 无差异（P>0.05）。
结论 早期胃癌患者的 RDW 水平高于正常对照组；高 RDW 组与年龄有差异，与性别、CA125、CA199 无差异。说明 RDW 在早期胃癌的诊断中可作为一项辅助筛查指标 。

PU-3898

SIEMENS-AVIDA 2120 血细胞分析仪对新生儿白细胞计数的研究应用

程少杰
中国人民解放军联勤保障部队第 900 医院

目的 探讨 SIEMENS-AVIDA 2120 血细胞分析仪计数新生儿外周血白细胞的准确性，消除有核红细胞影响，并对其临床应用作以评价。
方法 选取我院新生儿病区 98 例新生儿静脉血样本，应用 SIEMENS-AVIDA 2120 血细胞分析仪和人工镜检法对每份样本中的白细胞进行计数，仪器法采集新生儿血液于 EDTA-K2 抗凝管中充分混匀，用质控品对 SIEMENS-AVIDA 2120 血细胞分析仪进行室内质控，在结果在控的情况下应用 SIEMENS-AVIDA 2120 血细胞分析仪，于 2h 内检测完毕；人工镜检法准确吸取 20ul EDTA-K2 抗凝全血，加入含有 0.38mL 白细胞稀释液的试管中，充分混匀，充入细胞计数池中，计数四个大方格中的白细胞数，同时制备血涂片，经瑞 - 吉氏染液染色后由专业检验人员在显微镜下直接计数，在血涂片体尾交界处，选择细胞分布均匀、细胞着色较好的部位，计数 100 个白细胞，同时记录 NRBC 的数量，并根据白细胞校正公式校正计算白细胞总数；两种方法各检测两次取均值比对，采用 SPSS 22.0 统计学软件分析数据，计量资料用(x±s)表示，采用配对 t 检验，做出统计学分析。
结果 在选取的 98 例受检样本中，白细胞计数结果低于 15.0×109/L 有 45 例，(15.0～20.0)×109 / L 有 39 例，大于 20×109/L 有 14 例。当白细胞计数低于 15.0×109/L 时，两种检测方法比较差异无统计学意义(P>0. 05)；在(15.0～20)×109/L 时，两种检测方法比较差异无统计学意义(P >0. 05)； 高于 20.0×109/L 时，两种检测方法比较差异有统计学意义(P <0. 01) 。
结论 SIEMENS-AVIDA 2120 型血细胞分析仪在对新生儿外周血白细胞计数的过程中，当遇到高值白细胞时出现有核红细胞概率增大，仪器会自动纠正 WBC 结果，有效降低复检率，具有较好的准确性。

PU-3899

脂血标本对血常规结果的影响及校正方法探讨

鲁君艳、姜志刚、王鹏
永州市中心医院

目的 研究不同浓度脂血标本对全自动血液分析仪血常规检测结果的影响，并比较血浆置换法与公式校正法消除脂血标本影响的校正效果。
方法 选取 32 例健康体检者无脂血、溶血、黄疸的标本作为对照组，进行血常规及三酰甘油（TG）检测。32 例标本每份平均分成三管，低速离心分离血浆，三管标本分别吸出 10、20、40μl 血浆，再加入同等量的脂肪乳制备脂血标本，进行血常规及 TG 检测。根据 TG 浓度水平分轻、中、重度脂血（A、B、C）三组，将检测结果与对照组进行比较分析。脂血标本经血浆置换法和公式校正法进行校正，校正后结果与对照组及脂血组结果进行比较分析。
结果 A 组血常规参数与对照组比较，结果略有升高，差异无统计学意义（P＞0.05），B 组中 HGB、MCH、MCHC 水平与对照组相比，差异均有统计学意义（P＜0.05）。C 组中 HGB、MCH、MCHC、WBC、HCT、MCV 水平与对照组相比，差异均有统计学意义（P＜0.05）。三组中 RBC、PLT 水平与对照组相比，差异都无统计学意义（P＞0.05），脂血标本经血浆置换法和公式校正法处理后基本可消除乳糜微粒对检测结果的影响，校正后结果与对照组比较差异无统计学意义（P＞0.05）。
结论 不同浓度脂血会对全自动血液分析仪血常规结果产生不同的影响，尤其是 HGB 结果，中、高浓度脂血影响更明显。脂血标本经血浆置换法和公式校正法处理后基本可消除乳糜微粒对检测结果的影响，但血浆置换法步骤繁琐，公式校正法更为简便易行。

PU-3900

BC-6800 Plus 血细胞分析仪血小板光学通道在纠正血小板假性减少中的应用

郭平
上海交通大学医学院附属瑞金医院

目的 评估 BC-6800 Plus 血细胞分析仪光学血小板通道对乙二胺四乙酸（EDTA）依赖性血小板假性减少样本的血小板聚集解离效果。
方法 经知情同意后收集血细胞分析仪出现“血小板聚集”报警信息且镜检确认血小板聚集的 EDTA 抗凝样本及其对应枸橼酸钠抗凝样本 20 例，同时收集经确认无血小板聚集健康对照 EDTA 抗凝样本及其对应枸橼酸钠抗凝样本 20 例。采用 BC-6800 Plus 血细胞分析仪阻抗通道（PLT-I）与光学血小板通道（PLT-O）检测上述样本。采用配对 t 检验比较 EDTA 抗凝样本与枸橼酸钠抗凝样本 PLT-I 与 PLT-O 通道间血小板计数的差异是否存在统计学意义，并计算 EDTA 抗凝样本血小板计数解离率与提升率。解离率=EDTA 抗凝样本 PLT-O 血小板计数/枸橼酸钠抗凝样本 PLT-O 血小板计数×100%；提升率=（EDTA 抗凝样本 PLT-O 血小板计数- EDTA 抗凝样本 PLT-I 血小板计数）/EDTA 抗凝样本 PLT-I 血小板计数×100%。
结果 健康对照 EDTA 抗凝样本与枸橼酸钠抗凝样本 PLT-I 与 PLT-O 通道间血小板计数的差异无统计学意义（P＞0.05）；血小板假性减少患者 EDTA 抗凝样本 PLT-I 通道血小板计数显著低于 PLT-O 通道（P＜0.05）及枸橼酸钠抗凝样本 PLT-O 通道结果（P＜0.05）。20 例样本中血小板计数解离率＞70%的有 17 例，血小板提升率中位数 173%。
结论 BC-6800 Plus 血细胞分析仪的光学血小板通道可有效纠正 EDTA 依赖的血小板假性减少，初步满足临床应用需求。

PU-3901

血管内皮生长因子反义寡核苷酸对小鼠肺癌的抑制作用

王颖、林春艳
哈尔滨医科大学附属第一医院

目的 探讨血管内皮生长因子 (Vascular endothelial growth factor， VEGF) 反义寡核苷酸的基因治疗方法。
方法 于 2001 年 5 月至 2002 年 1 月在哈尔滨医科大学第一临床医学院实验动物中心制作 C57BL/6 小鼠皮下肺癌模型 30 只，分为血管内皮生长因子反义寡核苷酸 (antisense oligodeoxynucleotide,ASODN)治疗组、VEGF 正义寡核苷酸(oligodeoxynucleotide ,SODN)治疗组及对照组。接种 Lewis 肺癌细胞后 24 小时内，用 ASODN 及 SODN 皮下注射进行治疗，对照组只注射生理盐水，观察小鼠肿瘤的生长情况以及组织形态学改变。标本常规石蜡切片，HE 染色，用免疫组化方法检测 VEGF 蛋白表达及微血管密度。通过 RT-PCR 检测 VEGFmRNA 的表达。
结果 对照组、VEGF 反义寡核苷酸治疗组、VEGF 正义寡核苷酸治疗组平均瘤重分别为（7.83±0.78）g、（4.49±0.43） g 和(7.73±0.69)g。VEGF 反义寡核苷酸治疗组、VEGF 正义寡核苷酸治疗组抑瘤率分别为 42.7%、5.9%。VEGF 反义寡核苷酸能明显抑制 VEGF 蛋白及 VEGFmRNA 的表达。
结论 原位注射 VEGF 反义寡核苷酸能抑制小鼠肺癌生长。

PU-3902

急性粒细胞性白血病中的 NOTCH 基因变异很少

毕莉、李琳
哈尔滨医科大学附属第一医院

在 12 例急性粒细胞白血病患者与 8 例急性粒细胞性白血病细胞株中寻找 Notch1 基因变异。应用 nested-PCR 法，银染色-sscp，direct sequencing 法分析。在患者 9 的白血病细胞中 PEST 部位发现点突变(7316C/T)，氨基酸也随之发生变异(Pro2439Leu)。本基因变异是首次在 AML 细胞中发现的 Notch1 基因变异。由于在此患者的完全缓解的骨髓细胞中没有发现本突变，因此本突变不是 SNP。有关本变异的具体作用机制还有待于进一步探讨。

PU-3903

应用 ROC 曲线评价三种 APTT 试剂对 LAC 的初筛价值

李琳、毕莉
哈尔滨医科大学附属第一医院

目的 探讨三种 APTT 试剂作为狼疮抗凝物质（LAC）初筛实验的临床价值。
方法 收集自 2017 年 11 月 1 日至 2018 年 3 月 31 日期间哈尔滨医科大学附属第一医院就诊 63 例 LAC 阳性患者作为观察组，同时期的 58 例 LAC 阴性患者作为对照组。采用三种试剂对其血浆进行 APTT 检测，并对结果进行分析比较。
结果 与对照组相比，观察组的三种试剂的 APTT 均较高并都有显著的统计学差异。ROC 曲线分析结果显示，三种试剂 ACTIN、FSL、SynthAsil 的线下面积分别为 0.726、0.777、0.800，均>0.7 而且 P 值都<0.0001；诊断敏感度分别为 0.581、0.613、0.468。
结论 APTT 依然是最为经济有效的狼疮抗凝物质阳性初筛试验。三种试剂中 SynthAsil 试剂对于 LAC 阳性的诊断效能最高。

PU-3904

多发性骨髓瘤患者首发临床特征、实验室检测及影像学检查分析

王甩艳[1]、木尼热•凯沙[2]
1. 深圳市罗湖医院集团医学检验实验室
2. 广东医科大学医学技术学院

目的 探究多发性骨髓瘤（MM）的首发临床特征，再结合实验室检测及影像学的检查，以此提高MM的诊断率。
方法 回顾性分析就诊深圳市罗湖区人民医院27例多发性骨髓瘤患者的临床资料，分析总结患者首发症状、实验室检测结果及影像学检查的特点。
结果 27例MM患者中首发临床表现有骨折、骨痛有13例，乏力有5例，肾功能不全有4例，贫血有2例，胸闷有1例，上肢麻木有1例，淀粉样变性有1例。首诊科室依次为骨外科、脊柱骨科、血液内科、肾内科、心血管内科、肿瘤内科、普外科等 。实验室检测结果可知有15例血红蛋白浓度降低，其中 2 例重度贫血，7 例中度贫血，6 例轻度贫血；血清肌酐增高有 11 例；血清钙增高有 4 例；β2-微球蛋白升高有4例，降低有5例；CRP升高有4例；外周血涂片中可见浆细胞有7例；成熟红细胞呈“缗钱”状排列有 14 例；骨髓增生活跃或明显活跃，浆细胞占有核细胞总数 10%以上，可多达80%。免疫固定电泳 M 蛋白分型为 IgG-Kappa 型 M 蛋白 8 例，IgG-Lambda 型 M 蛋白 6 例，IgA-Kappa 型 M 蛋白 5 例，IgA-Lambda 型 M 蛋白 5 例，轻链 Kappa 型 M 蛋白 1 例，轻链 Lambda 型 M 蛋白 2 例，阴性 2 例，其中同时有两种免疫表型有 2 例。流式细胞术免疫表型分析表明所有的骨髓瘤细胞均表达 CD38 和 CD138，93%的患者不表达 CD19，75%不表达 CD45，59%表达 CD56，33%表达 CD28， CD117、CD20 和 CD13 的阳性表达率均较低，分别为 22%、15%和 7%，cKappa 和 cLambda 的阳性表达率分别为 59.25%和 51.85%。通过 X 线、CT 检查结果可知主要有骨质破坏伴有病理性骨折，一般疾病出现为腰椎、盆骨、肋骨及股骨。
结论 了解 MM 患者首发临床表现，并依据实验室检查结果和影像学检查对临床初步诊断 MM 有很重要的作用，从而也可降低误诊误治率。

PU-3905

尿液干化学结果影响因素的探讨

董莉芹、刘兆杰
哈尔滨医科大学附属第一医院

目的 工作中我们认为所用仪器应掌握影响尿液干化学测定结果的多种因素及解决的方法。只有这样才能达到测定结果准确，以便发挥仪器应有的效能。
方法 新鲜尿液中酸碱度及蛋白质的变化直接影响比重的测定，尿蛋白浓度增高，病人尿比重偏高，尿试带实际上是测的尿中离子浓度尿比重偏高，尿纸条检测的是离子强度，尿液中的非离子化合物（如葡萄糖、造影剂等）对测定结果也有一定影响。
结果 pH 随温度的升高而降低；尿液中含有比色素还原能力更强的物质时，可见尿糖结果偏低，甚至可以出现假阴性；尿液中酸碱度及蛋白质的变化直接影响比重的测定；药物对尿中蛋白质的测定都有影响；当各种因素导致红细胞破裂时，可引起干化学结果和镜检结果不一致；细菌繁殖可以导致丙酮消失；用维生素 C 或亚硝酸盐时，可使尿胆红素、尿胆原测定出现假阴性结果；尿细菌生长，亚硝酸盐检测出现假阳性结果；尿中以淋巴细胞为主，白细胞检测会出现假阴性结果；当尿中有其他还原剂时，可使维生素 C 检测结果偏高。
结论 根据我们在多年的工作中对尿十项的经验总结，日常工作中易受尿液标本中化学成分干扰，所以对待特殊病人的尿液标本应该将试带与手工操作相结合，对于化学全阴性标本应采用显微镜检查，以免漏检。

PU-3906

心脑血管病患者中阿司匹林抵抗的探讨

张云平、付璐
哈尔滨医科大学附属第一医院

目的 研究哈尔滨地区心脑血管病患者中发生阿司匹林抵抗（AR）概况，并探讨其预测因子。
方法 110 例病情稳定的心脑血管病住院患者，每日服用阿司匹林 100mg，连服 10 天，第 11 天晨起采取空腹静脉血，分别以二磷酸腺苷（ADP）`花生四烯酸（AA）为诱导剂，检测血小板聚集功能。
结果 患者中 AR 发生率为 0，阿司匹林半敏感（ASR）者占 7.3%,女性较多（男：女，75.6%vs40.5%,p=0.002），吸烟者亦较多（37.5%vs17.5%,p=0.001）。
结论 阿司匹林用于抗血小板治疗及预防动脉粥样硬化事件的心脑血管患者中，若有 AR 或 ASR 存在可选用其他安全有效的抗血小板制剂，预测 AR 及抗血小板治疗个体化，将是抗血小板治疗的发展方向。

PU-3907

采血小板不良反应的原因及分析

徐海燕、杨秋月
哈尔滨医科大学附属第一医院

目的 提高血小板采集数量和质量，从而降低输血传播疾病的概率和输血反应率。随着血细胞分离机性能的不断提高，可从献血者血循环中一次采集 1～2 个治疗单位的血小板，这样，既可解决机采供者的短缺，缓解对医院供不应求的矛盾，还可节约耗材、试剂，降低成本。
方法 采集前将供者血小板计数、性别、身高、体重等数据输入机内设定程序，抗凝剂 ACD-A：全血为 1 : 11，预采血小板产品单治疗量≥2.5×1011/L，容积：单治疗量 220 ml。严格执行机采血小板操作规程。
结果 医护人员应具备熟练的采血技术，并选择粗大、弹性好的静脉
结论 保证一次穿刺成功，以减少献血者疼痛，缩短采集时间。

PU-3908

尿常规显微镜手工法与分析仪检验分析

徐海燕、张娜
哈尔滨医科大学附属第一医院

目的 手工法检验尿常规结果分析，进一步了解分析仪和传统的显微镜手工法在尿液分析中的优缺点，使检验工作者在实际工作中正确对待两种方法的应用，指导检验人员科学地把两种结合起来。
方法 用尿液分析仪检测只记录，尿蛋白、白细胞、红细胞结果，微量以上为阳性，微量以下为阴性。然后用加热醋酸法检测尿蛋白，再用离心试管取 10 ml 混匀的尿液以 1 500 r/min 离心 5 min，倾去上清液，留取 0.2 ml 沉渣，涂片镜检，记录尿蛋白、红细胞和白细胞结果，微量以上为阳性，微量以下为阴性。
结果 两种方法合理应用，取长补短，遇到可疑情况，还应及时询问病人，查找原因
结论 以便为临床疾病的诊断和治疗提供正确检验结果。

PU-3909

直方图中间型细胞异常情况浅析

杨秋月、徐海燕
哈尔滨医科大学附属第一医院

目的 血细胞计数已普遍使用于各医院实验室，尤其是三分类的血球计数仪更为普遍。这种计数仪的原理是电阻抗法，此原理是基于细胞在测试系统中产生的脉冲大小，与仪器内设定的阈值比较而得出的数据。
方法 用 EDTAK2 抗凝静脉血，其含量为 1.5 mg/ml 全血。将 EDTAK2 配成 150 g/L 的溶液，预先制备具塞塑料抗凝管，于每日清晨抽静脉血 0.5 ml 混匀抗凝，室温放置，并于 0.5—5.0 h 内测定。
结果 白细胞直方图中间细胞异常的分析，由于仪器型号不同，试剂不同等原因可能/一定会存在一定的差异。关键在于出现中间细胞异常时的合理处理，涂片染色镜检是最好的方法。
结论 在中间细胞正常时，若临床提示，如过敏症，传单增等疾病时，临检人员也应涂片镜检，以免异常细胞漏检。

PU-3910

抗凝剂引起血小板减少的成因

杨秋月、张娜
哈尔滨医科大学附属第一医院

目的 血液学一般检查最常用的检测仪器是血细胞分析仪，它以检测速度快、精确度高、操作简便的优势为临床提供着有用的实验指标，对疾病的诊断和治疗有重要的意义。
方法 血细胞计数用 EDTAK2 作抗凝剂，用量为 EDTAK2H2O 1.5 mg/ml～2 mg/ml 血液。近年来因 EDTA 引起血小板聚集发生血小板假性减少并不少见，下面是 1 例血小板减少患者，经试验分析为 EDTA 依赖性假性血小板减少（EDTAPTCT）。
结果 采用抽血后立即检测、手工计数血小板及血涂片镜检或采用其他种类抗凝剂来鉴别。
结论 有文献报道，当 EDTA 依赖性血小板减少时，可用其他抗凝剂作血小板计数，可避免血小板假性减少。

PU-3911

XN 系列血液分析仪 Q-flag 报警在判断血小板聚集中的应用

张景道、张晗钰、张金彪
河北省沧州中西医结合医院

目的 根据 XN1000 血球仪中 PLT clumps 的 Q-flag 报警值判断低值血小板结果的可靠性
方法 通过对 XN1000 血球仪分析的低值血小板标本进行推片镜检，积累标本 WDF 与 WNR 通道产生的 Q-flag 报警值的分布及对应的血小板聚集情况，做出敏感性和特异性分析并绘制 ROC 曲线
结果 1、200 例血小板聚集阳性的低值血小板标本 Q-flag 报警值分布区间为 20-300 2、收集 Q-flag 报警值小于 40 的 200 例低值血小板标本人工镜检，得出 Q-flag 报警值＜20 时标本未发生血小板的聚集的特异度为 100% 3、收集 400 例 Q-flag 报警值＞20 的低值血小板标本人工镜检，得出不同 Q-flag 报警值分组情况下检出标本阴性和阳性率差异有统计学意义（X^2=97.547,*P*=0.000）且随着 Q-flag 报警值增高，血小板聚集的阳性率增高，趋势性卡方检验有统计学意义（X^2=0.494，*P*=0.000），当 Q-flag 报警值＞250 时，血小板聚集阳性的敏感度为 95.0%。4、ROC 曲线提示以

Q-flag 报警值预测血小板聚集情况的最佳临界值为 100，此时 AUC 为 0.900，敏感度 86.5%，特异度为 75.6%。
结论 XN1000 血球仪 Q-flag 报警值可帮助检验工作者判断低值血小板结果是否需要纠正，从而减少工作量。

PU-3912

钙卫蛋白在结肠癌中的研究与应用

李晶
天津医科大学肿瘤医院

目的 研究粪便钙卫蛋白（FC）、癌胚抗原（CEA）、糖类抗原 19-9（CA19-9）、C 反应蛋白（CRP）在结直肠癌中的诊断价值。
方法 回顾性分析 2020 年 12 月至 2021 年 3 月天津市肿瘤医院确诊的 60 例结直肠癌患者（患病组）和 40 例排除结肠癌的健康人（对照组）病例资料，内容包括了粪便钙卫蛋白（Calprotectin）、联合癌胚抗原（CEA）、糖类抗原 19-9（CA19-9）、C 反应蛋白（CRP）。采用受试者工作特征曲线（ROC 曲线）分析钙卫蛋白对结直肠癌患者的诊断价值。
结果 患病组粪便钙卫蛋白检测结果高于对照组，差异存在统计学意义（P＜0.05）。钙卫蛋白、血清 CEA、血清 CA19-9 及血清 C 反应蛋白检测结直肠癌 ROC 曲线图中，AUC 分别为 0.794、0.631、0.750、0.611，其中 FC 的 ROC 曲线下面积最大，诊断价值最佳。且 FC 的 cut off 值为 36.66 比报告中的 0-50 更为准确；在 Dukes 分期中钙卫蛋白 A 期与 B、C、D 三期之间 FC 水平 $p < 0.05$,B、C、D 三期之间 FC 水平 $p > 0.05$，B、C、D 三期 FC 阳性率明显优于 A 期阳性率，但三期之间差异无统计学意义。而 CEA、CA19-9、CRP 阳性率差异无统计学意义；FC、CEA、CA19-9、CRP 的阳性率差异，在不同部位的结肠癌中没有统计学意义；FC 联合 CA19-9 与单独 FC 检测比较时 AUC 有所提高，但提高程度并不明显。FC 联合 CEA、CA19-9、CRP 与单独 FC 检测比较时 AUC 提高较多，且结果有明显差异。；FC 联合 CA19-9 和 FC 联合 CEA、CA19-9 及 CRP 联合法检测结直肠癌可以提高其敏感性,且四种方法联合检测较单种检测方法差异有统计学意义。
结论 检测粪便钙卫蛋白对结直肠癌有一定意义。临床中可考虑粪便钙卫蛋白联合和癌胚抗原、糖类抗原 19-9、C 反应蛋白提高诊断结直肠癌检测的准确度。若为减少工作量，可考虑选择粪便钙卫蛋白联合糖类抗原 19-9 进行检测，也具有较好的诊断效能。

PU-3913

静脉血 WBC 和超敏 CRP 测定在儿童感染性疾病诊断的临床探讨

张文忠
资阳市第一人民医院

目的 探讨超敏 C 反应蛋白(hs-CRP)、白细胞(WBC)检测在小儿感染性疾病中的诊断价值。
方法 选择 300 例临床确诊的感染患儿，分别测定 CRP、WBC 结果并进行统计学分析.
结果 细菌感染组患儿 hs-CRP、WBC 检测值显著高于正常对照组健康儿童(P＜0.05);细菌感染组患儿 hs-CRP、WBC 检测值高于病毒感染组(P＜0.05);病毒感染组患儿 hs-CRP 和 WBC 检测值稍高于正常对照组儿童,差异无统计学意义(P＞0.05).细菌感染组患儿 CRP、WBC 的阳性检出率均明显高于病毒感染组(P＜0.05).
结论 hs-CRP 结合 WBC 检测有助于儿科感染性疾病的早期诊断,并对于细菌感染和病毒感染的鉴别诊断为指导临床合理使用抗感染药物和判定疗效具有重要价值.

PU-3914

探讨妊娠期血小板减少症对孕产妇及新生儿的影响

吴章菊
资阳市第一人民医院

目的 探讨妊娠期血小板减少症对孕产妇及新生儿的影响.
方法 回顾性分析 2013 年 1 月—2020 年 1 月我院收治的 23 例妊娠期血小板减少症孕产妇及新生儿的临床资料.
结果 19 例妊娠期特发性血小板减少及全部血小板计数>50*109/L 的患者均于产后的 3-5 日内恢复正常血小板计数水平,4 例血小板计数≤50*109/L 者产后一周左右恢复正常.新生儿血小板减少 3 例(13.04％).
结论 妊娠期血小板减少症孕产妇分娩后其血小板计数可自行恢复,不会增加产后出血率以及影响临床分娩结局,但正确鉴别和处理妊娠期血小板减少症可以避免对产妇及新生儿造成的不良影响.

PU-3915

异常早幼粒细胞 Auer 小体发生率的影响因素分析

张景逍、张金彪、张晗钰、翟文燕、王晓静
河北省沧州中西医结合医院

目的 探讨急性早幼粒细胞白血病（APL）患者存在 Auer 小体的异常早幼粒细胞的比例具有差异的影响因素并分析 Auer 小体发生率在评估 APL 患者预后中的意义
方法 收集 2018 年 5 月至 2020 年 5 月河北省沧州中西医结合医院确诊的共 38 例急性早幼粒细胞白血病患者，计数出现 Auer 小体的异常早幼粒细胞的比例作为 Auer 小体发生率。采用非参数秩和（Mann-Whitney U）检验比较不同 PML/RARα 融合基因类型、CD56 与 HLA-DR 的表达、性别、年龄中 Auer 小体发生率的差异；采用皮尔逊相关系数检验分析异常早幼粒细胞各项流式表达率（CD13、CD33、CD117、CD38、CD64）及初诊 WBC、HB、PLT 计数和 PML/ABL 定量与 Auer 小体发生率之间的相关性，采用简单线性回归对 Auer 小体发生率进行单因素分析；综合各项统计数据初步分析 APL 患者的初诊异常早幼粒细胞 Auer 小体发生率对患者预后的影响，以 $P<0.05$ 为差异有统计学意义。
结果 1、CD56 阴性组患者的 Auer 小体发生率大于阳性组($P<0.05$)，PML/RARα 融合基链 L 型患者 Auer 小体发生率大于 S 型($P<0.01$)，差异均有统计学意义。2、线性相关分析显示 WBC 与 Auer 小体发生率的相关系数有统计学意义（$P=0.02$；r= -0.376）；将 WBC 引入线性回归分析，回归方程为：Y= -0.001X+0.079，可认为初诊 WBC 与患者 Auer 小体发生率存在负相关关系，但回归方程需要更大的样本量进行修正。
结论 CD56 的表达、PML/RARα 融合基因类型与患者初诊白细胞计数均可影响初诊 APL 患者 Auer 小体的发生；结合以往研究，本文三项研究结论对患者预后的指向一致即初诊 APL 患者异常早幼粒细胞 Auer 小体的高发提示患者预后良好。

PU-3916

血液检验在贫血鉴别诊断中的临床价值

王佳军
资阳市第一人民医院

目的 分析血液检验在贫血鉴别诊断中的临床价值。
方法 选择近一年我院接收的 90 例贫血患者作为案例，随机分为甲组和乙组，分别是地中海贫血和缺铁性贫血，同时收取健康体检的 50 例受检者作为丙组，对三组研究对象实施血液分析，对结果分析。
结果 对三组患者的数据资料分析后得知，丙组的参数趋于正常，对比后差异明显。
结论 血液检验在临床贫血诊断中有突出的作用，可以准确的对贫血的类型进行分析，整体作用明显。

PU-3917

SOX 家族在乳腺癌中的表达及预后的综合分析

孙继德
重庆医科大学附属第一医院

目的 SOX 家族是一组保守的转录因子，被认为是多种癌症类型的调控因子。越来越多的证据表明 SOX 家族参与了乳腺癌的肿瘤发生。本研究旨在分析 SOX 家族的 20 个成员在乳腺癌患者中的转录和生存数据。
方法 在本研究中，我们通过 Oncomine、基因表达谱交互分析(GEPIA)、Kaplan-Meier Plotter、人类蛋白图谱(HPA)和 cBioPortal 等一系列数据库研究 SOX 家族在乳腺癌患者中的不同表达谱和预后价值。
结果 我们发现乳腺癌患者中 SOX4 和 SOX12 的 RNA 表达水平高于正常人，而乳腺癌患者中 SOX5、SOX7-8、SOX10 和 SOX17-18 的 RNA 表达水平低于正常人。SOX6、SOX9、SOX11、SOX13、SOX15、SOX17-18、SOX30 的表达水平与肿瘤进展期相关。Kaplan-Meier Plotter 数据库的生存分析显示，SOX2、SOX4、SOX6、SOX11 和 SOX15 的高转录水平预测所有乳腺癌患者的总体生存期较低。相反，在这些患者中，高水平的 SRY、SOX10 和 SOX13 与高总生存率相关。
结论 我们的研究表明，SOX2、SOX4、SOX6、SOX11 和 SOX15 可能是乳腺癌患者潜在的治疗靶点，而 SRY、SOX10 和 SOX13 可能是乳腺癌新的预后生物标志物。

PU-3918

FA280 型粪便自动处理仪的临床性能评价

刘颖
重庆医科大学附属第一医院

目的 评价 FA280 型粪便自动处理仪对各种有形成份的识别能力及对便隐血的检出能力。
方法 选取镜检确认阳性（每种有形成分）新鲜临床粪便标本各≥50 例和镜检确认阴性新鲜临床粪便标本≥50 例，按照全国临床检验操作规程（第 4 版）要求进行手工涂片镜检，同时按照仪器标准操作流程进行上机检测，分别记录手工镜检结果及仪器检测结果并分析阳性符合率、阴性符合率、总符合率和各自的置信区间。随机选取新鲜临床粪便标本 200 例（阳性标本≥30%），分别按照试剂卡（沃文特和深蓝公司）手工检测的标准操作规程和仪器检测的标准流程检测。分别记录手工法及仪器法检测结果并进行统计分析。

结果 有形成分检出率红细胞在 0-2/HP、0-3/HP、0-4/HP 的检出率分别为 52.5%、77.5%、95%，白细胞在-2/HP、0-3/HP、0-4/HP 的检出率分别为 60%、80%、87.5%；红细胞浓度为 100 个/μL 和 300 个/μL 的 CV 值分别为 9.25%和 10.59%；有形成分和便隐血的携带污染率均为 0；便隐血可以检测血红蛋白浓度为 0.2μg/mL~2000μg/mL 的样本；便隐血的重复性好且与深蓝试纸条有较高的符合率；有形成分与人工镜检相比较的阳性符合率和阴性符合率均较高。
结论 FA280 型粪便处理仪具有较好的有形成分识别能力及对便隐血的检出能力。

PU-3919

女性不孕者阴道分泌物病原体感染情况分析

李小琴
重庆医科大学附属第一医院

目的 分析不孕女性生殖道病原体感染现状，了解支原体药敏情况，为临床的诊治提供参考依据。
方法 回顾性分析 2020 年 1 月-2020 年 11 月于重庆医科大学附属第一医院生殖中心的不孕女性患者 211 例临床资料。分为原发性不孕组和继发性不孕组，根据年龄分为<35 岁组和≥35 岁组（高龄女性不孕组），对所有患者进行阴道分泌物及宫颈分泌物的检查。
结果 不孕患者生殖道感染率为 54.0%；211 例患者中，未观察到革兰阴性双球菌感染，仅有 1 例滴虫感染，发生率为 0.47％；霉菌感染率为 5.21％；细菌性阴道病发生率为 7.58％；人乳头瘤病毒（HPV）感染率为 10.4%；解脲支原体（Uu）感染率为 37.44％；解脲支原体（Uu）和人型支原体（Mh）混合感染发生率为 4.74％，本研究未观察到单一人型支原体感染。霉菌感染、细菌性阴道病、Uu+Mh 感染的发生率在不同年龄段、以及原发不孕和继发不孕组患者中无明显差异；HPV 感染率在≥35 岁患者组（26.8%）明显高于＜35 岁患者组(6.5%)（P<0.05）；原发不孕组 Uu 感染率明显高于继发不孕组（P<0.05）。Uu 敏感率较高的药物为美满霉素、强力霉素、克拉霉素、阿奇霉素，耐药率较高的药物为诺氟沙星、环丙沙星、氧氟沙星； Uu+Mh 混合感染敏感率较高药物为美满霉素、强力霉素，耐药率较高的药物为诺氟沙星、阿奇霉素、壮观霉素、氧氟沙星、罗红霉素、环丙沙星、司帕沙星、左氧氟沙星、克拉霉素。
结论 不孕女性生殖道感染率较高，需加强生殖道感染检查，高龄不孕女性应重视 HPV 筛查。临床治疗支原体感染可首选美满霉素、强力霉素。

PU-3920

血常规和 CRP 检测结果应用

贾克鹏、王倩、程绍民、李新、张真
禹城市人民医院

目的 探讨 CRP 和血常规中白细胞计数联合检验在临床上的应用价值。
方法 CRP 和血常规均采用 PMC 血球计数仪，CRP 采用比浊法，血常规采用五分类计数法。
结果 细菌感染患者 CRP 升高程度更大(78.95%>50mg/L)，病毒感染患者 CRP 升高幅度较低（69.81%≤50mg/L），WBC 在细菌感染、急性心梗、外科术后均增高。
结论 CRP 与血常规中的白细胞计数联合检验有助于临床医生对患者病情进行初步诊断, 减少不必要的抗生素的应用, 有利于患者得到更好的治疗。

PU-3921

单纯血小板增多的 CML 研究分析

马骋赟
山东第一医科大学附属省立医院临床医学检验部

目的 原发性血小板增多症（ET）主要以外周血血小板显著升高，骨髓巨核细胞增生及特殊形态为特点，而慢性髓系白血病（CML）以外周白细胞升高，血涂片见幼粒细胞，骨髓有核细胞增生极度活跃，且多有脾脏肿大，仅有少数 CML 表现为单纯血小板增高，因此初诊时极易和原发性血小板增多症混淆，本研究主要探讨单纯血小板增的 CML 的特例。
方法 选择在山东省立医院 2015 年 1 月至 2021 年 6 月住院 100 例血液科抽取骨髓患者作为研究组，体检健康志愿者 100 例作为对照组，分别抽取血常规进行检验，观察研究组和对照组血常规以及骨髓涂片染色情况，进一步研究组超声以及染色体核型分析；
结果 总体进行分析发现，经过统计来看，仅有两例血常规白细胞仅轻度升高，外周血涂片偶见幼粒细胞，超声未见脾肿大，进一步完善分子生物学检查 BCR-ABL1 融合基因阳性，诊断为 CML，因仅以单纯血小板增多为临床表现，故最终诊断为单纯血小板增多的 CML，其他血小板增高案例并未检测到融合基因故诊断为 ET，差异之间有统计学意义（P<0.05）。
结论 以单纯血小板增多的 CML 患者发生无年龄差异，起病隐匿外周血血小板升高，部分患者可见幼粒细胞，有嗜酸嗜碱粒细胞升高，NAP 积分可呈现升高、不变、降低不同变化，多无脾脏肿大，与 ET 较难区分，早期易误诊，本研究主要强调对于所有血小板升高的患者，临床应进行 BCR-ABL1 融合基因以及染色体的检查，以便早期对患者进行对症治疗。

PU-3922

凝血因子 VIII 在血液透析患者高凝诊断中的应用价值

郭勇晖
南方医科大学珠江医院

目的 评估凝血因子 VIII 在血液透析患者高凝状态诊断中的应用价值，为预测获得性易栓症提供有价值的临床评估指标和可以应用的医学决定水平。
方法 通过对血液透析患者凝血因子 VIII 的检测以及临床表现的评价，比较发生血栓事件的患者凝血因子 VIII 的活性与未发生血栓事件患者之间的差异，探索凝血因子 VIII 在血液透析患者高凝状态诊断中的应用价值。
结果 只有 30.3%（44/145）的患者凝血因子 VIII 的活性在正常范围，而发生一次或多次血栓事件的患者为 17.9%（26/145）。
结论 肾病综合征患者由于肾功能严重受损，凝血因子 VIII 蓄积，凝血功能异常，体内呈高凝状态，在凝血因子活性高于 200%时，提示患者可能达到易栓状态，其发生血栓事件的可能性高，值得临床予以注意和预防。

PU-3923

检测外周血自然杀伤细胞、辅助性和调节性 T 细胞在不明原因复发自然流产中的临床意义

宋宏岩
南京大学医学院附属鼓楼医院

目的 通过检测不明原因复发性自然流产患者外周血中自然杀伤性细胞（NK 细胞）、辅助性 T 细胞（Th1/Th2）和调节性 T 细胞（Treg 细胞）的表达水平，探讨 NK、Th1、Th2 和 Treg 细胞在 URSA 中的临床意义。
方法 应用流式细胞术分别检测 385 例 URSA 患者外周血中 NK 细胞占淋巴细胞比例、CD3+CD4+INF-γ+细胞占 CD4+细胞（Th1）的比例、CD3+CD4+IL4+细胞占 CD4+细胞（Th2）的比例和、CD4+CD25+Foxp3+占 CD4+细胞（Treg）的比例和 NK 细胞占淋巴细胞比例。
结果 流产两次 URSA 患者 Treg 表达水平高于流产两次以上 URSA 患者（P<0.05）。175 例 Th1 正常的 URSA 患者 Treg（2.46%±0.84%）高于 165 例 Th1 高值的 URSA 患者 Treg（2.24%±0.78%）（P<0.05）。259 例 Th2 正常的 URSA 患者 Treg（2.26%±0.75%）低于 117 例 Th2 低值的 URSA 患者 Treg（2.47%±0.88%）（P<0.05）。259 例 Th2 正常的 URSA 患者 NK（20.16%±8.48%）高于 117 例 Th2 低值的 URSA 患者 NK（17.64%±7.73%）（P<0.01）。
结论 检测 URSA 患者外周血中的 NK、Th1、Th2 和 Treg 细胞表达水平有助于临床诊断及了解病情发生发展。[ml1] 结论有些宽泛，与结果缺乏较强的逻辑

PU-3924

临床医学检验中影响血液细胞检测质量的控制方法

李瑶
资阳市第一人民医院

目的 本文主要研究临床医学检验中影响血液细胞检测质量的有关因素及其控制方法。
方法 选取我院 2020 年 3 月-2021 年 3 月自愿进行血液细胞检测的 240 名普通人进行研究，这些人群的血型必须是一样的，随机进行分组研究（分为四组），然后对比对这些人群的白细胞、红细胞、血小板以及血红蛋白的含量进行比较。
结果 对照组 A 与研究组 A 结果进行对比，白细胞、红细胞、血小板以及血红蛋白的含量具有明显的差异性，且研究组 A 的含量更趋向于正常值（P<0.05），对照组 B 与研究组 B 比较白细胞、红细胞、血小板以及血红蛋白的含量具有明显的差异性，研究组 B 的含量更趋向于正常值（P<0.05）。
结论 抗凝剂的浓度以及过期的血液样本会影响血液细胞检测的质量，为了提高检测质量，需要配比准确的抗凝剂，并在规定的时间内检验血液样本。

PU-3925

人工镜检测尿红细胞与 MT600 尿分析仪方法学比较的探讨

李兴博
资阳市第一人民医院

目的 对尿液分析仪检测尿潜血反应和显微镜镜检红细胞（RBC）的结果进行分析比较。
方法 对 400 份门诊患者留取的随机尿液立即按照仪器操作说明进行尿液分析仪检验和尿沉渣显微镜检查。

结果 尿液分析仪潜血反应阳性，镜检有红细胞的有 210 例，镜检无红细胞的有 50 例。尿液分析仪潜血反应阴性镜检有红细胞的有 140 例，镜检无红细胞的有 120 例。两种方法结果出现差异。
结论 临床工作中尿液分析仪潜血反应与显微镜检查红细胞应联合进行，尤其是显微镜检查至关重要，不可忽视。

PU-3926

染色体 Dup(1q)异常在 MDS 中的细胞遗传学研究

史沛芹
连云港市第一人民医院

目的 观察 Dup(1q)染色体异常的核型变化在 MDS 中临床表现及细胞分子遗传学分析。
方法 应用 R 显带技术对患者进行核型分析；用流式细胞仪检测免疫表型；运用基因探针进行荧光原位杂交分析；定量 RT-PCR 融合基因测定白血病 43 种融合基因,高通量测序靶向检测髓系细胞白血病 42 种相关基因检测，
结果 核型分析结果显示患者异常克隆，其核型为 46,xy,dup(1)(q12q41)[10]。免疫分型检测血液肿瘤 30 种单抗，淋巴细胞 54.8%表型未见明显异常，骨髓活检红巨两系造血旺盛，轻度病态造血。荧光原位杂交融合基因阴性，定量 RT-PCR 融合基因未见阳性表达。高通量测序靶向检测 ASXL1,ETV6,FLT3,SH2B3,ZRSR2 基因突变。
结论 1 号染色体长臂的全部或部分重复异常在恶性血液病 MDS ，AML,淋巴瘤，ALL，MM 等中并不罕见，但常涉及其他染色体异常，作为唯一异常表现少见，回顾资料在 MDS 中作为唯一核型异常表现仅报告 15 例。1q21;1q32 作为两个重要的脆性位点，这种不稳定性可能源于该区域染色质的组织导致了起源和选择在肿瘤过程中具有功能意义的差异，引起染色体基因的缺失和扩增，对肿瘤的发展有显著的影响，这种不稳定性的分子遗传学分析，无疑对 MDS 及其他恶性血液病的发生具有重要意义，但染色体 Dup(1)作为唯一异常在 MDS 预后中能否成为独立危险因素，与基因突变有何影响，发病机制与预后的关系但仍需进一步研究 。

PU-3927

杜氏利什曼原虫与组织胞浆菌、马内菲青霉菌形态学鉴别

朱爱民
娄底市中心医院

杜氏利什曼原虫、组织胞浆菌和马内菲青霉菌在骨髓涂片中病原体形态相似，易造成误诊，并常导致严重后果。现通过我院 3 个病例对这三种病原体的形态学鉴别进行简要阐述，给骨髓细胞形态室检验技师提供帮助。

杜氏利什曼原虫无鞭毛体与组织胞浆菌、马内菲青霉菌分别是黑热病、组织胞浆菌病、马内菲青霉菌病的病原体，这三种疾病均为少见的感染性疾病，不但临床症状极为相似，如发热、肝脾淋巴结肿大，全血细胞减少等。且在骨髓涂片中病原体形态也相似，容易混淆，导致误诊[1]。

近十年来，我院骨髓细胞形态室发现荚膜组织胞浆菌 6 例，马内菲青霉菌 3 例，杜氏利什曼原虫 1 例（后转省人民医院确诊），现找出其中 3 个病例与大家分享：

PU-3928

Proteomic Screening of potential N-glycoprotein biomarkers for colorectal cancer by 2D-LC-MS/MS

Jin Wang、Jinjin Wang、Aifeng Liang、Guangang Tian、Mengjiao Yuan、Qing Ke、Yijun Cai、Qian Gong
Qingpu Branch of Zhongshan Hospital, Fudan University

Background and aims: Colorectal cancer (CRC) is one of the most common malignant tumors. At present, colonoscopy is a routine procedure in the diagnosis of CRC, but it is traumatic. Carcinoembryonic antigen, CA199, and CA242 are common serum markers for the diagnosis of CRC; however, they do not demonstrate satisfactory specificity and sensitivity for the diagnosis of CRC. Hence, it is necessary to screen many valuable serum biomarkers for CRC, proteomics Methods have been used to investigate PTMs such as glycosylation of proteins with prominent roles in the occurrence and development of tumors.
Methods This study screens altering glycosylated proteins of CRC tissues using high-performance liquid chromatography-mass spectrometry quantitative glycoproteomics, and then these candidate biomarkers for CRC are further validated by serum glycoproteomics.
Results The results of glycoproteomics and bioinformatics analysis suggest that these molecules are mainly involved in many biological processes, including collagen fibril organization and skeletal system development. the changing trends of 3 protein glycosylation were consistent with MS results of CRC tissues, including APOB, MPO, ICAM. Areas under the ROC curve (AUC) results confirm that APOB, MPO, ICAM as potential diagnostic markers of CRC have great sensitivity and specificity.
Conclusion The APOB (3411 site), MPO (355 site), ICAM1 (145 site), may serve as a potential tumor marker for CRC.

PU-3929

ApoE 基因多态性及血脂水平与动脉瘤性蛛网膜下腔出血的相关性

白垚
重庆医科大学附属第一医院

目的 探讨 ApoE 基因多态性及血脂水平与动脉瘤性蛛网膜下腔出血（Aneurysmal subarachnoid hemorrhage ,aSAH）的关系；
方法 采用病例对照研究方法，病例组为 2018 年 5 月～2020 年 4 月就诊于重庆医科大学附属第一医院的 aSAH 患者，对照组为同期住院患者，收集并统计分析 ApoE 基因多态性及血脂水平与 aSAH 的关系；
结果 1、ApoE 基因型和等位基因频率在 aSAH 组和对照组中无统计学差异(P >0.05)。2、病例组血清甘油三酯水平低于对照组（P <0.05）。3、ε2 /ε3 型受试者中，病例组血清低密度脂蛋白胆固醇水平高于对照组（P < 0.05），ε3 /ε3 型受试者中，病例组血清甘油三酯水平低于对照组（P < 0.05）；
结论 ApoE 基因多态性可能与 aSAH 之间存在关联，ApoE 基因多态性可能通过血脂水平影响 aSAH。

PU-3930

血液系统疾病造血干细胞移植后肝损伤的相关因素分析

黄敏
山东第一医科大学附属山东省立医院

目的 分析造血干细胞移植后肝脏损伤的相关因素，以便早期预防与诊断移植患者出现的肝损伤，以改善移植患者的预后情况。
方法 收集造血干细胞移植的病人 121 例，其中自体造血干细胞移植 30 例，异基因全相合造血干细胞移植 41 例，异基因半相合造血干细胞移植 50 例。记录患者是否出现发热、乏力、纳差、肝区疼痛、等肝功能相关症状，临床缓解情况。患者肝功能相关指标、肝炎病毒感染指标、巨细胞病毒、EB 病毒等实验室以及影像学相关指标结果至移植后 1 年。
结果 进行造血干细胞移植的患者中发生移植物抗宿主病、真菌感染、败血症、移植种类不同、原发病不同造成的肝功能损害不同。HBsAg(+)患者相较于 HBsAg(-)者对于肝功能的损害并没有明显不同，但是 HBV-DNA 水平增高患者发生重度以上肝损害的机率明显增高，年龄、性别以及从确诊到移植的时间间隔对患者肝脏功能没有明显影响。不同肝功能组的一年生存率及一年无事件生存率均有明显差异。
结论 造血干细胞移植患者的预后与肝功能损害程度紧密相关，早期预防与诊断移植患者出现的肝损伤可以提高移植后患者的生存质量。

PU-3931

Study on Nosocomial Infection and its Risk Factors in Patients with Acute Leukemia

min huang
Shandong Provincial Hospital Affiliated to Shandong First Medical University

Objective To investigate the characteristics of nosocomial infection in patients with acute leukemia and provide basis for its prevention and treatment .
Methods A retrospective review of the medical records of 311 patients with acute leukemia admitted between October, 2001 and October, 2003 was performed. 144 cases were regarded as nosocomial infection group（NI group）, the other 167 cases without any infections as non-NI group. The data were analyzed with the single factor X2 test and multifactor logistic-regression analysis.
Results The incidence of nosocomial infection was 46.3%(144/311), mainly consisting of respiratory tract, blood and oral infection. No recognized sites could be found in certain patients with nosocomial infection. The most common pathogens were gram-negative bacilli(46.6%), which were relatively sensitive to Imipenem/Cilastatin Sodium(TIENAM), Amikacin, Ceftazidine. The gram-positive cocci were relatively sensitive to Vancomycin and Ceftazidine. The analyzed results show that age, corticosteroids therapy, absolute neutrophil count in peripheral blood, cycles of chemotherapy, length of hospitalization, stages of treatment, the latest infections and seasons of hospitalization were found as independent risk factors of nosocomial infection.
Conclusions The incidence of nosocomial infection in patients with acute leukemia is high. In order to reduce the death rate, improve level of therapy and prolong survival periods of these patients, positive measures should be taken to prevent and treat nosocomial infection. The conditional pathogenic bacteria are the main pathogens in nosocomial infections in patients with acute leukemia, and most of them are resisted to antibiotics. As infections in these patients are usually severe and complicated, with poor prognosis, so antibiotics selection upon experiences should be taken rapidly. General principles of antimicrobial therapy should also be applied, including administration in time, high-effective, broad-spectral and bactericidal drug combination.

Adequate dosage and duration of antimicrobial therapy are also important. Age, corticosteroids therapy, absolute neutrophil count in peripheral blood, cycles of chemotherapy, length of hospitalization, stages of treatment, the latest infections and seasons of hospitalization are independent risk factors for nosocomial infection in patients with acute leukemia.

PU-3932

Clinical utility of circulating tumor cells in patients with esophageal cancer

Yang Li、Rao Fu、Tingting Zhang、Dawei Yang
Liaocheng People's Hospital

Purpose As one of the aggressive gastrointestinal tract cancers, esophageal carcinoma (EC) has the 10th morbidity and 6th mortality rate in the world in 2020. This study was conducted to investigate the diagnostic and prognostic value of circulating tumor cells (CTCs) in patients with EC.
Methods Peripheral blood was collected from one hundred and twenty-nine newly diagnosed EC patients, seventeen benign diseases, and seventy-five healthy donors for CTCs analysis using negative enrichment-immunostaining fluorescence in situ hybridization (NE-iFISH) approach. The correlation between CTCs and clinicopathological characteristics was then investigated. Moreover, overall survival (OS) and progression-free survival (PFS) were analyzed to evaluate the prognostic value.
Results CTCs detecting using NE-iFISH approach could differentiate EC patients from benign or healthy controls at a threshold of 2 per 3.2 mL peripheral blood with the sensitivity and specificity rate of 70.54% and 96.74%, respectively (AUC = 0.826, 95% CI 0.770-0.874, P < 0.001). CTC count was associated with tumor depth (P = 0.012), but there was no correlation with any other clinicopathological characteristics. Kaplan-Meier analysis showed that OS was significantly shorter for patients with CTCs ≥ 3 compared with patients with CTCs < 3. Univariate analysis showed that gender, vascular invasion, distant metastasis, tumor depth, lymph node metastasis, and TNM stage were significant prognostic factors for patients with EC. Multivariate analysis demonstrated that distant metastasis (HR 3.262, 95% CI 1.671-6.369, P = 0.001 for PFS; HR 3.759, 95% CI 1.867-7.571, P < 0.001 for OS) was significant prognostic factor for patients with EC.
Conclusions Our results suggest that CTCs detected using NE-iFISH could be helpful for the diagnosis of EC. CTCs ≥ 3 was an independent prognostic biomarker that indicates a worse prognostic for patients with EC.

PU-3933

晚期妊娠凝血功能检测的临床价值分析

陈春杰
宁津县人民医院

目的 分析晚期妊娠孕妇中凝血功能检测的临床价值。
方法 选择正常的非妊娠妇女 60 例为对照组，选择晚期妊娠孕妇 60 例为观察组，分析两组的凝血酶时间、血小板、纤维蛋白原等。
结果 观察组和对照组在血小板、凝血酶时间比较差异无统计学意义，但观察组纤维蛋白原明显高于对照组。
结论 孕妇在晚期妊娠时，体内会有高凝状态，因此在孕妇产前、分娩时一定要监测孕产妇的凝血指标，这对预防产后出血及血栓形成有重要意义。

PU-3934

单核细胞/淋巴细胞比值对溃疡性结肠炎的诊断价值

程迎迎、张桂红、闫静
南京中医药大学附属医院，江苏省中医院

目的 检测外周血中单核细胞/淋巴细胞比值（monocyte-lymphocyte ratio, MLR）在溃疡性结肠炎（ulcerative colitis, UC）及对照组中的表达水平，比较 MLR 与临床常用炎症指标 C 反应蛋白(C-reaction protein, CRP)单独和联合应用诊断 UC 患者的 ROC 曲线。评价 MLR 作为 UC 诊断标志物的效能。
方法 收集 2018 年 1 月至 2018 年 12 月在江苏省中医院住院的 UC 患者 99 例，另选取同期肠易激综合征（irritable bowel syndrome, IBS）患者 72 例作为对照组。收集患者临床资料，检测比较对照及 UC 患者 MLR 差异，采用 ROC 曲线的方法计算 MLR 最佳临界值及曲线下面积，并与临床常用指标白细胞(white blood cell, WBC)、C 反应蛋白(C-reaction protein, CRP) 、红细胞沉降率(erythrocyte sedimentation rate, ESR) 、血小板(platelet, PLT)、中性粒细胞/淋巴细胞比值（NLR）和血小板/淋巴细胞比值（PLR）进行比较，分析 MLR 等指标对诊断 UC 的效率差异。
结果 UC 组患者外周血中 MLR 明显高于 IBS 组（0.43 vs 0.26, p<0.01）；MLR 用于诊断 UC 的 cut-off 值为 0.35，灵敏度和特异度分别为 85%和 62%，曲线下面积（area under curve, AUC）为 0.766（95%CI: 0.695~0.837），优于 WBC(AUC: 0.687, 95%CI: 0.604~0.770)、PLT(AUC: 0.745, 95%CI: 0.670~0.819)、NLR(AUC: 0.758, 95%CI: 0.685~0.832)和 PLR(AUC: 0.759, 95%CI: 0.689~0.830)，稍逊于 ESR(AUC: 0.783, 95%CI: 0.715~0.851)和 CRP(AUC: 0.830, 95%CI:0.770~0.891)；MLR 联合 CRP 的诊断价值(AUC: 0.832, 95%CI: 0.772~0.893)优于独立的 MLR 和 CRP。
结论 与对照组相比，MLR 在 UC 患者外周血中的水平升高，差异具有统计学意义。MLR 诊断 UC 的效率优于常用指标 WBC、PLT、NLR 和 PLR，其与 CRP 联合应用可提高 UC 的诊断效能，可以作于诊断 UC 的额外标志物。

PU-3935

血小板相关因子及凝血因子与乳腺癌等转移的相关性研究

宋志纯
丽水市人民医院

目的 探讨乳腺癌细胞在介导因子血小板的作用下转移关系。
方法 采用回顾性调查方法，以同期 100 例健康体检者为对照。分析 248 例乳腺癌患者血小板增多与转移的关系。
结果 乳腺癌组血小板计数较正常组高，差异具有统计学意义（P<0.01）。临床分期乳腺癌肿瘤转移组又显著高于未转移组, 差异具有统计学意义（P<0.05）。
结论 血小板与乳腺癌转移关系密切，肿瘤细胞可激发并活化血小板，同时血小板可促进肿瘤细胞转移。测定血小板及其功能可作为恶性肿瘤患者的疗效监测的参考指标。

PU-3936

胃癌肿瘤标志物联合检测在胃癌诊断中的研究进展

王晶晶
吉林金域医学检验所有限公司

目的 胃癌是我国高发的恶性肿瘤之一,无特异性临床症状，早诊断、早治疗是临床提高生存期和降低病死率的关键。目前，肿瘤标志物联合检测在胃癌早期诊断中具有较好的应用前景，成为临床研究的热点。本文综合 CEA、CA19-9、 CA72-4 等的现状和最新研究进展，分析肿瘤标志物联合检测在提高胃癌早期诊断效率中的作用。
方法 通过查阅大量文献，了解各大医疗机构及第三方医检机构对胃癌肿瘤标志物的检测种类、频次及效果，分析胃癌肿瘤标志物检测的最新进展。
结果 常见胃癌肿瘤标志物包括：癌胚抗原（CEA）是目前研究最广泛的消化道肿瘤标志物之一。糖链抗原 72-4（CA72-4）是一种黏蛋白类癌胚抗原，其水平高低主要与肿瘤的位置大小、临床分期、转移有关，是胃肠道的一种非特异性肿瘤标志物。糖链抗原 19-9（CA19-9）是判断胃癌患者预后情况的重要指标。
结论 单一的肿瘤标志物检测没有足够的灵敏度和高特异性而存在一定的局限性，因此，选用不同性质、相对敏感的指标进行联合监测可以实现互补，能够明显提高胃癌的检出率。肿瘤标志物在胃癌的初期诊断、临床分期以及预后判断和疗效观察中发挥了较大的作用。大多数肿瘤标志物对肿瘤的诊断仅仅只有相关性并无特异性，所以肿瘤标志物的联合检测对胃癌的诊断意义重大，而且这种检测方法患者的接受能力强，具有较高的诊断价值。

PU-3937

浆细胞白血病 1 例并文献复习

李康
德州市人民医院

浆细胞白血病是一种罕见的浆细胞恶性增殖性疾病，以外周血中出现大量浆细胞为特征。WHO 的诊断标准为外周血中浆细胞至少 ＞ 20% 或绝对值 ＞ 2.0 × 109 /L。浆细胞白血病恶性程度高，缓解期短，生存期低，主要原因为其独特的发病机制及特有的分子遗传学异常。现报告浆细胞白血病 1 例，并结合文献进行复习。

PU-3938

全自动血细胞分析仪与血涂片细胞形态联合用于血常规检验的临床研究

刘可
乐至县人民医院

目的 分析全自动血细胞分析仪以及血涂片细胞形态联合用于血常规检验中的临床效果。
方法 选取我院接受血常规检验的 150 例患者作为本文的观察对，选取时间为 2018 年 3 月至 2018 年 9 月间，并将其按照检测方式的不同分成两组，一组为参照组，接受单一的血液涂片细胞形态进行检验，另一组为实验组，接受全自动血细胞分析仪联合血液涂片细胞形态进行检验，两组各有患者 75 例，并对血常规检验阳性率进行对比。

结果 实验组患者的血常规检验的阳性率为 20.00%（15 名），参照组患者的血常规检验的阳性率为 5.33%（4 名），从血常规检验的阳性率上看，实验组的阳性率明显高于参照组，两组对比差异显著，具有统计学意义（x2=7.292，p=0.007）。
结论 对行血常规检验的患者采取全自动血细胞分析仪联合血涂片细胞形态检查，可有效提高检查效果，值得推广。

PU-3939

血常规联合 C 反应蛋白检验对小儿细菌感染与小儿病毒感染的鉴别价值分析

刘可
乐至县人民医院

目的 分析血常规联合 C 反应蛋白检验对小儿细菌感染与小儿病毒感染的鉴别价值。
方法 选取我院 2017 年 12 月至 2019 年 1 月间收治的细菌感染患儿 40 例作为观察组，再将我院同期收治的病毒感染患儿 40 例作为对照组，对这两组患儿均采取血常规联合 C 反应蛋白进行检验，并分析两组的检验情况。
结果 从白细胞计数（WBC）以及 CRP 浓度水平上比较，两组的统计学对比结果为（p<0.05），差异具有统计学意义；从阳性率上对比，血常规联合 C 反应蛋白检验的阳性率明显优于血常规检验阳性率以及 C 反应蛋白检验阳性率，差异显著（p<0.05）；而血常规检验的阳性率与 C 反应蛋白检验的相比无统计学意义，（p>0.05），具有统计学意义。
结论 采取血常规联合 C 反应蛋白检验可提高小儿细菌感染以及小儿病毒感染的诊断准确性，具有较高的临床应用价值。

PU-3940

血常规检验在鉴别缺铁性贫血与地中海贫血的应用分析

熊杨
资阳市乐至县人民医院

目的 探讨贫血患者贫血类型鉴别中选用血常规检验的价值。
方法 纳入 2018 年 1 月-2019 年 12 月收治 25 例缺铁性贫血患者为观察 1 组、25 例地中海贫血观察 2 组，同期选择 25 例健康体检者为对照组，均实施血常规检验，分析检查结果、阳性率。
结果 （1）检查结果：观察组 MCH、MCV、Hb 低于对照组，RDW 高于对照组，且观察 1 组 MCH、Hb 低于观察 2 组，RDW、MCV 高于观察 2 组，组间对比 P<0.05。（2）阳性率：观察组高于对照组，组间对比 P<0.05。
结论 血常规检验在缺铁性贫血与地中海贫血鉴别中效果确切，可根据 MCH、Hb 等指标明确诊断，值得借鉴。

PU-3941

伴有体质性染色体异常的血液肿瘤患者四例及文献复习

张之芬
山东第一医科大学附属省立医院

目的 探讨血液病患者体质性核型与所患疾病的关系。
方法 骨髓细胞瑞氏染色、染色体 G 显带、融合基因、免疫分型检查。
结果 四例血液肿瘤患者，除了伴有与血液疾病有关的染色体异常外，还发现有体质性染色体异常。慢性粒细胞性白血病（CMML）患者获得了供体的体质性 t（4; 19）（q21; p13），一名急性早幼粒细胞白血病（APL）患者是 XYY 携带者， 慢性粒细胞白血病（CML）患者和另一位 APL 患者是 9 号染色体臂间倒位（inv（9））携带者。经过系统治疗，患者血液病缓解后，与血液肿瘤相关的染色体异常消失了，而体质染色体异常仍然存在。
结论 我们的病例提示体质性染色体异常与血液肿瘤无明显相关性，确定的结论需要更多的病例以进一步研究。

PU-3942

尿沉渣全自动分析仪与显微镜检测法在尿常规检验中的应用效果比照观察

宋晓君
乐至县人民医院

目的 分析尿沉渣全自动分析仪与显微镜检测法在尿常规检验中的应用效果对比。
方法 选取我院 2018 年 1 月中 2018 年 6 月间收治的 100 例患者的尿常规检验资料作为研究样本，并分别采取尿沉渣全自动分析仪以及显微镜检测法进行检验，并对比两种检验的结果。
结果 通过尿沉渣全自动分析仪检测出的白细胞阳性率为 33.00%，通过显微镜检测法检测出的白细胞阳性率为 50.00%，从白细胞的检测阳性率上看，尿沉渣全自动分析仪明显低于显微镜检测法，对比差异显著（x2=5.952，p=0.015）；通过尿沉渣全自动分析仪检测出的红细胞阳性率为 44.00%，通过显微镜检测法检测出的红细胞阳性率为 30.00%，从红细胞的检测阳性率上看，尿沉渣全自动分析仪明显高于显微镜检测法，对比差异显著（x2=4.204，p=0.040）。
结论 尿沉渣全自动分析仪以及显微镜检测法各有优势，建议临床可联合使用。

PU-3943

脂浊对 SYSMEX XN-9000 检测血红蛋白的影响

张连杰
苏州市独墅湖医院（苏州市独墅湖医院）

目的 探讨脂浊对 SYSMEX XN-9000 血液分析仪对测定 Hb（hemoglobin，血红蛋白）的影响。
方法 选取 45 例高脂 EDTA-K2 抗凝静脉血，进行血浆置换。用 SYSMEX XN-9000 血细胞分析仪重新测定，将 Hb 测定的结果与置换前进行比较，同时根据 HCT 值和血清 TG（triglyceride，甘油三酯）浓度算出全血 TG 浓度，统计分析不同脂浊程度对 SYSMEX XN-9000 测定 Hb 的影响差异。
结果 脂浊会使 SYSMEX XN-9000 测定的 Hb 结果假性增高，但 SYSMEX XN-9000 也有一定的抗脂浊干扰能力：当全血 TG 浓度<9.49mmol/L 时，血浆置换后测得的 Hb 结果与在乳糜血状态下测得的结果差异较小，差异无统计学意义（P>0.05）；而当全血 TG 浓度>9.49mmol/L 时，置换前后

结果差异显著，乳糜血状态下测得的 Hb 结果明显增高，差异有统计学意义（P<0.05），且随全血 TG 浓度的递增差异越大。
结论 脂浊在一定范围内会使 Hb 结果假性增高，当全血 TG 浓度>9.49mmol/L 时，需采取一定的措施如血浆置换等加以纠正，从而为临床提供正确的血常规分析结果。

PU-3944

BC-7500 CRP 微量模式检测系统性能验证及应用评价

张连杰、于鸿滨、陈艳、韩秀、韩清珍、王琳
苏州市独墅湖医院（苏州大学附属独墅湖医院）

目的 对迈瑞 BC-7500 CRP 血细胞分析仪微量模式检测系统进行性能验证，并探讨其在临床检测应用中的注意事项。
方法 根据 WS/T406-2012《临床血液学检验常规项目分析质量要求》和 WS/T246-2005《白细胞分类计数参考方法》的要求，对其进行性能验证，验证内容包括：本底计数、携带污染率、精密度（批内和日间）、正确度、白细胞分类参数正确度、线性范围、不同吸样模式间的可比性。
结果 本底计数三次检测结果均为 0；携带污染率除 RBC 为 0.12%外，其余参数携带污染率为 0；批内和日间精密度远小于行业标准，稳定性良好；正确度验证各参数合格率均≥80%，与靶机具有良好的一致性和可比性；仪器白细胞 5 分类结果与人工相比，所有参数合格率均≥80%；不同吸样模式间比对 5 个样本合格率为 80%，满足行标要求；线性范围验证所得回归曲线斜率均在 1±0.05 范围内，相关系数 r2 都大于 0.95。
结论 对 BC-7500 CRP 微量模式检测系统性能评价合格，其各项指标性能良好，符合厂家声明的要求，是目前市场上一款良好的能胜任末梢血分析的血细胞分析仪。但在临床检测中，为了提高检测结果的准确性，也有相应的注意事项。

PU-3945

正确采集检验标本的重要性

李梅、董莉芹
哈尔滨医科大学附属第一医院

目的 疾病诊疗治疗过程中临床医生拿到与病人病情不符的检验结果时，最先想到的是检验工作人员是否正确检验标本，而忽略了检验标本前的准备工作和标本的正确采集。
方法 检验标本均由护理人员采集、送检。检验者按有关收取标本的规定对检验标本进行查对验收，并通过观察标本外观、询问采集时间、检测分析、复查及联系医护人员等途径发现和确定不合格标本并详细登记。
结果 为临床提供准确、可靠的实验诊断依据，更好地为患者服务。
结论 因此，为确保检验结果的准确性和客观性，临床医护人员应更多的了解和学习标本采集的注意事项，加强基本功和理论知识的培训，加强责任心。

PU-3946

2 例抗凝血类灭鼠药中毒病例分析与思考

李庆
昆明医科大学第一附属医院

通过对抗凝血类灭鼠药中毒引起的人体继发性凝血功能障碍的临床表现及实验室检查结果的整理与研究，探讨和分析其临床诊断与治疗的有效性。
方法 通过对 2 例抗凝血类灭鼠药中毒患者研究，并对其临床资料、实验室检查结果以及相关文献进行回顾性分析。
结果 2 例均以反复鼻衄、血尿为首发临床症状，实验室检测凝血因子 7、9 的活性强度下降，而 5、8 因子的功能正常，PT、APTT 时间延长，TT、FIB、FDP、DD2、ATⅢ结果正常。
结论 1.本组研究资料中，两名患儿均来自农村，中毒原因均为误食，其中一名出现全家中毒的情况，这可能与父母文化程度不高导致对孩子的监管和日常安全教育不足有关。2.抗凝血类灭鼠药中毒的首要表现是凝血功能障碍和全身散在活动性出血，医生面对不明原因且反复鼻衄、口唇出血的患者时，应考虑是否为抗凝血类灭鼠药中毒，并仔细询问病史，完善相关实验室检查。3. 维生素 K1 对于解灭鼠药毒有特殊的治疗效果，其治疗剂量因根据患者的出血情况作调整，常规治疗是每隔 12 小时通过静脉滴注给予患者 10mg 维生素 K1，出血严重者可输注新鲜冰冻血浆 400ml。4.维生素 K1 的使用疗程应长达 2-3 个月，不然出院后停药则极易出现病情复发或加重。

PU-3947

提高门诊桡动脉血气分析的采血一次性成功率

李牧
复旦大学附属中山医院青浦分院

目的 提高门诊桡动脉血气分析采血的成功率。
方法 采用随机、对照的临床试验设计。将门诊 100 例需桡动脉采血的患者作为研究对象。随机分为两组，各 50 例，对照组采用针筒垂直法进行桡动脉采血，试验组采用一次性动脉采血器进行桡动脉采血。比较 2 组一次穿刺成功率，疼痛程度，动脉血气分析结果的差异性。
结果 两种采血方法血气分析结果无明显差异(P>0．05)，但一次性动脉采血器采血时间短、成功率高，病人疼痛低(P<0．01，P<0．05)。
结论 使用一次性动脉采血器采集血气分析标本检测数据准确、操作简便、成功率高。

PU-3948

尿液潜血的方法学比较

刘琰、鲁平
哈尔滨医科大学附属第一医院

目的 显微镜检查对鉴别肾小球性与非肾小球血尿有重要的临床价值，故有学者提出显微镜检查是尿液红细胞检验的“金标准”，是尿液分析仪无法替代的。
方法 尿液分析仪检测尿潜血 于混匀的 10ml 新鲜尿液中浸入尿试纸条 1s 后取出，上仪器进行测定，自动打印结果。
结果 报告分为：-、+/-、+、++、+++、++++。使用 URiSCANTM 尿液分析仪及其配套的尿分析试纸条。结果尿液分析仪法测定的阴性结果与镜检不一致的也应复查，以确保测定结果的准确可靠。

结论 迄今为止，没有一台仪器的检测结果能完全替代显微镜，尿沉渣镜检以其独特的临床价值仍是尿液分析中不可缺少的检查手段。

PU-3949

脑梗死患者红细胞体积分布宽度的变化及临床意义

李祯
山东第一医科大学附属省立医院

目的 探讨脑梗死患者红细胞分布宽度(red cell distribution width ,RDW)水平的变化及临床应用。
方法 收集 265 例脑梗死患者和 160 例健康对照组外周血，检测脑梗死组和健康对照者 RDW 水平，利用受试者工作特征曲线(ROC 曲线)确定 RDW 最佳截点并将脑梗死患者分为低 RDW-CV 组（RDW<12.65%）和高 RDW 组（RDW≥12.65%），分析两组间年龄、性别、活化部分凝血酶时间（activated partial thromboplastin time，APTT）、凝血酶原时间（prothrombin time，PT）、D-二聚体（d-dimer，D-D）差异。
结果 脑梗死患者 RDW 水平显著高于健康对照组，差异有统计学意义（Z=-6.518，P<0.001）；采用 ROC 曲线，将患者分为低 RDW-CV 组（RDW<12.65%）和高 RDW-CV 组（RDW≥12.65%），高 RDW 组患者的 APTT、PT 水平显著高于低 RDW 组（APTT Z=-2.331，P=0.020；PT Z=-2.062，P=0.039），而 D-D 水平差异无统计学意义（Z=-1.141，P=0.254）。
结论 脑梗死患者的 RDW 水平显著高于正常对照者，高 RDW 组 APTT、PT 水平显著升高提示 RDW 在脑梗死疾病辅助诊断中有重要意义。

PU-3950

尿液细胞学检测的方法学解析

刘琰、王琳琳
哈尔滨医科大学附属第一医院

目的 临床上最常用的重要的检测项目之一，主要用于泌尿生殖系统疾病、肝胆疾病、代谢性疾病及其他系统疾病的诊断和鉴别诊断、治疗监测及健康普查。干化学分析仪已广泛应用于临床，流式技术的沉渣分析仪也逐步应用于临床。本文探讨流式尿沉渣定量分析仪、Clinitek 200 尿干化学分析仪、涂片显微镜镜检进行对照研究。
方法 我院来诊患者随机 200 例，用一次性洁净尿杯收集患者尿液 15 ml 左右，先进行尿干化学测定，再进行涂片显微镜镜检，最后做尿沉渣定量分析(用双盲法判读)，操作由丰富临床经验的专业技术人员在 1 h 内完成。流式尿沉渣定量分析仪测定红细胞(RBC)、白细胞(WBC)的正常值为 RBC 0 个/μl~1 个/μl，WBC 0 个/μl~3 个/μl，Clinitek 200 尿干化学分析仪 RBC、WBC 正常值为阴性，涂片显微镜镜检正常值为 RBC 0 个/μl~1 个/HP，WBC 0 个/μl~2 个/HP，超出正常值范围则视为阳性。
结果 三种方法检测 RBC、WBC 的检出率较一致，对 RBC 而言检出率高低分别为 Clinitek 200＞sysmex1000i>涂片镜检，对 WBC 而言检出率高低分别为 sysmex1000i ＞Clinitek 200＞涂片镜检。
结论 在临床应用上把 3 种方法有机地结合起来，干化学的快捷简便和流式沉渣定量的准确性及自动化、手工镜检的金标准，从而可增加检测结果的敏感度和准确性，为临床对泌尿系、循环系、内分泌系的清晰鉴别诊断、疗效观察及预后观察提供可供参考的实验数据。

PU-3951

胃癌患者中性粒细胞与淋巴细胞比值及血小板与淋巴细胞比值的变化及临床意义

李祯
山东第一医科大学附属省立医院

目的 探讨胃癌患者中性粒细胞与淋巴细胞比值(neutrophil-to—lymphocyte ratio，NLR)及血小板与淋巴细胞比值(platelet-to-lymphocyte ratio，PLR)水平的变化及临床应用。
方法 收集 224 例胃癌患者和 135 例健康对照组外周血，检测胃癌组和健康对照者 NLR 和 PLR 水平，利用受试者工作特征曲线(ROC 曲线)确定 NLR 和 PLR 最佳截点并将胃癌患者分为低 NLR 组（NLR<2.975）和高 NLR 组（NLR≥2.975）;PRL 组（PLR<157.74）和高 PLR 组（NLR≥157.74）分析两组间年龄、性别、癌胚抗原（carcino-embryonic antigen CEA）、(carbohydrate antigen,CA199)、(carbohydrate antigen,CA724)的差异。
结果 NLR、PLR 胃癌患者水平显著高于健康对照组，差异有统计学意义（NLR Z=-6.588，P<0.001；PRL Z=-7.446，P<0.001 ）；采用 ROC 曲线，将患者分为低 NLR 组(NLR<2.975) 、高 NLR 组（NLR≥2.975）和低 PLR 组(PLR<157.74) 、高 PLR 组（PLR≥157.74）。高 NLR 组患者的 CA724 水平显著高于低 NLR 组（Z=-2.983，P=0.003），而 CEA、CA199 水平差异无统计学意义（CEA Z=-1.266，P=0.205；CA199 Z=-0.869，P=0.385 ）。高 NPLR 组患者的 CA724 水平显著高于低 PLR 组（Z=-2.057，P=0.04），而 CEA、CA199 水平差异无统计学意义（CEA Z=-1.111，P=0.267；CA199 Z=-0.956，P=0.339 ）。
结论 胃癌患者的 NLR 和 PLR 水平显著高于正常对照者，高 NLR 和 PLR 组 CA724 水平显著升高提示 NLR 和 PLR 在胃癌疾病辅助诊断中有重要意义。

PU-3952

血细胞参数在多发伤患者中的指导作用

王琳琳、刘琰
哈尔滨医科大学附属第一医院

目的 由于创伤急救技术的不断提高和急救系统不断完善，严重创伤患者伤后急速病死率已明显下降，但是伤后危及生命的并发症的发生率和各种伤残率却无明显减少。正确判断多发伤患者的创伤严重程度和预后是目前危重病医学领域中创伤诊治方面所面临的一个重要课题，亦是进一步降低多发伤患者病死率的关键。本研究试图通过观察多发伤患者外周血血细胞参数的动态变化,探讨其在多发伤发生、发展及预后中的作用。
方法 多发伤患者 34 例，于创伤后 24h 内采集静脉血，作为第 1 天标本，并分别在入院后的第 3 天和第 7 天清晨空腹采血。工作特征曲线(ROC 曲线)分析曲线下面积(AUC)；AUC 0.5～0.7 诊断价值较低，0.7～0.9 中等诊断价值，0.9 以上有较高诊断价值。采用 SPSS 11.5 统计软件，数据以(x±s)表示，多组均数间的比较采用单因素方差分析。
结果 本研究显示，WBC、HB、PC/WBC 比值在第 1、3、7 天差异有显著性，另外，PC/WBC 比值均数逐步上升。本研究利用 ROC 曲线下面积评价外周血血细胞参数在评估多发伤患者预后不良时的准确性，结果显示，PC/WBC 在第 3 天 AUC 为 0.820 (0.634～1.006)，第 7 天为 0.948 (0.844～1.051)
结论 应用血细胞参数对创伤患者进行评价具有广阔的前景。并且观察 PC/WBC 在第 3 天和第 7 天的 AUC 对临床诊疗具有较高的应用价值。

PU-3953

骨髓细胞染色体核型分析在恶性血液病的诊断治疗预后中的重要意义

李祯、张之芬
山东第一医科大学附属省立医院

目的 研究分析骨髓细胞染色体核型分析在恶性血液病的诊断治疗及预后中的临床应用情况。
方法 选取我院 2016 年 12 月到 2017 年 12 月收治的恶性血液病 100 例，在各患者治疗前均进行骨髓图片相关检查，流式细胞，融合基因及骨髓细胞染色体核型分析。
结果 本组 100 例患者中染色体核型异常者为 58 例，阳性率约为 58%。其中急性白血病 21 例.骨髓增生异常综合征 9 例，慢性粒细胞白血病 14 例，多发性骨髓瘤 4 例，淋巴细胞白血病 10 例，再生障碍性贫血 0 例。
结论 骨髓细胞染色体核型分析在恶性血液病的诊断治疗及预后中效果明显，具有重要意义值得广泛应用。

PU-3954

尿液显微镜手工方法比较分析仪法

王琳琳、鲁平
哈尔滨医科大学附属第一医院

目的 手工法检验尿常规结果分析，进一步了解分析仪和传统的显微镜手工法在尿液分析中的优缺点，使检验工作者在实际工作中正确对待两种方法的应用，指导检验人员科学地把两种结合起来。
方法 我们对 500 份尿样分别用两种方法进行检测对其结果分析，一种方法用尿液分析仪检测记录尿蛋白、白细胞、红细胞结果，微量以上为阳性，微量以下为阴性。另一种方法用加热醋酸法检测尿蛋白，再用离心试管取 10 ml 混匀的尿液以 1 500 r/min 离心 5 min，倾去上清液，留取 0.2 ml 沉渣，涂片镜检，记录尿蛋白、红细胞和白细胞结果，微量以上为阳性，微量以下为阴性。
结果 分析仪检测尿蛋白和白细胞的阳性率（8.85%和 10.20%）不及手工法阳性率（9.10%和 11.85%）高，但分析仪检验红细胞的阳性率（11.85%）高于手工法红细胞阳性率（9.80%）。阳性结果不能相吻合，两种方法虽然存在一定的差异，但经统计学处理（P>0.05）差异无显著性。
结论 结果说明两种方法均可为临床使用。分析仪检测尿蛋白阳性率低于手工法阳性率，分析仪检测白细胞阳性率不如显微镜检测尿中白细胞阳性率高。但分析仪对尿中红细胞的检测比显微镜阳性率高。两种方法合理应用，取长补短，以便为临床疾病的诊断和治疗提供正确检验结果。

PU-3955

迪瑞尿液分析工作站 FUS3000 尿沉渣复检规则的制定

王学军、续薇
吉林大学第一医院

目的 对尿液分析 16 条自动审核规则进行验证,分析应用适宜性并进行完善。
方法 收集来自吉林大学第一医院检验科 2021 年 5 月 6 日至 2021 年 5 月 20 日期间的尿液分析常规样本共 324 例。进行人工镜检及 Sysmex UC-3500 尿液全自动干化学分析仪、Sysmex UF-5000 尿液有形成分分析仪双盲法检测。计算假阴性率、假阳性率、真阴性率、真阳性率及自动审核通过正确率,并与自动审核规则建立时验证数据进行率的比较。

结果 自动审核通过率、真阴性率、真阳性率及通过正确率高于规则建立组,假阴性率及假阳性率低于规则建立组。
结论 应用 16 条尿液分析自动审核规则能够保证尿液分析检验结果的准确及工作效能,具有较好的应用适宜性。

PU-3956

青浦区胃癌患者凝血-纤溶系统标志物检测的功能研究

王金金、高霏、林见敏、袁梦娇、龚倩
复旦大学附属中山医院青浦分院

目的 观察胃癌患者在肿瘤不同分期的凝血-纤溶系统标志物的变化,以探索其在胃癌患者中的诊断、预后判断中的意义。
方法 对 70 例胃癌（实验组）患者和 30 名体检健康者（正常对照组）的进行检测。检测项目包括 PLT、PT、APTT、TT、FIB、D-D 以及凝血酶一抗凝血酶复合物 (TAT)、血浆血栓调节蛋白(TM) 、纤溶酶一 α2 抗纤溶酶复合物(PIC)、组织型纤溶酶原激活剂-纤溶酶原激活物抑制剂-1 复合物(t—PAI-C)等反映凝血-纤溶系统分子标志物指标。
结果 胃癌患者组 FIB 和 D-D 高于正常对照组，二者间比较差异有统计学意义(P < 0. 05)；在胃癌患者组中 PLT、PT、APTT、TT 与正常对照组比较差异无统计学意义（p>0.05）；在胃癌患者中 TM、TAT、PIC、t-PAI-C 与正常对照组比较差异均有统计学意义（P<0.05）；
结论 胃癌患者体内存着凝血，纤溶系统的常规止凝血指标和分子标志物指标的改变，这些凝血纤溶标志物的指标改变可作为胃癌病情进展、疗效观察以及预后判断的指标之一。

PU-3957

三种仪器法和显微镜法在低值血小板计数中的比较

焦瑞宝、陈继中
安徽省铜陵市人民医院

目的 探讨三种仪器法和显微镜法在低值血小板计数时之间的差异及相关性。
方法 选取 2020 年 8 月至 9 月在铜陵市人民医院住院、血小板减少症患者 104 例，利用 Sysmex XN-A1 型全自动血液分析仪红细胞通道（RBC/PLT-I 通道）、网织红细胞通道（RET/PLT-O 通道）、血小板通道（PLT-F 通道）共三种通道同时检测血小板，并采用显微镜法人工计数血小板。按照电阻抗法（PLT-I）计数结果进行分为四组,A 组 [(PLT≤15)×109/L] 18 例；B 组 [(16＜PLT≤30)×109/L] 28 例；C 组 [(31＜PLT≤45）×109/L] 23 例；D 组 [（46＜PLT≤60）×109/L] 35 例；采用配对资料 t 检验，分析三种仪器法与显微镜法差异及相关性。
结果 除了 C 组 PLT-O 与 PLT-M 比较，差异有统计学意义（t=2.857，*P＜0.01），其他组内三种仪器法与显微镜法间配对检验，差异均没有统计学意义（P＞0.05）；A 组 PLT-I 与 PLT-O、PLT-F、PLT-M 之间相关系数（r）分别为 0.912、0.917 和 0.940；PLT-O 与 PLT-F、PLT-M 之间 r 分别为 0.981 和 0.960；PLT-F 与 PLT-M 之间 r 为 0.984；B 组 PLT-I 与 PLT-O、PLT-F、PLT-M 之间 r 分别为 0.654、0.663 和 0.680；PLT-O 与 PLT-F、PLT-M 之间 r 分别为 0.983 和 0.955；PLT-F 与 PLT-M 之间 r 为 0.982；C 组 PLT-I 与 PLT-O、PLT-F、PLT-M 之间 r 分别为 0.659、0.680 和 0.666；PLT-O 与 PLT-F、PLT-M 之间 r 分别为 0.964 和 0.952；PLT-F 与 PLT-M 之间 r 为 0.942；D 组 PLT-I 与 PLT-O、PLT-F、PLT-M 之间 r 分别为 0.352、0.344 和 0.311；PLT-O 与 PLT-F、PLT-M 之间 r 分别为 0.924 和 0.868；PLT-F 与 PLT-M 之间 r 为 0.907。

结论 B、C、D 三组患者 PLT-I 与 PLT-O、PLT-F、PLT-M 均呈中、低度相关；而 PLT-O、PLT-F、PLT-M 三种方法在四组内始终保持高度相关。四种计数方法各有优缺点，临床上需在适当时候采取恰当方法确保检测结果客观准确。

PU-3958

尿红细胞研究型参数在血尿鉴别诊断中的作用

焦瑞宝、陈继中
安徽省铜陵市人民医院

目的 探讨 Sysmex UF-1000i 尿有形成分分析仪提供尿红细胞研究型参数在血尿鉴别诊断中的作用。
方法 回顾性收集 2020 年 5 月至 8 月在铜陵市人民医院住院肾脏病患者 21 例，设为肾病组；泌尿系统结石等患者 37 例，设为尿结石组。比较分析两组患者尿液 10 项红细胞相关参数的差异性。
结果 肾病组的溶血 RBC%中位数(17.2%)为明显高于尿结石组(2.4%)，肾病组未溶血 RBC%低于尿结石组，差异均有统计学意义（P＜0.001）；小 RBC%肾病组中位数（83.6%）明显高于尿结石组（10.4%），差异有统计学意义（P＜0.001）；肾病组的尿 70%红细胞前散射光强度（RBC-P70Fsc）中位数（64.0ch），明显低于尿结石组（122.0ch）差异有统计学意义（P＜0.001）；肾病组和尿结石组红细胞前散射光分布宽度（RBC-Fsc-DW）比较，差异没有统计学意义（P＞0.05）。
结论 利用这些参数可对血尿的鉴别诊断起到很好的帮助作用，并且在肾脏病的疾病监测与随访中具有重要的意义。建议将上述红细胞参数纳入尿液常规分析报告单，为临床有需要的科室提供参考信息。

PU-3959

铜陵市 29 例新型冠状病毒肺炎患者流行病学及实验室检测结果分析

焦瑞宝、陈继中
安徽省铜陵市人民医院

目的 分析铜陵市 29 例新型冠状病毒肺炎（COVID-19）患者流行病学资料及实验室检测结果。
方法 回顾性收集 2020 年 1 月至 2 月在铜陵市人民医院住院治疗 29 例新冠肺炎，设为新冠肺炎组，选择在本院住院、诊断为其他肺炎患者 31 例设为其他肺炎组，另设置 28 例征兵体检男性作为健康对照组，拟对三组的血常规中白细胞总数及五分类绝对值及百分比进行对比研究。
结果 29 例新冠肺炎患者 21 例来自武汉，2 例来自上海，6 例为本地常住人口；潜伏期 1~19d，中位数及四分位数为 5（3，9）d，住院日为 5~29d，平均为（16.2±7.3）d；无家庭聚集接触史 18 例（占 62.07%），有家庭聚集接触史 11 例（占 37.93%）；29 例新冠肺炎患者 24 例（占 82.76%）出现症状，无症状筛查发现者 5 例（占 17.24%）；新冠肺炎组血常规中白细胞总数（WBC）、淋巴细胞绝对值（L#）、嗜酸粒细胞百分比（E%）及绝对值（E#）、嗜碱粒细胞百分比（B%）及绝对值（B#）均低于正常健康组，差异有统计学意义（P＜0.05）;新冠肺炎组的 WBC、中性粒细胞绝对值（N#）、单核细胞绝对值（M#）、B#低于其他肺炎组，两个肺炎组的单核细胞百分比（M%）大于正常健康组，差异有统计学意义（P＜0.05）。
结论 铜陵市 2020 年 1 月至 2 月发生的新冠肺炎具有疫源性，且具有明显家庭聚集性，流行病学特征明显。与其他肺炎和健康对照组比较，新冠肺炎可引起白细胞总数及淋巴细胞绝对值减少，但是这些改变是非特异性的，对诊断新冠肺炎具有帮助，特异性诊断还需要依靠新冠病毒核酸检测。

PU-3960

新生儿网织红细胞仪器法系列参数参考区间的调查

焦瑞宝、陈继中
安徽省铜陵市人民医院

目的 调查新生儿网织红细胞系列参数的正常参考区间。
方法 回顾性收集 2019 年 1 月至 12 月在铜陵市人民医院新生儿科住院的新生儿患者 424 例，采用参考区间取 95%置信区间（P2.5,P97.5）调查参考值，并按照性别不同、日龄不同进行组间比较，探讨网织红系列参数的变化情况。
结果 424 例新生儿所有 6 项参数均呈非正态分布，网织红细胞百分比（RET%）95%置信区间为（0.66~5.80）%，网织红细胞绝对值（RET#）95%置信区间为（25.72~284.56）×109/L；男性与女性新生儿 RET#和 RET%比较，女性均高于男性，差异有统计学意义（P＜0.05）；按日龄分组，组 1（≤7d）、组 2（8~14d）、组 3（15~28d）比较，网织红细胞系列参数 RET#、RET%、HFR、LFR、IRF 组间比较，差异均有统计学意义（P＜0.05）；组 1 与组 2 比较，只有 RET#、RET%差异有统计学意义（P＜0.05）；组 2 与组 3 比较，只有 IRF 差异有统计学意义（P＜0.05）。
结论 新生儿网织红细胞仪器法系列参数参考区间不完全与成人及儿童相同，期待早日建立新生儿网织红细胞仪器法系列参数，服务于临床。

PU-3961

2017-2020 年某综合性医院输入性疟疾流行病学及实验检测结果分析

焦瑞宝、陈继中
安徽省铜陵市人民医院

目的 分析某综合性医院近四年输入性疟疾流行病学及实验室检测结果。
方法 回顾性收集 2017 年 1 月至 2020 年 8 月在铜陵市人民医院门诊或住院就诊的输入性疟疾 16 例门诊或住院患者，设为疟疾组，另选择我院住院、无境外流行病学史、临床症状疑似疟疾而未检测疟原虫、由其他原因引起发热的患者 23 例设为发热非疟疾组，并设置 30 例健康征兵人员设为健康对照组。拟对三组实验室检测结果进行对比分析。
结果 16 例输入性疟疾均为男性，年龄为 31~71 岁，平均年龄为（48.0±8.2）岁；年度分布：2017 年 3 例，2018 年 3 例，2019 年 10 例，2020 年前 8 月 0 例；其中 3 月和 6 月分别有 3 例，7 月和 12 月分别有 2 例；国家及地区分布为刚果（金）1 例，加蓬 1 例，赞比亚 6 例，尼日尼亚 8 例；疟原虫虫种分布为间日疟原虫 1 例（占 6.25%），卵形疟原虫 2 例（占 12.50%），其余 13 例（占 81.25%）均为恶性疟原虫；16 例患者 RBC、HGB 和 HCT 共出现 5~7 例下降，占比在 31.25%~43.75%之间；血小板下降更为厉害，15 例患者下降，占比为 97.75%，其中轻度、中度和重度分别为 6、6 和 3 例，占比为 37.5%、37.5%和 18.75%。疟疾组、发热非疟疾组及健康对照组比较，淋巴细胞百分比及绝对值、单核细胞百分比及绝对值以及嗜酸粒细胞绝对值比较，差异均有统计学有意义（P＜0.05 或 0.001）。红细胞三项参数和血小板三组间比较，差异均有统计学意义（P＜0.001）。
结论 输入性疟疾感染对血细胞影响主要表现在红细胞和血小板计数上，常明显造成红细胞相关参数的下降，以及血小板计数明显降低，而血小板计数过低可能是重症疟疾的表现形式之一，需重点关注。

PU-3962

阴道分泌物对尿常规临床检验结果的影响及对策研究

邹航
安岳县人民医院

目的 因女性阴道口与尿道口较近，阴道分泌物能够影响尿常规检查结果,对女性患者采取阴道分泌物抑制尿液采集法检验，对其检测结果的影响予以探究。该检测方法能够对肾小球肾炎，糖尿病，血液病等疾病的治疗提供有利的依据.
方法 57 例患者选自 2018 年 2 月-2019 年 2 月期间。将上述患者随机分为实验组 29 例（阴道分泌物抑制尿液采集法）；参照组 28 例（传统尿液采集法）。对比 2 组尿常规指标。
结果 实验组红细胞（RBC）、白细胞（WBC）、 上皮细胞（Epithelial Cell）、亚硝酸盐（Nitrite）检出率低于参照组；实验组蛋白质、pH 值、比重以及尿糖指标与参照组对比差异具备统计学含义（P<0.05）。
结论 本次研究中对患者采取阴道分泌物抑制尿液采集法。可有效确保尿常规检测的准确度，该方法可推广应用。

PU-3963

不同品牌血细胞分析仪结果可比性研究

战然
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 实验室分别采用迈瑞 BC-5180 与 Sysmex XN-10 血细胞分析仪进行新鲜血检测，对两者结果的一致性和相关性进行分析，提高实验室检测结果的准确性。
方法 以参加室间质评的 Sysmex XN-10 为参考仪器，选取 20 例标本（覆盖白细胞、红细胞和血小板高、中、低值）分别采用迈瑞 BC-5180 与 Sysmex XN-10 进行血细胞分析，记录结果并分析。
结果 两台仪器 8 项检测比对项目（白细胞、红细胞、血红蛋白、红细胞压积、平均红细胞体积、平均血红蛋白含量、平均血红蛋白浓度、血小板）的比对符合率≥80%，两组检测结果的差异无统计学意义。
结论 迈瑞 BC-5180 血细胞分析仪检测结果稳定准确，与 Sysmex XN-10 结果相比一致性良好，可用于实验室检测及临床诊断。

PU-3964

外周血未成熟粒细胞检测在菌血症诊断中的作用研究

焦瑞宝、陈继中
安徽省铜陵市人民医院

目的 探讨外周血未成熟粒细胞检测在菌血症中变化及对菌血症的预测效能。
方法 回顾性收集 2020 年 2 月至 8 月在铜陵市人民医院住院、血培养阳性 108 例患者（设为菌血症组）血常规及未成熟粒细胞检测结果，并设置健康对照组 65 例，比较两组血常规中白细胞计数(WBC)、中性粒细胞百分比（NEUT%）、中性粒细胞百分比/淋巴细胞百分比(NLR)及未成熟粒细胞百分比（IG%）。
结果 菌血症组的 WBC、NEUT%、NLR 及 IG%均高于健康对照组，Z 值分别为-4.662、-8.370、-8.761 和-9.781，差异均有统计学意义（P＜0.05）；以健康对照组为参照，WBC、NEUT%、NLR、IG%四项参数对菌血症患者的 ROC 曲线下面积（AUC）分别为 0.712、0.880、0.898 和 0.943，

临界值分别为 9.44×109/L、71.0%、3.19 和 0.45%，四项指标对预测菌血症有效性均具有统计学意义（P＜0.001）;其中 AUC、约登指数及敏感度以 IG%为最高。
结论 菌血症患者 WBC、NEUT%、NLR、IG%均呈不同程度的上升，对于预测菌血症具有不同效能，其中 WBC 最低，IG%最高。

PU-3965

凝血四项指标、FDP、D-二聚体在妊娠期糖尿病患者中的相关性研究

翁立艳
资阳市安岳县人民医院

目的 探讨凝血四项指标、纤维蛋白(原)降解产物(FDP)及 D-二聚体(DD)在妊娠期糖尿病孕晚期患者中的相关性研究。
方法 选择 2018 年 2 月—2021 年 2 月收治的妊娠期糖尿病晚期孕妇 120 例作为妊娠期糖尿病组,正常妊娠孕妇 120 例作为正常妊娠组,体检健康妇女 120 例作为正常对照组。妊娠期糖尿病组和正常妊娠组于孕晚期检测凝血功能指标、DD、FDP,正常对照组于体检时检测以上指标。凝血功能指标、D-D 及 FDP 比较采用单因素方差分析,两两比较采用 LSD-t 检验,P0.05 为差异有统计学意义。
结果 妊娠期糖尿病组、正常妊娠组、正常对照组这三组 PT、APTT、TT、FIB 及 D-D、FDP 比较差异有统计学意义(均 P0.05),妊娠期糖尿病组以上指标变化最明显(均 P0.05)。
结论 妊娠期间对凝血功能及 D-D、FDP 进行检测,可为预防血栓提供参考，因此对于这些孕妇应常规检测凝血功能。对于患有妊娠期糖尿病的孕妇，应着重监测其凝血功能。

PU-3966

我院血常规检测及复检的程序在日常工作中的应用

陈婕
西安医学院第一附属医院

血液分析仪是目前临床血液一般检查最常用的检测仪器，仪器的品牌与型号也是多种多样的，我院现用的全自动血液分析仪是 SYSMEX XN2800、SYSMEX XN3000、SYSMEX XN350。但尽管如此，仍然有时会出现某些检测项目的结果异常，而这些异常有可能并不是标本本身的真实结果，为了能够准确无误的发放报告，此时必须要对标本进行复检。

PU-3967

血清鳞状细胞癌抗原联合铁蛋白、癌胚抗原检测在宫颈癌临床研究进展

周婷婷
吉林金域医学检验所有限公司

目的 宫颈癌是由宫颈上皮内瘤变缓慢进展而来，是女性生殖系统第二大恶性肿瘤。临床对于早期宫颈癌患者主要以冷冻技术、线圈电切、子宫全切等治疗方式，可有降低宫颈癌复发率，经治疗 5 年生存率高达 69%-95%。但由于在患宫颈癌早期无明显临床症状，部分患者在发现明显阴道流血或接触性出血后到院就诊，大部分患者经确诊属后以属于晚期，错过最佳治疗时机。目前，临床一

直认为多种肿瘤标志物联合检测和提高宫颈癌的准确性，且对临床治疗提供可靠疗效判定以及预后评价。但是对多种肿瘤标志物的最佳联合检测方式尚无确切定论，为此本文就血清鳞状细胞癌抗原（SCCA）、铁蛋白（SF）以及癌胚抗原（CEA）联合检测宫颈癌，旨在为临床诊断提供新思路。
方法 选取 98 例疑似宫颈癌患者作为观察组，正常健康对照组 95 例作为对照组，采用酶联免疫吸附法检测 SCCA、SF、CEA 水平。
结果 观察组血清 SCCA、SF、CEA 以及联合检测水平均高于对照组（*P<0.05*），且三者联合检测特异性与灵敏度均高于单一检测（*P<0.05*）。
结论 肿瘤标志物是反应肿瘤生长与生存的一组蛋白质，水平可提示肿瘤的发生与发展。SCCA 主要分布在鳞状上皮细胞细胞质。SF 是由肿瘤细胞分泌，CEA 属于一种高分子可溶性糖蛋白，参与胚胎细胞的有关基因调控其水平不仅与肿瘤大小、性质和部位有关，且与病情进展有关。SCCA、SF、CEA 三者联合检测具有较高的灵敏度和特异性，可作为宫颈癌辅助诊断的首选标志物。同时也是宫颈癌临床分期、病理分型、疗效评价重要指标。

PU-3968

血清肿瘤标志物联合检测在非小细胞肺癌中的研究进展

李雨艳
吉林金域医学检验所有限公司

目的 肺癌为全球性发病率极高的恶性肿瘤，其肿瘤细胞具有异质性和生物学复杂性，但由于影像学检查无法明确肺癌分期，病理组织学检测虽然具有较高的特异性，但是取材存在一定的难度，导致敏感性不高，为此血液肿瘤标志物逐渐成为临床理想目标。为弥补肿瘤标志物单一检测的特异性和敏感性的不足，提高临床诊疗水平，本文探讨血清肿瘤标志物联合检测在非小细胞肺癌中的研究进展。
方法 选取 121 例疑似非小细胞肺癌患者作为观察组，正常健康对照组 98 例作为对照组。采用癌抗原 125(CA125)、癌胚抗原（CEA）、非小细胞肺癌相关抗原(CYFRA21-1)联合检测其血清内 CA125、CEA、CYFRA21-1 水平。
结果 经检测后，观察组 CA125、CEA、CYFRA21-1 水平均高于对照组（*P<0.05*）。且患者临床分期越高，且肿瘤标志物水平越高（*P<0.05*）。CA125、CEA、CYFRA21-1 联合检测阳性率高于单一检测（P<0.05）。
结论 癌抗原 125(CA125)作为肿瘤糖类抗原，储存于细胞中，当其血清浓度降低，可提示组织发生恶性病变或肿瘤侵入组织所引起的组织破坏而入血，助于高发病风险的非小细胞癌患者的检测。癌胚抗原（CEA）属于酸性糖蛋白，是由胰腺、肝脏、小肠合成，当血清中 CEA 水平为正常水平 3 倍或以上，提示肿瘤有全身转移的可能性。非小细胞肺癌相关抗原(CYFRA21-1)是上皮细胞表达细胞片段，主要分布于复层肿瘤细胞胞质内，血清含量降低时，提示恶性肿瘤细胞凋亡，肿瘤体积缩小。血清肿瘤标志物联合检测对非小细胞肺癌临床诊断、复发监测、预后以及疗效分析有重要的意义，可提高诊断敏感性与诊断率。

PU-3969

基于 Tim4-PS 捕获分离系统的微流控芯片 HBEV-Chip 检测肿瘤源性小细胞外囊泡用于泛癌筛查

杨柳、邓昆
重庆医科大学附属第三医院（捷尔医院）

目的 为了快速分离高质量的肿瘤源性小细胞外囊泡即磷脂酰丝氨酸阳性小细胞外囊泡（PS+sEV）用于泛癌筛查

方法 直接用 Tim4 对鱼骨状微流控芯片功能化捕获的 PS+sEV，通过钙离子螯合剂 EDTA 释放通道内捕获的 PS+sEV，构建基于 Tim4-PS 捕获分离系统的鱼骨状微流控芯片(即 HBEV-Chip)；基于质谱鉴定的小细胞外囊泡蛋白质组学运用生物信息分析 PS+sEV 与肿瘤的相关性；在 8 例结直肠癌、8 例胰腺癌、8 例非小细胞肺癌、6 例健康人的血浆中验证 PS+sEV 作为泛癌筛查标志物的诊断效能；

结果 1.构建 HBEV-Chip 的最适合功能化蛋白 Tim4 的浓度为 125ng/mL，洗脱液 EDTA 的为 20mM，最佳血浆上样量为 200uL；2.HBEV-Chip 的捕获效率为 90.43 ± 2.12%，释放效率为 78.36 ± 11.73%；HBEV-Chip 获取 sEV 的纯度为 75.32 ± 2.25%，sEV 蛋白含量占比为 70.38%，超速离心获取的 sEV 的纯度为 67.48 ± 3.18%，sEV 蛋白含量占比为 68.81%；3.PS+sEV 与肿瘤发生发展的信号通路即 Cdc42 protein signal transduction, neuropilin signaling pathway, and Wnt signaling pathway 具有高度相关性（P<0.01）；4.PS+sEV 含量在结直肠癌、胰腺癌、非小细胞肺癌血浆中含量为 2.92×108 ± 2.61×107 particles/mL, 3.64×108 ± 5.26×107 particles/mL, 4.48×108 ± 4.62×107 particles/mL,在对照组血浆中为 2.10×108± 2.24×107 particles/mL，存在显著统计学差异（P<0.05），进一步综合为肿瘤组 PS+sEV 含量为 4.23×108±6.04×107 particles/mL，统计学差异更为显著（P<0.01）。根据 PS+sEV 含量绘制 ROC 曲线的相应 AUC 值为 0.85。

结论 构建了一种优于传统小细胞外囊泡分离方法的 HBEV-Chip，其快速分离的 PS+sEV 可作为泛癌筛查物，为临床泛癌筛查和实验室肿瘤功能研究提供了一个多功能平台。

PU-3970

尿液 mALB,α1-M 和 NAG 联合检测在糖尿病患者肾脏早期损伤诊断研究进展

路放
吉林金域医学检验所有限公司

目的 患 2 型糖尿病患者中，25%以上存在不同严重程度损伤，而 DN 发病机制较为复杂，微量白蛋白尿是糖尿病肾病早期主要表现，被临床最为重要诊断依据广泛应用在临床中。然而，由研究报道，部分糖尿病肾病患者的微量白蛋白尿（mALB）可存在自行缓解消失等现象，且无微量蛋白尿患者出现肾病理改变，严重者出现肾实质或功能性改变，由此说明微量白蛋白年灵敏度和特异性有待考究，不能作为糖尿病肾脏早期损伤的标志物，因此寻找由价值的尿液标志物检测方式成为临床研究热点。为此本文通对糖尿病肾病尿液检测标志物联合检测的最新研究进展进行深入探讨，旨在为临床早期诊断和治疗提供可靠依据。

方法 搜集 92 例糖尿病伴肾脏早期损伤患者以及 119 例同期健康体检者尿液标本作为研究样本，采用乳胶增强免疫比浊法检测患者 mALB,α1-M 以及 NAG 水平。

结果 糖尿病伴肾脏早期损伤患者 mALB,α1-M 以及 NAG 浓度均高于健康对照组（*P<0.05*）。三者联合检测灵敏度和特异性均高于单一检测（*P<0.05*）。

结论 糖尿病肾病是糖尿病最严重的微血管并发症之一，是糖尿病发展到一定阶段的必然损伤，也是是终末期肾病的主要危险因素。在国外，糖尿病肾病已经成为血液透析治疗的首要病因。α1-微球蛋白（α1-M）为低分子糖蛋白，由淋巴细胞和肝脏合成。指标升高表示为肾功能不全，可作为早期肾损伤的敏感性指标。尿液 N-乙酰 β-D-氨基葡糖苷酶（NAG）可反应肾实质病变，可用于早期肾损伤病程观察与监测。三者联合检测能够提高检测水平，提高检测灵敏度和特异性。

PU-3971

陕西地区 2810 例遗传咨询者外周血染色体核型分析

李文妮
西安金域医学检验所有限公司

目的 分析陕西地区 2810 例遗传咨询者的染色体异常与疾病的关系，探讨细胞遗传学检查在临床诊断中的应用价值。
方法 采用外周血淋巴细胞培养法，基础 G 显带法进行染色体制备。采取患者外周血进行淋巴细胞培养， 37℃培养箱恒温培养 72h，按常规方法进行染色体制备及 G 显带分析。每例计数 20 个中期分裂象，分析 5 个核型，如有异常加大计数分析。必要时加做 C 带和 N 带分析。
结果 陕西地区 2810 例遗传咨询者中检测出染色体异常 262 例，异常核型比率为 9.3%，其中染色体多态性 100 例，占 38.2%，性染色体异常 37 例，占 14.1%，唐氏综合症为 49 例，占 18.7%，其余常染色体异常 76 例，占 29%。遗传咨询者常见病因有不良孕产史、习惯性流产、无精子、少精子和弱精子、原发或继发闭经史、智力低下、不孕不育症、先天畸形、第二性征异常等。
结论 染色体异常是导致生育障碍、智力低下、新生儿缺陷的主要原因，因此对高危人群进行染色体检查，对优生优育及提高人口素质具有重要意义。

PU-3972

一株糖尿病患者体内分离到的 Dysgonomonas 菌及其物种分类

高小娟、韦洁宏、郝同雨、李萌萌
深圳市罗湖医院集团医学检验实验室

本研究首次从糖尿病伴并发症及肺部感染患者的血液中分离得到一株少见菌。对其进行富集培养后，用布鲁克 MALDI-TOF 进行物种鉴定时，未匹配到准确度较高的菌株。然后使用菌落 PCR 的方法扩增得到其 16S rRNA，通过 Sanger 测序的方法得到其序列信息，然后在 NCBI 上检索到该菌株属于 Dysgonomonas 属微生物，其与 Dysgonomonas oryzarvi 、Dysgonomonas mossii 相似度最高，一致性分别为 99.64%、99.57%。D.oryzarvi 是从微生物燃料电池中分离得到，具有将有机物中的化学能直接转化成电能的功能。D. mossii 是从一位乙肝复发性肝细胞癌患者的血培养中分离得到。本文分离得到的 Dysgonomonas 菌株命名为 D.oryzarvi Wh21。Wh21 在哥伦比亚血平板上生长的克隆表面光滑，形态呈针尖儿状。革兰氏染色鉴定出该菌株属于革兰氏阴性杆菌，其在有氧和厌氧的环境下皆可以生长，属于兼性厌氧菌。在透射电镜下观察到的形态大小为 0.45-0.55×0.95-1.52μm，短杆状，无鞭毛。使用二代测序的方法得出其包含多种抗生素的耐药基因 rpoB2、APH(3')-Ia、tet(C)、optrA 等，分别与利福霉素、氨基糖苷类抗生素、氟喹诺酮类抗生素、大环内酯类抗生素耐药性相关。本研究发现的 D.oryzarvi Wh21 属于一种少见菌，在免疫力低下的患者的血液中分离得到，属于机会致病菌。

PU-3973

The urinary peptidome as a noninvasive biomarker for screening of kidney disease

Zewen Li
Zhu jiang hospital, southern medical university, Guangzhou

Introduction Chronic kidney disease (CKD) is a worldwide-prevalent public health problem, with a low awareness rate. In clinical practice, the existing laboratory tests barely meet the needs of

early screening for KD. Urine peptides are derived from the circulation by the kidney and excreted under physiological conditions. With detectable change before failure of the glomerular filtration barrier, it has gradually emerged as one of the most attractive topics in biomarker discovery. Urinary peptidome has potential as an indicator of screening for kidney disease (KD) in healthy individuals.
Problems the question remains as to whether urinary peptidome could be used in healthy individuals to make early diagnose for kidney disease.
Results In the present study, we conducted one discovery cohort and two independently validation cohorts. By using next generation MALDI-TOF MS, urinary peptidome patterns in KD participants was characterized and kidney-related peptide risk score (PRS) was applied to prospectively screen for KD. We observed significant and consistent shifts in urinary peptidome between KD and control participants among three cohorts. Using 423 kidney-related urine peptides based on the discovery cohort, we conduct a kidney related peptide risk score (PRS) for representing and quantifying KD. Extrapolating this index to an independently validation cohort, we found higher PRS in KD patients and the association between PRS and kidney-related risk factor and clinical manifestations. Appling this index to a median of 6.5 years follow-up cohort, we observed a consistent trend between groups and associations with risk factors and clinical manifestations indicating PRS may act as a biomarker of KD. Furthermore, at the point of enrollment of the perspective cohort, PRS had prospectively significant increased in those participants who developed KD after a median of 6.5 years follow-up and the participants with highest quartile PRS had 86% (RR: 1.86, 95%CI: 1.01-3.43, P = 0.043) higher risk for KD compared with the lowest quartile.
Conclusion we proposed that PRS could be applied as one indicator to assess the risk of kidney disease

PU-3974

血涂片中胀亡淋巴细胞形态与临床

李德来、赵广明、沈兴娅、杨立顺
天津市北辰区中医院

目的 描述胀亡淋巴细胞形态，检测血涂片中胀亡淋巴细胞并应用于临床。
方法 对血常规分析提示有异常血细胞者做形态学复检，对疑似 IM 及胀亡淋巴细胞明显增高者纳入本调查资料，对细胞进行拍照、分析、描述胀亡淋巴细胞的形态学特点及与临床的相关性。
结果 1.胀亡淋巴细胞胞体及胞核明显胀大、胞核常胀出胞体并常起泡、核变薄、核边聚、核膜破裂、核染色质分散、核染色质均质化或不全均质化溶解、胞膜通透性增强、细胞质渗透到胞体外、细胞质内起泡等。2.胀亡淋巴细胞常检出于：⑴见于 IM，35 例 IM 病例中有 16 例检出以胀亡淋巴细胞为主的异淋细胞；⑵其它胀亡淋巴细胞增高病例，如腹痛、脑梗死等；⑶围产期妇女有较高的检出率。3.相关问题：⑴在胀亡淋巴细胞增高的病例中常可检出胀亡中性粒细胞、胀亡单核细胞、胀亡嗜酸性粒细胞和胀亡嗜碱性粒细胞；⑵35 例 IM 病例中未检出幼稚样异淋细胞。
结论 胀亡淋巴细胞是不可忽视的异淋细胞，常规血涂片瑞-姬氏染色，在油镜下可完成胀亡淋巴细胞检测，适于临床应用。

PU-3975

The Podocyte Count Detected by an Improved Immunocytochemical Method has Higher Diagnostic Efficiency than Enzyme-Linked Immunosorbent Assay and Serum Cystatin C to Evaluate the Early Stage Damage of Glomerular

Li Li
Provincial Hospital Affiliated to Shandong First Medical University

Backgroud In renal diseases, earlier injury to glomerular may lead to the abscission of podocyte. The number of podocyte in urine may reflect the severity of glomerular damage. Podocalyxin (PCX) was considered as a podocyte marker. Many Methods were used to detect podocyte. Applications of these Methods were limited by tricky, expensive and low accuracy. Here we improved an immunocytochemical method to count the number of podocyte in urine.
Methods In this study, we counted the numbers of podocyte in urine by our improved method and detected the PCX levels in urine by enzyme-linked immunosorbent assay (ELISA) in glomerulopathy patients and healthy controls. The serum levels of cystatin C (CysC), blood urea nitrogen (BUN), creatinine (CR), uric acid (URIC), and β2-Microglobulin (β2-MG) in all subjects were detected. Correlation analysis and diagnostic efficiencies comparisons between immuocytochemical method, ELISA and the biochemistry index were also performed.
Results The podocyte counts in patients were significantly higher than controls. Podocytes counts positively correlated with PCX concentrations and the serum CysC. The podocyte count had higher diagnostic efficiency than PCX concentrations detected by ELISA and serum CysC.
Conclusion The podocyte count detected by our improved method had higher diagnostic efficiency than ELISA and serum CysC.

PU-3976

网织血小板检测在妊娠合并 ITP 与妊娠期血小板减少症鉴别诊断中的价值

宋广浩
南京大学医学院附属鼓楼医院

目的 探讨网织血小板比率（RP%）在妊娠合并特发性血小板减少性紫癜（ITP）与妊娠期血小板减少症（GT）鉴别诊断中的作用。
方法 选取 2019 年 1 月至 2020 年 1 月南京鼓楼医院收治的妊娠合并 ITP 患者 25 例（ITP 组），GT 患者 80 例（PT 组）与同期体检中心健康体检孕妇 30 例（对照组）作为研究对象，比较 3 组外周血 RP%的变化。采用受试者工作特征（ROC）曲线评价 RP%诊断妊娠合并 ITP 与 GT 的效能。
结果 ITP 组 RP%显著高于 GT 组及健康对照组（P<0.001； P<0.001），而 GT 组 RP%与对照组比较，差异无统计学意义（P=0.23）；以健康对照组为对照，RP%诊断 ITP 与 GT 的 AUC 分别为 0.867，0.557；以 GT 组为对照，RP%鉴别诊断 ITP 的 AUC 为 0.820，最佳临界值为 5.40%，敏感性为 76.00%，特异性为 82.50%；RP%与 PLT 联合检测鉴别诊断 ITP 的 AUC 为 0.905，敏感性为 88.00%，特异性为 81.25%。
结论 RP%在妊娠合并 ITP 患者中高表达，在妊娠合并 ITP 与 GT 患者的鉴别诊断中具有较高的临床运用价值。

PU-3977

Estrogen promotes B cell activation in vitro through down-regulating CD80 molecule expression

Li Li
Provincial Hospital Affiliated to Shandong First Medical University

Backgroud Estrogen is the main female hormone of women. It has diverse effects on cell growth, differentiation and homeostatic functions. Accumulated evidence has indicated that estrogen may regulate multiple immune functions and the immune status of women. However, there is little report on the effect of estrogen on mature B cell functions.
Method In this study, we observed the effect of 17b-estradiol (E2) on the proliferation, apoptosis, antibody production and differentiation of splenic B cells of mice in vitro. Splenocytes of female BALB/c mice were isolated and cultured with E2.
Result E2 treatments decreased the expression of CD80 molecule on splenic B cells but enhanced the total IgG antibody production of splenocyte, without promoting the differentiation of B cells to plasma cells. E2 protected splenic B cells from the serum-deficiency-induced apoptosis but had no influence on the proliferation of B cells.
Conclusion These results suggest that estrogen may promote the activity of B cells through down-regulating the expression of CD80 molecule on B cells.

PU-3978

伴 WT1、MLL-PTD、EVI1 基因幼儿急性巨核细胞白血病的诊断与遗传学分析

赵理平
广东省珠海市妇幼保健院

目的 对一例伴 WT1、MLL-PTD、EVI1 基因幼儿急性巨核细胞白血病(acute megak-aryoblastic leukemia，AMKL)进行诊断与遗传学分析。
方法 采集 EDTA-K_2 抗凝静脉血进行血常规及血细胞形态分析；抽取骨髓进行细胞形态学、免疫表型、染色体核型及融合基因分析(骨髓 MICM)。
结果 血常规白细胞计数（WBC）12.3×109/L、血红蛋白（Hb）73g/L、血小板计数（PLT）13×109/L；血细胞形态分析发现幼稚细胞胞体大小似原始幼稚淋巴细胞，呈圆形或不规则形，部分可见明显伪足；胞浆嗜碱性，着色不均，内有颗粒；核染色质细致，可见核仁 1-3 个，此类细胞约占 40%；骨髓细胞形态分析符合急性白血病，过氧化物酶（POX）染色阴性，酯酶双染色 AS-DNCE 阴性，α-NBE 阴性；流式结果可见约 52%的原始细胞，伴明显的巨核细胞相关标记表达(cCD41+，CD61+部分，CD36+)；染色体核型 46,XX,der(3)add(3)(p21)add(3)(q25),add(9)(q22),-13,+mar[4]/46,XX,
del(13)(q12q22)[3]/46,XX[3]；融合基因 WT1 过表达、MLL-PTD 阳性、EVI1 阳性。
结论 急性巨核细胞白血病具有独特且复杂的实验室检查特点及遗传学特征。临床需加强对 AMKL 的形态学认识，积极开展 MICM 检查，在分子遗传水平上进一步深入研究，以提高对 AMKL 的诊断水平。

PU-3979

红细胞分布宽度与冠状动脉病变相关性的初步研究

陈克平
东南大学附属中大医院

目的 探析红细胞分布宽度变异系数（RDW-CV）和红细胞体积分布宽度标准差（RDW-SD）与冠状动脉病变程度相关性，辅助患者的诊断与治疗。
方法 检索 2017 年 8 月至 2017 年 10 月间在本单位接受冠脉造影检查的患者共 258 例，收集其冠脉造影结果、肝功能、肾功能、病毒八项等临床基本资料，以及血细胞分析等检测指标。根据冠脉造影结果，计算 CAD 患者 Gensini 积分狭窄程度与动脉病变支数，借助 t 检验等统计学方法处理数据。
结果 CAD 与非 CAD 患者 RDW-CV 和 RDW-SD 水平 P 值均大于 0.05，差异无统计学意义;冠状动脉狭窄程度（最大值）与 RDW-CV 和 RDW-SD 无统计学意义。3. CAD 患者冠状动脉狭窄程度>25%时，病变支数（单支病变，多支病变）与 RDW-CV 存在相关性; CAD 患者冠状动脉造影 Gensini 积分与 RDW-CV 水平存在相关性。
结论 RDW-CV 水平与冠脉病变支数及 Gensini 积分相关。

PU-3980

A novel differential diagnosis method by flow cytometry from hypoproliferative MDS with Aplastic anemia

Li Li
Provincial Hospital Affiliated to Shandong First Medical University

Backgroud Myelodysplastic syndromes (MDS) are a group of clonal haematopoietic stem cell diseases characterized by cytopenia, dysplasia in one or more of the major myeloid lineages.Some hypoproliferative MDS (hypoMDS) patient is difficult to identified from aplastic anemia (AA) patient.
Method In our study, four-color flow cytometry was used to analyze the proportion of bone marrow myeloid progenitor cells, lymphocytes, neutrophils and nucleated red blood cells of patients without lymphoid and hematopoietic system tumors and AA (as control group), hypoMDS patients, puncture dilution and AA patients. The lymphocyte to granulocyte ratio (LGR), myeloid progenitor cell to lymphocyte ratio (BLR), lymphocyte to nucleated red blood cell ratio (LER) and granulocyte to nucleated red blood cell ratio (GER) were also analyzed.
Results The results showed that the proportion of bone marrow myeloid progenitor cells combined with BLR can effectively identify the control population, hypoMDS patients, puncture dilution patients and AA patients.
Conclusion This method only needs a small amount of monoclonal antibodies and bone marrow samples. The sample processing time is short and the result analysis is simple, which is very conducive to clinical laboratory application.

PU-3981

Genetic variants of cyclin-dependent kinase 5 regulatory subunit associated protein 1-like 1 and transcription factor 7-like 2 are not associated with polycystic ovary syndrome in Chinese women

Li Li
Provincial Hospital Affiliated to Shandong First Medical University

Backgroud Polycystic ovary syndrome (PCOS) is a common disorder in women that shares many genetic features with type 2 diabetes mellitus. Novel risk loci for type 2 diabetes, single nucleotide polymorphism (SNP) rs7756992 in cyclin-dependent kinase 5 (CDK5) regulatory subunit associated protein 1-like 1 (CDKAL1), rs290487 and rs11196218 in transcription factor 7-like 2 (TCF7L2), were recently identified. The aim of this study was to test whether these loci are also associated with PCOS.
Method We recruited 826 patients with PCOS and 620 healthy controls for case–control analysis. The genotypes of these three SNPs were identified. The relationships between PCOS-related clinical endocrine and metabolic features and genotypes were also analyzed. Genotype distribution of these three loci in case and control groups showed no deviation from the Hardy-Weinberg equilibrium. No significant differences in genotype and allele frequencies were found between patients with PCOS and healthy controls.
Results No associations were observed between genotypes of the three SNPs and the clinical endocrine and metabolic features of patients with PCOS in case group after adjustment for body mass index.
Conclusion We concluded that rs7756992 in CDKAL1, rs290487 and rs11196218 in TCF7L2 have no associations with PCOS or PCOS-related clinical features.

PU-3982

凝血酶原时间与血小板检验方式对肝硬化疾病患者诊断的价值研究

张丽丽
资阳市雁江区人民医院

目的 探讨在肝硬化诊断的过程中采用凝血酶原时间与血小板检验方法对患者的诊断效果及价值研究。
方法 我院 2018 年 3 月至 2020 年 6 月进行检查诊断的肝硬化疾病病人 50 例作为观察组，同期在我院实施健康体检的 50 例作为对照组。采集静脉血进行检验，比较分析两组研究对象的血小板参数以及凝血酶原时间。
结果 观察组病人血小板压积比对照组明显要低，血小板计数比对照组要小，血小板体积和血小板宽度比对照组明显要大，凝血酶原时间比对照组明显要长（P<0.05）。
结论 在肝硬化疾病病人实施凝血酶原时间与血小板检验，其应用的价值显著，能够精确的检测病人的肝功能损伤程度，值得应用于推广。

PU-3983

双鞘液与惯性聚焦的联合作用提高循环肿瘤细胞的分离效率和纯度

李博文、魏昆、孙献歌、苏宁、李文满、尚美云、黄庆
陆军特色医学中心（大坪医院）

目的 外周血循环肿瘤细胞(*circulating tumor cells, CTC*)含量极少，因此 CTC 的分选富集是鉴定分析的必要前提。尽管微孔过滤器等临床上普及开展技术在 CTC 的分选富集领域展示出良好应用性能，但仍存在分选富集效率低、细胞纯度和活性差、检测成本高且耗时等问题。为克服上述不足，本研究拟研制有效提高 CTC 分选富集效能的基于惯性聚焦原理的双螺旋微流道。
方法 (1)通过 COMSOL 多物理场仿真软件计算和优化微流道参数，构建双螺旋微流道。(2)采用 10.4 和 16.5μm 两种不同粒径的荧光微球分别模拟外周血的血细胞和 CTC，优化微流道各入口的流速等相关物理参数。(3)不同浓度(*1.0×10*^{5}、1.0×10^4、1.0×10^3/mL)Hela、MCF-7 和 K562 肿瘤细胞株经免疫荧光染色后分别加入健康成人外周血，模拟含有 CTC 的临床肿瘤患者样本，评价双螺旋微流道分选富集 CTC 的多项方法学参数。(4) 收集不同临床肿瘤患者全血样本进行分选富集，检验双螺旋微流道的实用性。
结果 (1)双螺旋微流道主通道的最佳宽度和深度分别是 500 和 170μm，可分选富集粒径尺寸~12μm 以上的细胞(如：CTC)或粒子。(2)与现有的单螺旋微流道相比，双螺旋微通道分选的两种颗粒间隔扩大了四倍以上，模拟 CTC 的 16.5μm 荧光微球的分选效率、回收率和纯度均值分别达到了 98%、96%、90%。(3)模拟肿瘤患者外周血标本的 CTC 分选通量为 $1x10^8$ 个细胞/分钟，CTC 纯度高达到 88%，细胞活性~100%。(4)从临床患者(*n=12*)的 2ml 全血中分选出 5~57 个 CTCs。
结论 本研究所述双螺旋微流道直接进行全血分选，可有效降低 CTC 丢失、活性低等风险，并具有良好的分选纯度和回收率等性能，操作简便快捷，整体耗时远低于现有技术，对临床肿瘤的诊断、转移复发监测、疗效评估具有良好的应用前景。

PU-3984

实验室拒收不合格标本及纠正对策分析

张丽丽
资阳市雁江区人民医院

目的 分析临床基础实验室对不合格标本拒收的原因，并采取有效的纠正对策；
方法 采用回顾性分析，对我院临床基础实验室 2020 年 3047 份不合格标本拒收原因进行分析，并提出纠正对策；
结果 从结果来看，当年标本不合格比率为 0.82%，1 月不合格率为 1,2%，6 月不合格率为 1.3%，其他月份的不合格率均低于 1%；不合格原因为无采集时间、标本凝固、标本量不足、非本实验室标本、医嘱停止、样本号被占用及其他（包含信息错误、条码不清等）。
结论 针对不合格标本原因采用沟通、绩效考核及培训等对策进行纠正，有助于控制检验前的质量，提高检验效率。

PU-3985

红细胞参数与网织红细胞参数在巨幼细胞贫血与溶血性贫血鉴别诊断中的应用价值

张丽丽
资阳市雁江区人民医院

目的 研究红细胞参数与网织红细胞参数在巨幼细胞贫血患者（MA）与溶血性贫血患者（HA）病情鉴定中的判定价值。
方法 将我院收治的 70 例巨幼细胞贫血患者和溶血性贫血患者（各 35 例）作为研究组，35 例正常体检人员作为对照组，比较两组人员红细胞参数 MCV、MCH、MCHC、RDW 和网织红细胞参数 RET%、IRF、HLR%的差异。
结果 研究组患者网织红细胞参数 RET%、IRF、HLR%和 RDW 均高于对照组，且 MA 网织红细胞参数参数均低于 HA（P<0.05）；研究组患者红细胞参数 MCV、MCH、MCHC 均低于对照组，且 MA 患者红细胞参数 MCV、MCH、RDW 高于 HA（P<0.05）有统计学意义，而 MCHC 参数 MA 患者与 HA 患者差异不显著。
结论 红细胞和网织红细胞参数可用于临床判断区别 MA 患者和 HA 患者，能为患者病情诊断提供依据，值得推广。

PU-3986

细针穿刺细胞学对甲状腺肿物分类的研究分析

贺爱丽、陶贵华
德州市第二人民医院

目的 通过甲状腺肿物穿刺细胞学涂片的分析，对甲状腺肿物各种临床常见疾病进行分类研究。
方法 甲状腺肿物细针穿刺或 B 超引导下细针穿刺，瑞氏一姬姆萨复合染液染色进行分类诊断，对手术病人与病理组织学对照,对良性反应性疾病病人进行跟踪随访。
结果 根据多年细胞学经验进行总结，对甲状腺各类常见疾病进行分析、研究、比对、得出正确结论。
结论 技术操作越熟练，诊断经验越丰富，操作过程实行全程质量控制，提高诊断结果的正确性。甲状腺是人体最大的内分泌腺， 位于颈前部,紧贴在喉与器官上端。其主要功能是合成和分泌甲状腺激素，当甲状腺肿大，出现肿瘤，达到一定程度时可压追气管，使气管软化，出现呼吸困难，吞咽困难等症状。甲状腺针吸细胞学检查，操作简便，不需麻醉，安全，经济实用，制片阅片快速，对于病人来说痛苦小，易于接受，极少有并发症，诊断较准确。适用于肿瘤的诊断和随访及筛查,能够早期发现癌症，其诊断的敏感性和特异性均较好。甲状腺肿物的针吸细胞学检查，为临床治疗提供可靠的依据，而且操作越熟练，经验越丰富，对于较小的病灶，我们均采用 B 超或 CT 引导下穿刺,也取得了较好的效果，具有重要意义。对于操作中的每一个环节我们都实行了质量控制，并采取了一个病例，多人同时阅片，同时诊断，对于疑难病例，到上级医院请专家会诊等形式。一个正确的诊断结果,需要多年经验的积累,不断地学习，随着免疫组化等新技术的开展,我们的形态学将会更上一个新的台阶。

PU-3987

血常规检验结果准确性的影响因素探讨

杨超
资阳市雁江区人民医院

目的 对影响血常规检验结果准确性进行分析，并提出有效的整改措施。
方法 以我院临床血液检验室 2020 年 1 月-2020 年 2 月送检血常规 3600 例为研究对象，结合临床诊断，对存在误差样本再次复检，统计存在误差的次数，分析影响准确性的因素。
结果 从结果来看，有 360 例检验假结果值，占比 10%；仪器因素为 64 例，占比 17.78%；生理因素 164 例，占比 45.56%；人为因素 132 例，占比 36.66%；因此生理因素影响最大，必须要高度重视。
结论 血常规检验属于复杂多变的过程，影响因素比较多，有时难免出现疏漏，因此应该采取相应整改措施，有效避免或减低这些因素影响准确性，才能确保血常规检验的可靠性与准确性。

PU-3988

联合应用干化学法和尿沉渣镜检的应用研究

汪德宇
资阳市雁江区人民医院

目的 分别应用干化学法和联合尿沉渣镜检对尿液进行检查，比较两种方法的阳性率及总体符合率，探讨尿液检查过程中联合应用尿沉渣镜检的必要性。
方法 随机选择我院门诊及住院病人共 600 例的新鲜尿液，每份标本均在 2 小时内分别单独应用干化学法和联合尿沉渣镜检对尿液进行检查，并以红细胞、白细胞为例，对所得结果进行统计学分析、对比。
结果 从统计分析结果可以看出单独应用干化学法和联合应用尿沉渣镜检两种方法对红细胞、白细胞的总体检出率及符合率有一定的差异，除此以外，在这 600 例尿液标本中用镜检法还检出 14 例管型、9 例病理性结晶、37 例上皮细胞等，而这些有形成分是尿干化学法无法检测的。
结论 联合应用干化学法和尿沉渣镜检，二者结果互为参照，并密切结合临床，才能得到客观、准确的评价。

PU-3989

岳阳地区 1150 例辅助生殖技术患者外周血染色体核型分析

蒋华科、向阳海、徐锦波、龚燕飞
岳阳市一人民医院

目的 对辅助生殖技术患者进行细胞遗传学分析，探讨这类患者与染色体异常的关系，为临床诊疗和遗传咨询提供依据。
方法 回顾分析 2019 年 3 月至 2021 年 5 月在岳阳市一人民医院生殖中心进行辅助生殖技术的 1150 例患者，进行外周血淋巴细胞培养、染色体制备及核型分析，并统计异常核型的类型及发生率。
结果 1150 例辅助生殖技术患者共检出染色体异常 26 例，异常核型检出率 2.26%（26/1150），其中男性染色体异常 1.86%(11/591)，明显低于女性的 2.68%(15/559)。性染色体异常 15 例，占异常核型的 57.69%（15/26），其中性染色体数目异常 11 例，包括 47,XXY 克氏综合征 5 例、45,X 特纳综合征 3 例、47,XXX 超磁综合征 3 例，性染色体结构异常 4 例；常染色体异常 9 例，占异常

核型的 34.62%（9/26），包括平衡易位 4 例，倒位 3 例，罗氏易位 1 例，染色体插入 1 例，染色体重复 1 例；检出其他染色体异常性反转 1 例，标记染色体 1 例。共检出染色体多态变异 192 例，多态率 16.69%（192/1150），其中男性多态占 73.44%（141/192），显著高于女性多态 26.56%（51/192），染色体多态变异以 Y 染色体长臂异染色质区长短和 D/G 组短臂、随体区变异检出率最高。

结论 染色体异常是不孕不育及不良孕产史的重要影响因素，临床上对辅助生殖技术患者进行染色体检查，为临床诊断与辅助生殖技术提供依据。

PU-3990

肺部感染与血小板减少的相关性研究

唐光织
资阳市妇幼保健院

目的 探讨肺部感染与血小板减少的相关性。

方法 收集临床肺部感染的患者共 232 例(所有病例肺部感染诊断明确，并排除血液系统疾病及其他可能引起血小板减少的继发因素)。分别统计血小板正常组人数与血小板减少组人数。入选血小板减少组的肺部感染人群满足至少两次血常规检查血小板计数<100×109/L。收集同期间相关样本数量健康人群 235 例作为对照组。分别统计血小板正常组人数与血小板减少组人数。采用 Sysmex-XN550 全自动血液分析仪分别检测外周血血小板的数量，并对其检测结果进行统计学分析。

结果 肺部感染患者血小板计数减少发病率为 19%，而对照组血小板计数减少率为 6%，感染患者血小板减少发生率明显高于对照组，差异有统计学意义，因此血小板减少与肺部感染有关。C 反应蛋白、降钙素原、纤维蛋白原检测结果与血小板计数成负相关。

结论 肺部感染可能会引起血小板数目减少，血小板数目与 C 反应蛋白、降钙素原、纤维蛋白原呈负相关。

PU-3991

白细胞、C-反应蛋白和降钙素原三项联合检测对预测婴幼儿肺炎临床诊断的临床价值

黄杰
资阳市雁江区人民医院

目的 探讨白细胞（WBC）、C-反应蛋白（CRP）和降钙素原（PCT）三项联合同时检测对预测婴幼儿肺炎临床诊断的重要价值。

方法 对 2015 年 1 月至 2015 年 12 月，我院 868 例 0-3 岁的不同肺炎病原体感染患儿进行 WBC、CRP、PCT 测定。

结果 比较阳性比率结果 868 例病人标本中，细菌性肺炎 436 例，病毒性肺炎 241 例。其中细菌性肺炎 WBC、CRP、PCT 阳性比例分别为 51.6%、60.3%、87.6%，病毒性肺炎 WBC、CRP、PCT 阳性比例分别为 26.5%、9.5%、15.0%，两组比较有统计学意义。在细菌感染组中 WBC 的灵敏度为 51.6%，特异度为 73.4%；在细菌感染组中 CRP 水平的灵敏度为 55.3%，特异度为 90.5%；在细菌感染组中 PCT 灵敏度为 87.6%，特异度为 85.1%。

结论 WBC、CRP、PCT 水平均可作为早期诊断婴幼儿肺炎感染类型的重要指标。且对早期诊断与评估预后有重要意义。

PU-3992

高荧光强度网织红细胞占比与终末期肾病患者生存质量的关系

苏洋、曹杰贤
昆明医科大学第一附属医院

高荧光强度网织红细胞（HFR）是晚幼红细胞发育成为成为成熟红细胞的最初阶段，是骨髓造血活性较敏感的指标。红细胞生成素（EPO）系主要由肾脏产生的糖蛋白，为促进骨髓红系祖细胞生长、增殖、分化、发育为成熟红细胞的主要刺激因子，同时加速网织红细胞的释放，EPO 与 HFR 之间有着密切联系。肾病进展至终末期会导致 EPO 生成减少，对骨髓红系刺激降低，骨髓造血活性减弱，严重影响患者生存质量。HFR 占比检测对于临床应用 EPO 治疗终末期肾病导致的贫血有极其重要的意义。

PU-3993

应用静脉采血法及末梢采血法为患者进行血常规检验对提升检验准确率的价值分析

杨姗
资阳市雁江区中医医院

目的 分析静脉采血法及末梢采血法在血常规检验中的对提高检验准确率的价值。
方法 以我院 2019 年 1 月至 2020 年 1 月间接受体检的 98 例健康人员作为此次的观察对象，将采取静脉采血法所得检验结果设为实验组，将末梢采血法所得检验结果设为对照组，所有患者先行静脉采血，再行末梢采血，并对检验结果进行对比分析。
结果 从红细胞相关指标检测结果上看，实验组的 HGB、HCT、MCHC 以及 PLT 水平较高，与对照组相比差异具有统计学意义（$p<0.05$）；从血小板相关指标检测结果上看，实验组的 WBC 水平明显较低，与对照组相比差异显著（$p<0.05$）；观察白细胞相关指标检测结果，实验组的 NE 水平明显较低，对比具有统计学差异性。
结论 静脉采血法以及末梢采血法在血常规检验中均可得到较为准确的结果，但是静脉采血法更为准确，值得推广。

PU-3994

阴道分泌物对尿常规临床检验结果的影响及干预研究

陈婷
资阳市雁江区中医医院

目的 分析阴道分泌物对尿常规临床结果的影响。
方法 以 2019 年 3 月至 2020 年 3 月间在我院接受尿常规检验的 38 例女性临床资料作为此次的研究样本，所以观察对象均接受尿常规检验，共计采集两份标本，其中 38 例为常规采集尿液标本，并命名为参照组，其余 38 例在参照组的基础上，做阴道分泌物剔除处理，并命名为研究组，分析两组尿液标本检验结果。
结果 观察两组的各指标检出率，结果显示（$p<0.05$），研究组的蛋白质、红细胞、白细胞以及上皮细胞检出率均较低，对比具有统计学差异性（$p<0.05$）；观察两组各项指标检出水平，结果（$p<0.05$），研究组的 pH、尿糖以及蛋白质均较低，对比具有统计出差异性。
结论 临床尿常规检验结果会受阴道分泌物的影响，导致检验结果准确性下降。

PU-3995

肿瘤患者治疗前后 TBNK 淋巴细胞亚群变化情况及临床意义

常艳红
吉林金域医学检验所有限公司

目的 探讨肿瘤患者治疗前后 TBNK 淋巴细胞亚群变化情况及临床意义。
方法 统计吉林金域医学检验所有限公司，在 2020 年 1 月-2021 年 1 月接收的肿瘤患者 3500 例治疗前后的样本检测 TBNK 淋巴细胞亚群的数据结果，比较患者在治疗前后 TBNK 淋巴细胞亚群的变化情况并进行统计分析。
结果 正常人 CD3 范围为 67.88±9.22，CD4 范围为 39.52±3.66，CD8 范围为 29.50±2.11，通过统计分析发现，3500 例肿瘤患者在治疗前的 T 细胞 CD3 的范围为 46.23±12.47，CD4 的范围为 22.43±9.44，CD8 的范围为 28.64±7.59，结果明显低于正常水平（P＜0.05）。接受治疗后，肿瘤患者 T 细胞 CD3 的范围为 55.64±9.07，CD4 范围为 36.87±6.40，CD8 范围为 26.98±6.28 比例有显著的提升（P＜0.05）。不难发现，治疗后有效果的患者 CD4/CD8 较治疗前有所升高（P＜0.05）。
结论 淋巴细胞亚群是检测细胞免疫和体液免疫的重要指标，反映的是机体当前的免疫功能和状态情况。由于肿瘤患者的细胞免疫功能处于免疫抑制状态，患者对识别和杀伤突变细胞的能力下降，故 T 细胞（CD3、CD4、CD8）比例明显低于正常人。随着治疗的进程，治疗有效果的患者 T 细胞会有所上升，而治疗无效果的患者 T 细胞反而会下降。表明通过检测 TBNK 淋巴细胞亚群变化，可以来监测治疗效果是否有效以及判断预后都有一定的帮助。目前肿瘤的发病率越来越高，临床急需一种检测手段来辅助诊断，而 TBNK 淋巴细胞亚群的变化情况就是反应机体当下的免疫情况，故可以广泛应用于临床，来辅助诊断及监测肿瘤患者的病情。

PU-3996

限制性输血方式对创伤性脑损伤患者 临床转归的预后影响

黄通位
资阳市雁江区中医医院

目的 对创伤性脑损伤患者应用限制性输血方式后临床转归的预后影响进行研究分析。
方法 选取我院 2014 年 10 月—2016 年月 10 月收治的 138 例创伤性脑损伤患者作为研究对象，按照入院顺序将其随机分为对照组和观察组，各 69 例。对照组应用开放性输血方式，观察组患者应用限制性输血方式。对比分析两组患者的临床转归和预后影响情况。
结果 对照组不良反应发生率为 24.64%，观察组的不良反应发生率为 4.35%，观察组比对照组明显低。对照组有 6 例患者治愈，观察组有 19 例患者治愈，观察组明显高于对照组。两组患者在康复治疗、看护、机械通气治疗等方面无明显差异。
结论 应用限制性输血方式对创伤性脑损伤患者进行治疗，能取得较好的治疗效果，能降低不良反应发生率，提高治愈率，临床转归预后较好，临床上具有较高的应用价值。

PU-3997

临床检验中影响尿液检验的因素分析

王潘
资阳市雁江区中医医院

目的 分析临床检查中影响尿检结果的因素，提出有效的预防和干预措施。

方法 随机抽取 200 例患者进行尿常规检查。所有患者均按检测要求采集晨尿作为检测样本，采集后尽快送实验室。采用尿液分析仪进行尿常规检查，结合患者的身体状况和后期临床诊断结果判断尿常规结果的准确性。本文详细分析总结了影响尿样采集、保存和检查分析结果的因素，并提出了有效的干预措施，以提高尿检的可靠性，为临床实践提供准确的依据。
结果 200 例中 15 例异常，占 7.50%（15/200）。最容易引起误差的环节是尿样检测 66.67（4/15），其次是尿样采集 26.67（4/15），影响较小的因素是尿检申请 0 和尿样转移申请 6.67（1/15）。
结论 影响尿检结果准确性的关键因素包括：尿检申请、尿样采集、转移和检测。影响这个过程的因素很多。只有患者和医务人员才能规范操作，这样才能保证尿检过程中不出差错，得到最准确的尿检结果，才能帮助医生准确鉴别疾病，希望引起重视。

PU-3998

临床检验中便常规检验的临床应用价值分析

王潘
资阳市雁江区中医医院

目的 分析临床检验中便常规检验的临床应用价值。
方法 120 例进行便常规检验患者,随机分为查虫卵试验组与便潜血试验组,每组 60 例。查虫卵试验组患者采用查虫卵试验进行检验,便潜血试验组患者采用便潜血试验进行检验。对比两组诊断有效率、疾病检出率、疾病诊断符合率。
结果 便潜血试验组患者诊断总有效率为 93.33%,高于查虫卵试验组的 80.00%,差异有统计学意义（P<0.05）。便潜血试验组患者疾病总检出率为 93.33%,高于查虫卵试验组的 80.00%,差异有统计学意义（P<0.05）。
结论 临床检验中便常规检验的临床应用价值突出,潜血试验的诊断效果更好,值得临床医护人员高度重视并推广利用。

PU-3999

Evaluation of Serum Exosomal LncRNA-Based Biomarker Panel for Diagnosis and Recurrence Prediction of Bladder Cancer

Shujun Zhang、Chuanxin Wang
The Second Hospital of Shandong University

Background Long non-coding RNAs (lncRNAs) embedded in circulating exosomes may serve as diagnostic biomarkers for a variety of tumors. We aimed to develop a panel consisting of serum exosomal lncRNAs for diagnosis and recurrence prediction of bladder cancer (BC).
Methods Exosomes were isolated from serum of BC patients and healthy controls and validated by transmission electron microscopy (TEM), nanoparticle tracking analysis (NTA) and Western blotting analysis. qRT-PCR was performed to analyze the expressions of 11 candidate lncRNAs using a training set (n=200) and a validation set (n=320). Receiver-operating characteristic (ROC) curves were employed to evaluate the diagnostic performance of the identified lncRNAs. Multivariate logistic regression model was used to construct an lncRNA panel. Moreover, we determined the correlation between lncRNAs and recurrence-free survival (RFS) of patients with non-muscle-invasive bladder cancer (NMIBC) by Kaplan-Meier analysis, univariate and multivariate Cox analysis.

Results Three lncRNAs (PCAT-1, UBC1 and SNHG16) were significantly up-regulated in serum exosomal samples of BC patients, and a panel was established based on these three lncRNAs. The three-lncRNA panel provided high diagnostic accuracy for BC with an the area under the ROC curve (AUC) of 0.857 and 0.826 in the training set and validation set, respectively, which was significantly higher than that of urine cytology. The corresponding AUCs of this panel for patients with Ta, T1 and T2–T4 were 0.760, 0.827 and 0.878, respectively. Kaplan-Meier analysis showed that NMIBC patients with high UBC1 expression had significantly lower RFS (p=0.01). Univariate and multivariate Cox analysis demonstrated that UBC1 was independently associated with RFS (p = 0.018).
Conclusions Our study established a distinctive three-lncRNA panel with considerable diagnostic value and identified lncRNA UBC1 as a potential biomarker for prediction of NMIBC recurrence.

PU-4000

遗传性蛋白 S 缺陷症家系的临床表现及遗传背景研究

李蕾、吴希、武文漫、丁秋兰、王学锋
上海交通大学医学院附属瑞金医院

目的 蛋白（PS）作为活化蛋白 C（APC）和组织因子途径抑制物（TFPI）的辅因子在体内发挥重要的抗凝功能。PS 缺陷症是我国 VTE 患者最主要的危险因素之一，受累患者众多。然而，国内尚缺少针对 PS 缺陷症的大样本研究。本研究对 55 个 PS 缺陷症家系的临床表现，危险因素及遗传背景进行研究。
方法 收集 55 个 PS 缺陷症家系的临床资料，检测止凝血相关指标，对 55 例遗传性 PS 缺陷症患者的临床特征、实验室表型和基因检测结果进行总结；通过凝血酶生成实验检测 32 例 PS 缺陷症患者的 APC 和 TFPI 辅因子功能；采用二代测序联合 AccuCopy 拷贝数检测技术对包含 PROS1 在内的 35 个基因组成的易栓症基因检测 panel 进行点突变、小插入/缺失或大插入/缺失的检测，并对检出的突变进行致病性分析。
结果 该研究的 55 例 PS 缺陷症家系的先证者中，52.7%的患者经历多次或多部位血栓发生，以下肢 DVT 或 PE 为主（82.7%），40%的患者合并其他遗传性或获得性 VTE 危险因素，这些患者首次发生 VTE 的年龄更小且 VTE 复发的比例更高。共有 50 例患者被检出携带致病性的 PROS1 突变，高于国际报道的 50%的突变诊断率；共发现 38 种不同的 PROS1 杂合突变，其中有 17 种为国际首次报道；首次发现三种中国人群特有的 PROS1 热点突变（E67A, R561W 和 Y560*）；通过凝血酶生成实验首次发现两种不影响 PS 的 APC 辅因子活性但导致 TFPI 辅因子活性减弱的 PROS1 突变（R233K 和 G308E）；体外蛋白表达及功能试验进一步证实 R233K 和 G308E 突变型 PS 的表达和分泌正常、APC 辅因子活性正常但 TFPI 辅因子活性仅分别为野生型的 80%和 69%；未来对自然发生的导致 TFPI 辅因子活性减弱的 PS 突变进行深入研究有助于揭示 PS 发挥 TFPI 辅因子抗凝功能的可能机制，对完善目前 PS 缺陷症的临床诊断具有重要意义。
结论 作为国内较大规模的 PS 缺陷症研究，本研究首次对中国 PS 缺陷症患者临床特征、合并其他血栓危险因素的情况、实验室表型和基因型特征进行了详细总结；PS 缺陷症患者合并其他遗传性或获得性血栓危险因素时，首发静脉血栓的年龄更年轻且血栓复发比例更高；首次发现了三个不同于其他种族的 PROS1 热点突变（E67A，R561W 和 Y560*）；首次发现两种不影响 PS 的 APC 辅因子活性但导致 TFPI 辅因子活性减弱的 PROS1 突变（R233K 和 G308E），未来对自然发生的导致 TFPI 辅因子活性减弱的 PROS1 突变进行深入研究有助于揭示 PS 发挥 TFPI 辅因子抗凝功能的机制并进一步完善目前 PS 缺陷症的临床诊断。

PU-4001

结直肠癌外周血单个核细胞 DNA 甲基化检测可实现结直肠癌的早期诊断

谢艳
山东大学第二医院

目的 本研究初步建立起结直肠癌外周血单个核细胞（PBMC）DNA 甲基化图谱，对外周血 PBMC 进行提取，筛选出用于结直肠癌诊断的 cg 位点，探究其作为肿瘤标志物的诊断效能，为阐明甲基化位点在结直肠癌发生发展中的作用机制研究提供思路。
方法 研究前期对结直肠癌患者及健康对照者外周血 PBMC 进行 850K 芯片分析，初步筛选出在差异最大的 10 个位点作为候选。通过焦磷酸测序在训练集（20 对结直肠癌患者及 20 对健康对照者）样本中检测候选 cg 位点的甲基化情况。同时采用受试者工作特征曲线（ROC）分析外周血 PBMC 中差异甲基化位点对结直肠癌的诊断效能。训练集样本中表达趋势与测序结果一致的 cg 位点进入验证阶段。随后在另一独立样本集，即验证集样本（30 对结直肠癌患者及 30 对健康对照）中检测候选 cg 位点的甲基化情况，并评估其诊断价值。在模型建立阶段，除去关联性分子，建立诊断 pancel，并评估其诊断价值。
结果 在训练和验证阶段，我们通过焦磷酸测序证实 cg06469890、cg27077475、cg09072601 在结直肠癌外周血 PBMC 均低甲基化。在训练集样本中， 3 个位点对结直肠癌的诊断效能分别为 0.75、0.72、0.80；在验证集样本中， 3 个位点对结直肠癌的诊断效能分别为 0.74、0.75、0.79。最后构建诊断 logestuc 诊断模型。
结论 本研究通过分析、验证结直肠癌外周血 PBMC 的 cg 位点甲基化情况，并建立诊断 pancel，对结直肠癌的诊断具有良好的敏感性和特异性，可以较好地区分结直肠癌患者和健康对照者，因此可作为结直肠癌诊断的潜在生物标志物。

PU-4002

一种基于流体力学的单细胞捕获微流道的研究

孙献歌、李博文、魏昆、尚美云、苏宁、李文满、黄庆
陆军特色医学中心（大坪医院）

目的 本文基于流体力学最小流阻原理设计了单细胞捕获微流道，单个细胞快速高效的捕获在相应的位置，获得高效的单细胞捕获效率满足单细胞分析的需要。
材料与方法 （1）采用 COMSOL 多物理场仿真软件模拟了三维微通道中速度场分布，获得细胞捕获前和捕获后的流率比值，优化微通道的几何参数，并通过软光刻技术制备 PDMS 材质的单细胞捕获微流道。（2）采用注射泵 1.0×10^5 个/mL K562 细胞悬液以一定的流速注入微通道内进行细胞捕获，验证该微通道单细胞捕获的可行性以及评价构建的单细胞捕获微流道的捕获效率以及捕获细胞的活性。
结果 （1）仿真得到微流道的主通道的宽度 25um，高度 25um，捕获通道圆形区域的半径 50um，捕获区域的长度 12um，宽度为 7um，适用于捕获尺寸大于 10 um 的细胞。（2）细胞捕获过程中，细胞优先流向流阻较小的捕获区域被捕获，同时细胞捕获后捕获通道的流阻急剧增加，随后的细胞将绕过该捕获区域流向主通道，从而基于通道流阻的动态变化实现单细胞的捕获形成单细胞阵列。（3）细胞实验表明该单细胞捕获微通道能够高效且快速地完成单细胞捕获，单细胞捕获效率可高达 85%，并且捕获的细胞保持良好的细胞活性，证实了该微通道捕获单细胞的可行性。
结论 该单细胞捕获微流道无需复杂的集成，蛇形弯曲通道的设计能够增加主通道的流阻，同时圆形结构的设计能够减少捕获通道的流阻，不仅有效缩小了整个微流控装置的尺寸，可快速高效地实现高通量的单细胞捕获，在单细胞分析中具有潜在的应用价值。

PU-4003

罕见先天性嵌合体血型所致混合视野的分析

梁路石
东南大学附属中大医院

目的 对一例微柱凝胶法 ABO 血型鉴定反定型为 B 型（与标准 Ac 凝集强度为 4+、与标准 Bc 和 Oc 均不凝集）、正定型出现混合视野（与单克隆抗-B 凝集强度为 4+ mixed field、与单克隆抗-A 不凝集）的样本进行进一步检测，加以分析以明确原因。
方法 结合临床资料，对本例中出现混合视野的可能原因逐项鉴别。采用试管法复检 ABO 血型，检测亲和力，并增加与抗-H 的反应。应用毛细管离心技术，对远、近心段红细胞分别进行 ABO 正定型检测。对与单克隆抗-B 血清不凝集部分的红细胞以及凝集部分且经二硫苏糖醇处理后的红细胞分别进行 ABO 正定型的检测。对本例样本进行分子生物学检测。
结果 患者非血液系统疾病、无输血史。试管法 ABO 血型鉴定反定型结果同微柱凝胶法，正定型与单克隆抗-A 不凝集，与单克隆抗-B 多次离心后出现“油煎蛋”样混合凝集外观。与单克隆抗-B 表现为正常亲和力。与抗-H 呈强阳性反应。毛细管离心后近心端和远心段结果相同，均仍表现出与原始结果相同的混合视野。与单克隆抗-B 不凝集部分的红细胞再次检测为 O 型，与单克隆抗 B 凝集部分的红细胞经二硫苏糖醇处理后再次检测为 B 型。该样本经过 ABO 测序虽未检测到 3 个以上等位基因，但发现 B 基因特征突变点位置出现小峰，B 基因扩增强度较其他基因更弱，说明 B101 等位基因的拷贝数比 O01 等位基因低，不同于 B101/O01 杂合。
结论 血液病、造血干细胞移植、非同型输血均可导致血型鉴定出现混合视野，可通过临床资料以及毛细管离心技术进行排除。先天性嵌合体血型是导致混合视野的一个罕见原因，本例为 B/O 嵌合体血型在排除上述后天因素后需要与 B3 亚型进行鉴别，B3 亚型亲和力显著减低，基因检测可发现特征性突变。正确对嵌合体血型进行识别对输血安全及亲子鉴定有重要意义。

PU-4004

遗传性易栓症患者非血栓急性期时血浆标志物的变化及意义

李蕾、吴希、武文漫、丁秋兰、王学锋
上海交通大学医学院附属瑞金医院

背景 遗传性抗凝蛋白缺陷症患者具有多部位或反复血栓形成倾向，因此，及时准确地诊断静脉血栓栓塞形成（VTE）对该类患者的管理和治疗至关重要。
方法 选取 100 例未在 VTE 急性期的遗传性抗凝蛋白缺陷患者（TPs）和 100 例健康对照（HCs），检测以下指标：凝血酶-抗凝血酶复合物（TAT），纤溶酶-α2-纤溶酶抑制剂复合物（PIC），组织型纤溶酶原激活物/纤溶酶原激活物抑制物-1 复合物（t-PAIC）和可溶性血栓调节蛋白（sTM），比较上述指标的组间差异。
结果 虽然 TPs 组的 TAT，PIC，t-PAIC 和 sTM 的水平显著高于 HCs 组，但是 70％TPs 的上述四种生物标志物结果属于正常参考范围。26％的 TPs 检测到 PIC 升高（伴或不伴 TAT 升高），这表明患者体内存在纤溶和凝血功能的激活。与无 VTE 史的 TPs 相比，有 VTE 史的 TPs 血浆中 sTM 水平显著降低，而其他三个生物标志物仅显示出轻度升高。与发生反复血栓事件的 TPs 相比，发生单次血栓事件的患者 tPAI-C 水平明显降低，而 TAT，PIC 和 sTM 水平与血栓事件次数无关。
结论 大多数遗传性易栓症患者在 VTE 非急性期时，体内的凝血、纤溶和内皮功能处于代偿状态；男性易栓症患者发生凝血和纤溶系统同时激活的可能性高于女性患者，而女性患者更容易出现内皮细胞损伤。四种生物标志物（TAT、sTM、PIC 和 t-PAIC）的单次检测结果难以预估易栓症患者的血栓形成风险，未来的研究应重点关注其在易栓症患者 VTE 非急性期的动态监测，探究该四项生物标志物在 VTE 的早期诊断、推测病情进展和监测预后中的作用。

PU-4005

某品牌微柱凝胶卡漏检 cisAB 型 1 例

梁路石
东南大学附属中大医院

目的 对一例某品牌微柱凝胶法全自动血型仪判读为正常 AB 型而玻片法提示为疑似 AB 亚型（AB_{weak}）的标本进行进一步鉴定并加以分析。
方法 采用试管法复检 ABO 血型并增加与抗-A_1 和抗-H 的反应，检测亲和力并进行分子生物学检测
结果 试管法与抗-A 凝集强度为 4+，与抗-A_1 不凝集，与抗-B 凝集强度为 2+，自身对照为阴性，通过二次离心、4℃孵育等增强实验检出弱的不规则抗-B，血清学格局为 A_2B_x。H 抗原增强，与对照 O 细胞与抗-H 的凝集强度相近。与单克隆抗-B 标准血清凝集时间显著延长，表现出低亲和。基因型为 CisAB01/O01。
结论 微柱凝胶卡存在因填充的单克隆抗体效价过高和/或使用了增强剂以致检测体系灵敏度过高的问题，其可能导致部分亚型的弱凝集表现为正常凝集强度而不能被正确识别，是一种易被忽视的且可能直接导致临床不良后果的 ABO 亚型漏检原因，一味追求高效价、高灵敏度是误区，必须引起重视。当前 ABO 血型鉴定质控品及质控规则存在漏洞，仅设置强阳性和阴性为靶值不能识别出这种失控状态。若单独使用单一品牌微柱凝胶卡检测 ABO 血型即使正反定型一致、质控在控仍可能出现错误结果，存在安全隐患。玻片法 ABO 血型鉴定与非常规试验的亲和力检测手法相似，一定程度上可以通过反应出的弱凝集或相异于微柱凝胶卡的凝集结果和低亲和表现而提示出 ABO 亚型的可能，合理的利用“不灵敏”的玻片法作为微柱凝胶卡的补充，是解决此问题的一个选择。

PU-4006

不同程度的溶血对同型半胱氨酸检测结果的影响

王波、张明亮
合肥金域医学检验实验室有限公司

目的 探讨标本溶血对同型半胱氨酸（Homocysteione，Hcy）检测结果的影响。
方法 选取 2020 年 3 月-2020 年 6 月送检合肥金域医学检验实验室同型半胱氨酸 20 例，其中血清 10 例，肝素抗凝全血 10 例，20 例标本均无溶血、脂血、黄疸，溶血标本采用两种方法制备。方式 1：分别为将 10 例正常血清采用 BecKman Coulter AU5800 全自动生化分析仪检测 HCY 结果，然后用血红蛋白液按不同浓度配置成溶血程度为 5g/L、10g/L、15g/L、20g/L、25g/L、30g/L 的系列血清标本；方式 2：将 10 例肝素钠抗凝全血标本离心后采用 BecKman Coulter AU5800 全自动生化分析仪检测 HCY 结果，然后采用注射器抽打混匀，根据美国临床和实验室标准化协会(CLS I)的文件要求制备轻度溶血及重度溶血的血清标本。采用 BecKman Coulter AU5800 全自动生化分析仪检测上述 40 例血清 Hcy 浓度变化，并与正常血清标本 Hcy 浓度进行对比。
结果 两种方法制备的溶血标本相对与未溶血标本均处于增高趋势，差异具有统计学意义 $P<0.05$
结论 检验工作中，影响临床结果准确性的有很多因素，其中以溶血最常见，了解标本溶血对检验结果的影响及溶血后的处理方法，可以更好地进行检验工作，并提高检验结果的准确性和可信性。

PU-4007

高通量易栓症基因检测 PANEL 的临床应用研究

李蕾、吴希、武文漫、丁秋兰、王学锋
上海交通大学医学院附属瑞金医院

目的 易栓症是指由于遗传性或获得性危险因素导致患者易发静脉血栓栓塞症（VTE）的一类疾病，其中遗传性抗凝蛋白缺陷症是亚洲静脉血栓患者最主要的危险因素。及时准确的表型和基因诊断不仅对易栓症患者的血栓预防和诊疗至关重要，还为发现新的致栓机制奠定基础。研发高效、准确、简单、实用的易栓症遗传性危险因素的基因检测方法，有助于我国易栓症患者的病因诊断和治疗指导。本研究遵循“临床诊断-家系调查-表型检测-基因分析-分子发病机制探究”的研究模式，对 411 例易栓症患者的表型及遗传背景进行分析。

方法 收集上海交通大学医学院附属瑞金医院血栓与止血门诊 411 例静脉血栓患者的临床及家系资料，并对其进行遗传性及获得性易栓症表型检测；通过文献研究和人类孟德尔遗传学数据库检索，遴选出 35 种与血栓发生相关的基因，组成易栓症基因检测 Panel，采用二代测序及 CNVplex®高通量拷贝数检测技术对该 Panel 进行点突变、小缺失/插入及拷贝数变异检测。

结果 411 例静脉血栓患者中有 267 例携带基因突变，突变检出率为 65.0%。其中，62.2%的患者携带单一基因突变，13.5%携带单基因的复合杂合突变，另有 24.3%携带 2 种及以上的基因突变。在 267 例携带基因突变的患者中，有 220 例患者携带抗凝蛋白基因（SERPINC1、PROS1 和 PROC）的突变，有 47 例患者携带其他 22 种基因（F2、F5、F9、F12、PROCR、THBD、SERPIND1 及 PLG 等）的突变，其中部分突变（F2 基因 R596Q 及 R541W、F9 基因 R384Q 突变及 JAK2 基因 V617F 突变等）被证实与静脉血栓发生相关。拷贝数检测发现，有 31 例患者存在拷贝数变异，以 PROS1 及 PROCR 基因为主。另外，在 82 例存在获得性血栓危险因素（抗磷脂综合征、手术或妊娠等）的患者中，61.0%的患者携带遗传性血栓危险因素。56 例患者实验室表型检测结果均为正常，而易栓症基因检测 Panel 结果显示，其中 20 例患者携带致病性基因突变。72 例患者因处于血栓急性期或口服抗凝药物期间，无法进行表型检测，经易栓症基因检测 Panel 分析发现，其中 32 例患者携带致病性基因突变。

结论 本研究建立的易栓症基因检测 Panel 可以快速、有效及准确地对遗传性静脉血栓危险因素进行筛查。对存在获得性血栓危险因素的患者仍有必要进行遗传分析。根据基因检测结果，可评估患者及其家系成员血栓发生风险的大小，制定相应的预防治疗方案，预防血栓的发生或复发，减少血栓后综合征的发生，值得在临床上广泛推广应用。

PU-4008

BNP、MYO、D-D 水平对慢性心衰患者心衰程度的临床意义分析

刘琳琳
陆军军医大学第二附属医院（新桥医院）

目的 探讨血浆 BNP、MYO、D-D 水平及 LVEF 对慢性心衰患者心衰程度的临床意义分析。

方法 选择 2016 年 1 月—2018 年 1 月于新桥医院心内科住院的慢性心力衰竭患者 77 例作为心衰组，根据美国纽约心脏病学会（NYHA）心功能分级标准，本研究中心功能Ⅰ级患者 15 例，心功能Ⅱ级患者 19 例，心功能Ⅲ级患者 22 例；心功能Ⅳ级患者 21 例；选取同期体检的健康老年人 80 例作为对照组。比较各组 B 型利钠肽（BNP）、肌红蛋白（MYO）、D-二聚体（D-D）水平及左心室射血分数（LVEF），分析 BNP、MYO、D-D 水平、LVEF 的相关性。

结果 心衰组 BNP、MYO、D-D 水平高于对照组，差异有高度统计学意义（P < 0.01）。心功能分级由Ⅰ级到Ⅳ级，血浆 BNP、MYO、D-D 水平逐渐升高，LVEF 逐渐降低，差异有高度统计学意义（P < 0.01）；按心脏射血分数<55%、55%-65%、>65%分组，血浆 BNP、MYO、D-D 水平逐渐升高，LVEF 逐渐降低，差异有高度统计学意义（P<0.01）；心力衰竭患者血浆 MYO、D-D 水平与 BNP 均呈正相关（r = 0.65、0.74），与 LVEF 均呈负相关（r =-0.52、-0.66），差异有统计学意义（P< 0.01）；ROC 曲线分析显示，血浆水平联合检测诊断心功能Ⅲ级、Ⅳ级 CHF 的灵敏度、特异度、约登指数、ROC 曲线下面积较各指标单项诊断时高。
结论 心力衰竭患者的 BNP、MYO、D-D 水平明显升高，且三者与心功能分级呈正相关，与 LVEF 呈负相关，因此可作为评估心力衰竭严重程度的重要指标。

PU-4009

TCT 联合 HPV 分型检测对宫颈癌筛查的应用价值探讨

鲍渝霞
昆明医科大学第一附属医院
云南省实验诊断研究所
云南省检验医学重点实验室

目的 比对薄层液基细胞学（TCT）检查、人乳头瘤病毒（HPV）分型检测及二者联合检测在宫颈病变筛查中的差异，经宫颈病理学组织检查确诊，探讨上述两种方法及其联合使用在宫颈病变筛查中的诊疗价值。
方法 收集 2018 年—2020 年里，我院收治并行 HPV、TCT 和宫颈活检的 173 例患者检查资料，以组织学检查为确诊标准，回顾性分析两种检测方法在宫颈病变中的早期筛查效果。
结果 173 例患者，组织活检呈阳性 166 例，阴性 7 例。HPV 检测呈阳性 145 例（阳性率 83.82%）；TCT 阳性 139 例（阳性率为 83.24%）。当两者联合检测时，其阳性率（93.6%）和与病理诊断的符合率（95.95%）均大于 HPV、TCT 单独检测，且其假阴性率、假阳性率相较独立检测均明显减低。
结论 HPV+TCT 联合检查提高早期宫颈病变筛查的准确度、阳性率和阳性预测值，并降低其筛查的假阴性率、假阳性率；对早期宫颈病变及宫颈癌的发现具有重要意义，在临床诊治方面应用价值高，推荐广泛应用。

PU-4010

血浆凝血因子活性测定临床应用的初步调查

鲍渝霞
昆明医科大学第一附属医院
云南省实验诊断研究所
云南省检验医学重点实验室

目的 通过对昆明医科大学第一附属医院 2015 年 5 月至 2016 年 3 月做血浆凝血因子活性检测的标本数量统计调查，探讨临床医师对血浆凝血因子活性检测的应用状况。
方法 调查性研究，对我院做凝血因子活性检测的标本数量分别做总体、分组、分布情况做统计分析。
结果 调查期间，70894 份凝血检测标本中仅有 253 份检测血浆凝血因子活性，占总数的 0.36%。所有检测凝血因子活性标本中，凝血四项正常的占 15.2%，凝血四项异常的占 84.98%。凝血因子活性检测主要集中在血液内科 45.45%，儿科 13.04%，EICU 12.65%，急诊输液 10.28%，方便门

诊 9.09%,其他科室占 9.49%。20 例确诊为血友病 A 的住院患者住院期间做 FⅧ检测一次的有 4 例，大于两次的有 16 例。

结论 1.临床医师对血浆凝血因子活性测定的临床意义不甚了解，在临床工作中使用极少。2.临床科室中血浆凝血因子测定主要集中在小部分科室，如血液内科及儿科，其余应常规检测凝血因子活性的科室，如血管外科、消化内科等，在调查期间凝血因子活性因子测定标本极少。3.临床对血友病患者凝血因子检测仍存在不规范现象。

PU-4011

血清外泌体 circRNAs 的测序分析示 circ-PNN 可作为结肠直肠癌潜在的生物标志物

谢艳、王传新、杜鲁涛
山东大学第二医院

目的 本研究初步建立起结直肠癌血清外泌体 circRNAs 差异表达谱，对血清外泌体进行提取、鉴定，筛选出用于结直肠癌诊断的 circRNAs 分子，探究其作为肿瘤标志物的诊断效能，为阐明 circ-PNN 在结直肠癌发生发展中的作用机制研究提供思路。

方法 研究前期对结直肠癌患者及健康对照者血清外泌体 circRNAs 进行测序分析，初步筛选出在多个测序样本中均具有表达的 circRNAs 分子作为候选分子。随后，我们通过沉淀剂法从结直肠癌患者及健康对照者血清中分离并提取外泌体。并通过透射电子显微镜、免疫印迹技术、纳米粒径分析技术对所提取外泌体进行鉴定。针对候选 circRNAs 分子环化位点设计 divergent 引物，通过琼脂糖核酸凝胶电泳验证引物的特异性，sanger 测序检测 circRNAs 环化位点，放线菌素 D 实验证明 circRNAs 较 mRNAs 稳定性强。随后，通过实时荧光定量 PCR(RT-qPCR)技术在训练集（88 对结直肠癌患者及 88 对健康对照者）样本中检测候选 circRNAs 分子的表达情况。同时采用受试者工作特征曲线（ROC）分析血清外泌体中差异表达的 circRNAs 分子对结直肠癌的诊断效能。训练集样本中表达趋势与测序结果一致的 circRNAs 分子进入验证阶段。随后，在另一独立样本集，即验证集样本（58 对结直肠癌患者及 58 对健康对照）中检测候选 circRNAs 表达情况，并评估其诊断价值。最后，我们用 Targetscan 和 Miranda 等软件预测出和 circ-PNN 有结合靶点的 miRNAs 分子及其下游 mRNAs，并通过 RT-qPCR 验证 miRNAs 与 circ-PNN 在结直肠癌血清外泌体中表达水平之间的关系。

结果 在训练阶段，我们通过 RT-qPCR 实验技术分析证实 circ-PNN 在结直肠癌血清外泌体中高表达。在训练集和验证集中， circ-PNN 对结直肠癌的诊断效能分别为 0.855 和 0.826。最后我们构建出 circRNA-miRNAs-mRNAs 互作网络图，并验证得出结直肠癌患者血清外泌体 hsa-miR-6833-3P、hsa-let-7i-3p and hsa-miR-1301-3P 的表达水平与 circ-PNN 呈负相关。

结论 本研究通过分析、验证血清外泌体的 circRNAs 高通量测序结果，发现 circ-PNN 在结直肠癌外泌体中高表达，对结直肠癌的诊断具有良好的敏感性和特异性，可以较好地区分结直肠癌患者和健康对照者，因此可作为结直肠癌诊断的潜在生物标志物。

PU-4012

急性脑梗死患者氯吡格雷抵抗现象的临床研究

朱兵兵、刁艳君、刘家云
空军军医大学西京医院

目的 研究急性脑梗死患者的氯吡格雷的发生率，探讨其临床相关因素。

方法 收集急性脑梗死 102 例患者，服用氯吡格雷 75mg/d，连续 7 天进行治疗，抑制血小板聚集，预防血栓再发。服用最后一天于 24h 内空腹抽取静脉血，使用血小板功能分析仪（Verify Now）检测其血小板抑制情况，
结果 102 例急性脑梗死患者中氯吡格雷抵抗发生率为 26%。抵抗组和参照两组患者的性别构成比、糖尿病史、高血压史，血脂的 差异均有统计学意义(P ＜0. 05) ，氯吡格雷抵抗组中以男性居多，高血压，高血脂患者出现氯吡格雷抵抗的比例明显升高。
结论 氯吡格雷抵抗在急性脑梗死服用氯吡格雷的患者中是存在的，氯吡格雷在临床使用中患者响应程度存在个体差异，本研究显示在男性，有糖尿病史、高血压史，高血脂的患者应警惕氯吡格雷抵抗的发生，在临床治疗过程中如果发现氯吡格雷抵抗存在应及时调整用药。对服用氯吡格雷的患者进行血小板功能分析，明确药物是否达到预期治疗效果，避免心脑血管不良事件的发生。

PU-4013

急性脑梗死患者 CYP2C19 基因多态性与凝血指标相关性研究

朱兵兵、刁艳君、刘家云
空军军医大学西京医院

目的 探讨急性脑梗死患者 CYP2C19 基因多态性与凝血指标的相关性。
方法 选取我院 2019.4-2020.4 年急性脑梗死患者常规服用氯吡格雷超过 1 个月的 108 例为研究对象，采用 DNA 微阵列芯片法检测其 CYP2C19 基因型，运用 CS5100 分析仪凝固法检测凝血指标 PT APTT FIB，免疫比浊法检测 D-dimer FDP。观察 CYP2C19 基因多态性与凝血指标的相关性。
结果 108 例急性脑梗死患者中快代谢型（快代谢组，CYP2C19*1/*1）患者为（49）例，占比 45.4%；中代谢型（中代谢组，CYP2C19*1/*2、CYP2C19*1/*3）为（35）例，占比 32.4%；慢代谢型（慢代谢组，CYP2C19*2/*2、CYP2C19*2/*3）最少，为（24）例，占比 22.2%。
慢代谢组 FIB 及 D-dimer FDP 水平高于快代谢组及中代谢组，差异有统计学意义（P＜0.05）。
慢代谢组 PT APTT 水平低于高于快代谢组及中代谢组。
结论 使用常规剂量的氯吡格雷治疗存在个体化差异，CYP2C19 基因慢代谢型急性脑梗死患者，可考虑更换新的药物或增加剂量进行治疗。CYP2C19 基因型与 PT APTT FIB 和 D-dimer FDP 凝血指标具有一定相关性，检测急性脑梗死患者的 CYP2C19 基因多态性与凝血指标相结合，可以评估患者预后及心脑血管事件风险，为临床诊断提供思路。

PU-4014

临床常用药物对血浆纤维蛋白原水平的影响分析

颜楠
空军军医大学西京医院

目的 通过观察与探讨临床上两种常用蛇毒类凝血酶制剂，白眉蛇毒血凝酶（邦亭）、东菱迪芙(巴曲酶)与两种肝毒性药物，丙戊酸(valproate，VAP)、培门冬酶(pegaspargase，PEG—ASP)四种药物在用药治疗前后有显著差异的凝血指标纤维蛋白原（FIB）水平的变化，为临床提供用药指导参考，并对因该四种药物导致严重低纤维蛋白血症可能发生出血风险的病人向临床医生做出提示。
方法 回顾性分析 2018 年 10 月 31 日至 2020 年 l0 月 31 日在空军军医大学附属西京医院住院治疗的 200 例 FIB 降低(<1．5g／L)的患者的临床资料变化。分为有产物组与无产物组。将泌尿外科与耳鼻喉科使用蛇毒类凝血酶制剂药物的病例 70 例定为有产物组（其中使用邦亭的患者 38 例，使用巴曲酶的患者 32 例）；再将神经科与血液科使用肝毒性药物的病例 130 例定位无产物组（其中使用 VAP 的患者 60 例，使用 PEG—ASP 的患者 70 例）。分别于患者使用药物治疗前后检测常规凝血六项指标，做好记录并观察其水平变化。

结果 两组病例用药治疗前与治疗后的凝血相关指标结果比较。FIB 水平在用药治疗前后比较差异有统计学意义（P＜0.05）。
结论 FIB 水平在使用该四种药物前后的显著差异变化可以为临床提供用药指导参考，并且可以帮助提醒临床医生一定要掌握其适应症及使用剂量并且严密观察临床表现及凝血功能,避免导致严重的低纤维蛋白血症引起的出血风险。当遇有严重的凝血功能改变时，应及时减少药物用量或是停止用药，有必要时使用 FIB 浓缩物、新鲜冰冻血浆或输注冷沉淀等方法以纠正凝血功能的异常状态，以避免临床发生严重的出血性事件。

PU-4015

CircKLHL8, a potential biomarker of gastric cancer, promotes the proliferation and metastasis of gastric cancer cell lines by sponging hsa_miR_29a_3p through PI3K-AKT signaling pathway

Mei Tao
Affiliated Hospital of Nantong University

Background Gastric cancer (GC) is a malignant tumor with insidious onset and more prevalent in East Asian populations. It ranks the fifth most frequent cancer and is the third leading cause of cancer mortality. Upper gastrointestinal endoscopy is the gold standard for GC diagnosis, with a high detection rate. Since this method is invasive and has the risk of bleeding and perforation, it is necessary to search for non-invasive markers for auxiliary diagnosis. Circular RNA (circRNA) is a novel non-coding RNA with a circular structure. CircRNAs are expected to be potential biomarkers due to their high abundance and good stability. Our aim is to find an effective and non-invasive method to distinguish gastric cancer (GC) patients from healthy persons and other stomach diseases such as gastritis patients.
Methods Structure characteristic of circKLHL8 was verified by Sanger sequencing, Actinomycin D assay and RNase R assay. Relative expression of circKLHL8 in GC cells, plasma and tissues was detected by quantitative real-time polymerase chain reaction (RT-qPCR). Besides, we conducted CCK8 assay and clone formation assay to confirm the ability of proliferation in vivo. Transwell assays including migration and invasion were used to show the ability of metastasis. Finally, data were analyzed by Graph Prism software 6.0 and SPSS software 20.0. The data were shown as the means±SD obtained in triplicate assays.
Results Our present work shows that circKLHL8 (has_circ_0002538) is more stable than their linear transcript. CircKLHL8 is markedly up-regulated in 72 pairs of GC tissues, 82 GC plasma samples and 60 gastritis plasma samples, while down regulated in 39 postoperative plasma specimens from GC patients. The receiver operating characteristic (ROC) curve analysis shows that circKLHL8 appears to be more sensitive and specific at diagnosing GC patients from both healthy (sensitivity: 79%, specificity: 88%) and gastritis individuals (sensitivity: 75%, specificity: 82%) than CEA and CA199. The combination of circKLHL8, CEA and CA199 rather than a single index improves the diagnostic efficiency in GC. CircKLHL8 levels in GC tissues and plasma are also associated with clinical characteristics and severity, including age, histological differentiation, the T stage, lymphatic metastasis as well as TNM stage in GC patients. Moreover, in-vitro experiments show that circKLHL8 facilitates the proliferation and metastasis of GC cells via sponging hsa-miR-29a-3p through PI3K-AKT signaling pathway.
Conclusions Overall, this study provides new evidence that circKLHL8 can be a diagnostic biomarker of GC and reveals the potential carcinogenic mechanisms of circKLHL8, providing a novel target for GC treatment.

PU-4016

干化学法检测尿微量白蛋白与尿肌酐比值与生化免疫透射比浊法/酶法检测结果的对比分析

王玲玲、曹宝华
中山大学附属第三医院

目的 尿液分析是临床上最常见的三大常规之一，采用干化学试纸检测尿微量白蛋白与尿肌酐的比值（albumin-to-creatinine ratio, ACR）对临床上快速筛查早期肾脏损伤和糖尿病等疾病具有重要意义。本文通过对比分析干化学检测 ACR 与生化标准方法免疫透射比浊法/酶法的结果，评价干化学法测定 ACR 的准确性，建立临床使用干化学法快速筛查早期肾损伤等疾病的可行方法。
方法 收集 121 例新鲜尿液标本，离心后平均分为两份，一份采用日立 7600 及免疫透射比浊法/酶法检测尿微量白蛋白与尿肌酐的比值（ACR），并作为标准方法；另一份采用 Sysmex UC3500 尿液分析仪和其配套 NY-UC-11A 干化学试纸条检测尿 ACR。通过计算其敏感度、特异度、误诊率、约登指数等评价干化学法检测 ACR 的能力；通过 Kappa 检验评价结果的一致性。
结果 与免疫透射比浊法/酶法相比，干化学法检测 ACR 的灵敏度为 92.31%，特异度为 85.37%，误诊率为 14.63%，漏诊率为 7.69%；约登指数为 0.78；阳性预测值 75.00%，阴性预测值 95.89%；阳性似然比为 363，阴性似然比为 0.09；Kappa= 0.732，P<0.001。
结论 结果证明干化学和免疫透射比浊法/酶法检测尿 ACR 诊断结果具有较高的一致性，且干化学法具有较高的灵敏度，可以快速提示临床对阳性结果及时采取进一步检查。总之，干化学法检测尿微量白蛋白与尿肌酐比值的方法可作为临床早期快速筛查糖尿病前期和早期肾脏损伤的可靠筛选工具。

PU-4017

浅谈体液常规细胞学检查在痛风性关节炎诊断中的应用

唐丽红、柴树红
乌鲁木齐市友谊医院

目的 探讨体液常规细胞学检查在痛风性关节炎中的临床意义。
方法 常规送检的关节腔积液离心浓集细胞，制片，染色，镜检进行形态学检查。
结果 关节腔积液常规细胞学检查检出尿酸钠结晶。
结论 在关节腔积液中查见尿酸钠结晶，可及时为临床对患者的病情诊断提供可靠依据，并且通过早发现早诊断早治疗使患者获得更好的治疗效果。

PU-4018

血常规及凝血指标对骨创外科患者下肢深静脉血栓形成的预测价值

唐莹莲
云南省第二人民医院

目的 探究骨创患者血常规和凝血指标对其下肢深静脉血栓形成的预测价值 。
方法 收集 2018 年 1 月至 2020 年 12 月期间骨创外科发生下肢深静脉血栓的患者 160 例(DVT 组)，随机筛选同期没有发生下肢深静脉血栓的患者 170 例(非 DVT 组)为对照组。采用 t 检验、Mann-Whitney U 检验比较两组血常规（白细胞计数、中性粒细胞计数、淋巴细胞计数、中性粒细胞/淋巴细胞、单核细胞计数、红细胞计数、红细胞分布宽度、血红蛋白、血小板计数、血小板计数/淋巴

细胞、红细胞分布宽度/血小板计数）和凝血指标（D-二聚体、纤维蛋白(原)降解产物、凝血酶原时间、活化部分凝血活酶时间、纤维蛋白原），对两组有差异的影响因素进行 logistic 回归分析。
结果 两组患者中性粒细胞/淋巴细胞（NLR）、血小板计数/淋巴细胞（PLR）、红细胞分布宽度/血小板计数（RPR）、D-二聚体、纤维蛋白(原)降解产物（FDP）差异均存在显著性（P<0.05），多因素 logistic 回归分析显示中性粒细胞/淋巴细胞（NLR）、血小板计数/淋巴细胞（PLR）、纤维蛋白(原)降解产物（FDP）升高可能是骨创患者发生下肢深静脉血栓的主要危险因素。
结论 中性粒细胞/淋巴细胞（NLR）、血小板计数/淋巴细胞（PLR）、纤维蛋白(原)降解产物（FDP）三项指标对于预测骨创患者下肢深静脉血栓的形成有一定的提示作用。

PU-4019

Serum glycocholic acid-to-total bile acids ratio is negatively associated with non-alcoholic fatty liver disease: a retrospective cross-sectional study

Hu Li、Jin Ma、Li Chen、xinxin Zhang
Department of Infectious Disease, Research Laboratory of Clinical Virology, Ruijin Hospital, Shanghai Jiaotong University, School of Medicine

Background Bile acids play an essential role in the progression of non-alcoholic fatty liver disease (NAFLD). This study aimed to investigate the association of serum glycocholic acid (GCA) level, total bile acids (TBA) level, and the GCA-to-TBA ratio with NAFLD in the general population.
Methods A total of 6708 individuals were recruited retrospectively from our hospital, and 2859 (42.6%) were diagnosed with NAFLD. NAFLD diagnosis was based on evidence of fatty liver by abdominal ultrasonography without excessive alcohol consumption or other known liver diseases. Demographic characteristics and biochemical data were compared between individuals with NAFLD and those without NAFLD. Multivariate logistic regression analysis was performed to determine the association of serum TBA level, GCA level, and GCA-to-TBA ratio with NAFLD.
Results The serum TBA and GCA levels were significantly higher in individuals with NAFLD than in those without NAFLD [2.8 (2.0-4.2) μmol/L vs. 2.5 (1.8-3.7) μmol/L, and 1.30 (1.10-1.53) μg/mL vs. 1.28 (1.08-1.50) μg/mL, respectively, all p<0.001], whereas the serum GCA-to-TBA ratio was lower in individuals with NAFLD than in individuals without NAFLD [0.44 (0.33-0.60) vs. 0.48(0.36-0.64), p<0.001]. Logistic regression analysis showed GCA-to-TBA ratio was negatively associated with NAFLD after adjusting for confounding factors [odds ratio: 0.81, 95% confidence interval (CI): 0.71-0.92, p<0.001]. The area under the receiver operating characteristic of GCA-to-TBA ratio-based model for NAFLD diagnosis was 0.84 (95% CI: 0.83-0.85).
Conclusion The serum GCA-to-TBA ratio is negatively associated with NAFLD and may serve as a risk indicator.

PU-4020

初步研究谷氨酸的摄入对血小板聚集率的影响

何穗芬[1]、郭勇晖[1]、刘思洁[2]
1. 南方医科大学珠江医院
2. 南方医科大学

研究目的 血小板活化时对谷氨酸的摄入显著升高，已知此作用由血小板膜上的兴奋性氨基酸转运体（excitatory amino acid transporters，EAATs）所介导，鉴于 EAATs 对血小板活化的作用和意义至今尚不清楚，本研究设计在体外抑制正常血小板的 EAATs 活性，以探究谷氨酸的摄入对血小板聚集功能的影响。

方法 以健康成人的血小板为研究对象，使用非选择性 EAATs 抑制剂——DL-TBOA（D, L-threo-β-benzyloxyaspartate）预处理富血小板血浆（platelet rich plasma，PRP），分别选择凝血酶（thrombin，TH）、花生四烯酸（arachidonic acid，AA）、二磷酸腺苷(adenosine diphosphate，ADP)、胶原（collagen，Coll）和肾上腺素（Epinephrine，EPI）为诱导剂，以散射比浊法为原理的血小板聚集仪检测血小板的最大聚集率，进而初步探讨 EAATs 介导的谷氨酸摄入对血小板聚集反应的作用和意义。
结果 a）越高浓度的 DL-TBOA 对 TH 诱导的血小板聚集率抑制作用越强；b）TH 诱导下，男性的血小板聚集功能对 DL-TBOA 的可耐受浓度较女性明显降低；c）当正常血小板暴露于 8 mM DL-TBOA 时，ADP、Coll 和 EPI 诱导的血小板聚集反应可被完全抑制，AA 诱导的血小板最大聚集率也明显降低。
结论 EAATs 参与调控血小板的聚集反应，其介导的谷氨酸摄入可能是血小板实现正常聚集的必要条件。

PU-4021

北京某地区 5 岁以下腹泻患儿 A 群轮状病毒感染分析

凌云映[1]、赵国军[2]
1. 北京华信医院（清华大学第一附属医院）
2. 河北北方学院

目的 回顾性分析本院儿科门诊 5 岁以下腹泻患儿 A 群轮状病毒感染的好发季节、年龄分布、性别差异，以了解 A 群轮状病毒感染的现状，为预防、鉴别诊断和治疗婴幼儿腹泻提供参考依据。
方法 收集来自 2017 年 1 月至 2019 年 12 月 6367 例儿科门诊 5 岁以下腹泻患儿的粪便样本，用胶体金方法进行 A 群轮状病毒抗原检测并显微镜观察便常规，采用 SPSS22.0 软件进行分析，阳性率的比较采用卡方检验，轮状病毒阳性率与便常规镜检检测结果采用 Kappa 一致性检验。
结果 在 6367 腹泻患儿标本中有 2313 例 A 群轮状病毒呈阳性，阳性率为 36.33%，男女阳性率分别为 35.63%和 37.28%，差异无统计学意义（P>0.05）；0~<1 岁、1~<2 岁、2~<3 岁、3~<4 岁、4~<5 岁 A 群轮状病毒阳性率分别为 32.15%、42.22%、37.06%、26.83%、17.93%，其中 0~<1 岁、1~<2 岁、2~<3 岁腹泻患儿 A 群轮状病毒阳性率明显高于其他年龄组，尤其以 1~<2 岁的阳性率最高，差异有统计学意义（P<0.05）；A 群轮状病毒感染季节分布明显，以 11、12、1、2、3 月为发病高峰，阳性率分别为 42.41%、51.04%、50.21%、48.45%、40.34%；轮状病毒阳性便常规性状以黄色糊状为主，占 52.01%，水样便或蛋花汤性状便次之，占 32.34%；经 Kappa 一致性检验，A 群轮状病毒阳性率与便常规中的红细胞、白细胞的检出率一致性差，与脂肪滴的检出率有较弱一致性。
结论 A 群轮状病毒感染是婴幼儿腹泻的重要原因，该地区 11~12 月和 1~3 月为高发期，3 岁以下是其易感人群，其粪便中脂肪滴的检出率与轮状病毒阳性率有相关性。

PU-4022

VWF 相关检测作为肝脏疾病预后指标的价值探讨

杨铭康[1,2]、刘禹[1]、许冠群[1]、梁茜[1]
1. 上海交通大学医学院附属瑞金医院检验科
2. 上海交通大学医学院检验系

目的 全面评估血管性血友病因子（von Willebrand factor，VWF）及其相关检测与肝脏疾病严重程度的相关性，为该类疾病患者预后及转归提供有价值的非侵入性实验室参考指标。

方法 收集 2020 年 12 月至 2021 年 3 月上海交通大学医学院附属瑞金医院收治的肝病患者共计 147 例，其中轻症组肝病患者 68 例（包括慢性肝炎（未检出肝硬化）组 35 例，肝硬化代偿组 33 例），重症组肝病患者 79 例（包括肝硬化失代偿组 40 例，肝衰竭组 39 例）。检测 VWF 抗原水平（VWF:Ag）、VWF 与胶原结合能力（VWF:CB）、VWF 前肽水平（VWFpp）、VWF 多聚体结构分析、VWF 糖基化修饰差异，并分析各指标与肝脏疾病严重程度的相关性。
结果 VWF:Ag 检测值分别为慢性肝炎（未检出肝硬化）组 162.80%（123.60% ~ 196.10%）、肝硬化代偿期组 163.00%（132.70% ~ 218.25%）、肝硬化失代偿期组 269.35%（212.55% ~ 345.65%）、肝衰竭组 232.30%（171.00% ~ 368.20%），且重症患者组 VWF:Ag 水平显著高于轻症患者组[260.90%（191.5% ~ 349.7%）vs 166.00%（133.03% ~ 209.75%），P＜0.05]。VWF:CB/VWF:Ag 比值在各组间差异无统计学意义（P>0.05）。重症患者组 VWFpp/VWF:Ag 显著高于正常对照组[1.459（1.153 ~ 1.840）vs 1.057（0.907 ~ 1.127），P＜0.05]，提示重症患者组 VWF 清除加快，且可能与 VWF 糖基化修饰变化有关（O 型糖链末端脱唾液酸以及半乳糖残基的暴露）。ROC 曲线分析显示， VWF:Ag 检测值诊断重症肝病的 AUC 为 0.783（95% CI:0.708~0.859，P＜0.05），当界值为 218.3%时，其诊断的敏感度为 68.4%，特异度为 84.8%，阳性预测值 92.7%，阴性预测值 48.7%，诊断准确率为 72.7%。
结论 随着肝病进展，患者的 VWF:Ag 水平表现为进行性升高，且伴 VWF 清除速率加快。相比常规肝功能指标，血浆 VWF 水平在肝病诊断与预测疾病进展过程具备更优的性能。

PU-4023

全自动血凝仪 ACT TOP 700 性能验证

覃月华
南方医科大学珠江医院

近年来，随着现代医学对血栓与出血方面不断地深入认识，临床实验室对该方面有关的检测项目指标不断增多[1]。全自动血凝分析仪在各大医院应用广泛，为临床实验室在血栓与出血方面疾病的预防、诊断以及治疗提供了更加精准的指标。根据 ISO15189《医学实验室质量和能力的专用要求》规定，实验室全自动设备应通过性能验证，并符合相关检验所需要求，方可使用。本研究根据对 ACT TOP 部分凝血项目进行精密度、准确度、携带污染率、线性以及同型号仪器间比对等结果进行系统性的验证。结论各项目中样本针携带污染率 K1 小于 10%，精密度 CV≤15%，均符合要求，参考区间验证基本通过。

PU-4024

血栓弹力图相关参数与短暂性脑缺血后进展为脑梗死的相关性分析

张静、吕毅、陈派强、李明月、高秀叶
郑州颐和医院

目的 短暂性脑缺血发作(TIA)是临床常见的缺血性脑血管疾病，反复的 TIA 可发展为脑梗死，具有较高的致残率和致死率。其纤溶障碍和血液高凝状态是 TIA 进展或反复发作的主要因素。血栓弹力图（下文简称 TEG）能够一定程度上动态反应凝血因子、纤维蛋白原、血小板功能及纤溶情况等，是评价凝血功能状态较为敏感的指标，本文主要探讨 TEG 相关参数与短暂性脑缺血后进展为脑梗死的相关性。
方法 收集 2019 年 12 月至 2020 年 12 月本院诊治的 96 例 TIA 患者，所有患者均经过 MRI 或 CT 确诊，并对以上患者随访 3 个月，按疾病进展分为脑梗死组与非脑梗死组。所有患者均在就诊 24h 之内进行 TEG 检测，比较 2 组 TEG 各参数指标：凝血因子反应时间（R）、血细胞凝块形成时间

（TK）、血细胞凝块形成速率（Angle）及最大振幅（MA）差异，并进行相关性分析。采用 SPSS18.0 医学统计软件进行统计分析，计数资料采用 χ2 检验；计量资料以()表示，比较采用 t 检验，；以 P＜0.05 表示差异具有统计学意义。
结果 脑梗死组的 R 值和 TK 较非脑梗死组低(P<0.05)，Angle 和 MA 较非脑梗死组高(P<0.05)；R 值和 TK 值与脑梗死发生呈负相关性(P<0.05)，Angle 和 MA 与脑梗死呈正相关(P<0.05)。
结论 R 值和 TK 值越长，发生脑梗死风险越低，Angle 和 MA 越低，发生脑梗死风险越低。由此表明，TEG 检测对脑卒中、脑梗死及血栓塞等疾病具有重要的指导价值。临床上应将 TEG 检测和凝血功能检查相结合，更全面有效用于缺血性脑血管疾病的诊断及病情的评估。

PU-4025

获得性血友病 A 的临床分析

刘禹、许冠群、丁秋兰、毛恩强、王学锋、盛慧球
上海交通大学医学院附属瑞金医院

目的 提高临床医师对获得性血友病 A(AHA)的认知。
方法 结合 2019 年 9 月至 2020 年 12 月收治于上海交通大学医学院附属瑞金医院的 3 例 AHA 患者的临床诊治过程及相关文献报道，对 AHA 的临床症状、实验室检查结果、治疗方案及转归情况等进行总结及讨论。
结果 3 例患者均无血友病家族史，无明确诱因下出现皮肤瘀斑、肌肉血肿及肉眼血尿等出血症状。实验室检查结果示活化部分凝血活酶时间(APTT)延长，凝血因子Ⅷ活性(FⅧ:C)下降及凝血因子Ⅷ(FⅧ)抑制物阳性。经止血治疗及抑制物清除治疗后，2 例获得完全缓解，1 例获得部分缓解。
结论 AHA 发病率低，常伴有不同程度的出血症状，给予抑制物清除治疗，以提高其治愈率。

PU-4026

乳腺癌标志物研究进展

张莹
山东大学第二医院

乳腺癌是全球女性死亡率第一的恶性肿瘤。癌胚抗原（CEA）、糖类抗原（CA）15-3、CA125 等血清肿瘤标志物异常表达提示肿瘤的发生风险。CA15-3 过表达被认为与乳腺癌的疾病进展有关,不同临床分期乳腺癌患者血清 CA15-3 的阳性检出率对诊断临床分期有显著优势,灵敏度和特异度较低。但目前认为,某项血清肿瘤标志物单独检测对乳腺癌的阳性检出率较低,对早期筛查及诊断的意义不大,因此,多主张血清肿瘤标志物联合检测以对乳腺肿瘤进行早期筛查和早期诊断。本文将讨论已在临床一定范围内得到应用的肿瘤标志物以及新发现的用于指导乳腺癌临床决策及治疗方案的肿瘤生物标志物与乳腺癌诊断、治疗及预后相关的临床研究。

PU-4027

Bioinformatics Analysis of High Frequency Mutations in Myelodysplastic Syndrome-related Patients

Kun Wu 、Shenju Cheng、Mingxia Shi
First Affiliated Hospital of Kunming Medical University

Myelodysplastic syndrome (MDS) is a group of hematological malignancies that may progress to acute myeloid leukemia.Bioinformatics-based analysis of high-frequency mutationgenes in MDS-related patients is still relatively rare, so we carry out research in order to explore whether high-frequency mutation genes in MDS-related patients can play a reference role in clinical guidance and prognosis. Next generation sequencing (NGS) technology was used to detect 32 mutations of 64 MDS-related patients. We classified the patients'genes and analyzed them by gene ontology (GO) analysis,Kyoto encyclopedia of genes and genomes (KEGG)analysis,protein-protein interaction (PPI) analysis, and combined with gene survival curve of high-frequency mutations. Wediscoveredsome high frequency mutation genes such as ASXL1,DNMT3A,KRAS, NRAS, TP53,SF3B1, and SRSF2. Theoverall survival (OS) of these genes decreased significantly after mutation. These genes play a significant role in biological processes not only play a role in MDS, but also in the occurrence and development of other diseases.Through retrospective analysis, genes associated with MDS-related diseases were found and their effects on the disease were predicted, which provided theoretical basis for clinical and scientific research and opened up the research scope of MDS.

PU-4028

迈瑞 6800 血细胞分析仪在肿瘤患者异型淋巴细胞检出中的应用价值

邓瑶、吴菡、曾丹丹
四川省肿瘤医院

目的 探讨迈瑞 6800 血细胞分析仪异型淋巴细胞报警提示在肿瘤患者异型淋巴细胞检出率中的应用价值.
方法 对 2019 年-2020 年四川省肿瘤医院迈瑞 6800 血细胞分析仪检测到"异型淋巴细胞"报警提示的 712 例肿瘤患者外周血标本和"异型淋巴细胞"未报警的 695 例肿瘤患者外周血标本进行人工涂片复检，将复检结果与仪器异型淋巴细胞报警信息，HFC%百分率进行分析。
结果 迈瑞 6800 血细胞分析仪对肿瘤患者异型淋巴细胞临床检测敏感度为 97.3%,检测特异性为 92.9%，其中阳性检出率为 92.7%,阴性预测值为 97.4%。经复检显示异型淋巴细胞标本组的 HFC%明显增多，且 HFC%>3%，异淋检出率大于 93.5%。
结论 迈瑞血细胞分析仪根据"异型淋巴细胞"和 HFC%高值检出异型淋巴细胞具可靠性，与人工镜检相结合可以更好地应用临床。

PU-4029

肿瘤患者血液异型淋巴细胞检测结果的实验分析

邓瑶、李贤兵、邓克刚、吴菡
四川省肿瘤医院

目的 探讨肿瘤患者血液中异型淋巴细胞比例增高的临床意义。

方法 回顾性分析 2018 年至 2020 年来四川省肿瘤医院首诊的五类癌症（胃癌、食管癌、结直肠癌、宫颈癌、肺癌）患者的血常规结果，按 HFC%＞3%为异型淋巴细胞比例增高，分析这些癌症患者异型淋巴细胞增高的比例。并收集 81 例异型淋巴细胞增高的食管癌及胃癌患者以及 45 例健康体检者的 EDTA 抗凝全血，采用流式细胞技术分析其淋巴细胞亚群。
结果 2018 年至 2020 年五项癌症共 74293 例，其中胃癌患者 3033 例，异型淋巴细胞增高的患者比率为 12.793%；食管癌患者 2882 例，异型淋巴细胞增高的患者比率 9.924%；结直肠癌 17445 例，异型淋巴细胞增高的患者比率 1.800%；宫颈癌患者 23778 例，异型淋巴细胞增高的患者比率 0.833%；肺癌患者 27155 例，异型淋巴细胞增高的患者比率 0.961%。淋巴细胞亚群分析显示：81 例异型淋巴细胞增高的胃癌和食管癌患者的 B 细胞和 NK 细胞的比例分别为（16.36±10.98）%和（13.1±6.64）%，明显高于健康对照组（P＜0.05），而 T 细胞比例及 CD4/CD8 的比值与健康对照组之间的差异无统计学意义（P＞0.05）。
结论 胃癌和食管癌患者较其他类型癌症患者较易发生异型淋巴细胞比例增高，与病毒感染引起的异型淋巴细胞比例增高主要以 T 细胞增加不同，此类患者的淋巴细胞亚群分析以 B 细胞和 NK 细胞增加为主。

PU-4030

A pro-survival role of ADCY7 in chronic myeloid leukemia

wenjun tian
shandong provincial hospital

Chronic myeloid leukemia (CML) is a principle section of chronic leukemia with blood system disorder happened mainly in adults. It has been reported that the inverse function of adenylyl cyclase 7 (ADCY7) in acute myeloid leukemia (AML). However, expression of ADCY7 in (CML) further to explore. To verify the mechanism of ADCY7, K562 cells, a human myeloid leukemia cell line, were transfected with ADCY7 interference plasmid (ADCY7-KD group). Our results indicated that interference of ADCY7 decreased the proliferation and invasion in CML cells compared to the NC group, but had no effect on cell cycle and apoptosis. Thus, targeting ADCY7, which in turn affects the expression of its downstream channels, represent an effective treatment strategy for CML patients. These results prompt us that ADCY7 participate in CML cell pathogenesis, such as cell proliferation and invasion. ADCY7 may be a promising candidate for clinical and pro-clinical treatment.

PU-4031

网织红细胞参数对慢性肾病患者缺铁性贫血诊断的临床检验价值

宋威
天津市第一中心医院

目的 探讨网织红细胞（RET）相关参数对网织红细胞参数对慢性肾病患者缺铁性贫血诊断的临床检验价值。
方法 选取我院 2020 年 1 月至 2021 年 1 月收治的 40 例慢性肾脏疾病伴缺铁性贫血患者作为观察组，同时选取 40 例慢性肾脏病不伴缺铁性贫血患者作为对照组，评价两组患者网织红细胞参数情况。
结果 观察组患者的 LFR 指数高于对照组，而 RET%、HFR、RET-He、IFR 水平低于对照组（P＜ 0.05）。Logistic 回归分析显示 Ret-He（β=0.28,OR=1.41,95% CI:1.18～1.69） 与 ACD 合并 IDA 独立相关（P<0.05）。Ret-He 预测 ACD 合并 IDA 的曲线下面积（AUC）为 0.96（95%CI:0.95～0.97）。

结论 对于慢性肾病伴缺铁性贫血患者，网织红细胞（RET）相关参数对其诊断具有一定临床价值，Ret-He 可作为其预测指标。

PU-4032

336 例乙肝肝硬化患者止凝血参数检测结果分析

段正军、李彩东、李惠军、梁新宇、刘学梅、田鹏飞、陈俏丽、雷志萍、张旭强、靳克俭、张雅琦
兰州市第二人民医院

目的 探讨乙肝肝硬化患者止凝血参数检测结果。
方法 选取 2019 年 1 月～2021 年 3 月入院的 336 例乙肝肝硬化患者作为观察对象，通过检测 PLT、MPV、PDW、PCT；以及 WBC、RBC、血红蛋白含量（HB）；另检测凝血酶原时间（PT），凝血酶原比率（PT-Ratio），凝血酶原活动度（PT%），国际标准化比值（INR），活化部分凝血活酶时间（APTT），凝血酶时间（TT），纤维蛋白原（FIB）等并与 60 例正常对照组进行比较。
结果 乙肝肝硬化组中 PLT、PCT 水平显著低于正常对照组；而 PDW、MPV 水平显著高于正常对照组，有显著性差异（P#<0.01；P*<0.05）。另外，乙肝肝硬化组的 WBC、RBC、HB 水平显著低于正常对照组，有显著性差异（P▲<0.05）。在凝血参数中 PT、PT-Ratio、INR、APTT、TT 时间明显延长；FIB、PT%明显降低，与正常对照组比较有显著性差异（P<0.05）。
结论 对乙肝肝硬化患者进行上述临床参数检测可以早期发现凝血机制障碍，各参数的变化间接反映着肝损伤的程度，有助于乙肝肝硬化患者病情的预后和治疗。

PU-4033

WBC-D 及 WBC-N 与有核红细胞的相关性研究

周荣
东南大学附属中大医院

目的 对迈瑞 BC7500 血液分析仪，在血细胞分析中存在有核红细胞时，DIFF 和 WBN 两种通道测得白细胞结果进行分析探讨。
方法 收集 2021 年 4 月到 6 月我院新生儿血常规 NRBC%>1%的标本 64 例，采用 DIFF 通道和 WBN 通道进行血细胞分析，对 TNC-D WBC-D 差值 和 TNC-N WBC-N 差值两组数值进行统计分析。
结果 DIFF 通道测得 TNC-D WBC-D 的差值和 WBN 通道测得 TNC-N WBC-N 的差值结果有统计学意义(P<0.05)。
结论 仪器在血细胞分析中，存在有核红细胞时，WBN 通道能识别有核红细胞并去除有核红细胞，而获得准确的白细胞数值;DIFF 通道不能识别有核红细胞，会误判成白细胞数，但给出的参数 WBC-D 数值与 WBC-N 数值有着一致性。说明仪器自动根据 WBN 通道识别的细胞数据对 WBC-D 结果进行了优化处理。

PU-4034

中性粒细胞/淋巴细胞比值等参数在 SLE 活动性评价中的应用

胡伟
南京大学医学院附属鼓楼医院

目的 分析 NLR、MLR、PLR 和淋巴细胞数在 SLE 活动性评价中的作用。

方法 本研究对我院 2016 年 1 月至 2018 年 6 月收治的 145 例系统性红斑狼疮患者和 150 例健康对照者进行回顾性分析。分析 NLR、MLR、PLR 和淋巴细胞计数结果与 SLEDAI 的相关性。
结果 NLR、MLR、PLR 和淋巴细胞计数均与对照组有显著性差异。而“SLEDAI≤9”与“SLEDAI>9”患者相比，淋巴细胞计数和 PLR 之间而非 NLR 和 MLR 有统计学差异。进一步的回归分析得出 PLR 为“R=0.17，p=0.04”，淋巴细胞计数与 SLEDAI 的相关性为“R=-0.41 和 p<0.0001”分数。对这四个参数的 ROC 曲线分析表明，淋巴细胞计数显示最大的 AUC（0.75,95%可信区间：0.67-0.83）。
结论 淋巴细胞计数与 SLEDAI 的相关性优于 NLR、MLR 和 PLR，因此它更适合于 SLE 疾病活动性的评价。

PU-4035

A novel O allele with a mutation c.859G>T was identified in an ABO discrepancy individual

Hang Lei
Ruijin Hospital, Medical School of Shanghai Jiao Tong University

BACKGROUND Mutations of ABO gene may cause the dysfunction of ABO glycosyltransferase that can result in weak ABO phenotypes. Here, we identified one novel weak ABO subgroup alleles and explored the mechanisms that caused subgroup phenotype.
Methods and Materials. The routine serologic tests were performed by tube method and adsorption-elution test. All the coding regions of the ABO gene were amplified and sequenced. The haplotypes of the ABO gene were identified by cloning.
RESULTS The serologic results of ABO typing showed a discrepancy between the forward and reverse typing, The subject was suspected as O subgroup. According to the directly sequencing and cloning results, there was a heterozygote of ABO*O.01.01 and a novel O allele on the ABO* O.01.02 with a mutation c.859G>T.
CONCLUSION A novel allele with c.859G>T on the ABO*O.01.02 was identified in a Chinese pregnant woman. In this woman, weak A antigen was detected in peripheral RBCs, and the mechanisms underlying this phenomenon need to be clarified in future

PU-4036

南京地区成人 RET 参数参考区间的建立

王贤
南京大学医学院附属鼓楼医院

目的 分析并建立南京地区成人的网织红细胞（RET）参数的参考区间。
方法 选取 1188 例本院健康体检的健康成年人，空腹抽取 EDTA-K2 抗凝静脉血，用 SYSMEX-5000 全自动血液分析仪对所有标本进行 RET 参数测定。参照中华人民共和国卫生行业标准（WS/T405 -2012）《血细胞分析参考区间》中的推荐方法，建立 RET 参数的参考区间。
结果 RET-He、LFR、MFR、HFR 检测数据为非正态分布，其 95%参考区间采用百分位点法（P2.5～P97.5）表示。RET-He、LFR、MFR、HFR 按照性别分组，组间比较,差异有统计学意义；RET-He、LFR、MFR、HFR 按照不同年龄段分为三组，各年龄组间两两比较，差异有统计学意义。
结论 首次建立了南京地区成年人 RET 参数的参考区间,为本地区 RET 检测的临床应用提供了准确的依据。

PU-4037

血栓标志物对骨性关节炎（OA）患者全膝关节置换术（TKA）后深静脉血栓（DVT）形成的诊断价值

袁博
西安医学院第一附属医院

目的 探讨新型血栓标志物对骨性关节炎（OA）患者全膝关节置换术（TKA）后深静脉血栓（DVT）形成的诊断价值。
方法 79 例 OA 患者行 TKA 术，根据术后 DVT 的形成分为血栓组（39 例）和对照组（40 例），检测其血栓调节蛋白（TM）、凝血酶抗凝酶复合物（TAT）、纤溶酶-抗纤溶酶复合物（PIC）、组织型纤溶酶原激活剂-抑制剂 1 复合物（t-PAIC）和 D 二聚体（D-D）的表达， ROC 曲线评估其对 DVT 的诊断效能。
结果 血栓组中 TAT (34.91±15.84)ng/ml 和 D-D (2.70±2.69)ng/ml 高于对照组的 TAT (27.75±12.10)ng/ml 和 D-D (1.68±1.79) ng/ml，而 TM (10.94±2.51)mg/ml 低于对照组 (13.33±5.51)mg/ml，P＜0.05；PIC 和 t-PAIC 无统计学意义(P＞0.05)。TM、TAT、D-D 单独诊断术后 DVT 的 ROC 曲线下面积（AUC）分别为 0.654、0.631、0.630；TM、TAT、D-D 联合诊断术后 DVT 的 AUC 为 0.687，敏感性为 52.63，特异性为 79.49。
结论 TM、TAT、D-D 联合检测对 OA 患者 TKA 术后 DVT 的形成具有良好的辅助诊断价值，可作为 DVT 的早期诊断标志物用于临床。

PU-4038

A novel mutant-Cys328-terminator in severe coagulation factor XIII deficiency:A case report

Ruimin Cai 、Yi Li、Wenyang Wang、Qiang Feng
Taian City Central Hospital

Factor XIII (FXIII) deficiency is an extremely rare bleeding disorder, which is due to mutations in the FXIIIA subunit gene,commonly. We evaluated a patient with umbilical cord bleeding after birth,an intracerebral haemorrhage at age 6, hematuria and cephalohematoma, who suffered from a lifelong haemorrhagic diathesis. The clot solubility test showed that the clot of patient was dissolved in the urea solution after 10h. Genetic testing identified a novel homozygous mutation, c.984C>A, resulting in a premature stop codon in exon 8 of the F13A1 gene, that was p.Cys328stop. The results of clusterX software showed that Cys328 of exon 8 of F13A1 is highly conservative among species.

PU-4039

外周血形态复检规则设定在白血病中的应用

高晓玲、吴惠玲、黄琪富、马巧芬
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨白血病初诊血细胞参数、散点图变化特征，设定推片规则，进行外周血细胞形态观察，及早发现白血病，防止漏检、漏诊及误诊。
方法 回顾分析 2016 年 9 月至 2019 年 2 月我院已确诊白血病 97 例，按白细胞数分为（1）白细胞增多组：白细胞＞10.0×109/L，（2）白细胞正常组：4.0×109/L≤白细胞≤10.0×109/L，（3）白细胞减少组：白细胞＜4.0×109/L，观察首次血细胞参数白细胞(WBC)、血小板(PLT)、有核红细胞

(NRBC)、幼稚粒细胞（IG）、单核细胞(M)、嗜碱性粒细胞（B）、无白细胞分类（DC）结果或DC不全及散点图，设定推片规则是否能推片。
结果 按设定推片规则：白细胞增多组 63 例，推片率为 96.83%（61/63），2 例未触碰规则占（3.17%），一例淋巴细胞百分比为 90.64，另外一例细胞参数及散点图均正常；白细胞正常组 14 例，推片率为 100%（14/14）；白细胞减少组 20 例，推片率为 100%（20/20）。
结论 通过设定推片复检规则，进行外周血细胞形态观察，能有效的筛查出白血病。

PU-4040

细胞形态学异常用于骨髓增生异常综合征的诊断价值研究

詹学良
玉溪市人民医院医学检验科（昆明医科大学 第六附属医院医学检验科）

目的 探讨细胞形态学异常用于骨髓增生异常综合征的诊断价值。
方法 选取 2012 年到 2016 年于我院就诊的骨髓增生异常综合征患者共 42 例，将其作为观察组；另选择同期非克隆性疾病患者 42 例，将其作为对照组。比较两组患者外周血极其骨髓细胞的形态特征。
结果 依据原粒细胞、幼粒细胞、幼红细胞、及巨核细胞系形态异常状况分析外周血细胞形态学病态检查结果时，观察组患者的形态异常发生比例明显高于对照组，且组间数据对比存在显著差异，具统计学意义（P＜0.05）；另从骨髓粒细胞系指标、红细胞系指标及巨核细胞系指标分析骨髓细胞形态特征时，观察组患者的相关比例发生率均明显高于对照组，且组间数据对比亦存在显著差异，数据对比具统计学意义（P＜0.05）。
结论 细胞形态学异常是临床上诊断骨髓增生异常综合征最基础和重要的手段，能够为临床诊断和治疗提供有效依据，具有临床推广及应用价值。

PU-4041

肺炎支原体、冷凝集致红细胞参数假性降低 1 例探讨

刘艳[2]、普永冰[1]、普好业[1]
1. 玉溪市中医医院
2. 玉溪市中医医院

在临床检验工作中发现有很多因素会干扰血细胞分析仪计数，出现异常检测结果。本文发现 1 例肺炎支原体感染及冷凝集引起红细胞参数计数假性降低的病例，即在 37°C 水浴不同孵育时间上，冷凝聚对于白细胞和血小板及其分类影响不大，而对于红细胞计数结果明显偏低，由此所致 HCT.MCV.MCH. MCHC 结果均显示异常，引起检验人员注意。

PU-4042

D-二聚体增高的原因分析

王进
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨 D-二聚体增高的原因，为血栓性疾病的诊断和鉴别提供参考依据。
方法 回顾性分析我院 2019 年一季度 7875 例 D-二聚体增高的标本，分析其增高的原因。
结果 合并 FDP 增高 FDP>DD 的有 3672 例，占 46.04%；FDP 正常范围且 FDP>DD 的有 4271 例，占 53.55%；DD>FDP 的有 32 例，占 0.40%。

结论 D-二聚体作为交联纤维蛋白的降解产物，阴性可排除深静脉血栓和肺栓塞，增高可认为是活动性静脉血栓形成的标志，由于检测方法的局限性和对项目意义认识的局限性，会给血栓性疾病的诊断及治疗带来困扰，明确其增高的原因对血栓性疾病的诊断和鉴别诊断具有重要意义。

PU-4043

AVE-562 全自动粪便分析仪临床应用评价

陈穆群、张兴锋
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 评价 AVE-562 全自动粪便分析仪检测粪便标本的临床应用价值。
方法 采用手工镜检法和 AVE-562 全自动粪便分析仪同时检测 3006 例患者的粪便标本，以手工镜检法为金标准[仪器自动隐血（OB）检测与珠海贝索 OB 试纸条人工检测结果比较，对粪便常规检测结果进行比较分析，计算 AVE-562 全自动粪便分析仪检测的敏感性、特异性、准确率。
结果 仪器自动 OB 检测与珠海贝索 OB 试纸条一致率为 97.85%（kappa=0.918）。以手工镜检法为金标准，AVE-562 全自动粪便分析仪检测红细胞（RBC）、白细胞（WBC）的敏感性分别为 86.05%、80.95%；特异性分别为 99.63%、99.80%；准确率分别为 99.44%、99.54%；kappa 值分别为 0.810、0.827。
结论 AVE-562 全自动粪便分析仪粪便常规检测 RBC、WBC 等指标与手工镜检法一致性较好，仪器操作简单，自动化程度高，有较高的临床应用价值。

PU-4044

沃文特 F280 全自动粪便分析仪的临床应用评价

王成
深圳市罗湖医院集团医学检验实验室

目的 评估沃文特 F280 全自动粪便分析仪检测粪便标本的临床应用价值。
方法 收集 2020 年 3 月份至 5 月份我院 2364 份粪便样本，分别用手工镜检法与 F280 全自动粪便分析仪进行检测,以手工镜检为金标准,通过灵敏度、特异度、符合率及方法间一致性指标评估 F280 的临床应用价值。
结果 F280 全自动粪便分析仪检测的理学性状、红细胞（RBC）、白细胞 （WBC）、脂肪球、酵母样真菌、虫卵和隐血的灵敏度分别为 83.97%、95.51%、97.53%、97.92%、92.59%、88.89%和 98.92%；特异度分别为 99.5%、99.61%、99.87%、99.55%、99.61%、98.89%和 99.77%；符合率分别为 98.5%、99.32%、99.28%、99.45%、99.53%、98.6%和 99.7%；Kappa 值分别为 0.87、0.91、0.90、0.95、0.82、0.32、0.98。
结论 F280 全自动粪便分析仪在 F160 的基础上有所提高，结果可靠，工作效率高，生物安全风险低，有较高的临床应用价值。

PU-4045

血浆置换法校正乳糜血干扰血常规测定结果 15 例结果分析

周利、陈剑、李春梅、黄奕然、冯磊
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨乳糜血对血常规结果的干扰及处理方法。

方法 收集 2018 年 12 月至 2021 年 5 月我院收治的 15 例乳糜血干扰血常规结果标本，采用等量血浆置换法重测对结果进行校正，并对校正前后标本进行分析。
结果 校正前后 RBC、Hb、MCH、MCHC 结果有显著性差异，校正后结果明显低于校正前。
结论 乳糜血对血常规结果 RBC、HGB、MCH、MCHC 有明显干扰，对 WBC、PLT 结果干扰较小，在检验工作中应对重度乳糜血标本采用等量血浆置换法进行结果校正。

PU-4046

外周血细胞形态学在儿科疾病诊断中的价值

刘梦云、林喜荣、莫红梅
深圳市罗湖医院集团

目的 分析外周血细胞形态学在儿科疾病诊断中的价值。
方法 选取 2019 年 11 月-2020 年 1 月我院儿科住院部及门急诊的 444 例患者为研究对象，对其进行外周血细胞形态观察，分析统计结果。
结果 444 例患儿外周血细胞形态，同一例可包含几种异常结果。正常血象共 37 例；红细胞异常 39 例，确诊地中海贫血 25 例、缺铁性贫血 14 例；原始细胞 1 例，确诊急性淋巴细胞白血病；中性粒细胞比例增高 179 例，中性粒细胞核左移 13 例，中性粒细胞毒性改变 63 例，均提示细菌感染；异型淋巴细胞增多 40 例，包括流感 10 例、传染性单核细胞增多症 10 例、肺炎支原体感染 20 例；淋巴细胞比例增高 123 例，考虑病毒感染；血小板增多 136 例；血小板减少 3 例；单核细胞比例增高 60 例；嗜酸粒细胞比例增高 20 例；嗜碱粒细胞增高 1 例。
结论 外周血细胞形态观察可为临床诊断儿科疾病提供有力线索，具有重要的临床价值。

PU-4047

巢式聚合酶链反应在白血病微小残留病检测中的应用

何穗芬、刘思洁
南方医科大学珠江医院

目的 探讨巢式逆转录聚合酶链反应（reverse transcription-polymerase chain reaction，RT-PCR）在白血病微小残留病检测中的应用价值。
方法 回顾多篇文献，综合分析巢式 RT-PCR 在各类白血病检测、危险度分析、预后判断等方面的应用价值。
结果 应用巢式甲基化特异性 PCR（nMS-PCR）可以准确检测恶性血液病细胞株 APC 基因的甲基化状态；应用巢式 RT-PCR 能够对白血病多种融合基因进行检测并可显著提高微小残留病（minimal residual disease，MRD）的检出敏感性；应用一步法 RT-PCR 和两步法 RT-PCR 两种巢式 PCR 检测骨髓移植后 CML 微小残留病，一步法 RT-PCR 检测出阳性的最长移植时间较两步法长；
结论 MRD 检测方法需要灵敏度高和有效覆盖范围广，因而聚合酶链反应（polymerase chain reaction，PCR）目前被广泛使用。已知巢式逆转录聚合酶链反应（巢式 RT-PCR）具有省时高效的优点，是分子生物学检测方法的代表。MRD 指白血病患者经诱导缓解治疗后达到临床缓解标准，但体内残留的微量白细胞无法使用形态学方法检出，是白血病复发的根源。巢式 RT-PCR 可半定量白血病治疗后的微小残留，敏感度可达 1/106，是监测 MRD 的良好方法。并且 nMS-PCR 检测与 APC 基因甲基化相关的基因突变的敏感度比 MS-PCR 更高。综上，巢式 RT-PCR 能够提高 MRD 检出敏感度，反映白血病个体治疗效果及预后，对于制定个体化治疗方案具有重要意义。

PU-4048

Sysmex XN-9000 全自动血细胞分析流水线复检规则及 3R 规则在综合医院应用的评估

权衡[1]、伍均[2]
1. 上海市第一人民医院
2. 上海市第一人民医院嘉定分院

目的 建立本实验室的 Sysmex XN-9000 全自动血细胞分析流水线的复检规则及 3R 规则并进行验证评估，以提高工作质量和效率。
方法 依据国际血液学学会推荐的“41 条复检规则”和国内 XE-2100 血液分析仪复检标准制定协作组推荐的“23 条复检规则”及 XN-9000 的性能初步建立本实验室的复检规则及 3R 规则,在此规则指导下对 1032 例样本进行分析，统计涂片复检率，对此规则进行评估并不断优化，规则建立后，选择 500 例样本（主要为血液病和肿瘤化疗患者病例）进行验证，评价规则的可行性和有效性。
结果 初步建立了本实验室的 25 条血常规复检规则及 sysmex XN-9000 的 11 条 3R 规则，对评估检测结果进行统计分析，真阳性率 21.70%（224 例），假阳性 4.85%（50 例），真阴性 72.00%（743 例），假阴性 1.45%（15 例），无病理性细胞漏检。对验证检测结果进行统计分析，结果显示准确率为 93.70%；推片复检率为 18.99%（196 例），假阳性率 4.85%（50 例），假阴性 3.00%（15 例）。
结论 本复检规则下假阴性率为 3.00%，符合国际规定的标准（小于 5.00%），所建立的复检规则和 3R 规则有效地提高了检测效率，减少了漏检率、误检率，符合本实验室质量及工作效率的要求。

PU-4049

136 例儿童急性白血病流式细胞术免疫分型分析

凡慧慧
永州市中心医院

目的 了解儿童急性白血病中的抗原表达特点。
方法 采用流式细胞术四色荧光标记，CD45/SSC 双参数散点图设门方法，对 136 例儿童急性白血病患者进行免疫分型检测分析，并将免疫分型结果与形态学分型结果比较分析。
结果 136 例儿童急性白血病中，ALL 检出 83 例，ALL 中各抗原的表达情况:CD19>CD10>CD20>CD7>CD3>CD13>CD33、CD16，其中 B-ALL 74 例，占 89.16%，T-ALL 9 例，占 10.84%，My+ALL 发生率 7.23%；AML43 例，AML 中各抗原的表达情况：CD13>CD33>CD117>CD19>CD7>CD14，Ly+AML 发生率 46.51%；HLA-DR 和 CD34 在 AML 和 ALL 中表达无显著差异，CD117 在 AML 和 ALL 中的表达有显著性差异（P<0.001）；流式细胞术免疫分型与 FAB 分型的符合率为 88.24%，免疫分型检出 5 例 B-M 混合，3 例 T-M 混合。
结论 流式细胞术免疫分型在白血病分型中有重要的作用，是 FAB 的重要补充和修正,尤其对于 MAL、抗原交叉表达和形态、化学染色特征不明显的病例有重要的意义；CD117 有助于儿童 AML 和 ALL 的鉴别诊断。

PU-4050

腹痛难忍，原是鞭虫

凡慧慧
永州市中心医院

患者，女， 45 岁，因“右侧腹痛 4 天余，无发热，无便血和黑便， 肛门排气排便通畅” 入院。查体：急性痛苦面容，腹膨隆（肥胖），未见胃肠型和蠕动波，右侧腹肌稍紧张，右侧上腹有压痛，反跳痛不明显，未触及肿块，肝脾肋下未及， Murphy 征（—）。 CT 示：升结肠及横结肠右侧水肿明显。 WBC9.56 10^9/L，N76.2%，嗜酸粒不高， CRP25.4mg/L。患者在全麻腹腔镜下行肠粘连松懈+右半结肠切除术+腹腔冲洗引流术（超声刀）， 于横结肠远端断端吻合前见横结肠中段及远端有较多细条状寄生虫，取出绝大部分寄生虫送检至我科。术后标本剖视见升结肠一穿孔，直径 0.3cm，右半结肠腔内密密麻麻满布数千条上述寄生虫。 我科夜班值班人员收到标本后取虫制片观察，发现数条寄生虫成虫缠绕一起，难以分开，虫体较长约 3-5cm，两端粗细不均， 拍照后上传检验科科室群讨论，先后排除了蛔虫、蛲虫、粪类圆线虫、钩虫等肠道常见的寄生虫。最后我科周老师建议寻找雌虫的尾部是否有虫卵，以虫卵来鉴别更有效。因晚班一个人值班，工作量大且经验有限，同临床协商后次日清晨发报告。第二天，在周老师的指导下，成功找到雌虫并戳破虫体找到虫卵，最后鉴定为鞭虫成虫及鞭虫虫卵。同时建议临床送检粪便寄生虫检查， 3 日后在粪便中找到鞭虫虫卵

PU-4051

D-二聚体动态监测对多发性骨髓瘤患者治疗效果及预后影响分析

杨瑞芳
天津医科大学肿瘤医院

目的 监测多发性骨髓瘤患者在疾病诊断和治疗过程中 D-二聚体含量，探讨 D-二聚体检测及使用硼替佐米后对治疗效果评价和预后的意义。
方法 本研究收集 61 例多发性骨髓瘤患者的多项病历信息（均来自于天津医科大学附属肿瘤医院），20 名健康人入院时临床指标作为对照组。经过临床、骨髓、流式细胞学、免疫固定电泳等检查确诊为多发性骨髓瘤。采用法国生物梅里埃的 VIDAS 检测仪，通过定量全自动 ELISA 法检测多发性骨髓瘤患者血液中 D-二聚体的含量。使用 SPSS 25.0 软件分析包进行实验数据的统计学分析。其中计量单位用均数±标准差表示，以 P＜0.05 差异具有统计学意义。
结果 在经过对比分析后结果显示多发性骨髓瘤患者血液中 D-二聚体含量 FDP 含量要明显高于健康对照组，具有统计学意义（P 值＜0.05）。AT-Ⅲ含量较对照组明显减低，具有统计学意义（P 值＜0.05）在 DS 分期分期中Ⅱ期和Ⅲ期患者 D-二聚体和 FDP 含量明显高于Ⅰ期患者，差异有统计学意义（P 值＜0.05）。根据对比肌酐含量未升高的复发概率明显降低，差异具有统计学意义（P 值＜0.05）。初发时 D-二聚体含量升高的患者在使用硼替佐米治疗后血液中 D-二聚体含量有明显的降低，差异具有统计学意义（P 值＜0.05）。但对于初发时 D-二聚体水平高低与生存期变化未得出统计学意义。D-二聚体升高患者 FISH 结果阳性例数明显增多。
结论 多发性骨髓瘤患者血液中 D-二聚体含量明显升高，并且在疾病发展过程中存在动态变化，随着疾病分期增加 D-二聚体含量升高，D-二聚体含量与患者病情密切相关。硼替佐米对多发性骨髓瘤患者 D-二聚体有一定降低作用，尤其对 D-二聚体高浓度患者有较好的疗效。D-二聚体的变化与疾病归转密切相关，D-二聚体有望作为多发性骨髓瘤患者治疗和预后的危险因素。

PU-4052

中性粒细胞与淋巴细胞比值、血小板平均体积等炎症指标在 T2DM 中的变化分析

龙璐
中南大学湘雅医院

目的 探讨中性粒细胞与淋巴细胞比值（neutrophil-to-lymphocyte ratio，NLR）、血小板平均体积（mean platelet volule,MPV）、中性粒细胞绝对值等指标在 2 型糖尿病（Type 2 diabetes mellitus，T2DM）中的诊断价值。
方法 选取中南大学湘雅医院住院确诊为 2 型糖尿病的 544 例患者作为研究对象，设为 T2DM 组。其中男 289 例，女 255 例。另选同一时间段在中南大学湘雅医院接受体检的 126 例正常人为健康对照组。比较两组间 NLR、MPV、中性粒细胞绝对值和淋巴细胞绝对值水平等指标。采用全自动血液分析仪检测的血常规以及生化常规项目。
结果 (1)T2DM 疾病组全血中性粒细胞比例（NEUT%）水平显著高于健康对照组（P＜0.01），而 T2DM 疾病组全血中淋巴细胞比值（LY%）低于对照组有统计学意义。T2DM 组中性粒细胞计数为（69.26±9.066），高于于对照组的（54.53±5.701）；观察组 MPV 为（10.59±1.54）fL，高于对照组的（10.09±0.69）fL；而 T2DM 淋巴细胞为（20.12±4.02），低于对照组的（35.59±5.81）差异均有统计学意义（P<0.05）；(2)在 T2DM 组中，NLR、MPV 水平随着病程越长而显著升高（P＜0.01）；(3)通过相关性分析可得出随着患者患病时间越长，其微血管病变和炎症反应也明显加强。
结论 1.全血中的 NLR、MPV 随着疾病的进展而增高，在疾病的监测治疗方面有一定临床价值。2.logistics 回归分析得出 NLR、MPV 为 2 型糖尿病的危险因素。

PU-4053

智慧型仿生纳米药通过有氧糖酵解重编辑介导线粒体结局：一种有前景治疗淋巴瘤的新方法

赵强强、桂嵘、聂新民
中南大学湘雅三医院

目的 化疗药物引起的毒性和耐药性已成为治疗肿瘤的瓶颈。基于纳米载体的抗癌药物的递送被认为是解决前述问题的理想途径。
方法 本研究设计构建了一种新的抗淋巴瘤纳米药物 CD20 适配子-RBCm@Ag-MOFs/PFK15(a-RAMP)，它由两部分组成：1.金属-有机框架 Ag-MOFs(AM)负载肿瘤有氧糖酵解抑制剂 PFK15(P)，形成核心部分(AMP)；2.将靶向分子 CD20 适配子(A)插入红细胞膜(RBCm)，形成外壳部分(A-R)。在 CD20 适配子指导下的 A-RAMP 在体外和体内均主动靶向 B 细胞淋巴瘤。
结果 A-RAMP 不仅明显抑制对肿瘤生长的影响，而且对治疗的裸鼠未见明显副作用，表明 A-RAMP 能准确靶向肿瘤细胞，重编程有氧糖酵解并通过 Ag + 和 PFK 15 发挥协同抗肿瘤作用。进而探讨 A-RAMP 通过凋亡途径和靶向代谢组学在体内的抗肿瘤机制。
结论 A-RAMP 作为一种智能、安全、有效、协同的抗淋巴瘤制剂具有广阔的应用前景。

PU-4054

2-Mercaptoethanol (2-ME)-based IATs or Polybrene method mitigates the interference of daratumumab on blood compatibility tests

Xiaohong Cai
Ruijin Hospital, Shanghai Jiaotong University School of Medicine,Shanghai

Objectives Treating red blood cells (RBCs) with dithiothreitol (DTT) is a wildly-recommended to overcome the interference of the daratumumab (DARA) with blood compatibility testing. Nevertheless, DTT can be hard to obtain in the clinical laboratory, while its use in routine practice may be time-consuming. In the following study, we explored the feasibility of using a commercial 2-mercaptoethanol (2-ME) working solution or the time-saving Polybrene method to mitigate DARA interference.
Methods Antibody screening and cross-matching were performed using 2-ME or DTT-based indirect antiglobulin tests (IATs) and Polybrene method (with human IgG anti-E same IATs titer as DARA as positive control) on 37 samples. Most clinically important blood group antigens on RBCs were detected after treatment with 2-ME or DTT.
Results Treating RBCs with 2-ME eliminates the DARA interference with the antibody screening or cross-matching; yet, K antigen is denatured during treatment. DARA does not interfere with antibody screening and cross-matching via Polybrene method, while 2+ agglutinations of anti-E antibody with the same titer (IATs method) as DARA could be observed in the positive controls via this method.
Conclusion 2-ME-based IATs or Polybrene method could replace DTT-based IATs to mitigate DARA interference.

PU-4055

仿生修饰的纳米银构建及其靶向抗淋巴瘤的应用

赵强强、桂嵘、聂新民
中南大学湘雅三医院

目的 淋巴瘤是人体众所周知的恶性肿瘤。虽然人们开发了许多抗癌药来提高患者的生存率，但约40%的患者持续复发或难治，这是一个需要补救措施的关键问题。因此，有必要确定替代治疗方法，以降低该病的死亡率。
方法 为此，以 AgNPs 为纳米颗粒的核心同时以靶向分子叶酸插入红细胞膜为外壳，制备了一种新型的抗淋巴瘤纳米复合物 FA@RBCm-AgNPs。
结果 红细胞膜(RBCm)的仿生特性赋予 F-RAN 良好的生物相容性以及逃避网状内皮系统清除的能力。此外，用叶酸修饰 F-RAN，主动、选择性地鉴定肿瘤细胞。体内外实验证明，F-RAN 在促进淋巴瘤凋亡的同时，能抑制淋巴瘤细胞，诱导干细胞凋亡，且无明显副作用。
结论 因此，F-RAN 可作为淋巴瘤的一种新的治疗方法。

PU-4056

Correlation between the prognosis of peripheral blood nucleated red blood cells in patients with tumor intensive care

Shusheng Hu
Clinical Laboratory Department,Tianjin Medical University Cancer Institute and Hospital

Objective To explore the case characteristics of peripheral blood nucleated red cells (NRBC) in tumor intensive care patients and the correlation analysis between NRBC and prognosis of tumor intensive care patients, so as to provide data support for doctors to judge prognosis of current tumor intensive care patients and reduce the mortality of patients.
Methods Intensive care patients in the tumor hospital of tianjin medical university from January to December 2018 were selected, and patients with peripheral blood NRBC>0 during intensive care were retrospectively studied, and the patients were divided into death group and survival group. Collect the basic information of the tumor in intensive care patients (age, gender), the condition of prognosis (dead or alive), survival time, monitoring during the period of peripheral blood in patients with NRBC absolute value (NRBC#) and peripheral blood NRBC ratio (NRBC %) to the highest level, clinical diagnosis of the comparative analysis between groups, using logistic regression analysis to determine the NRBC can the independent risk factors of death in patients with as, choose Kapian - meier method explored survival time for patients, Then, ROC curve was used to evaluate the predictive efficacy of NRBC# and NRBC% as prognosis of cancer intensive care patients.
Results Among 183 patients with peripheral blood NRBC>0, 53 died and 130 survived in tumor intensive care. NRBC# and NRBC% in the death group were significantly higher than those in the survival group (P<0.05). Logistic regression analysis showed that NRBC# and NRBC% were risk factors for death in tumor intensive care patients. Kapian - meier survival analysis results show: the peripheral blood in patients with high of NRBC ´ at 0.1×/L for the boundary is divided into two groups, NRBC < 0.1×/L and NRBC > 0.1×/L survival time with statistical significance (P < 0.01). NRBC# and NRBC% have statistical significance in predicting the prognosis of tumor intensive care patients, and the area under the ROC curve is 0.773 and 0.777, respectively (P<0.01). NRBC# to the prognosis of patients with intensive care in the diagnosis of tumor boundary value of 0.0350´/L (sensitivity and speciality rate were 64.2% and 81.5%, respectively), the best diagnostic boundary NRBC % value of 0.1500/100 white blood cells (WBC), sensitivity and were 84.9% 63.8%), NRBC# acuity 0.0350´/L or NRBC % 0.1500/100WBC can be used as a judgment in intensive care patients with poor prognosis of tumor "red line".
Conclusion NRBC is a risk factor for the death of patients with severe tumors, and with the gradual increase of NRBC in peripheral blood, the risk of death of patients with severe tumors also increases gradually, and NRBC may be used as a clinical indicator to judge the prognosis of patients.

PU-4057

同源肿瘤细胞膜伪装纳米递药系统的构建及其抗淋巴瘤的应用

赵强强、桂嵘、聂新民
中南大学湘雅三医院

目的 非霍奇金淋巴瘤(NHL)在细胞遗传学、免疫表型和临床特征上具有很大的异质性，目前化疗作为主要的治疗方式。虽然采用单克隆抗体靶向药物显著提高了其总体疗效，但仍有许多患者遭受耐药或复发的困扰。为了解决这些临床难题，寻找治疗 NHL 的替代和可靠的治疗策略势在必行。

方法 本研究提出了基于载中药异欧前胡素(ISOIM)的介孔二氧化硅纳米颗粒(MSNs)的纳米平台的构建，该纳米平台被称为 CCM@MSNs-ISOIM 的癌细胞膜(CCM)所伪装。
结果 该纳米递药系统具有免疫逃逸、抗吞噬作用、高载药率、pH 反应、良好的生物相容性和主动靶向肿瘤部位、阻断淋巴瘤细胞周期和促进线粒体介导的细胞凋亡等特点。
结论 本研究为寻找淋巴瘤新的临床治疗方法提供了理论依据。

PU-4058

Whole transcriptome analysis of platelet concentrates during storage

Hasiyati Heililahong
Ruijin Hospital, Shanghai Jiaotong University School of Medicine,Shanghai

Background Platelets, while anucleate, contain RNA. Whole transcriptome analysis applies to platelet biology during storage, providing insights into platelet function change and the mechanisms of platelet storage lesion.
Objective To explore the changes in the whole transcriptome expression profile of platelet concentrates during storage and the potential biological functions of the differential expression of mRNA, lncRNA and circRNA in platelet storage damage.
Methods Apheresis platelets were collected from three healthy blood donors, each 50 mL of Apheresis platelets, stored with shaking at (22±2) ℃, and using RNA- sequencing technology(RNA-seq)detects the changes in the expression profiles of long no coding RNA (lncRNA), circular RNA (circRNA) and mRNA in machine-harvested platelets stored for 0, 2, and 4 days; GO analysis and KEGG analysis are used to predict the functional distribution of differential expression of mRNAs, and cis-regulation analysis is used to predict that lncRNAs and circRNAs regulate adjacent protein-coding genes molecular mechanisms of expression; GSEA analysis is used to analyze the differential expression of gene pathway.
Results RNA-sequencing: Compared with platelet storage for 4th day and 0 day, the expression levels of 222 mRNAs changed significantly, 59 continually increased and 146 continually decreased; 44 468 lncRNAs had obvious expression levels, and the expression levels of 43 species increased and 28 species decreased; Besides, the 4th day compared with the 0 day, the expression levels of 198 species of circRNA changed significantly, 14 species changed continually. GSEA, GO and KEGG analysis: Differentially expressed mRNA, lncRNAs and circRNA may be involved in physiological processes such as platelet activation, platelet aggregation, endocytosis, apoptosis, metabolism, DNA repair, cell cycle, actin fiber aggregation, and regulation of the actin skeleton; we observed that among the up-regulated lncRNA, STXBP5-AS1 and ZNF667-AS1 were reported to be related to apoptosis, and can provide important basis and entry points for the study of platelet storage damage and apoptosis in vitro.
Conclusion Platelets contain a large amount of mRNA, lncRNA and circRNA, and its expression changes with the prolonged platelet storage time. Generally speaking, the number of down-regulated RNAs is larger, and the magnitude of the down-regulation is larger. Some changes in mRNA, lncRNA and circRNA may be closely related to the physiological functions of platelets, and play a role in platelet storage leison.

PU-4059

仿生纳米疗法：基于中性粒细胞膜的核壳结构纳米药靶向治疗淋巴瘤

赵强强、桂嵘、聂新民
中南大学湘雅三医院

目的 非霍奇金淋巴瘤(NHL)是淋巴组织的恶性疾病。目前化疗仍是治疗 NHL 的主要方法。R-CHOP 可明显提高患者生存率。遗憾的是，DOX 是 R-CHOP 中的主要细胞毒性药物，它可导致不良反应。因此，发现 NHL 新的治疗方案尤为重要。
方法 本研究设计并构建了新型抗肿瘤纳米颗粒复合物 Nm@MSNs-DOX/SM。以载多柔比星(DOX)和抗炎药山栀苷甲酯(SM)的介孔二氧化硅纳米粒(MSNs)为纳米粒的核心。中性粒细胞膜(Nm)可包被多个纳米核作为外壳。
结果 DOX 联合 SM 可增强抗肿瘤作用，并诱导淋巴瘤细胞凋亡，抑制与肿瘤发生有关的炎症因子的表达依赖于 Bcl-2 家族介导的线粒体通路的调控，如 TNF-α、IL-1β 等。因此，对肿瘤微环境(TME)进行了重塑，并放大了 DOX 的抗肿瘤作用。此外，Nm 具有良好的生物相容性，能增强 Nm@MSNs-DOX/SM 的 EPR 效应，增加主动靶向肿瘤的作用。
结论 Nm 修饰的药物递送系统 Nm@MSNs-DOX/SM 是一种很有前途的靶向化疗和抗炎治疗纳米复合物，可作为一种特异性、高效的抗淋巴瘤治疗药物。

PU-4060

粪便中检出灵芝孢子、酵母样真菌 3 例与常见寄生虫卵的鉴别分析

陈剑、周利、黄奕然、冯磊
玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨粪便镜检下灵芝孢子、酵母样真菌与常见寄生虫卵大小、形态以及临床表现的区别。
方法 将灵芝孢子粉保健品、两例口服灵芝孢子粉保健品患者及一例粪便真菌感染患者的粪便分别以 0.9%氯化钠溶液涂片镜检，在显微镜下观察灵芝孢子的大小及形态特点，并结合临床表现与常见寄生虫卵标本图例进行比较。
结果 灵芝孢子、酵母样真菌与寄生虫卵有相似之处，但也各有特点。
结论 在检验工作中，粪便中查到大量类寄生虫卵实体时，应认真观察, 仔细分析,详细询问患者的病史、生活习惯、服药情况及饮食结构，再密切联系临床表现，结合显微镜下的大小、形态及特征来做出鉴别。

PU-4061

肺栓塞 25 例临床分析

陈剑[2]、周利[1]、于属灵[1]、白张弘蕾[1]、冯磊[1]
1. 玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）
2. 玉溪市人民医院医学检验科（昆明医科大学第六附属医院医学检验科）

目的 探讨极易误诊误治的肺栓塞早期诊断及干预治疗。
方法 对我院 2 年来已确诊的 22 例肺栓塞进行回顾性分析。

结果 经抗凝、溶栓治疗，其中 19 例 3-6 月低分子肝素抗凝治疗，2 例终身抗凝，4 例大面积栓塞溶栓治疗。23 例好转及治愈占 91%，2 例恶化及死亡占 8%。
结论 临床工作中应注意肺栓塞可能，发现疑似病例要早诊断、早干预、早治疗，能很好的提高治愈率。

PU-4062

The proteasome inhibitor bortezomib disrupts tumor necrosis factor-related apoptosis-inducing ligand (TRAIL) expression and natural killer (NK) cell killing of TRAIL receptor-positive multiple myeloma cells

Xiaoli Feng
Clinical laboratory center of the second hospital of Shandong university

Bortezomib, a potent 26S proteasome inhibitor, is approved for the treatment of multiple myeloma (MM) and clinical trials are under way to evaluate its efficacy in other malignant diseases. However, cytotoxic effects of bortezomib on immune-competent cells have also been observed. In this study, we show that bortezomib downregulates cell surface expression of tumor necrosis factor-related apoptosis-inducing ligand (TRAIL) on primary human interleukin (IL)-2-activated natural killer (NK) cells. Pharmacological inhibition of the transcription factor, NF-kappaB also profoundly decreased TRAIL expression, suggesting that NF-kappaB is involved in the regulation of TRAIL expression in activated human NK cells. Furthermore, perforin-independent killing of the human MM cell lines RPMI8226 and U266 by NK cells was markedly suppressed following bortezomib treatment. In addition, blocking cell surface-bound TRAIL with a TRAIL antibody impaired NK cell-mediated lysis of the TRAIL-sensitive MM cell line, RPMI8226. In conclusion, the proteasome is likely to be involved in the regulation of TRAIL expression in primary human IL-2-activated NK cells. Proteasome inhibition by bortezomib disrupts TRAIL expression and TRAIL dependent and/or independent pathway-mediated killing of myeloma cells, suggesting that bortezomib may potentially hamper NK-dependent immunosurveillance against tumors in patients treated with this drug.

PU-4063

一例双克隆的慢性淋巴细胞白血病的实验室检查特征分析并文献复习

李良梅
四川金域医学检验中心有限公司

目的 探讨一例双克隆的慢性淋巴细胞白血病的实验室检查结果分析并文献复习。
方法 对一例双克隆的慢性淋巴细胞白血病的临床资料、骨髓细胞形态学、骨髓活检、颈部淋巴结活检、流式细胞学及分子生物学检查的结果分析。
结果 骨髓细胞形态学分析提示成熟小淋巴细胞占 93.5%；骨髓活检与颈部淋巴结活检免疫表型符合 CLL/SLL，骨髓流式检测到约 82.54%单克隆 B 淋巴细胞，表达 CD19、CD20、CD5，部分表达 CD23、CD200、CD22、CD79b、HLA-DR，不表达 CD10、FMC7、CD103，但是 CD19 阳性 B 细胞分两群，一群 CD19 相对较弱，sKappa 轻链呈限制性表达；一群 CD19 相对较强，sLambda 轻链呈限制性表达；表型符合 CD5+CD10-成熟小 B 细胞淋巴瘤/白血病。分子生物学检测到 TP53 基因突变，突变位于 exon8,突变频率 76.4%，位点测序深度 2415X；检测到 IGHV 单

克隆重排（2 个克隆），一个克隆突变程度＞2%，另一克隆突变程度≤2%；结合临床表现及 MICM 相关检查结果，综合诊断为 CLL。
结论 表达双克隆的慢性淋巴细胞白血病较为罕见，当肿瘤细胞同时表达 Kappa、Lambda 轻链时，需根据肿瘤细胞表型的差异进行精确设门，仔细辨别其克隆性，以免导致疾病漏诊或误诊。疾病的临床表现、完善的免疫表型、形态学及病理活检、分子生物学等相关检查有助于该类疾病的精准诊断及预后评估。

PU-4064

红细胞分布宽度对系统性红斑狼疮疾病活动度的评估价值

谢婷彦、丘世飏
中南大学湘雅医院

目的 探讨红细胞分布宽度（RDW）与系统性红斑狼疮（SLE）疾病活动度之间可能存在的关系。
方法 收集 70 例 SLE 患者及 60 例健康体检者 RDW、ESR、CRP 及 24h 尿蛋白结果等相关临床数据，对 SLE 患者进行 SLEDAI-2K 评分并按评分划分为活动期和缓解期两组，观察 RDW 在各组中的差异，分析 RDW 与 SLEDAI-2K 评分、ESR、 CRP 及 24h 尿蛋白之间的相关性，绘制 ROC 曲线探索 RDW 对 SLE 疾病活动性的评估价值。
结果 RDW 值在 SLE 活动期高于缓解期，且均显著高于健康对照组，三组之间两两比较，差异均具有统计学意义（P＜0.05）；RDW 与活动期组 SLEDAI-2K 分值、CRP、ESR 呈正相关（r=0.588、0.405、0.382，P<0.05），与 24h 尿蛋白之间无明显相关关系；RDW 对 SLE 病情活动性评估的 ROC-AUC 为 0.840，当 RDW 取 13.9%为诊断界值时，评估效价最高。
结论 RDW 的测定对评估 SLE 疾病活动度具有一定的临床应用价值。

PU-4065

肝素酶纠正的血栓弹力图对肝素应用后凝血功能监测的临床研究

康海全、马萍
徐州医科大学附属医院

目的 通过肝素酶纠正的血栓弹力图（hmTEG）研究不同肝素残留情况对凝血功能的影响。
方法 回顾分析徐州医科大学附属医院 2019 年 1 月-2020 年 12 月心胸外科患者术后肝素残留检测样本 89 例（术前凝血功能均正常）。分别分析①非肝素残留组、肝素残留组、肝素过量组三组内 CK-TEG 和 CKH-TEG 的 R、K、α 角、MA、CI 五组参数间有无差异。②非肝素残留组、肝素残留组、肝素过量组三组间 CKH-TEG 的 R、K、α 角、MA、CI 五组参数间有无差异。
结果 非肝素残留组中，CK-TEG 和 CKH-TEG 各参数比较，K 值、α 角、MA 值、CI 值差异无统计学意义,R 值差异有统计学意义(P<0.001)。 肝素残留组中，CK-TEG 和 CKH-TEG 各参数比较，MA 值差异无统计学意义，R 值、K 值、α 角、CI 值差异均有统计学意义(P 值均<0.001)。肝素过量组中，CK-TEG 和 CKH-TEG 各参数比较，R 值、K 值、α 角、MA 值、CI 值差异均有统计学意义(P 值均<0.001）。非肝素残留组、肝素残留组、肝素过量组三组间 CKH-TEG 各参数比较 R 值、K 值、α 角、MA 值、CI 值组间整体均有统计学差异(P 值分别为<0.001、0.002、0.002、0.042、<0.001)。经组间两两比较发现，MA 值三组间无差异，R 值、K 值、α 角、CI 值在肝素残留组和肝素过量组均与在非肝素残留组差异显著(P<0.05)。
结论 非肝素残留组肝素仅影响凝血因子功能，肝素残留组肝素影响凝血因子功能和纤维蛋白原功能，肝素过量组肝素影响凝血因子功能、纤维蛋白原功能和血小板功能。纠正肝素影响后，肝素残留组和肝素过量组相较于非肝素残留组凝血因子功能、纤维蛋白原功能、综合凝血功能仍明显减弱。

PU-4066

巨核细胞异形性改变与骨髓增殖性肿瘤诊断分型相关性研究

张凤、郑朱鑫、陈丹红、李景岗、刘声平、高飞
福建医科大学附属协和医院

目的 收集 88 例 MPN 患者及 187 例中老年正常对照骨髓涂片，研究骨髓巨核细胞增多程度及形态特征在 MPN 四种常见亚型 CML、PV、ET、PMF 中是否具有特征性改变，为骨髓涂片中巨核细胞计数、形态特征在 MPN 诊断分型提供一定参考。
方法 纳入符合标准的 88 例确诊 MPN 患者及 187 例正常对照组的骨髓涂片。染色后计数全片巨核细胞及 20mm×15mm 框内巨核细胞总数，并分类 200 个巨核细胞。分类计数骨髓粒系、红系、单核细胞及 NAP 化学染色等骨髓细胞分类计数结果，对巨核细胞发育阶段及形态异型性分类计数并统计。
结果 计数骨髓涂片单位面积内与全片巨核细胞有同等意义，四种 MPN 巨核细胞较对照组数量增多，但差别无统计学意义，巨核细胞各发育阶段百分比在正常对照组及 4 型 MPN 中差异无统计学意义。4 型 MPN 亚型 1~5 分叶颗粒型巨核细胞均低于正常对照组，PV 组 6-10 分叶颗粒巨核细胞较正常对照及其他 3 型 MPN 明显增多；细胞质/细胞核空泡型巨核细胞在 4 型 MPN 中增多而正常对照组罕见，可用于 MPN 初筛；巨核细胞核质比明显缩小为 ET 特征性改变，占 40%，其他组罕见。
结论 骨髓涂片巨核细胞计数及发育阶段分类在 MPN 患者诊断价值有限，巨核细胞形态分类可辅助 PV、ET 诊断。

PU-4067

蠊缨滴虫致慢性咽炎感染一例

朱云波
芷江侗族自治县人民医院

本例患者咽痒、哽噎感、轻咳吐白色泡沫痰半年；取痰液加生理盐水直接涂片，在光学显微镜下观察，可见活动的蠊缨滴虫；针对病原体予以甲硝唑治疗后，患者症状消失。目前，蠊缨滴虫导致慢性咽炎的病例较少，且基层检验人员对蠊缨滴虫的形态认识不足，在临床诊治过程中需提高警惕和认识，以防漏诊。

PU-4068

阿加曲班治疗进展性缺血性卒中疗效的影响因素分析

唐小童
中国人民解放军北部战区总医院

目的 在进展性缺血性卒中患者中探讨影响阿加曲班给药 2 小时后 APTT 水平及疗效的因素。
方法 我们对 50 例急性缺血性卒中患者基本信息及入院/出院 NIHSS 评分进行统计。计算阿加曲班给药 2 h 后 APTT 升高水平，以反应阿加曲班抗凝治疗是否有效。根据入院时年龄、性别、体温、收缩压、舒张压、吸烟史、饮酒史、肝肾功、合并疾病情况进行分类比较。
结果 发现以 3.0μg/kg/分钟的初速度静脉泵入阿加曲班时，以 ATPP 值提高 1.5 倍为目标值,给药后 2 小时 APTT 比值达标患者与不达标患者，年龄存在显著差异（63.81±10.65 vs 56.62±10.14，P<0.05）。采用二元逻辑回归，把肝功和性别纳入模型，年龄仍与 APTT 达标情况具有相关性（b=0.08,sE=0.04, OR=1.09, CI=10.1-1.17, P<0.05）。结果显示首次 APTT 是否达标与 NIHSS

评分改善程度无显著差异。性别、体温、收缩压、舒张压、吸烟史、饮酒史、肝肾功、合并疾病情况对阿加曲班早期起效的影响无统计学差异。
结论 阿加曲班用于治疗急性缺血性卒中时，给药后 2 h APTT 是否达标与年龄相关，提示对于青年及老年前期患者可以给予更快的给药速度，以尽快发挥抗凝作用。

PU-4069

TAT 和 tPAI·C 联合 D-二聚体用于肺癌转移患者的诊断价值

吴楠楠[1]、项羽坤[2]、侯敏[1]
1. 天津胸科医院
2. 天津医科大学

目的 比较肺癌转移与非转移患者间血栓四项的差异，探讨血栓四项联合 D-二聚体在肺癌患者转移中的诊断价值。
方法 收集 2020 年 10 月至 2020 年 12 月于天津市胸科医院就诊的 288 例患者，其中包括 201 例肺癌患者、57 例肺良性疾病患者及 30 例健康对照者，分别检测血浆血栓四项血浆血栓调节蛋白(TM)、凝血酶－抗凝血酶复合物(TAT)、组织型纤溶酶原激活物－纤溶酶原激活物抑制剂复合物(tPAI·C)、纤溶酶－α2 纤溶酶抑制剂复合物(PIC)及 D-二聚体水平，绘制 ROC 曲线判断 TAT 和 tPAI·C 联合 D-二聚体用于肺癌转移患者的诊断价值。
结果 转移组 TAT、PIC 水平明显高于非转移组（P＜0.01），ROC 曲线显示 D-二聚体、TAT、tPAI·C 对肺癌转移的诊断价值。TAT 和 tPAI·C 联合 D-二聚体诊断的 AUC 高于单项检测(0.835 vs. 0.809、0.781、0.774)。
结论 TAT 和 tPAI·C 联合 D-二聚体可作为诊断肺癌转移的新标记物。

PU-4070

地中海贫血与缺铁性贫血患者的血常规结果的研究

朱志强
南方医科大学珠江医院

目的 对厚街镇缺铁性贫血与非复合型地中海贫血患者的血常规结果分析，根据其血液学指标的主要分布情况，探究其在地贫与缺铁贫的鉴别和地贫初筛的临床意义。
方法 将 52 例缺铁性贫血患者设定为缺铁贫组，52 例非复合型地中海贫血患者设定为地贫组，52 例健康体检者设定为对照组。比较 3 组血细胞参数 HB、HCT、MCV、MCH、RDW 水平并确立各参数的可信区间（95%）分布。
结果 经方差分析 SNK-q 检验的两两比较，地贫组、缺铁贫组、对照组的 HB、HCT、MCV、MCH、RDW 均有统计学差异（P＜0.05）；根据均数的可信区间分析，地贫组、缺铁贫组与对照组的可信区间(95%)无交叉重叠。
结论 红细胞参数在缺铁性贫血的临床鉴别和地中海贫血的初筛诊断有重要意义，可根据其血常规参数值大小作出初步的筛查。

PU-4071

Acquired hemophilia A secondary to autoimmune pancreatitis with elevated IG4

Qiang Feng[1]、JIANMIN LI[2]
1. Taian Central Hospital
2. 山东省泰安市中心医院

Acquired hemophilia A (AHA) is a rare disease resulting from autoantibodies against factor VIII (FVIII) that leads to bleeding. AHA associated with IgG4 related diseases is even rarer. The patient was diagnosed with IgG4 associated autoimmune pancreatitis in January 2019, and the condition improved after two hospitalizations. However, 22 months later, the patient was admitted to hospital due to generalized bleeding points. After laboratory tests, he was diagnosed with AHA. He recovered quickly after hormone therapy and plasma exchange. Although IgG4 is associated with IgG4-related disease and AHA, its relevance to the etiology of both diseases is not well understood.

PU-4072

M 蛋白阳性临床特点分析

林艳、林倩、刘亭莉、何春容、杨清
成都市第三人民医院

目的 探讨血清蛋白电泳筛查在筛查 M 蛋白中的意义及 M 蛋白阳性病例临床特点分析。
方法 收集 2019 年 3 月至 2021 年 2 月住院病人的血清蛋白电泳中，异常尖峰图形病例样本，通过免疫分型确认其中 M 蛋白为阳性的病例，并整理分析病人临床资料。
结果 与同期 100 例住院对照病人的临床资料相比 ，M 蛋白阳性病例在在血红蛋白浓度，白细胞比例，总蛋白定量，白蛋白定量，白球比，免疫球蛋白 IgG、IgA、IgM 定量，尿蛋白/肌酐并无显著差异。
结论 血清蛋白电泳在筛查 M 蛋白阳性病例方面，相对多发性骨髓瘤、单克隆球蛋白疾病的其他生化指标，具有无法比拟的优势。

PU-4073

冷凝集素对血常规结果的影响及处理方法

戚佩谊
南方医科大学珠江医院

血细胞分析结果的准确直接影响临床疾病的诊断和治疗，但准确与否，除了标本采集、仪器性能、操作人员等因素外，还有一个重要原因即某些血液标本自身存在干扰血细胞分析仪检测结果准确性的因素，如冷凝集、脂血、溶血、寄生虫感染等。冷凝集素是一种红细胞自身免疫性抗体，绝大多数为 IgM，少数为 IgG 或 IgA。在正常生理条件下，冷凝集素可以低活性存在于健康人的血清中，其滴度不超过 1:16，因此不会出现血细胞凝集现象，但是当温度低于某一温度时，冷凝集素浓度将升高，处于循环中的自身抗体可与红细胞表面抗原结合，使血液凝集，4-27 ℃为其在体外的最适温度，4℃时出现明显红细胞凝集现象。

目前常见的冷凝集消除方法

1. 水浴法：将标本置于 37℃水 浴箱中水浴 30 分钟后立即上机检测。

2. 血浆置换法：将标本低速（500r/min）离心 2 分钟，用加样器取出约 3/4 的血浆，用已预温 10 分钟的生理盐水等量置换血浆，充分混匀，如此置换 3 次后上机检测。

3. 提高室温法：将室内温度提高至 25～30℃并稳定 1 小时，同时将标本置 37℃水浴箱中水浴 30 分钟后上机检测。

PU-4074

血液分析仪在急慢性白血病检验中的应用价值

周重阳
滨州医学院烟台附属医院

目的 研究血液分析仪在临床中对急慢性白血病检验的应用价值，避免白血病患者漏检，为临床分析和同步病情指导提供有效信息 。

方法 选用 2019 年 5 月到 2020 年 5 月期间本医院确诊的成年急性白血病患者 15 位作为急性白血病组，慢性白血病患者 15 位作为慢性白血病组，和同期进行健康体检的 15 位作为参照组，所有研究对象采取静脉全血后使用血液分析仪进行检验，对检验结果进行统计学分析，比较三组测定的实验数据得出结论。

结果 急性白血病的白细胞数为(90.1±0.4)×109/L，C 反应蛋白为(113.4±5.3)mg/L 均高于对照组，急性白血病血红蛋白为(35.5±6.2)g/L 低于对照组，俩组对比均具有统计学意义，P＜0.05。慢性白血病的白细胞数为(105.2±0.4)×109/L，C 反应蛋白为(185.6±4.2)mg/L 均高于对照组，慢性白血病血红蛋白为(34.3±7.3)g/L 低于对照组，俩组对比均具有统计学意义，P＜0.05。急慢性白血病的白细胞计数，C 反应蛋白，血红蛋白三组数据之间不具有统计学意义，P＞0.05。

结论 血液分析仪对于急慢性白血病临床检验具有极高的应用价值，能较为准确的诊断出急慢性白血病，具有自动化程度高，检测参数多，精密度高，速度快，智能化程度高等优点，可作为急慢性白血病检查的首选方法，为患者临床治疗提供有效参考。

PU-4075

医院获得性肺血栓栓塞症的临床特征和危险因素分析

梁湘辉[2]、杨奥烽[3]、赵声远[1]、唐红英[4]
1. 中南大学湘雅医院检验科
2. 中南大学湘雅医院检验科
3. 中南大学湘雅医学院
4. 中南大学湘雅医院生殖医学中心

目的 了解医院获得性肺血栓栓塞症（Hospital-acquired Pulmonary Thromboembolism，HA-PTE）患者的临床特征；探究 HA-PTE 的危险因素及其导致的医疗和经济负担；评估实验室检验项目对于 HA-PTE 的预测价值。

方法 回顾性收集并分析某三甲医院 2018 年度 HA-PTE 患者的临床资料并采用 1：1 配对的病例-对照研究，收集 HA-PTE 患者（病例组）和匹配的非 HA-PTE 患者（对照组）的临床资料和实验室检验数据。应用条件 Logistics 回归模型对 HA-PTE 的危险因素、导致的医疗和经济负担以及实验室检验项目的预测价值进行分析。

结果 该中心 2018 年确诊 HA-PTE 患者共 68 例，男性多于女性（54.41%vs45.59%），高龄患者（≥65 岁）占 47.06%。循环系统疾病为最常见的基础疾病（88.24%）。内外科患者数相同（48.53%），2.94%来自 ICU。患者总住院时长为 1-52 天（中位天数 17 天），19.1%的患者曾入住 ICU。最常见的侵入性操作为外科手术（48.53%）和留置导尿管（48.53%）。患者的总医疗花销为 6106.04-357176.5 元。入住 ICU（OR=7.800，95%CI 1.687-36.061，P=0.009）和抗生素使

用史（OR=2.964，95%CI 1.282-6.855，P=0.011）为 HA-PTE 的危险因素。HA-PTE 患者的总住院时长和总医疗花销显著高于非 HA-PTE 患者（P<0.001/P=0.008）。HA-PTE 患者的纤维蛋白（原）降解产物浓度显著高于非 HA-PTE 患者（P=0.002）。
结论 ICU 入住史和抗生素使用史是 HA-PTE 的危险因素。HA-PTE 会给病人带来更重的医疗和经济负担。纤维蛋白（原）降解产物浓度对于 HA-PTE 具有预测价值。

PU-4076

全自动尿有形成分分析仪的使用过程遇到的问题

才玥
吉林大学第一医院

目的 为了了解 sysmex UF-5000 全自动尿有形成分分析仪的主要性能，探讨应用过程中出现的问题。
方法 采用随机选择标本的方法，对该仪器主要检测参数红细胞、白细胞、上皮细胞、管型及细菌等影响因素进行测试。
结论 sysmex UF-5000 全自动尿有形成分分析仪作为尿有形成分检查的仪器，可为临床提供快速准确的结果。

全自动尿有形成份分析仪 UF-5000 用蓝色半导体激光束照射经过核酸荧光染色后在鞘流贯流分析池中形成的鞘流样本，并通过对从各粒子产生的前方散射光、侧向散射光、消偏振的侧向散射光以及侧向萤光信号转换成的光电信号进行分析，从而对各个粒子进行识别。

流式细胞计数法: 流式细胞术（FCM）采用将激光照射至细胞等粒子的方法测定产生的散射和荧光以确定粒子的特性。对细胞中的特定物质进行荧光染色，将细胞置于悬浮状态并包裹在鞘液中，继而通过喷嘴排出。然后用紧密聚焦的激光束照射到细胞上，这会产生散射光和荧光。使用这些光信号作为参数，可以生成基于光强度的一维直方图以及基于荧光强度和散射光强度的二维散点图，从而对细胞进行详细的测定。前向和侧向散射的入射激光被称为散射光，散射光的强度可指示细胞的大小和表面状况。根据从细胞中染色元素发出的荧光可基于荧光标记抗体和荧光颜料的属性对细胞表面、胞浆属性和细胞核（RNA 和 DNA 数量）等细胞特性进行定量测定。基于流式细胞仪原理，全自动尿有形成份分析仪 UF-5000 可将尿液中的粒子分离为 RBC （红细胞） 、WBC（白细胞）、EC （上皮细胞）、Squa.EC （上皮细胞）、CAST （管型）和 BACT （细菌）等，并予以定量标示。

PU-4077

乳腺癌外周血循环肿瘤细胞的检测及临床意义

李小月
安庆市第一人民医院

目的 探讨乳腺癌患者外周血循环肿瘤细胞水平及其与临床病理特征的关系。
方法 选取本院 2018 年 1 月至 2018 年 12 月经病理组织学证实的乳腺癌患者 16 例，清晨空腹抽取其肘正中静脉血 10ml，24h 内检测。用氯化铵裂解血液中的红细胞，离心弃上清留取 5ml，再将磁珠微粒加入沉淀中充分结合白细胞，用分离溶液分离出被磁珠结合的白细胞。并行免疫荧光原位杂交检测，有两个或者两个以上的探针信号即为肿瘤细胞， 记录肿瘤细胞个数，计算 CTCs 阳性率并分析其与临床病理特征的关系。 选取同期的 16 例乳腺良性病变患者作为阴性对照组，用同样的方法检测肿瘤细胞数，并进行统计学分析。

结果 乳腺癌组外周血 CTCs 阳性率为 87.5%（14/16），明显高于对照组外周血 CTCs 阳性率 6.25%（1/16），差异具有统计学意义（p＜0.05)；乳腺癌患者 CTCs 水平不仅与年龄无关，同时与乳腺癌 ER、PR、HER-2 表达均无关（p＞0.05)。
结论 乳腺癌患者外周血中 CTCs 水平与年龄及临床病理特征无关，乳腺癌早期阶段外周血中便可检出 CTCs，提示可能在肿瘤早期阶段即发生微转移。

PU-4078

STA Compact Max 全自动凝血仪检测 PLG、AT-Ⅲ、PC、PS 的性能验证

宋洪平、解兴欣、方美懿、唐喻春、王灵禧、赵璐、王榕
重庆金域医学检验所有限公司

目的 评价 STA Compact Max 全自动凝血仪检测 PLG、AT-Ⅲ、PC、PS 四个项目性能。
方法 参照美国临床和实验室标准化协会(CLSI)系列指南文件、科室质量体系文件和仪器厂家标准对 STA Compact Max 全自动血凝仪的精密度、线性范围、携带污染率、参考区间进行性能验证。
结果 STA Compact Max 检测 PLG、ATIII、PC、PS 的项目批内精密度 ATⅢ≤5.0%，PLG≤6.25%，PC≤5.0%，PS≤6.25%，批间精密度 ATⅢ≤6.67%，PLG≤8.33%，PC≤6.67%,PS≤8.33%。四个项目不准确度均小于 10%。PLG 线性验证试验理论值和实测值的回归方程 Y=0.9994X+3.0452,r2=0.9973,，ATⅢ线性验证试验理论值和实测值的回归方程为 Y=1.0102X-1.415,r2=0.9994,PC 线性验证试验理论值和实测值的回归方程为 Y=0.9931X-2.3756,r2=0.9978,PS 线性验证试验理论值和实测值的回归方程为 Y=1.0471X-1.1268,r2=0.9895。均符合斜率在 1±0.05 范围内,相关系数 r2≥0.95，验证结果表明 PLG、ATIII、PC、PS 实测值和理论值之间线性关系良好。实验仪器携带污染率合格，实验结果 3SD1-X2+X1>0,满足 X2-X1<3SD1。参考范围验证结果 PLG、ATIII、PC、PS 无离群值，PLG 的 R 值为 0.9，超出 95%置信区间的点数 0 个；ATIII 的 R 值为 1.0，超出 95%置信区间的点数 0 个；PC 的 R 值为 1.0，超出 95%置信区间的点数 0 个；PS 的 R 值为 1.0，超出 95%置信区间的点数 0 个。
结论 STA Compact Max 全自动凝血仪检测 PLG、AT-Ⅲ、PC、PS 项目性能验证均符合质量要求，方法学的稳定保证了检测结果的准确可靠，可以满足临床检测的要求。

PU-4079

全自动阴道分泌物分析仪性能评价方式的建立

王琪
东南大学附属中大医院

目的 对全自动阴道分泌物检测仪 AVE320 的有形成分检测，及配套的联合检测试剂盒进行性能评价。
方法 有形成分的日内重复性：从临床上取得有形成分浓度高的样本若干份，混合均匀后，均分成 10 管依次检测。记录仪器检测结果。有形成分的日间重复性：使用仪器配套的高低 2 个水平的质控品，按要求将其混匀后分别进行检测，每天检测 4 次，连续检测 5 天。记录每天的结果。有形成分的正确度验证：同批号质控高低值混匀后各检测 10 次，记录结果。 有形成分的方法学比对：连续 4 天，每天抽取 5 个新鲜样本进行仪器的有形成分识别和人工镜检，计算两者的符合率，所选择样本中阳性占 80%。有形成分的携带污染率：人工镜检筛选出有形成分浓度高的样本 10 份。将样

本混合并混匀，分装在五只试管内。取去离子水，分装在五个试管内。10 份标本穿插检测，记录所有结果。
联检试纸阴性阳性符合率：使用同批试纸条，将 AVE320 阴、阳性质控品，分别检测 10 次，计算符合率。联检试纸条日间重复性：使用同批试纸条，连续 5 天，将 AVE320 阴、阳性质控品，记录所有结果。联检试纸的批间重复性：随机抽取 5 个新鲜样本，使用两个不同批号的试纸， 每个批号每个样本做 5 次，记录所有结果。联检试纸的携带污染率：人工镜检选出有形成分浓度高 10 个样本。混合并充分混匀，分装在五只试管内。取去离子水，分装在五个试管内。将 10 份标本穿插检测，记录所有结果。
结果 本组实验初步建立了用于评估 AVE320 全自动阴道分泌物检测仪的方案。形态学项目：红、白细胞、杂菌、杆菌、鳞状上皮细胞，线索细胞、滴虫、霉菌的日内、日间重复性实验、正确度验证、方法学比对、携带污染率，联检试纸：PH 值，过氧化氢、白细胞酯酶、b-葡萄糖醛酸苷酶、唾液酸苷酶、乙酰氨基葡萄糖苷酶，的阴阳性符合率，日间、批间重复性，携带污染率，均符合仪器本身技术要求和临床应用检测技术指标实际要求。可为临床提供准确可靠的检测结果。

PU-4080

肾移植后微小病毒 B19 感染导致纯红细胞再生障碍贫血 2 例实验室结果分析

李倩、杨昆荣
昆明市第一人民医院甘美医院

目的 通过相关实验室指标特点，探讨肾移植术后人类微小病毒 B19 感染导致的纯红细胞再生障碍性贫血（PRCA)诊断，提高纯红再障的诊断率。
方法 2021 年 3 月共诊断肾移植术后人类微小病毒 B19 感染导致的纯红细胞再生障碍性贫血 2 例。排除出血、溶血等情况，对患者的临床资料、血常规、骨髓象等检查，提示典型 PRCA 表现，微小病毒 B19DNA 阳性。
结果 2 例纯红再障患者均有贫血的症状和体征，一例血红蛋白中度减低，一例血红蛋白重度减低，网织红细胞严重减低，血小板正常，骨髓中红系严重减少。
结论 肾移植术后出现顽固性贫血，应考虑 HPV B19 感染导致的 PRCA。骨髓细胞学检查及 HPV B19DNA 检测结果是诊断纯红再障的依据。

PU-4081

血清外泌体 hsa_circ_0007989 在胃癌中作用机制及临床价值研究

侯杰
江苏大学

目的 本研究的目标是在胃癌患者血清外泌体中寻找差异表达的环状 RNA，探讨其作为胃癌早期诊断标志物的价值，深入探讨在胃癌发生发展中的作用机制以及作为治疗靶点的可行性。
方法 收集 3 对健康体检者及胃癌患者的血清，进行外泌体环状 RNA 表达谱芯片分析。通过血清外泌体及组织样本的大规模临床标本验证选定差异表达的环状 RNA，ROC 曲线及生存曲线分析用于评价其诊断效能。在体外胃癌细胞系模型和体内动物模型中过表达及沉默环状 RNA 研究其生物学功能。机制方面，我们通过生物信息学预测可能结合的 miRNA。RNA 免疫共沉淀实验和双荧光素酶报告基因实验验证。回补实验探讨环状 RNA 通过调节 miRNA 的下游途径发挥其生物学作用。

结果 外泌体环状 RNA 表达谱芯片分析显示有 2798 个差异性表达的环状 RNA ，其中 187 个上调，2611 个下调。50 对胃癌组织和 25 例血清外泌体标本结果表明 hsa_circ_0007989 呈现下调趋势，其 ROC 曲线下面积分别为 0.64 及 0.78，提示 hsa_circ_0007989 具有一定诊断价值，。沉默 hsa_circ_0007989 后胃癌细胞增殖、迁移能力增强，凋亡比例下降。生物信息学预测显示 hsa_circ_0007989 存在潜在的 miRNA 结合位点，有可能通过结合 miRNA 发挥调控作用。
结论 血清来源的外泌体环状 RNA hsa_circ_0007989 在胃癌早期诊断方面有一定优势，体外实验初步显示其具有抑制胃癌作用，可能成为胃癌诊断与治疗的新靶点。

PU-4082

临床肝癌患者 PD-L1 表达水平与索拉非尼药效的相关研究

牛蕾蕾
山东大学第二医院

目的 肝癌发病率位居全球癌症前列，临床试验表明多靶点激酶抑制剂索拉非尼(sorafenib)是唯一可以有效延长中晚期肝癌患者总生存期的药物，遗憾的是，大多数肝癌患者对索拉非尼存在原发性耐药，大大降低了索拉非尼的临床疗效和利用率，加之该药价格昂贵，因此，找到可以指示索拉非尼药效的肿瘤分子标记物变得尤为重要。
方法 在本研究中，我们搜集了 65 例于 2012-2015 年间经手术切除后接受索拉非尼化疗的肝癌患者的临床资料，利用免疫组化技术检测肝癌组织中 PD-L1 的表达水平，并将染色结果划分为阴性，弱阳性，阳性与强阳性，将阴性与弱阳性的肿瘤组织定义为 PD-L1 低表达，阳性与强阳性的肿瘤组织定义为 PD-L1 高表达，利用生存 分析观察索拉非尼在 PD-L1 表达水平不同的肝癌患者中的疗效。
结果 约 38.5%(25/65)的患者肿瘤组织为 PD-L1 低表达，61.5%(40/65)的患者肿瘤组织为 PD-L1 高表达。在 PD-L1 低表达组，患者总生存期为 15.6 个月; 而在 PD-L1 高表达组，患者总生存期为 12.7 个月。生存分析结果显示该差异具有统计学意义($p<0.05$)。
结论 PD-L1 或许可以作为潜在的肿瘤分子标记物，有助于临床医生将对索拉非尼敏感的患者从中筛选出来，进而接受有效的治疗，检测肿瘤组织中 PD-L1 的表达可以预测患者对索拉非尼的敏感性。

PU-4083

长链非编码 RNA MGC27382 检测水平指示肺癌患者预后的相关研究

牛蕾蕾
山东大学第二医院

目的 流行病学资料表明非小细胞肺癌高病死率与肿瘤组织持续异常增殖及远处转移有关，因此，找到调控这两方面的作用机制并以此为靶点治疗非小细胞肺癌是目前人们关注的热点，长链非编码 RNA 与肿瘤细胞增殖、侵袭转移密切相关，在本研究中，我们期望明确长链非编码 RNA 在这其中的作用。
方法 利用 RT-qPCR 技术，我们检测了长链非编码 RNA MGC27382 在 30 组肿瘤组织和癌旁组织中的表达水平，利用慢病毒过表达/敲除系统构建 MGC27382 的稳转/稳敲细胞株，利用 western blot 实验检测上调/下调 MGC27382 对细胞周期蛋白和 AKT/GSK3β 的调控，利用 MTT 和 Transwell 实验检测 MGC27382 表达水平对细胞增殖和侵袭能力的影响。

结果 实验结果表明 80%（24/30）的非小细胞肺癌低表达 MGC27382，过表达 MGC27382 能抑制 cyclin D1、cyclin E 以及 AKT/GSK3β 信号通路的表达，此外，MGC27382 稳转细胞株的增殖能力和侵袭能力减弱。
结论 MGC27382 在非小细胞肺癌中低表达，上调 MGC27382 抑制细胞增殖和侵袭，靶向 MGC27382 或许有助于提高非小细胞肺癌患者预后。

PU-4084

嗜血细胞综合征与 EB 病毒感染的相关分析

石洪琼
昆明医科大学第一附属医院

目的 探讨嗜血细胞综合征与 EB 病毒感染的相关分析。
方法 选取 2014 年 12 月～ 2017 年 8 月本院收治的嗜血细胞综合征(HPS)患者 31 例，对其 EB 病毒感染情况进行回顾性分析。
结果 31 例患者中 EB 病毒阳性有 22 例。
结论 EBV- HPS 是 HPS 中常见的一种类型，在临床工作中应该引起高度重视。

PU-4085

多发性骨髓瘤实验室诊断分析

马晓波
云南省昆明医科大学第一附属医院

目的 研究多发性骨髓瘤(Multiple Myelome，MM)细胞形态学及其他实验室相关指标特征, 提高对多发性骨髓瘤的认识。
方法 回顾性分析 22 例多发性骨髓瘤患者的实验室检查资料, 其中瘤细胞比例按照 Greipp 标准〔1〕, 重新进行评估。
结果 22 例多发性骨髓瘤中, 贫血者 20 例，血沉增快 15 例,平均为 106.5 mm /h。。, 蛋白尿 9 例平均为(++)，尿酸>90 umol/L 者 22 例。尿本周氏蛋白的检查者 6 例。尿轻链比值异常 17 例，血清轻链比值异常 22 例。22 例患者进行了骨髓穿刺镜检，浆细胞比例>=10%者 21 例，原始浆细胞型及幼稚型浆细胞 22 例(100%),其中原始浆及幼稚浆细胞>15%者 12 例。红细胞缗钱状排列 22 例， 12 例进行了骨髓活检，骨髓增生活跃，浆细胞片状分布 11 例，17 例患者进行了影像学 CT 检查，14 例患者骨代谢异常，虫噬状骨质破坏及不规则骨质吸收破坏。
结论 多发性骨髓瘤细胞形态学诊断结合实验室相关指标检查, 能够提高多发性骨髓瘤诊断的准确性, 为临床诊断提供可靠依据。

PU-4086

25 例低纤维蛋白原的肛肠科患者的回顾性分析

张婴嫱
联勤保障部队第 903 医院

目的 探讨因白眉蛇毒血凝素的应用，肛肠科低纤维蛋白原患者的低纤维蛋白情况，为临床用药提供指导意见。
方法 回顾分析 25 例低纤维蛋白原患者的用药、性别、年龄及低纤维蛋白情况。

结果 应用白眉蛇毒血凝酶治疗两天左右患者出现不同程度的低纤维蛋白原血症:其中 17 例明显降低（<1.0 g/L 但≥ 0.50 g/L），8 例达危急值（<0.5 g/L）。25 例患者中，男 16 例，占 64%；女 9 例，占 36%；年龄 22-78 岁，其中大于 70 岁 2 例，40-70 岁 19 例，小于 40 岁 4 例。
结论 白眉蛇毒血凝素应用广泛，但易导致纤维蛋白原降低,临床应用中要合理使用，特别注意给药期间凝血功能的监测,保证患者用药安全。

PU-4087

CRP、胆红素等指标在新生儿黄疸早期检测的临床意义

张敏
滨州医学院烟台附属医院

目的 研究探讨血清淀粉样蛋白 A（SAA）、γ-谷氨酰基转移酶(γ-GGT)、C-反应蛋白(CRP)检测浓度与胆红素实验室检测浓度之间存在什么关系以及早期检测有什么临床意义。
方法 选取 2019 年 7 月到 2020 年 1 月期间，滨州医学院烟台附属医院的新生儿 144 例，其中高胆红素血症 114 例，健康新生儿 30 例，分析各组新生儿的血清淀粉样蛋白 A（SAA）、γ-GGT、CRP 浓度的改变与 TBIL 浓度、DBIL 浓度的之间的关系。
结果 高胆红素血症组患儿 CRP、γ-GGT、TBIL、DBIL 检测指标的浓度均高于健康新生儿组，差异有统计学意义（P<0.05）。SAA 浓度实验组和对照组差异无统计学意义（P>0.05）。病理组 CRP 浓度、γ-GGT 浓度与 TBIL、DBIL 呈正相关（P<0.05），SAA 浓度与 TBIL 浓度呈正相关，与 DBIL 浓度呈负相关。
结论 实验组 CRP、γ-GGT 浓度的改变与胆红素浓度的改变之间的关系是呈正相关的，且对临床早期新生儿黄疸病程的监测及诊疗方案具有重要的参考意义；而 SAA 与胆红素之间的关系仍需要我们进一步研究证实。

PU-4088

IL-6 表达水平与非霍奇金淋巴瘤的相关性研究

方文硕
滨州医学院烟台附属医院

目的 研究非霍奇金淋巴瘤 (NHL)患者血清 IL-6 含量变化，并探讨其临床意义。
方法 利用电化学发光免疫分析检测 110 例非霍奇金淋巴瘤患者及 70 例健康对照组血清中 IL-6 的含量，并分析其与非霍奇金淋巴瘤的临床分期、肿瘤负荷的关系。
结果 患者组血清中 IL-6 含量较正常对照组均明显升高，差异有显著性 （P＜0.01）。根据 NHL 临床分期标准对研究组患者进行临床分期，Ⅲ、IV 期患者血清中 IL-6 水平较Ⅰ期和Ⅱ期明显升高（P ＜ 0.01），Ⅱ期患者血清 IL-6 含量亦比Ⅰ期患者高，其差异有显著性（P ＜ 0.01），IV 期患者血清 IL-6 显著高于 III 期患者血清 IL-6 含量（P ＜ 0.01）。随着临床分期增加，患者血清中 IL-6 含量呈递增趋势，各期间比较均有显著性差异 (P<0.01)。
结论 细胞因子 IL-6 的免疫失调与人类非霍奇金淋巴瘤的发病机制有非常紧密的关系。IL-6 血清表达水平与非霍奇金淋巴瘤的病程有重要相关性， NHL 患者血清中 IL-6 的含量，能够反映患者的肿瘤负荷，对非霍病情的判断具有重要意义。

PU-4089

LJ-5000 粪便分析仪与手工法检测对比分析

赵丹
滨州医学院烟台附属医院

目的 观察 LJ-5000 全自动粪便分析仪与手工操作结果的相一致性，评价全自动粪便分析仪的临床实用性。
方法 使用 LJ-5000 自动化粪便分析仪对 1000 份住院患者的粪便标本进行检测，包括标本的理学性状、病理有形成份和粪便隐血试验。同时，通过有经验的检验人员使用显微镜和手工方法对两种方法进行比较，比较两种方法结果的一致性，并以人工显微镜检验作为本次检验的金标准，与自动化粪便分析仪的结果进行比较，分析自动化粪便分析仪的临床实用性。
结果 自动化粪便分析仪与手工法的粪便理学性状检测结果之间无统计学差异（P＞0.05）；使用自动化粪便分析仪检出红细胞 150 例、白细胞 123 例、脂肪滴 70 例、霉菌 67 例、虫卵 6 例，检测结果与手工方法的镜检结果无统计学差异（P＞0.05）；自动化粪便分析仪隐血试验阳性 369 例，与手工法符合率为较相符。
结论 LJ-5000 自动化粪便分析仪检测结果与手工法检测结果一致性较好，并且有检测过程标准化、流程化，实验过程和工作环境更加洁净卫生，操作简便等优点，可以取代手工法进行推广使用。

PU-4090

对人工镜检作为 AML 患者外周血原始细胞复检“金标准”的思考

孙德华
南方医科大学南方医院

目的 本研究首次建立患者真实疾病情况的评价标准，以当前主流血液细胞分析仪和人工镜检为评价对象，分析其在 AML 患者诊疗过程不同阶段中对外周血原始细胞的检出能力及其差异。
方法 参考 NCCN 指南 AML 患者诊疗过程模型，制定患者疾病状态阳性和阴性判断标准，回顾性分析南方医院血液科 303 例 AML 患者的外周血样本，其中阳性组 76 例、阴性组 227 例。对明确分组的样本，使用人工镜检和 BC-6800Plus 血液分析仪这两种实验室外周血原始细胞筛查的方法进行检测并比较评估各自优劣性。
结果 以人工镜检为 Blast 检出的“金标准”进行分析， BC-6800Plus 血液细胞分析仪的 Blast 报警灵敏度可达 90.6%；以临床对患者疾病状态的定性判断为参照进行分析时，BC-6800Plus 对 Blast 的检出灵敏度分别为 97.4%，显著高于人工镜检 78.9%（P<0.05），当扩大人工镜检细胞到 500 时，灵敏度可显著提高至 94.7%；而在 Blast 检出特异性上，人工镜检特异性为 91.6%，显著高于 BC-6800Plus 的 68.3%（P<0.05）；在初始诊断和巩固治疗阶段，血液细胞分析仪对 41 例 AML 初诊样本和 5 例 AML 复发样本无一漏检，而人工镜检 12.5%（5/41）初诊假阴性样本和 20%（1/5）复发假阴性样本；应用 ROC 对 BC-6800Plus 和人工镜检的诊断效能进行评价，AUC 依次为 0.916 和 0.881，灵敏度和特异性分别为 97.4%和 68.3%、73.7%和 98.1%。
结论 高端血液细胞分析仪在 Blast 检测上具有高灵敏度的特性，能通过报警实现对 AML 患者外周血原始细胞的高效检出，为临床早期疾病早期预警提供依据；人工镜检可通过提高白细胞数量从而弥补原始细胞检出灵敏度低的问题，值得临床实验室思考常规人工镜检方法作为原始细胞复查“金标准”时的合理性及替代方法的可能性。

PU-4091

多发性骨髓瘤骨髓微环境中 B 细胞发育模式的研究

位金洺
滨州医学院烟台附属医院

目的 通过研究多发性骨髓瘤（Multiple myeloma，MM）患者骨髓微环境中 B 细胞各亚群的分布特点及发育模式，了解该疾病的发病机制，并讨论针对该疾病的可能存在的研究靶点。
方法 采用流式细胞学对其骨髓中各细胞群体进行测定和分析以明确 MM 患者骨髓微环境中 B 细胞的发育模式。通过对微环境中 NK 细胞和活化的 NK 细胞进行分析，明确 B 细胞和 NK 细胞在 MM 患者的疾病进展和预后中的作用。
结果 1.相对于“非 MM 患者”对象，MM 患者骨髓幼稚（Naive）B 细胞占总 B 细胞（CD19+）的比例明显减低，而记忆（Memory）B 细胞和活化（Activated）B 细胞占总 B 细胞的比例增高；2. MM 患者骨髓微环境中 NK 细胞占有核细胞的比例与“非 MM 患者”人群相比没有明显差异，但 MM 患者的活化 NK 细胞（CD27+ NK）比例明显低于正常人。3.与初诊时相比，经治疗后获得缓解的 MM 患者骨髓中的幼稚（Naive）B 细胞可出现一定升高，活化（Activated）B 细胞降低。
结论 MM 患者骨髓微环境 B 细胞分化发育异常，且整体处于免疫无应答状态；虽然记忆（Memory）B 细胞和活化（Activated）B 细胞的比例虽然较正常人有所增高，但并不能执行免疫功能，且增高的记忆 B 细胞可能与 NK 细胞的免疫抑制有关。

PU-4092

以急性胰腺炎为特征的肝吸虫病一例

闫平
吉林大学第一医院

目的 探讨肝吸虫性急性胰腺炎的临床特征，分析漏诊原因并提出减少漏诊的方法。
方法 对我院收治的 1 例因急性胰腺炎住院治疗的临床资料进行回顾性分析。
结果 本例患者因 4 天内无明显诱因出现上腹部疼痛,首次就诊于韩国首尔国立医院并住院接受治疗,诊断为急性胰腺炎，后回国于我院继续检查治疗。连续三天对患者粪便进行检查，其中两次查出肝吸虫虫卵，后详问病史，患者十余年前有食生鱼史，考虑肝吸虫病诊断明确,此前行腹部 CT 见肝内外胆管扩张，炎性可能，均考虑与肝吸虫病有关，予对症治疗后好转出院。电话随访半年,患者未再复发。
结论 肝吸虫感染诱发急性胰腺炎的病例并不常见,易发生漏诊情况,而全面细致分析病情,正确认识肝吸虫病,了解急性胰腺炎发作的诱因有利于减少肝吸虫病的漏诊。而粪便对肝吸虫卵筛查的重要性往往被轻视，关注急性胰腺炎的患者粪便筛查也是减少肝吸虫漏诊的关键。

PU-4093

乳腺癌化疗后继发急性髓系白血病 2 例

林慧君、候云龙
河南周口骨伤医院

目的 报道乳腺癌治疗后继发性白血病 2 例。
方法 报道 2 例乳腺癌继发急性髓系白血病患者的临床资料。
结果 2 例患者均为急性髓系细胞白血病(AML)，均有乳腺癌化疗史，其中 1 例化疗方案含环磷酰胺和表柔比星，潜伏期为 7 个月，继发急性髓系白血病 M2a,患者治疗效果好，嘱定期复查。另外 1

例潜伏期为 1 年半，行 IA(去甲氧柔红霉素和阿糖胞苷)化疗方案，继发急性髓系白血病 M4EO，该患者放弃治疗，要求自动出院。
结论 放化疗是目前肿瘤患者主要的治疗方案，而放化疗又是诱发白血病的主要因素，临床实际工作中应该严格掌握化疗药物的应用指征和剂量，从而降低治疗相关性白血病的发病率。

PU-4094

疟疾阳性病例血象分析及血片中疟原虫的镜检

曹阳阳
滨州医学院烟台附属医院

目的 归纳疟疾患者血象变化的一般规律，熟悉显微镜下查找并区分疟原虫，为早期临床治疗及预后判断提供参考数据和技术支持。
方法 回顾性分析 6 例疟疾患者一天的和 1 例疟疾患者数天的病例、检验报告单、厚薄血涂片信息。
结果 前 6 例患者 TBIL、DBIL、ALT、AST、γ-GT、BUN、Cr 个别患者有所升高，WBC 正常或降低，Lymph#、Lymph%、PLT、MPV、PCT 有所降低，Gran#及 Gran%变化高低不同，HGB、RBC 出现 2 例升高者，PDW 都升高，后 1 例患者随着治疗，各指标趋于正常。
结论 当 TBIL、DBIL、ALT、AST 越高，RBC、HGB、PLT 越低，患疟疾的可能性就越大。

PU-4095

肺癌患者外周血 ctDNA 和外泌体中 SHOX2 基因甲基化水平比较及临床应用价值评估

聂娜、沈燕
郑州大学第一附属医院

肺癌是全球范围内癌症死亡的主要原因。目前，临床上对肺癌的诊断和治疗方面取得了一定的成就，但在全球控制肺癌的发展中仍然存在许多问题。因此，早发现和早治疗仍是现在面临的重要问题。人矮小同源盒基因 2（shortstaturehomeobox2，SHOX2）属于 SHOX 基因家族成员，许多研究表明 SHOX2 基因甲基化与肺癌有关。本研究探讨以外泌体样本作为检测 SHOX2 基因甲基化的可行性，从而建立一种简便快速的检测方法。通过检测肺癌患者外周血 ctDNA 和外泌体中 SHOX2 基因甲基化，分析 SHOX2 基因在 ctDNA 和外泌体中甲基化水平是否一致。检测肺癌患者血清中 NSE、CYFRA21-1、ProGRP、CEA 和 SCC 水平，分析 SHOX2 基因甲基化联合五项血清肿瘤标志物检测在肺癌诊断中临床敏感性和鉴别小细胞肺癌和非小细胞肺癌的准确性。分析患者临床病理特征与外泌体中的 SHOX2 基因甲基化有无关联。研究发现，肺癌患者外周血 ctDNA 和外泌体中 SHOX2 基因甲基化水平检测结果较一致，其水平的增高与肺癌有关，外泌体中 SHOX2 基因甲基化与 NSE、CYFRA21-1、ProGRP、CEA、SCC 联合检测可提高诊断效能。这将为临床上肺癌的辅助诊断、治疗判断和预后监测提供依据。

PU-4096

有核红细胞数量与重症 ICU 死亡率的相关性研究

郑建蕊、郭翀
昆明医科大学第一附属医院

目的 分析外周血中有核红细胞(NRBC)与重症 ICU 患者死亡率的相关性 。
方法 回归性研究，收集 2020 年 1-8 月份在昆医大附一院重症 ICU 住院且做过血常规检查以及 NRBC 阳性的数据，收集患者的基本信息，包括性别，年龄，临床诊断，出院或者死亡，以及血常规检查中 NRBC#、NRBC%的最大值。
结果 收集到 NRBC 阳性的重症 ICU 患者共 133 例。分为死亡组和出院组。采用 Logistic 多因素回归对年龄、NRBC#、NRBC%分析，发现 NRBC # 、NRBC% 以及年龄为死亡的独立危险因素，每增加 1 个单位的 NRBC 计数，患者的死亡风险成 5.902 倍增长；每增加 1 个单位的 NRBC 百分比，患者的死亡风险成 0.440 倍增长。 利用 ROC 曲线对 NRBC#、NRBC%对预后评价效率进行评估。NRBC NRBC#和 NRBC%的曲线下面积分别为 0.704 和 0.683。当 NRBC#的临界值为 0 .025 0 × 10 9 /L 时，Sen 和 Spe 分别为 88%和 52.8%，当 NRBC%的临界值为 0 .350/100WBC 时，Sen 和 Spe 分别为 76% 和 61.1% 。 所以，当 NRBC # ≥ 0 .025 0 × 10 9 /L 或者 NRBC% ≥ 0 .350 时，可能会被作为判断患者预后的临界值 。
结论 本次研究结果表明，患者的 NRBC 水平高的死亡率也高，本次研究的患者死亡率为 18.8%。患者的死亡风险及预后评估与患者的性别无关，与患者的年龄有关，患者年龄越大，则死亡风险就越大，预后越差外周血 NRBC 数量的增高预示了患者可能预后不良、死亡风险增加、对临床早期发现不良预后有一定的指导意义。对急危重症特别是 NRBC 升高的患者，应密切监测，可对 NRBC 数量进行常规监测，及时发现患者的病情变化，以便进行相关治疗，从而降低死亡风险，预防不良后果的发生几率。

PU-4097

不同血液检测指标在冠心病临床诊治中的应用价值

赵中建
江苏省人民医院（南京医科大学第一附属医院）

目的 分析冠心病患者不同血液检测指标的价值。
方法 选取我院 2019 年 1 月至 2020 年 2 月期间接诊的冠心病患者 63 例，作为观察组，选择同时期健康体检者 63 例，作为对照组。两组均接受血液检测，分析不同血液检测指标两组的差异性。
结果 观察组血小板参数（包括血小板分布宽度、平均血小板体积、血小板体积、红细胞分布宽度）与对照组相比，（P＜0.05）具有统计学意义；观察组的心肌肌钙蛋白参数（包括心肌肌钙蛋白 T、高敏心肌肌钙蛋白 T、肌酸激酶同工酶、心肌肌钙蛋白 I）与对照组相比，（P＜0.05）具有统计学意义。
结论 不同血液检测指标在冠心病临床诊治中具有重要意义，可以为冠心病的临床症状提供有效依据，值得进行使用和推广。

PU-4098

血常规标本采集对检验结果的影响

文秋洁
雅安市人民医院

目的 了解静脉血与末梢血对血细胞检测结果的影响，探讨其检测结果的差异性。
方法 对 30 例住院患者同时采集静脉血和末梢血，用全自动细胞计数仪测定血常规，将所得两组数据进行重复性实验和比对实验，经统计学分析，比较静脉血和末梢血的差异。
结果 全自动细胞计数仪测定静脉血和末梢血血常规结果显示，两组白细胞（WBC）、红细胞（RBC）、血红蛋白（HGB）、血小板（PLT）均有极显著差异。
结论 血细胞分析应以静脉血为主，应对引起末梢血结果的诸多因素予以重视。

PU-4099

分析初发急性白血病凝血和纤溶指标

唐明霞
雅安市人民医院

目的 本文主要对急性白血病患者的凝血改变情况以及纤溶指标改变情况进行探讨和分析，以便为急性白血病患者提供最佳的治疗方法。
方法 本文选取本院 2019 年收治的 66 例急性白血病患者以及同期到医院体检的 50 例体检者作为研究对象，其中急性白血病患者为研究组，体检者为对照组，采用全自动凝血分析仪对实验组患者以及对照组的体检者的凝血酶时间以及凝血酶原时间进行分析，除此之外，还检验两组患者纤维蛋白原和 D-二聚体含量。
结果 急性白血病患者的出血倾向比较明显，并且治疗期间纤溶处于亢奋状态，检验急性白血病患者的 PT、FIB、D-二聚体等指标，有助于对急性白血病患者存在出血倾向的诊断，对病情的判断以及采取科学的治疗方法有着重要意义。

PU-4100

Research progress of correlation of platelet and its signaling pathway in the occurrence and development of acute myeloid leukemia

jianying zhang
East Hospital of Sichuan Provincial People, Hospital

Platelet is an important component of the hematopoietic system, which has special physiological functions and participates in the pathological process of many serious diseases.While its generation signaling pathway thrombopoietin(TPO) and its receptor MPL not only affects the normal platelet production, but also is closely related to the occurrence, development and prognosis of a variety of myeloid tumors. However, abnormal platelet and TPO / MPL signaling pathway occur in many hematologic malignancies or in the early stage of hematologic malignancies,these abnormalities are involved in or reflect the pathogenesis of hematological malignancies, which may affect the prognosis of hematological malignancies.Therefore, TPO / MPL signaling pathway and myeloid hematologic malignancies have a relationship of mutual promotion, development and interaction. This article reviews molecular mechanism of platelet production and its function, and the research progress of TPO

/MPL in myeloid malignancies, hoping to find a new target for the treatment of myeloid malignancies, even whether thrombocytopenia can play an early warning role in the occurrence of hematologic malignancies.

PU-4101

不同程度脂血标本对血常规血小板计数和血红蛋白检测结果的影响

孟静
山东大学第二医院

目的 探讨不同程度脂血标本对血常规血小板计数和血红蛋白含量检测结果的影响。
方法 全自动血细胞分析仪检测 EDTA-K2 抗凝全血脂血标本 100 例。分别采用电阻抗和血涂片镜检的方法检测血小板计数，采用比色法检测血红蛋白含量。对 100 例不同程度的脂血标本进行处理前后的血小板计数和血红蛋白检测结果进行比较。
结果 100%的标本血小板计数和血红蛋白检测结果处理前后结果相差悬殊。血小板计数假性增高 200-500%；血红蛋白假性增高 75-150%。
结论 脂血标本的血常规血小板计数和血红蛋白含量检测结果需矫正后发布到临床。

PU-4102

红细胞参数和网织红细胞参数在新生儿缺血缺氧性脑病中的变化及意义

孔虹、韦丽坚
中国医科大学附属盛京医院

目的 探讨新生儿缺血缺氧性脑病(Hypoxic-ischemic encephalopatly, HIE)中红细胞参数（FRC、MCV、MCH、MCHC、HGB、RDW、MicroR 和 MacroR）和网织红细胞参数(RET、IRF、HFR、MFR、LFR)的变化及临床意义。
方法 选择中国医科大学附属盛京医院已确诊为 HIE 的新生儿 52 例作为观察组，正常健康新生儿 44 例作为对照组，应用 Sysmex XN9000 全自动血液分析仪检测外周血红细胞参数和网织红细胞参数，将患者的参数与健康新生儿的参数进行比较，分析 HIE 患儿红细胞参数和网织红细胞参数的变化。
结果 经全自动血液分析仪检测发现，观察组红细胞参数中 RDW-CV、FRC 和 MicroR 比对照组高,HGB、MCV、MCHC、MacroR 比对照组低，差异具有统计学意义（$p<0.05$）；观察组网织红细胞参数 RET#、IRF 比对照组高，LFR 比对照组低，差异具有统计学意义（$p<0.05$）。
结论 全自动血液分析仪检测血细胞参数速度快、操作简单、准确度高，分析红细胞参数和网织红细胞相关参数的变化在临床 HIE 的筛查和辅助诊断方面具有一定的价值，但 HIE 的确诊需要多种手段联合检测。

PU-4103

雅安地区网织红细胞血红蛋白含量参考区间的初步建立

黄滔[1]、刘雨欣[2]、陈涛[1]、郑悦[1]、何霞[1]
1. 雅安市人民医院检验科
2. 雅安职业技术学院药学与检验学院

目的 初步建立和验证雅安地区健康成人网织红细胞血红蛋白含量（Ret-He）的参考区间。
方法 回顾性分析我院 2018 年 9 月至 2020 年 11 月体检人群，严格按照纳入和排除标准选取了 3105 位体检健康对象。使用 Sxsmex XN1500 全自动血液分析仪检测 Ret-He，按照性别、年龄和地区分组比较，最后采用非参数方法建立 95%参考区间，IBM SPSS 20.0 软件的 bootstrap 程序计算 P2.5 和 P97.5 处的 95%置信区间。
结果 Ret-He 呈现男性高于女性，其差异有统计学意义（P<0.05）；不同年龄组间的差异无统计学意义（P=0.194）；不同地区间的差异有统计学意义（P<0.05）,但两两比较后发现其差异均无统计学意义（P>0.05），故本地区应该单独建立男性和女性的参考区间，不同年龄和地区使用合并参考区间。健康成年男性和女性的参考区间分别为：26.5～37.2，25.1～36.1。
结论 本研究成功建立和验证了雅安地区 Ret-He 参考区间，对诊断和治疗贫血相关疾病有重要意义。

PU-4104

网织红细胞血红蛋白含量的测定在缺铁性贫血中的应用

尹正
中国医科大学附属盛京医院

目的 探究网织红细胞血红蛋白含量，在缺铁性贫血诊断的应用价值，以便于尽早确定贫血类型，准确的对缺铁性贫血进行治疗和预后服务。
方法 随机抽取 50 例缺铁性贫血患者、50 例非缺铁性贫血患者和 50 例健康体检人群。其中缺铁性贫血和非缺铁性贫血为实验组，健康体检人群为对照组。使用 HXL_XE2100-a 作为检验仪器进行检验，测量试验组和对照组的红细胞计数（RBC）、红细胞平均体积（MCV）、红细胞平均血红蛋白含量（MCH）、红细胞血红蛋白含量（HB）、平均红细胞血红蛋白浓度（MCHC）及网织红细胞血红蛋白含量（RET-HE），运用 spss26.0 统计软件对测量结果进行分析统计评价。
结果 对三组试验对象 RET-HE、MCV、MCHC、MCH、Hb、RBC 结果分析，A 组的（RET-HE、MCV、RBC.、MCH、MCHC）与其他两组相比是有差异的，差异具有统计学意义（P＜0.05）。A 组的 HB 含量与 B 组相比，差异无统计学意义（P＞0.05），与 C 组相比，差异有统计学意义（P＜0.05）。对 A 组数据进行灵敏度、特异性、准确度、阴性预测值和阳性预测值分析计算，RET-HE 的灵敏度与特异性均高于其他数据。使用 A 组数据绘制 ROC 曲线，RET-HE 曲线下面积最高为 0.928.
结论 RET-HE 在贫血的诊断中具有一定的临床应用价值，尤其对缺铁性贫血缺铁性病人的早期诊断具有重要的临床意义。

PU-4105

复发性流产患者中血小板参数与血小板聚集率的相关性

佟威威、华志阳
中国医科大学附属盛京医院

目的 分析复发性流产患者中，血小板参数与血小板聚集能力的相关性。探讨血小板参数预测复发性流产患者高血凝状态的应用价值。
方法 根据 LIS 系统数据，共选取 218 例诊断为复发性流产患者，依靠其花生四烯酸诱导的血小板聚集率分组，分为聚集率大于 80%组、70%-80%组与小于 70%组。再根据患者二次检测结果，血小板聚集率大于 20%为治疗抵抗组，血小板聚集率小于 20%为治疗有效组。比较两组的血小板参数差异。将治疗前患者的血小板参数与治疗后患者血小板参数进行差异性分析。最后，将治疗前患者的血小板参数与治疗有效的患者治疗后的血小板参数进行差异性分析。使用 SPSS 组间进行 T 检验与方差分析，判断差异是否具有统计学意义。
结果 血小板聚集率大于 80%组、70%-80%组和小于 70%组的血小板数量，组间具有显著差异，结果具有统计学意义（F=11.40，P＜0.01）。血小板聚集率大于 80%组、70%-80%组与小于 70%的血小板压积，组间差别有统计学意义（F=14.45，P＜0.01）。治疗有效组与治疗抵抗组，血小板数量（P＜0.01），差异具有统计学意义。治疗组与非治疗组差异不明显，无统计学意义。
结论 临床使用血小板参数预测血小板聚集能力具有可行性；可以通过血小板参数预测复发性流产患者的治疗效果；治疗前后血小板参数差异未有明显统计学意义，后续希望使用更多数据再次验证。

PU-4106

实验室指标、骨髓细胞形态学及流式细胞术对多发性骨髓瘤的诊断价值分

周颖、杨晓东、刘金彪
三峡大学附属仁和医院

目的 探讨实验室指标、骨髓细胞形态学及流式细胞术对多发性骨髓瘤（MM）的诊断价值。
方法 选取三峡大学附属仁和医院 32 例经临床诊断确诊的 MM 患者为研究对象，通过实验室检查血红蛋白、红细胞沉降率、球蛋白及免疫球蛋白含量，同时显微镜下观察骨髓中瘤细胞形态特征，结合骨髓流式细胞免疫表型进行分析。
结果 32 例 MM 患者中，轻度贫血者占 9.37%，中度贫血者占 71.87%，重度贫血者占 18.76%；红细胞沉降率升高的达 96.87%；血清球蛋白含量升高的达 84.38%，血清球蛋白含量正常的占 9.37%，血清球蛋白含量减低的占 6.25%；血清免疫球蛋白为 κ 轻链型的比例大于 λ 轻链型，差异有统计学意义（P<0.05）；MM 患者骨髓增生程度较多为增生活跃，且疾病分期越高，骨髓增生程度越活跃，形态学检测骨髓瘤细胞中位数比例为 37.00%（8.00%-95.00%），流式细胞术检测中位数 27.66%（4.10%-88.67%）；对骨髓瘤细胞抗原 CD138、CD38、CD56、CD27、CD19、cKappa、cLambda 进行分析，结果发现：32 例 MM 患者 CD138、CD38 阳性表达率均为 100%，其他抗原阳性表达阳性率为 CD56 93.75%、CD27 56.25%、CD19 21.87%，κ 轻链型占 37.50%，λ 轻链型 31.25%。
结论 由于多发性骨髓瘤（Multiple myeloma，MM）恶性程度高，临床症状复杂，容易漏诊和误诊，临床诊断 MM 时如结合血红蛋白、红细胞沉降率、球蛋白及免疫球蛋白含量、骨髓细胞形态学检查给到一定的提示作用，若联合流式细胞术检查，则诊断和鉴别诊断的水平一定可以得到提高。

PU-4107

NLR、MLR 在急性胰腺炎中的诊断价值研究

冉桥生
陆军军医大学第二附属医院检验科

目的 探讨中性粒细胞/淋巴细胞比值（Neutrophil to lymphocyte ratio，NLR）、单核细胞/淋巴细胞比值（Monocyte to lymphocyte ratio，MLR）检验检测指标在急性胰腺炎（acute pancreatitis，AP）中的诊断价值。
方法 回顾性选取 2018 年 1 月至 2019 年 10 月在陆军军医大学第二附属医院急诊科病区确诊为 AP 的住院患者 110 例作为病例组，选取陆军军医大学第二附属医院健康体检中心性别和年龄与病例组相匹配的健康体检人员 110 例作为对照组，对病例组就诊首次血常规测定项目与对照组血常规测定项目进行分析比较，并进行 Spearman 相关性分析和 ROC 曲线的绘制。
结果 1）AP 组与健康对照组比较， MPV、NLR、MLR 差异有统计学意义（P<0.05）。 2）Spearman 相关性分析，NLR、MLR 与白细胞（White blood cell，WBC）、中性粒细胞（Neutrophils，NEUT）、单核细胞（Monocytes，MON）、红细胞分布宽度（Red blood cell distribution width，RDW）均呈正相关（P<0.05）。3）ROC 曲线结果分析，NLR、MLR 共同联合检测诊断 AP 时，ROC 曲线下面积（Area under curve，AUC）为 0.963，敏感性和特异性较好（敏感性为 92.7 %，特异性为 94.6 %）。
结论 NLR 和 MLR 均可作为急性胰腺炎快速诊断的有效检测指标，且 2 项指标联合检测诊断价值较好，为急性胰腺炎的临床诊断提供了一种价格低廉、简便快速的实验室诊断方法。

PU-4108

江西省首例输入性新冠病毒 B.1.1.7 变异株感染患者的救治防控体会

刘洋、张伟、向天新
南昌大学第一附属医院

目的 探索输入性新冠病毒 B.1.1.7 变异株感染病例的临床特点及救治防控体会。
方法 对 2021 年 3 月 16 日江西省九江市第三人民医院收治的 1 例输入性新冠病毒 B.1.1.7 变异株感染患者的发病过程、临床表现、实验室检查、影像学改变及救治防控等进行总结。
结果 患者鼻咽拭子新冠病毒核酸检测阳性，经过中国 CDC 全基因组测序确认为输入性的新冠病毒 B.1.1.7 变异株，确诊为新冠病毒 B.1.1.7 变异株感染病例。患者男，34 岁，72kg 体重，由津巴布韦回国途中感染新冠病毒 B.1.1.7 变异株。早期为无症状感染者，后经发热、头痛进展为新冠肺炎（普通型），干扰素雾化吸入治疗，口服阿比多尔，口服江西特色抗新冠中药，丙种球蛋白静脉治疗。病程进展较快，病程第 3 天胸部 CT 呈现多发性感染灶，体温升高至 39.2℃，静脉应用甲强龙 40mg（0.56mg/kg/d）。被子、枕头、面罩存在大量病毒残留，环境消杀彻底。病程第 7 天病情有所好转，肺部病灶部分吸收。病程第 11 天，病毒核酸转阴，各种炎性及酶学指标恢复正常，肺内病灶明显吸收；病程第 14 天患者好转出院。
结论 新冠病毒 B.1.1.7 变异株潜伏期长，核酸载量增长快，病情进展速度快，环境病毒核酸残留污染严重，环境消杀与核酸监测齐头并进；早期各种指标监测及预判其重型化是治疗的重点，糖皮质激素对肺部病灶吸收有一定疗效，使用剂量有待进一步探讨。

PU-4109

红细胞分布宽度和血小板分布宽度对判断弥漫大 B 细胞淋巴瘤患者疗效和预后的价值

柳洪周
成都市第三人民医院

目的 探讨红细胞分布宽度（RDW)和血小板分布宽度（PDW）在弥漫大 B 细胞淋巴瘤(DLBCL)患者疗效及预后中的价值。
方法 回顾性分析 116 例 DLBCL 患者初诊时的 RDW、PDW 与临床特征及疗效预后的关系，根据 RDW、PDW 正常参考范围将患者分为低 RDW 组(≤15％)和高 RDW 组(>15％)、低 PDW 组(PDW≤14fL)和高 PDW 组(PDW>14fL)，比较 2 组患者疗效、总生存期（OS）及疾病无进展生存期（PFS），单因素和多因素回归分析各指标与疗效及预后的关系。
结果 高 RDW 组较低值组患者在疗效(P<0.001)、OS(P=0.017)和 PFS(P=0.038)均较差。高 PDW 组与低 PDW 组相比，高值组在疗效(P<0.001)、OS(P=0.014)和 PFS(P=0.030)均较差。多因素回归分析显示，高 RDW 和高 PDW 是影响 DLBCL 患者疗效的独立危险因素(OR=2.232，95％CI=1.181, 3.834，P=0.030)和(OR=2.560，95％CI=1.363, 4.728，P=0.027)。
结论 高 RDW 和高 PDW 与 DLBCL 患者的化疗疗效和不良预后相关。

PU-4110

Metabolomic profiling of cerebrospinal fluid reveals an early diagnostic model for central nervous system involvement in acute lymphoblastic leukemia

Zhiqiang Song[1,2]、Gusheng Tang[1]、Mian Wang[1]、Diya Lv[2]、Guihua Lu[1]、Jie Meng[1]、Zhenyu Zhu[2]、Jianmin Yang[1]、Yue Liu[2]、Yifeng Chai[2]
1. Changhai Hospital
2. 第二军医大学药学系

Central nervous system involvement (CNSI) is a common disease in patients with acute lymphoblastic leukemia (ALL). Currently, the pathogenesis of CNSI remains unknown and the robust biomarker for early diagnosis of CNSI is absent. An untargeted cerebrospinal fluid (CSF) metabolomics study was performed to identify the biomarkers that could early discriminate between ALL patients with CNSI and without CNSI in two independent ALL cohorts. In addition, we tracked the changes of the identified biomarkers in different stages of patients with CNSI, including before CNSI, CNSI and remission after treatment. 33 significantly altered metabolites of CNSI were identified, which were primarily associated with phenylalanine, tyrosine and tryptophan biosynthesis, synthesis and degradation of ketone bodies, D-Glutamine and D-glutamate metabolism, alanine, aspartate and glutamate metabolism, phenylalanine metabolism, citrate cycle (TCA cycle), tyrosine metabolism, arginine biosynthesis and butanoate metabolism. Then, CNSI evaluation score (CES) based on five biomarkers was constructed to predict the risk of CNSI, which could diagnose CNSI with positive prediction values of 97.2% and 86.1% in training and validation sets, respectively. Finally, we further validated the CES by tracking the changes of the CES in different stages of patients with CNSI, showing good ability of monitoring the development of CNSI. Our results revealed the metabolic changes of CSF related to CNSI and the CES could predict the CNSI well. This unique CSF metabolomics study help us understand the pathogenesis of CNSI and diagnose CNSI in early stage.

PU-4111

Relation of neutrophil-to-lymphocyte ratio and platelet-to-lymphocyte ratio to survival in patients with laryngeal squamous cell carcinoma

Xi Zhang
Department of Clinical Laboratory, Caner Hospital of Yunnan Province, the Third Affiliated Hospital of Kunming Medical University

Aims Although previous researches have demonstrated that preoperative complete blood count (CBC) and inflammation-associated blood cell markers may correlate with prognosis in patients with laryngeal squamous cell carcinoma (LSCC). However, the independent prognostic value of neutrophil-to-lymphocyte ratio (NLR) and platelet-to-lymphocyte ratio (PLR) based on multivariate analysis still remains controversial and needed be elucidated. we investigated the possible effect and particular prognostic importance of NLR and PLR in LSCC.
Methods Information including preoperative CBC parameters，clinical/ pathological materials and 5-year follow-up data were obtained retrospectively in 151 LSCC patients underwent primary surgery from December 2008 to October 2015. Cutoffs for NLR and PLR were optimized by receiver operating characteristic (ROC) curve. Overall survival (OS) was confirmed by Cox proportional hazards models and Kaplan-Meier method. Survival curves were obtained by Kaplan-Meier survival analysis and compared by log-rank test. Correlation of NLR and PLR with clinic/pathological parameters was analyzed using non-parametric tests.
Results In our study, PLR with cutoff 97.72 and NLR with cutoff 2.22 had independent prognostic significance for OS, while both PLR-high and NLR-high predicted a poor prognosis. In addition, NLR was strongly associated with cervical lymph node metastasis, preoperative neutrophil/Lymphocyte count, platelet distribution width (PDW) and stage, whereas PLR was also strongly associated with cervical lymph node metastasis, preoperative neutrophil/Lymphocyte count and PDW.
Conclusion Preoperative NLR and PLR can be used as independent factors affecting the survival of laryngeal cancer patients after operation, and have an important significance for the prognosis evaluation of laryngeal cancer.

PU-4112

加热灭活血清样本对新型冠状病毒不同检测方法所测抗体滴度的影响

张如意、胡秀梅、郑磊、王前
南方医科大学南方医院

目的 评估传统 56℃加热 30 分钟灭活血清样本后对 ELISA 法检测 SARS-CoV-2 IgM 及 IgG 抗体的影响
方法 收集 2020 年 2 月 26 日至 2020 年 3 月 6 日在武汉市汉口医院就诊的新型冠状病毒肺炎确诊患者住院患者血清 62 例，作为病例组。健康医护人员血清标本 18 例作为对照组。留取双份血清标本，一份 56℃ 30 min 热灭活，另一份未灭活。采用商品化新型冠状病毒（SARS-CoV-2）抗体检测试剂盒（ELISA 法）对分别对灭活前后的血清标本进行特异性 IgM 和 IgG 抗体检测。采用配对 kappa 检验对血清灭活前后 SARS-CoV-2 IgM 和 IgG 抗体检测检测结果差异进行统计学分析。
结果 灭活后的 IgM 及 IgG 水平整体高于灭活前，但其诊断阳性率并无明显改变；灭活前后 IgM 的阳性符合率、阴性符合率及总体符合率分别为 100.00%（55/55）、96.00（24/25）、98.75%

（79/80）（κ=0.971，P＜0.001）；而灭活前后 IgG 的阳性符合率、阴性符合率及总体符合率分别为 98.21%（55/56）、91.67%（22/24）及 98.75%（79/80）（κ=0.910，P＜0.001）。
结论 加热灭活法不影响 SARS-CoV-2 抗体的检测，可在临床中应用采用加热灭活的方法对病毒进行灭活以减少检测人员的感染风险。

PU-4113

白细胞介素-6 联合 PCT 与 CRP 评估儿童脓毒血症患者预后的价值

周觅
山东大学第二医院

目的 探讨血清 IL-6、PCT 与 CRP 变化在儿童脓毒血症中的临床意义,探寻儿童脓毒血症患者预后的评估价值.
方法 选取我院 2020 年 1 月～2020 年 10 月儿内重症监护室收治的 145 例脓毒血症患者,根据患者一个月内存活情况分为存活组(130 例)和死亡组 15 例),比较两组入院时 IL-6、PCT 与 CRP 水平、入院 3 天 IL-6、PCT 与 CRP 水平,采用受试者工作特征(ROC)曲线评价患者入院时 IL-6、PCT 与 CRP 对脓毒血症预后的评估价值.
结果 存活组入院时 PCT 与 CRP 水平低于死亡组,差异有统计学意义(P＜0.05);存活组患者入院时及入院 3 天 IL-6 水平均高于死亡组,并且迅速恢复正常,差异有统计学意义(P＜0.05);但是死亡组 IL-6 后续升高后一直维持一定水平难以恢复正常；两组入院时 IL-6、PCT 水平与入预后水平呈正相关(P＜0.05);ROC 曲线显示,IL-6、PCT 与 CRP 减少值单独及联合评估患者预后的曲线下面积分别为 0.829、0.848、0.933,两者联合诊断的曲线下面积、灵敏度、特异度、阳性和阴性预测值均高于单一指标.
结论 IL-6、PCT 与 CRP 联合检测对脓毒血症患者病情危重程度及预后的评估具有重要意义,可作为患者病情评估及预后的指标.

PU-4114

82 例初诊多发性骨髓瘤的临床特征及实验室检查分析

刘杭敏[1]、于鹏飞[2]、李谦[3]、曹颖平[1]
1. 福建医科大学附属协和医院检验科
2. 福建省级机关医院检验科
3. 福建医科大学医学技术与工程学院

目的 探讨影响初诊多发性骨髓瘤患者总生存的便捷有效预后因素。
材料和方法 筛选我院 2017 年 1 月至 2020 年 12 月初诊多发性骨髓瘤患者的病历资料共 82 例。1.确定 NLR、MLR 与总生存期的 ROC 截断值；2.单因素分析性别、年龄、白蛋白、乳酸脱氢酶、钙、肌酐、NLR、MLR、血红蛋白、血小板、β2 微球蛋白、ISS 分期、FISH 结果异常与总生存预后的关系；3.将有统计学意义的单因素变量纳入多因素分析。应用 SPSS23．0 统计软件处理所有资料数据，以 P<0.05 为差异有统计学意义。
结果 1.82 例患者年龄范围 40-88 岁（61.87±9.99 岁），其中男患者 46 例，女患者 36 例。首发症状骨痛 51 例，贫血 16 例，其他 15 例。IgG-κ 型 21 例，IgG-λ 型 22 例，IgA-κ 型 12 例，IgA-λ 型 9 例，κ 型 5 例,λ 型 9 例，不分泌型 2 例。ISSⅠ期 15 例，Ⅱ期 24 例，Ⅲ期 43 例。2.外周血 NLR 的 ROC 曲线截断值为 1.75，曲线下面积 0.509，敏感性 62.5%，特异性 43.1%（95%CI(0.358～0.660）。外周血 MLR 的 ROC 曲线截断值为 0.225，曲线下面积 0.614，敏感性 70.8%，特异性 56.9%（95%CI(0.471～0.758）。3.单因素分析显示性别、年龄、白蛋白、乳酸脱氢酶、浆细胞比

例、血清钙、血肌酐、血红蛋白、血小板、NLR、FISH 与总生存期 OS 之间无统计学差异（P>0.05），MLR、LDH、β2 微球蛋白、ISS 分期与总生存期 OS 之间有统计学差异(P<0.05)。4. 以 MLR、LDH、β2 微球蛋白和 ISS 分期因素进行 COX 模型分析，结果显示 MLR≥0.225 是影响 MM 患者 OS 的独立不良预后因素(P<0.05)。

结论 本研究表明 MLR≥0.225 是预测 MM 患者总生存期降低的独立危险因素，可以为临床更早更准确评估 MM 患者预后提供客观依据。

PU-4115

粪便隐血定量和肿瘤标志物诊断结直肠癌的临床研究

高丹、韦汇祯
中国医科大学附属盛京医院检验科

目的 探讨粪便隐血定量和肿瘤标志物检测结直肠癌的临床应用价值。

方法 本课题通过收集 2020 年 4 月至 2021 年 4 月中国医科大学附属盛京医院消化内科、肛肠肿瘤外科住院患者中的通过内镜检查及病理活检的患者的粪便标本及血清标本，分别做粪便隐血定量及肿瘤标志物检测，分析不同病理诊断类型中粪便隐血定量、癌胚抗原（CEA）、糖抗原 19-9（CA19-9）、糖抗原 72-4（CA72-4）这些指标的变化。以病理活检的患者为实验组，以同时期体检的健康人作为对照组,对统计的数据进行统计学分析。

结果 单独检测粪便隐血定量、CEA、CA19-9、CA72-4 在 CRC 组、良性肿瘤组、IBD 组及对照组中阳性率相对较低，粪便隐血定量联合肿瘤标志物检测的阳性率增高，在 CRC 组、良性肿瘤组、IBD 组及对照组的阳性率分别为 100%、36.7%、70%、0%。粪便隐血定量联合肿瘤标志物检测的灵敏度为 100%，单独粪便隐血定量、CEA、CA19-9、CA72-4 检测的灵敏度分别为 76.9%、73.1%、65.4%、53.8%。联合检测的特异度为 46.7%，阳性预测值 44.8%，阴性预测值 100%。

结论 粪便隐血定量联合肿瘤标志物检测可以提高检测的敏感性，在结直肠癌的诊断中具有重要的临床应用价值。

PU-4116

血清淀粉样蛋白联合白细胞、C 反应蛋白在小儿呼吸道感染诊断中的应用

谭珊[2]、王诗琪[1]
1. 湖南师范大学医学院
2. 湖南省人民医院

目的 分析血清淀粉样蛋白联合白细胞、C 反应蛋白在小儿呼吸道感染诊断中的应用。

方法 选取 2020 年 5 月至 2021 年 4 月内，湖南省人民医院收治的 100 例呼吸道感染儿童作为观察组，观察组包括细菌感染组 50 例，病毒感染组 50 例，同时选取同期在我院接受健康体检的 50 例健康儿童作为对照组，比较其 SAA、CRP 以及 WBC 的检验结果。

结果 观察组 CRP、SAA、WBC 阳性率分别为 51.00%、82.00%、46.00%。细菌感染组、病毒感染组 SAA、CRP、WBC 均高于对照组,细菌感染组 SAA、CRP、WBC 高于病毒感染组,数据有统计学差异,差异有统计学意义(P<0.05)。三项指标联合检验阳性结果分布：观察组 WBC、CRP 双项联合检验结果阳性率为 67.00%；WBC、CRP、SAA 三项联合检验阳性率为 86.00%。

结论 血清淀粉样蛋白联合白细胞、C 反应蛋白水平变化能够更好地反映小儿感染的病情变化，发挥良好的临床作用。

PU-4117

ALIFAX-Roller 20 全自动血沉仪性能评价及生物参考区间建立

邓中华[1]、孙文豪[1]、陈宇[2]、陈玮[1]、彭剑桥[1]、曹友德[1]
1. 湖南省人民医院（湖南师范大学附属第一医院）
2. 湖南师范大学医学院

目的 评估 ALIFAX Roller 20 全自动血沉仪检测性能并建立该方法不同性别及年龄人群的生物参考区间。
方法 选取 9 份临床样本连续检测评估仪器的重复性；采用质控品连续检测 20 天评估仪器的日间精密度；严格按照纳入排除标准收集健康体检人群静脉血标本上机检测，计算各人群生物参考区间，正态分布数据选（X±1.65S）为该人群生物参考区间，非正态分布数据选 P95 作为该人群生物参考区间；生物参考区间建立后，随机选取 20 份健康体检样本进行生物参考区间的验证，符合率达 90%则验证通过。收集 50 份临床样本，分别采用魏氏法和 Roller 20 同时进行血沉检测，比较两种检测方法的相关性。
结果 重复性评估结果显示 CV 小于 6%。日间精密度评估结果显示 CV 小于 5%。各性别和年龄组 Roller 20 全自动血沉仪检测生物参考区间分别为：男性，0-10 岁 2-23mm/h、11-20 岁为 2-24 mm/h，21-30 岁为 2-23 mm/h，31-40 岁为 2-24 mm/h，41-50 岁为 2-22 mm/h，51-60 岁为 2-31 mm/h，> 60 岁为 2-37 mm/h；女性，0-10 岁为 2-25 mm/h，11-20 岁为 2-25 mm/h，21-30 岁为 2-25 mm/h，31-40 岁为 2-28 mm/h，41-50 岁为 2-32 mm/h，51-60 岁为 2-34 mm/h，> 60 岁为 2-38mm/h；参考区间经验证，符合率 95%；Roller 20 全自动血沉仪法与魏氏法检测结果相关性分析显示两种方法检测相关系数为 R=0.932。
结论 ALIFAX-Roller 20 全自动血沉仪检测重复性和日间精密度良好，不同性别和年龄段人群的血沉生物参考区间稍有差异，女性高于男性，年龄越大血沉值越高。本研究建立的生物参考区间经验证可用于临床。

PU-4118

血栓弹力图联合常规凝血检测对 60 岁以上人群心脑血管疾病的评估价值

于鹏跃、赵凤莲、庞孟煜、王莹、张晓华、赵丽娟
The Second Hospital of Jilin University

目的 探讨 60 岁以上人群心脑血管疾病血栓弹力图(thrombelastoraphy,TEG)各项指标与常规凝血检测指标的相关性，以及上述指标对心脑血管疾病的评估价值。
方法 选取 2016 年 1 月至 2018 年 12 月期间就诊于吉林大学第二医院，年龄≥60 岁，脑血管疾病患者 113 例，心血管疾病患者 172 例，健康体检者 83 例，收集其治疗前的血栓弹力图、凝血常规、血小板计数等检测数据并进行回顾性分析。
结果 1.脑血管疾病组的活化部分凝血活酶时间(APTT)、血小板计数和平均血小板体积(MPV)高于对照组，心血管疾病组的 TEG-K、MPV 和 MPV/PLT 高于对照组，凝血酶原时间(PT)和纤维蛋白原(Fib)低于对照组；
2.脑血管疾病组和心血管疾病组 TEG-R 均与 APTT 呈正相关（相关系数分别为 0.295 和 0.176)，TEG-K 与 Fib 呈负相关(相关系数分别为-0.293 和-0.310)，TEG-α 与 Fib 呈正相关（相关系数分别为 0.345 和 0.271），TEG-MA 与 PLT 计数正相关(相关系数分别为 0.540 和 0.420)，TEG-MA 与 Fib 正相关（相关系数分别为 0.417 和 0.418）,TEG-MA 与 MPV/PLT 呈负相关(相关系数分别为-0.444 和-0.295)；
3.两组间 D-dimer 的分布趋势无明显差别，脑血管疾病组 FDP 高于心血管疾病组，而 D-dimer/FDP 低于心血管疾病组。

结论 1.大于 60 岁的心脑血管疾病人群中 TEG 检测指标与传统凝血常规指标存在明确的相关性，其中 Fib 对于 TEG-MA 的贡献可能高于文献所提到的 20%；
2.D-dimer 与 FDP 的联合检测对于 60 岁以上人群心脑血管疾病的凝血状态评估更具有价值；
3.MPV/PLT 和 D-dimer/FDP 可以作为机体止凝血功能的评价指标。

PU-4119

中性粒细胞／淋巴细胞比值与狼疮肾炎肾损伤的相关性研究

刘宇思
中国医科大学附属第一医院

目的 探讨中性粒细胞／淋巴细胞比值与狼疮肾炎肾损伤的相关性。
方法 选取在中国医科大学附属第一医院就诊的系统性红斑狼疮（SLE）患者 88 例。根据有无合并肾损伤将 88 例 SLE 患者分为 SLE 无 LN 组（43 例）和 LN 组（45 例）。另外，在同期本院体检中心选取性别、年龄相匹配的 55 名体检人员作为健康对照组。收集三组受试者完整的病史资料、相关检验指标，包括年龄，尿素，肌酐，血胱抑素 C（CysC），肾小球滤过率（eGFR），中性粒细胞计数，淋巴细胞计数，中性粒细胞比例，淋巴细胞比例，计算 NLR。并收集 SLE 患者的 C 反应蛋白（CRP），补体 C3，补体 C4，24 h 尿蛋白定量（UTP），尿微量白蛋白（UPRO），ds-DNA 抗体水平。采用单因素方差分析和 Kruskal-Wallis H 检验比较三组各项指标的差异性，通过 Spearman 分析 NLR 与狼疮肾炎肾损伤的相关性。采用 logistic 回归分析 NLR 与 LN 的关系，通过受试者工作特征曲线（ROC）评估 NLR 对 LN 的诊断效能。
结果 三组受试者的 NLR 值比较，差异具有统计学意义（P<0.05）。SLE 组的 NLR 值均高于健康对照组，且 LN 组的 NLR 高于 SLE 无 LN 组，差异均有统计学意义（P 均<0.05）。在 LN 患者中，NLR 与 UPRO 和 UTP 呈正相关（r 分别=0.386，0.309， P 均<0.05），与补体 C3 呈负相关（r=-0.325， p<0.05）。logistic 回归分析显示，NLR 是 LN 发病的危险因素（OR=1.618，P<0.05）。ROC 曲线分析结果表明，NLR 鉴别诊断未累及肾脏的 SLE 患者和 LN 患者的曲线下面积（AUC）为 0.732，最佳截断值为 2.07，灵敏度为 88.9%，特异度为 51.2%。
结论 外周血 NLR 与 LN 肾损伤密切相关，可作为评估 LN 肾功能损伤的指标。

PU-4120

Application of ion mobility spectrometry and data-mining to profile vaginal cleanliness: a hospital-based study in Xiamen

Zhenguo Lin[1]、guolin Hong[2,3]
1. 厦门大学公共卫生学院
2. 厦门大学附属第一医院检验科
3. 厦门市基因检测重点实验室

Objectives Vaginal cleanliness is an important clinical indicator for the evaluation of vaginal microecological state and the diagnosis of vaginal inflammatory diseases. We came up with a quick on-site solution to characterize the pattern of vaginal cleanliness and explore the related potential clinical significance based on ion mobility spectrometry for mini clinics or community hospitals, where the microscopic examination as the detection of vaginal cleanliness is not easy to be achieved.
Methods Testing of the vaginal secretions of 100 participants with vaginal cleanliness Grade 2, Grade 3, and Grade 4 was conducted by ion mobility spectrometry. Based on the ion mobility spectrometry sum spectra, we used the data-mining workflow composed of the principal

component analysis, Boruta, t-SNE, Radviz, heatmap, self-organized mapping, decision tree and Spearman correlation to profile the pattern characterization of vaginal cleanliness.
Results TC4, TC6 and TC10 as 3 key principal components were extracted and screened from the ion mobility spectrometry sum spectra. Then the pattern recognition and characterization analysis showed that vaginal cleanliness Grade 3 and Grade 4 tending to have smaller TC4 were similar in pattern, but they were relatively evidently different from vaginal cleanliness Grade 2 tending to have smaller TC6. And there was a negative correlation between TC4 and vaginal cleanliness ($p < 0.001$), a positive correlation between TC6 and vaginal cleanliness ($p < 0.001$), and a negative correlation between TC10 and vaginal cleanliness ($p < 0.05$).
Conclusion The clinical application of ion mobility spectrometry can provide a new idea for vaginal cleanliness detection.

PU-4121

细胞学检查对乳腺癌的诊断价值

刘婕
山东大学第二医院

目的 对细胞学检查诊断乳腺癌的价值进行系统综述。
方法 计算机检索 Pubmed,中国知网数据库、万方数据库,系统检索国内外公开发表的细胞学检查诊断乳腺癌的临床研究。
结果 临床上常用的细胞学检查包括细针抽吸细胞学和乳头溢液涂片细胞学。细针抽吸细胞学是诊断乳腺病变的基本方法之一，作为对患者临床病情初步评估的一种方法，对指导是否行手术治疗具有重要意义。乳头溢液进行细胞学检查适用于对临床评估有导管内恶性高风险病变患者进行诊断。
结论 细胞学检查是一种敏感性及特异性较高，易操作且经济的检查方法。

PU-4122

人外周血单个核细胞非同源端连接修复活性体外测定方法的开发与应用

浣西莎
中南大学

背景 非同源端连接(Non-homologous end joining, NHEJ)是维持遗传完整性和 DNA 双链断裂(DNA double-strand breaks, DSBs)修复的关键。体外 NHEJ 活性检测方法可测定 DSBs 修复活性，被认为是一种有价值的人类生物标志物。但由于缺乏标准化、操作流程复杂，且对细胞量的要求高(＞1-5 × 108)，体外 NHEJ 活性检测通常仅用于细胞系实验，很少用于临床血液样本的直接检测。
目的 建立一种检测人体血液样本非同源端连接修复活性的常规实验室方法。
方法 建立和优化适用于人外周血单个核细胞检测的体外 NHEJ 修复活性检测方法，并将其应用于健康人及鼻咽癌患者标本检测。
结果 所建立的方法将分析所需的细胞数量减少到 2×106，采用优化后的方法基于 179 例健康献血者样本建立了正常人的参考区间。对鼻咽癌患者的样本进行分析，结果表明，鼻咽癌患者的 NHEJ 体外活性平均值显著低于健康对照组($P<0.05$)。此外，经过 3 个月的随访，我们的研究发现，NHEJ 在 PBMCs 中的活性与正常组织的辐射副作用相关($P<0.01$)，而与治疗效应无明显关联($P>0.05$)。这是首次直接使用血液样本提取细胞，并评估 NHEJ 在大样本人群中的活性。

PU-4123

冠状动脉粥样硬化性心脏病患者凝血酶激活的纤溶抑制物（TAFI）及其编码区基因 CPB2（Thr325Ile）多态性的研究

徐成伟
山东大学第二医院

目的 探讨 TAFI 及其编码基因单核苷酸多态性与冠状动脉粥样硬化性心脏病之间的联系。
方法 应用 PCR-RFLP 检测 210 例冠心病患者和 190 例正常对照者的 TAFI 基因型，应用发色底物法和 ELISA 法分别测定 TAFI 的活性及抗原，并进一步分析基因多态性与 TAFI 的活性及抗原之间的关系。
结果 TAFI 的活性及抗原在心肌梗死组、心绞痛组和对照组中的浓度分别为（51.4±9.3）ug/ml、（145.6±33.5）%，（47.6±8.4）ug/ml、（128.3±28.7）%及（26.4±6.5）ug/ml、TAFI Ag（79.2±25.8）%。经方差分析，心肌梗死组及心绞痛组血浆中 TAFI 抗原与活性水平均较对照组显著增高（p＜0.0001），而冠心病组之间则无统计学意义（p＞0.05）。CPB2 基因的 3 种基因型（Thr325Thr、Thr325Ile、Ile325Ile）频率分布在心肌梗死组、心绞痛组和对照组分别为 32（32%）、53（53%）、15（15%），31（28.2%）、58（52.7%）、21（19%）和 64（33.6%）、92（48.4%）、34（17.8%），等位基因 C、T 频率在心肌梗死组、心绞痛组和对照组分别为 117（58.5%）、83（41.5%），120（54.5%）、100（45.5%）和 220（57.9%）、160（42.1%），三组之间基因型及等位基因频率分布无统计学差异且均符合 Hardy-Weinberg 平衡。在冠心病组和对照组不同的基因型对 TAFI 活性没有影响（p＞0.05）；对 TAFI 抗原含量的影响，则以 Thr325Thr 纯合基因型者血浆 TAFI 抗原浓度最高（p＜0.05）。
结论 TAFI 具有抑制纤溶的作用，可能是冠心病发病的危险因子。TAFI 编码区 CPB2 基因的多态性对血浆中 TAFI 抗原水平有明显影响，但与冠心病的发生没有明显的相关性。

PU-4124

肺癌患者凝血与纤溶系统分子标志物的检测及其临床意义

徐成伟
山东大学第二医院

目的 探讨血浆血栓调节蛋白（TM）、凝血酶抗凝血酶复合物（TAT）、组织型纤溶酶原激活物-纤溶酶原激活物抑制剂-1 复合物（t-PAI-C）、纤溶酶-α2 纤溶酶抑制剂复合物（PIC）等 4 项指标与肺癌病情发展及预后的关系。
方法 采用化学发光酶免疫法测定 158 例肺癌患者（NSCLC 患者 113 例，SCLC 患者 45 例）、53 例肺良性疾病患者及 60 例健康对照者血浆 TAT、TM、t-PAI-C、PIC 水平，分别比较肺癌组、肺良性疾病组与健康对照组，肺癌组有无转移，以及肺癌患者手术前后 4 项指标的差异。
结果 肺癌组血浆 TAT、TM、t-PAI-C、PIC 水平均显著高于肺良性疾病组和健康对照组（P<0.01），但肺良性疾病组与健康对照组比较无显著性差异（P>0.05）；NSCLC 患者血浆 TAT、TM、t-PAI-C、PIC 水平均显著高于肺良性疾病组和健康对照组（P<0.01），SCLC 患者血浆 TAT、TM、PIC、t-PAI-C 水平均显著高于肺良性疾病组和健康对照组（P<0.01）；肺癌转移组血浆 TAT、TM、t-PAI-C、PIC 水平均显著高于无转移组（P<0.01 或 P<0.05），其中 SCLC 组有无转移组血浆 t-PAI-C 水平未见显著性差异（P>0.05）；肺癌手术后 7～10 天血浆 TAT、TM、t-PAI-C、PIC 水平较术前明显下降，差异具有统计学意义（P<0.001）。
结论 肺癌患者存在不同程度的血管内皮损伤及凝血与纤溶系统功能紊乱，导致患者体内高凝状态容易并发血栓形成。检测血浆 TAT、TM、t-PAI-C、PIC 水平有助于评判恶性肿瘤并发血栓栓塞症的病情进展、疗效观察及预后判断。

PU-4125

2 型糖尿病患者 TAFI、PAI-1、t-PA、F1+2 与尿微量蛋白之间关系的研究

徐成伟
山东大学第二医院

目的 探讨 TAFI 和 PAI-1 在 2 型糖尿病患者中纤溶抑制的作用机理，并分析 TAFI、PAI-1、t-PA、F1+2 等凝血、纤溶的指标与尿微量蛋白之间的关系。
研究对象和方法 64 例 2 型糖尿病患者以尿蛋白排泄量分微量蛋白尿组（MAU）和正常蛋白尿组（NAU）2 组。凝血酶激活的纤溶抑制物（TAFI）、纤溶酶原激活物抑制剂-1（PAI-1）、组织型纤溶酶原激活剂（t-PA）及凝血酶原片段 1+2（F1+2）等凝血纤溶指标测定用酶联免疫吸附双抗体夹心法（ELISA），并分析上述指标与尿微量蛋白、血压、血糖、血脂、功能参数之间的关系。
结果 与对照组比较，血浆 TAFI 仅在 MAU 组显著性升高（P＜0.05）；血浆 t-PA 在 T2DM 的两组中增高均无显著性；而血浆 PAI-1 和 F1+2 在 NAU 和 MAU 组均显著性增高，差异具有统计学意义（P＜0.01）。但 TAFI、PAI-1、t-PA、F1+2 在 NAU 和 MAU 两组之间无显著性差异。
结论 2 型糖尿病患者的纤溶功能降低主要是由于 PAI-1 的作用，随着蛋白尿的出现，其进一步的低纤溶状态则是由 TAFI 介导的，故 TAFI 和 PAI-1 在抑制纤溶系统功能上的作用是独立的。

PU-4126

2 型糖尿病合并下肢骨折患者凝血分子标志物的变化及其与血栓形成的关系

徐成伟
山东大学第二医院

目的 探讨骨折对 2 型糖尿病患者凝血活性的影响及其与发生血栓性疾病的关系。
方法 测定 90 例 2 型糖尿病合并下肢骨折患者、90 例 2 型糖尿病患者及 90 例性别、年龄、体质指数均具有可比性的健康对照者的血浆纤维蛋白原（Fib），D-二聚体（D-dimer），血管性血友病因子（vWF）、血小板膜颗粒糖蛋白 140（GMP-140）、凝血酶原片段 1+2（F1+2），凝血酶激活的纤溶抑制物（TAFI）及组织因子途径抑制物（TFPI）等含量或活性水平，并进行组间比较。
结果 糖尿病合并骨折组 Fib、D-dimer、vWF、GMP-140、F1+2 和 TAFI 测定值分别是（5.3±1.4）g/L、（1350.1±88.3）ng/mL、（161.9±6.6）IU/dL、（21.8±2.5）μg/L、（1.6±0.5）nmol/L、（30.5±3.8）μg/mL，糖尿病组的相应测定值分别为（4.1±1.2）g/L、（880.5±35.6）ng/mL、（123.6±5.5）IU/dL、（18.9±2.3）μg/L、（1.3±0.3）nmol/L、（28.3±2.9）μg/mL，对照组的相应测定值分别为（2.5±0.6）g/L、（145.7±22.5）ng/mL、（96.8±4.5）IU/dL、（13.8±2.1）μg/L、（0.8±0.2）nmol/L、（26.4±2.5）μg/mL，前两组的测定值均较对照组显著增高，且糖尿病合并骨折组较糖尿病组显著增高（P<0.001）；糖尿病合并骨折组血浆 TFPI 活性为（16.2±1.3）U/ml，糖尿病组为（17.3±2.1）U/mL，均低于对照组（18.5±2.7）U/ml，且糖尿病合并骨折组较糖尿病组降低，差异均有显著性（F=26.68，P<0.001）。
结论 骨折可导致糖尿病患者的凝血活性增强，高凝状态加剧，进而更容易发生血栓栓塞性疾病。

PU-4127

Expression of serum free light chain in patients with lymphoma in Western China

Juan Zhang、jiaqiang wang、dan li
Sichuan Provincial People's Hospital

In abroad, Serum immunoglobulin free light chain (FLC) elevations in patients with Hodgkin lymphoma (HL) and non Hodgkin lymphoma (NHL) are associated with an inferior outcomes. However, there is limited data on serum FLC in lymphoid malignancies in China, especially, in west China. In this article, we will focus on lymphoma FLC in the west China.We analyzed the FLC results and the association of elevated FLC with clinical characteristics in 122 cases from Sichuan Provincial People's Hospital with newly diagnosed lymphoma. We found that the FLC elevation was common in lymphoma, but varied by types of FLC secretion (monoclonal or polyclonal), lymphoma types, geography and race. Furthermore, the patients with elevated FLC had adverse clinical characteristics more frequently, such as old age, more males, higher AMC and ALC, and etc. We demonstrated that the FLC was a new, useful, easily measured, serum biomarker in west china lymphoma population.

PU-4128

血清铁蛋白与血常规水平变化在诊断孕中期贫血中的意义

梁福燕
联勤保障部队 970 医院

目的 分析育龄期妇女的孕中期的血清铁蛋白和血常规检测项目之间水平变化，找到孕中期血清铁蛋白与血常规报告中各个数值之间变化的相关性，为预防孕期因血容量增大而引起的贫血及临床诊断、治疗孕中期贫血提供帮助并总结数值变化规律在孕中期贫血中的意义。
方法 选取 42 例孕中期贫血的孕妇作为研究对象，提取她们在怀孕前和孕中期的血清铁蛋白（SF）和血常规[红细胞比容（HCT）、红细胞计数 (RBC)、平均红细胞血红蛋白浓度 (MCHC)、 平均红细胞体积 (MCV)、血红蛋白（HB）、红细胞体积大小变异系数（RDW-CV）]数据，计算出怀孕前与怀孕中期的各项指标差值，以血常规报告的六组数据作为自变量，整理好借助 SPSS 数据分析软件，以此建立出各数值变化与血清铁蛋白变化的线性模型。阐述了孕中期血常规报告中六项指标，血清铁蛋白，孕中期贫血间的相关性，总结各变量之间的相互影响和意义。
结果 通过 SPSS 软件进行数据分析的线性建模，得出红细胞计数（RBC）、平均红细胞血红蛋白浓度（MCHC）与血清铁蛋白呈正性正相关（P＞0.05），红细胞比容（HCT）、血红蛋白（HGB）与血清铁蛋白呈负性正相关（P＞0.05），平均红细胞体积(MCV)和血清铁蛋白呈负性负相关（P＞0.05）。
结论 血常规报告中的六组数据都与孕中期贫血的血清铁蛋白存在一定的线性关系，所以在确诊孕中期贫血时可借助相关血常规报告中的检测指标及血清铁蛋白数据提示孕妇贫血，及时补充铁剂。

PU-4129

系统性红斑狼疮患者狼疮抗凝物和凝血功能检测的应用价值

刘红春、黄国虹
新疆维吾尔自治区人民医院

目的 探讨狼疮抗凝物(LA)及凝血功能指标在系统性红斑狼疮(SLE)患者血栓形成中的应用价值。
方法 收集 64 例 SLE 患者和 60 例健康体检者临床资料，比较 SLE 患者与健康对照组 LA 标准化比值、凝血功能指标（活化部分凝血活酶时间(APTT)、凝血酶原时间(PT)、纤维蛋白原(FIB)、D 二聚体(D-D)、抗凝血酶Ⅲ(AT-Ⅲ)）水平的差异，分析 LA 和凝血功能指标对 SLE 患者血栓形成的影响，研究在 SLE 血栓患者中各凝血指标与 LA 的相关性。
结果 SLE 患者中 LA 阳性占比为 31.25%，与健康对照组相比，SLE 患者组 LA 标准化比值、APTT、D-D、AT-Ⅲ水平均高于正常对照组，差异有统计学意义（P＜0.05）。SLE 血栓率为 18.75%，发生血栓事件的 SLE 患者的 LA 标准化比值和 APTT 水平均高于 SLE-非血栓组，差异有统计学意义（P＜0.05）。Pearson 直线相关分析结果显示，APTT 与 LA 呈正相关（r=0.63，P＜0.05），AT-Ⅲ与 LA 呈中度负相关（r=-0.58，P=0.05）。
结论 SLE 与 LA 及凝血功能部分指标密切相关，LA 比值增高和 APTT 延长造成 SLE 患者血栓形成风险增加，早期测定 SLE 患者的 LA 和凝血功能水平，有利于对 SLE 患者高凝状态的预防，为 SLE 患者并发血栓的早期诊断提供参考指标。

PU-4130

成都市正常妊娠女性血小板及相关参数参考范围的建立

杨婷
四川省人民医院东院

目的 检测成都地区不同孕期的正常妊娠女性血小板及其相关参数，建立该地区孕早、中、晚期女性的血小板及其相关参数的参考范围。
方法 选取 2019 年至 2020 年在四川省人民医院产科进行孕期检查的正常妊娠女性 819 例进行回顾性研究，其中孕早期 270 例，孕中期 289 例，孕晚期 260 例，同时选取 333 例健康体检的非妊娠育龄妇女作为对照。以上选取的妊娠及非妊娠女性的全血血小板计数（PLT）、血小板平均体积（MPV）、血小板分布宽度（PDW）及大血小板比例（p-LCR）水平结果均采用 Sysmex-XN 血细胞分析仪检测所得。对检测结果进行分析，比较正常妊娠妇女与非妊娠妇女以及各孕期之间血小板及相关参数的差异，建立该地区妊娠妇女 PLT、MPV、PDW、p-LCR 的参考范围。
结果 正常妊娠女性与正常非妊娠女性的 PLT、MPV、PDW、p-LCR 比较，差异有统计学意义（P＜0.05）。正常妊娠女性孕早期与孕中、晚期的 PLT、MPV、PDW、p-LCR 比较，差异均有统计学意义（P＜0.05）；孕中期与孕晚期的 PLT、MPV、p-LCR 比较，差异均有统计学意义（P＜0.05）；但孕中期与孕晚期的 PDW 比较，差异无统计学意义（P＞0.05）。正常妊娠女性孕早、中、晚期 PLT 参考范围分别为（112.0～312）、(103～294）、（93～284），MPV 参考区间分别为（9.1～14.1）、（9.1～14.6）、（9.0～14.3），PDW 参考区间分别为（9.0～21.9）、(9.4～23.5）、（9.4～23.5），p-LCR 参考范围分别为（17.5～57.9）、（18.1～58.4）、（18.1～57.5）。
结论 正常妊娠女性与正常非妊娠女性的血小板及相关参数有明显变化，且孕早期与孕中期、孕晚期也有所差异，各地区应建立适合本地区的正常妊娠女性血小板及相关参数参考范围。

PU-4131

异型淋巴细胞在 CMV 感染患儿中的临床应用

张富蕊
滨州医学院烟台附属医院

目的 为了探讨异型淋巴细胞变化水平在巨细胞病毒感染患儿中的诊断价值，异型淋巴细胞的水平是否与巨细胞病毒感染患儿具有相关性，对临床是否有诊断价值。
方法 实验组为滨州医学院附属医院在儿童门诊及病房 CMV 感染患儿 100 例，年龄在 4 岁左右，无其他血液系统等并发症；对照组为滨州医学院附属幼儿园健康儿童，年龄在 6 岁左右。对所有实验对象进行外周血涂片染色镜检，筛查异型淋巴细胞的数量对异型淋巴细胞数目统计分类，两组间数据比较采用卡方检验。同时运用流式细胞技术检测患儿组外周血淋巴细胞中的 pp65 抗原进行对比分析。
结果 巨细胞病毒感染的婴幼儿发病后，机体免疫系统紊乱，异形淋巴细胞水平增高，X2 值为 95.998，P<0.01。
结论 异型淋巴细胞变化水平与巨细胞病毒感染有相关性。异型淋巴细胞的检出对于婴幼儿感染巨细胞病毒具有明确的诊断价值，异型淋巴细胞的检查方法对于诊断巨细胞病毒感染具有一定的临床意义，准确性较高，是值得作为辅助临床诊断婴幼儿感染 CMV 的一项技术。

PU-4132

基于血小板参数建立区分肺结节良、恶性模型的真实世界研究

祖瑞铃
四川省肿瘤医院

目的 利用真实世界数据，基于血小板参数建立用于区分肺结节良、恶性的模型，对该模型的诊断效率进行验证，并与其他临床模型进行比较。
方法 纳入 2018 年至 2020 年在四川省肿瘤医院就诊的肺结节患者，所有纳入患者的治疗和相关检查均由临床医生决定，本研究者不做任何干预。回顾性收集纳入患者的 CT、临床和血小板数据，使用 XGBoost 构建预测模型。利用 ROC 曲线、IDI、NRI 和 NB 对模型进行评估并与其他模型比较。
结果 纳入人群被随机分入训练组和测试组，其中训练组包括 295 名肺结节患者（213 名恶性结节），测试组包括 124 名患者（90 名恶性结节）。最终年龄、血浆样本中的血小板计数 (pPLT)、富血小板血浆样本中的血小板比容（pPCT）、结节大小、全血样本中的血小板比容（bPCT）被纳入 XGBoost 模型。与 VA、MC、BU 模型相比，XGBoost 模型在 AUC 上有更好的表现（0.6365, 95%CI: 0.5786-0.6944; 0.6504, 95%CI: 0.5907-0.7101; 0.6232, 95.60425 ，分别为 95%CI:0.6946-0.7971)，从 NRI (0.1906, 95%CI:0.0955 - 0.2857; 0.2053, 95%CI: 0.1177 - 0.29217, 0.29217, 0.29217; 0.2928）和 IDI（分别为 0.07；95% CI，0.06-0.08；0.1274，95%CI：0.0909 - 0.1638；0.06，95% CI，0.05-0.06）来看，XGBoost 模型在对良、恶性结节的重新分类上要优于其他模型。根据决策曲线所示，XGBoost 模型也可以为患者带来更多益处。
结论 在本研究中，基于血小板参数的 XGBoost 模型被证明是一种区分恶性结节和良性结节的准确方法。

PU-4133

如何减轻患者静脉穿刺的疼痛

官余蕊
山东大学第二医院

1、建立有效沟通,给予心理支持,减轻患者的恐惧感
患者紧张的心理状态和对以往静脉穿刺时疼痛记忆,会使患者在采血过程中产生恐惧感。因此,护士在与患者的沟通过程中要面带微笑,语气温和,言词简单易懂,减少患者的紧张情绪,争取在轻松愉快的沟通过程中进行穿刺。因患者分散了注意力,对穿刺时的疼痛敏感性也随之降低。
2、提高穿刺技术,减轻患者疼痛
2.1 改进穿刺方法,减轻穿刺引起的疼痛
采用常规静脉穿刺法采血时,进针角度小(针头与皮肤成 30 度角) ,针头在血管旁边直刺或斜刺后再进入血管, 因此针头与皮肤接触面积较大,同时针头所穿过的皮肤组织较多,牵涉组织及神经末梢也相对较多,表皮到达血管的距离相对较长。
如果操作者进针速度越慢,对神经末梢刺激时间也就越长,表皮受损范围越大,所以患者疼痛感明显。同时, 由于穿刺时血管受推动压力的作用,易滑动,从而在一定程度上会降低穿刺的成功率,这样既增加了患者的痛苦又延长穿刺时间。要减轻穿刺引起的疼痛,就要减弱刺激,缩短刺激时间和减少刺激面积。即减少皮肤机械性损伤面积和缩短针尖斜面在皮内的刺激时间。采用改良的采血方法,即加大进针角度(头皮针与皮肤成 40~60 度角) ,针尖沿静脉上方直接快速进入静脉腔, (血管越充盈粗大则进针穿刺角度越大, 且穿刺速度越快),见回血后即接上真空采血管。这种方法可直入主题,由皮肤直接进入血管,不需要潜行进入针头,避免针头在皮下穿梭损伤皮下组织和加重痛感。
2.2 采用辅助措施,减轻患者疼痛感
采血前,将止血带较常规扎得稍紧,可起到麻痹扎止血带下段肢体神经的作用,有效减轻痛感。
3、采用合适的采血针,减轻患者恐惧感
采血时,根据患者血管情况,选用大小合适的采血针。一般情况下成人使用 6 号采血针,而小儿则使用 5 号半的头皮针。小号针头因其针尖斜面小,尖锋利,刺破皮肤时阻力小,刺破血管时机械切面小,对血管内膜损伤轻,在人的痛阈内完成操作从而减轻患者痛苦。

PU-4134

儿童末梢采血的技巧

孟义
山东大学第二医院

在我们日常采血工作中，儿童末梢采血是必不可少的，但是儿童自主配合特别低，有的小朋友一看到采血的工作人员就非常抗拒，有的直接跑，有的攥住拳头不松开，有的藏进妈妈的怀抱。面对孩子的反抗，所以在采集过程中，相比成人采血成功率低，因此在实践工作中总结了一些技巧。
向患儿家长核对患儿的信息，核对项目，执行执行单。
准备合适的试管，执行单贴在试管上，检查乳胶吸头，取一次性微量吸管，采血针。
嘱咐家长抓好儿童手腕，并告知家长用大拇指按住儿童大拇指根部。
用 75%酒精消毒，待干。
用左手大拇指和食指固定采血部位使皮肤紧绷，右手用一次性末梢采血器扎入指腹，然后立即拔出。
用无菌干棉签擦去第一滴血。
用一次性微量吸管吸血，如果血流不畅，可用左手大拇指和食指稍微施压使血流流出，用无菌干棉签按压伤口止血。
用乳胶吸头将一次性微量吸管中的血液排进试管中，颠倒混匀，切勿大力振荡。

PU-4135

急性髓细胞白血病中 CEBPA 基因突变特点分析

韩雪莹、朱丽蒙、张慧、张暨
郑州金域临床检验中心有限公司

目的 探究 CCAAT/增强子结合蛋白 α (CEBPA)在急性髓系白血病（AML）中的突变特点、CEBPA 胚系突变对 AML 预后的影响及胚系验证的必要性；
方法 收集郑州金域 2018 年 5 月至 2021 年 5 月用高通量测序方法检测 AML 相关基因突变（检测范围：30 基因全外显子）的患者数据共 803 例，通过生信分析就人员突变位点筛选、临床意义分级发现其中发生 CEBPA 突变患者共 329 例，患者年龄范围 11-92 岁。分析 CEBPA 双等位基因突变、单突变等不同突变模式下伴随基因的分布情况。在 CEBPA 突变的患者中，经验证得出具有家族遗传史的案例为 2 例，并分析胚系突变的发生特点及临床影响。
结果 329 例阳性患者中双突变为 212 例，单突变为 117 例，主要以双突变形式存在（65%）。且突变发生的年龄范围主要集中在 31-70 岁之间，占比达到 79%。CEBPA 双突变的患者中，更易伴随 GATA2、TET2、WT1、DNMT3A 基因的突变。在伴随基因分类中，双突变的高危标志基因伴随率为 23.88%，CEBPA 单突变患者的高危基因伴随率为 37.84%。这些高危分子标志的累积叠加可能进一步导致不良预后。伴 CEBPA 突变的遗传相关 AML 通常表现为显性遗传且完全外显，但胚系突变的来源不局限于之前研究发现的 N 端，DNA 结合区域也会有致病胚系突变的检出。
结论 CEBPA 单突变比双突变患者具有更多的预后不良相关基因突变，可能与 CEBPA 两种突变的致病性差别而导致预后差异相关。CEBPA 的胚系突变会导致家族性 AML 的发生，且在伴随其他致病体细胞突变时会加快疾病出现进程，对 CEBPA 突变检出阳性的患者，要对符合胚系突变特征的阳性位点进行胚系验证，提高检出率和正确率，如果先证者得到验证，需进一步进行家族突变谱筛查，以提供家族 AML 风险管理和早期诊断的依据。

PU-4136

302 例胎儿超声异常的遗传病因学分析

李毅、查斌斌、张帅、范晓宇、孙晶
泰安市中心医院

目的 从细胞和分子水平探讨胎儿超声异常的遗传病因学。
方法 选取 2004 年 6 月～2019 年 7 月 302 例以胎儿超声指标异常为指征进行侵入性产前诊断的病例，对其染色体及微阵列检查结果进行回顾性总结分析。
结果 302 例胎儿超声异常中，染色体核型异常 62 例，总异常检出率 20.53%；羊膜腔穿刺胎儿染色体异常检出率 26.77%（53/198）；脐血穿刺胎儿染色体异常检出率 8.65%（9/104）。超声指标异常染色体异常检出率依次为：结构畸形合并软指标异常 33.33%＞软指标异常 27.21%＞结构畸形 15.79%；胎儿颈部淋巴水囊瘤病例，染色体异常检出率最高为 58.33%，其次为颈项透明层增厚，异常核型检出率为 38.36%。合并三项及以上软指标异常组中，胎儿染色体异常检出率 36.36%高于单纯一项或两项组，伴有胎儿超声指标异常的高龄孕妇组染色体异常检出率高于低龄孕妇组。65 例同时进行染色体核型及染色体微阵列分析的病例中，核型正常而染色体微阵列分析异常 13 例，其中 6 例致病性微缺失微重复综合征。
结论 孕早中期超声筛查有助于更早地检出染色体异常胎儿，超声指标异常种类和数量越多及孕妇高龄合并胎儿超声指标异常时，发生染色体异常的机率增高；21-三体、性 CS 异常及 18-三体是最常见的超声异常胎儿的染色体异常类型；颈项透明层增厚、颈部淋巴水囊瘤等指标对染色体异常有重要提示价值，染色体微阵列分析在分子水平对染色体核型分析提供有力补充。

PU-4137

氧化石墨烯结合适配体酶切循环用于细胞外囊泡的快速检测

黄蓉蓉
南京鼓楼医院

目的 结合信号放大机制实现胃癌细胞外囊泡的定量检测，为胃癌的早期筛查、临床诊断和预后评估提供快速、灵敏、简便、成本低廉的新方法。
方法 一种以氧化石墨烯（Graphene oxide，GO）为检测平台的胃癌细胞外囊泡荧光检测法，首先将 GO 作为载体用于吸附修饰荧光基团的适配体，此时荧光信号被猝灭，当待测样品中存在细胞外囊泡时，适配体与细胞外囊泡结合而从氧化石墨烯上脱离，当氧化石墨烯吸附适配体后，适配体碱基与氧化石墨烯之间的 π-π 堆积相互作用能保护其不被脱氧核糖核酸酶 I（Deoxyribonuclease Ⅰ，DNase Ⅰ）降解，当待测样品中存在靶细胞外囊泡时，适配体与细胞外囊泡结合并从氧化石墨烯表面脱离，此时适配体能被 DNase Ⅰ降解并释放细胞外囊泡，游离的细胞外囊泡重新与氧化石墨烯上吸附的适配体结合，引发下一轮酶切反应。上述酶切循环能产生大量的短链核酸片段，由于短链核酸与氧化石墨烯之间的分子间作用力较弱，无法吸附到氧化石墨烯表面，因此能维持强烈的荧光的信号，且信号强弱与细胞外囊泡浓度呈正相关，通过检测反应体系最终的荧光信号，可以达到定量靶细胞外囊泡的目的。
结果 经过分析，当胃癌细胞外囊泡浓度在 3.2 × 107 ~ 1 × 1011 个/mL 的范围内时，检测体系的荧光强度与细胞外囊泡浓度呈现良好的线性关系，此时的线性方程为荧光值 F = 2570 × logC − 16007，其中 C 为细胞外囊泡浓度，单位为个/mL，线性相关系数 R2 = 0.9728，LOD 为 1.69 × 106 个/mL。
讨论 我们制备的氧化石墨烯结构稳定且包含大量的含氧官能团，传感器在引入酶切循环后信号增幅明显（约 4 倍），传感器的线性方程线性相关系数 R2 = 0.9728，检测限为 1.69 × 106 个细胞外囊泡/mL。

PU-4138

WBC、CRP、SAA、ESR 联合检测在冠心病诊断中的应用

喻岚
华中科技大学协和深圳医院

目的 探讨 WBC、CRP、SAA、ESR 在冠心病诊断中的临床价值，讨论这四个血液指标之间的关系，联合检测是否能够提高冠心病的阳性率。
方法 收集在深圳南山人民医院行冠状动脉造影的冠心病患者、来院进行体检的健康者的病例资料及血液标本 117 例。通过筛查，将符合本次实验研究标准的 75 例冠心病患者的病历资料及血液样本纳入冠心病组；42 例健康体检者的病历资料及血液样本纳入对照组；冠心病组再根据冠状动脉狭窄累积病变支数分为单支病变组 27 例、双支病变组 20 例及三支病变组 28 例。最后分别检测各分组中的 WBC、CRP、SAA 及 ESR。
结果 冠心病组与对照组的 WBC、CRP、SAA 存在显著性差异，具有统计学意义（P<0.05）;但冠心病组与对照组的 ESR 差异无统计学意义。检测项目 WBC、CRP、SAA、ESR 具有一定的相关性(P＜0.01)，CRP 与 SAA 成高度相关。各项项目检测指标的阳性率：SAA > CRP > WBC > ESR。
结论 冠心病与 WBC、CRP、SAA 具有一定的相关性，可通过检测这三个指标提早发现冠心病；SAA 与 CRP 具有高度相关性，且各项指标之间阳性率比较结果为 SAA 高于其他指标，表明 SAA 具有较好临床诊断价值；联合检测这四个指标可以提高冠心病的检出率。

PU-4139

浅谈环境温湿度对染色体 G 显带制片影响

陈超、翟贺
吉林金域医学检验所有限公司

目的 探讨环境温湿度对染色体 G 显带制片的影响，从而改善外周血 G 显带制片中出现的问题，提高制片质量、TAT 时间及降低退单率。
方法 随机选取近一周的 70 例外周血 G 显带样本进行接种，培养箱培养 72h 后细胞处于分裂的不同时期，加入秋水仙素可获得大量的中期分裂相细胞。用固定液甲醇:冰乙酸（3:1）进行固定，目的是维持染色体的固有形态及细胞膜。固定后获得一定沉淀细胞将细胞调制合适浓度进行滴片，在三种不同温度及湿度下对 70 例样本进行滴片，A 组：温度 25°C 湿度 50.0％-55.0％；B 组：温度 25°C 湿度 45.0％-50.0％；C 组：温度 27°C 湿度 50.0％-55.0％，滴片后统一放在 75°干燥箱内烤片 1h 烤片后进行吉姆萨染色。镜下随机选取 100 组分裂相观察其染色体形态及条带，记录较好的分裂相组数。
结果 对三种不同温湿度下的 70 例样本进行镜下分析后，结果如下图。A 组环境下较好分裂相为 61 组、B 组环境下较好分裂相为 73 组、C 组环境下较好分裂相为 57 组。
结论 在 B 组：温度 25°C 湿度 45.0％-50.0％的环境下，低倍镜下可看见中期分裂相，进而转至高倍镜及油镜下观察，可见染色体较为饱满，分布均匀，着色较好，沿染色体长轴可显出深浅不同的 G 带横纹条带清晰（如图）。且 B 组所得较好分裂相占比 73%，远高于 A 组 61%与 C 组 57%。由此可见，环境温湿度对制片有一定的影响，且温度 25°C 湿度 45.0％-50.0％的环境下制片效果最佳。

PU-4140

发热伴血小板减少综合征（SFTS）危重型案例一篇

张源达
江苏省人民医院（南京医科大学第一附属医院）

目的 分析实验室指标对诊断发热伴血小板减少综合征疾病的重要价值。
方法 跟踪分析一例发热伴血小板减少综合征（SFTS）危重型患者从初步诊断到最终确诊的过程。分析患者资料包括主诉、临床表现及体征、实验室指标（血液细胞学、生化、心肌标志物、凝血功能等常规指标，入院后炎症指标、免疫球蛋白等完善性检查指标，以及病原微生物学、分子生物学等特异性检查指标）、影像学检查。本案例重点分析常规实验室指标对初步诊断及最终确诊的指导价值。
结果 患者女，67 岁，入院前一周余无明显诱因下出现发热，最高达 39℃，伴全身乏力，经当地医院抗生素抗病毒药物治疗后，体温恢复正常。2021-3-18 患者突发意识障碍，言语不清，行走困难，遂至我院就诊。相关实验室检查及影像学检查结果见附件。根据患者主诉，结合患者发热、腹股沟可触及肿大淋巴结、血小板下降等相关临床症状，临床初步考虑为发热伴血小板减少综合征。根据急诊脑脊液检测结果，病毒性脑膜炎诊断明确。发热伴血小板减少综合征病毒 RNA 检测结果为阳性最终确诊为发热伴血小板减少综合征(SFTS)。
结论 发热伴血小板减少综合征是由新型布尼亚病毒感染所引起的经蜱传播传播的自然疫源性疾病，临床主要表现为发热、血小板减少、白细胞减少、消化道症状及多脏器功能损伤等，病情严重者可出现抽搐、昏迷、休克、全身弥漫性血管内凝血等，甚至导致死亡。该患者因合并有病毒性脑膜炎，以及慢性胆囊炎、慢性乙型病毒性肝炎等基础性疾病，实验室指标反映多脏器功能受损，病情较为复杂，增加了最终确诊的难度，而入院初期的一系列常规实验室指标检查的综合指向性较为符合 SFTS 的临床特征，进而为特异性实验室指标确诊指明了思路，提高了临床诊疗效率。

PU-4141

全血红细胞相关参数在肠梗阻的诊断和鉴别诊断中的应用价值研究

何亚琼、束国防
东南大学附属中大医院

目的 探究全血红细胞相关参数在肠梗阻的诊断和鉴别诊断中的应用价值。
方法 收集我院 2019 年 1 月—2021 年 5 月诊断为肠梗阻的住院病人共 170 例，作为研究组，根据肠梗阻的程度和病情，分为不完全性肠梗阻（109 例）、完全性肠梗阻（32 例）和粘连性肠梗阻（29 例）。选取同期健康人 100 名，作为对照组。采用非参数 K 检验比较各组平均红细胞体积(MCV)、平均红细胞血红蛋白含量(MCH)、平均红细胞血红蛋白浓度(MCHC)及红细胞体积分布宽度((RDW-CV、RDW-SD)的水平。
结果 研究组 MCV、MCH、MCHC、RDW-CV、RDW-SD 的水平明显低于正常对照组，且差异均有统计学意义（P<0.05）.不完全性肠梗阻患者的 MCHC 水平明显高于完全性肠梗阻患者，差异有统计学意义（P<0.05）。不完全性肠梗阻患者的 MCV、MCH、MCHC 水平高于粘连性肠梗阻患者，而 RDW-CV 低于粘连性肠梗阻患者，差异均有统计学意义（P<0.05）。
结论 不同类型肠梗阻患者的红细胞相关参数具有不同特征，红细胞参数水平能够为临床肠梗阻的诊断和鉴别提供较为有效的参考依据。

PU-4142

FUS-2000 全自动尿液分析仪性能验证的结果分析

肖婷
陆军军医大学第一附属医院（西南医院）

目的 探讨已使用过 4 年的 FUS-2000 全自动尿液分析仪性能，验证其是否能满足国家相关规定的要求，以便在临床正常使用。
方法 依据《中华人民共和国医药行业标准》YY/T 0475-2011 验证尿干化学模式试纸条的重复性检测、准确度测试、携带污染率、生物参考区间；依据《中华人民共和国医药行业标准》YY/T 0996-2015 验证尿有形成分模式的检出限、准确性、重复性、携带污染率、线性范围、识别率、假阴性率、可报告范围、生物参考区间。
结果 FUS-2000 全自动尿液分析仪尿液干化学纸条 12 个项目的重复性变异系数均小于 1%；准确度测试 12 个项目均满足要求；携带污染率阴性样本未出现阳性结果；尿干化学生物参考区间符合要求。尿有形成分准确性绝对偏差为 1.64%；红白细胞检出限 10/ul；红细胞低值、高值浓度重复性的变异系数分别为 8.7%、6.1%；白细胞低值、高值浓度重复性的变异系数分别为 8.4%、4.9%；携带污染率为 0.00%；红细胞的线性范围的相关回归方程 y=0.9928x+10.5563；红细胞的可报告范围为 10-16000*256/ul；白细胞符合率为 96%、红细胞符合率为 92%、管型符合率为 90%；假阴性率为 5.5%；尿有形成分生物参考区间符合要求。
结论 FUS-2000 全自动尿液分析仪性能验证的结果尿有形成分假阴性率不符合要求，其它参数符合国家要求。假阴性的结果会让临床漏诊一些疾病，所以应停止使用该仪器，及时查找原因并采取纠正措施，纠正后并重新进行性能评价，性能验证通过后才能再次应用于临床。总之在临床工作中我们应按要求在规定的时间内做好仪器的性能验证，以便了解其最佳的性能状态，为临床提供准确的报告，减少漏诊及误诊。

PU-4143

尿路感染诊断中尿常规检验的临床意义与结果分析

徐亚敏
山东第一医科大学第一附属医院（山东省千佛山医院）

目的 观察尿路感染诊断中尿常规检验的结果,分析其临床价值.
方法 选取我院 2020 年 9 月-2020 年 12 月收治的 100 例疑似尿路感染患者作为观察组,100 例健康体检人员作为对照组,对两组研究对象均进行尿常规检测和尿细菌培养,比较两组研究对象中白细胞计数以及亚硝酸盐阳性率,尿液细菌培养阳性率，以及检出的革兰阳性球菌和革兰阴性杆菌的百分比.
结果 观察组白细胞计数(5.98±1.32)个/HP,亚硝酸盐阳性 69 例,阳性率 69%;对照组白细胞计数(0.44±0.32)个/HP,亚硝酸盐阳性 0 例,阳性率为 0,观察组白细胞计数及亚硝酸盐阳性率明显高于对照组,差异具有统计学意义(P〈0.05).观察组尿液细菌培养阳性 90 例,阳性率 90.00%，其中有 17 例患者检出革兰氏阳性球菌,有 73 例患者检出革兰氏阴性杆菌,阳性球菌检出率显著低于阴性杆菌检出率(P<0.05);对照组尿液细菌培养均为阴性,阳性率为 0;观察组尿液细菌培养阳性率明显高于对照组,差异具有统计学意义(P〈0.05).
结论 对尿路感染患者进行尿常规检验,疾病检出率较高,对临床诊断具有一定的价值,可为临床医师诊断病情提供依据，值得进一步研究.

PU-4144

血清淀粉样蛋白 A（SAA）的临床应用

黄金英
柳州市妇幼保健院

目的 血清淀粉样 蛋白 A（SAA）在肝脏中合成，是一个炎症标志物，特异性及敏感性均高于传统 C 反应蛋白（CRP），健康人在 10mg/L 以下，当细菌、病毒感染、心血管疾病、肿瘤、类风湿性关节炎以及移植排异等多种疾病时增高。SAA 在病毒和细菌感染中均可升高，而 CRP 在病毒感染中几乎不升高或升高不明显。对于微弱的炎症刺激，SAA 也较 CRP 更敏感。所以 SAA 是反映感染性疾病早期炎症的敏感指标，也因此受到临床研究学者们的青睐，与 CRP 的组合检测更能体现优势互补，对细菌、病毒感染鉴别更有临床增值意义。
方法 采用乳胶增强免疫比浊技术，首先将血液样本和试剂 1 充分混匀，试剂 1 中含有的溶血剂会破碎血细胞，防止血细胞形成的浊度对检测结果的影响。然后向试剂 1 和样本的混合液中加入试剂 2，试剂 2 由抗体标记的乳胶构成。加入试剂 2 后，抗 SAA 抗体标记的乳胶和血液中的 SAA 抗原结合形成抗原抗体复合物，使反应液体出现浊度。利用测量仪对浊度进行测定从而检测抗原含量。
结果和结论 血常规、CRP、SAA 为代表的早期检测指标，在疾病感染中的应用各有优缺点，多指标联合连续监测，有助于感染性疾病的早期诊断、疗效判断以及预后评估 。作为疾病感染的三大常规,通过联合检测可以有效、快速的进行细菌感染和病毒感染的诊断，能让医生更好的针对性用药，指导抗菌药物的合理利用。易于在各级医院中开展,有效的诊断、合理的用药可以缩短病程，有助于患者的恢复。

PU-4145

Red blood cell distribution width as a diagnosis biomarker of acute mesenteric ischemia: a meta-analysis

Luyao Yang[1]、Qingying Hu[2]
1. Chengdu University of Traditional Chinese Medicine
2. Hospital of Chengdu University of Traditional Chinese Medicine

Background Red cell distribution width (RDW) is a standard parameter in routine hematological examination. Some studies have revealed that RDW could serve as a prognostic marker of several diseases, such as acute mesenteric ischemia (AMI). However, different studies have reported various diagnostic values. In our paper, we present a systematic review and meta-analysis conducted to evaluate the diagnostic accuracy of RDW for AMI.
Methods We systematically searched the PubMed, FMRS, and EMBASE databases, the Cochrane Database of Systematic Reviews, the Chinese Biomedical Literature Database, the China Academic Journals Full-text Database, and the Chinese Scientific Journals Database for potential studies. Studies were included if they were related to red cell distribution width (RDW) and acute mesenteric ischemia and reported diagnostic outcomes. Diagnostic value analysis was used to summarize the overall diagnostic performance of RDW.
Results Six studies were included in the meta-analysis. The ranges of the metrics of diagnostic performance of RDW for AMI were as follows: sensitivity, 0.41~0.76; specificity, 0.49~0.92; positive likelihood ratio, 1.9~5.2; negative likelihood ratio, 0.36~0.60; and diagnostic odds ratio, 4~13. The assessments revealed significant risk of bias (Chi-square: Q=26.588, df=2.00, P=0.000) and inconsistency (I-square: I2 = 92%, CI = 86~99). The asymmetry test indicated significant publication bias (P<0.05).
Conclusions As a diagnostic biomarker, AMI may not be effective, and there are several limitations to the reviewed studies.

PU-4146

免疫监控在肿瘤免疫治疗不良反应中的应用价值

袁小庚[1]、赵晓武[1]、王涛[2]
1. 郑州金域医学检测中心
2. 河南省中医药大学第一附属医院

目的 免疫检查点抑制剂治疗肿瘤过程中发生的免疫相关不良反应（Immune-Related Adverse Events，irAE）严重者会威胁患者生命，为了及早的判断病情、指导药物应用及预后评估，需要评估患者的免疫状态，包括淋巴细胞亚群和细胞因子水平的检测。
方法 对 60 例应用 PD1 抑制剂的非小细胞肺癌（NSCLC）患者， 在治疗前及治疗每周期（21 天），应用流式细胞术的方法检测淋巴细胞亚群变化水平，应用流式荧光的方法检测血清细胞因子的水平。
结果 1、流式细胞术的方法检测淋巴细胞百分比和绝对值检测（T/B/NK、CD3＋CD4＋T、CD3＋CD8＋T、CD4/CD8 比值）评估患者用药前及初次用药后机体的整体免疫状态；
2、通过检测 T 淋巴细胞活化亚群检测（标记:CD69/CD25/HLA-DR）（T 早期、中期、晚期活化指标）和功能/耗竭 T 细胞检测（标记 CD3/CD4/CD8/CD28）（功能 T 细胞，分化/耗竭 T 细胞），评估用药前患者机体免疫细胞的活化水平，指导用药时机及预测用药后发生免疫相关不良反应的风险。
3、细胞因子检测（14 因子）（IFN-γ、IL-1B、IL-2、IL-4、IL-5、IL-6、IL-8、IL-10、IL-12p70、IL-17A、IL-17F、IL-21、TNF-γ、TNF-β），评估免疫相关不良反应发生的风险及指导用药。

结论 监测 NSCLC 患者应用 PD1 抑制剂发生免疫相关不良反应，尤其是发生细胞因子风暴的重症患者其免疫因素的作用，为肿瘤免疫治疗不良反应的发生及临床效果的预测，提供诊断检测指标，避免病情恶化并为临床能够及时用药处理、降低不良事件发生具有重要指导作用。该项检测一定程度上填补了肿瘤免疫治疗相关不良反应的空白，为临床预防、监控和治疗提供新思路。

PU-4147

一例 CD103 阳性伴 HCL 相关基因阴性的小 B 细胞淋巴瘤的诊断及鉴别

邹丽萍
四川金域医学检验中心有限公司

目的 探讨一例 CD103 阳性伴 HCL 相关基因阴性的病例诊断及鉴别诊断并文献复习。
方法 对病例的临床资料、骨髓细胞形态学、流式细胞学、遗传学及分子生物学结果进行综合分析。
结果 患者全血细胞减少、脾大，血清免疫固定电泳为 IgM-Lambda；骨髓涂片成熟小淋巴细胞增生为主占 90%，部分可见绒毛状突起。骨髓流式免疫分型检测到单克隆 B 淋巴细胞占淋巴总数的 40.77%，FSC 小至中等，表达 CD19、CD20、HLA-DR、FMC7,部分表达 CD103、CD11c，不表达 CD5、CD10、CD25、CD23、CD200、CD34、CD117，胞膜免疫球蛋白 Lambda 轻链呈限制性表达。骨髓活检结果提示符合成熟 B 细胞淋巴瘤/白血病。染色体检查提示为正常核型，分子生物学检测 HCL 相关基因突变 ARID1A、BRAF、CCND3、EZH2、JAK3、KDM6A、KMT2C、KRAS、MAP2K1、NF1、NRAS、TP53、U2AF1 均为阴性；结合临床表现及 MICM 相关检查结果，综合诊断为 SLVL。
结论 HCL、HCL-v、SLVL、LPL、PLL、T-ALL 均可出现 CD103 阳性；当 CD5-CD10-成熟小 B 细胞淋巴瘤/伴 CD103 阳性时，需鉴别 HCL、HCL-v、SLVL；出现单克隆 IgM 需鉴别 LPL、SLVL；完善相关检查并结合临床表现有助于此类疾病的鉴别与诊断。

PU-4148

新冠肺炎康复者恢复期血浆治疗 COVID-19 患者清除体内病毒核酸效果

段丽、林国跃、蔺志强、王泉、秦莹、木尼热·库尔班、李远达、屈晓娟、赵豆豆、张弛、何雪
新疆医科大学第八附属医院检验科

目的 探讨康复者恢复期血浆治疗 COVID-19 患者后体内核酸基因 ORF1ab、N 转阴变化规律以及临床治疗效果。
方法 应用康复者恢复期血浆对临床 75 例快速发展型、重型和危重症 COVID-19 患者进行输血治疗，未输血组 200 例作对照，同时检测观察这 2 组 COVID-19 患者体内核酸基因 ORF1ab、N 清除状况、住院时间及临床效果，并统计比较分析。
结果 99 例快速发展型、重型和危重症 COVID-19 患者接受康复者恢复期血浆治疗，共输注血浆 107250ml，平均每人 1083.33ml，其中快速发展型使用康复期血浆最多占 47.0%，重型和危重型分别为 25.9%和 27%，而危重型还使用大量普通冰冻血浆、红细胞悬液、血小板和冷沉淀治疗。临床输血有效率 100%,治愈率 100%，总输血率达 9.31%（99/1064），无严重输血不良反应。输血组新冠肺炎核酸基因 ORF1ab、N 清除率（63.89%）明显高于未输血组（26.50%）（$p<0.005$）；且同期第 7-14d 基因 ORF1ab 和 N（-）转阴率（22.67%）、基因 ORF1ab（-）转阴率（17.33%）、基因 N（-）转阴率（21.33%）较未输血组（分别是 10.50%、7.50%、8.50%）较明显的高，差异均具有统计学意义（$p<0.01$）。输血组内 COVID-19 快速发展型、重型和危重型

3 型患者之间，随着病情发展程度加重患者住院天数越来越长差异均有显著性（P＜0.05）；未输血组内快速发展型与重型患者之间，随病情发展程度严重其住院天数也越来越长，差异有显著性（P＜0.05）。输血组快速发展型和重型患者住院天数均较未输血组患者明显缩短，差异有统计学意义（P＜0.05）。

结论 应用新冠肺炎康复者恢复期冰冻血浆治疗 COVID-19 患者，可有效增强重型和危重型住院患者免疫功能、加快病毒清除及核酸转阴率，有明显促进病情早日好转的作用。

PU-4149

基于新冠肺炎康复者恢复期血浆治疗 COVID-19 患者增强其体内免疫抗体 IgM 和 IgG 浓度变化研究

段丽、林国跃、蔺志强、秦莹、李远达、张弛、屈晓娟、白山、王子璠、王钒
新疆医科大学第八附属医院检验科

目的 探讨康复者恢复期血浆治疗 COVID-19 患者体内抗体 IgM、IgG 变化及治疗效果。

方法 对 COVID-19 患者进行康复者血浆治疗、观察，并检测抗体 IgM、IgG ct 值，与未输血组比对分析。

结果 （1）99 例快速发展型、重型和危重症 COVID-19 患者共输注康复者血浆 107250ml，平均每人 1083.33ml，其中快速发展型使用血浆 47.0%，重型和危重型分别为 25.9%和 27%，临床有效率 100%,治愈率 100%，总输血率 9.31%，无严重输血不良反应。（2）康复者血浆 229 袋（200ml）抗体检测平均抗体 IgG ct 值 31.61±23.28（1:64），IgM 为 7.19±11.94（1:8）。（3）在输血组中，输注血浆后患者体内抗体 IgG 和 IgM 的 ct 值（68.70±69.14 和 47.89±64.63）分别高于输血前（4.46±13.99 和 4.46±13.99），二者比较差异均具有显著性（p＜0.05）；在未输血组中，患者出院时体内抗体 IgM 和 IgG ct 值分别显著高于患者入院时体内抗体含量 ct 值（p＜0.05）；总体上输血组 IgM 和 IgG 抗体 ct 值含量明显高、浓度大，比未输血组分别高出 1-3 倍，但均无统计学差异（p＞0.05），但输血组重型患者出院时抗体 IgG 和 IgM 含量均明显高于未输血组出院时差异有统计学意义（P＜0.05）。（4）输血组内和未输血组内 COVID-19 快速发展型、重型和危重型 3 型患者之间住院天数都随病情发展程度加重越来越长，输血组快速发展型和重型患者住院天数均较未输血组患者明显缩短，差异有统计学意义（P＜0.05）。

结论 应用新冠肺炎康复者恢复期血浆治疗 COVID-19 患者可大幅提高重型和危重型患者抗体含量，有效增强免疫功能，缩短住院时间，加快病情早日好转的作用。

PU-4150

血栓弹力图对恶性肿瘤患者凝血功能的检测及意义

宁茜
天津医科大学肿瘤医院

目的对血栓弹力图对恶性肿瘤患者凝血功能的检测效果进行分析,并探讨实际应用价值与意义。血栓弹力图（thrombelastography, TEG）为一种凝血功能检测手段,能够全面地反映血液凝固及纤维蛋白溶解的过程,目前临床上主要将其应用于凝血功能监测、凝血障碍疾病的诊断、指导成分输血和监测抗血小板药物疗效。本文对 TEG 在恶性肿瘤患者中 VTE 发生的预测价值进行综述。

PU-4151

2015-2019 我院成分输血的情况分析

普菊华
昆明市中医医院

目的 通过对我院临床成分输血的分析，指导临床科学、合理用血，节约血 源，提高输血疗效，减少不良反应，最大限度地降低经血液传播疾病的发生。
方法 对我院近 5 年（2015～2019 年）成分用血情况进行统计。
结果 成分输血(红细胞类、 单采血小板、血浆、冷沉淀)使用量逐年增加, 但与现代国内外输血相比, 我院在血浆、 冷沉淀、血小板的使用上还存在着一定的差距和不合理性。
结论 加强成分输血管理, 降低血浆使用率,合理应用冷沉淀、血小板，开展自体输血

PU-4152

临床检验分析前质量控制因素分析

李云芬
昆明市中医医院

临床检验分析质量控制，分检验前、检验中、检验后三个主要环节，有数据表明，临床检验结果错误大多与临床检验分析前质量控制有关，由于影响临床检验分析前质量控制的相关性因素较多，贯穿于医生、患者、护士、检验人员的全流程，任何一个环节出了问题，都不可能得到合格的检验结果，因此高度重视临床检验分析前质量控制，最大限度的减少检验前不合格标本流入的数量，提高检验准确率，对于提升医院医疗服务质量，减少患者不必要支出，塑造良好医风医德有着十分重要的意义。

PU-4153

白带常规联合 BV Set 试剂盒诊断细菌性阴道病的临床分析

纪凤卿、陈君颖、滕菁 （通讯作者）
厦门市中医院

目的 分析研究白带常规联合 BV Set 试剂盒诊断细菌性阴道病的临床分析。
方法 取我院 2019 年 11 月—2020 年 7 月收治的阴道炎患者 600 例作为研究对象，将这 600 例阴道炎患者全部采用白带常规检查和 BV Set 试剂盒检查，最后将 600 例阴道炎患者的检查结果进行比较分析。
结果 根据研究表明发现，采用 BV Set 试剂盒检查的患者的阳性率为 7.00%，采用白带常规检查的患者的阳性率为 5.00%，差异无统计学意义（P > 0.05）；根据研究表明发现，BV Set 试剂盒检查中过氧化氢阳性率为 576（96.00%），唾液酸酶阳性率为 42（7.00%），白细胞酯酶阳性率为 180（30.00%）；并且过氧化氢阳性 576 例标本，其在白带常规各级清洁度患者中均有分布，其中 I 度、II 度、III 度、IV 度阳性率分别为 4.00%、20.00%、24.00%、52.00%。
结论 采用白带常规检查和 BV Set 试剂盒检查联合能够有效提高细菌性阴道病的检出率，从而提高患者的生活质量，为患者带来益处，值得大力推广。

PU-4154

低蛋白血症伴低 Hb 的高龄老人血清可溶性尿酸水平分析

蒋理、蔡针针
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨自然寿命地区普通人群中高龄老人可溶性尿酸水平与营养相关指标的相关性分析。
方法 回顾性分析 2017 年 1 月至 2019 年 12 月来我院健康管理中心参加体检的 80 岁以上老人 4686 例，分析血清尿酸(UA)、白蛋白（Alb），血红蛋白（Hb）水平及各指标间相关性分析。
结果 女性低尿酸比率明显低于男性，差异有统计学意义（P<0.05)。按白蛋白水平四分位数分组。高蛋白组（Q4 组）尿酸水平高于低蛋白组（Q1 组），两组尿酸水平差异显著（P<0.01）；且低蛋白组低尿酸比率明显高于高尿酸组，差异显著（P<0.01）。按 Hb 水平四分位数分组。高 Hb 组（Q4 组）尿酸水平高于低 Hb 组（Q1 组），两组尿酸水平差异显著（P<0.01）；且低 Hb 组低尿酸比率明显高于高 Hb 组，差异显著（P<0.01）。分析低蛋白组、低 Hb 组及 Hb、ALB 均低组与正常组之间尿酸水平及低尿酸比率的差异，Hb、ALB 均低组尿酸均值最低、低尿酸比率最高，差异有统计学意义。
结论 表明营养状态差的高龄老人其尿酸水平也会低下，提示我们关注高龄老人营养状况的同时也要关注其尿酸水平，可以适当补充能升高尿酸的食物。

PU-4155

南京市区未孕育龄女性医务人员贫血患病率的初步调查

蒋理、蔡针针
江苏省人民医院（南京医科大学第一附属医院）

目的 初步调查南京市区未孕育龄女性医务人员贫血患病率。
方法 选择 2020 年 3 月至 7 月在我院进行健康体检的 18~45 岁未孕女性共 5672 人，分析贫血相关指标。其中 2798 例未孕育龄女性医务人员为实验组，其余 2874 例未孕育龄非医务职业女性为对照组。
结果 未孕育龄女性医务人员贫血总体患病率为 7.22%，其中 18~24 岁年龄段患病率为 4.91%，25~29 岁年龄段患病率为 6.18%，30~34 岁年龄段患病率为 7.52%，35~39 岁年龄段患病率为 9.96%，40~45 岁年龄段患病率为 8.06%；未孕育龄非医务职业女性贫血总体患病率为 14.20%，对应的年龄段患病率分别为 9.83%、10.89%、14.41%、20.07%、16.15%。两组的总体及各年龄段患病率差异均有统计学意义（P<0.05）。贫血类型均以小细胞低色素性贫血为主，贫血严重程度均以轻度贫血为主。
结论 南京市区未孕育龄女性医务人员贫血患病率低于同地区未孕育龄非医务职业女性，表明职业背景对贫血患病率有一定的影响，其具体机制有待进一步探讨。

PU-4156

PLR、D-二聚体和 CA125 对上皮性卵巢癌诊断的研究

蔡针针、蒋理
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨血小板（Platelet，PLT）/ 淋巴细胞（Lymphocyte）、D-二聚体（D-dimer）和糖类抗原 125（CA125）在上皮性卵巢癌诊断中的应用价值。

方法 回顾性分析南京医科大学第一附属医院 2015 年 1 月−2020 年 12 月收治的上皮性卵巢癌患者 136 例[年龄：57.00(49.00,64.00)]、卵巢良性疾病患者 126 例[年龄：40.00(29.00,51.00)]。首先采用单因素分析和多因素 Logistic 回归分析与上皮性卵巢癌诊断相关实验室指标。其次用 ROC 曲线分析 PLR（PLT/Lymphocyte)、D-dimer、CA125 单独检测和联合检测对上皮性卵巢癌的诊断效能，最后分析上皮性卵巢癌患者 PLR、D-dimer、CA125 水平与其临床病理特征的关系。
结果 经 Logistic 回归分析，患者年龄、PLR、D-dimer 和 CA125 水平为上皮性卵巢癌独立危险因素。PLR、D-dimer 和 CA125 联合检测时诊断效能最好（AUC=0.955, 95%CI 0.922～0.977)。在上皮性卵巢癌组中，PLR 和 D-dimer 水平与肿瘤大小显著相关（P<0.05)；晚期患者与早期患者相比，PLR、D-dimer 和 CA125 水平均显著升高（P<0.05)；腹水<1000ml 的上皮性卵巢癌患者，PLR 水平明显低于腹水≥1000ml 的患者（P<0.05)；PLR、D-dimer 和 CA125 水平与上皮性卵巢癌淋巴结转移有关，有淋巴结转移的患者 PLR、D-dimer 和 CA125 水平均升高（P<0.05)。
结论 联合 PLR、D-dimer 和 CA125 有利于上皮性卵巢癌的诊断。

PU-4157

C 反应蛋白和淋巴细胞比例对重症急性胰腺炎患者的预后价值

陈颖、黎青
江苏省人民医院（南京医科大学第一附属医院）

目的 重症急性胰腺炎（SAP）是重症监护病房（ICU）的一种高死亡率常见病。疾病 严重程度的早期评估对于 SAP 预后很重要。 因此，我们旨在评估 C 反应蛋白（CRP）与淋巴细胞（LY）比率对 SAP 患者的预后价值。
方法 收集 2016 年 1 月至 2020 年 12 月期间，共有 154 例 SAP 患者被送入 ICU。根据患者 30 天的预后，将这些患者分为生存组和非生存组。用普门全自动特定蛋白分析仪检测血清中的 CRP，用血细胞分析仪测量外周血中的淋巴细胞。对这些危险因素进行逻辑回归分析， 用 ROC 曲线和 Kaplan–Meier 曲线评估 CRP / LY 的预后价值。
结果 单因素分析显示两组间的 CRP / LY 显著不同。 多元 logistic 回归分析显示 CRP / LY 可作为预测 SAP 患者住院死亡率的独立危险因素。CRP/ LY 的 ROC 曲线下面积为 0.831（敏感性：70.1％，特异性：88.2％）。根据 Kaplan–Meier 曲线分析，CRP / LY> 4.481 的患者的院内累积生存率明显高于 CRP / LY≤4.481 的患者。
结论 CRP / LY 是预测 SAP 患者住院死亡率的独立，有效且有前途的生物标志物。

PU-4158

对孕妇在妊娠晚期的纤维蛋白原参考区间的研究

马亮、李洁
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨并建立适用于全自动血凝分析仪希斯美康 CS5100 的健康妊娠晚期孕妇的纤维蛋白原（FIB）浓度的参考区间。
方法 收集 2019 年至 2020 年在江苏省人民医院河西分院产科门诊进行正常产检的妊娠妊娠晚期孕妇 907 例，使用希斯美康 CS5100 全自动血凝分析仪检测血浆 FIB 浓度。运用 SPSS 22.0 软件，对结果数据进行正态性分析并建立新的参考区间，将新的参考区间与原参考区间进行一致性检验并计算 Kappa(K)值。将 907 例样本分为高龄组（>34 岁，250 例）和适龄组（19~34 岁，657 例），分别分析两组数据并对两者的结果进行 t 检验以比较不同年龄段的参考区间有无差异。
结果 使用 Kolmogorov-Smirnov 法对数据进行检测，P＜0.001，数据分布符合正态分布，靶值 3.87，标准差 0.75。参考范围按均值±1.96 标准差计算，本次研究的参考值范围为 2.40~5.34 g/L。

使用 McNemar-Bowker 法对新参考区间与原参考区间（2~4 g/L）进行卡方检验，Kappa=0.060，P＜0.05，认为两个参考区间的一致性较差。对适龄组和高龄组分别进行分析，并对两组结果进行两独立样本的 t 检验，t=0.576，P=0.564＞0.05，认为适龄组和高龄组间的差异无统计学意义。
结论 正常健康人群纤维蛋白原浓度的参考区间不适用于妊娠晚期孕妇，因此需要单独建立孕晚期妇女 FIB 的参考区间，以提高临床对孕妇生理状态评估的准确性。

PU-4159

新生儿外周血有核红细胞检测的结果分析

葛高霞、蔡针针
江苏省人民医院（南京医科大学第一附属医院）

目的 分析新生儿外周血有核红细胞（NRBC），来探讨其临床应用价值。
方法 观察本院住院的 1000 例新生儿患者，利用 XN-9000 血液分析流水线，测定新生儿静脉血 NRBC 的比例、绝对值计数。
结果 69.8%（698/1000）的新生儿外周血检出 NRBC,且与性别无关。诊断为新生儿窒息的患儿外周血 NRBC 检出率 98%； 检出 NRBC 的患儿胎龄低于未检出 NRBC 的患儿（P＜0.01）；NRBC 的比例和绝对值，早产儿高于足月儿（P＜0.01），低体重高于体重正常的新生儿。
结论 早产儿、低体重儿、新生儿窒息的外周血 NRBC 比例和绝对值计数均会升高，测定新生儿外周血 NRBC 可以评估新生儿健康状况。

PU-4160

新生儿的末梢血与静脉血在血常规检验结果的比较分析

葛高霞、黎青
江苏省人民医院（南京医科大学第一附属医院）

目的 比较分析新生儿末梢血与静脉血的血常规检验结果的差异，为临床新生儿血常规检验的标准化操作提供理论和实验依据。
方法 选取在我院出生的健康足月新生儿 94 例，同时采集末梢血和静脉血在全自动血细胞分析仪上进行检测，并对检测结果中白细胞计数（WBC）、中性粒细胞计数（NE）、淋巴细胞计数（LY）、单核细胞计数（MO）、嗜酸性粒细胞计数（EO）、嗜碱性粒细胞计数（BA）、红细胞计数（RBC）、血红蛋白含量（HGB）、红细胞压积（HCT）、血小板计数（PLT）10 项主要指标进行统计分析。
结果 新生儿末梢血与静脉血的 WBC、NE、RBC、HGB、HCT 和 PLT 6 项指标平均水平差异具有统计学意义（P<0.05）；LY、MO、EO、BA 4 项指标平均水平差异无统计学意义（P>0.05）。
结论 新生儿末梢血并不能完全反映循环系统血液的整体情况，因此临床遇到结果存疑时，建议进行静脉采血复查，以免造成误诊。

PU-4161

HELLP 综合征 78 例临床特征分析

蔡针针、葛高霞
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨 HELLP 综合征患者临床特征及实验室检查指标变化，以便疾病早期诊断和及时干预。

方法 选取 2015 年 1 月至 2019 年 12 月于我院住院的 HELLP 综合征患者 78 例为病例组；对照组随机选取同期无妊娠合并症的健康分娩产妇作为对照组，收集患者年龄、妊娠信息、孕周、出血情况、临床表现、母婴结局、并发症、分娩后恢复情况等临床资料，以及血常规、肝酶、心肌酶、胆红素、白蛋白、凝血功能等实验室指标。
结果与对照组相比,HELLP 组入院时 RBC、PLT、PCT、PLR 均偏低，WBC、PDW、NE、NLR 值偏高，两组数据进行非参数检验，差异有统计学意义（P＜0．05）。与对照组相比，HELLP 组 AST、ALT、TBIL、IBIL、Cr 均明显升高，血清白蛋白降低，非参数检验 P 均＜0.05，差异具有统计学意义。HELLP 组较对照组 PT 及 APTT 均延长，FIB 偏低（P＜0．05），差异有统计学意义。
结论 HELLP 综合征患者在血常规、生化指标上有其独特的改变，往往需要多学科协助诊治。 在临床工作中，需要我们对患者异常的临床表现及化验指标变化提高警惕，对疾病进行早期诊断，以便及时干预，改善母婴预后。

PU-4162

由 APTT 纠正试验不能纠正发现抗磷脂抗体综合征 1 例

孟荣
西安医学院第一附属医院

抗磷脂抗体综合征（antiphospholipid antibody syndrome）是指由抗磷脂抗体（antiphospholipid antibody，APL 抗体）引起的自身免疫性疾病。APL 抗体是一组作用于磷脂、磷脂结合蛋白或两者的复合物，主要由狼疮抗凝物(lupus anti-coagulant，LA)、抗心磷脂抗体(anti-cardiolipid antibody，ACL 抗体)和抗 β2 糖蛋白 I（β2GP I）抗体组成。与 APL 抗体有关的临床表现主要为血栓形成、习惯性流产、 血小板减少和神经精神症状等，部分患者还可出现网状青斑、心瓣膜赘生物及溶血性贫血。本实验室通过常规凝血六项筛查出 APTT 异常增高患者一例，且通过 APTT 纠正实验不能纠正，提示临床患者体内存在自身抗体或抗磷脂抗体，进一步追踪检查，及时诊断出 1 例临床症状不典型的抗磷脂抗体综合征患者.

PU-4163

科宝 S120 型尿液有形成分分析仪检测 RBC、WBC 的性能评估

杨华、杨晓东、秦诗睿
三峡大学附属仁和医院

目的 对科宝 S120 型尿液有形成分分析仪检测 RBC、WBC 的性能进行评价，证实其性能满足临床要求。
方法 按照国家实验室 ISO15189 认可要求，分别对 S120 型尿液有形成分分析仪检测 RBC、WBC 的精密度、准确度、携带污染率、检出限、稳定性能、线性范围进行评价。
结果 RBC、WBC 的批内及日间精密度分析结果显示，批内及日间变异系数均小于 10%；质控品的测定值与理论值比较，RBC 高值和低值的平均相对偏差分别为 3.53%、4.0%，WBC 高值和低值的平均相对偏差分别为 4.71%、4.0%；RBC 的携带污染率为 0.02%，WBC 的携带污染率为 0.01%；红细胞、白细胞的检出率均为 95%；仪器在 2h 内测定 RBC、WBC 的重复性，稳定性良好；RBC、WBC 线性回归方程及相关系数分别为：y=0.9897x-8.3347 和 0.9993、 y=1.0013x-13.21 和 0.9994 。
结论 S120 型尿液有形成分分析仪检测 RBC、WBC 的各项性能良好，完全可满足临床实验室要求。

PU-4164

全自动血液推片系统对异型淋巴细胞形态学复检的影响

王科勇
西安医学院第一附属医院

目的 分析全自动推片机不同推片角度和速度下对异型淋巴细胞形态学复检的影响。
方法 选取 2019 年 9 月至 2020 年 9 月间淋巴细胞百分率>50%且异淋散点图异常的 50 例门诊患者，单纯淋巴升高者 30 例，健康对照 30 例，均采集 EDTA 抗凝全血标本。每份样本手工和仪器各制备血涂片 1 张，同时随机选取 20 例阳性标本使用推片机在 20°（100mm/s，150 mm/s）和 30°（100mm/s，150 mm/s）条件下制备血涂片 4 张并染色。对异型淋巴细胞进行计数，以人工涂片为标准进行比较分析。
结果 数据分析显示，仪器自动推片异型淋巴（10.36±3.15）明显高于手工推片（5.24±1.85），统计具有显著性差异（P<0.05）。而对照组仪器与手工推片异淋为（0.46±0.13 VS 0.40±0.16），淋巴升高组（1.42±0.24 VS 1.04±0.19），两种方法均无统计学差异（p>0.05）。且随着推片角度增大，异型淋巴细胞计数逐渐升高。
结论 推片角度会对仪器涂片的淋巴细胞形态产生影响，导致异淋假性升高，从而干扰血细胞形态学复检，因此在日常工作中需要优化涂片参数，减小对复检的影响。

PU-4165

探讨新、旧尿液复检规则对降低假阴性率的重要作用

唐良洪
宝鸡高新医院

目的 对本科室目前使用的尿液复检规则进行再评估，以此为依据重新建立更为严格的尿液复检规则并验证，对提高镜检率，降低假阴性率有重要的作用。
方法 对 2019 年 11 月 14 日至 2019 年 11 月 24 日共 1500 分临床尿液样本在优利特 1600 尿干化学分析仪和 sysmexUF-1000i 尿有形成分分析仪进行检测，并对这 1500 份尿液标本分别按照新、旧复检规则进行镜检，计算真阴性率、假阴性率，真阳性率、假阳性率。以验证新的复检规则在降低假阴性率方面的有重要性。
结果 旧规则 880 份阳性标本中，真阳性标本 682 份，真阳性率为 95.5%，假阳性标本 198 份，假阳性率为 22.8%。阴性标本 620 份，真阴性标本 587 份，真阴性率 94.7%，假阴性标本 33 份，假阴性率 4.6%。新规则 880 份阳性标本中，真阳性标本 743 份，真阳性率为 98.8%，假阳性标本 137 份，假阳性率为 18.3%。阴性标本 620 份，真阴性标本 611 份，真阴性率 98.5%，假阴性标本 9 份，假阴性率 1.19%。
结论 本实验室制定的新旧复检规则满足行业标准假阴性率≤5%的要求，新的复检规则假阴性率和假阳性率均比旧的复检规则低，结果更准确可靠。

PU-4166

Sysmex XN-2800 全自动血细胞分析复检规则的验证

杨亚琼
宝鸡高新医院

目的 对本实验室 Sysmex XN-2800 全自动血细胞分析设立的复检规则进行验证，确保检验结果的准确性，提高工作效率。

方法 依据国际血液学复检专家组推荐的 41 条自动 CBC 和 DC 复检规则和国内协和医院 Sysmex 系列涂片复检规则[1]，根据本实验室具体情况制定了本实验室的显微镜复检规则，选择 2020 年 4 月 1 日至 4 月 27 日期间的临床样本共计 324 例，涵盖本院主要疾病，阳性标本 163 份，阴性标本 161 份。以血细胞分析复检规则为评估基础，同时做显微镜核实，并以显微镜镜检结果为金标准，对检测结果进行统计分析。
结果 本次复检规则阳性标本共计 163 份，假阳性标本 16 份，真阳性标本 147 份。阴性标本 161 份，检出异型淋巴细胞共计 4 份，异淋比例大于 5%的标本为零份，检出有幼稚细胞的标本为 7 份，其中晚幼粒大于 3%的标本占 1 份，血小板聚集的标本占 6 份。共计假阴性标本 7 份。
结论 本实验室血细胞形态复检规则验证假阳性率为 9.8%，假阴性率为 4.3%，达到“＜5%假阴性率”的行业要求[2]，验证通过。

PU-4167

阴道分泌物对尿常规检验结果的影响分析

李程华
空军军医大学西京医院

目的 研究阴道分泌物对尿常规检验结果的影响。
方法 选取我院 2020 年 11 月-2020 年 12 月 280 例妇产科门诊患者，随机分为两组，实验组和对照组，每组患者 140 例，对照组的患者采用常规留取尿液的方式采集尿液标本，实验组的患者在检验人员的指导下，规范留取中段尿液，然后进行尿常规检测，并比较实验组和对照组尿液中的红细胞、白细胞、尿蛋白和上皮细胞的检测结果并进行统计学分析。
结果 尿常规检验结果显示，实验组患者尿液的红细胞和白细胞的检出率分别为 16％和 8％，明显低于对照组患者尿液的红细胞和白细胞的检出率（32％和 36％），两组尿常规检验结果之间的差异是显著的（P<0.05）。另外，实验组尿蛋白和上皮细胞的检出率分别为 7％和 19％，显著低于对照组的 23％和 39％，两组差异明显（P<0.05），具有统计学意义。
结论 阴道分泌物对尿常规检验结果有一定程度的影响，因此，为了提高尿常规检验结果的准确性，应规范尿液标本的留取方式，减少阴道分泌物对检验结果的干扰。

PU-4168

头孢哌酮钠舒巴坦钠对凝血的影响一例分析

朱兵兵、刁艳君、刘家云
空军军医大学西京医院

患者男性，49 岁，右下肢肿胀一周入院，既往有高血压 5 年，2007 年因外伤行肝破裂修补术，双侧下肢无畸形，双侧下肢完整无外伤创口，右侧下肢较对侧肿胀，无浅静脉曲张，无皮肤色素沉着，双侧足背，胫后动脉搏动良好。左侧下肢无异常。

实验室检查 下肢静脉超生提示左侧胫后静脉，肌静脉内径增宽伴血栓形成，2 月 4 日随收入院予以治疗，入院后进行检查血常规，血凝，生化指标均基本正常，给予克赛治疗，2 月 6 日进行凝血功能检查，PT 15.3s APTT 56.3s ,患者出现皮肤的瘀斑瘀点，随后停用克赛，2 月 8 日患者复查凝血结果有所恢复，PT 13.6s ，APTT 45.9 s ，由于患者存在抗凝指征，于是改用普通肝素泵入，2 月 10 日凝血功能检查，发现 APTT 延长至 106.6 s ，随后停用了肝素，患者 2 月 10 号进食后出现腹痛，发热 37.8，查体：全腹压痛，右上腹明显，Murphys 症（+） 彩超：胆囊大小约 7.6x3.4cm,壁增厚，胆汁淤积，诊断为：急性胆囊炎。治疗：头孢哌酮钠舒巴坦钠（舒普森） 3g q8h。2 月 11 日检测 APTT 为 73.6，再次复查 71.4 s ，APTT 出现居高不下的情况。

PU-4169

SYSMEXCS5100 全自动血凝分析性能验证

朱兵兵、刁艳君、刘家云
空军军医大学西京医院

目的 对 SYSMEXCS5100 全自动血凝分析仪进行性能验证。
方法 按照 ISO15189 的要求，参照美国临床实验室标准化协会（CLSI）和美国临床实验室改进法案 CLIA'88 的质量要求，本文针对 7 个常规检测项目：PT（凝血酶原时间），INR(国际标准化比值)，APTT（活化部分凝血活酶时间），FIB（纤维蛋白原含量），TT（凝血酶时间）,D-dimer（D 二聚体）的精密度、正确度、线性范围、携污率、参考区间进行性能评价。
结果 批内精密度小于 CLIA'88 标准限值要求的四分之一，合格；批间精密度小于 CLIA'88 标准限值要求的三分之一，合格；正确度不超过 CLIA'88 标准限值要求的二分之一的要求；各检测项目引用的线性范围、参考区间符合要求。
结论 CS5100 全自动分析仪检测符合质量要求，可以为临床提供可靠的依据。

PU-4170

采血人员职业暴露调研

刘康悦
山东大学第二医院

目的 了解我采血人员职业暴露发生情况，提出预防控制措施。
方法 对该院 2016 年 1 月一 2019 年 12 月采血中心发生的职业暴露情况进行统计分析。
结果 4 年共有 213 名采血人员发生职业暴露 70 例，职业暴露发生率为 32.8%,其中实习人员职业暴露发生率达 45.89%,工作年限四年的采血人员职业暴露发生率 为 49.54%。发生职业暴露的采血人员岗位主要是门诊采血中心(占 39.27%),暴露类型以采血针头刺伤、血液和体液污染皮肤黏膜为主，占 75. 87%。2016-2019 年我院采血人员职业暴露发生率分别为 52. 50% (21/40)、43.47% (20/46) .26. 23% (16/61) .21.21% (14/66),呈下降趋势(f = 12. 286,FV0. 01)。发生职业暴露后按医院感染管理科要求上报仅 23 例，漏报率达 68. 06% (49/72),正确规范处理率达 80. 56% (58/72)。
结论 应加强采血人员医院感染管理教育培训，提高安全防护意识，规范处理流程，强化上报意识,减少采血人员的职业暴露和暴露后感染的发生。

PU-4171

神奇的"眼镜核"

张铮
江苏省人民医院（南京医科大学第一附属医院）

探讨临床一例疑似血液科病人的外周血象结果，通过外周血象特征分析 Pelger-Huet 畸形与慢性粒单核细胞的关系。该患者散点图 WDF 图异常，单核淋巴区为灰区，中性粒细胞散点群左移，可能存在幼稚粒细胞。DI-60 读片仪中外周血涂片显示中性粒细胞颗粒减少，核发育不良，呈杆状或仅分为 2 叶，杆状核形则类似花生样，肾形或哑铃形，眼镜形，分叶核的分叶之间以细丝状连接，细胞质较为致密、深染，聚集成小块或条索状，其间有空白间隙。（Pelger-Huet 畸形）该患者后续骨髓细胞检查提示粒系病态单核比例增高，可见幼稚单核细胞，慢性粒单核细胞白血病待定。

PU-4172

一例 EB 病毒感染相关的低白细胞血症

王茸茸
江苏省人民医院（南京医科大学第一附属医院）

目的 一例 EB 病毒感染相关的低白细胞血症案例
方法 抽取患者外周血 2ml 于 EDTA 抗凝管中，在 SYSMEX XN-2000 上机检测血常规，并在 SP-10 自动推片仪上推片、瑞氏染色后用 DI60 阅片仪镜检。
结果 患者 1.29 血常规结果 WBC 0.94×109/L，HGB 98g/L，PLT 77×109/L，镜下见核左移、幼稚粒细胞，偶见疑似原幼细胞，实际为反应性淋巴细胞
结论 白细胞降低可能与用药和病毒感染相关，血培养结果阴性可排除细菌感染。三系减低、发热、幼稚型反应性淋巴细胞易误认为原始细胞，通过骨髓和流式分型可排除血液病，最终确诊为 EB 病毒感染。所以病毒感染往往与血液病难以鉴别，流式分型很重要。

PU-4173

全自动尿液分析仪检测尿液中管型的结果分析

杨若凡
空军军医大学西京医院

目的 探讨全自动尿液分析仪检测尿液中管型的准确性。
方法 选取 300 例新鲜尿液标本，采用 Sysmex UF-5000i 全自动尿液分析仪和显微镜检法分别检测，以显微镜检结果为标准，进行分析。
结果 300 例标本中，全自动尿液分析仪检测尿液中管型的阳性率为 53%,显微镜检查的阳性率为 31.67%，全自动尿液分析仪检测尿液中管型的假阳性率为 38.54%,假阴性率为 15.79%。
结论 全自动尿液分析仪对尿液中管型的检测存在一定的误差，必要时应用显微镜复检，以保证检验结果的准确性。

PU-4174

血栓弹力图联合氯吡格雷基因检测在颅内未破裂动脉瘤的应用

黄晨蕾、余潇、李小宁
皖南医学院弋矶山医院

目的 探讨血栓弹力图联合氯吡格雷基因检测在颅内未破裂动脉瘤中应用的意义
方法 选取皖南医学院第一附属医院神经外科 2019.01-2019.12 行支架辅助弹簧圈栓塞（stent-assisted coiling，SAC）治疗颅内未破裂宽颈动脉瘤患者 126 例，行 TEG 和氯吡格雷基因药物检测，通过对 CYP2C19 基因和 ABCB1-3435C 基因的四个位点进行临床分型并联合 ADP 抑制率的结果制定合理的抗血小板用药方案，来减少支架植入所引起的并发症。
结果 68 例患者基因型正常且 ADP 抑制率≥30%，予以常规剂量双抗治疗；58 例患者基因型异常且 ADP 抑制率＜30%，更改双抗治疗方案后 ADP 抑制率≥30%后予以手术。其中 2 例患者出现术中动脉瘤破裂和支架内血栓的并发症。
结论 临床上仅使用氯吡格雷基因检测来指导 SAC 术后抗血小板治疗是不足的，而 TEG 是检测抗血小板药物疗效的重要方法，两者联合对支架辅助弹簧圈栓塞治疗颅内未破裂动脉瘤的个体化双抗治疗用药有着指导作用。

PU-4175

临床常用蛇毒类凝血酶制剂对部分凝血指标的影响分析

颜楠
空军军医大学西京医院

目的通过观察与探讨泌尿外科相关疾病术后用于止血的注射用白眉蛇毒血凝酶（邦亭）与耳鼻咽喉头颈外科用于改善微循环障碍治疗突发性耳聋的东菱迪芙(巴曲酶)，二者在用药治疗前后有显著差异的凝血指标纤维蛋白原含量（FIB）与纤维蛋白/纤维蛋白原降解产物（P-FDP）水平的变化为临床提供用药指导参考，并对因该两种药物导致严重低纤维蛋白血症可能发生出血风险的病人向临床医生做出提示。

PU-4176

两种肝毒性药物对纤维蛋白原浓度的影响分析

颜楠
空军军医大学西京医院

目的通过观察与探讨神经内、外科抗癫痫药物丙戊酸(valproate，VAP)与用于血液病化学治疗药物培门冬酶(pegaspargase，PEG—ASP)两种药物在用药治疗前后有显著差异的凝血指标纤维蛋白原（FIB）水平的变化，为临床提供用药指导参考，并对因该两种药物导致严重低纤维蛋白血症可能发生出血风险的病人向临床医生做出提示。方法回顾性分析 2017 年 10 月 31 日至 2019 年 l0 月 31 日在空军军医大学附属西京医院住院治疗的 130 例 FIB 降低(<1．5g／L)的患者的临床资料变化。其中神经内、外科使用抗癫痫药物 VAP 药物的患者 60 例，血液科使用化疗药物 PEG—ASP 的患者 70 例，并且分为神经内、外科组与血液科组。分别于患者使用药物治疗前后检测常规凝血六项指标做好记录并观察其水平变化。

PU-4177

探讨两代尿沉渣分析仪在血尿来源鉴别中的应用

闫宏斌
空军军医大学西京医院

目的 探讨全自动尿沉渣分析仪 sysmex UF-1000i 和 sysmex UF5000 在鉴别血尿来源中的应用价值。
方法 用 sysmexUF-1000i 和 sysmex UF5000 分别检测 189 例和 301 例不同来源血尿样本的红细胞。
结果 应用 UF-1000i 检测变异性尿红细胞对肾小球性血尿诊断的敏感性为 85%,特异性为 78%。应用 UF- UF5000 检测变异性尿红细胞对肾小球性血尿诊断的敏感性为 89%,特异性为 88%。
结论 两种尿沉渣仪在血尿来源鉴定上具有一定的过筛作用，UF5000 的初筛能力优于 UF1000i。

PU-4178

反复呼吸道感染患儿血微量元素含量分析

徐晓丽、刘家云、周磊、刁艳君、何娟、袁冲
空军军医大学西京医院

目的 探讨反复呼吸道感染（RRI）患儿血微量元素缺乏情况，为合理补充微量元素，防治小儿反复呼吸道感染提供临床指导。
方法 选取 2020 年 1 月-2020 年 12 月西京医院儿科门诊就诊的 RRI 患儿 112 名作为观察组，其中男 62 名，女 50 名，1-3 岁 63 名，3-6 岁 37 名，6-12 岁 12 名，平均年龄（2.6±0.5） 岁；同期选取儿童保健门诊健康儿童 100 名作为对照组，其中男 56 名，女 44 名，1-3 岁 51 名，3-6 岁 34 名，6-12 岁 15 名，平均年龄（2.5±0.3）岁。两组患儿均取空腹末梢血，由专人采用北京博晖生产的五通道原子吸收光谱仪进行检测，检测项目为铜、锌、钙、镁及铁水平

PU-4179

C 反应蛋白、白细胞在社区获得性肺炎病原鉴别诊断中的临床应用价值

徐晓丽、刁艳君、刘家云、周磊、何娟、袁冲
空军军医大学西京医院

目的 社区获得性肺炎是儿童常见感染性疾病，鉴别细菌性、还是非细菌性肺炎对临床合理应用抗生素、有效治疗社区获得性肺炎有重要意义。本文旨在探讨 C 反应蛋白（CRP）联合血常规的白细胞检测，在鉴别诊断儿童社区获得性肺炎病原中的临床应用价值。
方法 选取 2019 年 9 月—2020 年 3 月在西京医院儿科住院的 101 例社区获得性肺炎患儿，出院时确诊为细菌性感染患儿 56 例为细菌组，非细菌性感染患儿 45 例为对照组，两组患儿均在用药前取静脉血液测定血清 CRP 浓度和血液常规。阳性判断标准： CRP>5mg／L；WBC>10.0×109／L。

PU-4180

探讨血浆蛋白 C、S、抗凝血酶Ⅲ和狼疮抗凝物检测在复发性自然流产中的价值

肖凤静、朱兵兵、 晁真真、刁艳君
空军军医大学西京医院

目的 探讨血浆蛋白 C、S（PC、PS）、抗凝血酶Ⅲ（ATⅢ）和狼疮抗凝物（LA）检测在复发性自然流产患者中的应用价值。
方法 选取 65 例复发性自然流产患者、50 例同一时期正常产检孕妇以及 50 例健康查体女性，分别进行血浆 PC、PS、ATⅢ和 LA 检测并进行统计学分析。
结果 与健康体检组相比，复发性流产患者组的 PC、PS、ATⅢ活性降低，差异有统计学意义($P < 0.05$)，复发性自然流产患者组 LA 阳性检出率明显增高，差异均有统计学意义($P < 0.05$)；与正常产检孕妇组相比，复发性自然流产患者组的 LA 阳性检出率增高，差异无统计学意义($P > 0.05$); 复发性自然流产组的 PC、PS、ATⅢ活性降低，差异有统计学意义($P < 0.05$)。

结论 复发性自然流产患者具有高凝倾向，与血栓前状态有关，联合检测血浆 PC、PS、ATⅢ和 LA 等指标对复发性自然流产患者的血栓前状态筛查以及改善妊娠结局具有重要的临床指导意义。

PU-4181

血栓弹力图与常规凝血实验和血小板参数的相关性分析

马跃飞
福建医科大学附属第一医院

目的 探讨血栓弹力图（TEG）与常规凝血实验（CCT）和血小板参数的相关性及其在评估凝血状态中的应用价值。
方法 选择住院患者 300 名，采集空腹静脉血同时进行 TEG、CCT 和 PLT 参数检测，分析 TEG 各指标与 CCT、PLT 参数的相关性；筛选临床明确诊断的高、低凝血功能状态的患者共 209 例，比较 TEG 与 CCT、PLT 检测的敏感性。
结果 反应时间(R)与 PT、APTT、TT 均成正相关(r=0.429，0.695，0.351；P<0.01)，与 APTT 相关系数最高。凝块形成时间(K)与 FIB、PLT、PCT 成负相关。最大切角(α)与 FIB、PLT、PCT 成正相关，与 MPV 成负相关。最大振幅(MA)与 FIB、PLT、PCT 均成中度正相关(r=0.676，0.647，0.675；P<0.01)，与 FIB 相关系数最高。当 PLT>280×109 个/L 时，MA 与 MPV 无相关性；当 PLT<160×109 个/L 时，MA 与 MPV 呈低度相关，相关性略高于 PLT（r=0.323 vs r=0.299）。R 在 PT、APTT 延长的样品中的阳性率分别为 33.3%、41.7%；K、α、MA 在 FIB< 1.8 g/L 和 PLT<150×109 个/L 时的阳性率分别为 47.4%、31.6%、63.2%和 18.5%、11.1%、25.9%。TEG 在高凝组检测敏感性高于低凝组，在两组中的敏感性均高于 CCT、PLT。
结论 TEG 与 CCT、PLT 参数存在相关性；MA 主要反应 PLT 功能；TEG 对异常凝血状态的敏感性高于 CCT 和 PLT。正确理解 TEG 与 CCT、PLT 的相互关系，有助于临床对凝血功能异常疾病的诊断、治疗和预后判断。

PU-4182

不同类型流感病毒患者的血常规分析

郭文静
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨不同类型流感病毒患者的炎性指标 。
方法 选取 2019 年 1 月—2020 年 6 月在江苏省人民医院住院的流感患者 300 例作为观察组，随机选择同期 100 例健康体检者作为对照组，分析两组血常规的差异。观察组中甲型流感患者 100 例，乙型流感患者 100 例，甲乙流同时感染患者 100 例，分析甲型流感组、乙型流感组、甲乙型流感组 3 组患者的血常规特点。
结果 观察组患者白细胞计数 (P＜0. 05) 、中性粒细胞绝对值及其百分比(P＜ 0. 01) 均高于对照组，差异有统计学意义; 而淋巴细胞绝对值及其百分比 (P＜0. 01) 明显低于对照组(P＜0. 05) 。
结论 血常规结果对流感的鉴别诊断具有一定的指导意义

PU-4183

浆细胞富集的 FISH 技术在多发性骨髓瘤检测中的意义

高菲
四川金域医学检验中心有限公司

目的 探究浆细胞富集的荧光原位杂交（fluorescence in situ hybridization, FISH）技术在多发性骨髓瘤（Multiple Myeloma, MM）检测中的意义。
方法 收集统计分析 2018 年至 2021 年 4 月送检我实验室明确诊断为 MM 的骨髓样本 406 例，应用探针组合（1q21、P53、IGH/FGFR3、IGH/MAF）进行 FISH 检测。其中 211 例应用 CD138 磁珠分选进行浆细胞富集后行 FISH 检测，为富集组（A 组），195 例直接进行 FISH 检测，为非富集组（B 组）；从 A、B 组筛选骨髓涂片结果浆细胞比例<15%的样本分别为低比例富集组（C 组)42 例和低比例非富集组（D 组）23 例。分析 A、B 两组及 C、D 两组细胞遗传学异常检出率及各个探针异常检出率。
结果 A 组异常检出率(63.51%)显著高于 B 组(31.28%)，C 组检出率(50.00%)显著高于 D 组检出率（13.04%），差异有统计学意义；对于各探针而言，A 组 1q21、P53、IGH/FGFR3 异常检出率（分别为 54.03%、9.48%、14.22%）显著高于 B 组（28.72%、3.59%、7.18%），差异有统计学意义；A 组 IGH/MAF 异常检出率（1.90%）高于 B 组（0.51%）；而在浆细胞比例<15%的 C、D 两组，C 组 1q21 的异常检出率（38.10%）显著高于 D 组检出率（3.0%），差异有统计学意义；C 组 P53、IGH/FGFR3、IGH/MAF 异常检出率分别为 19.0%、9.52%、0%，而 D 组均未检出（异常检出率为 0%）。
结论 浆细胞富集的 FISH 技术检测在多发性骨髓瘤诊断中可以显著提高细胞遗传学异常检出率，尤其是对骨髓涂片中浆细胞比例低于 15%的患者，该方法的应用可以大幅提高其阳性检出率，对临床诊断、治疗与预后评估有重要意义，应常规进行开展。

PU-4184

Sysmex XS-800i 血细胞分析仪血小板计数性能评价

马跃飞、杨滨
福建医科大学附属第一医院

目的 评价 Sysmex XS-800i 血细胞分析仪血小板（PLT）计数性能。
方法 遵照行业指南验证 Sysmex XS-800i 血细胞分析仪 PLT 计数的精密度、线性、携带污染率和正确度;以显微镜计数法为参考方法对仪器低值 PLT 检测一致性、小红细胞（RBC）和大 PLT 的干扰性和仪器报警有效性进行评价。
结果 精密度、线性、携带污染率、正确度均符合行业标准。对于 11×10955×109 L-1 范围内的低值 PLT,Sysmex XS-800i 检测相关性（r=0.923 9）优于 ADVIA 2120i（r=0.908 0）;平均红细胞体积（MCV）<70fL 或 MCV<75fL 且 PLT 直方图异常时、平均血小板体积（MPV）>x+2s 即 MPV>12fL 时,仪器检测 PLT 结果均有显著性差别（P<0.05）。特异性较高的报警为"RBC 大小不一"和"小 RBC",分别为 89.47%和 83.87%;阳性预测值较高的报警为"RBC 大小不一"（92.00%）。
结论 Sysmex XS-800i 血细胞分析仪的 PLT 计数性能符合行业标准要求;对低值 PLT 计数准确性良好,但抗小 RBC、大 PLT 干扰能力较差。日常使用应结合仪器各相关报警的有效性,建立合适的人工镜检复检规则。

PU-4185

某品牌阴道分泌物检测仪检测结果的比对性分析

李永辉
山东第一医科大学第一附属医院

目的 对某品牌阴道分泌物检测仪的检测结果与手工法（显微镜镜检结果和三联法）结果进行比对分析，研究其在阴道感染疾病中的临床价值。
方法 随机选择 2020 年 7 月在我院进行阴道分泌物检查的 100 例标本作为研究对象，分别对其进行仪器检测与手工法检查，对结果进行记录统计并分析。
结果 仪器法结果重在有统一的标准，手工法受主观因素影响较大，尤其是对于临界结果。仪器法结果中，白细胞酯酶的阳性率为 56%，唾液酸苷酶的阳性率为 18%，过氧化氢阳性率为 43%，乳酸杆菌阳性率 38%；手工法结果中，白细胞酯酶的阳性率 48%，唾液酸苷酶的阳性率为 15%，过氧化氢阳性率为 40%，线索细胞的阳性率为 13%，乳酸杆菌阳性率 45%。
结论 阴道分泌物检测仪检测结果可以作为诊断阴道感染性疾病的依据，同时仪器法相较手工法来说，具有操作简单快捷、生物安全防护性强的特点，值得在检验科室及临床科室推广和应用。

PU-4186

CellaVision DM96 自动成像系统在异常外周血分类计数中的应用

华诗
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 探讨 cellavision DM 96 自动成像系统在异常外周血分类计数中的应用价值。
方法 连续收集四川省人民医院检验科临检组 2020 年 12 月份共计 300 份异常且需要进行细胞分类复查的外周血标本, 通过 SP-1000i 全自动推片染色仪自动涂片染色。首先，用 DM96 对外周血中白细胞进行预分类，由经验丰富的形态学辨认人员审核再分类，以再分类结果作为“最终结果”；同时对每一份标本进行人工显微镜镜检，分类结果作为“金标准”；最后用 SPSS23.0 对“最终结果”与“金标准”两组数据进行差异性性分析。
结果 中性粒细胞、淋巴细胞、单核细胞通过 t 检验 P>0.05 无统计学差异,嗜酸性粒细胞、嗜碱性粒细胞通过非参数秩和检验 P>0.05 无统计学差异,未成熟粒细胞、原始幼稚细胞通过非参数秩和检验 P<0.05 有统计学差异。 CellaVision DM96 系统外周血分类结果与显微镜手工分类有着很好的相关性, Pearson 相关性分析其中中性分叶核粒细胞、中性杆状核粒细胞、淋巴细胞及嗜酸性粒细胞的相关系数分别达到 0.91、0.93、0.95 和 0.92。
结论 DM96 在异常外周血分类计数中能提供准确、可信的分类数据，有助于提高实验室形态学报告的一致性及工作效率，同时对于有核细胞较少的血片 DM96 阅片较显微镜人工镜检可以很大程度缩短细胞分类时间，具有较好的临床应用价值；但由于仪器阅片的机械化，DM96 读取细胞的区域对分类结果影响较大，血片制作染色还需要标准化，且需与传统的人工显微镜镜检相结合。

PU-4187

618 例住院患者血栓弹力图与常规凝血七项相关性分析

华诗
电子科技大学附属医院•四川省人民医院临床医学检验中心

目的 回顾性分析我院 618 例住院患者 TEG 检测结果，比较不同科室其检测结果与常规凝血七项分析结果的相关性，探讨其在评估患者凝血状态中的应用价值。
方法 通过 LIS 系统(Laboratory Information System)收集 2019 年 9 月 1 日～2019 年 12 月 31 日同时检测血栓弹力图（thromboelastogram，TEG）、常规凝血七项（PT、APTT、 FIB、 TT、D-Dimer、FDP 及血常规血小板（platelet，PLT））的住院患者检测结果共计 618 例，对检测结果进行 Pearson 相关性分析。
结果 618 例住院患者 TEG 检查中 R、K、Angle、MA、CI 皆与 APTT、D-D（MA 除外）和 FDP 相关；K、Angle、MA、CI 皆与 FIB、PLT 相关。按科室分类统计分析：293 例神经外科患者 TEG 检查中 R、K、Angle、MA 和 CI 皆与 FIB（CI 除外）、PLT（R 除外）相关；R、CI 与 PT 和 APTT 相关；此外，K 还与 TT、DD 和 FDP 相关。149 例肝胆外科患者 TEG 检查中 R、K、Angle、MA、CI 与 APTT、FIB、FDP（K 除外）和 PLT（R 除外）相关；R、CI 与 DD 相关，MA 还与 TT 相关。131 例胸外科患者 TEG 检查中 R 仅与 APTT 相关；K、Angle 仅与 FIB 相关；MA、CI 与 APTT（MA 除外）、FIB、TT、PLT 相关。45 例中医骨科患者 TEG 检查中 R、Angle 与常规凝血检查 7 项均无相关，K、CI 与 FIB、FDP 相关， MA 与 FIB、PLT 相关。
结论 TEG 检查与常规凝血七项检查的结果具有相关性，不同科室患者因所患疾病、患者凝血功能影响因素等的不同，两种检测方法结果的相关性也不尽相同，因此两者不能互相代替，在临床上两种方法结合使用，能够更加准确了解患者凝血功能，为临床的诊疗工作提供更大的帮助。

PU-4188

基于队列的急性缺血性脑卒中预后评价的研究

和珂莉
常德市第一人民医院

随着我国人口老龄化的增高，缺血性脑卒中已成为危害我国中老年人身体健康和生命的 主要疾病之一。临床工作中预测 AIS 患者的病情进展的一个挑战在于显著的个体差异，根据患者早期的变化，预测预后情况是一个亟待解决的难题。
目的 评价 S-100β 蛋白的切点对缺血性脑卒中预后评价价值；建立更简易、高效的预后评价系统；通过高通量测序比较分析预后差异性基因， 来完善缺血性脑卒中预后评价方式。帮助临床更好的判断患者的病情的严重程度，尽早 识别高死亡风险的患者，进而实现及时的给予患者最佳的临床处理来改善疾病的预后。
方法 本研究采用患者住院病历随访和电话随访等方式，随访终点为发病后 90 天止。收集脑卒中患者一般资料，临床治疗资料，实验室相关检查资料以及预后及不良结局事件并对患者血清 S100B 蛋白含量的测定采用 ELAISA 法测定。连续变量以均值±SD。表示,分类变量用频率(%)描述。组间均值的比较采用单因素方差分析,率的比较采用卡方检验。采用平滑曲线拟合 分析 S-100β 水平与脑梗塞预后的相关性。采用 ROC 曲线评估 S-100β 对评定脑梗塞预后的诊断价值,ROC 曲线 AUC 越大,诊断价值越大。 比较 ROC 曲线上每个 S-100β 切点的敏感性、特异性、阳性预测值、 阴性预测值和约登指数。约登指数等于敏感性+特异性-1,定义约登指 数最大的点为最佳诊断切点。统计分析采用双侧检验,以 P<0.05 为差异具有统 计学意义。
结果 统计分析正在进行中。

结论 S-100β 是一个较好脑卒中预后评价指标，通过测序筛选出了相关预后差异性基因。帮助临床更好的判断患者的病情的严重程度，尽早识别高死亡风险的患者，进而实现及时的给予患者最佳的临床处理来改善疾病的预后。

PU-4189

64 例单克隆丙种球蛋白血症临床分析

张月、何淑娅
四川省肿瘤医院

目的 了解 M 蛋白的分型及其临床意义，提高对 M 蛋白的认识，减少漏诊和误诊率。
方法 本文回顾性分析 2016 年和 2017 年两年期间就诊于四川省肿瘤医院的初诊 M 蛋白阳性者，对 M 蛋白进行分型，并分析其来源。
结果 64 例 M 蛋白阳性者中 IgG 型 22 例（占 34.3%），IgA 型 11 例（占 17.2%），IgM 型 2 例（占 3.1%），IgD 型 6 例（占 9.4%），游离轻链型 12 例（占 18.8%），双克隆型 10 例（占 15.6%），64 例 M 蛋白阳性者中，MM 51 例，非 MM 13 例：MGUS 1 例，髓外浆细胞瘤 5 例，非霍奇金淋巴瘤 4 例，浆母细胞淋巴瘤 1 例，骨髓转移癌 1 例。
结论 M 蛋白不仅出现在 MM 中，还可以出现在 WM、MGUS、非霍奇金淋巴瘤中，MM 患者的 M 蛋白主要是以 IgG 型为主，IgA 型其次，IgM 型、IgD 型、IgE 型、双克隆型极少量。

PU-4190

微小颗粒急性早幼粒细胞白血病（M3V）骨髓形态学及实验结果分析

李玉芹
四川省医学科学院·四川省人民医院

目的 探讨微颗粒急性早幼粒细胞白血病（M3V）形态学特点。
方法 收集 2016 年 1 月-2020 年 12 月 102 例符合 APL 诊断标准的初诊 APL，按 FAB 和国内分型分为 M3a、M3b 和 M3v 三组，对三组患者的外周血常规、凝血全套、骨髓象及骨髓细胞形态学特征进行分析比较。
结果 M3V 与 M3a 和 M3b 的 WBC、Hb、PLT 比较，WBC 均值 M3V>M3b>M3a，M3v 与 M3a 比较,有统计学差异(P<0.05)；凝血全套中 PT M3v 与 M3a 有统计学差异，D2 聚体 M3v 与 M3b 有统计学差异；骨髓检查 M3v 原粒高于 M3a 和 M3b,异常早幼粒低于 M3a 和 M3b；具有内外浆细胞比例 M3v 高于 M3a，与 M3b 相似，具有瘤状突起细胞比例 M3v 高于 M3a 和 M3b，含 Auer 小体细胞比例 M3v 低于 M3a 和 M3b，M3v 细胞核畸形易见，与典型 M3a 和 M3b 相似。
结论 微小颗粒急性早幼粒细胞白血病（M3v）细胞形态学特征不及 M3a 和 M3b 典型，易与 M2a、M4、M5 混淆，因此我们在做骨髓分析时应仔细观察细胞形态特征，寻找 M3 细胞的特征性证据，结合细胞化学染色及 ICM 进行综合诊断，以避免 M3 的漏诊和误诊。

PU-4191

RDW 在胃癌诊断及转移中的应用价值研究

唐亮、赵静静、王京京、彭亮
上海市松江区中心医院

目的 探讨红细胞分布宽度（red blood cell distribution width，RDW ）在提示胃癌及转移中的临床应用价值。
方法 回顾性分析上海市松江区中心医院 2019 年 1 月至 2020 年 12 月 130 例初诊胃癌患者的病历资料和外周血 RDW 数据， 对全部 130 例患者根据有无转移分为转移组和无转移组，并进一步对其中有转移者的根据转移程度分为近端转移组与远端转移组。 多组间计量资料的比较用单因素方差 ANOVA 分析,绘制受试者操作特征（receiver operating characteristic curve, ROC）曲线分析 RDW 对胃癌及转移的诊断价值。
结果 胃癌组患者的 RDW 水平为[13.81±1.91]%，显著高于良性胃病组[12.37±0.67]%，差异有统计学意义（P＜0.001)；胃癌转移组患者的 RDW 水平为[14.51±2.19]%，显著高于胃癌未转移组[13.02±1.12]%，差异有统计学意义（P＜0.001)；胃癌远端转移组患者的 RDW 水平为[15.30±2.51]%,显著高于胃癌近端转移组[13.64±1.35]%，差异有统计学意义（P=0.001）。方差分析趋势性检验的线性项（Linear Term）, F =195.193，P＜0.001，可认为随着胃癌的发生、转移及转移程度加重，RDW 值呈上升的线性变化趋势。ROC 曲线分析表明，RDW 诊断胃癌的曲线下面积(AUC)为 0.810 ，此时诊断的敏感度为 64.1%，特异度为 84.3%；RDW 鉴别诊断胃癌是否转移的 AUC 为 0.744，此时诊断的敏感度为 53.6%，特异度为 85.2%；RDW 鉴别诊断胃癌是否远端转移的 AUC 为 0.710，此时诊断敏感度为 83.3%，特异度为 57.6%。
结论 外周血 RDW 值的变化对胃癌的诊断及是否发生转移情况有一定的应用价值。

PU-4192

结外 NK/T 细胞淋巴瘤患者治疗前红细胞分布宽度与预后的相关性研究

廖钰霖
四川省肿瘤医院

目的 探讨结外 NK/T 细胞淋巴瘤（extranodal natural killer/T-cell lymphoma,ENKTL）患者治疗前红细胞分布宽度值（red blood cell distribution width, RDW）与预后的关系。
方法 回顾性分析四川省肿瘤医院收治的结外 NK/T 细胞淋巴瘤患者 191 例，收集患者的临床资料和血液分析、CPR 及生化检测等数据并随访，使用受试者工作曲线(ROC)确定 RDW 的阈值，将患者分为低 RDW 和高 RDW 两组，比较两组的临床特征及总生存期（OS）的差异。
结果 低 RDW 组（≤46.2）5 年累计生存率高于高 RDW 组（>46.2），差异有统计学意义，P<0.05。单因素及多因素分析显示，RDW 是结外 NK/T 细胞淋巴瘤预后的独立因素。
结论 结外 NK/T 细胞淋巴瘤患者治疗前高 RDW 和高 CRP 与不良预后显著相关，RDW 以及 CRP 是结外 NK/T 细胞淋巴瘤预后的独立因素。

PU-4193

Confirmed Cryoglobulinemia and Hyperviscosity Syndrome Secondary to Multiple Myeloma-IgA Kappa from Routine Blood Test: a Case Report

于培霞[1]、Junfeng Zhang[2]、Weiwei Tian[1]、Yaolong Kang[1]
1. 山西医学科学院山西白求恩医院
2. 山西省健康教育中心

Cryoglobulins and hyperviscosity syndrome (HS) occur in multiple myeloma (MM), which are considered clinical emergencies. A case of cryoglobulinemia and HS associated with advanced MM was reported, which is initially confirmed by aspiration failure in a routine blood test with sufficient sample,which could not be analyzed because of high viscosity and poor liquidity. A peripheral blood smearshowed numerous non-cellular clouds,which were identified as cryoglobulins.This case provides an effective way to deal with this kind of abnormal sample and laboratory evidence to establish diagnosis of cryoglobulinemia and HS secondary to MM.

PU-4194

Sirdah 公式在红细胞参数异常群体筛查中的应用

薛丽[1]、张丽霞[2]
1. 江苏省人民医院（南京医科大学第一附属医院）
2. 江苏省人民医院

目的 评价 Sirdah 公式在红细胞参数异常群体筛查中的价值。
方法 收集南京医科大学第一附属医院 183218 例体检人群血常规结果，分析红细胞（RBC）升高，血红蛋白（Hb）正常或降低，平均红细胞体积（MCV）降低为特征的红细胞参数异常人群，随机选取 100 例进行铁蛋白测定，运用 RBC、Hb 和 MCV 联合参数以及 Sirdah 公式（MCV-RBC-3×Hb）分别与铁蛋白水平作 ROC 曲线。选取 50 例进行外周血红细胞形态分析和血红蛋白电泳测定。
结果 红细胞参数异常人群共 1535 例，占研究人群 0.84%。根据 100 例铁蛋白结果和 RBC、Hb 和 MCV 联合参数以及 Sirdah 公式值做 ROC 曲线，AUC 分别为 0.955（0.901-0.991）和 0.946（0.910-1.000）（P＝0.527），选取 Sirdah 公式 cut off 值 24.1，敏感性为 100%，特异性为 76.19%。40 例样本根据 Sirdah 值分为两组，<24.1 组外周血红细胞形态分析可见靶形红细胞 20 例，HbA2 升高 8 例，>24.1 组可见靶形红细胞 18 例；HbA2 升高 3 例。
结论 Sirdah 公式可用于红细胞参数异常人群确诊前的大规模筛查，可用于轻型地中海贫血和缺铁性贫血的鉴别诊断。

PU-4195

A Rare case of Pseudo Grey Platelet Syndrome: EDTA-dependent Aggregation and Degranulation of Platelets in a Patient with Bladder Urothelial Carcinoma

Lixia Zhang
The First Affiliated Hospital of Nanjing Medical University

A 64-year-old man was hospitalized with bladder urothelial carcinoma and cholecystectomy. The patient’s routine admission examination revealed platelet aggregation. The platelet count

was only 9 ×109/L in EDTA tube and corrected to 95×109/L in sodium citrate tube detected by hematology analyzer. Although sodium citrate and heparinusually prevented the aggregation of platelets in EDTA-dependent pseudothrombocytopenia patients, heparin anticoagulants failed in this case (Fig 1 A). It was interest that the EDTA anticoagulant caused the degranulation of platelets (Fig 1 B), which is a rare artifact pseudo grey platelet syndrome due to the degranulation of platelets caused, in vitro, by EDTA. This phenomenon is likely to disturb the platelet numeration and it is essential not to mistake it for a grey syndrome platelet, which is a constitutional thrombopathy with macrothrombopenia, in order to avoid specialized tests, or even misdiagnosis. As far as we know, pseudo grey platelet syndrome is first reported in patient with malignant in this case.

PU-4196

哮喘时肺内细胞因子 25 表达改变的研究

汪沛
空军军医大学西京医院

由于近年来环境污染的持续存在，哮喘的发病率居高不下，已成为严重危害国民身体健康的疾病之一，也是我国儿童常见的呼吸道疾病。目前哮喘的发病机制学说众多，但气道重塑是哮喘较为公认的病理改变之一。IL-25 是重要的气道上皮细胞源性细胞因子，可参与哮喘的发生发展。研究者及其他研究者报道哮喘时患者血清中白细胞介素 25（IL-25）含量增加，IL-25 可促进大鼠气道平滑肌细胞的增殖活性，是导致气道重塑的重要因素之一。但是哮喘患者及卵清白蛋白（OVA）致敏的动物模型中 IL-25 表达增加的分子机制尚不明确。本研究在前期研究的基础上，以 OVA 致敏的哮喘大鼠模型和人支气管上皮细胞为研究对象，探讨 IL-25 表达增加的分子机制，明确表达调控的转录因子，为进一步阐明哮喘的发病机制提供实验依据。

PU-4197

Variations on Leukocyte Volume, Conductivity and Scatter Parameters During Sample Storage

Lixia Zhang
The First Affiliated Hospital of Nanjing Medical University

Introduction To evaluate the reliability of leukocyte volume, conductivity and scatter (VCS) parameters during storage of blood samples.
Methods A total of 32 voluntary blood samples were collected in EDTA-K2tubes and measured on Beckman Coulter hematology analyzer. The complete blood count (CBC) with differential tests(including the leukocyte VCS parameters) were performed at 1 (as soon as possible), 15, 30, 60 and 120 minutes after sampling blood. Morphological analysis of peripheral blood at different time from one case was identified by CellaVision DI60 analyser.
ResultsNo obvious morphological changes were observed under light microscope in different storage time. With the prolongation of sample storage time, the position and shape of each cell scatter group changed until to 30 minutes. After that, the change was slight. VCS parameters changed significantly during sample storage. Different trends were found in different type of leukocytes over storage time. The storage time of 30-60 minutes was relatively stable from an overall viewpoint, which was a suitable time point to evaluate VCS parameters.
ConclusionA uniform, optimal storage time should be adhered to ensure the reliability of VCS test results in evaluating VCS parameters in the scenarios of clinical practice.

PU-4198

热射病患者肾功能损伤及凝血功能障碍的血清学指标监测在治疗中的应用

屈慧、皇海
空军军医大学西京医院

目的 探讨热射病患者的血清学指标。
方法 回顾性分析 2016 年 6 月-2020 年 8 月收入本院急诊或麻醉 ICU 诊断为热射病的 11 例患者的资料，分析实验室检查的血清学指标，回顾疾病的治疗及转归。
结果 1, 11 例患者均为男性，劳力型热射病 6 例，年龄 19~26 岁， 平均（21.333±2.944） 岁。经典型热射病 5 例， 年龄 48~70 岁， 平均（58.2±7.981）岁。入院时间均在每年的 6 月至 8 月。两组一般资料比较，差异有统计学意义（P＜0.05）。2,患者入院后 11 例（100%）出现血清肌酸激酶（CK）增高，血清乳酸脱氢酶（LDH）增高，血清肌红蛋白增高。10 例（90.9%）患者肾功能异常，血清肌酐升高，8 例（72.7%）凝血功能障碍，纤维蛋白原降解产物 FDP、D-Dimer 升高，部分活化凝血酶原时间 APTT 延长，纤维蛋白原 FIB 消耗减低，血小板降低。3，患者转归情况劳力型热射病平均住院时间（14.833±9.745）d，经典型热射病平均住院时间（6.2±7.381）d，两组住院时间比较，差异有统计学意义（P＜0.05）。好转出院 11 例， 治愈率 100%。
结论 热射病患者血清肾功能指标和凝血功能指标的动态监测可以评估预后，提高对热射病的认识，早期识别和恰当处置对改善预后有帮助。

PU-4199

化学发光免疫测定技术检测对甲状腺肿瘤患者甲状腺球蛋白水平及检出准确度、敏感性的影响

屈慧、皇海
空军军医大学西京医院

目的 探讨化学发光免疫测定技术检测对甲状腺肿瘤患者甲状腺球蛋白水平及检出准确度、敏感性的影响，为临床提供参考。
方法 选取我院 2019 年 1 月至 2020 年 12 月收治的 100 例甲状腺肿瘤患者作为研究对象，采用化学发光免疫和放射免疫两种检测方法，对研究对象进行检测分析，将病理结果视为金标准，对比两种检测方法甲状腺球蛋白水平和个数，比较两种检测方法的准确度、敏感性和特异性。
结果 化学发光免疫检测法，检测出的甲状腺球蛋白水平高于放射免疫检测法，甲状腺球蛋白个数多于放射免疫检测法，差异有统计学意义（P＜0.05）。根据病理结果金标准，化学发光免疫检测法的准确度为 89.00%，敏感性为 92.31%，特异度为 77.27%；放射免疫检测法的准确度为 74.00%，敏感性为 76.47%，特异度为 60.00%，化学发光免疫检测法均高于放射免疫检测法，差异有统计学意义（P＜0.05）。
结论 化学发光免疫测定技术，应用在甲状腺肿瘤患者的甲状腺球蛋白水平的检测中效果明显，检出准确度、敏感性和特异度高，值得临床广泛推广及应用。

PU-4200

华支睾吸虫病的诊断、流行和防控

周锡铧、毕燕玲
广东省人民医院

华支睾吸虫病是分布最广、感染率高、发展最严重的食源性寄生虫病之一,危害着人民的健康与财产。是目前我国和部分东南亚国家重要的公共卫生问题。可引起人类肝吸虫病的肝吸虫包括华支睾吸虫、麝猫后睾吸虫和猫后睾吸虫，但流行于我国的华支睾吸虫感染人数最多，特别以广东、广西两地区尤为严重，这与当地的一种传统饮食文化和习俗有关，当地喜欢吃鱼生或未煮熟的淡水鱼。尽管政府对肝吸虫防控工作投入了大量的人力、物力和财力，但华支睾吸虫感染率居高不下，说明肝吸虫防控工作任重道远。本文针对华支睾吸虫病原学检测和诊断、传播和流行、以及防控等进行综述，指出了未来华支睾吸虫病防控工作的重点和难点。

PU-4201

不同类型肿瘤化疗药物治疗后患者外周血血小板聚集分析

王黎
江苏省人民医院（南京医科大学第一附属医院）

Our previous study showed that platelet clumps usually occur in patients with malignancies. The aim of this study was to evaluate the significance of platelet clumps in patients receiving various chemotherapy drugs. In 1235 patients with platelet clump interpretive program messages and 70 other patients with malignancies with significant PTCP. 70.4% of patients with platelet clump IP messages were found to have malignancies. PTCP occurred after chemotherapy in 50% of the 70 patients. We suggest that increased platelet activation in the tumor may induce platelet clumps; These clumps may occur in the early stage and be promoted by chemotherapy drugs. Thus, the phenomenon of platelet clumps may be a sensitive and real-time indicator of cancer development.

PU-4202

浅谈如何做好检验血液标本的采集工作

刘婵婵
山东大学第二医院

在临床检验血液标本工作过程中有三个阶段：分析前（申请单、患者准备、采血标本、标本存放和运送等）、分析中（标本测定、结果计算等）和分析后（检验结果的发出至临床应用）。为保证检验结果的准确性， 分析前质量管理至今未引起足够重视， 有研究表明， 实验前误差频率占总误差的 46.0%~68.2%，为保证减少误差，血液标本采集的方法显得尤为重要。血液标本的采集是检验人员常规的操作之一，正确掌握血液标本采集，是为临床提供准确可靠的诊断依据的根本，在工作中应掌握标本类型、采集部位及影响标本质量的因素检验前质量控制是检验医学中心开展 ISO 15189 医学实验室质量和能力认可的一项重要内容。

PU-4203

一次性采血针与注射器采血在婴幼儿股静脉采血中的应用

于淇
山东大学第二医院

目的 比较一次性采血针与注射器采血两种方法采婴幼儿股静脉血标本采集的效果比较。
方法 将 106 例危重患者按抛硬币法分为观察组和对照组，分别采用一次性采血针和一次性注射器采血，比较两组在婴幼儿股静脉采血时血管损伤情况及血液标本合格情况。
结果 对照组采血成功率为 54.7%（29/53），血液标本溶血率为 24.5%（13/53）；观察组采血成功率为 79.2%（41/53），溶血率为 1.9(1/53)，两组比较差异均有统计学意义（P＜0.05）。
结论 使用一次性采血针进行婴幼儿股静脉采血成功率高，减少了对婴幼儿血管的损伤和疼痛感，有效保证了血液标本采集的质量。

PU-4204

浅谈静脉采血和末梢采血两种采血方法对血常规检测结果的影响

鞠振宇
山东大学第二医院

目的 浅谈静脉采血和末梢采血两种采血方法对血常规检测结果的影响，为选择正确的血常规采血方法提供依据。
方法 选择 2018 年 6 月—2020 年 2 月在山东大学第二医院住院的 236 例患者，同时采集每例患者的静脉血和末梢血血样，使用血细胞自动分析仪进行血常规各项结果检测，通过对比判断哪种采血方法更具有优越性。
结果 末梢采血和静脉采血血样的血常规各项结果比较， 差异均有统计学意义 （P＜0.05）， 末梢采血血样的白细胞 （WBC） 高于静脉采血， 红细胞（RBC）、 血红蛋白 （HGB）、 血小板（PLT）、 血细胞比容 （HCT） 和红细胞平均体积 （MCV） 均低于静脉采血。
结论 末梢采血血常规检测结果与静脉采血血常规检测结果不一致，末梢采血法受多种因素影响不如静脉采血结果更有意义，静脉采血应作为血常规结果检测的主要采血方法。

PU-4205

Sysmex 尿液流水线筛查细菌性尿路感染的仪器报警信息和几种筛查方案的准确性评价

荆晶[1]、张志珊[2]、林振忠[2]、吴一波[2]、赵媛[1]、陈雅斌[2]
1. 空军军医大学西京医院
2. 福建省泉州市第一医院检验科

目的 研究 Sysmex UC3500 尿干化学分析仪和 UF5000 尿液有形成分分析仪组成的尿液流水线在筛查细菌性尿路感染中的作用。评价 UF5000 提示尿路感染的仪器报警信息、以及建立的几种筛查方案的准确性。
方法 选取 2000 例疑似尿路感染患者的中段尿尿液标本，同时进行细菌培养、Sysmex UC3500 和 UF5000 尿液流水线检测，分别记录细菌培养结果、UC3500 上白细胞酯酶（LEU）、亚硝酸盐（NIT）和 UF5000 上白细胞计数（WBC）、细菌计数（BACT）的检测结果。Kappa 一致性检验评价尿路感染仪器报警信息、LEU、NIT 和细菌培养结果的一致性；根据菌落生长数量将细菌分为 3 组（阴性组、104CFU/ml 组和 105CFU/ml 组），比较各组之间 WBC、BACT 水平的差异；绘制

ROC 曲线，计算 WBC、BACT 用于判断尿路感染的 cut-off 值。以 WBC、BACT 大于 cut-off 值做为阳性值，设计 6 种筛查方案：⑴单独 WBC 参数阳性；⑵单独 BACT 参数阳性；⑶WBC、BACT 两项参数同时阳性；⑷WBC、BACT、LEU 三项参数同时阳性；⑸WBC、BACT、NIT 三项参数同时阳性；⑹WBC、BACT、LEU、NIT 四项参数同时阳性。另外选取 600 例中段尿尿液标本对 6 种筛查方案筛查尿路感染的准确性进行性能评价。

PU-4206

Sysmex UF5000 全自动尿沉渣分析仪能提高上皮细胞检测的准确性

荆晶[1]、张志珊[2]、林振忠[2]、吴一波[2]、赵媛[1]、陈雅斌[2]
1. 空军军医大学西京医院
2. 福建省泉州市第一医院检验科

目的 研究 Sysmex UF5000 和 UF1000i 全自动尿沉渣分析仪检测尿液标本的 RBC、WBC、CAST、EC、X'TAL、YLC 等参数的一致性以及结果的准确性评价。
方法 选取 1059 例尿液标本同时在 UF5000 和 UF1000i 仪器上进行比较，并进行人工显微镜检查，记录三种模式下 RBC、WBC、CAST、EC、X'TAL、YLC 等参数的检测结果。以人工镜检作为金标准，对两台仪器的敏感性、特异性、阳性预测值、阴性预测值等准确性性能进行评价，并计算各参数检测结果和镜检结果是否一致的 Kappa 值。Deming 回归、一致性相关系数和 Kappa 一致性检验分别对 UF5000 和 UF1000i 的定量参数（RBC、WBC、CAST）和定性参数（X'TAL、YLC）进行一致性检验。并对各仪器的假阳性影响因素进行比较分析。
结果 UF5000 和 UF1000i 在 RBC、WBC、X`TAL 检测上与人工镜检的一致性较强（Kappa 值=0.597-0.784），但 CAST、YLC 和人工镜检一致性差（Kappa 值=0.143-0.332）。各检测参数上均有较好的特异性、阴性预测值和符合率（83.95 %-99.61 %），假阴性率低（0.38 %-7.27 %）。UF5000 相对 UF1000i 上多项参数准确性能有所提升，特别是 EC 检测的准确性能（敏感性、阳性预测值等）、一致性提升明显（Kappa 值从 0.317 到 0.752）。仪器之间的一致性比较，仅 RBC、WBC 检测参数表现出较好的一致性（RBC：r=0.9842，CCC=0.9693；WBC：r=0.9955，CCC=0.9711）。

PU-4207

血浆蛋白 C 及蛋白 S 的临床应用

江岩
空军军医大学西京医院

血浆蛋白 C（PC）、蛋白 S（PS）是维生素 K 依赖的一种蛋白，在凝血调节过程中起重要的作用。其缺乏会使人体的凝血及纤溶平衡受影响,使凝血亢进,从而易发生血栓性疾病。因此血浆蛋白 C、蛋白 S 检测对疾病的诊断预防及观察预后有重要价值。本文对血浆蛋白 C、蛋白 S 的临床应用作一综述。

PU-4208

消化病医院血细胞分析复检规则的建立后的持续改进

贾晶媛
空军军医大学西京医院

目的 以国际 41 条为准则，在我院门诊血细胞复检规则的基础上进行调整和优化，通过对数据进行分析，制定适合院中院消化病医院的血细胞复检规则。使用一年后对复检规则进行评估,以达到持续改进的目的。
方法 1.挑选 200 例血细胞相关分析阳性标本，使用消化病医院血细胞分析仪检测，进行规则判断以查看阳性标本是否存在漏复检现象。2.在 SYSMEX 仪器的 Laboman 中查看复检规则进而分析规则中假阳性率较高的规则。进行评估是否需要修改复检规则。3.通过日常工作查看复检规则是否存在问题，及时进行补充。
结论 通过验证复检规则未发生挑选阳性标本的漏检情况，未发现假阳性率过高的规则，日常工作中未发现标本漏检的情况。复检规则的持续改进可以为我们日常的血细胞分析复检工作进行保驾护航，缩短阴性标本 TAT 时间，提高阳性标本的复检质量，提高工作效率，使患者在较短的时间内取得较为准确的报告，保证工作的质量和安全。

PU-4209

不同保存方法对尿沉渣检测结果的影响

何娟、刘家云
空军军医大学西京医院

目的 探讨不同尿液保存方法对尿沉渣检测结果的影响。
方法 选取 2020 年 7 月至 8 月于我院进行尿常规检测的患者新鲜尿液标本 100 例，每例标本分为两份，分别于冷藏（2~8℃）环境下、室温（18～28℃）环境下，在收到标本后 0h、2h、4h、6h 进行尿液沉渣检测，比较不同保存方法下尿液红细胞、白细胞、上皮细胞、细菌检测结果。
结果 室温保存 2 h 及冷藏保存 2h 的尿沉渣检测结果与 0h 检测结果比较，差异均无统计学意义（P>0.05），室温保存 4h、6 h 的尿沉渣检测结果与 0h、2h 检测结果比较，具有统计学意义（P<0.05），冷藏保存 4h、6 h 的尿沉渣检测结果与 0h、2h 检测结果比较，具有统计学意义（P<0.05）。
结论 不同保存方法会对尿沉渣检测结果有一定影响，为保证尿液检测结果确定性，应于收到尿液标本后应于 2h 内完成检测。

PU-4210

血液分析仪提示疟原虫感染的 2 例病例探讨

高倩
空军军医大学西京医院

疟疾是一种经按蚊传播的常见于热带、亚热带和温带地区的急性发热性疾病，是一个严重威胁着人类健康的公共卫生问题，中国维和医务人员以及军队在国际交流学习时需要注意警惕[1-3]。疟原虫为孢子虫，在脊椎动物的细胞内寄生，种类很多，但寄生于人体的疟原虫共有四种，分别是间日疟原虫，恶性疟原虫、三日疟原虫和卵形疟原虫，我国主要是间日疟原虫和恶性疟原虫，三日疟原虫和卵形疟原虫罕见[4, 5]。疟疾的治疗是全世界关注的问题，中国科学家屠呦呦及其研究团队从黄花蒿中分离得到抗疟疾的药物—青蒿素，在世界治疗疟疾的过程中发挥了重要的作用[6, 7]。

本研究通过血液分析仪器提示疟原虫感染的 2 例病例分析，探讨合理应用仪器信息进行疟原虫检测，避免漏诊或误诊。

PU-4211

尿液干化学分析仪 UC-3500 及其适配试纸条性能评估

程翔、王刚强、何娟、卢佩、李程华、杨若凡、郑善銮、刁艳君、刘家云
空军军医大学西京医院

目的 评估尿液干化学分析仪 UC-3500 及其适配试纸条的性能，探讨其临床应用可靠性。
方法 根据中华人民共和国医药行业干化学尿液分析仪（YY/TO475 2011）和尿液分析试纸条（YY/TO478 2011）的行业标准，对仪器的重复性、稳定性、携带污染率，适配试纸条的准确度、重复性、检出线、分析特异性、批间差进行验证，验证项目包含酸碱度（PH）、比重（SG）、白细胞（LEU）、隐血（ERY）、亚硝酸盐（NIT）、蛋白质（PRO）、葡萄糖（GLU）、胆红素（BIL）、尿胆原（URO）、酮体（KET）；随机挑选门诊病人新鲜尿液标本 620 例在干化学尿液分析仪 AX-4030 平行检测，计算两种仪器 PH，SG 的成对差异百分率及其余项目阳性检出率及符合率；结果仪器的稳定性、重复性、携带污染率及与适配试纸条的准确度、重复性、检出线、分析特异性、批间差、稳定性均符合行业标准要求；干化学尿液分析仪 UC-3500 与 AX-4030 PH 均值差异百分率<10%，SG 均值差异百分率<1%，一致性符合要求， LEU，ERY，NIT，PRO，GLU，BIL，URO，KET 一般符合率>80%，Kappa>0.4，结果一致性良好。
结论 干化学尿液分析仪 UC-3500 及其适配试纸条性能良好，可满足临床需要。

PU-4212

凝血试验分析前质量控制中采血因素的影响及对策

晁真真
空军军医大学西京医院

目的 讨论凝血实验分析前质量控制中采血因素的影响及对策。
方法 将前来我院进行体检的 60 名健康体检者作为研究对象，收集比例不同的采血量与溶血，即 1:10、1:9、1:8、1:5 和 1：3，其中标准组血液收集比例为 1:9，观察组为 1:10、1:8、1:5 和 1：3。对比分析凝血检验效果。
结果 观察组的检验效果由于标准组，差异有统计学意义（P＜0.05）；溶血组的 PT、TT、APTT 与标准组相比，差异有统计学意义（P＜0.05）；Fib 与 AT-Ⅲ两组对比后无差异（P＞0.05）。
结论 凝血试验质量与采血人员的认知情况和操作技术有着直接关系，应引起采血人员的高度重视。

PU-4213

Dysentery Caused by Balantidium coli in China

Peixia Yu、JianRong Rong、Yan Zhang、Jingjing Du
Shanxi Bethune Hospital & Shanxi Academy of Medical Sciences

Balantidium coli human infection predominantly occurs in tropical and subtropical regions in the world. Human case is extremely rare in China. This report details a case of B. coli infection in a 68-year-old man in China, who presented with a 1-week history of abdominal pain, tenesmus, diarrhea with blood and mucus stools. He also reported symptoms of nausea, vomiting and anorexia and a 4-month history of working as a pig farmer. Routine wet-preparation stool

examination showed both red blood cells and white blood cells 4+/ high power field. Surprisingly, Large mobile trophozoites of Balantidium coli exhibiting rapid rotary-type and boring motion were captured and their somatic cilia was visible (Video. S1 in the Supplementary Appendix). The tapering anterior end has a cytostome and the posterior end is broadly rounded (Panel A). Many trophozoites were observed in the Wright-Giemsa stained smear on lower power (Panel B). A smaller round micronucleus nestled against a larger kidney-shaped macronucleus within the trophozoite was displayed. (Panel C). Diagnosis of dysentery caused by B. coli was established. Treatment of oral metronidazole for 2-weeks led to a full recovery. There was no recurrence after 6-months of follow-up. Our case indicates possible occurrence of Balantidium coli-related disease in cooler climates. This case is presented not only because of its rarity but also for future references.

PU-4214

血栓弹力图分析前影响因素的探讨

马跃飞
福建医科大学附属第一医院

目的 探讨分析前因素对血栓弹力图（TEG）检测的影响。
方法 采集健康志愿者和住院患者标本,分析标本状态如溶血/脂血、检测时间、标本采集量和人员等因素对 TEG 检测的影响。
结果 标本溶血和脂血导致反应时间（R）降低、凝块形成时间（K）升高、最大切角（α）降低、最大振幅（MA）降低,除脂血标本的 K 值外,各参数差异有统计学意义（P <0. 05）。R、K、α 在 5 min～30 min 内呈现趋势性变化（P <0. 05）。MA 在 60 min 内成"∧"型波动。R 在 30 min 后、MA 在 1 h 后、K 和 α 在 2 h 后检测结果差异无统计学意义（P> 0. 05）。与正常采集量 2. 0 ml 相比,标本量 2. 3 ml 时 K 值升高,差异有统计学意义（P <0. 05）,其他参数在 1. 7 ml～2. 3 ml 差异无统计学意义（P> 0. 05）。不同实验人操作时各参数的变异系数（CV）均高于同一实验人。
结论 溶血、脂血对结果影响较大,TEG 应在 1 h～4 h 内检测,不同实验人应严格遵循相同的操作程序。

PU-4215

Identification of RHOBTB2 aberration as an independent prognostic indicator in acute myeloid leukemia

Xiaoning Zhang
Shandong Provincial Qianfoshan Hospital

Rho-related BTB domain (RhoBTB) proteins belong to Rho guanosine triphosphatases (GTPases). Their putative role implicated in carcinogenesis has been supported by accumulating evidence. However, their expression pattern and potential role in acute myeloid leukemia (AML) remain unclear.

We profiled RHOBTB mRNA expression via the Gene Expression Profiling Interactive Analysis 2 (GEPIA2) database. Survival analysis was conducted with GEPIA2 and UALCAN. Univariate and multivariate Cox regression analyses were performed to validate RHOBTB genes as independent prognostic indicators in the LAML cohort from The Cancer Genome Atlas (TCGA). Data regarding expression in different subtypes and relationships with common disease-related genes were retrieved from UALCAN. Co-expressed genes were screened out and subsequently subjected to functional enrichment analysis.

We observed aberrant transcription levels of RHOBTB genes in AML patients. RHOBTB2 was identified as a prognostic candidate for overall survival (OS), independent of prognosis-

related clinical factors and genetic abnormalities. Moreover, RHOBTB2 expression was increased in non-acute promyelocytic leukemia (APL) subtypes, patients without FLT3 mutation and PML/RAR fusion, and imparted a positive correlation with the expression of FLT3, FHL1, and RUNXs. Co-expressed genes of RHOBTB2 were enriched in functional pathways in AML.

Our findings suggest that RHOBTB2 might be a novel biomarker and independent prognostic indicator in AML and provide insights into the leukemogenesis and molecular network of AML.

PU-4216

vWF 与 TM 联合检测在糖尿病肾病诊断中的应用价值

范小斌
广东省人民医院

目的 探讨血管性血友病因子（vWF）和血栓调节蛋白（TM）联合检测在糖尿病肾病（DN）诊断中的应用价值。
方法 选择 2018 年 12 月至 2019 年 12 月入住广东省人民医院的 31 例 2 型糖尿病（T2DM）患者的临床资料进行回顾性研究，患者分为单纯糖尿病组（DM）和糖尿病肾病组（DN），收集患者抗凝治疗前凝血功能相关指标的检查结果进行组间比较并分析其特征。
结果 DN 组的 vWF 和 TM 水平分别是 206.50±88.52%和 20.06±8.70TU/mL，单纯 DM 组的 vWF 和 TM 水平 114.80±47.43%和 10.38±2.52TU/mL，DN 组患者的 vWF 和 TM 水平均明显高于单纯 DM 组，两组差异具有统计学意义（P＜0.05），DN 组患者的 APTT 水平（38.13±5.12s）明显比单纯 DM 组（43.40±6.82s）低（P＜0.05），两组在其他凝血功能指标 PT、FIB、TT、AT-Ⅲ、FDP、PLG、、D-DI 水平上的差异均无统计学意义（P＞0.05）；vWF、TM 值诊断 DN 的 ROC 曲线下面积分别为 0.835 和 0.885；cut-off 值分别为：150 %和 10.9 TU/mL；灵敏度分别为：75.0%和 93.8%；特异度分别为 80.0%和 73.3%，采用联合检测后，灵敏度和特异度分别为 75.0%和 100.0%。
结论 血浆 vWF 和 TM 联合检测对于诊断 DN 效能良好，有一定的临床应用价值。

PU-4217

Neutrophil-to-lymphocyte ratio (NLR) and platelet-to-lymphocyte ratio (PLR) as promising biomarkers to predict clinical outcome of gastric cancer

Fuyan Han
Department of Clinical Laboratory, The Second Hospital of Shandong University

Objectives The neutrophil-to-lymphocyte ratio (NLR) and platelet-to-lymphocyte ratio (PLR) have been presented to be a prognostic indicator in several types of cancer. The purpose of the present study was to detect whether the preoperative NLR and PLR can be used to distinguish patients with (GC) from the healthy controls and predict the progression and prognosis of the GC.
Methods The NLR and PLR values of 222 patients wgastric cancerith GC were retrospectively analyzed comparing with 153 healthy controls which were enrolled in the Second Hospital of Shandong University from January 2013 to April 2018. In addition, the clinicopathological features, survival curves and prognosis of the patients with GC were compared between the high and low groups according to the NLR and PLR cutoff values.
Results Significant higher NLR and PLR were detected in patients with GC compared to the healthy controls (all P<0.05). A higher NLR was significantly associated with male, older age, a larger tumor diameter, Lymph node metastasis, advanced pStage and elevated CEA (all P<0.05). A higher PLR was also significantly associated with older age, a larger tumor diameter, deeper

tumor infiltration, Lymph node metastasis, advanced pStage and elevated CA199 (all P<0.05). A patient who had a distance metastasis was inclined to have an elevated NLR after surgery (P=0.012). The patients with a higher NLR possessed a significantly poorer OS and DFS compared to those with a lower NLR (P=0.017 and P=0.005, respectively). Similarly, the patients with a higher PLR showed a significantly worse OS and DFS than those with a lower PLR (P<0.001 and P<0.001, respectively) . Univariate and multivariate survival analysis showed that PLR could act as an independent prognostic factor for OS (P=0.027) and DFS (P=0.041) in GC.
Conclusion The preoperative NLR and PLR were simple and convenient predictive factors for the progression and prognosis of patients with GC. The PLR could act as an independent prognostic indicator for OS and DFS in GC.

PU-4218

Neutrophil-to-lymphocyte ratio (NLR) and red blood cell distribution width (RDW) as promising biomarkers to predict clinical outcome of esophageal cancer

Fuyan Han
Department of Clinical Laboratory, The Second Hospital of Shandong University

Backgroud Recent studies have borne out claims that inflammation has a vital role in the development and progression of many diseases, including cancers. It has been reported that neutrophil-lymphocyte ratio (NLR) and red blood cell distribution width (RDW) could act as independent prognostic factors for several malignant tumors. The present study aimed to evaluate the diagnosis and prognosis values of preoperative inflammatory indicators, including NLR and RDW in esophageal cancer (EC).
Methods We retrospectively analyzed the clinical data of 284 EC patients and 220 early esophageal cancer (EEC) undergoing potentially curative esophagectomy in the Second Hospital of Shandong University between January 2011 and April 2015. Meanwhile, we chose 101 age and sex-matched healthy volunteers as the control group. We compared the clinicopathological features, survival curves and prognosis of the EC patients between the high and low groups according to the cutoff values of NLR and RDW.
Results Significant higher preoperative NLR and RDW values were detected in patients with EEC and EC compared to the healthy controls (P<0.05). A high RDW were significantly associated with an older age and distance metastasis (P<0.05). NLR and RDW values after surgery in EC group were significantly higher than those before surgery (P<0.001 and P<0.001, respectively). For EEC group, a higher RDW value only showed a significantly worse disease-free survival (DFS) (P=0.041). For EC group, an increased NLR indicated a significantly association with poor overall survival (OS) (P=0.035) and DFS (P=0.011). Preoperative NLR can act as an independent prognostic indicator for EC.
Conclusion The preoperative NLR and RDW are convenient, practical easily measured biomarkers of clinical diagnosis and prognostic assessment of patients with EC. Furthermore, NLR was more effective than RDW acting as an independent prognostic biomarker for EC.

PU-4219

肺泡灌洗液细胞学分析在肺炎患者中的临床意义

朱红艳
西安市第三医院

探讨支气管肺泡灌洗液（Bronchoalveolar lavage fluid,BALF）细胞学分析在肺炎患者中的临床意义。

方法 收集从 2019 年 7 月至 2021 年 2 月期间于西安市第三医院诊断为肺炎，住院期间所做项目包括 BALF 细胞学检查、血常规（Blood routine examination,血 RT）、C-反应蛋白（C-reactive protein, CRP）、降钙素原（Procalcitonin, PCT）,以及一般细菌培养的患者 160 例,比较它们之间的差异。

PU-4220

中性粒细胞参数在肺部感染性疾病中的临床应用研究

陈小剑、林潮庆、蒋伟燕、陈碧
温州医科大学附属第二医院、育英儿童医院

目的 探讨中性粒细胞参数(NEUT-X、NEUT-Y)在肺部感染性疾病中的变化及其应用价值。
方法 收集 123 例肺部感染患者的外周血液样本，其中 20 例为病毒感染组，103 例为细菌感染组，另收集 133 例健康体检者（对照组）的外周血样本，在 Sysmex XE-5000 上对其 NEUT 参数进行检测。
结果 肺部感染组与对照组相比 NEUT-Y 参数结果差异有统计学意义(P＜0．05)，NEUT-X 参数结果差异无统计学意义(P > 0.05)；细菌组 NEUT-X、NEUT-Y 值较对照组均升高，差异有统计学意义(P<0.05)；细菌组 NEUT-Y 值与病毒组比较，差异有统计学意义(P<0.05)；细菌组中 WBC>10×109/L 组别 NEUT-X、NEUT-Y 升高程度高于 WBC<10×109/L 组；>70%组 NEUT 参数均高于≤70%组。
结论 中性粒细胞参数 NEUT-Y 值对有无肺部感染的判断有价值；由细菌感染引起的肺炎其 NEUT-X、NEUT-Y 值均升高。

PU-4221

Evaluation of immature platelet fraction as a novel biomarker in psoriasis: association with platelet activation

Zhijia Fan、Li Wang、Dandan Li、Zhicheng Wang
Department of Laboratory Medicine, Huashan Hospital, Fudan University, Shanghai

Background Platelet activation that involved in the pathophysiology of psoriasis could link persistent inflammation and the formation of thrombus contributing to the increased risks of cardiovascular complications. The studies about markers of platelet activation in the association with psoriasis activity have still been controversial and there is a paucity of data examining which markers are appropriate. We aim to evaluate the association between platelet activation and psoriasis severity by investigating the values of novel activation markers.
Methods A total of 120 patients with psoriasis and 120 sex-matched healthy controls were enrolled in the study. K2-EDTA anticoagulated peripheral venous blood specimens were tested on a Sysmex XN 9000 hematology analyzer. The levels of immature platelet fraction (IPF), immature platelet count (IPC), mean platelet volume (MPV), and platelet distribution width (PDW) were estimated in all study populations. The relationships between these platelet indexes and disease severity measured by the Psoriasis Area and Severity Index (PASI) were assessed. Univariate and multivariate logistic regression analyses, with adjustment for potential confounding factors such as age, gender, age at onset, history of hypertension, diabetes, arthritis, smoking, and alcohol, were performed to evaluate whether platelet parameters could be associated with the psoriasis severity.
Results A marked increase in white blood cell (WBC) count suggested the inflammatory response of patients. And we observed significant platelet activation in psoriasis, as demonstrated by the elevation in platelet indexes, the psoriasis group showed higher values of

IPF, IPC, PDW, and MPV with statistical significance when compared with those in the control group. Platelet activation markers except for MPV had positive correlations with PASI. And in the multivariate analysis, following adjustment for confounding factors, only IPF and IPC could emerge as available markers to evaluate the severity of psoriasis, whereas MPV and PDW were no longer significantly associated with psoriasis severity. After treatment, the PASI score markedly decreased accompanied by the significant reduction of IPF and IPC.
Conclusion Our results indicate that there is significant platelet activation in psoriatic patients measured by specific platelet indexes, especially when linked to the increasing disease severity. Different levels of platelet markers are found in psoriasis with an increase in mean platelet volume and platelet distribution width and, particularly the immature platelet parameters, which could contribute to increased risks of cardiovascular complications. IPF may be the most sensitive biomarker of all studied platelet parameters. Given the simple convenience of this parameter for routine clinical laboratories, considerably more work will be needed to confirm the value of IPF in the management of psoriasis, and there should be also some further research to explore such as the mechanisms of platelet activation in psoriasis.

PU-4222

淋巴细胞计数对新型冠状病毒肺炎的临床诊断价值

杜岩青、秦中华、张丽霞
天津市海河医院检验科

目的 通过评价感染指标淋巴细胞计数（LYM#）在新型冠状病毒肺炎的诊断效能，以期为新冠肺炎的临床诊断提供参考。
方法 收集 2020 年 1-2 月在天津市海河医院收治的 84 例新冠肺炎确诊患者的临床资料，根据疾病临床分型分为普通组（n=61）和重症组（n=23），30 例体检健康者作为健康组。考察新冠肺炎患者外周血细胞分析的特征并进行 ROC 分析，考察其 AUC 面积、cut-off 值、灵敏度和特异度。
结果 新冠肺炎患者 NEU%显著上调，WBC、LYM#、LYM%显著下调（P 均<0.05），重症型患者 RBC（女性）、NEU%、中性粒细胞/淋巴细胞比值（NLR）显著高于普通型，LYM#和 LYM%显著低于普通型（P 均<0.05）。普通型患者 LYM#的 ROC 曲线的 AUC 面积、灵敏度、特异度、cut-off 值分别为 0.9626、88.52%、93.33%、1.75，重症型患者上述指标分别为 0.9942、100%、93.33%、1.69。
结论 LYM#与新冠肺炎疾病进展具有较强的相关性，具有一定的临床诊断价值。

PU-4223

Sysmex UC3500 联合 UF5000 尿液流水线审核报告流程的建立和验证

陈雅斌
福建医科大学附属泉州第一医院

目的 建立并验证 Sysmex UC3500 联合 UF5000 尿液流水线的审核报告流程。
方法 选取 1000 例尿液标本在 Sysmex UC3500 和 UF5000 尿液流水线上进行检测，同时进行人工显微镜检查。建立尿液审核报告的流程和触发显微镜镜检的复检规则，以人工镜检的结果作为金标准，计算流程的复检率、真阳性率、真阴性率、假阳性率和假阴性率，在此基础上进行规则的改进。进一步选取 300 例尿液标本验证改进后的审核报告流程，并进行性能评价。
结果 1000 例标本中复检率 23.00 %，未触发复检规则标本真阳性率 21.20 %、真阴性率 50.40 %、假阳性率 1.30 %、假阴性率 4.10 %。根据结果进行了规则的追加，改进后复检规则共 8 条。300

例验证标本中复检率 27.66 %，未触发复检规则标本真阳性率 21.67 %、真阴性率 47.67 %、假阳性率 0.67 %、假阴性率 2.33 %。规则改进后复检率有所提高，但假阴性率降低，避免了肾脏相关疾病的漏诊率。假阳性干扰因素分析中，结晶、细菌、上皮细胞和粘液丝是主要的干扰因素。假阴性标本主要集中在 RBC 和 WBC 检测项目上，建立和验证实验中分别有 11 例和 2 例的肾相关疾病。
结论 本实验室建立的尿液流水线审核报告流程假阴性率<5 %，符合 ISO15189 实验室认可和通用的复检规则评估标准，适用于本实验室在临床工作中审核尿液报告。

PU-4224

311 例体检者尿液结晶检测结果及其与性别、年龄的关系分析

王春苗、龚彩平、杨玉静、周茂华
广东省人民医院（广东省医学科学院）

目的 分析尿液结晶检测阳性率与性别、年龄的关系，为泌尿系结石的预防工作提供依据。
方法 随机收取广东省人民医院 2020 年 6 月~11 月 311 例体检者晨尿，采用人工镜检对尿液结晶进行诊断和分类，并进行性别分组、年龄分组的比较分析。
结果 311 例尿液样本中，结晶阳性 27 例，阳性率 8.69%，所检测出结晶主要是草酸钙结晶，占 88.89%，其他结晶占 11.11%。男性组尿液结晶检测阳性率明显高于女性组（x2= 4.954，P<0.05）。随着年龄增长，尿液结晶检测阳性率呈上升趋势，并且老年组尿液结晶检测阳性率明显高于青年组，差异有统计学意义（x2= 10.979，P<0.05）；尿液结晶检测阳性率在青年组与中年组、中年组与老年组之间差异无统计学意义（x2=0.996；x2= 2.682，P 均>0.05）。
结论 尿液结晶检测阳性率在不同性别、年龄存在一定的差异，该研究为泌尿系结石的预防工作提供一定的参考依据。

PU-4225

双重荧光染色在妇科阴道炎诊断中的应用价值

李翠、应春妹
复旦大学附属妇产科医院

目的 探讨双重荧光染色系统在妇科门诊患者阴道分泌物常规检测中的应用价值
方法 搜集复旦大学附属妇产科医院黄浦分院 2020 年 12 月至 2021 年 5 月妇科门诊阴道炎患者，同时用传统显微镜湿片法和双重荧光染色系统对阴道炎患者阴道分泌物进行检测分析。依据显微镜下形态报告孢子、假菌丝、线索细胞、滴虫、脓细胞、杂菌 6 项检测项目；并用卡方检验分析该染色系统相较传统显微镜湿片法的一致性及优势。
结果 5625 例阴道炎患者中，菌群失调病例 694 例，占 12.3%，显著高于直接镜检的 315 例，p<0.001；
念珠菌性阴道炎（含孢子及假菌丝）1490 例，占 26.5%，显著优于直接镜检法的 1226 例，p<0.001；
细菌性阴道炎病例 1602 例，占 28.5%；滴虫性阴道炎 77 例，占 1.4%，显著优于直接镜检法的 1017 例，p<0.001；
非特异性阴道炎 2012 例，占 35.8%，与直接镜检法的 2004 例一致性较好，无明显差异，p>0.05。
结论 妇科阴道炎患者中单纯性白细胞增多病例占比较高；双重荧光染色系统简便高效，可清晰显示致病菌及患者阴道分泌物菌群分布情况；双重荧光染色系统作为一项新技术，可提高妇科阴道炎患者阴道疾病诊断，值得在妇科门诊中应用推广。

PU-4226

SAA and CRP are potential indicators in distinction and severity assessment for children with Influenza

seyin zou[1]、jinjie liu[2]、zhiyong yang[1]、danxia xiao[1]、donglin cao[1]
1. Guangdong Second Provincial General Hospital
2. 广东医科大学

Purpose Laboratory indicators are essential to diagnosing and monitoring influenza infection.The clinical values of C-reactive protein (CRP) and serum amyloid A (SAA) to distinguish non-severe from severe children with influenza are rarely reported.
Methods Baseline characteristics and laboratory results were collected and analyzed. Receiver operating characteristic (ROC) curve analysis was used to combined detection of indicators for children with influenza, and the scatter-dot plots was used to compare the differences between non-severe and severe children.
Results 263 influenza cases were included, 183 of those with influenza A and the remaining 80 with influenza B. There was no statistical difference in the sex ratio between the influenza A group and influenza B group (P = 0.54). The mean age was significantly higher among children with influenza A than those with influenza B(P = 0.003). Children with influenza B had more bronchitis and pneumonia (P < 0.05),while children with influenza A had more other serious symptoms (P = 0.015). Among children aged under 4 years, a significant difference was observed in lymphocyte count, neutrophil count ,NLR(neutrophil-to-lymphocyte ratio),CRP and SAA between children with influenza(A and B) and healthy individuals, but there were no statistically significant differences among children with influenza A and those with influenza B. Of children over 4 years old, significant differences were observed in lymphocyte count, neutrophil count ,NLR,CRP and SAA among children with influenza A and healthy individuals; while only lymphocyte count and NLR did significant differences among children with influenza B and healthy children; Moreover, the neutrophil count, NLR, CRP, and SAA were significantly higher in children with influenza A than those with influenza B(P < .05). Compared with NLR and SAA, the ROC curve analysis showed that the combined of NLR and SAA for distinguishing healthy children from children with influenza A was better than detection of NLR or SAA alone; compared with lymphocyte count and SAA, the ROC curve analysis showed that joint detection of lymphocyte count and SAA could better separate healthy children from children with influenza B than single indicator detection, no matter with <4y group or ≥4y group. Both the levels of CRP and SAA were significantly higher in children with influenza A and severe influenza B infection than healthy controls, and they also showed a significant difference among children with severe influenza A and B infection(P < .05), but there were no statistical differences between the non-severe influenza B group and control group. In addition, both CRP and SAA in children with influenza A were significantly higher in the severe group than those in the non-severe group(P < .05);while the levels of CRP among children with influenza B didn't show a significant elevation in the severe group, compared with the non-severe group (P > .05).However, the neutrophil count, lymphocyte count, and NLR were not statistically different among non-severe and severe children both in influenza A and B group.
Conclusions There were several differences in clinical symptoms and laboratory indicators among children with influenza A and B. SAA and CRP could be potential indicators in distinction and severity assessment for children with influenza, but the age should be taken into account when using in children with influenza B.

PU-4227

血清 cTnT 与 NT-proBNP 联合检测在肝癌化疗相关心肌损伤中的早期预测价值研究

周楚琦
南华大学附属第一医院

目的 探究血清超敏心肌肌钙蛋白(cTnT) 与脑利钠肽前体(NT-proBNP) 联合检测在肝癌化疗相关心肌损伤中的早期预测价值。
方法 选择于本院 2017 年 1 月至 2019 年 6 月收治的中晚期肝癌患者 135 例作为研究对象。患者进行彩色多普勒超声检查并记录左室射血分数(LVEF) ，根据超声诊断结果分为对照 A 组（无心肌损伤事件发生）和实验 B 组（有心肌损伤事件发生）。采用化学发光法检测化疗前后血清 cTnT 与 NT-proBNP 水平。绘制受试者工作曲线（ROC），通过曲线下面积（AUC）评价血清 cTnT、NT-proBNP 以及联合检测在肝癌化疗相关心肌损伤中的早期预测价值。
结果 B 组中 cTnT 与 NT-proBNP 阳性率均高于 A 组水平，差异具有统计学意义（P<0.05）；cTnT、NT-proBNP 及联合检测诊断肝癌化疗相关心肌损伤的 AUC 分别为 0.913，0.900，0.921，其中联合检测诊断价值最佳。
结论 血清 cTnT、NT-proBNP 在肝癌化疗相关心肌损伤早期诊断中具有一定价值，且二者联合检测对肝癌化疗相关心肌损伤诊断最佳。

PU-4228

UA-5800 和 AE-4020 尿液分析仪尿蛋白试纸条结果的一致性及其与尿蛋白/肌酐比值（ACR）的相关性研究

王悦[2]、杨唯唯[2]、张聪[2]、张晨[2]、赵博禹[1]、王国洪[2]
1. 吉林市中心医院
2. 北京肿瘤医院

目的 比较迈瑞公司 UA-5800 和日本爱科来公司 AE-4020 尿液分析仪试纸条检测尿蛋白的一致性并验证其测定的敏感性和特异性。
方法 随机收集 2016 年 10 月某肿瘤专科医院门诊及住院尿液标本共 721 例，同时采用 UA-5800 和 AE-4020 尿液分析仪行尿蛋白定性检测，其后采用生化分析仪检测尿白蛋白含量和肌酐水平，计算尿白蛋白/肌酐比值（ACR）。以 ACR≥30 mg/g Cr 作为尿蛋白阳性的诊断标准，以尿试纸条阴性组 ACR<30 mg/g Cr 的阴性率作为特异性，以尿试纸条结果微量、1+、2+和 3+组 ACR≥30 mg/g Cr 的阳性率作为敏感性。
结果 UA-5800 和 AE-4020 的尿蛋白定性结果具有一致性（κ=0.65），两者检测尿蛋白的特异性分别为 85.19%和 83.41%。UA-5800 和 AE-4020 检出蛋白尿的敏感性在尿蛋白微量组、1+组、2+组和 3+组分别为 35.53%和 34.27%、86.79%和 73.69%、100%和 100%、100%和 92.31%。
结论 国产 UA-5800 和日本 AE-4020 尿分析仪尿蛋白干化学检测具有较高的一致性和良好的诊断蛋白尿的特异性和敏感度。二者均具有良好的蛋白尿筛查性能。

PU-4229

A simple electrochemical sensor for PCSK9 detection based on signal-on responses using aptamer with methylene blue label at specific internal thymine

Guolin Yuan
Department of Laboratory Medicine, Shiyan Taihe Hospital, Hubei University of Medicine

Proprotein convertase subtilisin/kexin 9 (PCSK9) serves a key regulatory function in the metabolism of low-density lipoprotein (LDL)-cholesterol (LDL-C) through interaction with the LDL receptor (LDLR) followed by its destruction that results in the elevation of the plasma levels of LDL-C. Hence, design an effective method to detect serum PCSK9 is meaningful for the prevention, monitor and diagnosis of cardio- vascular diseases. In this work, a novel, ultrasensitive electrochemical immunosensor has been fabricated for the determination of PCSK9 in human serum. Glassy carbon electrode was used as the working electrode on which gold nanoparticles (AuNPs) was electrodeposited. This approach provided a high content of Au surface suitable for the direct covalent binding of PCSK9 aptamer. Usually, the redox tag is placed on aptamer terminal, however, sometimes the terminal label may be insensitive to target-binding and fail to generate sensitive responses. The redox tag methylene blue (MB) labeled on different sites of aptamer may experience distinct changes in local environment, distance to electrode, or interactions with aptamer bases during affinity binding, which affect the current signal. Thus, it is possible to construct aptamer electrochemical sensors with sensitive and significant responses to targets by screening a series of sites (here we use internal thymine T) of the aptamer and placing MB tag on a specific site of the aptamer. With this strategy, we successfully fabricated an electrochemical aptamer sensor by using a DNA aptamer with MB on an internal T site (e.g., 10th T) and a thiol moiety at 5' terminal. This sensor generated remarkable signal-on responses to PCSK9 and enabled detection of PCSK9 in human serum samples. The results for real sample analysis in human serum demonstrated that the newly constructed aptamer sensor provided a rapid and simple assay with low detection limits for clinical applications and provide a novel strategy for the detection of serum molecular.

PU-4230

血小板可否作为肿瘤生物标志物？

苏海翔、王涛、郭欢、江秀娟
甘肃省医学科学研究院，甘肃省肿瘤医院

目的 了解肿瘤环境中诱导的血小板（TEP）作为 RNA 生物标记物在癌症检测应用中的研究进展。
方法 文献检索。
结果 血液是肿瘤相关生物标志物的丰富来源，一些以血液为基础的生物分子如 cfDNA、cfRNA、蛋白质、CTC 和外泌体等已被探索用于新肿瘤标志物开发。TEP 被认为是局部和全身对肿瘤反应后的一类血小板亚群。剪接的 TEP-RNA 信号可以提供肿瘤存在、位置和分子特征的具体信息。目前已有对来自肺癌、脑癌和乳腺癌患者血液样本进行 TEP-RNA 测试结果的文献报道，表明来自癌症患者的 TEP-RNA 与来自炎症和非肿瘤疾病患者的不同。
结论 TEP-RNA 可能作为液体活检诊断的生物来源分子，用于早期癌症的检测，促进无创性监测技术的进步。但有关肿瘤导致血小板内 RNA 剪接的机制以及这类特定血小板亚群是如何影响肿瘤发生发展的，还有待研究。

PU-4231

利多卡因与硬膜外出血进展的研究

史大隆
潍坊医学院附属医院

目的 通过利多卡因对硬膜外出血进行不同浓度干预，评估其对凝血功能的影响。
方法 采集全血标本，研究其离体凝集与不同浓度的利多卡因稀释液，采用血栓弹力图及凝血常规检测。使用方差分析及重复测量进行统计分析。
结果 高浓度利多卡因能够引起低凝和/或纤溶变化。高浓度利多卡因能够加快硬膜外出血的进展。
结论 高浓度利多卡因能够引起低凝和/或纤溶变化。

PU-4232

肿瘤患者放化疗后外周血细胞形态改变的研究进展

朱晓、娄加陶
上海市胸科医院

恶性肿瘤现如今在中国的发病率和死亡率仍然高居不下，除了手术以外，主要的治疗手段有放射治疗以及化学药物治疗。当其杀死肿瘤细胞的同时对正常组织和细胞也会造成不良影响。主要影响之一的骨髓抑制可以通过观察外周血细胞形态来发现，其主要的异常形态有细胞体积巨型变或小型变、中毒颗粒、核右移、核左移、低分叶、未成熟细胞、退行性变化、异型淋巴、核分叶异常及大颗粒淋巴、破碎细胞、有核红细胞、红细胞形态异常、大血小板。而形成骨髓抑制的机制有损伤 DNA 导致细胞凋亡、衰老以及骨髓细胞周期异常；损伤造血微环境中的微血管、造血生长因子（HGF）及骨髓基质细胞。通过观察外周血细胞形态出现的异常改变可以发现骨髓抑制损伤情况并为临床医生提供参考依据做出相应的改善治疗措施。

PU-4233

有核红细胞与感染的关系的研究进展

徐阳飚、李欣、娄加陶
上海市胸科医院

有核红细胞是未成熟的红细胞。除新生儿期外，有核红细胞极少出现在正常人的外周血中。外周血中出现有核红细胞往往提示病理状态。感染时，患者机体存在炎症反应，组织细胞缺氧刺激促红细胞生成素的合成，导致有核红细胞释放增加。近年来，多项研究揭示了外周血有核红细胞与感染的关系。有核红细胞的数量与阶段分类对于各类疾病感染及其严重程度的辅助诊断与预后判断有重要的意义。现将国内外有核红细胞与感染的关系的研究综述如下。

PU-4234

CD73 在急性淋巴细胞白血病、急性髓系白血病及伴原始细胞增多的骨髓异常增生综合征中的表达特点及临床意义

肖思颖、李海艳、刘格格、彭德志、王佳佳、韦杰
济南金域医学检验中心有限公司

本研究旨在探究 CD73 在不同类型白血病中的表达情况。采用多参数流式细胞术分析 33 例急性 B 淋巴细胞白血病（B-ALL）、51 例急性髓系白血病（AML）、24 例伴原始细胞增多的骨髓增生异常综合征（MDS-EB）中 CD73 的阳性表达率。结果表明在 B-ALL 中 29（87.88%）例表达 CD73，AML 中 4（7.84%）例表达 CD73，MDS 中 1（4.17%）例表达 CD73，B-ALL 与 AML 及 MDS 有显著的统计学差异，AML 与 MDS 无明显统计学差异，CD73 可以作为白血病分型确定 B 系、髓系系别的辅助指标。

PU-4235

The clinical value of neutrophil to lymphocyte ratio in the diagnosis and treatment of Crohn's disease

Chu Chu
The First Affiliated Hospital, Nanjing Medical University, Nanjing, Jiangsu Province, China

Background To evaluate the clinical value of neutrophil to lymphocyte ratio in the diagnosis and treatment of Crohn’s disease.
Methods Between March 2018 and April 2020, patients diagnosed with CD at the First Affiliated Hospital of Nanjing Medical University were identified. A total of 128 patients with definite diagnosis, and 123 healthy people as the control group at the same time. The data of these patients were extracted retrospectively from their medical record. counts of white blood cells (WBC), counts of Neutrophils (NE), counts of lymphocyte (LY), hypersensitive C-reactive protein (hs-CRP), erythrocyte sedimentation rate (ESR) were recorded at the same time of colonoscopy. The IBM SPSS 20.0 software was used for the statistical analysis of data.
Results Levels of NLR in CD with ileocolon lesions were significantly higher than those in CD patients with ileum lesions (3.13 vs 2.72) (Z=-2.326, P=0.02). Levels of NLR in CD with colon lesions were higher than those in CD patients with ileocolon lesions (4.07 vs 3.13) (Z=-2.409, P=0.04). The levels of NLR, WBC, hs-CRP in activity stage were significantly higher than those in remission stage (P < 0.05), ESR levels in activity stage was higher than that in remission stage. the optimal cutoff point for the NLR level in order to predict the diseases was 2.18, and a highest AUC equal to 0.762 (0.700-0.823, P < 0.001). the optimal cutoff point for the WBC level in order to predict the diseases was 5.51 109/L, and a highest AUC equal to 0.634 (0.565-0.703, P < 0.05), the optimal cutoff point for the hs-CRP level in order to predict the diseases was 3.02 mg/L, and a highest AUC equal to 0.676 (0.606-0.746, P < 0.05), the optimal cutoff point for the ESR level in order to predict the diseases was 8.5 mm/h, and a highest AUC equal to 0.726 (0.660-0.793, P < 0.05).
Conclusions Neutrophil to lymphocyte ratio can be used as a sensitive and reliable noninvasive marker in the course of Crohn’s disease.

PU-4236

血栓弹力图分析在晚期重度子痫前期中的应用价值

卢帅军、汪芳、朱虹、王卫华
宁波大学医学院附属医院

目的 分析血栓弹力图在晚期重度子痫前期患者中的特点并与常规凝血项目对比，探讨其在监测晚期重度子痫前期患者凝血功能中的应用价值。
方法 选择 2018 年 10 月至 2020 年 7 月在宁波大学医学院附属医院收治的妊娠晚期重度子痫前期患者 75 例，其中 31 例血小板计数＜100×109/L，44 例血小板计数≥100×109/L，相同孕期正常孕妇 50 例作为对照组。收集各研究对象的血栓弹力图（TEG）、凝血功能检测以及血常规的检测结果。
结果 重度子痫前期组的 TEG 各参数与对照组相比，均有显著差异（P＜0.01）；重度子痫前期合并血小板减少组与重度子痫前期组及正常对照组相比，R 值和 K 值均显著增大（P＜0.01），α 角、MA 值和 CI 值则均显著减小（P＜0.01）。正常妊娠组的 PT 值高于[华为 1] 重度子痫前期组，差异具有统计学意义（P＜0.01），但该参数在正常参考范围内，其余凝血检测的各项参数在三组间均无统计学意义（P＞0.05）。ROC 曲线分析显示，R 值和 K 值（AUC 分别为 0.92、0.82）对诊断重度子痫前期的参考价值优于 APTT、D 二聚体、Fbg[华为 2] 、AT[华为 3] （AUC 分别为 0.55、0.51、0.55 和 0.61）。
结论 晚期重度子痫前期合并血小板减少患者的凝血功能差，出血风险大，TEG 参数在鉴别和监测此类患者中相比常规凝血检测具有更大优势。

PU-4237

尿液细胞形态学在 1 例急性髓系白血病肝脾及泌尿系统浸润患者诊断中的指导作用

杜园园
长治医学院附属和平医院

目的 探讨尿液细胞形态学检查在 1 例急性髓系白血病肝脾及泌尿系统浸润患者诊断中的指导作用。
方法 回顾性分析 1 例以血尿为症状的急性髓系白血病肝脾及泌尿系统浸润患者的诊治过程，患者，33 岁男性，入院前 1 周出现头晕、恶心，未重视，3 天前患者剧烈呕吐后出现右侧鼻腔出血，出血量较多，不易自止，自行填塞治疗，继而出现排黑便 2 次，总量约 500ml，输注新鲜冰冻血浆 200ml 后转诊我院急救中心，以“白血病”收住入院。分别行相关实验室指标检查、尿液细胞形态学检查、超声及骨髓细胞形态检查等。
结果 入院查血常规：WBC 33.0×109/L，RBC 2.13×1012/L，HGB 65.6g/L，PLT 15.6×109/L，尿常规：尿液外观：红色浑浊，尿蛋白 2+，尿血红蛋白定性试验 2+，RBC 34759 个/μL，WBC 1729 个/μL；粪便隐血试验：3+；泌尿系彩超示：肝脾大、双肾及膀胱肿大。膀胱刺激症明显，考虑膀胱炎症。行尿液细胞形态学检查发现可见大量原始幼稚细胞，考虑白血病浸润可能；随后做骨髓室尿液沉渣涂片可见原始血细胞，比例占 65%，部分胞浆含有 Auer 小体。
结论 该患者白血病病史，病情较重，后期出现持续肉眼血尿、膀胱刺激症状、肝脾大、双肾及膀胱肿大等表现，尿液细胞形态学检查发现异常细胞，结合病史、相关检查及骨髓细胞检测，考虑急性白血病肝脾及泌尿系统浸润。提示尿液细胞形态学检查在该例患者中具有一定的临床实用性及诊断优势。

PU-4238

COVID-19 感染导致凝血功能障碍的机制研究

张舒阳、王宏
江苏省人民医院（南京医科大学第一附属医院）

多项研究显示，绝大多数 COVID-19 感染患者具有凝血功能障碍，而出凝血相关疾病是导致死亡的重要原因之一。本文结合 COVID-19 的临床特征和感染的高危因素，收集了多项相关研究的实验室检查结果，包括凝血功能指标和炎症细胞因子水平等，总结了可能存在的凝血功能障碍机制。

PU-4239

血清 PCT、CRP 在小儿脓毒症早期诊断中的价值

万芙荣
山东第一医科大学第一附属医院

目的 探讨血清 PCT、CRP 水平在小儿脓毒症早期诊断中的价值。
方法 随机选取我院 2018 年 1 月-2020 年 1 月收治的 SIRS（全身炎症反应综合症）患儿外周血标本 90 例，作为观察组。于同期选择 100 例非脓毒症患儿标本，作为对照组。采用荧光法定量法检测血清 PCT 水平，采用免疫比浊方法检测血清 CRP 水平。
结果 观察组患儿血清 PCT、CRP 测定水平与对照组比较均显著升高，差异有统计学意义（P<0.05），其中 SIRS 休克组患儿 PCT、CRP 水平显著高于严重 SIRS 组和对照组（P<0.05），严重 SIRS 组患儿 PCT、CRP 水平亦高于对照组（P<0.05）。
结论 联合检测血清 PCT、CRP 水平可用于早期诊断小儿脓毒症，有利于疾病的分层诊断，值得临床推广。

PU-4240

血栓弹力图在缺血性脑卒中临床诊治中的应用价值

闫彬[1]、刘坤[2]
1. 南阳市中心医院
2. 河南大学附属南石医院

目的 探讨血栓弹力图（TEG）检测在缺血性脑卒中中的临床价值。**方法** 收集 183 例急性缺血性脑卒中（AIS）患者，分为不同的亚组比较 TEG 的差异。
结果 （1）与≤50 岁 AIS 患者相比，51-70 岁 AIS 患者和≥71 岁 AIS 患者的 K 值显著降低，而 Angle 值和 CI 值则显著升高，且年龄越高，K 值越低、Angle 值和 CI 值越大，差异有统计学意义（*P*<0.05）。（2）≤50 岁的 AIS 患者的 TEG-K 值与 PLT 值之间成负相关（*r*=-0.281，*P*=0.013）；Angle 值与 PLT 值之间成正相关（*r*=0.277，*P*=0.015）；MA 值与 PLT 值、FIB 值之间成正相关（*r* 分别为 0.496、0.365，*P* 均<0.001）；CI 值与 PLT 值之间成正相关（*r*=0.272，*P*=0.017）；G 值与 PLT 值和 FIB 值之间成正相关（*r* 分别为 0.496、0.362，*P* 均<0.001）。（3）与未合并冠心病的 AIS 患者相比，合并冠心病的 AIS 患者的 K 值显著地降低，而 Angle 值则显著升高；与无脑卒中病史的 AIS 患者相比，有脑卒中病史的 AIS 患者的 K 值显著降低，而 Angle 值、MA 值、CI 值和 G 值则显著升高，差异均有统计学意义（*P*<0.05）。（4）大动脉粥样硬化型和小动脉闭塞型在 TEG 各项参数之间的差异无统计学意义（*P*>0.05），但大动脉粥样硬化型脑卒中患者的住院天数要显著长于小动脉闭塞患者住院天数（19.04±13.25 vs. 14.01±8.01），两者之间的差异有统计

学意义（*P*=0.031）。（5）TEG 参数对 AIS 的预测价值较低，AUC 最大的是 G 值（AUC=0.648，*P*=0.001），其次是 MA 值（AUC=0.647，*P*=0.001）。
结论 高龄 AIS 患者机体的高凝状态更为显著，≤50 岁的 AIS 患者的血栓弹力图和常规凝血指标之间的相关性较弱，且 TEG 参数对 AIS 发生的预测价值较弱。

PU-4241

血栓弹力图与传统凝血指标在深静脉血栓形成中的相关性及应用研究

闫彬、胡天喜、杜伟鹏
南阳市中心医院

目的 探讨血栓弹力图（TEG）在深静脉血栓形成（DVT）中的临床价值。
方法 收集在我院确诊的 60 例下肢静脉曲张和 142 例 DVT 患者。评估 TEG 和传统凝血指标在 DVT 中的相关性和一致性分析 TEG 的临床价值。
结果 DVT 患者的 R 值与 APTT 和 TT 呈正相关（*r*=0.289，*r*=0.337，P 均<0.05）；K 值与 TT 呈正相关（*r*=0.375，*P*<0.001），而与 PLT 和 FIB 呈负相关（*r*= -0.434，*r*=-0.503，*P* 均<0.05）；Angle 值、MA 值、CI 值、G 值均分别与 PLT 和 FIB 呈正相关（*r*=0.437，*r*=0.508，*r*=0.530，*r*=0.679，*r*=0.382，*r*=0.469，*r*=0.560，*r*=0.638，*P* 均<0.05），而与 TT 呈负相关（*r*= -0.353，*r*=-0.348，*r*=-0.409，*r*=-0.388，*P* 均<0.05）。TEG 对低凝和高凝状态的检出率分别为 23.94%、6.34%，而传统凝血指标分别为 3.52%、1.41%，其检出率之间的差异有统计学意义（*P*<0.05）。TEG 中 R 值判断 PT>14s 的敏感度和特异度分别是 38.5%和 95.3%，AUC 为 0.671（*P*=0.043）；K 值预测 PLT<125×10^9/L 的敏感度和特异度分别是 68.4%和 66.7%，AUC 为 0.709（*P*=0.003）；Angle 值、MA 值、CI 值和 G 值均对 TT<14 s、FIB>4 g/L 显示的高凝状态有预测价值，AUC 分别为 0.670、0.715、0.671、0.815、0.716、0.698、0.681 和 0.794（*P* 均<0.05）。
结论 TEG 和传统凝血指标检测在 DVT 中的相关性和一致性较弱，但 TEG 在预测传统凝血指标异常方面价值较大，且更易检出 DVT 患者凝血状态的改变。TEG 检测将有助于推动 DVT 患者的精准化抗凝治疗。

PU-4242

血常规和凝血常规联合检测对重症新型冠状病毒肺炎的诊断效能

闫彬、段金霞、杜伟鹏
南阳市中心医院

目的 探讨血常规和凝血常规联合检测在重症新型冠状病毒肺炎（COVID-19）患者中的诊断效能。
方法 回顾性分析在我院就诊的 53 例 COVID-19 患者，纳入其血常规和凝血常规各项指标，分为 35 例非重症组（包括轻型和普通型）和 18 例重症组。
结果 （1）与非重症组患者相比，重症组患者的年龄更大，合并糖尿病和冠心病的比例更高；（2）重症组患者的白细胞和中性粒细胞计数水平显著高于非重症患者，而淋巴细胞计数则显著低于非重症患者，差异有统计学意义。重症患者的 PT 值、FIB 值和 D-二聚体水平都显著高于非重症组患者，两组之间的差异有统计学意义（*P* 均<0.05）；而 TT 值显著低于非重症组患者（15.60±2.41 vs. 17.23±1.53，*P*=0.002），两组之间的差异有统计学意义。（3）白细胞、中性粒细胞和淋巴细胞单独检测对判断重症 COVID-19 患者的 AUC 曲线分别为 0.690、0.779 和 0.853，约登指数分别为 0.384、0.498 和 0.575（*P* 均<0.05）；PT 值、FIB 值、TT 值和 D-二聚体值单独检测对判断重症 COVID-19 患者的 AUC 分别为 0.699、0.922、0.759 和 0.83，约登指数分别为 0.463、0.748、0.51 和 52.54（*P* 均<0.05）。（4）中性粒细胞计数和淋巴细胞计数与 TT 值、FIB 值和 D-二聚体

联合检测能够显著提高对重症 COVID-19 患者的诊断效能（联合检测的 AUC 均>0.800，*P* 均<0.001），其中淋巴细胞计数和 FIB 值联合检测的 AUC 曲线最大可达 0.942，灵敏度和特异度分别为 88.89%、94.29%（*P*<0.001）。

结论 血常规和凝血常规的联合检测能够更好地帮助临床医师判断 COVID-19 患者病情程度，尤其是淋巴细胞计数和 FIB 值的联合检测能够尽早地帮助识别重症患者，从而及时采取措施预防病情恶化。

PU-4243

精子 DFI、精子 HDS 测定联合精液常规在男性不育患者中的应用

程少杰
中国人民解放军联勤保障部队第 900 医院

目的 观察分析男性不育患者精液常规检查及精子 DFI、精子 HDS 测定结果分析,为临床男性不育患者诊治提供参考依据。

方法 选取 2020 年 6 月至 2020 年 12 月我院收治的男性不育患者 70 例作为观察组,选取同期进行健康体检的正常男性 50 例作为对照组,两组受检者均行精液常规检查和精子 DFI、精子 HDS 测定,统计分析两组受检者的精液常规检查的异常项目及精子 DFI、精子 HDS 测定相关性变化。

结果 观察组的精液液化时间大于对照组,精子活动力、精子存活率、精子计数均低于对照组,异常精子率高于对照组,差异均有统计学意义(P<0.05); 精子 DFI、精子 HDS 与精子活动力、精子存活率负相关,即精子 DFI、精子 HDS 越高, 精子活动力、精子存活率越低;与不动精子率正相关,即精子 DFI、精子 HDS 越高,不动精子所占比列相对应的也越高。

结论 男性不育患者的精液常规检查结果主要体现在精子活力下降、精子存活率降低、精子计数降低、液化时间延长等方面,但是存在不可控因素如患者留取精液标本时未完全收集全部精液，液化时间延长但精液常规其他指标正常，对临床判断造成一定影响，患者在精液常检测同时联合测定精子 DFI、精子 HDS 测定有助于更全面反应精子质量，在男性不育的诊断治疗有重要意义。

PU-4244

Hemoglobin to red blood cell distribution width ratio predicts in-hospital mortality in patients with type A acute aortic dissection

Yaman Wang、jun zhou
Jiangsu Provincial People's Hospital (First Affiliated Hospital of Nanjing Medical University)

Objective Acute type B aortic dissection (BAAD) is a life-threatening emergency, which is associated with high morbidity and mortality rates. The aim of this study was to assess the value of serum hemoglobin (HB) to red blood cell distribution width (RDW) ratio (HRR) in predicting in-hospital mortality in type B AAD patients.

Methods A total of 126 type B AAD patients were included in this retrospective investigation from April 2017 to November 2019. Admission blood routine parameters were gathered and HRR was computed. The outcome was all cause in-hospital mortality within 30 days.

Results The average levels of serum HRR were significant higher in survivor group than those in non-survivor group (10.54 ± 1.73 vs 8.62± 2.36, p <0.001) and serum HRR was an independent factor associated with in-hospital mortality (hazard ratio (HR): 5.158; 95% confidence interval (CI): 1.501–17.719; p = 0.009). In addition, the area under the ROC curve (AUC) was 0.773 (95% CI 0.640–0.886, p < 0.001).

Conclusion Admission serum HRR can be used as an independent predictor of in-hospital mortality in patients with type B AAD.

PU-4245

红细胞参数检验在贫血鉴别诊断中的价值

江家红、李洁
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨红细胞相关参数在贫血鉴别诊断中的价值。
方法 选取 15 例地中海贫血和 20 例缺铁性贫血作为实验组,另选 40 例健康人群作为对照组,对比两组红细胞参数。
结果 实验组 HB、MCV、RBC、MCH 均低于对照组,而实验组的 RDW 水平显著高于对照组,但是实验组中,缺铁性贫血患者 RDW 和 MCV 水平高于地中海贫血,而 RBC 和 HB 水平低于地中海贫血患者,且 P<0.05。
结论 红细胞参数可作为贫血鉴别诊断的指标,还可以鉴别地中海贫血和缺铁性贫血,从而为贫血的治疗提供依据。

PU-4246

食管胸膜瘘 1 例并文献复习

汪勇、张晓辉
苏州大学附属第一医院

患者凡某，男性，63 岁，主诉“咳嗽 1 月余，加重气短 1 天”于 4 月 28 日入院。既往 2020 年 10 月因进食后哽噎行胃镜检查发现食管新生物，病理示鳞状细胞癌，多次行放化疗及免疫治疗，末次化疗时间 2021 年 4 月 15 日，末次放疗时间 2021 年 1 月 13 日。2021 年 3 月 9 日查颈胸腹增强 CT：提示多发转移。入院查体：体温 36.5℃，脉搏 135 次/分，呼吸 25 次/分，血压 93/62mmHg（1.3μg/kg/min）；听诊右肺呼吸音低，两肺可闻及散在湿性啰音；胸部 CT 示：右侧液气胸；右肺渗出液；左肺肺气肿；右侧主支气管内痰栓可能。实验室检查：代谢性酸中毒；CRP 增高；心功能不全；肾功能不全；电解质代谢紊乱；4 月 29 日穿刺胸水，性状乳糜样、乳糜试验阳性、离心沉渣染色镜检发现鳞状上皮细胞，细菌及杆菌，提示食管胸膜瘘；结合病史以及相关检查，利用亚甲蓝鼻饲试验确诊食管胸膜瘘。患者经过治疗一般情况较好至 18 日出院随访。讨论：食管胸膜瘘是指各种原因导致食管与胸膜腔异常沟通而形成瘘管，污染的消化液及食物残渣经纵隔进入胸腔，导致纵隔、胸腔和肺部的化学性炎症和细菌性感染；可以通过食管造影、亚甲兰试验、胸部Ｘ线检查、胸部 CT、MRI、内镜检查进行诊断。本例患者胸水中发现有限的蛛丝马迹，第一时间与临床沟通，早期诊断和及时正确的处理提高治愈率。体液细胞学检查越来越受临床重视和喜爱，应该大力推广以及提高与临床的沟通水平。细微处发现线索，更好服务临床！

PU-4247

超敏 C-反应蛋白联合凝血功能检测对于新生儿败血症诊断价值探讨

张立涛、李洁
江苏省人民医院（南京医科大学第一附属医院）

目的 探讨超敏 C-反应蛋白(hsCRP)联合凝血酶原时间(PT)、活化部分凝血酶时间(APTT)对于新生儿败血症的诊断价值。
方法 收集 2016 年 1 月至 2021 年 1 月江苏省妇幼保健院儿科新生儿收治的 95 例败血症患儿作为研究对象，根据血培养的结果，将血培养阳性患儿归为败血症 A 组(38 例)，血培养阴性患儿归为败血症 B 组(57 例)，另选取同期出生的 48 例正常新生儿归入对照组。检测并比较 3 组受试对象 hsCRP、PT 和 APTT 值；绘制受试者工作曲线(ROC)，计算各检测指标 ROC 曲线下面积(AUC)以及灵敏度、特异度、阳性预测值和阴性预测值，用二项分类 Logistic 回归法建立新的变量 CPR+ PT+ APTT，继续绘制 ROC 曲线，计算新变量的 AUC、灵敏度、特异度、阳性预测值和阴性预测值。
结果 对照组、败血症 A 组、败血症 B 组的 CPR、PT 和 APTT 实验室检测结果均依次升高(F=10.616、6.155、5.243,P=0.000、0.000、0.000),差异具有统计学意义。4 项指标中，CPR+ PT+ APTT 的 AUC 最高(0.94)，灵敏度最高(93.42％)，特异度最高(91.66％)，阳性预测值最高(92.60％)，阴性预测值最大(78.55％)。
结论 在血培养未能及时诊断新生儿败血症的情况下，联合检测 CPR+ PT+ APTT，可以为临床进行败血症早期诊断提供重要依据。

PU-4248

炎症指标在早期诊断大肠癌手术吻合口漏中的作用

田春迎、于秀艳
吉林省肿瘤医院

目的 白细胞（WBC）、血沉、降钙素原（PCT）和 C 反应蛋白（CRP）是诊断术后感染的常用炎症指标。吻合口漏是大肠癌手术后一种令人担忧的并发症，早期诊断可改善临床结局。关于吻合口漏的诊断已经做了大量的研究，但是关于吻合口漏的早期诊断，尚无有效的炎症指标作鉴别诊断。本研究的目的是调查 WBC、血沉、PCT 和 CRP 在早期诊断大肠癌手术吻合口漏中的应用价值。
方法 本研究选取 2018 年 5 月至 2020 年 12 月在我院接受大肠癌手术的 126 例患者作为研究对象，主要研究终点为吻合口漏，回顾性分析患者相关临床病理参数、在术后第 1 天至第 5 天抽取的血样中确定 WBC、血沉、PCT 和 CRP 数值。统计分析使用 SPSS 20.0 版进行。定量变量的比较使用 t 检验和 Pearson 相关分析，定性变量用 χ2 检验，采用受试者工作曲线（ROC）分析并计算曲线下面积（AUC），以评估诊断的预测值。
结果 在 126 例大肠癌病例中，10 例患者发生了吻合口漏。吻合口漏患者的 PCT 和 CRP 水平显著高于非吻合口漏患者，差异具有统计学意义（P<0.05），而吻合口漏患者的 WBC 水平更高，但差异无统计学意义（P>0.05），血沉的比较无明显差异。PCT 可以将吻合口漏患者和非吻合口漏患者区分开（AUC：0.952），而 CRP 不能很好的区分吻合口漏患者和非吻合口漏患者（AUC：0.583）。CRP 截止浓度为 172mg/L 时可产生 89％的敏感性，83％的特异性和 99％的阴性预测值（NPV）。PCT 截止浓度为 2.34ng/mL 时，灵敏度为 88％，特异性为 95％，阳性预测值为 46％，NPV 为 98％。
结论 血清 PCT 和 CRP 能够有效鉴别诊断大肠癌手术后吻合口漏，具备早期诊断价值。

PU-4249

血细胞参数对儿童病毒性肺炎病情判断价值评估

李娟、甘月滨、张晶、陈甜花、黄回滨
厦门市妇幼保健院

目的 探讨血细胞参数对病毒性肺炎轻型与重型，急性期与恢复期鉴别的价值。
方法 选取该院收治的 95 例病毒性肺炎患者，按照病情轻重程度分为轻型组（20 例），重型组（75 例）。采用 t 检验与非参数秩和检验分析比较两组患者在发病早期血细胞参数的差异性以及重型病毒性肺炎患儿急性期与恢复期血细胞参数的差异性；应用受试者工作特征（ROC）曲线分析不同指标对病情的预测价值。
结果 (1)疾病早期，与轻型组相比，重型组患儿淋巴细胞计数(Lym）、血小板计数（PLT）显著升高（P<0.05），中性粒细胞计数（Neu）、血小板分布宽度（PDW）、Neu 与 Lym 比值（NLR）显著降低（P<0.05）; (2) 与恢复期相比，重型病毒性肺炎急性期白细胞计数（WBC），Neu，C 反应蛋白（CRP）和 NLR 显著升高（P<0.05），Lym 显著降低（P<0.05）;(3) ROC 曲线分析结果显示，NLR 诊断重型病毒性肺炎的曲线下面积（AUC）为 0.763,敏感度和特异度分别为 75%和 72%;由 Neu 和 NLR 联合预测重型病毒性肺炎的恢复期的 AUC 为 0.718，敏感度和特异度分别为 72%和 70%.
结论 Neu，Lym 和 NLR，可辅助判断病毒性肺炎病情轻重程度和药物治疗效果。

PU-4250

Can we reduce the interference of vitamin C and PH in urinalysis?

danqin feng[1]、jinbiao lin[2]、jianguo cai[3]、xiaoli chen[4]、huiming ye[5,6]
1. Women and Children's Hospital, School of Medicine, Xiamen University
2. Women and Children's Hospital, School of Medicine, Xiamen University
3. Women and Children's Hospital, School of Medicine, Xiamen University
4. Women and Children's Hospital, School of Medicine, Xiamen University
5. Women and Children's Hospital, School of Medicine, Xiamen University
6. School of Medicine, and Department of Laboratory Medicine, School of Public Health, Xiamen University

Objectives To evaluate the interference of vitamin C and PH in urinalysis, and minimize the risk to make the effective communication.
Design and Methods 732 leftover urine samples in which the concentration of vitamin C was 0.0mmol/L and either of the test-strip results (Glucose, Blood, Bilirubin, Leucocyte, Nitrite, Protein, Ketone) was positive that were collected. The interference test checked out using these leftover urine samples. When the chemical protein module was positive, the sulfosalicylic acid test performed to confirm the positive Results
Results About 27% of urine samples were vitamin C positive. Adequate vitamin C would interfere with the chemical result of GLU, BIL, and BLD, but not KET, PRO, WBC, NIT(p-value<0.05). False-positive protein occurred at any samples, but higher when urine PH is greater than or equal to 8.0.
Conclusion To minimize the risk of vitamin C and PH in urinalysis, the laboratory should pay more attention to its conditions. Also, do more to help guarantee the accuracy of the urinalysis results and to give more comments to doctors to achieve effective communication.

PU-4251

脓毒血症患者血栓弹力图与凝血指标和血小板参数的相关性分析

陈思宇
成都市双流区第一人民医院四川大学华西空港医院

目的 分析脓毒血症患者血栓弹力图、凝血指标及血小板参数的变化及其相关性。
方法 以 2019 年 6 月至 2020 年 6 月成都市双流区第一人民医院重症医学科的 54 例脓毒血症患者为研究对象进行回顾性横断面调查研究,其中男性 40 例,女性 14 例;年龄 39-96 岁,平均(68.72±14.45)岁。收集患者住院期间一般资料、TEG 指标为凝血反应时间(R 值,反应凝血因子情况)、纤维蛋白原时间(K 值，反应纤维蛋白原的功能和水平)、最大血块强度(MA 值,反应血小板功能)、α 角（α 角）、凝血指标及血小板相关参数。根据血栓弹力图的 CI 指标结果将纳入的患者分为正常组(-3≤ CI≤+3)、低凝组(CI＜-3)和高凝组(CI＞+3)。采用 Pearson 相关方法分析 TEG 与凝血指标和血小板参数之间的相关性。
结果 低凝组患者，R 值和 K 值都明显延长，α 角和 MA 值明显缩短。高凝组患者 R 值和 K 值明显缩短，而 α 角和 MA 值则明显延长。 低凝组患者血小板计数（PLT）明显低于正常组和高凝组（P＜0.05），高凝组患者的 P-LCR 明显高于低凝组和正常组（P＜0.05）。高凝组患者 D-二聚体明显高于低凝组和正常组。脓毒血症患者 TEG 各指标与凝血常规检测指标间无相关性；而与血小板参数具有一定的相关性（K 值与 PLT、P-LCR 呈负相关；α 角与 PLT、P-LCR 呈正相关，与 PDW 呈负相关；MA 与 P-LCR 呈正相关）。
结论 TEG 更能有效监测脓毒血症患者凝血功能改变，并对脓毒血症严重程度具有鉴别能力，能够识别高凝、低凝状态，客观评价脓毒血症患者病情严重程度，指导临床风险评估和疾病的治疗。

PU-4252

大鼠出生后第一周血清蛋白质组学研究

魏利龙、周允、曹永彤
中日友好医院

背景 血浆是最复杂的体液之一，包含大量物质，这些物质是通过主动分泌或从组织和细胞渗漏释放出来的。因此，血浆变化在很大程度上可以反映机体状态。为了研究早期生命中血浆蛋白的变化，本实验使用 LC-MS / MS 技术比较了新生大鼠和生后第一周大鼠的血浆蛋白质组。
方法 分别收集 6 只新生鼠和 6 只出生后一周大鼠的血浆蛋白。对血浆蛋白进行 LC-MS/MS 质谱鉴定，获得血浆蛋白的定量信息。采用双侧 T 检验，寻找显著差异的蛋白。对差异蛋白进行功能分析。
结果 在两个发育阶段的大鼠血浆中共鉴定出 570 种蛋白质。通过非标记定量比较了生后第一周大鼠和新生大鼠的血浆蛋白质组。 发现 75 种蛋白质显着增加，而 22 种蛋白质显著减少。通过差异蛋白质 GO 数据库分析，可以很容易地分离出两个发育阶段的血浆蛋白质组。通过使用 Ingenuity Pathway 分析工具， LXR ／ RAR 反应通路、急性期反应信号传导、补体系统、一氧化氮生成和活性氧物种等通路被显着活化。
结论 与新生大鼠相比，出生一周后大鼠的血浆蛋白质组明显不同。这些变化将使新生鼠更容易存活。这是首次使用 LC-MS / MS 研究新生大鼠血浆蛋白质组发育的研究，可为研究动物发育提供基础和线索。

PU-4253

改良细胞形态学联合生物学标志物在结核性胸膜炎中诊断价值

杜园园
长治医学院附属和平医院

目的 探讨联合胸腔积液改良细胞形态学检查、腺苷脱氨酶检测(ADA)、结核感染 T 细胞检测(TB-IGRA)、结核基因检测(TB-DNA)和结核抗体检测(TB-Ab)对结核性胸膜炎的诊断价值评价。
方法 选取 2019 年月 6 月至 2020 年 6 月临床病例 230 例(包括结核组 120 例，非结核组 110 例)，进行胸腔积液细胞形态学检查、腺苷脱氨酶检测(ADA)、结核感染 T 细胞检测(TB-IGRA)、结核基因检测(TB-DNA)和结核抗体检测(TB-Ab)，分析其单项检测结果及联合应用诊断效能。
结果 改良细胞形态学检查、ADA、TB-IGRA、TB-DNA 和 TB-Ab 五项指标组成不同组合中，五项指标组合并联检测的诊断结核性胸膜炎的敏感性最高(达 97.50%)；三项指标组合细胞形态学+TB-IGRA+ADA 并联检测敏感性较高(94.17%)；两项指标组合细胞形态学+TB-IGRA 并联检测敏感性较高(91.67%)，均高于单一指标检测敏感性，差异有统计学意义($\chi2=174.885$，$P<0.001$)；串联检测组合中，五项指标组合串联检测对诊断结核性胸膜炎的特异性最高(达 99.09%)；三项指标组合 TB-IGRA+TB-DNA+TB-Ab 串联检测特异性较高(92.73%)；两项指标组合细胞形态学+TB-DNA 检测特异性较高(90.00%)，均较单一指标检测时特异性明显提高，差异有统计学意义($\chi2=35.242$，$P<0.001$)。且各组合之间比较均有统计学差异($\chi2=36.073$、107.085，$P<0.001$)。
结论 改良细胞形态学检查、ADA、TB-IGRA、TB-DNA 和 TB-Ab 并联检测可提高对结核性胸膜炎诊断敏感性，串联检测可提高其特异性，并可根据实际情况合理选择多项指标的不同检测组合，具有很好的诊断效能及临床实用性。

PU-4254

血小板与淋巴细胞比值与消化道肿瘤的相关性研究

刘菁菁、何挚、吴国球
东南大学附属中大医院

目的 本研究通过观察血小板与淋巴细胞比值（PLR）与消化道肿瘤的相关性，探讨 PLR 对于消化道肿瘤的诊断价值，为临床消化道肿瘤的诊断提供帮助。
方法 收集 316 例明确诊断的消化道肿瘤纳入实验组，收集 367 例同期表观健康人群纳入对照组。分析患者临床资料，比较 2 组 PLR 水平差异，采用临床受试者工作特征（ROC）曲线计算 PLR 最佳临界值及曲线下面积（AUC）。
结果 消化道肿瘤组患者外周血 PLR 明显高于对照组（$P<0.05$）。PLR 用于诊断消化道肿瘤的最佳临界值为 159.61，灵敏度和特异度分别为 77.2%和 89.0%，AUC 为 0.925。
结论 消化道肿瘤患者 PLR 显著提高，PLR 对消化道肿瘤患者具有较好的诊断价值。

PU-4255

血小板与淋巴细胞比值对急性胰腺炎的诊断价值

何挚、刘菁菁、吴国球
东南大学附属中大医院

目的 本研究通过观察血小板与淋巴细胞比值（PLR）与急性胰腺炎的相关性，探讨 PLR 对于急性胰腺炎的诊断价值，为临床急性胰腺炎的诊断提供帮助。

方法 收集 104 例明确诊断的急性胰腺炎纳入实验组，收集 112 例同期表观健康人群纳入对照组。分析患者临床资料，比较 2 组 PLR 水平差异，采用临床受试者工作特征（ROC）曲线计算 PLR 最佳临界值及曲线下面积（AUC）。
结果 急性胰腺炎组患者外周血 PLR 明显高于对照组（P＜0.05）。PLR 用于诊断急性胰腺炎的最佳临界值为 148.215，灵敏度和特异度分别为 76.9%和 87.5%，AUC 为 0.912。
结论 急性胰腺炎发生时，PLR 显著升高，PLR 对急性胰腺炎患者具有较好的诊断价值。

PU-4256

血小板与淋巴细胞比值与宫颈癌的相关性研究

何挚、刘菁菁、吴国球
东南大学附属中大医院

目的 本研究通过观察血小板与淋巴细胞比值（PLR）与宫颈癌的相关性，探讨 PLR 对于宫颈癌的诊断价值，为临床宫颈癌的辅助诊断提供帮助。
方法 收集 167 例宫颈癌患者纳入实验组，收集 183 例同期表观健康人群纳入对照组。分析患者临床资料，比较 2 组 PLR 水平差异，采用临床受试者工作特征（ROC）曲线计算 PLR 最佳临界值及曲线下面积（AUC）。
结果 宫颈癌组患者外周血 PLR 明显高于对照组（P＜0.05）。PLR 用于诊断宫颈癌的最佳临界值为 168.38，灵敏度和特异度分别为 78.4%和 86.7%，AUC 为 0.848。
结论 宫颈癌患者的 PLR 水平显著高于正常人群，PLR 对宫颈癌患者具有较好的预测及辅助诊断价值。

PU-4257

血小板与淋巴细胞比值对类风湿性关节炎的诊断价值

何挚、刘菁菁、吴国球
东南大学附属中大医院

目的 本研究通过观察血小板与淋巴细胞比值（PLR）与类风湿性关节炎（RA）的相关性，探讨 PLR 对于 RA 的诊断价值，为临床 RA 的诊断提供帮助。
方法 收集 152 例类风湿性关节炎患者纳入 RA 组，收集 170 例同期表观健康人群纳入对照组。分析患者临床资料，比较 2 组 PLR 水平差异，采用临床受试者工作特征（ROC）曲线计算 PLR 最佳临界值及曲线下面积（AUC）。
结果 RA 组患者外周血 PLR 明显高于对照组（P＜0.05）。PLR 用于诊断 RA 的最佳临界值为 161.33，灵敏度和特异度分别为 64.5%和 88.2%，AUC 为 0.861。
结论 PLR 与 RA 活动性密切相关，对 RA 患者具有较好的诊断价值。

PU-4258

血小板与淋巴细胞比值及中性粒细胞与淋巴细胞比值对慢性肾衰竭的诊断价值

刘菁菁、何挚、吴国球
东南大学附属中大医院

目的 本研究通过观察血小板与淋巴细胞比值（PLR）及中性粒细胞与淋巴细胞比值（NLR）与慢性肾功能衰竭（CRF）的相关性，探讨 PLR 及 NLR 对于 CRF 的诊断价值，为临床 CRF 的诊断提供帮助。
方法 收集 409 例慢性肾功能衰竭患者纳入 CRF 组，收集 449 例同期表观健康人群纳入对照组。分析患者临床资料，比较 2 组 PLR、NLR 水平差异，采用临床受试者工作特征（ROC）曲线计算 PLR 及 NLR 最佳临界值及曲线下面积（AUC）。
结果 CRF 组患者外周血 PLR、NLR 均明显高于对照组（P＜0.05）。PLR 用于诊断 CRF 的最佳临界值为 122.445，灵敏度和特异度分别为 73.0%和 56.2%，AUC 为 0.716，NLR 用于诊断 CRF 的最佳临界值为 2.28，灵敏度和特异度分别为 84.1%和 47.2%，AUC 为 0.673。
结论 PLR 及 NLR 对 CRF 患者均有一定的诊断价值，且 PLR 略优于 NLR。

PU-4259

Application of SF-Cube 2.0 technology in platelet count in patients with EDTA-dependent pseudothrombocytopenia

Zhi He、Guofang Shu、Huixia Lu
Zhongda Hospital, Southeast University

Background To explore the application of SF-Cube 2.0 technology in platelet count in patients with EDTA-dependent pseudothrombocytopenia (EDTA-PTCP).
Methods Twenty-two out-patients and in-patients with EDTA-PTCP in our hospital were selected from February 1, 2020, to August 31, 2020. With the permission of each patient, blood samples of EDTA and sodium citrate anticoagulant tubes were collected. EDTA anticoagulant samples were tested by using the "complete blood cell count and white blood cell differential count"(CD) mode, and "complete blood cell count, white blood cell differential count, and reticulocyte count" (CDR) mode of the Mindray BC-6800Plus automated hematology analyzer, and the platelet counts were compared with the sample of sodium citrate anticoagulant from this patient.
Results As SF-Cube 2.0 technology (implemented by using the CDR mode of the Mindray BC-6800Plus) was used, the platelet count of EDTA-PTCP sample was consistent with that of sodium citrate anticoagulant, which was significantly higher than that of CD detection mode.
Conclusions SF-Cube 2.0 technology can effectively correct the platelet counts in people with known or suspected EDTA-PTCP.

PU-4260

血小板与淋巴细胞比值对溃疡性结肠炎的诊断价值

何挚、刘菁菁、吴国球
东南大学附属中大医院

目的 本研究通过观察血小板与淋巴细胞比值（PLR）与溃疡性结肠炎（UC）的相关性，探讨 PLR 对于 UC 的诊断价值，为临床 UC 的诊断提供帮助。

方法 收集 114 例溃疡性结肠炎患者纳入 UC 组，收集 105 例肠易激综合征(IBS)患者纳入 IBS 组，收集 120 例同期表观健康人群纳入对照组。分析患者临床资料，比较 3 组 PLR、白细胞计数（WBC）及 C-反应蛋白（CRP）水平差异，采用临床受试者工作特征（ROC）曲线计算 PLR 最佳临界值及曲线下面积（AUC）。
结果 UC 组患者外周血 PLR 均明显高于 IBS 组和对照组（P＜0.05）。PLR 用于诊断 UC 的最佳临界值为 135.395，灵敏度和特异度分别为 90.4%和 66.2%，AUC 为 0.819，诊断价值优于 WBC（AUC 为 0.731）和 CRP（AUC 为 0.703）。
结论 PLR 对 UC 患者的诊断价值优于 WBC 及 CRP 等传统炎症指标。

PU-4261

TEG 联合 D-Dimer/FDP 比值检测在脓毒症并发 DIC 患者中的研究

赵启波
昭通市第一人民医院

目的 探讨 TEG 联合 D-Dimer/FDP 比值对脓毒症并发 DIC 预后的预测价值.
方法 选取 2020 年 1 月-2021 年 1 月我院收治的 107 例脓毒症患者,其中 41 例患者发生 D1C(DIC 组),66 例未发生 DIC(非 DIC 组).追踪 DIC 组临床结局,分为死亡组(14 例)和存活组(27 例)..受试者工作特征曲线(ROC)分析 TEG 各参数和 D-Dimer/FDP 比值预测 DIC 患者预后的价值.
结果 DIC 组 R、K、LY30、FDP 高于非 DIC 组(P＜0.05),α 角、MA 值、C1、D-Dimer、D-Dimer/FDP 比值低于非 DIC 组(P＜0.05).=死亡组 R[(9.21±0.72)min vs.(6.53±1.42)min]、K[(5.32±2.42)min vs.(3.85±0.69)min]、LY30[(7.42± 1.63) % vs.(5.29±1.52) %]、FDP[(10.64±1.67)mg/L vs.(8.54±2.34)mg/L] 高于存活组 (P ＜ 0.05),D-Dimer[(0.40±0.03)mg/L vs.(0.49±0.03)mg/L]、D-Dimer/FDP 比值(0.10±0.02 vs.0.16±0.03)]低于存活组(P＜0.05).ROC 分析结果显示 MA 值、α 角、D-Dimer/FDP 比值具有预测脓毒症并发 DIC 患者预后的价值,联合三项指标预测脓毒症并发 DIC 患者预后的 AUC 为 0.960(95％CI:0.909?1.000),大于 MA 值、α 角、D-Dimer/FDP 比值(P＜0.05).
结论 TEG 联合 D-Dimer/FDP 比值有利于监测脓毒症并发 DIC 患者凝血状态,对病情评估和预后判断均有较高价值.

PU-4262

环境温湿度变化对染色体滴片效果的影响研究

陈士威
吉林金域医学检验所有限公司

目的 分析环境温湿度变化对染色体滴片效果的影响，推断环境温湿度与分裂相伸展和分散之间的关系，为选择合适的滴片环境，提高染色体制片质量提供参考依据。
方法 选取 2020 年 1 月至 2020 年 3 月送检我公司的 5 例合格样本，通过人工干预，采用空调、加湿器、除湿机、水浴箱以及电磁炉烧水等方式控制环境温湿度，分别在湿度小于 50%、温度小于 22℃；湿度 50%-60%、温度 22℃-26℃；湿度大于 60%、温度大于 26℃三种不同环境下滴片，进行对比验证。
结果 湿度小于 50%，温度小于 22℃时的 5 例样本，所滴玻片干燥很快，分裂相还未完全伸展开玻片已干，分裂相成团，染色体重叠较多，分散效果差，且染色体本身短小。湿度大于 60%，温度大于 26℃时的 5 例样本，所滴玻片干燥很慢，染色体长度和粗细合格，染色体重叠较少，但有胞

浆，且分裂相过于分散，个别分裂相内染色体丢失。通过人工干预，湿度在 50%-60%，温度 22℃-26℃时的 5 例样本，分裂相分散程度适宜，染色体伸展较好，长度和粗细也较好。

结论 环境对染色体滴片效果起着决定性作用，冬夏季温差较大，环境温湿度差别大，滴片效果有所不同。通过实验对比结果可以看出，使环境保持在湿度 50%-60%，温度 22℃-26℃时，制片质量最好。因此，可以通过对失控的环境进行有效的人为干预，控制滴片环境温湿度，有效提高染色体制片质量，降低退单率，使染色体诊断更为精准，出结果更为迅速。

PU-4263

Sysmex XN-9000 全自动血细胞分析流水线血小板聚集警示值的研究探讨

林乘龙、肖伟欢、张嘉琳
广东省人民医院

目的 探讨 Sysmex XN-9000 全自动血细胞分析流水线血小板聚集的最佳警示值。

方法 选取 2020 年 10 月至 2021 年 4 月广东省人民医院血常规标本 105 例份，采用 XN-9000 的 WNR、WDF、PLT-F 检测通道、人工镜检判断血小板聚集情况。以人工镜检结果为金标准，分析 XN-9000 警示值对血小板聚集的判断价值，两种方法的相关性。绘制受试者工作特征（ROC）曲线，研究探讨 XN-9000 血小板聚集的最佳警示值。

结果 XN-9000 检测 105 例份血常规标本中，WNR 通道血小板聚集阳性 7 例份，阴性 98 例份；WDF 通道阳性 9 例份，阴性 96；PLT-F 通道阳性 36 例份，阴性 69 例份；人工镜检阳性 14 例份，阴性 91 例份。WNR 通道警示判断血小板聚集特异性最好为 94.51%；PLT-F 通道敏感性为 78.57%，在三个通道中最高。且经 Pearson 相关分析，对于血小板聚集报警 PLT-F 通道与手工镜检确认聚集的相关性呈正相关（r=0.469，P<0.05）。 以手工镜检做对照，ROC 曲线分析显示 PLT-F 通道 AUC 为 0.784，在三通道中，以 PLT-F 通道最优。

结论 XN-9000 中 PLT-F 通道警示值判断血小板聚集的可信性较高。最佳血小板聚集报警阈值为 80。

PU-4264

流式细胞术两种不同试剂检测淋巴细胞亚群的结果比较

鞠颖慧、吴蕙、陈朴、王蓓丽、潘柏申、郭玮
复旦大学附属中山医院

目的 评估国产试剂与进口试剂在流式细胞术检测外周血淋巴细胞亚群的差异性，比对其效果。

方法 收集三家医院共 200 例入院患者的全血标本，分别使用美国 BD 公司进口试剂和北京同生时代公司国产试剂，采用流式细胞术检测其淋巴细胞亚群百分比及绝对计数，分析两者检测结果的相关性和一致性。

结果 与 BD 试剂相比，同生时代试剂在检测 CD3+细胞、CD3+CD8+细胞、CD3+CD4+细胞、CD19+细胞、CD16+CD56+细胞的百分比结果上无显著差异(P＞0.05), 相关性分析结果显示两者结果之间呈现良好线性相关（R＞0.95，P<0.05）。

结论 流式细胞术国产试剂与进口试剂间检测结果具有良好的相关性，可用于临床淋巴细胞亚群分析。

PU-4265

全自动血液分析仪检测浆膜腔积液常规细胞计数的可行性研究

王冲、朱捷、顾梅秀、郭玮、王蓓丽
复旦大学附属中山医院

目的 探讨 Sysmex XN-9000 全自动血液分析仪体液模式在浆膜腔积液标本细胞计数及白细胞分类的检测中代替人工计数法的可行性。
方法 收集本院住院患者共 284 例浆膜腔积液标本（168 例胸水、65 例腹水、25 例腹透液及 26 例心包积液标本），分别使用显微镜人工计数法和 Sysmex XN-9000 血液分析仪检测法进行红细胞（RBC）和白细胞（WBC）计数以及白细胞分类。采用 t 检验及方差检验，以显微镜人工计数法为金标准，对血液分析仪检测浆膜腔积液细胞计数及白细胞分类的准确性进行评估。
结果 WBC 人工计数法 400~15000 个/ul 的标本，相关性较好，R2 为 0.993，P 为 0.000；RBC 人工计数法数值 400~150000 个/ul 的标本，相关性较好，R2 为 0.994，P 为 0.000；252 例白细胞分类的标本，仪器法结果与金标法结果的符合率高，两种方法相比，单个核细胞、多个核细胞、嗜酸性粒细胞的 P 值均 <0.01。
结论 Sysmex XN-9000 血液分析仪检测体液细胞具有快速、准确、重复性好等优势，在 RBC、WBC 一定线性范围内可以取代人工计数法计数。

PU-4266

MYC protein expression does not correlate with MYC abnormalities but predicts an unfavorable prognosis in de novo acute myeloid leukemia

Pu Chen[1]、Lucas Redd[2]、Prasad Koduru[2]、Franklin Fuda[2]、Weina Chen[2]
1. Department of Laboratory Medicine, Zhongshan Hospital, Fudan University
2. Departments of Pathology, University of Texas Southwestern Medical Center, Dallas, TX, USA

Aims MYC is a crucial proto-oncogene that has not yet been extensively studied in acute myeloid leukemia (AML). We investigated the significance of MYC protein expression by immunohistochemistry (MYC-IHC) regarding its correlation with MYC abnormalities and prognosis in de novo adult AML.
Methods MYC-IHC in bone marrow of patients with untreated AML (n= 58) was assessed and scored as MYClow (0-40% of blasts) or MYChigh (> 40% of blasts) and correlated with MYC abnormalities by fluorescence in situ hybridization (FISH) and prognosis in the context of cytogenetic risk stratification. Residual myeloid disease at the end of induction was assessed by flow cytometry.
Results MYClow and MYChigh were detected in 24 (41%) and 34 cases (59%), respectively. Extra copies of MYC was present in 12% cases and was not correlated with level of MYC-IHC. No cases had MYC translocation or amplification. Compared to MYClow patients, MYChigh patients had a shorter overall survival in all cytogenetic risk groups (68 vs. 21 months, p=0.006) and in the intermediate risk group (61 vs. 21 months, p = 0.046). MYChigh patients had a tendency towards detected residual disease at the end of induction in all cytogenetic risk and intermediate risk groups.
Conclusions Regardless of the underlying mechanisms of MYC dysregulation, high level of MYC protein is expressed in the majority of AML and correlated to worse prognosis. Further studies on MYC dysregulation in leukemogenesis and therapy targeting MYC aberration are warranted.

PU-4267

贝克曼 Power Express 流水线血细胞分析人工智能审核的应用及规则验证

王东红、郭锐芳
长治医学院附属和平医院

目的 制定贝克曼 Power Expres（PE）血细胞分析流水线自动审核规则，并对自动审核系统进行验证。
方法 选取 1056 份乙二胺四乙酸二钾(EDTA-K2) 抗凝的静脉全血标本，在贝克曼 DXH800 上进行检测并对所有标本进行人工镜检，根据仪器检测结果及人工镜检结果对自动审核规则预期方案进行评估，另选取 21990 份标本结果使用自动审核软件(Remisol Advance Data Manager) 进行样本审核，统计自动审核通过率及未通过的样本构成；并对 1056 份样本采用自动审核软件和样本审核与全部采用人工审核的实验室内周转时间中位数及 90%位数进行对比。
结果 通过检测 1056 份标本，其中假阴性率为 0.85，低于国际血液学复检专家组要求的 5% 的最大允许范围。其假阴性主要集中于核左移、血小板聚集、有核红细胞及红细胞形态 4 个项目。用自动审核软件对 21990 份标本结果进行分析，通过自动审核的标本占 62.5% ，需人工审核确认的占 37.5% ，主要包括: 白细胞(WBC) 超出范围、红细胞平均体积（MCV）超出范围、血小板(PLT) 超出范围、HB 超出范围、未成熟粒细胞报警提示、原始细胞等仪器旗标报警。
结论 采用自动审核软件对样本审核可以确保较低的假阴性率，减少差错，大大提高检验医生的工作效率，缩短报告时间，提高了患者满意度。

PU-4268

重型和危重型 COVID-19 患者体内免疫细胞及细胞因子反应状况

林国跃[2]、宋玉霞[1]、舒占钧[1]、蔺志强[1]、何雯雯[1]、段丽[1]、赵豆豆[1]、何雪[1]、张蕊[1]
1. 新疆医科大学第八附属医院（新疆新冠肺炎医疗救治定点医院）
2. 解放军第 474 医院

目的 探讨新疆地区 COVID-19 不同临床分型患者体内炎性免疫细胞和细胞因子的反应水平及其临床意义。
方法 收集整理 2020 年 1 月 31 日-2 月 19 日在新疆维吾尔自治区第六人民医院定点救治的 46 例 COVID-19 患者临床与实验数据资料，按照《新型冠状病毒感染的肺炎诊疗方案》（试行第七版）诊断标准分型，总结 COVID-19 患者临床流调基线特征，分析比较患者病情严重程度时体内多种免疫细胞及细胞因子免疫状况。
结果 新疆乌鲁木齐市 COVID-19 流行病学特点以输入性汉族为主 40 例（87.0%），其他各民族也有感染，多为聚集性接触发病；COVID-19 患者的 CRP、PCT 和 WBC 检测结果在重症型和危重型组中比普通型组、疑似组明显的高，差异均具有统计学意义（P＜0.001），CRP 定量检测和 CRP 升高的病例数，WBC 计数和 WBC 计数降低病例数及 N 降低病例数在≥45 岁组明显高于＜45 岁组（P ＜0.05），而淋巴细胞百分率在 ≥45 岁组中明显低于 ＜45 岁组（P ＜0.05）；淋巴细胞亚群 CD3+T、CD4+T、CD8+T、CD45+T、CD4+T/CD8+T 和细胞因子 IL-4、IL-6、IL-10、IL-17、TN-α、INF-γ 6 项检测结果在重症型和危重型组中明显高于普通型及疑似组，组间比较存在显著差异（P ＜0.001）。
结论 实时监测 CRP、PCT、白细胞和淋巴细胞及细胞因子等指标对 COVID-19 临床病情严重程度具有明确的分型诊断作用；免疫细胞和细胞因子渐进快速升高可及时预警病情重症化发展与转归以及指导临床精准救治。

PU-4269

定点医院输血科救治危重症 COVID-19 患者输血保障作用

秦莹 1[1]、段丽 [1]、木尼热·库尔班 [1]、蔺志强 [1]、付玉华*[2]、李菲 [3]、陈苒 [4]、邓茜 [5]、林国跃*[1]
1. 新疆医科大学第八附属医院（新疆新冠肺炎医疗救治定点医院）
2. 新疆维吾尔自治区儿童医院输血科
3. 新疆维吾尔自治区人民医院输血科
4. 新疆维吾尔自治区第三人民医院输血科
5. 新疆维吾尔自治区第八人民医院检验科

目的 总结探讨定点医院输血科在保障新冠肺炎康复者血浆救治 COVID-19 危重症患者中的重要作用及保障能力。
方法 通过回顾性分析新疆第二波新冠疫情 1064 例新冠肺炎住院患者救治，99 例“临床快速发展型、重型和危重型”康复者恢复期血浆治疗创新性保障做法和一些有益经验，并统计分析。
结果 输血科分批接收来自武汉、大连、哈尔滨等国内支援的新冠康复者恢复期血浆 4 批次合计 122650ml，完成交叉配血 891 人次，ABO 和 Rh 血型鉴定各 1782 人次，不规则抗体 891 人次，临床发血 297 人次。对临床 99 例危重症 COVID-19 患者开展新冠肺炎康复者恢复期血浆的治疗以及 5 例血浆置换，共输注新冠康复者血浆 107250ml，平均每人 1083.33ml；乌市血液中心提供的新鲜普通冰冻血浆 39570ml，平均 399.7ml；红细胞悬液 144.5 单位，以及血小板 31 治疗量、冷沉淀 73.3 单位，免疫球蛋白 150 支的保障治疗任务；发生轻型输血反应 6 例，无严重输血不良反应；临床输血有效率 100%,治愈率达到 100%，总输血率达 9.31%（99/1064）。
结论 对 COVID-19 危重症患者使用康复者恢复期血浆和红细胞悬液救治输血科发挥了特殊时期重要的保障作用，保证了临床输血高效、及时和安全。

PU-4270

COVID-19 患者临床病情发展中重要血液学指标动态监测分析

林国跃 [1]、张弛 [1]、屈晓娟 [1]、宋玉霞 [1]、舒占钧 [1]、蔺志强 [1]、张蕊 [1]、秦莹 [1]、段丽 [1]、木尼热·库尔班 [1]、赵豆豆 [1]、何雪 [1]、王珂 [2]
1. 新疆医科大学第八附属医院（新疆新冠肺炎医疗救治定点医院）
2. 广东省广州市天河区黄埔大道石牌村广东省结核控制中心

目的 探讨 COVID-19 患者病程进展中体内血液细胞免疫动态变化及诊断意义。
方法 应用流式细胞等技术连续动态监测 COVID-19 住院患者外周血重要血液学免疫指标动态变化和心、肺、凝血功能等主要指标反应水平，统计比较分析。
结果 （1）连续监测入院当天、第 7 天、第 14 天、第 21 天、出院前的外周血象，结果白细胞、血小板系统所有血液学指标均有显著改变（$P < 0.05$）；其中白细胞入院第 7d 升高最大，出院前比入院当天要高；EOS 和 EOS% 在入院时最低，在第 21d 和出院前均升高明显；BASO 和 BASO% 在入院 14d 升幅最大；LYMPH 和 LYMPH % 在入院第 14d 与 21d 升高明显，且出院时明显高于入院时；MONO 及 MONO% 在入院 14d 升高最大，出院前高于入院当天。PLT 及 PCT (%) 在入院当天最低，在第 14d 升至最高；MPV (fL)及 PDW (fL)在入院时最高，出院时最低；NLR 和 PLR 在第 7d 最高，出院前已恢复到入院时水平。（2）WBC 在重症和危重型组中明显高于普通型、疑似组，并且在≥45 岁组明显高于＜45 岁组（$P<0.05$）；而中性粒细胞（%）在疑似组高于重症和危重型组，淋巴细胞百分率（%）在重危型组较低。（3）心功能指标 AST、ALT、LDH、CK 和 CKMB（除 cTnI、Myo 外），肺功能 PCO2、PO2 和 LAC，肾功能 UREA 和 CRE 和凝血功能 D 二聚体（DD）、PLT、FIB、TT、PT-INR、DD、PT-%和 PT-R（除 PT、APTT、TT 外）等重要指标在重型和危重型组明显高于在轻型组（$P<0.001$）；AT3 在轻型组显著高于重症和危重型组（$P<0.001$）。

结论 COVID-19 患者病情严重程度与血液学重要指标白细胞系统、血小板凝血系统关系密切，连续动态监测这些常见的免疫细胞指标变化对临床诊断、分型、病情预后判断等具有重要的指导作用。

PU-4271

血常规红细胞参数在贫血鉴别诊断的检验价值分析

张巍
郴州市第一人民医院

目的 分析血常规红细胞参数在贫血鉴别诊断的检验价值；
方法 此次研究对我院收治的 50 例贫血（贫血类型：地中海贫血 17 例，缺铁性贫血 33 例）患者进行诊断研究，并将同期 50 例体检者患者作为比较对象，分别纳入观察组和对照组，全部患者均取患者 2m1 静脉血，使用 EDTA 抗凝剂，使用全自动血液分析仪进行样本红细胞参数检测，比较两组红细胞参数结果，并对地中海贫血和缺铁性贫血患者红细胞参数进行分析；采用 SPSS21 软件进行统计学分析，计量资料采用均数±标准差表示，正态分布资料采用 t 检验，非正态分布资料采用秩和检验。组间样本率比较采用 X2 检验，采用 Logistic 回归分析对进行影响因素分析。均采用双侧检验，P<0.05 为差异有统计学意义。红细胞参数的预测价值通过受试者操作特征曲线（ROC 曲线）评估。
结果 观察组的血红蛋白 Hgb、红细胞平均体积 MCV、红细胞数量 RBC 低于对照组的血红蛋白、红细胞平均体积、红细胞数量，观察组的红细胞体积分布宽度 RDW 高于对照组，结果存在显著差异（P<0.05），地中海贫血患者的红细胞平均体积、红细胞数量和红细胞体积分布宽度高于缺铁性贫血患者，而血红蛋白低于缺铁性贫血患者，结果具有明显差异（P<0.05）；
结论 将血常规血红蛋白应用于贫血患者诊断中，可有效判断患者是否患有贫血，同时通过红细胞平均体积、红细胞数量和红细胞体积分布宽度等参数检验结果，利于进行贫血类型判断，该检验方式对患者贫血诊断具有指导作用。

PU-4272

PCT 与 CRP 联合检测对血流感染的诊断价值

黄津[1]、陈爽[2]
1. 天津市天津医院
2. 天津医科大学临床医学院

目的 探讨前降钙素（PCT）和 C-反应蛋白（CRP）在感染性疾病中的诊断价值，并观察两者联合监测对血流感染的诊断价值，为感染性疾病的早期、快速诊断提供科学依据。
方法 回顾性分析 2020 年 7 月 1 日至 2021 年 1 月 1 日在天津市天津医院进行治疗的 168 例疑似预防感染的患者病例资料，根据其血培养研究结果可以分为血培养试验阳性组和阴性组，其中血培养阳性组 71 例；血培养阴性组 97 例，同时收集血培养采集当天该患者血液标本中 PCT 和 CRP 浓度数据，采用 t 检验比较两个指标在两个实验组之间的差异，采用受试者工作特征曲线（ROC 曲线）分析每一个指标对血流感染诊断的应用价值。
结果 阳性组 CRP 和 PCT 水平分别为：（68.98±36.87）mg/L 和（18.15±28.18）ng/ml；阴性组 CRP 和 PCT 水平方面分别为：（17.51±16.67）mg/L 和（0.24±0.28）ng/ml，阳性组 CRP 和 PCT 水平均明显高于阴性组（P<0.05），CRP 诊断血流感染的敏感度为 77.5%、特异度为 93.8%、ROC 曲线下面积（AUC）为 0.811。血清中 PCT 水平诊断血流感染的敏感度、特异度、约登指数以及 AUC 分别为 84.5%、90.7%、0.752、以及 0.908；采用两者联合监测其敏感度、特异度、约登指数和 ROC 曲线下面积分别为 84.5%、97.9%、0.824、0.928，与单项检测相比(P<0.05),差异具有统计学意义。

结论 PCT 和 CRP 可作为感染性疾病的诊断指标，联合检测 PCT 和 CRP 可更快、更准确地早期诊断血流感染，从而有效、及时地指导临床合理用药。

PU-4273

Analysis of clinical application of automatic feces processing and analysis system FA280

Tingting Long[2]、Hong Jiang[1]
1. West China Hospital of Sichuan University
2. West China Hospital of Sichuan University

Objective To explore the application value of automatic feces processing and analysis system FA280 in routine feces inspection.
Methods The 904 routine results of fecal samples tested in FA280 in our laboratory were collected from April 20, 2020 to April 25, 2020. Combined with the review of manual identification images and the review of "direct smear microscopy", the clinical value of the automatic fecal detector was evaluated.
Results The instrument results of FA280 to identify the color and appearance of feces were consistent with manual results (Kappa value were 0.72 and 0.75, respectively). The detection rates of red blood cells, white blood cells, fungi and fat droplets reported by FA280 were all higher than the results of manual when recognizing the image information collected by the instrument, with the coincidence rates were 98.78%, 96.35%, 94.69% and 99.66%, respectively, and the Kappa values were 0.814, 0.718, 0.588 and 0.986, respectively. The sensitivity and specificity of FA280 for parasite detection were 88.89% and 87.93%, respectively, which were only 87.17% consistent with the artificial results, and the consistency is poor (Kappa value was 0.112). The coincidence rate between FA280 and the manual method was up to 99.78% when reading the results of occult blood reagent card, with very good consistency (Kappa value was 0.994).
Conclusion The results of automatic feces processing and analysis system FA280 are basically consistent with the results of manual identification in routine feces inspection, with a great clinical application value for sample screening.

PU-4274

Determination of plasma β-amyloids by rolling circle amplification chemiluminescent immunoassay for noninvasive diagnosis of Alzheimer’s disease

Danhua Wang、Yibei Dai、Xvchu Wang、Pan Yu、Shufang Qu、Lingyu Zhang、Ying Cao、Zhenping Liu、Ying Ping、Weiwei Liu、Zhihua Tao
the Second Affiliated Hospital of Zhejiang University School of Medicine

A rolling circle amplification chemiluminescence immunoassay (RCA-CLIA) was developed for precise quantitation of Aβ inplasma. Capture antibodies conjugated with magnetic beads and detection antibodies with collateral single-stranded DNA(ssDNA) were bound to Aβ42/Aβ40 antigens to form a typical double-antibody sandwich structure. The RCA reaction wastriggered by the addition of ssDNA, which generated products with a large number of sites for the binding of acridinium ester(AE)–labeled detection probes, thereby realizing the purpose of the amplification. The RCA-CLIA method had higher sensitivitythan conventional CLIA without loss of specificity. Under optimum conditions, the linear range of Aβ42 and Aβ40 detectionwas 3.9–140 pg/mL and 3.9–180 pg/mL, respectively, with corresponding low detection limits of 1.99 pg/mL and 3.14 pg/mL,respectively. Plasma Aβ42 and Aβ40 were detected in the blood of 21 AD patients and 22

healthy people, wherein this ratiocould significantly distinguish AD patients from healthy individuals with a sensitivity of 90.48% and specificity of 63.64% for acutoff value of 154. The Aβ42/Aβ40 ratio of plasma acts as an accurate indicator for AD diagnosis; therefore, detection ofplasma Aβ using the RCA-CLIA exhibits great potential in noninvasive diagnosis and progressive assessment of AD.

PU-4275

不同浓度诱导剂对血小板最大聚集率的影响

王宏
江苏省人民医院（南京医科大学第一附属医院）

目的 观察不同浓度的两种常用血小板聚集诱导剂二磷酸腺苷（ADP）和花生四烯酸（AA）对血小板最大聚集率检测结果的影响
材料与方法 收集阿司匹林用药者和正常人的枸橼酸钠抗凝标本，使用 Sysmex CS5100 全自动血凝仪检测血小板聚集率，两种诱导剂的浓度分别为：ADP 选择 2.0uM、2.5uM、5.0uM；AA 选择 0.5uM、1.0uM、1.5uM。
结果 不同浓度诱导剂对阿司匹林用药者的血小板聚集率影响很大，但是对于正常人不同浓度诱导剂影响很小。对于 ADP，5.0uM 和 2.5uM 相关性（R2=0.785）要高于 5.0uM 和 2.0uM（R2=0.585）。对于 AA，1.5uM 和 1.0uM 相关性（R2=0.895）要高于 1.0uM 和 0.5uM（R2=0.700）。
结论 血小板最大聚集率结果和所选择的诱导剂浓度有关。

PU-4276

微流控模型对血栓形成的研究

林晶英
成都上锦南府医院

目的 本研究旨在通过查阅与体外微流控技术及动脉血栓相关的文献，研究血栓形成与血管几何形状和剪切力变化的血流动力学关系，对比总结 2D 与 3D 打印微流控模型的区别及优缺点，同时对微流控模型在血栓形成等方面的应用研究进行详细叙述。
方法 使用 PubMed 和知网数据库检索了 2007 至 2021 年的中英文文章，截至 2021 年 5 月，所有搜索均为最新。使用的搜索词包括“microfluidic”、“platelet aggregation”、“剪切力”、 “动脉血栓”等。
结果 经查阅文献发现，目前较为常见的 3D 打印技术主要有微立体光刻、双光子聚合效应、基于数字光处理 3D 打印技术及熔融沉积技术等，有着体积小、速度快、成本低及通量高等特点。通过模拟健康血管和狭窄冠状动脉的微流控模型发现，血小板聚集通常发生在狭窄顶部及血栓形成下游的低剪切区，聚集体的稳定依赖于膜系绳的动态重组。此外，稳定的盘状血小板聚集在血栓形成中起主要作用，而可溶性激动剂在血小板聚集的不可逆阶段起次要作用。微流控技术可广泛应用于多个方面，在动脉血栓方面可研究血栓形成的原理及形成的预测，在血小板聚集方面得出血小板聚集程度与剪切微梯度的大小密切相关。血小板黏附功能方面发现血小板系绳形成是一个动态的过程，包括初始形成、伸长和收缩重构的不同阶段。血凝块力学分析方面发现，通过控制、测量组织形成，可以在血管内剪切微梯度存在的情况下再现凝块形成的动态过程，并实时监测凝块力学的性质变化。在剪切力研究方面，剪切力的变化会导致血小板的激活聚集以不同方式出现。抗血栓药物的选择方面，可利用微流控技术筛选评估各类药物疗效。

结论 微流控技术的出现，极大地促进了对血栓形成的研究，而决定血栓形成的因素主要在于流体流速梯度、微小的再循环、固有的凝血途径和剪切率的增加等。对比总结国内外 3D 微流控模型的研究发现，微流控技术有着广泛的应用范围。

PU-4277

血栓弹力图评估肝癌患者手术前凝血状态的临床研究

王浩
天津市肿瘤医院（天津医科大学肿瘤医院）

目的 应用血栓弹力图(thrombelastogram，TEG) 评估肝癌患者手术前凝血状态。
方法 选择 2020 年肝癌手术的患者 100 例作为手术组，同时选取同时期入院进行体检的健康人 50 例作为对照组，比较术前手术组和对照组患者术前常规凝血四项和 TEG 指标，包括凝血酶原时间（PT）、活化部分凝血活酶时间（APTT）、纤维蛋白原（FIB）、凝血酶时间（TT）、血凝时间（R 值）血块形成时间（K 值）血凝速率（a）和血块强度（MA）。
结果 手术组和对照组 R 值相比，差异无统计学意义（P>0.05）。手术组的 K 值显著低于对照组（P<0.05），a 和 MA 显著高于对照组（P<0.05）， TEG 图像显示 手术组 100 例肝癌患者中 73%的肝癌患者为高凝状态，5%的患者表现为低凝状态。凝血四项结果显示手术组 100 例肝癌患者中 35%的患者表现为高凝状态。
结论 肝癌患者的血液多数处于高凝状态 TEG 和凝血四项均能对肝癌患者手术前血液的高凝状态进行分析，血栓弹力图(TEG)更为敏感。

PU-4278

肺癌患者 AB0 血型、血管性血友病因子及血栓风险的关联

葛鹏
天津医科大学肿瘤医院

目的 探讨肺癌患者血浆 vWF 水平与 O 型/非 O 型血以及血栓风险的关联性。
方法 回顾性分析 2017-2018 年天津市肿瘤医院收治的 82 例肺癌患者、17 例正常健康者的血凝常规指标 vWF、D-D 含量以及 CEA、C19-9 浓度。采用两独立样本资料的 t 检验分析比较两组研究变量的差异。再将病例组和对照组按血型分为 O 型血和非 O 型血，分析比较两组 vWF 是否有差异。
结果 病例组的肺癌患者 D-D、vWF 水平高于健康对照组，结果有显著性差异，P<0.05.病例组和对照组中的非 O 型血人 VWF 水平高于 O 型血人，P<0.05. 病例组中的肺癌患者 vWF 水平高于对照组，其 CEA、CA19-9 水平亦高于正常人，P<0.05。
结论 肺癌患者比正常健康人患血栓的风险更高，非 O 型血的人存在血浆中 vWF 水平升高的风险。而 vWF 水平升高容易导致肺癌的发生和转移。

PU-4279

Electrophoresis- and dialysis-based method for isolating serum derived extracellular vesicles

Meng Yang、Fuxiang Chen
Shanghai Ninth People's Hospital, Shanghai JiaoTong University School of Medicine

Objective There are tremendous scientific and clinical interests in extracellular vesicles (EVs) for cancer diagnosis and therapy over the past decades. Isolation of EVs is the prerequisite for

downstream researches. In this paper, electrophoresis was combined with molecular weight cut-off (MWCO) of 300 kDa dialysis bag (named ELD) for serum EVs isolation.
Methods Under electric field, the particles of biological fluids were endowed with different mobility depending on their sizes and charges. With 300 kDa dialysis tubing, contaminant biomolecules passed through the membrane. The fresh electrophoresis buffer was changed, and electric direction was reversed per 30 min for avoiding membrane pore blocked by EVs.
Results Using ELD, we could isolate serum derived EVs, which were characterized with western blot, nano sight, transmission electron microscopy (TEM). Then, we compare the protein content of serum derived EVs isolated by ELD and ultracentrifugation (UC), and the results indicated that ELD has 140 proteins common with UC which contributed 74% (140/188), and 84% (140/ 165) of total proteins respectively. To demonstrate the application of the ELD method in cancer diagnosis and therapy, we selected the following two cases: microRNA-155 derived from serum EVs was used for oral squamous cell carcinoma (OSCC) diagnosis, and data indicated the area under a receiver operating characteristic (ROC) curve is 0.7592 compared with 35 healthy control and OSCC patient.
Conclusion ELD is a robust method for the isolation of serum derived EVs isolation and will have extensive applications in the growing field of EVs.

PU-4280

超敏 C 反应蛋白和纤维蛋白原在急性冠状动脉综合症患者的水平研究

范小斌
广东省人民医院

目的 探讨急性冠状动脉综合征患者血清超敏 C 反应蛋白(hs-CRP)和纤维蛋白原(FIB)血浆水平测定及临床意义。
方法 选取我院 56 例急性冠状动脉综合征患者、51 例稳定型心绞痛患者、50 例健康正常人（对照组）作为研究对象。通过免疫比浊法测定各组 hs-CRP 和 Clauss 磁珠法测定 FIB 水平作比较。
结果 急性冠状动脉综合征患者血清 hs-CRP 和血浆 FIB 水平显著高于稳定型心绞痛患者组及对照组。急性冠状动脉综合征患者血清 hs-CRP 和 FIB 呈正相关性。
结论 hs-CRP 和 FIB 可以作为急性冠状动脉综合征事件的指标。

PU-4281

某三甲医院三年住院患者肠道寄生虫检出状况回顾调查

谢恒
四川大学华西医院

目的 通过对四川大学华西医院 2017—2020 年住院病人大便常规寄生虫检出情况的回顾性分析，了解四川地区乃至西南地区的肠道寄生虫感染情况，为有效预防和控制肠道寄生虫感染提供实验室数据。
方法 对 2017 年-2020 年四川大学华西医院住院病人的大便常规寄生虫检查阳性的病例进行记录，统计肠道寄生虫的检出率和各感染虫种的检出率。同时收集患者的血常规结果，观察钩虫感染患者贫血相关参数的变化以及蠕虫感染患者嗜酸性粒细胞计数的情况。
结果与讨论 1 肠道寄生虫感染的总检出率是 0.64 %；各虫种的检出率分别为：钩虫卵检出率 0.34% 占比 53.8%；人芽囊原虫检出率 0.12%占比 19.02%；蓝氏贾第鞭毛虫包囊检出率 0.07%占比 10.32%；肝吸虫卵检出率 0.05%占比 7.6%；带绦虫卵检出率 0.03%占比 4.89%；结肠内阿米巴包囊检出率 0.01%占比 2.17%；鞭虫卵检出率 0.01%占比 1.63%；蛔虫卵检出率 0.004%占比 0.54%。

2.感染病例的年龄段分布主要集中在 50-79 岁之间；女性占 48%，男性占 52%。
3 钩虫贫血特点呈低色素小细胞贫血，本次调查钩虫感染患者的红细胞检查参数中血红蛋白降低者占 62.6%；红细胞计数降低者占 66.7%；55.5%感染者平均红细胞压积降低；平均红细胞体积(MCV)降低者占 20.2%。由于钩虫病贫血程度与感染轻重相关，所以红细胞相关参数可作为感染程度的参考指标。
4 肠道蠕虫感染患者中嗜酸性粒细胞升高者占 16.7%，大多数感染者该指标在参考范围内，故嗜酸性粒细胞升高是否能作为蠕虫感染有价值的参考指标还有待商榷。
结论 我国人口基数巨大，即使感染率不高，但总体感染人数依然庞大。寄生虫病作为危害我国居民身体健康重要公共卫生问题，加强对寄生虫病防治宣传和教育，定期开展寄生虫病调查是非常必要的。

PU-4282

婴幼儿末梢血稀释样本放置时间对血细胞分析结果的影响

谢曦
天津医科大学朱宪彝纪念医院

目的 了解婴幼儿末梢血稀释标本放置时间对血细胞分析结果的影响，降低婴幼儿采血量少对检验工作所带来的不便，为临床提供可靠数据。
方法 选取 2018 年 8 月到 2019 年 3 月期间天津医科大学第二医院 50 例 0-5 岁患儿末梢血，按照一定比例（1：7）与稀释液混匀，在室温下（20-25℃）分别于即刻,10 分钟，30 分钟，60 分钟，2 小时用 Sysmex XN1000 分析仪在预稀释模式下检测各血细胞值，利用 t 检验进行统计学分析。
结果 室温下，随着婴幼儿末梢血稀释标本放置时间的延长，血红蛋白(HGB)、平均红细胞体积（MCV)、平均血红蛋白含量（MCH）、平均血红蛋白浓度（MCHC）略有变化，但无统计学意义(P＞0.05)，白细胞(WBC)、红细胞(RBC)在 2 小时有统计学意义(P<0.05)血小板(PLT)、血小板压积(PCT)、平均血小板体积（MPV），各参数差异均有统计学意义(P<0.05)。
结论 婴幼儿末梢血稀释标本在室温下放置时间长短对血常规检测中的一些参数有影响，尤其是 PLT 相关（PCT、MPV）的指标差异较大。合理安排时间，减少婴幼儿稀释末梢血放置时间对血常规的影响，应在 10-60 分钟内完成测试。

PU-4283

迈瑞血细胞分析仪检测全血超敏 CRP 方法的性能评价

孙召东
江苏省连云港市第一人民医院

目的 对迈瑞 BC-5390 CRP 血细胞分析仪检测超敏 CRP 结果的性能评价
方法 对超敏 CRP 的精密度和携带污染率进行评价，同时评价溶血程度及红细胞压积变化对超敏 CRP 检测的影响，并对迈瑞血细胞分析仪检测超敏 CRP 结果与 beckman coulterImmage800 特定蛋白仪的超敏 CRP 结果过进行比对
结果 血细胞分析仪检测超敏 CRP 的批内精密度分别为 2.02（=3.8mg/l）和 1.83(=43.5 mg/l) ；批间精密度分别为 2.45（=6.0mg/l）和 2.01(=44.2mg/l)，携带污染率为 0.08%；溶血对超敏 CRP 的检测的影响，轻度溶血(HGB=6g/L)偏差为 2.2%，中度溶血(HGB=12g/L)偏差为 5.4%，重度贫血(HGB=23g/L)的偏差为 11.8%；高红细胞压积（HCT>50%）标本和低红细胞压积（HCT<30%）标本与正常红细胞压积（30%<HCT>50%）标本检测全血超敏 CRP 的结果偏差在允许的范围之内；血细胞分析仪全血超敏 CRP 与特定蛋白检测血清超敏 CRP 的回归曲线是 y = 1.1186x - 0.4142，

相关系数 R2= 0.9908，具有良好的相关性，医学决定水平处，两者的结果偏差均在允许的范围之内。
结论 血细胞分析仪检测全血超敏 CRP 的性能够满足临床使用要求，结果与血清超敏 CRP 有良好的一致性，且不受到红细胞压积的影响，但要重度溶血对全血超敏 CRP 检测有影响，因此应该避免溶血标本。

PU-4284

进入西藏高原人群血常规参数的调查研究

史清海[1]、米哲[2]
1. 新疆军区总医院
2. 陆军第 957 医院

目的 高原自然环境的主要特点是低压缺氧、高寒，对人体血细胞的生成与功能将产生极大影响。本研究目的是调查进入西藏高原人群静脉血血常规参数指标的变化情况，为科学保障进藏人群健康提供依据。
方法 选取不同时段进入海拔 4300 米西藏高原的 5717 名人群作为调查对象，进入高原时间为 6-8 个月，同时选取平原人群 2820 例作为对照组，分别空腹采集静脉血，进行血常规检测并进行统计学分析。
结果 与平原人群比较，进入高原 8 个月后静脉血白细胞计数(WBC10^9/L)6.55±2.12、中性粒细胞计数(NEUT10^9/L)3.51±1.98、红细胞计数(RBC10^12/L)5.97±0.70、血红蛋白(HGBg/L)192.1±18.9、红细胞压积(HCT%)56.7±6.7 均上调，结果均有统计学差异。
结论 高原低氧环境显著增加人体血液红细胞数量和血红蛋白含量，增加程度与海拔高度、进驻高原时间有关；中性粒细胞数量增加，表明机体存在应激或炎症反应。

PU-4285

Establishment of reference intervals for the systemic immune-inflammation index, neutrophil to lymphocyte ratio, platelet to lymphocyte ratio and lymphocyte to monocyte ratio in healthy adults in Eastern China: a multi-centre study

Fumeng Yang、Qian Liu
The Second People's Hospital of Lianyungang

Background We preliminarily established the reference intervals for the systemic immune-inflammation index (SII), neutrophil to lymphocyte ratio (NLR), platelet to lymphocyte ratio (PLR) and lymphocyte to monocyte ratio (LMR) in healthy adults in Eastern China to guide the interpretation and application of these indicators in clinical practice.
Methods In total, 29,947 ostensibly healthy subjects (five regions) from December 2020 to March 2021 were included in this study. The distributions of the SII, NLR, PLR and LMR were analysed using the Kolmogorov-Smirnov test. According to the C28-A3 guidelines, the 2.5th and 97.5th percentiles (P2.5 to P97.5) of the SII, NLR, PLR and LMR were used to establish the reference intervals based on nonparametric Methods
Results All SII, NLR, PLR and LMR data were non-normally distributed. The levels of the SII, NLR, PLR and LMR in healthy adults were significantly different between males and females (all $P<0.05$). However, there were no significant differences in the SII, NLR, PLR or LMR among the different age groups, regardless of sex (all $P>0.05$). Therefore, the reference intervals for the SII,

NLR, PLR and LMR were established based on the Sysmex testing platform for males (162×109/L~811×109/L; 0.89~3.26; 63.15~191.34; 3.18~9.61) and females (165×109/L~792×109/L; 0.87~3.16; 69.04~205.62; 3.46~10.96).
Conclusions Reference intervals for the SII, NLR, PLR and LMR in adults in Eastern China were established based on the Sysmex detection platform and Big Data. It will be beneficial to promote the inclusion of these parameters in conventional complete blood count (CBC) reports and their widespread use in clinical practice.

PU-4286

C57 小鼠外周血单个核细胞 MHC 表达与 Lewis 肺癌发展关系的研究

景丽萍、庄学伟
山东省立第三医院

目的 通过动物实验探讨以外周血单个核细胞 MHC 为代表的宿主 MHC 表达在肿瘤发展和转移中的作用以及 Th1/Th2 漂移与肿瘤的相关性。
材料与方法 50 只 C57BL/6J 纯系小鼠随机分为：A 组即正常对照组，B 组即荷瘤对照组，C 组即环磷酰胺组+荷瘤组,D 组即干扰素-γ+荷瘤组，E 组即荷瘤+干扰素-γ 组。用药前采用流式细胞仪测外周血淋巴细胞表面 H-2Ks 和 H-2Db 表达。然后对 C 组和 D 组分别腹腔注射环磷酰胺和干扰素-γ7 天，其余两组用等量生理盐水。再测外周血淋巴细胞表面 H-2Ks 和 H-2Db 表达后，接种 Lewis 肺癌细胞株，C 组和 D 组停药而改用等量生理盐水，同时 E 组开始腹腔注射干扰素-γ7 天。14 天后处死再测外周血淋巴细胞表面 H-2Ks 和 H-2Db 表达；用 ELISA 法测各组各时期血浆细胞因子 IL-2、IL-4、TNF-α。
结果 ①环磷酰胺和干扰素-γ 影响小鼠外周血淋巴细胞 H-2Ks 表达。②接种肿瘤后，环磷酰胺组瘤重明显重于对照组，有显著差异（P<0.01）；干扰素及治疗组瘤重明显轻于对照组，有显著差异（P<0.01）。③接种肿瘤后，与接种对照组相比，环磷酰胺组肺转移灶数明显多于对照组，有显著差异（P<0.01）；干扰素组及治疗组肺转移灶数无显著差异（P>0.05）④接种肿瘤后，Th1 型细胞因子（IL-2）降低和 Th2 型细胞因子（IL-4）升高，TNF-α 显著升高（P<0.01）。
结论 肿瘤发生前宿主 MHC 状态与肿瘤发生发展密切相关，宿主 MHC 表达下降促进肿瘤的生成进展，宿主 MHC 表达增强时，肿瘤形成、发展和转移受到抑制。肿瘤发生后，Th1/Th2 模式向 Th2 漂移，机体的抗肿瘤免疫应答受抑制。

PU-4287

尿液手工方法与仪器分析的优劣

刘琰、王琳琳
哈尔滨医科大学附属第一医院

目的 手工法检验尿常规结果分析，进一步了解分析仪和传统的显微镜手工法在尿液分析中的优缺点，使检验工作者在实际工作中正确对待两种方法的应用，指导检验人员科学地把两种结合起来。
方法 我们对 500 份尿样分别用两种方法进行检测对其结果分析，一种方法用尿液分析仪检测记录尿蛋白、白细胞、红细胞结果，微量以上为阳性，微量以下为阴性。另一种方法用加热醋酸法检测尿蛋白，再用离心试管取 10 ml 混匀的尿液以 1 500 r/min 离心 5 min，倾去上清液，留取 0.2 ml 沉渣，涂片镜检，记录尿蛋白、红细胞和白细胞结果，微量以上为阳性，微量以下为阴性。

结果 分析仪检测尿蛋白和白细胞的阳性率（8.85%和 10.20%）不及手工法阳性率（9.10%和11.85%）高，但分析仪检验红细胞的阳性率（11.85%）高于手工法红细胞阳性率（9.80%）。阳性结果不能相吻合，两种方法虽然存在一定的差异，但经统计学处理（P>0.05）差异无显著性。
结论 结果说明两种方法均可为临床使用。分析仪检测尿蛋白阳性率低于手工法阳性率，分析仪检测白细胞阳性率不如显微镜检测尿中白细胞阳性率高。但分析仪对尿中红细胞的检测比显微镜阳性率高。两种方法合理应用，取长补短，以便为临床疾病的诊断和治疗提供正确检验结果。

PU-4288

外伤患者血细胞参数的指导意义

王琳琳、鲁平
哈尔滨医科大学附属第一医院

目的 由于创伤急救技术的不断提高和急救系统不断完善，严重创伤患者伤后急速病死率已明显下降，但是伤后危及生命的并发症的发生率和各种伤残率却无明显减少。正确判断多发伤患者的创伤严重程度和预后是目前危重病医学领域中创伤诊治方面所面临的一个重要课题，亦是进一步降低多发伤患者病死率的关键。本研究试图通过观察多发伤患者外周血血细胞参数的动态变化,探讨其在多发伤发生、发展及预后中的作用。
方法 多发伤患者 34 例，于创伤后 24h 内采集静脉血，作为第 1 天标本，并分别在入院后的第 3 天和第 7 天清晨空腹采血。工作特征曲线(ROC 曲线)分析曲线下面积(AUC)；AUC 0.5～0.7 诊断价值较低，0.7～0.9 中等诊断价值，0.9 以上有较高诊断价值。采用 SPSS 11.5 统计软件，数据以(x±s)表示，多组均数间的比较采用单因素方差分析。
结果 本研究显示，WBC、HB、PC/WBC 比值在第 1、3、7 天差异有显著性，另外，PC/WBC 比值均数逐步上升。本研究利用 ROC 曲线下面积评价外周血血细胞参数在评估多发伤患者预后不良时的准确性，结果显示，PC/WBC 在第 3 天 AUC 为 0.820 (0.634～1.006)，第 7 天为 0.948 (0.844～1.051)
结论 应用血细胞参数对创伤患者进行评价具有广阔的前景。并且观察 PC/WBC 在第 3 天和第 7 天的 AUC 对临床诊疗具有较高的应用价值。

PU-4289

尿沉渣细胞学检测方法与仪器分析的对比

王琳琳、徐海燕
哈尔滨医科大学附属第一医院

目的 临床上最常用的重要的检测项目之一，主要用于泌尿生殖系统疾病、肝胆疾病、代谢性疾病及其他系统疾病的诊断和鉴别诊断、治疗监测及健康普查。干化学分析仪已广泛应用于临床，流式技术的沉渣分析仪也逐步应用于临床。本文探讨流式尿沉渣定量分析仪、Clinitek 200 尿干化学分析仪、涂片显微镜镜检进行对照研究。
方法 我院来诊患者随机 200 例，用一次性洁净尿杯收集患者尿液 15 ml 左右，先进行尿干化学测定，再进行涂片显微镜镜检，最后做尿沉渣定量分析(用双盲法判读)，操作由丰富临床经验的专业技术人员在 1 h 内完成。流式尿沉渣定量分析仪测定红细胞(RBC)、白细胞(WBC)的正常值为 RBC 0 个/μl~1 个/μl，WBC 0 个/μl~3 个/μl，Clinitek 200 尿干化学分析仪 RBC、WBC 正常值为阴性，涂片显微镜镜检正常值为 RBC 0 个/μl~1 个/HP，WBC 0 个/μl~2 个/HP，超出正常值范围则视为阳性。
结果 三种方法检测 RBC、WBC 的检出率较一致，对 RBC 而言检出率高低分别为 Clinitek 200＞sysmex1000i>涂片镜检，对 WBC 而言检出率高低分别为 sysmex1000i ＞Clinitek 200＞涂片镜检。

结论 在临床应用上把 3 种方法有机地结合起来，干化学的快捷简便和流式沉渣定量的准确性及自动化、手工镜检的金标准，从而可增加检测结果的敏感度和准确性，为临床对泌尿系、循环系、内分泌系的清晰鉴别诊断、疗效观察及预后观察提供可供参考的实验数据。

PU-4290

脑脊液脱落细胞学在恶性黑素瘤脑转移瘤诊断中的价值

许志宇
复旦大学附属华山医院

脑脊液脱落细胞学在脑恶性肿瘤的细胞学诊断中具有较高特异度和灵敏度，而脑脊液细胞离心涂片技术的应用，再配合细胞免疫化学染色的筛选，使脑恶性肿瘤的诊断更具有诊断明确、高效等优势，值得临床应用的推广。

回顾分析一例复旦大学附属华山医院一例恶性黑色素瘤脑转移病人的脑脊液脱落细胞学，从临床病史以及其他实验室检查，确定患者颅内脑积水，蛛网膜下腔异常信号，在主治医生经验抗病毒、抗结核治疗无效后，送检一份脑脊液细胞学检查，在使用脑脊液细胞离心涂片技术后，能够将脑脊液中数量并不多的恶性肿瘤细胞或异型细胞聚集涂片，增加脑脊液细胞学检查阳性率。配合瑞氏染色，通过观察异性细胞形态及数量，可寻找出恶性黑色素瘤细胞特有的异型细胞胞浆中中等或大量的黑色素颗粒，再使用其他细胞免疫化学染色后，可观察出该类异型细胞 HMB45 染色阳性，S100 染色阳性，为临床缩小诊断方向。配合临床身体检查及脑脊液二代测序，明确诊断，积极治疗。

脑脊液脱落细胞学对于脑膜癌，脑转移癌等易脱落的脑部肿瘤，具有较高的敏感性、特异性和选择性，同时具有安全性、快速性，配合脑脊液脱落细胞流式细胞术、脑脊液肿瘤标志物等检测，能够有助于提高诊断的阳性率和鉴别能力

PU-4291

Use of mean reticulocyte volume improves the accuracy in diagnosing iron deficiency in pregnant women

Fengfeng Zhao
Department of Clinical Laboratory of Zhongda Hospital, Southeast University

Objective To evaluate the application value of mean reticulocyte volume (MRV) in diagnosing iron deficiency in pregnant women.
Methods (1) 20 healthy volunteers were selected to test MRV on the 1st, 4th, 7d,15d,21d and 30d. (2)282 cases of iron deficiency pregnant women (the study group) and 442 healthy pregnant women (the control group) were selected from our hospital to test the levels of mean reticulocyte volume (MRV), reticulocyte hemoglobin equivalent (RHE), red blood cell volume distribution width-standard deviation (RDW-SD) , mean corpuscular volume (MCV), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC) and serum ferritin(SF) (SF < 12μg /L as the basis for the iron deficiency).
Results (1) Compared with the 1st, the level of 20 healthy volunteers MRV had no significant difference on the 4th, 7d,15d,21d and 30d (the value of T test respectively is 0.544、1.644、1.482、1.482、1.239, P > 0.05). (2) MRV, RHE, RDW-SD , MCV, MCH, MCHC, and HCT of the two groups had significant differences(the value of T test respectively is 16.971, 16.829, 7.356 ,7.367, 7.807, 4.726, 3.659, P < 0.01). The area under the Receiver Operating Characteristic (ROC) curve respectively is 0.840, 0.837, 0.676, 0.654, 0.639, 0.602,0.571.
Conclusions MRV is a very stable incidence in healthy people, and has a much higher application value for diagnosing iron deficiency in pregnant women.

PU-4292

血液分析仪 XN-2000 中高荧光强度有核细胞对胸、腹腔积液性质的鉴别价值

俞萍丽
福建医科大学附属协和医院

目的 探讨血液分析仪研究参数中高荧光强度有核细胞（HF）对浆膜腔积液肿瘤细胞的筛选效能。
方法 收集本院胸腹腔积液标本 48 例，经仪器检测后收集其 WBC（白细胞总数）、MN %（单个核细胞百分比）、PMN%（多个核细胞百分比）、TC-BF（有核细胞总荧光强度）、HF-BF%（高荧光强度有核细胞百分比）和 HF-BF#（高荧光强度有核细胞绝对值）几个指标，运用两均数比较的 t 检验、独立样本的 U 检验，结合受试者工作特征曲线（ROC）[1]分析二分类变量指标对良恶性积液的鉴别价值。
结果 对积液性质的判别中，WBC、MN%、和 TC-BF 的差异不具有统计学意义（P>0.05）,而 HF-BF#、HF-BF%和 PMN%的差异具有统计学意义（P<0.05）。ROC 曲线分析表明 HF-BF#和 HF-BF%对鉴别积液性质诊断效能较好，PMN%对鉴别积液无诊断效能。对预测概率做 ROC 曲线分析，得到 HF-BF#的曲线下面积(AUC)为 0.813，P<0.05，灵敏度为 0.652，特异性为 1.00。得到 HF-BF%的 AUC 为 0.786，P<0.05，灵敏度为 0.826，特异性为 0.760。两种模型均体现出一定的诊断效能。
结论 在体液模式下，XN-2000 中 HF-BF#和 HF-BF%对积液中肿瘤细胞具有较为良好的筛查效能。

PU-4293

血液学指标在福建地区 α-地中海贫血筛查中的价值

谢屿平、曹颖平
福建医科大学附属协和医院

目的 分析福建省不同地区 α-地中海贫血（α 地贫）的基因类型与构成比，比较相应的血液学表型特征，探讨平均红细胞体积（MCV）、平均红细胞血红蛋白量（MCH）、血红蛋白量（Hb）、红细胞分布宽度/红细胞计数（RDW/RBC）对该地区 α 地贫初筛的价值。
方法 通过 Gap-PCR 法检测 α 地贫缺失型突变，反向点杂交法检测非缺失型突变位点，对 α 地贫基因型进行分型确定，并分析确诊的 α 地贫患者血液学数据，通过分析 ROC 曲线确定本地区 α 地贫的最佳截断值，分析血液学指标在 α 地贫中的筛查价值。
结果 纳入的 772 例 α 地贫患者中，共发现 16 种基因突变类型，以--SEA/αα 缺失型突变 521 例最为常见（67.49%）。与对照组相比，同性别不同分型的患者 MCV、MCH、Hb 之间的均值差异均有统计学意义，而 RDW/RBC 值在男性患者中标准型和 HbH 病 2 组与对照组相比差异有统计学意义，女性 α 地贫患者中仅有 HbH 病组与对照组差异有统计学意义。MCV<81.25 fl、MCH<27.30 pg、Hb 男性<128.5 g/L， Hb 女性<123.5 g/L 为本实验室 α 地贫的最佳截断值，具有较高的特异性与敏感性。
结论 由于地域异质性以及各个医院设备环境的不同，不同实验室应建立适宜本地区的 α 地贫初筛截断值。今后本实验室可选择 MCV<81.25fl、MCH<27.30pg、Hb 男性<128.5g/L、Hb 女性<123.5g/L 作为临床筛查 α 地贫初筛值。

PU-4294

对 Beckman Coulter 型号流式细胞仪的电压监测、管理及优化

董敏
四川省医学科学院·四川省人民医院

目的 通过监测 Beckman Coulter 的电压，达到对此仪器重要部分的管理。
方法 取一支干净试管，加入 0.5ml 蒸馏水，再加入 10 滴贝克曼公司提供的 Flow Check 粒子，于涡旋器上振荡混匀，配置成一定浓度的 Flow Check 悬液。配好后，置于暗盒中，避光，并置于 4℃冰箱冷藏保存（最长放置时间不超过 1 周）。每日于 Beckman Coulter 开机稳定后，拿出配置好的 Flow Check 悬液，置于室温半小时复温，再于涡旋机混匀后，上机。监测流速、各个通道的电压等指标，连续监测两周后，发现微粒流速变化差异较大，且时快时慢，分析后排除 Flow Check 浓度对流速的影响。考虑可能是仪器压力阀故障或者样品针内壁老化所致。与工程师商讨后，首先进行了压力阀的更换。采用上述方法继续监测微粒的流速，在监测两日后发现流速依旧波动，且个别检测项目用低速模式根本无法检测，在用清洁液冲洗后，在低速模式依旧测不出 Flow Check 悬液的流速。在此基础上更换了一根全新的样品针，继续上述方法监测。
结果 监测至今，Flow Check 悬液的流速可稳定在厂家提供的参考范围内。
结论 稳定的微粒流速与稳定的电压密切相关，甚至可影响阴性、阳性细胞群体分群在流式分析图中的展示。所以电压的监测及管理在日常检测中是非常基础且重要的。

PU-4295

对流式技术检测个别项目中抗体用量优化的尝试

董敏
四川省医学科学院·四川省人民医院

目的 适当减少检测细胞免疫功能计数中的抗体用量，可在一定程度上节约成本。
方法 按照细胞免疫功能检测标准方案，准备 10 支干净流式检测试管，分为 5 组，编号为 1A、1B、2A、2B……5A、5B，按顺序放在试管架上。在所有带有”A”编号的试管中加入复合抗体 CD3/CD4/CD8/CD457.5ul，在所有带有”B”编号 CD16/CD56/CD457.5ul，再分别加入 5 组相对应的全血样本，用量均为为 25ul，避光孵育 15min 后，取出试管架，在每支试管中加入提前配置好的溶血剂（迈瑞公司的商品化溶血剂 50ml 加入至 450ml 灭菌用蒸馏水中，使其充分混匀），使红细胞溶解，避光静置 5min 后上机检测，分析数据，作为标准的检测结果。然后依次减少抗体用量，分别设置梯度为 7ul、6.5ul、6ul、5.5ul、5ul，按照上述同样方法孵育、检测、分析。
结果 对加入不同用量抗体的每组样本做统计学分析（成对 T 检验方法），发现当抗体用量为 6.5ul、6ul、5.5ul 时，与标准方案相比，淋巴细胞计数值的差异没有统计学意义（$t<0.05$）（小样本量），考虑此时抗原抗体的结合都达到了饱和或过饱和程度，从成本优化的角度选择抗体用量为 5.5ul 的组别。
结论 在进行细胞免疫功能检测时，抗体用量可从最初用量 7.5ul 减至为 5.5ul，且在不影响最终结果的基础上适当降低了成本。

PU-4296

基于白细胞群落参数机器学习模型鉴别诊断活动性结核病与潜伏性结核的研究

邓少丽、孙婷婷
陆军特色医学中心（大坪医院）

背景 结核病是严重危害人类健康的重大传染病，现有的结核实验室诊断尚不能满足临床需求，临床广泛开展的 γ-干扰素释放试验（IGRAs）对结核杆菌感染具有较高的灵敏度和特异性，但不能鉴别潜伏性结核感染者和活动性结核，机器学习和深度学习方法在结核病的诊断中体现了巨大的潜力和优势。
目的 白细胞群落参数（cell population data ,CPD）是血细胞分析仪测量分析而来的不同类型白细胞体积、导电率及各角度光散射参数，我们前期结果提示，结核患者中 CPD 参数中单核细胞相关指标变化最为明显，单核细胞联合淋巴细胞、中性粒细胞 CPD 参数还可用于鉴别影像学难以区分的肺结核、肺炎及肺癌。我们拟基于 CPD 参数采用机器学习算法，建立鉴别诊断活动性结核病与潜伏性结核的模型，提高鉴别诊断准确率。
方法 纳入活动性结核患者、潜伏性结核感染者及健康对照组各 300 例，收集 CPD 数据（每例样本收集中性粒细胞、淋巴细胞、单核细胞等 70 项 VCS 参数），分别采用利用 Python 基于 logistic 分析、支持向量机（SVM）分类器、随机森林(RF)模型和最邻近分类算法（KNN）的机器学习算法，将各组随机选取 70%数据作为训练组，30%数据作为测试组，分别建立四种机器学习的结核病诊断模型，分析四种经典算法的鉴别准确率。
结果 四种经典机器学习法鉴别鉴别诊断活动性结核病与潜伏性结核的准确率都达到 85%以上。其中基于 logistic 分析的准确率最高，达到 93.65%。SVM 分类器、RF 模型和 KNN 机器学习算法的准确率分别为 88.88%，88.88%和 87.30%。
结论 机器学习模型对鉴别诊断活动性结核病与潜伏性结核有较高准确率，且诊断时间短，可用于辅助临床鉴别诊断结核病。

PU-4297

粪便钙卫蛋白与炎症性肠病的研究进展

刘韶语
潍坊医学院附属医院

目的 本研究以钙卫蛋白在体内的分布和生物学特性为依据，探讨粪便钙卫蛋白检测在炎症性肠病中的作用。
方法 本研究收集自 2019 年 1 月至 2021 年 1 月期间本院经结肠镜检查和组织病理检查确诊的 100 例溃疡性结肠炎和 100 例克罗恩病分别为第一组的 A1 和 B1，50 例术后恢复期的为第二组的 A2 和 B2，50 例经体检健康的人群为第三组，均进行粪便钙卫蛋白的检测。入选者均排除了严重的上消化道疾病,均无重大身心疾病。近期无免疫抑制剂及糖皮质激素使用史,无长期服用非甾体类抗炎药用药史,并排除酗酒者、孕妇。采集新鲜粪便标本 10-20g,进行钙卫蛋白的检测。
结果 一组的钙卫蛋白水平均高于二组和三组；二组的钙卫蛋白水平高于三组但低于一组；经正态检验，均为非正态分布，溃疡性结肠炎的粪便钙卫蛋白中位数 575ug/g，克罗恩病的粪便钙卫蛋白水平中位数为 175ug/g，健康人群中的钙卫蛋白中位数为 4.9ug/g。
结论 粪便钙卫蛋白作为一种新型的炎症标志物，在粪便中含量丰富, 不受环境、温度的影响, 可长期保持相对稳定而不被各种酶和细菌所破坏。经研究表明，在溃疡性结肠炎和克罗恩病中，钙卫蛋白水平呈明显升高。因其检验方便，成本低，弥补了结肠镜检查和组织活检侵袭性大，患者耐受低，花费高的缺点，这种简便的检测手段在临床炎症性肠病的研究中一定会有很大的发展潜力。

PU-4298

48 例传染性单核细胞增多症患儿高荧光强度淋巴细胞百分比检测的临床意义

刘娟
吉林大学第一医院

目的 高荧光强度淋巴细胞百分比检查对传染性单核细胞增多症的诊断意义，高荧光强度淋巴细胞百分比与异型淋巴细胞比例，EB 病毒含量的相关性。传染性单核细胞增多症(infectionmononucleosis,IM)是儿童常见病毒感染性疾病，诊断主要依据典型临床表现，外周血异型淋巴细胞比例增高和 EBV 抗体检测。尽管 IM 外周血异型淋巴细胞增高很常见，但也常见于其他病毒感染性疾病，不具有特异性。EBV-lgM 抗体检测为临床诊断 IM 最常用的方法，但受病程、患者年龄及机体免疫状况影响，具有一定假阴性率。本研究采用高强度荧光淋巴细胞百分比检测 IM 患儿，探讨高强度荧光淋巴细胞百分比对儿童 IM 的诊断意义
本研究采用高强度荧光淋巴细胞百分比检测 IM 患儿，探讨高强度荧光淋巴细胞百分比对儿童 IM 的诊断意义。
材料与方法 研究对象：48 例于本院收 治的 IM 患儿，其中男 23 例，女 25 例，男比女为 0.92：1。
研究方法 对 IM 患儿进行血常规检测，检测血液中高荧光强度淋巴细胞百分比；血细胞形态检查，检测患儿异型淋巴细胞比例；同时进行 EB 病毒含量检测。
统汁学处理 ：采用 SPSS18.0 进行显著性检验，用单因素方差分析及 t 检验。
结果 48 例 IM 患儿，高荧光强度淋巴细胞百分比有 47 例明显升高，高于正常参考值； 外周血细胞形态学检查中 bi36 例异型淋巴细胞比值大于 10%；EB 病毒含量升高与高荧光强度淋巴细胞百分比升高结果具有一致性。
结论 高荧光强度淋巴细胞百分比检测是一种更加省时省力的方法，能够在第一时间对 IM 患者进行筛查，对临床诊断具有重要意义。

PU-4299

1 例多次输血导致交叉配血失败的病案分析

袁改玲、李蓉
新疆生产建设兵团第五师医院

目的 探讨自身性疾病与多次反复输血引发直接抗人球蛋白实验阳性的患者关于输血的安全性。
方法 回顾性分析 1 例自身患有急性髓系白血病 M2 型且存在溶血性链球菌感染的患者接受输注去白细胞的悬浮红细胞治疗过程中的病程变化，结合临床用药及其诊疗方法对本病例进行分析。
结果 患者血型为 AB 性 RH+血，在住院期间曾多次间断进行输血治疗，均无输血反应，在反复输血 5 次后，再次要求输注 3U 的去白细胞的悬浮红细胞，在红细胞抗体筛查及血型均无异常结果的前提下，交叉配血次侧在显微镜下出现弱凝集反应，肉眼不可见，用微柱凝胶法查直接抗人球蛋白出现阳性反应。
结论 对于本身有基础性疾病，有多次输血史的患者在交叉配血后建议复查直接抗人球蛋白，以确保输血安全。

PU-4300

血小板/白蛋白比值，血小板/血红蛋白比值及 C-反应蛋白/白蛋白比值与糖尿病患病相关性分析

徐阳、刘莉君
西安交通大学第二附属医院

目的 探究血小板/白蛋白比值（Platelet/albumin ratio, PAR），血小板/血红蛋白比值（Platelet/hemoglobin, PHR）及 C-反应蛋白/白蛋白比值（C-reactive protein/albumin, CAR）与糖尿病之间相关性。
方法 基于中国健康与营养调查 CHNS2009 数据，通过 ID 进行性别、年龄匹配，纳入具有血清学检测结果的 8258 例人群样本数据，根据空腹血糖和 Hb1Ac 分为糖尿病组与对照组。
结果 糖尿病组中血尿酸、总胆固醇、甘油三酯及 LDL-C 较对照组显著升高，HDL-C 则显著降低。其次，糖尿病组中 PAR 与 PHR 相比对照组均无明显差异，而 CAR 则显著升高（0.48±0.18 vs. 0.08±0.23, P<0.001），并与空腹血糖（r=0.1818，P<0.001）、HbA1c（r=0.1866，P<0.001）及 HOMA-IR（r=0.1881，P=0.003）均呈显著正相关，但 CAR 并非糖尿病的独立危险因素。此外，红细胞计数（B=1.324，95%CI: 1.182-1.483，P<0.001）和白细胞计数（B=1.230，95%CI: 1.166-1.298，P<0.001）升高可能是糖尿病患病的独立危险因素。
结论 CAR 与糖尿病存在一定相关性，但并非其独立危险因素；血脂异常和白细胞、红细胞计数升高可能是糖尿病患病的独立危险因素，但仍需进一步研究。

PU-4301

尿干化学分析和尿沉渣定量分析在尿细胞测定中的价值对比

战伟
大连大学门诊部

目的 探讨尿干化学分析和尿沉渣定量分析在尿细胞测定中的价值。
方法 把尿沉渣离心镜检作为金标准，用 Mejer-700 尿液干化学分析仪、IQ200 尿沉渣定量分析仪和离心镜检三种方法，分别测定 500 例患者尿液标本的 RBC 和 WBC 值，分析上述两种仪器在尿液 RBC 和 WBC 测定方面的准确度、灵敏度和特异性。
结论 干化学分析法和尿沉渣定量分析法测定尿标本中红细胞和白细胞的准确度、灵敏度、特异性和阳性率相比，差异无统计学意义 (P＞0.05)。联合应用两种测定方法，在准确度、灵敏度和特异性上均高于两种方法独自测定 (P＜0.05)。
结果 干化学分析和尿沉渣定量分析在测定尿液细胞时均有不足。但二者联合应用，可增加测定的准确度和灵敏度，提高工作效率并减少误差。

PU-4302

TEG5000 血栓弹力图仪采用原装进口试剂与国产试剂的比对研究

李蕾、马静、杨旭、王晓琳、王培昌
首都医科大学宣武医院

目的 探讨 TEG5000 血栓弹力图仪使用原装进口试剂与国产试剂检测结果的相关性、一致性及临床可替代性。

方法 选取 30 例临床血浆样本，用 TEG5000 和重庆鼎润血栓弹力图仪以及两家公司生产的试剂进行平行交叉测定,分为 A 组、B 组、C 组，并分析三组数据 R、K、Angle、MA 四个参数的相关性和一致性。
结果 A 组、B 组与 C 组 R、K、Angle、MA 四个参数均具有高度相关性（r>0.9）；且 B 组、C 组与 A 组有良好一致性，二者相差幅度为临床可接受；TEG5000 采用国产试剂检测结果，与生物参考区间的符合率≥90%。
结论 TEG5000 血栓弹力图仪采用国产试剂可以替代进口仪器试剂进行血栓弹力图检测，能为临床诊疗提供可靠、准确、有价值的数据。

PU-4303

激光散色法测定血红蛋白的临床应用

窦敏、林燕辉
福建省立医院

目的 观察激光散色法测定血红蛋白能否解决脂血对血红蛋白的影响，从而替代实验室常用的血浆置换法。
方法 1.收集 30 例非脂血标本，分为 HB 低值组、HB 中值组、HB 高值组，分别用激光散射法和比色法测 HB，并对两者进行比较。2.非脂血标本 150 例，分为 HB 低值组、HB 中值组、HB 高值组，分别用不同浓度脂肪乳进行血浆置换，对置换后激光散色法 HB 与置换前比色法 HB 进行比较分析。3.脂血标本 90 例，分为 HB 低值组、HB 中值组、HB 高值组，对激光散色法 HB 与血浆置换后比色法 HB 进行比较。
结果 1.三组非脂血标本激光散射法 HB 与比色法 HB 偏倚均<6%（-0.58±2.34，0.16±1.52，1.15±1.56），在允许总误差范围内。2.低值组 TG8.2mmol/L 激光散射法 HB 结果与置换前非脂血标本比色法 HB 偏倚<6%（-2.93±1.25），中值组 TG<16.4mmol/激光散射法 HB 结果与置换前非脂血标本比色法 HB 偏倚<6%（-3.98±1.43），高值组 TG<65.6mmol/L 激光散射法 HB 结果与置换前非脂血标本比色法 HB 偏倚<6%（-3.50±2.24）。3.三组脂血标本激光散射法 HB 与血浆置换法 HB 结果差异无统计学意义（P>0.05），且两者具有很好的相关性（r2=0.968，0.948，0.87）。
结论 激光散色法能够有效降低脂血对血红蛋白测定的影响，能替代传统的血浆置换法，具有较高的临床应用价值。

PU-4304

肾病合并糖尿病患者血栓分子标志物水平分析

王贝
东南大学附属中大医院

目的 观察糖尿病肾病患者血浆 TM、TAT、PIC 及 tPAI-C 水平.
方法 选 2020 年 1 月—2020 年 12 月本院收治的 288 例肾病患者（A 组），265 例糖尿病患者（B 组）, 78 例肾病合并糖尿病患者（C 组），另选同期 200 例体检健康者作为对照组（D 组）。采用化学发光免疫分析两步法检测各组受检者血浆血栓调节蛋白(TM)、凝血酶-抗凝血酶复合物(TAT)、纤溶酶-a2 抗纤溶酶复合物(PIC)和组织型纤溶酶原激活剂抑制剂复合物(tPAI-C)水平并比较组间差异。
结果 各组 TM、TAT、PIC 和 tPAI-C 水平比较差异均有统计学意义，且均呈 D 组<A 组< C 组趋势，差异均有统计学意义(P<0.05 或 P<0.01)；A 组和 B 组各指标无统计学差异。
结论 肾病合并糖尿病患者均存在凝血和纤溶系统异常，监测血浆 TM、TAT、PIC 和 tPAI-C 水平对评估患者出凝血状态有重要临床意义。

PU-4305

动态监测抗凝血酶Ⅲ、D-二聚体、超敏 C 反应蛋白在脓毒症患者诊疗中的应用

王贝
东南大学附属中大医院

目的 通过动态监测抗凝血酶Ⅲ（AT-Ⅲ）、D-二聚体（DD）、超敏 C 反应蛋白(hs-CRP)的水平变化，以评价其在脓毒症患者诊断、治疗及预后判断的应用价值。
方法 选取 2018 年 1 月-2020 年 3 月我院重症医学科脓毒症患者 80 例，及非脓毒症患者 100 例为研究对象。脓毒症组按入室时降钙素原（PCT）水平分为 PCT＜2.00 ng/ml 组、2.00 ng/ml≤PCT＜10 ng/ml 组、PCT≥10 ng/ml 组。监测 AT-Ⅲ、DD、hs-CRP 水平。
结果 脓毒症各组治疗 AT-Ⅲ、DD、hs-CRP 水平与非脓毒症相比有显著性差异（P<0.01）；脓毒症 3 组在治疗后 3d、7d、14d、21d 的 AT-Ⅲ、DD、hs-CRP 水平与治疗后 12h 相比均有显著性差异（P<0.01）；
结论 通过连续监测脓毒症患者治疗期间的 AT-Ⅲ、DD、hs-CRP 水平，有助于指导脓毒症患者的治疗和预后判断，降低脓毒症患者并发症的风险。

PU-4306

降钙素原、超敏 C 反应蛋白、D-二聚体、抗凝血酶 III 与急性心肌梗死程度相关性

王贝
东南大学附属中大医院

目的 观察急性心肌梗死患者(AMI)降钙素原（PCT）、超敏 C 反应蛋白（hs-CRP）、D-二聚体（DD）、及抗凝血酶 III（AT-III）水平变化，探讨其临床意义。
方法 以 90 例 AMI 患者为 AMI 组，90 例健康体检者为正常组。比较 2 组受试者，轻度与中重度 AMI 患者血浆 PCT、hs-CRP、DD、AT-III 水平，并进行相关性分析。
结果 AMI 组血浆 DD、PCT、hs-CRP 水平显著高于正常组，其 AT-III 水平显著低于正常组（P<0.05）。轻度组 PCT、hs-CRP、 DD 水平低于中重度组（P<0.05），其 AT-III 水平高于中重度组（P<0.05）。Pearson 相关分析显示，DD、PCT、hs-CRP 水平与 AMI 病情呈正相关（r=0.825、r=0.712、 r=0.742)，AT-III 与 AMI 病情呈负相关（r=-0.729）。
结论 AMI 患者存在明显凝血功能异常、炎性因子高表达状态；PCT、hs-CRP、DD、AT-III 水平变化对 AMI 患者病情预测、预后评估等均具有价值。

PU-4307

流式细胞术和骨髓细胞形态学联合检测在非霍奇金淋巴瘤诊断与分型中的临床价值

佘仕金
乐山市人民医院

目的 分析流式细胞术（FCM）和骨髓细胞形态学（BMA）联合检测在非霍奇金淋巴瘤（NHL）诊断与分型中的临床价值。
方法 回顾性选择 2017 年 1 月至 2019 年 1 月在我院和四川省人民医院血液科诊治的 NHL 患者 138 例的 FCM 及 BMA 的检测结果，分析 FCM 联合 BMA 分析不同程度、不同形态淋巴瘤骨髓侵犯的临床价值。
结果 BMA 检测阳性率明显高于骨髓涂片（$\chi2=7.046$，$P=0.008<0.05$）与 FCM（$\chi2=4.062$，$P=0.043<0.05$），而 FCM 联合 BMA 检测阳性率明显高于 BMA（$\chi2=4.158$，$P=0.041<0.05$）、FCM（$\chi2=16.025$，$P=0.000<0.01$）。FCM 与 BMA 方法检测结果均为阳性者 18 例（13.04 %），以高比例瘤细胞骨髓浸润者为主；均为不确定者为 10 例（7.25 %），主要为二者均不能定的低比例轻度异形淋巴样细胞；均为阴性 86 例（62.32 %）；结果不一致的病例 24 例（17.39 %），主要为轻度瘤细胞骨髓浸润的病例。FCM 联合 BMA、FCM 以及 BMA 三者在临床分期 I→IV 期与 II→IV 期修正结果比较，无统计学意义（$P>0.05$）；而 FCM 联合 BMA 在临床分期 III→IV 期修正结果明显高于 BMA（$\chi2=4.164$，$P=0.041<0.05$）、FCM（$\chi2=4.726$，$P=0.029<0.05$），而 FCM、BMA 在临床分期 III→IV 期修正结果比较，无统计学意义（$P>0.05$）。
结论 FCM、BMA 检测方法不同形态淋巴瘤细胞侵犯的敏感性不同，有良好的一致性在高比例瘤细胞骨髓浸润者中，而在轻度瘤细胞骨髓浸润这表现出明显差异。FCM 联合 BMA 检测阳性率明显高于 BMA、FCM，以及在临床分期 III→IV 期修正结果明显高于 BMA、FCM。

PU-4308

Flipped Quick-Response Code Enables Reliable Blood Grouping

Hong Zhang、Ruining Liu、Yang Luo
重庆大学医学院智慧检验与分子医学中心

Background Rapid and reliable blood grouping plays an essential role in various biomedical and forensic scenarios. However, identification of weak blood group agglutinations remains challenging due to the inevitable environmental interference and low precision during the process of result readout.
Methods Herein, we invented a disposable and handheld microfluidic platform of flipping QR-code identification with prompt error-discrimination (FLIPPED) features for accurate blood grouping by using a commercially available smartphone. For better identification of weak agglutination samples, a linear regression curve between the blood HCT value and resultant color change was established via machine learning. Additionally, an automatic correction algorithm was designed to remove any potential errors from scanning angles and ambient light intensities.
Results Ultimately, a reliable blood typing platform was devised, which can detect ABO, Rh, MNS, P, Kell, Kidd, and Lewis blood groups within 30 s to 3 min. An accuracy of 100% was observed in a total of 450 clinical blood samples in varied ambient conditions, validating the robustness of the proposed FLIPPED assay. Additionally, no any mistyping was observed for blood samples with different HSA concentrations, bilirubin levels, and total cholesterol levels.
Conclusion The proposed FLIPPED blood grouping assay possesses the characteristics of enhanced and simplified workflow along with wireless transmission, offering the potential for

being developed into a highly compact, automatic, efficient, and low-cost universal platform for quantitative analysis of a variety of biological and pathological biomarkers.

PU-4309

外周血中反应性淋巴细胞的特点及临床意义分析

郑春毅[1]、张国恺[2]、陈泽杰[2]
1. 潮州市人民医院
2. 广东省潮州市人民医院

目的 研究分析外周血中反应性淋巴细胞（atypical lymphocyte）的形态特点和存在临床意义的分析。
方法 按照实验室要求，当血液分析仪直方图出现异常报警信号和淋巴细胞结果异常警示、图形时[1]，我们及时对外周血细胞进行涂片，染色分类检查。
结果 我们单位一年期间约有 3000 例外周血标本进行涂片染色人工分类检查，经过祥细分类复查，发现其中有 160 例标本分类可见有反应性淋巴细胞。
结论 在病理情况下反应性淋巴细胞可以出现在外周血涂片中，如当机体有病毒感染（如 EB 病毒、新型冠状病毒、SARS 冠状病毒、流感病毒、呼吸道合胞病毒、巨细胞病毒、腺病毒、肠道病毒 71 型、柯萨奇病毒、轮状病毒、非肿瘤性皮肤病等）、原虫（如弓形虫）感染、药物反应、结缔组织病、过敏性疾病、多种免疫刺激疾病、炎症与感染性疾病等，外周血都可出现反应性淋巴细胞，及时发现对症治疗，反应性淋巴细胞可慢慢恢复为正常细胞。

PU-4310

Establishment of improved review criteria for hematology analyzers in cancer hospitals

Xiaoyan Wang、xu wang、peng ge、xiaoqiang zhao、chong chen、shusheng hu、li ren
Tianjin Medical University Cancer Institute and Hospital

Background Although hematologic review criteria for general hospitals have been established, they may be insufficient for cancer hospitals. This study aimed to establish the appropriate review criteria for hematology analyzers in cancer hospitals.
Methods A total of 1003 samples from our hospital were randomly selected for blood smear preparation and microscopic review. The review criteria of the International Consensus Group for Hematology Review (ICGH) and Chinese consensus group were used to obtain the review, true-negative (TN), true-positive (TP), false-negative (FN), and false-positive (FP) rates, as well as the triggered rules. Our review criteria were established by comparing flag or numeric value information of TP and FP samples,
adjusting rules to obtain better efficiency, a low slide review rate, and an acceptable FN rate.
Results Overall, 197 (19.64%) samples showed positive smear findings. Compared to the ICGH criteria, the slide review rate of the newly established criteria declined from 51.25% to 39.28%, and the TP and TN rates increased from 17.85% and 46.06% to
23.13% and 55.83%, respectively. The FN rate of the newly established criteria was 3.69%. Another set of samples used to validate the newly established criteria yielded the review, FN, and FP rates as 33.49%, 1.86%, and 25.58%, respectively.
Conclusion The newly established review criteria for hematology analyzers enabled the prompt identification, smear, and further verification of doubtful specimens, without a significant increase in the workload, thus improving the efficiency of the
review process. This study provided data support for other cancer hospitals to establish review criteria.

PU-4311

乳糜血对血细胞检测的影响

朱时帅、史永胜
哈尔滨医科大学第一附属医院

目的 研究乳糜血对血细胞检测结果的影响，并探讨去除此种影响的方法。
方法 随机选取 300 例（男 200 例，女 100 例）非乳糜血标本进行血常规检测；将标本用脂肪乳进行血浆置换，混匀后进行血常规检测；将标本随机分为生理盐水组和血常规稀释液 EPK 组，每组 100 例，分别将乳糜血标本用等量生理盐水和 EPK 进行血浆置换两次，并分别进行血常规检测。用 SPSS22.0 对各组数据进行统计分析。
结果 1.乳糜血标本的白细胞计数（WBC）、血红蛋白含量（Hb）、血细胞比容（Hct）、平均红细胞容积（MCV）、平均红细胞血红蛋白量（MCH）、平均红细胞血红蛋白浓度（MCHC）与原始血标本检测值之间有显著差异（P<0.05）; 2.生理盐水组和 EPK 组血浆置换一次的检测值与原始血标本检测值有显著差异（P<0.05），而置换两次的检测结果与原始结果之间无显著差异；3.红细胞计数（RBC）在各组之间均无显著差异。
结论 1.严重乳糜血会对白细胞计数（WBC）、血红蛋白含量（Hb）、血细胞比容（Hct）、平均红细胞容积（MCV）、平均红细胞血红蛋白量（MCH）、平均红细胞血红蛋白浓度（MCHC）的检测结果产生干扰；2.用生理盐水或血常规稀释液 EPK 进行血浆置换两次后可消除此种干扰。

PU-4312

能量代谢在脓毒症急性肾损伤中的研究进展

史永胜、金英玉
哈尔滨医科大学第一附属医院

脓毒症已成为急性肾损伤患者的主要原因，慢性肾功能不全患者感染常导致肾功能进一步恶化(1)。目前更多的关注是预防急性肾损伤。当患者出现严重电解质紊乱，如水钠潴留、氮质血症、肝肾综合征等危及生命的病理生理改变时，肾脏替代治疗是唯一的选择。肾脏接收 20%的心输出量。但其耗氧量相当于机体耗氧量的 10%(2)。此外，肾脏线粒体和耗氧量仅次于心脏。线粒体功能受到缺血缺氧、毒素刺激、重金属离子、化疗药物等各种因素造成的细胞代偿范围和细胞损伤的严重影响和损害。因此，ATP 合成减少，导致细胞能量代谢紊乱，随后细胞死亡(3)。急性肾损伤期间线粒体发生巨大变化，特别是早期线粒体功能不能得到纠正，导致线粒体功能失衡，可能导致细胞能量代谢紊乱和各种病理生理变化(4)。近年来，除了细胞坏死和凋亡外，其它程序性细胞死亡途径，如铁螯合、自噬和焦亡也被发现在急性肾损伤发病机制中发挥重要作用(5)。这些细胞死亡途径与线粒体功能障碍密切相关。因此对线粒体损伤的完整分子理解已成为发展急性肾损伤新疗法的探索领域。在不同的环境状态下，线粒体可以对不同的状态做出反应，并融合成棒状或者环状结构。在这种情况下，线粒体网络保持密切连接，几乎所有细胞中的线粒体始终处于融合分裂的动态平衡(6)。然而，直到最近几年，肾小管上皮细胞线粒体动力学的特异性改变才变得更加突出，这可能与线粒体动力学大部分是在心肌细胞纤维骨架上进行的有关。既往研究表明肾小管上皮细胞含有大量线粒体融合分裂相关蛋白(7)。推测线粒体融合和分裂在维持心肌细胞稳态中也可能发挥重要作用。能量代谢过程中 ATP 耗竭可引起线粒体分裂，最近的研究表明，包括线粒体体积释放在内的线粒体损伤与多种细胞事件有关，包括自噬、焦亡或者程序性细胞死亡机制，而不限于凋亡(8)。

PU-4313

脑脊液流式细胞术检测微小残留病的临床意义

罗燕飞
广东省人民医院

目的 探讨脑脊液流式细胞术监测微小残留病在急性白血病复发预测及指导治疗中的临床意义。
方法 采用流式细胞术对 2015 年 1 月到 2016 年 10 月的 62 例急性白血病患者进行追踪检测，分析脑脊液及骨髓 MRD 与白血病复发之间的关系。
结果 62 例患者中有 11 例患者脑脊液 FCM 检查为阳性的检出率为 17.74%，其中发生复发的有 6 例（54.55%），脑脊液 MRD 阴性 51 例，其中 8 例（15.69%）复发，两者复发率具有统计学意义（$\chi 2=7.82, P<0.05$）。脑脊液 MRD 阳性预测白血病复发的时间比骨髓 MRD 阳性早 85.67 天。
结论 监测白血病患者脑脊液 MRD，在监测复发以及估计预后中具有重要临床价值。

PU-4314

不同 CRP 水平的细菌性肺炎患者凝血指标的变化研究

金亚雄、黄珣钡、牛倩、江虹
四川大学华西医院

目的 分析细菌性肺炎患者凝血指标（PT、APTT、FIB、TT）的水平变化，并通过观察炎症指标 CRP(C-reactive protein)水平与凝血指标的相关性来评价凝血功能的变化在肺炎病程发展中的临床意义。
方法 收集四川大学华西医院 2019 年 10 月至 2020 年 3 月期间确诊为细菌性肺炎的患者 147 例作为疾病组，根据患者入院第一次 CRP 的水平将疾病组分为 3 组：低水平组（5-50mg/l）、中水平组（50-100mg/l）和高水平组（>100mg/l）；另外收集同期我院健康体检者 33 例作为健康对照组。观察各组 CRP、PT、APTT、FIB、TT 的水平变化。
结果 PT、APTT、FIB 在各组中的水平差异具有统计学意义（$P<0.05$），并且低、中、高水平组的 PT、APTT、FIB 水平均高于健康对照组，差异具有统计学意义（$P<0.05$）。疾病组总体 CRP 水平与 PT、APTT、FIB 均呈正相关（r 分别为 0.294、0.420、0.401，$P<0.05$）。
结论 联合检测 PT、APTT、FIB 与 CRP 能有助于炎症严重程度的观察，动态监测凝血指标可以更准确的判断疗效。

PU-4315

细胞因子与 D-二聚体在慢性阻塞性肺疾病发病过程中作用

周宇捷、孙烨、任建平
山西省中医院

慢性阻塞性肺疾病是一种持续性气流受限的疾病，该病发病率高，严重影响患者的生存质量，并给病人家庭带来承重的经济负担。由于该病具有异质性，因此根据其临床表现、影像学变化等将其分为不同的表型，其中肺功能型和全身炎症反应型为主要表型。目前临床多通过肺功能检查评估病情发病情况，但该检查不能全面反映病情的发展，且对于急性加重期病人无法进行肺功能检查。研究发现 COPD 的发生发展是由于机体免疫力-抗炎能力失衡引起的，且在疾病的进展期炎症因子会明显升高，但对于抗炎因子在疾病中扮演的角色不是很清楚。此外由于缺氧等因素对血管内皮细胞的损伤，机体的 D-二聚体也会发生明显变化。本文主要通过阐述对细胞因子及 D-二聚体对 COPD 影响，了解 COPD 患者细胞因子变化对疾病的影响。

PU-4316

体液标本乳糜定性试验阳性结果分析

张春莹、陈月梅、谢恒、邓山鹰、蒋能刚
四川大学华西医院

目的 通过对乳糜定性试验结果进行统计分析, 总结成人乳糜性积液形成的病因。
方法 统计 2014-2018 年华西医院进行乳糜定性试验的住院患者的体液标本结果及病例资料，回顾分析体液标本的乳糜定性试验阳性检出率，阳性患者科室分布及主要疾病特征。
结果 共收集进行乳糜定性试验的住院患者体液标本 1295 例，包括腹腔积液 190 例（14.67%）、胸腔积液 797 例（61.54%）、随机尿 145 例（11.20%）、心包积液 7 例（0.54%）、引流液 143 例（11.04%）、其他标本 13 例（1.00%），乳糜定性试验阳性标本 997 例，阳性检出率 76.99%。除尿标本的阳性检出率较低为 33.79%外，以上标本检出率为 80-100%。阳性患者主要集中分布于心脏外科、胃肠外科、呼吸内科、泌尿外科、肺癌中心、ICU 等科室。
结论 不同的标本类型在科室分布中有一定的聚集性，外科术后最易出现积液乳糜性，心脏外科出现乳糜性腹腔积液最常见。

PU-4317

血液分析仪仪器参数在血小板复检中重要性研究

陈思、毛志刚、王双、郑沁
四川大学华西医院

目的 血小板准确计数有利于临床对疾病的准确诊治。目前，血小板分析中阻抗法测血小板常用，但结果易受红细胞碎片、小红细胞、大血小板等多种因素影响，需采用其他方法，如荧光法对血小板计数进行复检。本研究拟探讨红细胞参数和血小板参数对血小板计数的影响，寻找合适的参数和阈值，以确定血小板计数复检的标准。
方法 收集 2019 年 1-2 月间，四川大学华西医院实验医学科 2133 例标本，每例标本均使用阻抗法、光学法和荧光法三种方法进行血小板检测。计算阻抗法和荧光法血小板差值或差值比率，差值或差值比率大于 12.5%即需复检。使用回归分析寻找红细胞、血小板参数对血小板复检测的影响因素。
结果 2133 例标本中，507 例标本需用荧光法复检。低 MCV、高小红细胞计数(OR, 1.39; 95%CI: 1.08 to 1.79; p=0.011)和碎片红细胞水平(OR, 6883; 95%CI: 1472 to 32184; p<0.001)对血小板检测结果影响较大。复检组样本 PDW、MPV、P-LCR、PCT 和 IPF%均高于其他样本。ROC 分析显示，RBC 参数 RBC、microR#、FRC#具有更好的诊断效能，AUC 分别为 0.712 (95%CI: 0.687-0.736)、0.731 (95%CI: 0.707-0.754)、0.744 (95%CI: 0.720- 0.769)。
结论 自动化血细胞分析中 RBC 参数 RBC、microR#、FRC#对血小板结果影响较大，根据这些参数指标确定血小板复检所需的检测阈值，对血小板计数进行复检，以保证检测结果的准确性。

PU-4318

全自动血凝仪 ACT TOP 700 性能验证

覃月华
南方医科大学珠江医院

目的 近年来，随着现代医学对血栓与出血方面不断地深入认识，临床实验室对该方面有关的检测项目指标不断增多[1]。全自动血凝分析仪在各大医院应用广泛，为临床实验室在血栓与出血方面疾病的预防、诊断以及治疗提供了更加精准的指标。根据 ISO15189《医学实验室质量和能力的专用

要求》规定，实验室全自动设备应通过性能验证，并符合相关检验所需要求，方可使用。本研究根据对 ACT TOP 部分凝血项目进行精密度、准确度、携带污染率、线性以及同型号仪器间比对等结果进行系统性的验证。
方法 从精密度，精确度，携带污染率，线性可报告范围验证，参考区间验证等多角度验证和评价全自动血凝仪 ACT TOP 700 的性能。

PU-4319

γδT 淋巴细胞增殖性疾病的临床及实验室特征分析

蒋能刚
四川大学华西医院

目的 分析累及骨髓的 γδT 淋巴细胞增殖性疾病的实验室检查和临床特征。
方法 采用流式细胞术对 γδT 细胞增殖性疾病的患者骨髓标本进行免疫表型分析，其结果与细胞形态学、外周血血象及临床特征进行分组比较分析。
结果 在累及骨髓的 17 例 γδT 淋巴细胞增殖性疾病中，按照 2016 年 WHO 的描述，临床诊断为肝脾 T 细胞淋巴瘤（HSTL）的 8 例；诊断为大颗粒淋巴细胞白血病（LGLL）的 6 例；无明确临床诊断的 3 例。8 例 HSTL 中位年龄 30 岁（22-41 岁），临床均表现为发热、脾大，LDH 均明显升高（均值 561±211 IU/L）；外周血 7 例血小板数量降低，4 例白细胞数量降低，5 例为轻至中度贫血，骨髓细胞形态 5 例发现中等偏大的性质不明细胞；免疫表型除特征性表达 TCRγδ 外，多表达 CD56（7/8），不表达 CD57，异常细胞占淋巴细胞比例差异较大（2％-98％）。6 例大颗粒淋巴细胞白血病中位年龄 55 岁，与 HSTL 组比较有明显差异；仅 1 例脾长大，无发热，LDH 均值 201±67 IU/L，明显低于 HSTL 组；2 例为三系减少， 4 例为单纯红细胞减少，骨髓细胞形态学有 3 例描述成熟淋巴细胞形态改变，均伴有核红细胞减少。免疫表型除特征性表达 TCRγδ 外，部分表达 CD56（3/6），多表达大颗粒淋巴细胞相关标志 CD57（4/6），异常 γδT 细胞占淋巴细胞比例均明显增加（51％-86％）。此外，各类 γδT 淋巴细胞增殖性疾病 CD2、CD7 均表达，且表达强度与正常 T 淋巴无明显差异， CD5 均以阴性表达为主（HSTL 组阳性 1/8，LGLL 组阳性 1/6）。
结论 侵及骨髓的 γδT 细胞增殖性疾病临床表现形式以恶性程度较高的肝脾 T 细胞淋巴瘤和惰性的大颗粒淋巴细胞白血病为主。二者间可通过流式细胞免疫表型分析和临床特征进行明确区分。

PU-4320

地中海贫血与缺铁性贫血患者的血常规结果的应用研究

朱志强
南方医科大学珠江医院

目的 对缺铁性贫血与非复合型地中海贫血患者的血常规结果分析，根据其血液学指标的主要分布情况，探究其在地贫与缺铁贫的鉴别和地贫初筛的临床意义。
方法 将 52 例缺铁性贫血患者设定为缺铁贫组，52 例非复合型地中海贫血患者设定为地贫组，52 例健康体检者设定为对照组。比较 3 组血细胞参数 HB、HCT、MCV、MCH、RDW 水平并确立各参数的可信区间（95%）分布。
结果 经方差分析 SNK-q 检验的两两比较，地贫组、缺铁贫组、对照组的 HB、HCT、MCV、MCH、RDW 均有统计学差异（P＜0.05）；根据均数的可信区间分析，地贫组、缺铁贫组与对照组的可信区间(95%)无交叉重叠。
结论 红细胞参数在缺铁性贫血的临床鉴别和地中海贫血的初筛诊断有重要意义，可根据其血常规参数值大小作出初步的筛查。

PU-4321

血鉴别诊断中血液检验

吕艳丽
南方医科大学珠江医院

目的 研究贫血鉴别诊断中血液检验的应用价值与有效性，为临床诊断提供必要指导。
方法 随机将 2017 年 3 月～2019 年 3 月本院 25 例贫血患者作为实验组，同期选择 25 例健康体检者作为对照组，对比两组参与者血液检验结果。
结果 实验组 MCV 为（74.79±0.48）、RBC 为（3.71±0.44）、MCH 为（10.11±1.32）、Hb 为（86.61±4.48）、RDW 为（22.46±1.57），前四项指标均比对照组高，最后一项指标高于对照组，差异具备统计学研究意义（P＜0.05）。
结论 诊断贫血的过程中，选择血液检验方式，可有效提高诊断结果的准确性，临床应用相对广泛。

PU-4322

凝血因子 VIII 在血液透析患者高凝状态诊断中的应用价值

郭勇晖
南方医科大学珠江医院

目的 评估凝血因子 VIII 在血液透析患者高凝状态诊断中的应用价值，为预测获得性易栓症提供有价值的临床评估指标和可以应用的医学决定水平。
方法 通过对血液透析患者凝血因子 VIII 的检测以及临床表现的评价，比较发生血栓事件的患者凝血因子 VIII 的活性与未发生血栓事件患者之间的差异，探索凝血因子 VIII 在血液透析患者高凝状态诊断中的应用价值。
结果 只有 30.3%（44/145）的患者凝血因子 VIII 的活性在正常范围，而发生一次或多次血栓事件的患者为 17.9%（26/145）。
结论 肾病综合征患者由于肾功能严重受损，凝血因子 VIII 蓄积，凝血功能异常，体内呈高凝状态，在凝血因子活性高于 200%时，提示患者可能达到易栓状态，其发生血栓事件的可能性高，值得临床予以注意和预防。

PU-4323

Improving performance of recently introduced flow cytometry-based approach of malignant cell screening in serous cavity effusion

Jingfang Sun、Shuang Ding、Liqiang Zhu、Yun Liu、Qingqing Jiang、Shuang Song、Weimin Chen、Shibao Li、Ping Ma
Affiliated Hospital of Xuzhou Medical University

Introduction Microscopy has been recognized as the “gold standard” cellular analysis of serous cavity effusion. However, this method is time consuming, labor intensive, and requires accomplished skills. Here, we investigated the efficiency of hematology analyzer in screening malignant cells in serous cavity effusion.
Methods A total of 991 serous cavity effusion samples and 370 validation specimens collected from different departments were sent to the clinical laboratory for routine cell count using the automated hematology BF mode and exfoliative cytology simultaneously. High-fluorescent cells(HFCs) were measured as the relative count (HF%) and absolute count (HF#) by BF mode.

Receiver operating characteristic curve (ROC) analysis was combined with scattergram rules to screen malignant cells.
Results HF# and HF% in malignant samples (subgroup) were significantly higher than those in benign samples, and the HF# and HF% levels were different between ascites and pleural effusion (PE). The area under the curve values were also different between ascites and PE. Positive of malignant cells was very high when the ascites or PE sample touching Rule 1 positive and either Rule 2 negative or positive. The cut-off levels of HF# were 5.5 HFC/μL on the basis of Rules 1 and 2 negative, whereas 83.5 HFC/μL on the basis of Rule 1 negative but Rule 2 positive in ascites. By contrast, the cut-off levels of HF% were 0.55 HFC/100 WBC on the basis of Rules 1 and 2 negative, whereas 4.95 HFC/100 WBC on the basis of Rule 1 negative but Rule 2 positive in PE.
Conclusions Serous cavity effusion will be increasingly analyzed using the automated hematology analyzer BF mode in the future because of its rapidness and convenience. The combined application of HFC with scattergram rules is a feasible and useful approach to screen malignant cells in serous cavity effusion.

PU-4324

血液分析仪法血小板计数假性增高因素的探讨与处理

孙静芳、陈卫民、丁爽、蒋清清、刘云、王炜
徐州医科大学附属医院

目的 分析血液分析仪血小板假性增高的原因，探讨其解决办法以准确发放血小板计数报告。
方法 回顾性分析 14 例血小板假性增高的病例，对 14 例样本均进行血涂片显微镜镜检观察血小板数量及分布、PLT-O 和手工法复检血小板。
结果 14 例样本均为血小板假性增高，血小板直方图均出现异常，血涂片显微镜镜检结果与仪器计数结果不符，PLT-O 与手工计数法结果之间无统计学差异。
结论 血小板直方图异常时，请注意鉴别是否存在干扰血小板计数的因素，注意镜检，必要时进行 PLT-O/PLT-F 或者手工计数血小板以确保血小板结果的准确发放。

PU-4325

胶体金法检测粪便钙卫蛋白在炎症性肠病中的应用价值

单智惠
海军军医大学第二附属医院（上海长征医院）

目的 采用半定量的胶体金快速检测方法检测粪便中的钙卫蛋白，以探讨粪便钙卫蛋白与 IBD 活动度的关系，从而为 IBD 患者的管理提供有意义的检测指标。
方法 71 份 IBD 患者的粪便样本全部来源于上海长征医院样本库，同时收集 10 例健康人粪便样本作为对照，纳入的 IBD 患者均为 2015 年至 2020 年本院消化内科收治并确诊的病例。根据患者的疾病情况分为缓解组、活动组和健康对照组。活动组 44 例，缓解组 27 例，健康对照组 10 例。对比 IBD 患者与健康对照组的粪便钙卫蛋白含量及对比活动组与缓解组患者的粪便钙卫蛋白含量，并计算粪便钙卫蛋白用于诊断 IBD 的灵敏度、特异性。
结果 以 60 μg/g 作为临界值，IBD 患者与健康人的粪便钙卫蛋白含量差异有统计学意义（P<0.05）；与健康人相比，IBD 患者的 FC 含量明显升高；以 60 μg/g 作为临界值时，活动组与缓解组 IBD 患者的钙卫蛋白含量有显著差异（P<0.05），活动组的粪便钙卫蛋白含量高于缓解组；粪便钙卫蛋白用于诊断 IBD 的灵敏度为 67.61%，特异性为 80.00%。
结论 采用胶体金的方法检测粪便中的钙卫蛋白，可判断疾病的活动度，且具有耗时短、经济方便、痛苦小等优点。

PU-4326

Prognostic value of hematological pre-albumin to fibrinogen ratio in patients with glioma

Chunjing Jin[1]、Shiqaing Hou[1]、Minfeng Yang[2]、Haidan Chu[3]、Beitian Shi[1]、Ruiyu Xie[1]、Yinan Chen[4]、Ning Lin[1]
1. Affiliated Chuzhou Hospital of Anhui Medical University, The First People's Hospital of Chuzhou
2. 香港理工大学
3. 南通大学附属医院
4. 安徽省立医院

Hematologicalbiomarkers that reflect host nutritional and inflammation status have beenidentified to be independent prognostic factors in various malignancies.The aim of the present study was to determine the predictive value of preoperativealbumin (ALB), fibrinogen (FIB), pre-albumin (pALB), Albumin to fibrinogenratio (AFR) and pre-albumin to fibrinogen ratio (PFR) for the prognosis ofpatients with glioma. X-tile software was used to identify cut-off values ofthese parameters. Kaplan-Meier survival analysis, univariate and multivariateanalyses based on Cox proportional hazards regression model were used todetermine whether these markers were associated with the prognosis of patientswith glioma. In addition, the Harrell concordance index with variables was usedto evaluate the prognostic accuracy. The results indicated that PFR (HR = 2.827,95% CI: 1.353-6.122, *p* = 0.006) is the only independent prognosticfactor in patients of glioma along with clinicopathological grade and age. C-indexof predicted nomogram including PFR (0.719) for glioma patients was higher thanthat without PFR (0.699). Our findings demonstrated that circulating preoperativePFR, rather than the other four parameters, might be a potential negativeindependent prognostic biomarker for glioma individuals.

PU-4327

胸腹水中高荧光强度的有核细胞计数在肺癌筛查中的临床应用

蒋清清
徐州医科大学附属医院

目的 探讨高荧光强度的有核细胞计数联合肺癌相关肿瘤标志物在肺癌筛查的临床应用.
方法 利用 Sysmex XN-2000 血液体液分析仪体液模式测定浆膜腔积液(胸腹水)标本中的高荧光细胞计数(HF-BF#)和百分比(HF-BF%),同时送检验科科细胞室进行液基细胞学检查和核医学科肿瘤标志物筛查（包括血清和胸腹水两种）,以病理科报告为诊断标准,对所有数据进行统计学处理,建立 ROC 曲线,评估胸腹水高荧光细胞初筛恶性肿瘤的应用价值.
结果 144 份标本通过误差条图我们发现同一患者的胸腹水的 CEA 和 CA125 检测值明显要高于血清的检测值，通过受试者工作特征(ROC)曲线分析标本,参数 HF-BF#(×106/L)最佳临界值为 61.5，此时参数 HF-BF#对恶性细胞检出的灵敏度为 72.2%,特异度为 75%。若将 HF-BF#(×106/L)临界点设在 309.0，此时参数 HF-BF#对恶性细胞检出的特异度可以达到 91.7%。
结论 Sysmex XN-2000 体液分析模式对浆膜腔积液标本进行肿瘤细胞筛查可以起到很高的参考价值,特别是参数 HF-BF#具有较高的特异性,可为临床诊断提供重要价值。

PU-4328

脑梗死患者颈动脉病变程度与血常规检测结果相关性研究

王冬丽
漯河医学高等专科学校第三附属医院

目的 研究脑梗死患者颈动脉病变程度与血常规检测结果的相关性。
方法 本次研究对象为 2018 年 1 月至 2019 年 12 月收治的 100 例脑梗死患者、同期的健康体检者 100 名，依次纳入观察组、对照组，均进行血常规检查，对比两组的血常规检查结果；再根据颈动脉内中膜厚度(IMT)超声检测结果进行分组，将各组的血常规检查结果进行比较。
结果 观察组患者的 WBC、RBC、PLT、HCT、MCV、RDW、MPV 与对照组相比差异具有统计学意义（P＜0.05）；斑块形成患者的 PLT、HCT、RDW、MPV 高于内膜增厚患者，不稳定斑块患者的 RBC、PLT、MPV 水平高于稳定斑块者，差异具有统计学意义（P＜0.05）。
结论 脑梗死患者的血常规检测结果能对疾病的发生及颈动脉病变程度进行判断。

PU-4329

Reference Intervals for a Panels of 20 Plasma Steroids in Chinese Han Adults

Yanhua Zheng、Xujing Kong、Xiaomin Fan、Jun Yao、Huiying Sun、Baorong Chen
Beijing Kingmed Clinical Laboratory

Systemic steroid hormone measurements can assist diagnosis of endocrine hypertension, reproductive and developmental abnormalities. This study was aimed to establish reference intervals for a panel of 20 plasma steroids in Chinese Han adults. A total of 192 healthy volunteers (80 males and 112 females aged 18-63 years) were enrolled. Individuals with endocrine diseases or other systemic diseases or tumors were excluded in this study. Plasma steroids concentrations were measured by mass spectrometry, and data were analyzed by SPSS software. Graphical representation of the data was carried out with Graph prism software. According to the “CLSI guidelines for defining, establishing, and verifying reference intervals in the clinical laboratory”, reference intervals for the panel of 20 plasma steroids were established. Except for pregnenolone, corticosterone, 17 hydroxypregnenolone, 11 deoxycortisol, cortisol, dehydroepiandrosterone and estriol, the other steroids were significant associated with gender ($P < 0.05$). Thus, reference intervals of most steroids were established by gender in this study. Plasma levels of steroid profiles obtained in this study could be clinically used as reference intervals for diagnosis and subtyping of patients with endocrine hypertension or developmental abnormalities.

PU-4330

Prevalence and genotype distribution of HPV infection among 214,715 women from Southern China, 2012-2018: baseline measures prior to mass HPV vaccination

Lipei Luo、Li Wang、Shuling Min
ChenZhou NO.1 people's Hospital

Background The epidemiology on the human papillomavirus (HPV) among females in Southern China is not well-established. Baseline data on the prevalence of HPV infection in China prior to mass prophylactic HPV vaccinationwould be useful. Thus, this study aims to determine the type-

specific HPV prevalence and distribution amongfemales from Southern China prior to mass HPV vaccination.
Methods A retrospective cross-sectional study employing 214,715 women attending ChenZhou NO.1 People'sHospital for cervical screening during 2012–2018 was conducted prior to widespread HPV vaccination. HPVgenotype was detected using nucleic acid molecular diversion hybridization tests. The overall prevalence, age-specific prevalence, type distribution, and annual trend were analyzed.
Results The overall HPV prevalence was 18.71% (95% confidence interval [CI], 18.55–18.88%) among SouthernChina females. During 2012–2018, the prevalence of HPV infection showed a downward tendency, from 21.63%(95% CI, 21.07–22.20%) in 2012 to 18.75% (95% CI, 18.35–19.16%) in 2018. Age-specific HPV distribution displayed apeak at young women aged less than 21 years (33.11, 95% CI, 31.13–35.15%), 20.07% (95% CI, 19.70–20.44%) amongwomen aged 21–30 years, 17.29% (95% CI, 17.01–17.57%) among women aged 31–40 years, 17.23% (95% CI, 16.95–17.51%) among women aged 41–50 years, 21.65% (95% CI, 21.11–22.20%) among women aged 51–60 years, and25.95% (95% CI, 24.86–27.07%) among women aged over 60 years. Of the 21 subtypes identified, the top threeprevalent high-risk HPV (HR-HPV) genotypes were HPV52 (5.12%; 95% CI, 21.11–22.20%), − 16 (2.96%; 95% CI, 2.89–3.03%), and − 58 (2.51%; 95% CI, 2.44–2.58%); the predominant low-risk HPV (LR-HPV) genotypes were HPV81 (1.86%;95%CI, 1.80–1.92%) and − 6 (0.69%; 95% CI, 0.66–0.73%) respectively. Incidence of HR-HPV only, LR-HPV only andmixed LR- and HR-HPV were 15.17, 2.07 and 1.47% respectively. Besides, single HPV infection accounted for 77.30%of all positive cases in this study.
Conclusions This study highlights 1) a high prevalence of HPV infection among females with a decreasingtendency towards 2012–2018, especially for young women under the age of 21 prior to mass HPV vaccination; 2)HPV52, − 16 and − 58 were the predominant HPV genotypes, suggesting potential use of HPV vaccine coveringthese HPV genotypes in Southern China.

PU-4331

WGS analysis of of Carbapenem-Resistant Klebsiella pneumoniae ST11 strains in a tertiary hospital in southern China: Molecular characteristic, Antimicrobial Resistance, and Virulence

Yili Chen[1]、Lu Ai[1]、Yaqin Peng[1]、Pingjuan Liu[1]、Penghao Guo[1]、Kang Liao[1]、Runshi Yang[2]
1. The First Affiliated Hospital of Sun Yat-sen University
2. 广东省科学院微生物研究所

Sequence type 11 (ST11) carbapenem-resistant Klebsiella pneumoniae (CRKP) has become the dominant clone in China. It may cause severe infections which are difficult to treat with current antibiotics, and has attracted world-wide attention. In this study, the microbiological traits, antimicrobial resistance, and virulence of the Carbapenem-Resistant Klebsiella pneumoniae ST11 strains were investigated by WGS analysis.
Methods CRKP strains were consecutively collected in the First Affiliated Hospital of Sun Yat-sen University during 2019. Antimicrobial susceptibility testing was performed according to CLSI2020-M100. All of the strains were subjected to whole genome sequencing (WGS) using the short-read Illumina HiSeq platform for detecting genes of Carbapenemase, ESBL, OmpK35/36, virulence and analysing multi locus sequencing type(MLST) . Clonal relatedness was determined based on single nucleotide polymorphisms (SNPs).
Results A total of 64 strains of CRKP were collected in this study, including 47 strains of ST11, accounting for 73.4%. Among the 47 strains of ST11, they were mainly isolated from sputum samples, accounting for 48.9% (23 / 47). The results of antibiotics susceptible test showed that these strains were the most sensitive to tigecycline, colistin and ceftazidime / avibactam, which were 98.9%, 97.9% and 93.0% respectively. Overall, blaKPC-2 (97.9%) was the predominant

carbapenemase gene. One of the blaKPC-2 carring strains belonged to a KPC-2 variant, showing resistant to ceftazidime / avibactam. Notably, one isolate coharbored blaKPC-2 and blaNDM-1, and one isolate coharbored blaKPC-2 and blaNDM-4. Moreover, the carriage of ESBL genes was prevalent, and 76.6% of the strains carried CTX-M gene. The two KL virulence types KL47 and KL64 of CRKP ST11 accounted for 42.6% vs 57.4% respectively. Phylogenetic structures of the 47 strains of ST11 CRKP from present study showed that there was high homology among the same virulence type strains.
Conclusions Our study highlights the importance of coordinated efforts between clinical and molecular microbiologists and infection control teams to rapidly identify, investigate and contain nosocomial outbreaks. Routine surveillance with advanced sequencing technology should be implemented to strengthen hospital infection control and prevention measures.

PU-4332

Upregulation of PEDF predicts poor prognosis and promotes esophageal squamous cell carcinoma progression by modulating the MAPK/ERK signaling pathway

Ting Zhang[1]、Zui Chen[1]、Di Che[2]、Xiaoqiong Gu[2]、Banglao Xu[1]
1. Guangzhou First People's Hospital
2. 广州市妇女儿童医疗中心

Purpose Analyze the expression of pigment epithelium-derived factor (PEDF) in esophageal squamous cell carcinoma (ESCC) tissues and investigate the mechanism by which PEDF promotes esophageal cancer cells metastasis to search biomarker for the diagnosis and prognosis of ESCC.
Methods Sequencing data of invasive and non-invasive cells of esophageal carcinoma from the GEO database were used for analysis. Immunohistochemical staining of survival esophageal cancer pathology sections was utilized to visualize PEDF changes. The expression of PEDF in kyse140 and kyse510 ESCC cells was overexpressed or knocked down by plasmid or siRNA interference, respectively. ESCC cells migration and invasion changes were analyzed using transwell assay, scratch assay and invasion assay. The expressions of epithelial-mesenchymal transition (EMT) related proteins and key proteins of signaling pathways were detected by Western blotting. Cells overexpressing PEDF were treated with PD98059 or U0126 to observe the alteration of related indicators.
Results In the microarray analysis of GEO data, PEDF expression was significantly higher in the invasive group of ESCC cells compared with the non-invasive group. Immunohistochemical staining showed that the expression of PEDF was positively correlated with distant metastasis and TNM stage of ESCC, and patients with high PEDF expression ($P = 0.0001$) had a lower 5-year overall survival rate than those with low PEDF expression. PEDF was an independent risk factor for poor prognosis in patients with ESCC. Transwell assay, scratch assay and invasion assay showed that PEDF could promote the migration and invasion of ESCC cells. Western blotting showed that PEDF could downregulate the epithelial marker E-cadherin, α-catenin, and upregulate the mesenchymal marker N-cadherin, suggesting that PEDF could activate the EMT process. Overexpression of PEDF increased the expression of p-ERK in the group of proteins associated with EMT related signaling pathways, but the expression of p-Akt, and Akt were not changed. After inhibiting MAPK/ERK signaling pathway by adding PD98059 or U0126, the progression of EMT in ESCC cells evoked by overexpression of PEDF was reversed.
Conclusions PEDF promotes esophageal squamous cell carcinoma cells invasion and metastasis by regulating cell epithelial-mesenchymal transition through the MAPK/ERK pathway, and PEDF may serve as a potential biomarker for the diagnosis and prognosis evaluation of ESCC.

PU-4333

Aspergillus but Not Candida: Fatal Fungus Infection in Critical COVID-19 Patients

Yang Yang、Xinyi Xia
Institute of Laboratory Medicine, Jinling Hospital, Nanjing University School of Medicine

Objectives Earlier researches focused little attention on COVID-19 co-infection with fungus while some experts suggested COVID-19 patients should be routinely screened for bacteria and fungi infection after COVID-19 being confirmed. Here, we enrolled 236 patients with COVID-19 to present a detailed analysis of their clinical situation of fungal infection.
Methods A total of 236 COVID-19 patients from Huoshenshan Hospital were included in this study, and three common fungi (candida, aspergillus, cryptococcus neoformans) were mainly detected by specific serological identification. By combining above fungi detection results and clinical data, the basic characteristics, laboratory indicators, viral nucleic acid, antibody level were compared among COVID-19 patients.
Results Firstly, based on specific serological identification results, 236 patients were divided into serologically positive group including 80 (34%) patients and serologically negative group including 156 (66%) patients, serologically positive group contained 32 only candida positive, 31 only aspergillus positive, 17 candida with aspergillus positive patients, and there was no positive result in cryptococcus neoformans detection. It is noteworthy that 5 mortality in serologically positive group were all related to aspergillus infection while candida infection rarely caused death, aspergillus was most common in non-survivors while candida was most common in survivors. Additionally, in terms of laboratory indicators, interleukin-6 (IL6) showed a significant higher level in serologically positive group than that in negative group, while other indicators (white blood cell count, neutrophil absolute value, eosinophil absolute value, basophil absolute value, procalcitonin, hypersensitive c-reactive protein, total protein, blood glucose), viral nucleic acid loads, and antibody level are higher but not significant in serologically positive group than those in serologically negative group. Finally, imaging evidence was presented such as the “new moon sign” ,which is a specific pulmonary imaging characteristic of aspergillus infection. Histopathological biopsy was also presented from a COVID-19 patient co-infected with aspergillus, in which a large number of distinct mycelia were observed in the patient’s lung biopsy.
Conclusions According to our study, 5 non-survivors of COVID-19 with fungal infection were almost associated with aspergillus infection. Aspergillus infection, instead of candida infection might be fatal for critical ill patients with COVID-19. The main drawback is that identification results of fungus infection in our study are difficult to reach the clinical diagnostic level, because the gold standard of clinical diagnostic in invasive fungus infection must be a positive histopathology result. However, there is still of great significance to carry out routine rapid screening for fungal infection especially for critical COVID-19 patients to enable early treatment to be implemented and improve their clinical prognosis.

PU-4334

Efficacy and safety of tocilizumab treatment COVID-19 patients: A case-control study and meta-analysis

Weijun Jiang、Xinyi Xia
Department of Reproduction and Genetics, Institute of Laboratory Medicine, Jinling Hospital, Nanjing University School of Medicine, Nanjing 210002, P.R. China

Objective As the pandemic progresses, the pathophysiology of COVID-19 is becoming more apparent, and the potential for tocilizumab is increasing. However, the clinical efficacy and safety of tocilizumab in the treatment of COVID-19 patients remain unclear.

Methods Amid the shortage of robust evidence regarding the use of tocilizumab in COVID-19 patients, we aimed to evaluate the efficacy and safety of tocilizumab treatment to COVID-19 patients in a case-control study and meta-analysis, which will help inform clinical management of COVID-19 patients. The study was conducted, including 95 patients treated with tocilizumab plus standard treatment, and matched controls with 95 patients treated with standard treatment therapy by propensity score from Februarys to April 2020. We searched PubMed, Web of science, and MedRxiv using the search terms severe acute respiratory syndrome coronavirus 2, COVID-19, SARS-CoV-2, 2019-nCoV interleukin-6 inhibitors; tocilizumab, and coronavirus for studies published from January 1, 2020, to June 1, 2021.
Results Of all patients, 63 (66.32%) cases and 56 (58.95%) controls had coexisting conditions, including hypertension, hyperlipidemia, hyperuricemia, diabetes, chronic cardiac disease, cancer, etc. Our case-control study found a lower mortality rate in the tocilizumab treatment group than in the standard treatment group (9.47% versus 16.84%), but the results were not statistically significant. We also found that the mortality rate in tocilizumab treatment groups was significantly lower than the standard treatment group in the stratified ICU analysis (OR= 0.52, 95%CI= 0.44-0.61, P= 0.048 and OR= 0.31, 95%CI= 0.10-0.99, P= 0.044). In the subgroup without secondary infection, the tocilizumab treatment group's mortality rate was significantly lower than in the standard treatment group (OR= 0.35, 95%CI= 0.12-1.00, P= 0.040).
In total, 49 studies (including 6568 cases and 11660 controls) met the inclusion criteria and were selected for the meta-analysis. In the overall analysis, we performed the meta-analysis that significantly decreased mortality after patients received tocilizumab (OR= 0.81, 95%CI= 0.69-0.95, P= 0.008). We also revealed significant associations within some subgroups. For mortality, the number of patients did not reach the optimal information size. However, the blue cumulative Z curve crossed both the traditional boundary and the TSA boundary, showing no more tests are needed to reach a positive conclusion in advance. No significant associations were observed between tocilizumab and elevated secondary infection risk, discharge, adverse events, and mechanical ventilation in the overall analysis.
Conclusion Tocilizumab significantly decreased mortality and increased discharge in COVID-19 patients, but no increased secondary infection risk, adverse event, and mechanical ventilation in a meta-analysis. Our data suggest that clinicians should pay attention to tocilizumab therapy as an effective and safe treatment for COVID-19 patients.(Part of the study was revised by Infectious Diseases and Therapy)

PU-4335

The role of LINC01088 in prediction and treatment of recurrent spontaneous abortion

Hui Zhao
The second hospital of Shandong University

Objective Recurrent spontaneous abortion (RSA) is defined as two or more consecutive pregnancy losses and could be attributed to genetic causes, infection and other unknown factors. Due to the lack of early prediction and effective clinical treatment, RSA has become one of the important causes of infertility. Therefore, to explore the etiology and pathogenesis of RSA is the key to prevention and treatment of RSA. LncRNAs reveal critical roles in regulation of gene expression of many diseases. However, there are few studies on the role of lncRNAs in RSA. Therefore, it is urgent to explore effective lncRNAs as markers for early prediction and treatment of RSA, so as to provide a basis for the diagnosis and treatment of RSA and the development of related drugs.
Methods Quantitative real-time PCR was used to detect the expression of LINC01088 in villus tissue. The receiver operating characteristic curve (ROC curve) was further drawn and the area under the curve (AUC) was calculated. Then CCK-8, EdU and clone formation assays were used to detect the effect of LINC01088 on the proliferation of trophoblast cells. The effect of

LINC01088 on cell cycle and apoptosis of trophoblast cells was detected by flow cytometry. The influence of LINC01088 on invasion and migration of trophoblast cells and villus tissue was detected by Transwell and explants culture. The cytoplasmic and nuclear RNA of trophoblast cells were isolated, and quantitative real-time PCR was performed to determine the localization of LINC01088 in trophoblast cells. We used RNA pull-down to detect the proteins bound to LINC01088. The influence of LINC01088 on nitric oxide/nitric oxide synthase system was detected by western-blot and nitric oxide detection kit. The signaling pathways and molecules were detected by western-blot.

Results The expression of LINC01088 in villus tissue of RSA patients was higher than in normal pregnancy group and LINC01088 has good sensitivity and specificity in the diagnosis of RSA. In vitro LINC01088 reduced the proliferation, invasion and migration ability of trophoblast cells. LINC01088 could inhibit the cell cycle process and promote the apoptosis of trophoblast cells. In trophoblast cells, LINC01088 was mainly localized in the nucleus and could bind to arginase 1 and enhance the stability of arginase 1 protein. Meanwhile, LINC01088 inhibited the protein level expression of endothelial nitric oxide synthase, resulting in synchronous decrease of nitric oxide level. The activated JNK/P38 MAPK signaling pathways were observed after overexpressed LINC01088.

Conclusions Our study demonstrated for the first time that the expression level of LINC01088 is closely related to RSA, and the sensitivity and specificity of LINC01088 in the diagnosis of RSA is very high. LINC01088 inhibited the proliferation, invasion and migration of trophoblast cells and promoted the apoptosis of trophoblast cells. Furthermore, LINC01088 in trophoblast cells indirectly inhibited eNOS/NO system via binding and increasing arginase-1. The reduction of NO ulteriorly activated JNK and p38 MAPK signaling pathways and ultimately caused the dysfunction of trophoblast cells and the occurrence of RSA. Our findings supported that LINC01088 might be a potential diagnostic and therapeutic target for RSA.

PU-4336

OXA-181-Producing Carbapenem-Resistant Klebsiella pneumonia Sequence Type 16 Isolated from Active Intestinal screening of a MICU patient in South China

Yili Chen[1]、Kang Liao[1]、Runshi Yang[2]
1. The First Affiliated Hospital of Sun Yat-sen University
2. 广东省科学院微生物研究所

Carbapenemase-producing Enterobacteriaceae (CPE) are important factors to the global public health problem of antibiotic resistance. Oxacillinase (OXA)-181 is the second most common worldwide type of the OXA-48-like carbapenemase. Generally, OXA-48-like enzymes have low activity towards carbapenems, high hydrolyzing activity against penicillins and are not impressionable to β-lactamase inhibitors.

In this report, we present the first case of an OXA-181-producing carbapenem-resistant Klebsiella pneumoniae (K334) isolated from Enteric Colonization of a MICU patient in South China. K334 showed susceptible to extended-spectrum cephalosporins and aztreonam, but highly resistant to imipenem; and meropenem. By PCR amplification and sequencing, we confirmed that the K334 strain carried OXA-181 gene. Meanwhile, this strain also carried extended-spectrum β-lactamase(ESBL) genes(SHV-26) with the loss of OmpK36 in porin genes. Multilocus sequence typing (MLST) indicated that it belonged to sequence type 16(ST16). Further WGS using the Oxford Nanopore MinION and the Illumina NextSeq platform and subsequent de novo hybrid assembly revealed that K. pneumoniae K334 harbored a 5.22 Mb circular chromosomal DNA and three plasmids. The blaOXA-181 gene was located on a 51,479 bp plasmid designated as pK334_OXA181 of incompatibility group IncX3, this plasmid also carried quinolone resistance gene qnrS1.

This study reported for the first time that OXA-181-producing carbapenem-resistant Klebsiella pneumonia ST16 isolated from enteric colonization of a MICU patient in South China, suggesting that since the gastrointestinal tract is a major reservoir of antibiotic resistance genes, screening of fecal samples for blaOXA-181 is recommended to prevent its possible rapid dissemination via the IncX3-type plasmid.

PU-4337

Tumor-derived exosomes, myeloid-derived suppressor cells, and tumor microenvironment

Xinyu Tian
Nanjing Drum Tower Hospital

Plenty of immune cells infiltrate into the tumor microenvironment (TME) during tumor progression, in which myeloid-derived suppressor cells (MDSCs) represent a heterogeneous population of immature myeloid cells with immunosuppressive activity. Tumor cells and stromal cells facilitate the activation and expansion of MDSCs in TME via intercellular communication, and expanded MDSCs suppress anti-tumor immune responses through direct and indirect mechanisms. Currently, exosomes, which are a kind of extracellular vesicles (EVs) that can convey functional components, are demonstrated to participate in the local and distal intercellular communication between cells. Numerous studies have supposed that tumor-derived exosomes (TEXs), whose assembly and release can be modulated by TME, are capable of modulating the cell biology of MDSCs, including facilitating their activation, promoting the expansion, and enhancing the immunosuppressive function. Therefore, in this review, we mainly focus on the role of TEXs in the cell-cell communication between tumor cells and MDSCs, and discuss their clinical applications.

PU-4338

The SaeRS two-component system contributes to the age-dependent nasal colonization of Staphylococcus aureus

Qian Liu
Renji Hospital

Staphylococcus aureus is an important human commensal bacteria colonizing the human body, especially the nasal cavity. The nasal carriage can be a source of S. aureus bacteremia. However, it is not completely understood what bacterial factors contribute to nasal colonization of S. aureus. By analyzing S. aureus isolated from the nasal cavity of three age groups, the children, young adults, and seniors, we found that the SaeRS two-component system is an important determinant of nasal colonization in the nasal cavity of seniors. The senior group isolates of S. aureus showed rather distinct sequence type composition, as compared with other age group isolates.The senior group isolates showed not only a lower gene carriage of enterotoxins a, c, and q and hemolysin B (hlb) but also lower hemolytic activity against human red blood cells. Of regulators affecting hemolysin production, only the SaeRS TCS showed an age-dependent decrease of activity. The decreased virulence of the senior group isolates of S. aureus was confirmed in the mouse skin infection model, where the senior group isolates showed the lowest survival. However, in the murine nasal colonization model, the sae-deletion mutant showed higher colonization. S. aureus was not significantly killed by nasal secretions from either young adults or seniors; however, it survived better in the senior nasal secretions. These results indicate that senior nasal cavity environment favors colonization of S. aureus with lower virulence, to

which the reduced activity of the SaeRS TCS contributes. Also, they illustrate an example of bacterial colonization adapts to the changing host environment.

PU-4339

syphilis test results analysis

Yongsheng Shi、yingyu jin
The first affiliated hospital of Harbin medical university

Objective In July 2019-12 at the end of a total of 8440 cases of patients with preoperative patients and medical analysis of monitoring results of syphilis, and discuss its popular trend, clinical manifestation ,treatment and prevention.
Methods Enzyme-linked immunosorbent (ELISA) method in 8440 cases of patients with syphilis specific antibody (TP-Ab) detection.
Results To detect the positive patients a total of 180 cases, 2.1% detection rate.acquired syphilis in 171 cases, 9 cases of congenital syphilis.The number of acquired syphilis in the 21-40 years old age group significantly more than other age groups, 33.9% of the positive number.Congenital syphilis accounted for 5% of the number of positive Numbers are mostly distributed in pediatrics.
Conclusion Positive rate of syphilis was gradually on the rise, in recent years should be attached great importance to, and vigorously publicized safety education, improve the understanding of syphilis and damage, reduce the syphilis harm to the society, family and individual

PU-4340

The role of LINC01088 in diagnosis and treatment of recurrent spontaneous abortion

Hui Zhao
The second hospital of Shandong University

Objective Recurrent spontaneous abortion (RSA) is defined as two or more consecutive pregnancy losses and could be attributed to genetic causes, infection and other unknown factors. Due to the lack of effective clinical treatment, RSA has become one of the important causes of infertility. Therefore, to explore the etiology and pathogenesis of RSA is the key to prevention and treatment of RSA. LncRNAs reveal critical roles in regulating gene expression. However, there are still few studies on the role of lncRNAs in RSA. Therefore, it is necessary to explore more effective lncRNAs as markers for clinical diagnosis and treatment of RSA, so as to provide a basis for the diagnosis and treatment of RSA and the development of related drugs.
Methods Quantitative real-time PCR was used to detect the expression of LINC01088 in villus tissue. The receiver operating characteristic curve (ROC curve) was further drawn and the area under the curve (AUC) was calculated. Then CCK-8, EdU and clone formation assays were used to detect the effect of LINC01088 on the proliferation of trophoblast cells. The effect of LINC01088 on cell cycle and apoptosis of trophoblast cells was detected by flow cytometry. The influence of LINC01088 on invasion and migration of trophoblast cells and villus tissue was detected by Transwell and explants culture. The cytoplasmic and nuclear RNA of trophoblast cells were isolated, and quantitative real-time PCR was performed to determine the localization of LINC01088 in trophoblast cells. We used RNA pull-down to detect the proteins bound to LINC01088. The influence of LINC01088 on nitric oxide/nitric oxide synthase system was detected by western-blot and nitric oxide detection kit. The signaling pathways and molecules were detected by western-blot.
Results The expression of LINC01088 in villus tissue of RSA patients was higher than normal pregnancy group. The sensitivity and specificity of LINC01088 in the diagnosis of RSA are high. LINC01088 reduced the proliferation, invasion and migration ability of trophoblast

cells. LINC01088 could inhibit the cell cycle process and promote the apoptosis of trophoblast cells. In trophoblast cells, LINC01088 was mainly localized in the nucleus and could bind to arginase 1 and enhance the stability of arginase 1 protein. LINC01088 inhibited the protein level expression of endothelial nitric oxide synthase, resulting in synchronous decrease of nitric oxide level. The activated JNK/P38 MAPK signaling pathways were observed after overexpressed LINC01088.

Conclusions Our study is the first to find that the expression level of LINC01088 is closely related to RSA, and the sensitivity and specificity of LINC01088 in the diagnosis of RSA is very high. LINC01088 inhibited the proliferation, invasion and migration of trophoblast cells and promoted the apoptosis of trophoblast cells. Furthermore, LINC01088 in trophoblast cells indirectly inhibited eNOS/NO system via binding and increasing arginase-1. The reduction of NO ulteriorly activated JNK and p38 MAPK signaling pathways and ultimately caused the dysfunction of trophoblast cells and the occurrence of RSA. Our findings supported that LINC01088 might be a potential therapeutic and diagnostic target for the treatment of RSA.

PU-4341

Circulating Cytokines and Lymphocyte Subsets in Patients Who Have Recovered from COVID-19

Xin Li、chaolu Hasi
First Hospital of Shanxi Medical College

To investigate the immune status of people who previously had COVID-19 infections, we recruited two-week postrecovery patients and analyzed circulating cytokine and lymphocyte subsets. We measured levels of total lymphocytes, CD3+ T cells, CD4+ T cells,CD8+ T cells, CD19+ B cells, and CD56+ NK cells and the serum concentrations of interleukin- (IL-) 1, IL-4, IL-6, IL-8, IL-10,transforming growth factor beta (TGF-β), tumor necrosis factor alpha (TNF-α), and interferon gamma (IFN-γ) by flow cytometry. We found that in most postrecovery patients, levels of total lymphocytes (66.67%), CD3+ T cells (54.55%), CD4+ Tcells (54.55%), CD8+ T cells (81.82%), CD19+ B cells (69.70%), and CD56+ NK cells (51.52%) remained lower than normal,whereas most patients showed normal levels of IL-2 (100%), IL-4 (80.88%), IL-6 (79.41%), IL-10 (98.53%), TNF-α (89.71%),IFN-γ (100%), and IL-17 (97.06%). Compared to healthy controls, two-week postrecovery patients had significantly lower absolute numbers of total lymphocytes, CD3+ T cells, CD4+ T cells, CD8+ T cells, CD19+ B cells, and CD56+ NK cells, along with significantly higher levels of IL-2, IL-4, IL-6, IL-10, TNF-α, IFN-γ, and IL-17. Among postrecovery patients, T cells,particularly CD4+ T cells, were positively correlated with CD19+ B cell counts. Additionally, CD8+ T cells were positively correlated with CD4+ T cells and IL-2 levels, and IL-6 positively correlated with TNF-α and IFN-γ. These correlations were not observed in healthy controls. By ROC curve analysis, post recovery decreases in lymphocyte subsets and increases in cytokines were identified as independent predictors of rehabilitation efficacy. These findings indicate that the immune system gradually recovers following COVID-19 infection; however, the sustained hyperinflammatory response for more than 14 days suggests a need to continue medical observation following discharge from the hospital. Longitudinal studies of a larger cohort of recovered patients are needed to fully understand the consequences of the infection.

PU-4342

Clonal dissemination of KPC-2-producing Klebsiella pneumoniae ST11 and ST48 clone among multiple departments in a tertiary teaching hospital in Jiangsu Province, China

Ruru Bi
The Affiliated Dushuhu Public Hospital of Soochow University

The world-wide prevalence of carbapenem-resistant Klebsiella pneumoniae (CRKP) has been posing a threat to the public health. In this study, a total of 82 non-duplicated CRKP isolates were analyzed for the prevalence of resistant determinants including carbapenemase, extended spectrum β-lactamase (ESBLs), and AmpC as well as integrons and cassette regions by PCR and DNA sequencing. The genetic relatedness was investigated by pulsed field gel electrophoresis (PFGE) and multi-locus sequencing typing (MLST). Overall, blaKPC-2 (n = 75) was the predominant carbapenemase, accompanied with high prevalence of blaSHV (92.7%) and blaCTX-M (90.2%). PFGE profiles and MLST analysis revealed that 65 out of 68 KPC-2-producing CRKP ST11 isolates were involved in clone dissemination among multiple departments with the department of neurology ICU being the major one. Moreover, first report on clonal dissemination of KPC-2-producing CRKP ST48 clone in four departments and NDM-5-producing CRKP ST337 clone was also identified. Class I integron were detected in 17 (20.7%) of 82 isolates with aadA2 being the most common cassette. And a novel cassette array of integron, aac(6')-II-blaCARB/PSE-1 was identified. Taken together, KPC-2-producing CRKP ST11 and ST48 clone were widely disseminated in multiple departments of our hospital, which triggers the need for urgent and active surveillance and implementation of infection control measures.

PU-4343

SC-514 protects acute liver failure induced by LPS/D-Gal in mice

Zhentang Jing
The second hospital of shandong university

Objective To determine whether SC-514 is involved in the protective effect of LPS/D-Gal on acute liver failure in mice.
Methods A certain dose of LPS/D-Gal combined application can cause acute liver failure and even death in two different strains of BALB/c and C57BL/6 mice. BALB/c and C57BL/6 were divided into groups, and the inhibitory effect of SC-514 on LPS/D-Gal-induced acute liver failure in mice was explored through biochemical, pathological and molecular biological research
Methods Results The pretreatment of SC-514 can significantly reduce the mortality of mice with acute liver failure induced by LPS/D-Gal or prolong the death time of mice, reduce the pathological damage of the test group at the same time, and reduce the gluten C of the test group at the same time. Biochemical levels of aminotransferase (ALT) and aspartate aminotransferase (AST). Further studies have shown that SC-514 can inhibit the production of tumor necrosis factor TNFα in mice induced by LPS/D-Gal, and TNFα is the main factor that promotes apoptosis in LPS/D-Gal-induced acute hepatitis models; and SC Under the action of -514, the apoptosis rate of hepatocytes in the experimental group was significantly reduced.
Conclusion SC-514 inhibits the production of TNFα, reduces the impact of cytokine storm on liver cells, and reduces the mortality of experimental mice with acute liver failure. It is suggested that the reasonable application and development of SC-514 can reduce the liver injury and fatality rate induced by LPS/D-gal.

PU-4344

USP48 suppresses tumor growth by interacting with Gasdermin E and initiating pyroptosis

Yidan Ren、Yunshan Wang
The Second Hospital of Shandong University

Background Ubiquitination is an important item in post-translation. Its most well-known function is to guide the degradation of proteins. Ubiquitination is reversible and can be reversed by a large group of proteases called deubiquitinating enzymes (DUBs). USP48 is an important member of the USP family of deubiquitinating enzymes. Pyroptosis is a kind of programmed cell death, which is characterized by the activation of inflammatory caspase and the cleavage of Gsdermin protein. There is a close relationship between pyroptosis and cancer. In-depth study on the mechanism of pyroptosis and its relationship with cancer is helpful to understand the occurrence and development mechanism of cancer.
Methods In this study, we applied high-throughput small hairpin RNA (shRNA) screening technology to obtain a number of genes that have significant regulatory effects on cell pyroptosis, and found that USP48 has the most significant regulation on pyroptosis. The role of USP48 in pyroptosis was further clarified by detecting the indicators of pyroptosis. Use proteomics and protein mass spectrometry analysis techniques to analyze the downstream regulatory proteins of USP48, confirm the regulation of GSDME by USP48, and use immunoprecipitation experiments to confirm the physical interaction between USP48 and GSDME, and clarify that USP48 is involved in the regulation of pyroptosis molecules mechanism. Animal models of pancreatic cancer were used to clarify the role of USP48 in the development of pancreatic cancer. Single-cell RNA sequencing and flow cytometry were used to further confirm the effect of USP48 on pancreatic tumor immunity.
Conlusion In this study, we confirmed that USP48 can regulate the expression of GSDME to promote pyroptosis. pyroptosis is a natural immune response, which is closely related to tumor immunity. Pancreatic cancer cells have a very unique tumor immune microenvironment. In this study, we are scolded to confirm that USP48 can promote pancreatic cancer cell immunity through promoting the occurrence of pyroptosis, and ultimately inhibit the occurrence of pancreatic cancer.

PU-4345

USP48 is upregulated by Mettl14 to attenuate hepatocellular carcinoma via regulating SIRT6 stabilization

Yidan Ren、Yunshan Wang
The Second Hospital of Shandong University

Exploiting cancer metabolism for the clinical benefit of hepatocellular carcinoma (HCC) patients is a topic under active investigation. Ubiquitin-specific peptidase 48 (USP48), a member of the ubiquitin-specific protease family, is involved in tumor growth, inflammation, and genome stability. However, the role of USP48 in HCC tumorigenesis remains unknown. In this study, we report that expression of USP48 is downregulated in diethylnitrosamine-induced liver tumorigenesis in mice as well as in human HCC. USP48 physically bound and stabilized SIRT6 by K48-linked deubiquitination at the K33 and K128 sites of SIRT6, which impeded metabolic reprogramming to hamper HCC tumorigenesis. Moreover, methyltransferase-like 14 (Mettl14)-induced m6A modification participated in the regulation of USP48 in HCC by maintaining USP48 mRNA stability. Our work uncovers the tumor suppressive function of the Mettl14-USP48-SIRT6 axis via modulation of glycolysis, providing new insights into the critical roles of metabolic activities in HCC and identifying an attractive target for future treatment studies.

PU-4346

Evaluation of dynamic changes in peripheral blood lymphocyte and platelet counts in the diagnosis of influenza infections

Qingzhen Han、ruru bi、lin wang
Suzhou Dushu Lake Hospital (Dushu Lake Hospital Affiliated to Soochow University)

The dynamic changes in peripheral blood LYM and PLT counts in the diagnosis of influenza infections were evaluated. A total of 158 patients with influenza infections, 144 patients with bacterial infections, 83 patients infected with other viruses and 152 healthy controls were enrolled in Suzhou, Jiangsu Province from 2016 to 2019. Dynamic detection of LYMs and PLTs was conducted in three different stages (before, during and after treatment). The diagnostic and prognostic values were also estimated. The PLT and LYM counts in all groups were decreased. PLT counts gradually increased during treatment in patients with influenza. The AUCs of the relative PLT and LYM counts were higher than those of the absolute counts (PLT: 0.9358 vs 0.6375, LYM: 0.7447 vs 0.7068), with relative PLT counts having the largest AUC (0.9358). Moreover, the rate of increase in PLT count can predict the prognosis of patients with influenza infections. Compared with LYM counts, dynamic changes in peripheral blood PLT counts exhibited better performance in determining the diagnosis and prognosis of influenza infections.

PU-4347

Bacterial epidemiology and antimicrobial resistance profiles in children reported by the ISPED program, China, 2016-2020

Pan Fu 、Chuanqing Wang
Huashan Hospital, Fudan University

Infectious disease Surveillance of Pediatrics (ISPED) program was established in 2015 to monitor and analyze the trends of bacterial epidemiology and antimicrobial resistance in Chinese children. Clinical bacterial isolates were collected from 11 tertiary children hospitals in China during 2016 to 2020. Antimicrobial susceptibility testing was carried out using Kirby-Bauer method or automated systems interpreted according to the criteria of Clinical and Laboratory Standards Institute (CLSI) 2019 breakpoints, while penicillin susceptibility of streptococcus pneumonia was detected by E-test. A total of 288,377 isolates were collected, of which 42.1% and 57.9% were gram-positive and gram-negative organisms, respectively. The top-ten predominant bacteria were E.coli, S.pneumoniae, S.aureus, H.influenzae, K.pneumoniae, M.catarrhalis, S.pyogenes, S.epidermidis, P.aeruginosa and A.baumannii. In 2020 COVID19 pandemic year, we observed a significant reduction in the ratio of respiratory tract samples (from 56.9% in to 44.0%). A comparable reduction was also seen for the primary bacteria mainly isolated from respiratory tract, including S.pneumoniae, H.influenzae and S.pyogenes. Multi-Drug Resistant Organisms (MDROs) in children were commonly observed and presented higher drug resistance than sensitive strains. The rates of carbapenem resistant K.pneumoniae (CRKP), A.baumannii (CRAB) and P.aeruginosa (CRPA), and Methicillin resistant S.aureus (MRSA) were 19.7%, 46.4%%, 12.8% and 35.0%, respectively. Those of CRKP, CRAB and CRPA strains all showed a decreasing but fluctuating trend between 2015 and 2020. Compared with those of non-neonatal patients, carbapenem resistance Enterobacteriaceae (CRE) and CRPA posed the potential threaten to neonates. MDROs showed a very high level of antimicrobial resistance and

became the potential threaten to children, suggesting that effective monitoring and controlling of the antimicrobial resistance among children are thus required in China

PU-4348

PLUNC could inhibit the migration and invasion of NPC cells through inhibiting the activation of the Wnt/β-catenin signaling pathway

Meilin Chen[1]、yuqin yang[1]、yanbing qiu[1]、yijun liu[1]、yumei huang[1]、zhicheng wang[1]、xiayu li[1]、ying liu[1]、qing zhou[1]、ge gao[1]、chaoyang zeng[2]、wei xiong[2]、guiyuan li[2]、wenling zhang[1]
1. The Third Xiangya Hospital of Central South University
2. 中南大学肿瘤研究所

Objective To study whether PLUNC could regulate the migration and invasion of nasopharyngeal carcinoma (NPC) through Wnt/β-catenin signaling pathway and provide more sufficient evidence for PLUNC as a candidate tumor suppressor gene for NPC.
Materials and Methods NPC cell lines (5-8F and HNE2) were transiently transfected with overexpressed PLUNC and shRNA PLUNC plasmids. The scratch test and the transwell test were used to detect the migration and invasion ability of NPC cells. Western blot was used to detect the expression of key molecules of EMT and Wnt/β-catenin pathway, then the key molecules of EMT and Wnt/β-catenin pathway were detected after Wnt pathway inhibitor XAV-939 was added to NPC cells. Immunofluorescence test and western blot were also used to detect the expression of β-catenin protein in the NPC nucleus.
Results PLUNC could inhibit the migration and invasion ability of NPC cells and the key molecules'expression in EMT and Wnt/β-catenin pathway in NPC cells. The expression of β-catenin in the nucleus and p-GSK-β, β-catenin, TCF4, Twist, MMP9 protein decreased after overexpressing PLUNC, while the expression of β-catenin in the nucleus and p-GSK-3β, β-catenin, TCF, Twist, and MMP9 protein increased significantly after interference PLUNC expression. Moreover, XAV-939 reinforce the tumor inhibition ability of PLUNC. Immunofluorescence test suggested that PLUNC could inhibit β-catenin into the nucleus of NPC cells, but the result was opposite after interference with the expression of PLUNC.
Conclusion PLUNC inhibited the migration and invasion of NPC cells through inhibiting the activation of the Wnt/β-catenin signaling pathway.

PU-4349

Construction and application of a miRNAs prognostic risk assessment model of gastric cancer

Shuang Shi
The Second Hospital of Shandong University

Objective To identify microRNAs (miRNAs) biomarkers related to the prognosis of gastric cancer patients, and construct a miRNA risk assessment model for survival prediction.
Methods The miRNA expression profile of gastric cancer patients and relevant clinical data were obtained from the Cancer Genome Atlas (TCGA) database. Differentially expressed miRNA were identified with "DESeq2" package. The miRNA related to prognosis were screened with univariate Cox regression and Kaplan-Meier analysis, which were analyzed with multivariate Cox regression to construct a prognostic risk assessment model. A receiver operating characteristic (ROC) curve was drawn with "time ROC" package to evaluate the effectiveness of the model. Finally, the messenger RNAs (mRNAs) that miRNA might bind to were predicted with online database, and

the possible functions were predicted with gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG).
Results With log2 |Fold Change |＞1 and P＜0.05 as the standards, 248 differentially expressed miRNA in gastric cancer tissues were identified. Univariate Cox regression and Kaplan-Meier analysis screened out 6 differentially expressed miRNA which had significant correlation with prognosis to construct a prognostic risk assessment model. The risk score =0.04835 × miR-181b-1 + 0.11206 × miR-548d-1 + 0.06800 × miR-675 + 0.07587 × miR-708 + 1.17521 × miR-4640 + 0.08989 × miR-4709. Kaplan-Meier analysis showed patients with high risks had a poor prognosis (P＜0.001). The area under the ROC curve (AUC) of the 5-year overall survival rate was 0.776, indicating the model was able to predict the prognostic risk. GO and KEGG analysis showed miRNA were involved in a few signaling pathways of gastric cancer.
Conclusion A miRNAs prognostic risk assessment model was successfully constructed based on bioinformatics analysis, which was proved by Kaplan-Meier analysis and ROC curve to have good prediction effects on the survival of gastric cancer patients.

PU-4350

Pyroptosis, Metabolism and Tumor Immune Microenvironment

Tiantian Du
The Second Hospital of Shandong University

In response to a wide range of stimulations, host cells activate pyroptosis, a kind of inflammatory cell death (ICD) which is provoked by the cytosolic sensing of danger signals and pathogen infection. In manipulating the cleavage of gasdermins (GSDMs), researchers have found that gasdermin proteins serve as the real executors and the deterministic players in fate decisions of pyroptotic cells. Whether inflammatory characteristics induced by pyroptosis could cause damage the host or improve immune activity is largely dependent on the context, timing and response degree. Here, we systematically review current points involved in regulatory mechanisms and the multidimensional roles of pyroptosis in several metabolic diseases and the tumor microenvironment (TME). Targeting pyroptosis may reveal potential therapeutic avenues.

PU-4351

RNA-Seq Profiling of Serum Exosomal Circular RNAs Reveals Circ-PNN as a Potential Biomarker for Human Colorectal Cancer

Yan Xie
The second hospital of Shandong University

Circular RNAs (circRNAs) are emerging as cardinal areas of focus in the non-coding RNA field. Growing evidences have revealed exosomal circRNAs as potential biomarkers for detection of various cancers. However, the clinical importance of most serum exosomal circRNAs in colorectal cancer (CRC) have rarely been investigated. In this study, we examined the possible clinical application of serum exosomal circRNAs in the diagnosis of CRC. Firstly, we conducted RNA sequencing (RNA-seq) analysis using fifty CRC and fifty healthy control serum samples to identify CRC-related circRNAs. The sequencing data showed 122 differentially expressed circRNAs including 100 up-regulated and 22 down-regulated circRNA transcripts in CRC patients. Then, eight most dysregulated circRNAs were selected for validation by reverse transcription-quantitative polymerase chain reaction (RT-qPCR) assay. Validation analysis revealed that the

serum exosomal circ-PNN (hsa_circ_0101802) levels were significantly up-regulated in CRC cases compared with those in the healthy control groups. Receiver operating characteristic curve (ROC) analysis suggested that circ-PNN had significant value in CRC diagnosis with areas under the ROC curve (AUC) of 0.855 and 0.826 in the training and validation sets, respectively. We also found that the AUC of serum exosomal circ-PNN for early-stage CRC was 0.854. Finally, a network map based on circ-PNN was constructed to determine its potential miRNA-mRNAs binding. We also demonstrated that the expression of hsa-miR-6833-3P, hsa-let-7i-3p and hsa-miR-1301-3P were negatively correlated with circ-PNN in CRC patients. Collectively, our findings indicated that serum exosomal circ-PNN might be a potential non-invasive biomarker for the detection of CRC and may play a crucial role in the pathogenesis of CRC.

PU-4352

A m6A-mediated LNPPS suppresses tumorigenesis of bladder cancer via regulating the PDCD5/p53/MDMD2 signaling pathway

Yifan Wang
The Second Hospital, Cheeloo College of Medicine, Shandong University

Long non-coding RNAs (lncRNAs) play critical roles in tumor initiation and progression. However, little is known about the functional role of lncRNAs in the p53-related tumor inhibition. Here, through transcriptomic profiling analysis of primary bladder cancer (BC) tumor and adjacent non-tumor tissues, we discovered a lowly expressed lncRNA, which we named as LNPPS (LncRNA for PDCD5 and p53 stability), could inhibit BC cell viability by inducing programmed cell death 5 (PDCD5)/p53-related apoptosis in vivo and in vitro. Mechanistically, LNPPS, serving as a scaffold, could connect PDCD5 and p53 with nucleotides located at 121 to 251 and 252 to 306 of LNPPS, respectively. Furthermore, LNPPS protected PDCD5 from proteasomal degradation through blocking its K20 ubiquitination. On the other hand, the greatly increased interaction between PDCD5 and p53 displaced p53 from Mouse double minute 2 homolog (MDM2)-p53 ubiquitination complex, resulting in upregulation of p53 and the related apoptosis level. Moreover, LNPPS could induce the accumulation of PDCD5 and p53 in nucleus and plays a synergistical effect on protein degradation. Finally, we confirmed that the suppressed LNPPS was mediated by the lower level of m6A modification. To conclude, our present findings highlighted the suppressive role of LNPPS in BC tumorigenesis via the regulation of PDCD5-p53-MDM2 axis, suggesting its great potential to serve as effective therapeutic target for patients with BC.

PU-4353

The value of NLR as a marker of renal damage in patients with H type hypertension

Zhenni Chen[1,2]、Biqiong Ren[1,2]
1. The second people's Hospital of Hunan Province
2. 湖南中医药大学临床医学院

Objective To explore the relationship between neutrophils to lymphocyte ratio (NLR) and renal function impairment in patients with H-type hypertension, and to reveal the clinical application value of NLR.
Methods 618 hypertension patients were divided into two groups according to the level of serum Hcy: the hyperhomocysteinemia group (Hcy ≥ 15 μmol/L) and the non-H hypertension group (Hcy < 15 μ mol/L). The glomerular filtration rate was calculated by CKD-EPI equation suitable for

Chinese population. The total leukocyte count (WBC), neutrophil value (n), neutrophils to lymphocyte ratio (NLR), estimated glomerular filtration rate (eGFR), and the level of serum Creatinine, Uric acid, Urea between the two groups were compared. Meanwhile, HHcy group was divided into HHcy-L group (15 ≤ Hcy < 20 μ mol/L) and HHcy-H group (Hcy ≥ 20 μ mol/L). Compared with non-H type hypertension group, according to WBC, NLR level three quantile interval, each group was divided into WBC low value, middle value, high value group and NLR low value, middle value, high value group, for statistical analysis.
Results 1) there were significant differences in Cr, Urea, UA and eGFR between HHcy group and non-H type hypertension group ($P < 0.001$); there were no significant differences in WBC and neutrophil absolute values between HHcy group and non-H type hypertension group ($P > 0.05$), but there were significant differences in NLR ($P < 0.01$); 2) There was no correlation between WBC and renal injury in HHcy group and non-H hypertension group ($P > 0.05$). NLR was significantly correlated with renal injury in HHcy-L group and HHcy-H group ($P < 0.05$, $P < 0.01$); 3) The results of ROC curve analysis showed that in HHcy-H group, when NLR was 2.247, Jordan index was the highest (0.3962), corresponding sensitivity was 0.7746, specificity was 0.6216, area under ROC curve was 0.6799 [95% CI (0.4610, 0.7594)]; 4) linear regression analysis showed that eGFR in HHcy-L group was negatively correlated with serum NLR level ($r = - 0.185$, $P < 0.05$), There was a significant negative correlation between eGFR and NLR in HHcy-H group ($r = - 0.430$, $P < 0.001$); 5) logistic regression analysis showed that the risk of renal injury increased by 10% ($P < 0.001$) for each 1 μ mol/L increase of Hcy, and 51% ($P < 0.05$) for each 1.0 increase of NLR in HHcy-H group.
Conclusion the degree of renal injury in HHcy patients is significantly higher than that in non-H type hypertension patients. NLR can be used as a marker of renal injury in H-type hypertension patients except for renal function index. However, the WBC and neutrophil does not have such a suggestive effect. NLR should be included in the blood routine test report as an important index.

PU-4354

A rare case of Aspergillus terreus Endogenous Endophthalmitis in a Nonimmunocompromised Patient and Laboratory Research

Ying Zhao
Peking Union Medical College Hospital

Background Aspergillus terreus is a common soil saprophyte which is also clinically important, causing infections ranging from superficial infections, such as onychomycosis, to invasive aspergillosis (IA) in severe immunocompromised hosts. Endophthalmitis caused by A. terreus is rarely reported in the literature. We report a case of endogenous endophthalmitis caused by A. terreus in a nonimmunocompromised patient with hypertension, taking regular medications and blood pressure controlled in the normal range, but without prior intraocular eye surgery or history of immunosuppression.
Material/**Methods** A vitreous biopsy was taken for culture and direct smear microscopy and further identified the isolate from culture positive plates by phenotype observation and molecular Methods In vitro antifungal susceptibility test were done by Etest.
Results Fungal spores and septate hyphae were found in vitreous direct smear (Figure 1). Tiny hair-like colonies grew on SDA after 7days' culture but the colony morphology is still atypical after 10 days' culture (Figure 2). We found attached spores by using scotch tape to stick the colonies on the side to (Figure 3). After 2 times generation (nearly a month), the strain showed typical colony (Figure 4) and microscopic morphology (Figure 5). The isolate was final identified as A. terreus according to morphology and the results of phenotypic and molecular identification. The isolate's MICs (μg/mL) to itraconazole, voriconazole, amphotericin B were 0.25, 0.125, and 2, respectively.

Conclusions Early diagnostic and therapeutic vitrectomy is useful for obtaining sufficient samples for organism identification and also to reduce organism load and inflammatory mediators in the eye. Timely reporting the results of direct smear to clinical physician is very meaningful for the initial selection of antimicrobial agents. For the phenotype atypical but clinical important filamentous fungi, using ITS sequence analysis and other molecular identification Methods can help to identify the fungal pathogen promptly.

PU-4355

Successful treatment of plantar warts using topical Zijinding, a traditional Chinese medicine preparation: A case series

Ying Zhao
Peking Union Medical College Hospital

Introduction Plantar warts are associated with high transmissibility and morbidity. Among the available therapeutic options, none is uniformly effective or virucidal. Salicylic acid is the first-line therapy but approximately one-third of lesions could not resolve and become recalcitrant despite repeated treatment. Cryotherapy is widely accessible with low cost but may be complicated by pain, blister formation, hemor- rhage, infection, excessive granulation tissue formation, and hyper -/hypo-pigmenta- tion. Hence, alternative treatment modalities are essential.

Methods Three patients with debilitating plantar warts refractory or intolerant to cryotherapy were treated with a course of Zijinding (a traditional Chinese medicine preparation) paste prepared with white vinegar.

Results All three patients showed excellent clinical response with Zijinding applica- tion with evolution of lesions to scabs and subsequently healthy skin within 1.5 to 5 months of treatment. Treatment was well tolerated and had no significant side ef- fects with excellent compliance recorded for all three patients. There was no relapse for at least 10 months after stopping the treatment.

Conclusion Topical Zijinding could be a promising alternative modality for the treat- ment of plantar warts. Further clinical trials on the comparison of Zijinding and other treatment modalities of plantar warts are warranted. Further studies are required to investigate the mechanism of action of Zijinding and to isolate the active ingredient. KEYWORDS plantar warts, traditional Chinese medicine, Zijinding

PU-4356

Etiological Analysis Of Pemphigus Complicated With Infection

Ying Zhao
Peking Union Medical College Hospital

Background Pemphigus is a group of potentially lethal autoimmune blistering skin diseases. It is characterized by the production of pathogenic autoantibodies directed against different proteins of the desmosome, leading histologically to intraepidermal cleavage, and clinically to vesicles and erosions on the epithelium of the mucous membranes and/or the skin. Patient usually needs long-term treatment with glucocorticoids and immunosuppressants, which increasing the risk of

infection. In order to understand the infection situation of pemphigus patients, explore the etiology of infection, the clinical data of 76 patients with pemphigus in our department were analyzed retrospectively.
Materials/**Methods** 76 cases of pemphigus from Jan 2017 to Nov 2019 and their clinical microbiological examination results were analyzed retrospectively.
Results 164 specimens (including 53 wound secretion, 30 respiratory tract specimen, 11 midstream urine, 17 oral swab,10 pus, 10 throat swab, 5 peripheral blood, et al) were sent to clinical microbiology laboratory for etiological examination. 178 strains (including 76 gram positive bacteria, 55 gram negative bacteria, 46 fungi, 1 mycobacterium) were isolated from these specimens. The most common gram positive bacteria are Staphylococcus aureus (30), Coagulase negative Staphylococcus (22,including 14 Staphylococcus epidermidis), and Enterococcus faecalis (4). The most common gram negative bacteria were Klebsiella pneumoniae (12), Pseudomonas aeruginosa (11), Escherichia coli (6) and Acinetobacter baumannii (6). The most common fungi were Candida spp.(42, including 17 Candida albicans, 8 Candida tropicalis, 5 Candida parapsilosis). 5 patients got bloodstream infection and all of them were condition improved and discharged because of timely and effective treatment. One patient got multiple infection with Pseudomonas aeruginosa in the pus and his blood and Listeria monocytogenes in his blood and CSF.
Conclusions Pemphigus is often complicated with infection, which has been reported previously. Most often infection was skin and mucous membrane infection, followed by lung infection and urinary tract infection. In this study, skin infection was the most infection, Staphylococcus aureus and yeast from the colonization bacteria of skin and mucous membrane are the most common pathogens. Infection control is the key point of pemphigus treatment, and early detection of special infection is of great significance to reduce mortality.

PU-4357

TRPV6 promotes breast cancer metastasis by upregulating ADAMTS6

xiang xu、jun wu
Shanghai General Hospital Jiading Branch, Shanghai Jiao Tong University School of Medicine, Shanghai

Objective Calcium signaling plays important roles in cell adhesion, migration and invasion of tumor cells. However, the mechanism is still indistinct. This study aims to explore the effect of cellular calcium on breast cancer cell metastasis and reveal the intrinsic mechanism.
Methods First, we measured cellular calcium concentration in breast cancer cells with stable calcium channel TRPV6 over-expression. Wound healing and Transwell assay were then operated in breast cancer cells with stable TRPV6 over-expression and low-expression. The cellular location of NFATC2 was detected in breast cancer cells with stable TRPV6 over-expression by Western blot and immunofluorescence. The target genes of NFATC2 were predicted in website BioUML. The wound healing and Transwell assay were performed to evaluate the cell migration ability.
Results Kaplan–Meier analysis of the effect of TRPV6 mRNA expression on the overall survival of breast cancer patients revealed that TRPV6 is closely associated with poor prognosis in patients with breast cancer. Activation of calcium channel TRPV6 promoted migration and invasion ability of breast cancer cells. NFATC2, whose cellular location was regulated by cellular calcium concentration, transferred from cytoplasm to nucleus followed by TRPV6 over-expression in breast cancer cells. Moreover, the expression of ADAMTS6, one of the target genes of NFATC2, increased in high expression of TRPV6 in breast cancer cells. Meanwhile, the expression of ADAMTS6 is correlated positively with the migration ability of breast cancer cells.
Conclusion These observations suggested that TRPV6 promotes breast cancer metastasis by upregulating ADAMTS6.

PU-4358

Application of Next-generation sequencing in the differential diagnosis of Dubin-Johnson syndrome

Jianfeng Shen[1]、wenbing yue[1]、sumin yang[1]、jing li[2]、min zhang[1]
1. Zhengzhou Jinyu Clinical Laboratory Co., Ltd.
2. 新郑市人民医院

Objective To analyze the genetic etiology of a patient with clinical manifestations of jaundice, yellow sclera, persistent hyperbilirubinemia, hyperplastic anemia suggested by bone marrow smear and suspected diagnosis of Dubin-Johnson syndrome by pathological biopsy, and to sort out the idea of differential classification of hyperbilirubinemia.
Methods Proband peripheral blood genomic DNA target capture all exons group which application of next-generation sequencing through bioinformatics data analysis , compare to our database of the general population, evaluate correlation between genes and disease by OMIM database and HPO, literature search by by HGMD literature database pro, select the possible pathogenic mutations. At the same time, bioinformatics software was used to predict the function of the variation and the conserved variant was evaluated. Finally, Sanger sequencing was conducted to verify the suspected pathogenicity variation in the family.
Results High-throughput sequencing results showed that the protestors with clinical manifestations of hyperbilierythroxin carried ABCC2 gene p. Glu647* and p.Arg1210Leu, Sanger sequencing confirmed that their parents carried ABCC2 gene variation. The proband carried a complex heterozygous variant of ABCC2 gene, which was mutually trans, and was consistent with the genetic pattern of Dubin-Johnson syndrome (AR). Mother, sister and older son had a heterozygosity with p.Glu647* and a father and younger son had a heterozygosity with p.Arg1210Leu. According to the guidelines of the Clingen Working Group on Interpretation of Sequence Variations, the p.Glu647* mutation was determined to be pathogenic and could theoretically cause Loss of function (through meaningless-mediated mRNA degradation or premature termination of encoded amino acid sequences) leads to disruption of the protein translation process, truncated protein production and loss of biological function p.Arg1210Leu is an unknown mutation of clinical significance, which has not been included in domestic and foreign literatures. The ABCC2 gene variant p.Arg1210Leu carried by the patient and p.Glu647* constituted a complex heterozygosity. p.Arg1210Leu was located in the ABCC2 protein domain and the site was very conserved which may affect the function of ABCC2 gene.
Conclusion The ABCC2 gene p.Glu647* and p.Arg1210Leu are the suspected pathogenic causes of this patient, and the mutation of p.Arg1210Leu was found for the first time in Dubin-Johnson syndrome.

PU-4359

Transcription factor AR regulates prostate cancer 3D genome

Xiaoyu Liu、haiyang guo
The second hospital of shandong university

Background Chromatin organization is critical in the regulation of tumor-specific gene expression. Transcription factor AR plays an important role in prostate cancer development, but there is a lack of AR function in the prostate cancer 3D genome organization.
Aims To determine the function and mechanism of AR in prostate cancer 3D genome
Methods Computational prediction was used to assess the potential of AR in the formation of liquid condensate via phase separation. AR ChIP-Seq was used to determine the enrichment of genomic binding at the regions that were important for three-dimensional interaction of chromatin.

Prostate cancer cells and PDXs were utilized to investigate the function of AR. AR HiChIP assay was performed to access the role of AR in the regulation of genomic three-dimensional interaction. LLPS experiments were conducted to determine the phase separation ability of intrinsically disordered region (IDR) in AR protein. We further assessed the capability of AR IDR in regulating prostate cancer specific chromatin three-dimensional interaction by CRISPR/Cas9-induced knock-in mutations at AR IDR.
Results AR protein has a strong IDR domain; The AR IDR domain is required for the prostate cancer-specific chromatin interaction; The AR IDR domain is also required for the formation of liquid condensate via phase separation; AR-associated chromatin loops regulate prostate cancer-specific gene expression.
Conclusion Based on these findings, we proposed that AR mediates the remodeling of high-order chromatin architecture and oncogene expression in prostate cancer by liquid-liquid phase separation (LLPS).

PU-4360

Genetic Study of an X-linked Agammaglobulinemia pedigree caused by an BTK mutation

Chenxi Wei[1]、Rujing Yang[2]、Xiaogeng Yuan[1]、Shihui Yu[3]、Jianping Qin[1]、Xinxian Tian[2]、Min Zhang[1]
1. Zhengzhou KingMed Center for Clinical Laboratory
2. 郑州大学第三附属医院（河南省妇幼保健院）
3. 广州金域医学检验中心有限公司

Background X-linked agammaglobulinemia (XLA) is a gamma globulin deficient, X linked recessive disorder. XLA is characterized by failure to produce mature B lymphocytes and be associated with a failure of Ig heavy chain rearrangement. The clinical feature shows recurrent bacterial infections in affected males in the first two years of life. The most common infection before diagnosis is recurrent otitis and virus infection can't be found. XLA is known to be associated with Bruton tyrosine kinase (BTK), also known as ATK or BPK. The defective BTK impairs early B-cell development in XLA, resulting in a significant reduction of mature B cells in peripheral blood. This study was designed to research the genetic pathogenesis of agammaglobulinemia in a family with two young patients who had repeated infection, which might benefit for both clinical diagnosis and family counseling.
Methods Data were collected from the patients' family including: clinical information, blood immune globulin level, as well as classification and subgrouping of B lymphocytes. Gene mutations were screened with whole exome sequencing (WES) and guideline through next-generation sequencing (NGS), verified with Sanger sequencing.
Results The IgG/IgA/IgM levels of two sick children were significantly lower than those of the girl with similar age and their mother in family. Flow cytometry result showed that numbers of CD19+ B lymphocytes were obviously lower than girl and their mother in family. A novel causative variant BTK NM_000061:c.1627T>C (p.Ser543Pro) was found in the family pedigree by WES. Two patients had this hemizygous variant, 5 female family members carried heterozygous variant with no phenotype and other members not detected. The phenotype and variant were co-segregated in family. This variant was not found in massive population database, such as gnomAD, ESP6500 etc. The variant located in the kinase domain which was not associated with benign variants, variant location close to Ser543 had been reported to be pathogenic or likely pathogenic. Most of the bioinformatical analyses predicted this variant as deleterious in biological function and the REVEL score was as high as 0.841. The decrease of immunoglobulin, reduction of B lymphocytes and mode of inheritance of disorder in patients are well defined phenotype matching with the XLA clinical diagnosis guideline.
Conclusion Based on results and guideline, BTK NM_000061:c.1627T> C (p.Ser543Pro) was found retrospectively to be a pathogenic variant. The patients were diagnosed as XLA. The

pathogenic variant should be the major cause of XLA in these patients´ pedigree. Our finding could provide fertility guidance for this family's members.

PU-4361

Association between ABO blood groups and clinical outcome of coronavirus disease 2019: Evidence from two cohorts

Weixiao Fan、Xianfei Zeng
Xi'an area medical diagnostic lab center

Objective To examine the correlation between blood type distribution and SARS-CoV-2 infection, progression, and prognosis of COVID-19.
Methods Two retrospective cohorts diagnosed with COVID-19 were enrolled in this study between February 5 and March 20, 2020. The first cohort comprised patients with mild symptoms admitted in three hospitals in Xi'an, Beijing, and Wuhan. The second cohort comprised critically ill patients from the two hospitals in Xi'an and Wuhan. COVID-19 was defined according to the World Health Organization interim guidance. COVID-19 was confirmed by a positive real-time reverse transcriptase polymerase-chain-reaction test of SARS-CoV-2 on nasal and pharyngeal swab specimens from suspected patients.
Continuous variables were expressed as median (25th and 75th percentiles), while categorical variables were expressed as percentages. The Mann–Whitney U-test or the Kruskal–Wallis test, as appropriate, were used to compare the medians of continuous variables between or among groups. Categorical data were tested using a $\chi 2$ test or Fisher's exact test. The unadjusted associations of ABO blood type and SARS-CoV-2 infection, development of ARDS or AKI, and death were tested separately among the cohorts using Pearson's $\chi 2$ test. Odds ratios (ORs) and 95% confidence intervals (CIs) were calculated to describe the possible effect on the occurrence and development of COVID-19. Statistical analyses were performed using SPSS (version 22.0) for Windows. A p-value of <0.05 was considered significant.
Given the limitations of a single factor analysis, we used multivariable logistic regression to further adjust the association of ABO blood type with occurrence of ARDS, AKI, or death for potential confounders, including the common risk factors of age, sex, pre-existing pulmonary disease, history of cardiovascular disease, diabetes mellitus, hypertension, and chronic kidney disease in the critical cohort. The history of diabetes mellitus was selected as a crucial confounder that needs to be adjusted because diabetes was reported to be protective against the development of ARDS, but as a risk factor for AKI and death.
Results The proportion of blood group A in patients with COVID-19, being 35.76% in the mild cohort and 39.22% in the critical cohort, was significantly higher than that in the reference population ($p=0.000$ and $p=0.005$, respectively). These results imply that the blood group A population may be more vulnerable to SARS-CoV-2 infection. In addition, blood type A was associated with increased risk of SARS-CoV-2 infection compared with the non-A blood type, with an OR value of 1.40 (1.01-1.96) and 1.63 (1.10-2.42) in the mild and critical cohorts, respectively. However, similar results were not obtained for B and O blood types. These observations further demonstrated that the blood group A population may be more susceptible to SARS-CoV-2 infection. Besides, age was associated with a higher risk for ARDS, AKI and death while blood type distribution was not a relevant factor of ARDS, AKI, and mortality in COVID-19 patients.
Conclusion The current retrospective study of two cohorts confirmed that blood type A populations are more susceptible to SARS-CoV-2 infection. Additionally, our study identified that age is a risk factor for the development of ARDS or death in critically ill patients with COVID-19. However, the outcomes including ARDS, AKI, and death are poor irrespective of ABO blood group distribution in critically ill patients with COVID-19.

PU-4362

Determination of CR-HvKP and Hv-CRKP by mouse lethality test

Dakang Hu
Huashan Hospital, Fudan University

Objective To investigate epidemiology of carbapenem-resistant hypervirulent Klebsiella pneumoniae (CR-HvKP) and their traits.
Methods Totally 436 Klebsiella pneumoniae (K. pneumoniae) strains were collected from 7 hospitals in mainland China between 2017.01 and 2018.02. Sequencing types, serotypes, antibiotic-resistance gene (blaKPC) and virulence genes (wzy-K1, allS, entB, irp2, iroN, iucA, fimH, mrkD, p-rmpA2, c-rmpA, p-rmpA and peg-344) were analyzed among 436 strains. Additionally, string test, capsule stain, Periodic Acid Schiff stain, fitness analysis, quantitative real-time PCR and mouse lethality test were also performed.
Results Diverse detection rates were found for the 13 virulence genes, ranging from c-rmpA (0.0%) to entB (100.0%). According to molecular criteria, 127 (29.1%), 186 (42.7%), 9 (2.1%) and 26 (6.0) strains were putatively denoted as HvKP, blaKPC(+)-KP, blaKPC(+)-HvKP and Hv-blaKPC(+)-KP. Mouse lethality test confirmed 2 blaKPC(+)-HvKP strains (JS184 and TZ20) and none Hv-blaKPC(+)-KP. JS184 showed K2 serotype, thin capsule, positive exopolysaccharides and string test. TZ20 presented K20 serotype, thin capsule, negative exopolysaccharide and string test. Compared with the positive control NTUH-K2044, qRT-PCR confirmed equal manC and galF expressions, growth curves in JS184 and TZ20.
Conclusions Molecular determination of CR-HvKP and Hv-CRKP brings remarkable bias compared with mouse lethality test. The exact prevalence of CR-HvKP is slight, which of Hv-CRKP is slighter.

PU-4363

UHRF1 ameliorates podocyte injury in mice with adriamycin-induced focal segmental glomerulosclerosis

Quanxin Li
Department of Clinical Laboratory, The Second Hospital of Shandong University

Focal segmental glomerulosclerosis(FSGS) is a common glomerular disease in children andadult nephrotic syndrome(NS) and it is one of the main causes of end stage renal disease(ESRD). Podocyte injury is the main pathological manifestation of FSGS. Recently, studies have shown that UHRF1 is involved in the development of renal disease. Epigenetic regulator UHRF1 is a regulator of DNA methylation and histone ubiquitination, and plays a important role in embryonic development and tumor genesis, but its role in kidney disease is poorly understood. Our previous work confirmed that the expression of UHRF1 in FSGS podocytes significantly decreased and aggravated podocyte injury, and the overexpression of UHRF1 significantly reduced podocyte apoptosis and inhibited the expression of Notch1. This study explores the role and regulation mechanism of UHRF1 in FSGS.
Methods In this study, the role of UHRF1 in FSGS podocyte injury and the molecular regulation mechanism of autophagy signaling pathway in podocytes were studied deeply by means of constructing podocyte UHRF1 knockout mice using Cre-loxP technology.Furthermore, the overexpression of UHRF1 by adeno-associated virus as a vector was further explored as a preliminary treatment for FSGS.
Results The expression of UHRF1 was decreased in renal tissues of FSGS, knockout of UHRF1 could further aggravate adriamycin-induced renal injury, overexpression of UHRF1 could alleviate podocyte injury in FSGS, and UHRF1 could regulate podocyte injury by regulating autophagy of

podocytes. In FSGS, the absence of UHRF1 aggravates podocyte injury by regulating podocyte autophagy, and UHRF1 may be a potential target of FSGS therapy.

PU-4364

Risk factors and mortality for patients with Bloodstream infectious of Carbapenem resistance Klebsiella pneumoniae in a tertiary hospital in southern China

Yili Chen、Yao Chen、Pingjuan Liu、Zhongwen Wu、Penghao Guo、Kang Liao
The First Affiliated Hospital of Sun Yat-sen University

Background Recently, bloodstream infection (BSI) caused by Klebsiella pneumoniae (KP), especially carbapenem-resistant KP (CRKP), results in higher and higher morbidity and mortality. We sought to explore the risk factors of mortality and evaluate existing therapy.
Methods A total of 274 patients with KP-BSI who were treated in the First Affiliated Hospital of Sun Yat-sen University from 1 January 2018 to 31 December 2020 were enrolled in the study. We divide patients into the carbapenem-sensitive group and the carbapenem-insensitive group according to the drug sensitive test about carbapenems to identify the risk factors related to the CRKP-BSIs. The outcome was defined as death within 28days since the first positive blood culture, survivor and nonsurvivor subgroups were compared to explore the predictors of mortality.
Result In this study, 242 patients suffered CSKP-BSI and 32 CRKP-BSI. We found CRKP infection were independently associated with cardiovascular disease (OR: 6.475, 95%CI: 1.373-30.525, P=0.018), the empirical use of cephalosporins (OR: 4.452, 95%CI: 1.183-16.744, P=0.027), pathogen isolated from other parts (OR: 4.667, 95%CI: 1.234-17.651, P=0.023), the department of patients when KP isolation (OR: 24.447, 95%CI: 5.257-113.702, P<0.001). Additionally, we found that carbapenems resistance (OR: 3.564, 95%CI: 1.096-11.586, P= 0.035), admission to ICU (OR: 5.935, 95%CI: 2.141-16.451, P=0.001) were independent risk factors for the death of KP BSI by comparing clinical and demographic characteristics of survivor and nonsurvivor.
Conclusion Our findings may be helpful for the reduction of the mortality of patients with KP BSI and the prevention of developing CRKP BSI in hospitals.

PU-4365

Evaluation of a commercial immunoassay for autoantibodies in Chinese Han systemic sclerosis population

Chenxi Liu、yongzhe li
Peking Union Medical College Hospital

Objective Systemic sclerosis (SSc) is a systemic autoimmune disorder that leads to vasculopathy, tissue fibrosis, and production of autoantibodies. A lack of reliable biomarkers has been a challenge for clinical diagnosis of the disease. To undertake this challenge, we employed a protein array-based approach to identify and validate SSc-specific autoantibodies using a previously described a two-phase strategy.
Methods Phase I involved profiled autoimmunity using HuProt arrays (20,240 human proteins) with 90 serum samples collected from the following subjects: 40 patients with SSc, 30 patients diagnosed with autoimmune conditions such as rheumatoid arthritis (RA; n = 6), systemic lupus erythematosus (SLE; n = 7), Sjögren's syndrome (SS; n = 7), dermatomyositis (DM; n = 5), polymyositis (PM, n = 5), and 20 healthy subjects. Bioinformatics analysis allowed us to identify

113 candidate autoantigens that were significantly associated with SSc. To validate these candidates in Phase II, we constructed a focused array with 113 identified antigens, and used this to profile a much larger cohort comprised of serum samples collected from 400 patients with SSc, 160 patients with autoimmune conditions, 40 chronic disease controls, and 100 healthy controls. Finally, we used Western blot analysis to validate the serum of validated proteins with high signal values (>3 standard deviations of the mean compared to the healthy group).
Results This two-phase strategy allowed us to identify and validate small nuclear ribonucleoprotein polypeptide A (SNRPA) as a novel SSc-specific serological biomarker. The observed positive rate of anti-SNRPA antibody in patients with SSc was 11.25%, which was significantly higher than that of any disease control group (3.33%) or healthy controls (1%). The elevated activity of anti-SNRPA in the sera of patients with SSc was further validated with traditional Western blotting.
Conclusion In conclusion, anti-SNRPA autoantibody serves as a novel biomarker for SSc diagnosis and may be promising for clinical applications, especially as a good supplementary marker in the clinical applications of anti-Scl-70 antibody.

PU-4366

Association of GTF2I, NFKB1, and TYK2 Regional Polymorphisms with Systemic Sclerosis in a Chinese Han population

Chenxi Liu、yongzhe li
Peking Union Medical College Hospital

Objectives Systemic sclerosis (SSc) is an uncommon autoimmune disease that varies with ethnicity. Single nucleotide polymorphisms (SNPs) in the GTFSI, NFKB1, and TYK2 genes have been reported to be associated with SSc in other populations and in individuals with various autoimmune diseases. This study aimed to investigate the association between these SNPs and susceptibility to SSc in a Chinese Han population.
Method A case-control study was performed in 343 patients with SSc and 694 ethnically matched healthy controls. SNPs in GTF2I, NFKB1, and TYK2 were genotyped using a Sequenom MassArray iPLEX system. Association analyses were performed using PLINK v1.90 software.
Result Our study demonstrated that the GTF2I rs117026326 T allele and the GTF2I rs73366469 C allele were strongly associated with patients with SSc (P = 6.97E-10 and P = 1.33E-08, respectively). Patients carrying the GTF2I rs117026326 TT genotype and the GTF2I rs73366469 CC genotype had a strongly increased risk of SSc (P = 6.25E-09 and P = 1.67E-08, respectively), and those carrying the NFKB1 rs1599961 AA genotype had a suggestively significantly increased risk of SSc (P = 0.014). Moreover, rs117026326 and rs73366469 were associated with SSc in different genetic models (additive model, dominant model, and recessive model) (P < 0.05) whereas rs1599961 was associated with SSc in the dominant genetic model but not in the addictive and recessive models (P = 0.0026). TYK2 rs2304256 was not significantly associated with SSc in this study.
Conclusion GTF2I rs117026326 and rs73366469 SNPs were strongly associated with SSc in this Chinese Han population. NFKB1 rs1599961 showed a suggestive association with SSc, and no significant association was found between TYK2 rs2304256 and SSc in this Chinese Han population.

PU-4367

Several Genetic Variants Associated with Systemic Sclerosis in a Chinese Han Population

Chenxi Liu、yongzhe li
Peking Union Medical College Hospital

Background Systemic sclerosis (SSc) is a connective tissue disease with ethnic differences. Single-nucleotide polymorphisms (SNPs) in the ARID3A, CXCR5 and TNFSF8 genes have been reported to be associated with various autoimmune diseases. The aim of this study was to investigate the association between these SNPs and susceptibility to SSc in a Chinese Han population.
Methods A case-control study was conducted in 343 patients with SSc and 694 ethnically matched healthy controls. SNPs in ARID3A, CXCR5 and TNFSF8 were genotyped using a Sequenom MassArray iPLEX system, and allele association analyses were performed using the PLINK v1.90 software.
Results Our study demonstrated that the ARID3A rs10415976 G, CXCR5 rs77871618 T and TNFSF8 rs1555457 T alleles were suggestively associated with patients with SSc (P = 0.049, P = 0.024 and P = 0.003, respectively). Patients carrying the ARID3A rs350146 TT and TNFSF8 rs1555457 TT genotypes had a significant increased risk of SSc (P = 0.03 and P = 0.004, respectively). Moreover, rs10415976, rs77871618 and rs1555457 were associated with SSc in an additive genetic model (P < 0.05). rs62132345 and rs1555457 were associated with SSc in the dominant genetic model (P < 0.05). rs350146 was associated with SSc in the recessive genetic model (P = 0.029).
Conclusions ARID3A rs10415976, ARID3A rs350146 and CXCR5 rs77871618 were suggestively associated with SSc and TNFSF8 rs1555457 was strongly associated with SSc in the Chinese Han population in this study.

PU-4368

A meta-analysis of genome-wide association studies for Sjögren's syndrome identified novel loci and ansestral-specific effects

Chenxi Liu、yongzhe li
Peking Union Medical College Hospital

Sjögren's syndrome (SS) is a common autoimmune disease with a strong genetic background. To systematically identify susceptibility loci of SS, we combined four genome-wide association studies (GWAS) and performed a meta-analysis of GWAS. The subjects were mainly East Asian and European. We identified the susceptibility loci (Pmeta < 5e-8) across the major histocompatibility complex (MHC) class I, III and II regions and found HLA-C in MHC class I and EHMT2 in MHC class III as new susceptible loci for SS. Some of the MHC loci showed population heterogeneity between East Asia and Europe. We identified 12 non-MHC loci associated with SS, including FCGR2A, STAT4, IL12A, PTTG1, PRDM1, IKZF1, IRF5, BLK, DDX6-CXCR5, IQGAP2, GTF2I and TNIP1. The first 9 loci were significant in all subjects, the next 2 loci were significant in East Asia, and the last locus was significant in Europe. The four loci (FCGR2A, PTTG1, PRDM1 and IQGAP2) were novel for SS. Ingenuity pathway analysis (IPA) was performed, and the results showed that most molecules were involved in pathways such as the cellular immune response and humoral immune response, while the differences in pathways and networks between East Asia and Europe were small. Our study provided the overall susceptible loci of SS.

PU-4369

Intranasal immunization with a rNMB0315 and combination adjuvants induces protective immunity against Neisseria meningitidis serogroup B in mice

Zhenyu Li
Hengnan People's hospital

Objective Neisseria meningitidis (N. meningitidis) is a human-specific pathogen and a major cause of meningitis and septicemia with a high case fatality rate. N. meningitidis may penetrate the nasopharyngeal mucosal membrane and cause severe meningitis, a mucosal immune response plays a key role in the defense against meningococcal infections. Our previous study demonstrated that N. meningitidis serogroup B 0315 (NMB0315) was a vaccine candidate against N. meningitidis serogroup B (NMB) through parenteral immunization. In this study, immunopotentiators (C48/80 or CpG-ODN) were loaded into chitosan nanoparticle (Chi NP) to form combination adjuvants (Chi-CpG NP and Chi-C48/80 NP) and adopted to enhance the immunogenicity of NMB0315 through intranasal immunization.
Methods Transmission electron microscopy (TEM) was used to observe the morphology, the particles's zate potential and polydispersity index by Zetasizer Nano-ZS. The female BALB/c mices were intranasally immunized with rNMB0315+Chi-C48/80 NP, rNMB0315+Chi-CpG NP and the serum, nasal washes and vaginal washes samples were collected to detect the rNMB0315 specific serum antibodies IgG, IgG1 and IgG2a, as well as sIgA antibody levels in vaginal wash and nasal wash by indirect ELISA. Splenic lymphocyte cultured supernate was used to detect the levels of cytokine IFN-γ, IL-4 and IL-17A by using ELISA kits according to the manufacturer's instructions. The bactericidal titer of the immune serum was detected by serum bactericidal assay (SBA) and the immune protective effect was investigated with the recombinant protein vaccine in vivo.
Result TEM analysis showed that the Chi-CpG NP and Chi-C48/80 NP were spherical, with an average mean diameter of 150~200 nm; zeta potential were 11.25±0.052mv and 19.54±0.069 mv; polydispersity index were 0.286 and 0.415, respectively. In addition, rNMB0315 loading efficacy on nanoparticles, Chi-C48/80 NP(85.5％) was higher than Chi-CpG NP (71.2％) . The Chi-CpG NP and Chi-C48/80 NP are effective mucosal adjuvants for the induction of significantly higher rNMB0315-specific IgG, IgG1, IgG2a and sIgA antibodies. Meanwhile, Chi-CpG NP and Chi-C48/80 NP could change the ratio of IgG1/IgG2a, inducing a more balanced cellular/humoral immune response. Chi-CpG NP and Chi-C48/80 NP also boosted interleukin-4 (IL-4), interferon-γ (IFN-γ) and interleukin-17 A (IL-17A) production by splenocytes, showing that Th1 and Th2, Th17 cells were induced in vivo. At day 42, the serum bactericidal titers of rNMB0315 group, rNMB0315+Chi-CpG NP group and rNMB0315+Chi-CpG NP group reached 1:2, 1:4 and 1: 8 respectively, the protection rates of the three groups were 60%, 75% and 85% respectively against the N. meningitidis strain MC58.
Conclusion The combination adjuvants could be applicable to the development of a mucosal vaccine against Neisseria meningitides serogroup B (NMB).

PU-4370

Epidemiology of and risk factors for mortality due to carbapenemase-producing organisms (CPO) in healthcare facilities

Shengyuan Zhao[1,2]、Sharon Kennedy[3]、Meghan Perry[4]、Julie Wilson[5]、Margo Chase-Topping[6,7]、Eleanor Anderson[8]、Mark Woolhouse[2,9]、Michael Lockhart[3]
1. Department of Clinical Laboratory, Xiangya Hospital, Central South University, Changsha, Hunan, China
2. Usher Institute, University of Edinburgh, Edinburgh, UK
3. Public Health Scotland, Glasgow, UK
4. Regional Infectious Diseases Unit, Western General Hospital, Edinburgh, UK
5. Antimicrobial Resistance and Healthcare Associated Infection Scotland, NHS National Services Scotland, Glasgow, UK
6. Roslin Institute, University of Edinburgh, Edinburgh, UK
7. Royal (Dick) School of Veterinary Studies, University of Edinburgh, Edinburgh, UK
8. NHS Greater Glasgow and Clyde, Glasgow, UK
9. Centre for Immunity, Infection and Evolution, School of Biological Sciences, University of Edinburgh, Edinburgh, UK

Aim To evaluate clinical and molecular epidemiology and mortality associated with CPO among patients in Scotland since its first report in 2003.
Methods All CPO from clinical and long-term healthcare surveillance cultures across Scotland in 2003-2017 were reviewed retrospectively. Polymerase chain reaction was used to detect genes coding for carbapenemases. A generalized linear mixed model was used to identify risk factors for mortality.
Results In total, 290 individuals with CPO were identified. The overall incidence increased over time (P<0.001) from 0.02 to 1.38 per 100,000 population between 2003 and 2017. A total of 243 distinct CPO isolates were obtained from 269 isolations in 214 individuals with available metadata. The majority of the isolates were Enterobacterales (206/243, 84.8%), and Klebsiella pneumoniae (65/206, 31.6%) and Enterobacter cloacae (52/206, 25.2%) were the most common species. VIM (75/243, 30.9%) and NDM (56/243, 23.0%) were the most common carbapenemases. The crude 30-day mortality rate was 11.8% (25/211), while the case fatality rate was 5.7% (12/211). Age >60 years [adjusted odds ratio (aOR) 3.36, 95% confidence interval (CI) 1.06-10.63; P=0.033], presence of non-fermenters (aOR 4.88, 95% CI 1.64-14.47; P=0.005), and systemic infection or organ failure (aOR 4.21, 95% CI 1.38-12.81; P=0.032) were independently associated with 30-day mortality.
Conclusion The incidence of CPO in Scotland is low but increasing. Awareness is required that inpatients aged >60 years, patients with systemic infection or organ failure, and patients presenting with non-fermenters are at higher risk of death from CPO.

PU-4371

Changes of ER, PR and HER-2 status during the treatment of breast cancer patients and their clinical significance

Linzhang Li、Xueying Yu、Ying Cai、Chengwu Han、Jun Shen、Yongtong Cao
Department of Laboratory Medicine, China-Japan Friendship Hospital

Objective For initial diagnosis of early breast cancer patients, in the original site before and after neoadjuvant chemotherapy, use recurrence of a transfer transfer of ER, PR, HER-2 state for data statistics and analysis, to observe the above index expression level whether there are differences in different periods, and analysis the ER, PR, HER-2 state change with neoadjuvant therapy efficacy and long-term prognosis, in order to provide more reference for the clinical treatment of breast cancer.

Methods It was collected that basic data, uncture pathology and postoperative pathology data, treatment plan and process, efficacy evaluation and follow-up data of 153 cases of breast cancer patients treated at the tumor center of our hospital on March 1, 2009 and December 31, 2018. Statistical software SPSS 22.0 was used to analyze the changes of ER, PR and HER-2 status in the treatment of breast cancer, and to analyze the changes of molecular expressions of breast cancer during preoperative neoadjuvant chemotherapy and disease recurrence, as well as their effects on the efficacy and prognosis.

Results Among the 63 patients receiving preoperative neoadjuvant chemotherapy, the expression level of ki-67 after neoadjuvant chemotherapy was lower than that before neoadjuvant chemotherapy, and the difference was statistically significant, while the difference of ER, PR and HER-2 was not statistically significant. Among the 90 patients initially diagnosed with at least one recurrence and metastasis at early stage, the changes of ER, PR and HER-2 status before and after recurrence and metastasis were statistically significant ($P<0.001$). Among the 90 patients with breast cancer recurrence and metastasis, the survival analysis results indicated that the tumor ER status and tumor size were the factors affecting DFS, and the difference was statistically significant ($P<0.05$). Among the 90 patients with breast cancer recurrence and metastasis, ER status, HER-2 status and Ki-67 expression were independent risk factors affecting DFS ofbreast cancer patients ($P<0.05$), and ER status was independent risk factor affecting OS of breast cancer patients ($P<0.05$).

Conclusion After neoadjuvant chemotherapy, the expression level of ki-67 was significantly lower than before, and preoperative ER, PR and HER-2 were not related to the efficacy of neoadjuvant therapy. In patients with breast cancer recurrence and metastasis, the ER, PR and HER-2 states of the recurrence lesions were changed compared with the states of the original lesions, in which the PR was mainly changed from positive to negative.

PU-4372

Small mixtures reveal a diagnostic new vision——three cases associated with APTT mixing study

Yuna Du、Boqing Wu、Zhengyu Xie、Chen Yiguo、Li Rong*
Jiangxi Provincial People's Hospital

Mixed test is a test method by mixing the plasma of patients with the mixed plasma of normal people according to the specific proportion, and then re-testing the relevant items. The procedure of the APTT mixing study consists of a 1:1 mixture of patient plasma and normal mixed plasma to detect APTT immediately or after incubation, and obtained seven values of APTT, respectively are APTT1-7.

Evaluation of results mainly depends on the values of APTT3, APTT6 and APTT7. If APTT3, APTT6, and APTT7 are all corrected, means the patient has a deficiency of clotting factors, doesn't have the inhibitor. If APTT3 and APTT7 are corrected, APTT6 minus APTT7 exceeds 3 seconds, it indicates the presence of time and temperature dependent inhibitor. If APTT3 and APTT7 are uncorrected, APTT6 minus APTT7 doesn't exceed 3 seconds, indicates the presence of inhibitor, but the inhibitor isn't time and temperature dependent. If APTT6 minus APTT7 exceed 3 seconds, it suggests the inhibitor is time and temperature dependent. In addition, we can also use the correction results of immediate or incubation mixed plasma as a diagnostic auxiliary index, which named as Rosner Index(RI). When RI less than 10% indicates the absence of factors, exceeds 15% indicates the presence of coagulant inhibitors.

Next, we'll confirm the clinical significance of APTT mixing study through several cases.

Case 1, a patient with prolonged APTT, results of the APTT mixing study showed APTT3, APTT6 and APTT7 were uncorrected, Rosner Index was greater than 15%, and APTT6 minus APTT7 exceeded 3 seconds, suggesting the presence of time and temperature dependent inhibitor. The activity of coagulation Factor 8 was only 0.6%, and the inhibitor was 487BU, so the diagnosis is Hemophilia A with inhibitor, needed to be treated with recombinant coagulation factor 7.

Case 2, a patient with abnormal APTT, APTT mixing study results were uncorrected, which is similar to the results in Case 1. The activity of coagulation factor 9 was only 0.1%, and the activity of coagulation factor 11 and 12 were also affected. The amount of coagulation factor 9 inhibitor was about 8BU. Therefore, the diagnosis is Hemophilia B with inhibitor and the treatment of this patient also required recombinant coagulation factor 7.
Case 3 is a patient who admitted to hospital with broken bone, preoperative examination showed abnormal APTT. So we carried out the APTT mixing study to explore the reason, results showed a decrease in activity of coagulation factors 8, 9, 11 and 12. After dilution of patient's plasma, the activity of these coagulation factors increased slightly, the content of lupus anticoagulant is 1.88. So the final diagnosis is lupus anticoagulant positive patient.

In conclusion of above 3 cases, we find APTT mixing study is simple and easy in operation and needn't special condition. But obviously, the clinical significance of APTT mixing study is very helpful for diagnosis and treatment. Therefore, it's worth popularizing this mixing study, especially in grassroots units.

PU-4373

Comprehensive analysis of the aberrant lncRNA-miRNA-mRNA network associated with Lung adenocarcinoma

Jing Wang
Yantai Yuhuangding Hospital

Background Recently, there has been enlarged attention in lncRNAs owing to their varied functions in cancers. A growing studies have reported that lncRNAs exercise roles in tumors by functioning as miRNA sponges or competing endogenous RNAs (ceRNAs) cooperate with miRNAs to connect with mRNA. However, it is not clear that functional roles and regulatory mechanisms of lncRNA-intervened ceRNA in lung adenocarcinoma (LUAD), and their use for potentially predicting the prognosis of LUAD.
Methods The expression profiles of mRNA, lncRNA of 535 LUAD sample tissues and 59 adjacent non-tumor lung tissues, and miRNA expression information of 521 LUAD sample tissues and 46 adjacent no tumor lung tissues were achieved from the The Cancer Genome Atlas (TCGA) database. Meanwhile, Gene Ontology (GO) analysis were performed using DAVID database and R/Bio conductor package of GO plot, KEGG pathway analysis were performed using R packages RSQLite and org.Hs.eg.db, visualized using Cytoscape software.
Results We identified a total of 1665 lncRNA, 127 miRNA, and 2503 mRNA as differentially expressed profiles. We constructed an aberrant lncRNA-mRNA-miRNA ceRNA network in LUAD, it was composed of 140 DElncRNA, 22 DEmiRNA, and 36 DEmRNA. According to the overall survival analysis, 36 out of 140 lncRNA, 16 out of 33 mRNA, and 2 out of 22 miRNA functioned as prognostic biomarkers for patients with LUAD (P value < 0.05). We got he top five GO and KEGG pathway significant enrichment and targeting mRNA of 36 DEmRNA associated with LUAD.
Conclusion Taken above, using integrated bioinformatics analysis, we have identified lncRNA-related ceRNA network in LUAD, which could improve our understanding of the cause and underlying molecular events, and these candidate genes and pathways could be therapeutic targets for LUAD.

PU-4374

Identification of potential genes with prognostic value in smoking Lung Adenocarcinoma by bioinformatics analysis.

dajie zhou
Yantai Yuhuangding Hospital

Background Lung adenocarcinoma occupies the majority of NSCLC. Smoking is one of the most important factors leading to lung cancer. While it is far to know that the signal pathway and driven genes in smoking lung adenocarcinoma.
Methods In this study, we extracted 433 samples of smoking lung adenocarcinoma and 75 cases of non-smoking lung adenocarcinoma from the Cancer Genome Atlas (TCGA) database. Gene Ontology (GO) analysis were performed using DAVID database and R/Bio conductor package of ggplot2, KEGG pathway analysis were performed using KEGG online database and R packages RSQLite and org.Hs.eg.db. Differential expressed genes in smoking and non-smoking lung adenocarcinoma were candidate genes and GO/KEGG enrichment analyzed.
Results We identified a total of 374 mRNA were differentially expressed (|log2 fold change| ≥2.0 and $P < 0.01$). A total of 71 mRNA were down-regulated, 303 mRNA were up regulated. Then, these differentially expressed genes contain 28 significant Go functions ($P< 0.05$) and 11 significant enrichment KEGG pathways ($P< 0.05$). Then, we matched 238 proteins of the 374 different expression genes in the PPI network. We got one most significant module in the PPI network, containing 30 proteins correlated to smoking lung adenocarinoma. The survival analysis of these genes encoding proteins revealed that three proteins, HIST1H4A, HIST1H2BF and HIST1H2BO, were significantly associated with survival status. These proteins belong to histone family, histone modification acts on a variety of biological processes.
Conclusion These data suggested that these three genes may be used as therapeutic targets and diagnostic biomarkers of smoking lung adenocarcinoma.

PU-4375

Inhibin B expression in Head and Neck Cancer tissues and correlation with tumor immune cell infiltration

Ying Wu[1]、Nuoya Ma[1]、Yuanyuan Wu[1]、Qing Zhu[1]、Min Xu[2]、Gouying Zou[1]
1. 湖南省第二人民医院检验科
2. 湖南省第二人民医院病理科

Objective To investigate the expression of inhibin B(inhibin B, INHB) α subunit (inhibin α, INHA) and βB subunit (inhibin βB, INHBB) in Head and Neck Cancer tissues and the relationship with tumor immune cell infiltration.
Methods The expression levels of INHA and INHBB in Head and Neck Cancer tissues and their correlation with clinicopathologic indicators were analyzed clearly by Oncomine and UALCAN database. The survival curve of INHA and INHBB expression in patients with Head and Neck Cancer was plotted by Kaplan-Meier Plotter, and the relationship between INHA, INHBB and tumor immune cell infiltration was detected with TIMER database. The degree of INHA and INHBB expression in nasopharyngeal carcinoma tissues and chronic nasopharyngitis tissues was verified by immunohistochemistry. In the meantime, the relationship between INHBB and clinicopathologic indicators was also analyzed.
Results Compared with normal tissues, the expression of INHA and INHBB was significantly higher in Head and Neck Cancer tissues. Analysis of the UALCAN database showed that INHA expression was extremely associated with clinical stage, tumor grade, and lymphatic metastasis, while INHBB was only associated with clinical stage and tumor grade. The overall survival (OS) and recurrence-free progression (RFS) were significantly shorter in patients in high INHA and

INHBB expression group than that in low expression group ($p < 0.05$). At the same time, INHA and INHBB also promoted the invasion of tumor immune cells ($p < 0.05$), and the expression of INHA and INHBB in Head and Neck Cancer was related to each other(partial. cor = 0.282, P = 1.94 e-10), which were examined via TIMER database. Immunohistochemistry results showed there was no significant difference in INHA expression and INHBB had a low expression in nasopharyngeal carcinoma tissues, when compared with chronic nasopharyngitis tissues. In addition, the expression of INHBB was associated with lymphatic metastasis ($p = 0.001$) and clinical stage ($p = 0.026$) in nasopharyngeal carcinoma.

Conclusion Data mining based on multiple databases found that INHA and INHBB are highly expressed in Head and Neck Cancer tissues than that in normal tissues, but transcriptional expression of INHA in nasopharyngeal carcinoma tissues is not significantly different from that in chronic nasopharyngitis tissues, and INHBB is underexpressed in nasopharyngeal carcinoma tissues, which indicates that the expression of inhibin B could be heterogeneous in different diseases. It is also related to clinicopathologic parameters, which could be expected to be potential biomarkers for diagnosis and prognosis as well as immunotherapeutic targets of Head and Neck Cancer in the future.

PU-4376

IFNγ/PD-L1 signaling improves the responsiveness of anti-PD-1 therapy in colorectal cancer-an in vitro study

Wenli Yuan[1]、Deyao Deng[1]、Hanyu Li[1]、Xinghui Hu[1]、Xueqin Shang[1]、Xia Hou[1]、Hongchao Jiang[2]、Hongchun He[1]

1. The second hospital of Yunnan Province
2. The Kunming Children's Hospital

Programmed cell death 1 ligand 1 (PD-L1) can be upregulated on cancer cells via interferon gamma (IFNγ) in the tumor microenvironment. IFNγ/PD-L1 signaling is associated with the response to immune checkpoint blockade in melanoma patients. Our previous investigation indicated that the microsatellite instability-high (MSI-H) cell line might exhibit selective hyperresponsiveness to IFNγ treatment, which contributes to increased PD-L1 expression and may be a mechanism of response to anti-PD-1 therapy in colorectal cancer. The present study evaluated the expression of PD-L1 in a set of MSI and microsatellite stability (MSS) cell lines with IFNγ treatment. The differential signaling molecules associated with signal transducer and activator of transcription (STAT) contributing to hyperresponsiveness to IFNγ exposure were also investigated. Furthermore, we established a coculture assay containing CT26 cells with higher expression of PD-L1 and peripheral blood mononuclear cells (PBMCs) in vitro. Changes in cancer cell viability as well as apoptosis status in response to anti-PD-1 therapy were demonstrated. We further observed changes in the percentage of CD4+ and CD8+ lymphocytes after PD-1 immunotherapy in the coculture assay. Finally, the average extent of inflammation and adaptive immunity factors in the assay was also investigated. This in vitro study revealed that the MSI cell line might exhibit hyperresponsiveness to IFNγ exposure, and IFNγ induced upregulation of PD-L1 mainly through increased STAT1 and decreased STAT3 signaling. IFNγ/PD-L1 signaling participated in the response to anti-PD-1 therapy mainly through the CTL profile. Our findings reinforce previous knowledge of the fact that the response to immune checkpoint blockade occurs mainly in patients with a preexisting intratumoral IFNγ/PD-L1 signal, thus suggesting potential therapeutic strategies to enhance responsiveness to PD-1 blockade immunotherapy in most patients with colorectal cancer.

PU-4377

Fibrinogen Clauss and prothrombin time derived method ratio can differentiate dysfibrinogenemia from hypofibrinogenemia and hyperfibrinogenemia

Meiling Luo、Liqun Xiang、 Jie Yan、Lin Liao、Yangyang Wu、Xuelian Deng、Donghong Deng、Peng Cheng、Faquan Lin
The First Affiliated Hospital of Guangxi Medical University

Objectives To determine whether the ratio of Fibrinogen Clauss and prothrombin-time–derived method (FgClauss/PT-der or FgPT-der/Clauss) can distinguish congenital dysfibrinogenemia (CD) from hypofibrinogenemia and hyperfibrinogenemia.
Methods The Clauss, prothrombin-time–derived method, and other coagulation tests were assessed in a total of 220 people, 66 CD patients, 54 hypofibrinogenemia patients, 50 hyperfibrinogenemia patients, and 50 normal control subjects. All of the indexes were derived from measurements obtained using an ACL-TOP 700 Coagulation Analyzer. The fibrinogen Clauss and prothrombin-time–derived method ratio was also calculated.
Results FgClauss in the CD group significantly decreased than that in the other groups (P=0.000). However, there was no statistically significant difference between the FgPT-der of the CD group and that of the normal control group (P=0.99). FgClauss/PT-der was significantly lower (P=0.000) and FgPT-der/Clauss significantly higher (P=0.000) in the CD group than in other groups. The area under the ROC curve of FgClauss/PT-der for diagnosis of CD was 1, and the optimal critical diagnosis point was 0.47. When the FgClauss/PT-der was < 0.47, the sensitivity and specificity for the diagnosis of CD were 100% and 100%,respectively. The area under the ROC curve of FgPT-der/Clauss for diagnosis of CD was 1, and the optimal critical diagnosis point was 1.7. When the FgPT-der/Clauss was > 1.7, the sensitivity and specificity for the diagnosis of CD were 100% and 100%, respectively.
Conclusion Fibrinogen Clauss and the prothrombin-time–derived method ratio can be considered an ideal index to distinguish congenital dysfibrinogenemia (CD) from hypofibrinogenemia and hyperfibrinogenemia.

PU-4378

Combined ERK and MK2 inhibition exerts synergistic antitumor activity and overcomes acquired drug resistance in pancreatic cancer

Qing Wei[1]、Qiong Li[1]、Min Li[2]
1. Renji Hospital, School of Medicine, Shanghai Jiaotong University
2. 上海交通大学医学院附属仁济医院

Introduction Pancreatic cancer is one of the most aggressive solid malignancies, marked by aberrant activation of signaling through the RAS-RAF–MEK–ERK (MAPK) pathway. Targeting the MAPK pathway terminal master kinases (ERK1/2) is currently a promising approach investigated in clinical trials in different types of cancers. Ulixertinib is an ERK1/2 kinase inhibitor with potent antineoplastic activity.
Methods Firstly, we measured cytokine profiles using a PCR array to investigate the pathways that were activated by MEK or ERK inhibition in PDAC cells. Flow cytometry analysis and western blot were performed to discovery the contribution of TNFα/TNFR1 signaling and its main downstream pathways to determining cell fate. Then MAPKAPK2 (MK2) was knocked down by shRNA and apoptosis was detected in shMK2 versus WT cells following treatment with Ulixertinib by flow cytometry analysis. Combination index was performed to examine the effect of combined

inhibition of ERK/MK2 signaling on growth suppression in PDAC cells. Furthermore, the mechanism by which TNFα was activated by ERK inhibition was explored using reverse phase protein array (RPPA) pathway mapping and then confirmed by qPCR analysis. Finally, mice bearing xenograft tumors were treated with combined inhibitors of ERK/MK2 to analyze tumor regression.
Results We demonstrated that Ulixertinib can significantly trigger the expression and release of tumor necrosis factor-alpha (TNFα) in PDAC cells. TNFα can transduce distinct signaling pathways leading to either apoptosis or survival. The downstream MK2/Hsp27 was targeted for cell survival. Then we revealed that combined inhibition of ERK and MK2 exerted synergistic anti-tumor activity both in vitro and in vivo. Mechanistically, TAK1 activation is involved to mediate TNFα activation.
Conclusion We conclude that combination of pharmacologic inhibitors that concurrently block both ERK and MK2/HSP27 axis has therapeutic potential against PDAC and it should be evaluated in a preclinical and clinical studies.

PU-4379

Development of a Loop-mediated Isothermal Amplification Assay for the Rapid Detection of Six Common Respiratory Viruses.

Nianzhen Chen
Shanghai East Hospital, School of Medicine, TongJi University

Purpose Due to the highly contagious and spreads quickly of respiratory infectious diseases (ADR), the availability of rapid, sensitive, and reliable diagnostic Methods is essential for disease control. Here, we develop an approach based on loop-mediated isothermal amplification (LAMP) for the detection of influenza A virus (Flu A), Flu A subtypes H1N1and H3N2, influenza B virus (Flu B), respiratory syncytial virus (RSV) subtypes A and B, human adenovirus (HAdV), parainfluenza virus (PIV) subtypes 1 and 3, and human rhinovirus (HRV) simultaneously.
Methods We designed primers specific to detect respiratory viruses above, optimized the RT-LAMP assay, and evaluated it for its sensitivity and specificity of detection using real-time monitoring based on SYBR - Green I. We also evaluated the result of our RT-LAMP assay on 638 nasopharyngeal (NP) swab specimens collected from padiatric patients were signs and symptoms of respiratory infection with the commercial RT-PCR by Cohen's Kappa. The samples with inconsistent results between RT-LAMP and RT-PCR were verified by Sanger sequencing.
Results The developed RT-LAMP assay displayed a detection limit of 1×102 copies/ml RNA close to that of RT-PCR, no cross-reactivity was observed in the 10 kinds of viruses studied. The results obtained with 638 clinical samples indicate that the developed method has high specificity (0.988 - 1) and sensitivity (0.863 - 1) for viruses studied, and the Kappa value of all viruses were more than 0.85 revealed an excellent agreement between the two Methods To further demonstrate the advantage of the RT-LAMP assay, in the collected specimens, the antigens of Flu A and Flu B also were detected by commercial Colloidal Gold kit, only 85 and 131 were detected as Flu A and Flu B positive respectively. In meeting the demand of rapid diagnosis, compared to the RT-PCR, we note that the κ value of RT-LAMP for Flu A and Flu B were 0.881 and 0.927 respectively, while the values of the commercial Colloidal Gold kit were only 0.813 and 0.700 respectively. Also, the sensitivity of commercial Colloidal Gold kit was lower than the RT-LAMP, resulting in many positive specimens being missed.
Conclusions we developed a RT-LAMP-based method, optimized for the detection of common respiratory viruses. It will be a powerful tool for rapid and reliable clinical diagnosis of ADR in primary hospitals.

PU-4380

Evaluation of a rapid and simplified protocol for direct bacterial identification from positive blood cultures by using matrix assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS)

Yufeng Dai、Chuanhao Jiang
The second xiangya hospital of central south university

Early and rapid identification of microorganisms is critical for reducing the mortality rate caused by bloodstream infections (BSIs). The accuracy and feasibility of directly identifying pathogens in positive blood cultures by matrix assisted laser desorption ionization time-of_x0002_flight mass spectrometry (MALDI-TOF MS) has been intensely confirmed. In this study, we combined density centrifugation and extra chemical lysis-extraction to develop an optimized method in the blood culture process, which significantly improved the effectiveness of direct identification by MALDI-TOF MS. The accuracy was evaluated by 2,032 positive blood culture samples (115 species of microorganism). The overall MALDI_x0002_TOF MS based identification rate with scores ≥ 1.700 was 87.60%. 94.06% of gram_x0002_negative bacteria were identified consistently to the genus level, followed by anaerobes (93.33%), gram-positive bacteria (84.46%), and fungi (60.87%). This protocol could obtain results within 10–20 min at a cost of less than $0.1 per sample, which saved up to 24 h in identifying 87.60% of the microorganism from positive blood cultures. This rapid and simplified protocol facilitates the direct identification of microorganism in positive blood cultures, and exhibits the advantages of cost-effective, time-saving, and easy-to-use. It could provide the causative organism of the patient to clinicians in time for targeted treatment and reduce mortality.

PU-4381

Immunodominant regions prediction of nucleocapsid protein for SARS-CoV-2 early diagnosis: a bioinformatics and immunoinformatics study

Yufeng Dai、Hongzhi Chen、Lingli Tang
The second xiangya hospital of central south university

COVID-19 caused by SARS-CoV-2 is sweeping the world and posing serious health problems. Rapid and accurate detection along with timely isolation is the key to control the epidemic. Nucleic acid test and antibody-detection have been applied in the diagnosis of COVID-19, while both have their limitations. Comparatively, direct detection of viral antigens in clinical speci-mens is highly valuable for the early diagnosis of SARS-CoV-2. The nucleocapsid (N) protein is one of the predominantly expressed proteins with high immunogenicity during the early stages of infection. Here, we applied multiple bioinformatics servers to forecast the potential immunodominant regions derived from the N protein of SARS-CoV-2. Since the high homology of N protein between SARS-CoV-2 and SARS-CoV, we attempted to leverage existing SARS-CoV immunological studies to develop SARS-CoV-2 diagnostic antibodies. Finally, N229-269, N349-399, and N405-419 were predicted to be the potential immunodominant regions, which contain both predicted linear B-cell epitopes and murine MHC class II binding epitopes. These three regions exhibited good surface accessibility and hydrophilicity. All were forecasted to be non-allergen and non-toxic. The final construct was built based on the bioinformatics analysis, which could help to develop an antigen-capture system for the early diagnosis of SARS-CoV-2.

PU-4382

Epidemic and pathogenic characteristics of Parvovirus B19 in Kidney Transplant Recipients in China

Qian Huang、yanan wang、xiaowei ma、Min Li
Renji Hospital Affiliated to Shanghai Jiaotong University School of Medicine

Parvovirus B19 (B19V) is a human pathogen that can cause a variety of diseases. B19V infection may persist in immunosuppressed patients, especially in kidney transplant (KT) recipients, who are unable to respond effectively to humoral or cellular immunity. There is a lack of the epidemiological studies on the course and clinical characteristics of B19V infections in KT recipients. By characterizing infections caused by B19V in KT recipients in Shanghai, China, we found that the infection rate of B19V in KT recipients was high (10.17%), which can cause anemia, lymphopenia, liver and kidney function damage. Due to the lack of adequate protective antibodies, immunodeficient patients are still at risk of secondary infection. All the B19V isolates detected in this study belonged to type Ⅰa. The genetic relationship of these B19V strains was very close, indicating that there is an epidemic of B19V in the hospital environment. Our present study also showed that B19V exhibits point mutations after a period of infection and the occurrence of point mutations may contribute to the immune escape of B19V, while the mechanism remains to be further studied. In conclusion, the patients with immunodeficiency should be alert to B19V infection, and the combination of symptomatic treatment and intravenous immunoglobulin (IVIG) treatment, coupled with the adjustment of the use of immunosuppressants, can effectively control B19V infection.

PU-4383

Establishment of early diagnosis models for cervical precancerous lesion using cervical cancer screening data sets

Bo Meng
广州金域转化医学院有限公司
昆明金域医学检验所有限公司

Background Human papilloma virus (HPV) DNA test was applied in cervical cancer screening as an effective cancer prevention strategy. The viral load of HPV generated by different assays attracted increasing attention on its potential value in disease diagnosis and progression discovery. TCT test could provide information about cervical lesion stages and infection status. However, neither of the test could provide absolute accurate test result so far. Since nowadays, many patients choose to do both HPV DNA test and TCT test, to combine the most information from both test results could provide more accurate test results compared only from one.
Methods In this study, three HPV testing data sets were retrieved from our data sets and respectively assessed and compared, including Hybrid Capture 2 (HC2) (n=31954), Aptima HPV E6E7 (n=3269) and HPV Cobas 4800 (n=13342). Viral load values generated by each method, bacteria infection status from TCT result and age, ect. were collected as variable factors. Logistic regression models for diagnosing early cervical lesions of the three data sets were established and compared. The best variable factor combination (VL+BV) and dataset (HC2) were used for further six machine learning models establishment. The performance of these models was evaluated and compared, and the best performed model was validated.
Findings Our results showed that viral load value was significantly correlated with cervical lesion stages in all three data sets. Viral Load and Bacterial Vaginosis were the best variable factor combination for logistic regression model establishment, and models based on the HC2 dataset

performed best comparing with the other two datasets. Machine learning method Xgboost generated the highest AUC value of models, which were 0·915, 0·9529, 0·9557, 0·9614 for diagnosing ASCUS higher, ASC-H higher, LSIL higher, and HSIL higher staged cervical lesions, indicating the acceptable accuracy of the selected diagnostic model.
Interpretations Our study demonstrates that HPV viral load and BV status were significantly associated with early stages of cervical lesions, and the best-performed models can serve as a useful tool to help early diagnose cervical lesions. This study is a big data based retrospective analysis study. It not only provide new diagnosing tool for accurate screening cervical cancer but also strongly testified the value of big data set of clinical diagnostic result. More studies were suggested to be carried out on the long time generated data set to discover more valuable findings to help improving clinical diagnostic accuracy.

PU-4384

Genome-Wide lncRNA Microarray Profiling Identifies Novel serum-based lncRNA biomarkers of Triple Negative Breast Cancer

Yongyin He[1]、Bin Xiao[2]、Ting Lei[1]、Zhenzhan Kuang[1]
1. General Hospital of Southern Theatre Command of PLA
2. 清远市人民医院

Background Circulating long non-coding RNAs(lncRNAs) serve as potential serum-based biomarkers for cancer diagonsis. Here, we identified the clinical value and biological function of lncRNA T376626, which could be used for Triple negative breast cancer(TNBC) detection.
Method Genome-wide lncRNA microarray was used to screen promising serum-based lncRNA biomarkers using 12 serum samples of breast cancer with different molecular subtypes and three healthy control. The expression of candidate serum lncRNAs were validated in 190 subjects. The diagnostic value of serum lncRNA T376626 was determined by the receiver operating characteristic(ROC) curve and serum stability experiment. We also evaluated the effect of hypoxia and serum deprivation on the expression of serumlncRNA T376626. RNA Fluorescent In Situ (FISH) and RNAScope ISH assay were conducted to examined the expression and location of lncRNA T376626 in TNBC cells and BC tissue. Kaplan-Meier analysis was conducted to evaluate the relationship between lncRNA T376626 and the overall survival(OS) rate of BC patients. The relationship between lncRNA T376626 expression and clinical pathological characteristic of BC patients were analyzed. CCK8 assay, colon forming assay, wound healing assay and transwell assay were performed to investigate the biological function of lncRNA T376626 in two TNBC cell lines. Cell apotosis, cell cycle and epithelial-mesenchimal transition (EMT) related biomarkers were quantified by western blot. The lncRNA T376626 binding proteins were screened and identified by RNA pulldown and RNA immunoprecipitaton.
Results The serum levels of lncRNA T376626 was significantly higher in TNBC, lower in non-TNBC groups and the lowest in healthy control. The expression of lncRNA T376626 was also increased in BC tissues and cell lines. The higher levels of lncRNA T376626 were found to be associated with higher pathological differentiation stage, more aggressive molecular subtype and poor prognosis of BC patients. ROC curve showed that the area under curve(AUC) was 0.857 and the sensitivity and specificity were 76.50% and 90.60% for lncRNA T376626. Besides, lncRNA T376626 was stable in serum and could be secreted under hypoxic environment. Overexpression of lncRNA T376626 significantly promoted TNBC cells proliferation, migration and invasion possibly through regulating several cell cycle, cell apoptosis and EMT biomarkers. A total of 131 lncRNA T376626-binding proteins were mainly enriched in biological processes such as mRNA splicing, cell adhesion and RNA alternative splicing. Two Laminin subunit, LAMB3 and LAMC2 were further identified to be lncRNA T376626-binding proteins.

Conclusion LncRNA T376626 may serve as a TNBC serum-based diagnostic and prognostic biomarker and play an oncogenic role in TNBC progression

PU-4385

The diagnostic and prognostic value of circulating tumor cells on multiple cancers by imFISH analysis

Xiaowen Dou、Min Li、Dan Xiong、Xiuming Zhang
Shenzhen Luohu People's Hospital

Objective To investigate the clinical value of imFISH on multiple cancers.
Methods A retrospective analysis was performed in Medical Laboratory Centre of Shenzhen Luohu Hospital Group covering from June 2018 to November 2020. A total of 235 cases involving 13 cancers were reviewed. The most confirmed cases were 80 breast cancers, 53 lung cancers, 31 colorectal cancers and other cancers. The correlation was evaluated between CTC analysis by imFISH (the detection rate and enumeration data) and different time periods, clinical stages, as well as the classical tumor biomarkers. Besides, the relationship between nuclear profile of CTCs and clinical prognosis were reviewed.
Results The positive rate of CTCs in all cancers was 65.53%, while the ratio of 81.25% was found in recurrent and metastatic patients. No statistical significance was observed between the untreated group (54.17%) and the treated group (61.79%) ($c2=0.833$, $P=0.361$). The CTC enumeration in two predominate cancers showed the positive rate was 41.25% (33/80) in breast cancers and 73.58% (39/53) in lung cancers and the significant difference with $c2=13.425$, $P<0.05$ was observed. The positive rate in post-treatment of breast and lung cancer was found with a decreased trend. Except for common tumor biomarkers including CEA, CA153, CA125 ($P>0.05$), there were significant differences in the positive rate of CTCs with lesion size, lymph node metastasis, distant metastasis and clinical staging ($P<0.05$). A dynamic CTC monitoring in six cancer patients showed that the characteristics including the nuclear shape and number provided a valuable insight into different stages of disease progression related to the clinical prognosis.
Conclusion The CTCs detection with imFISH is related to clinical characteristics, and the nuclear profile is correlated with clinical prognosis. The detection of CTCs has a certain clinical value in predicting tumor recurrence, metastasis and treatment prognosis.

PU-4386

MicroRNA expression profling after recurrent febrile seizures in rat and emerging role of miR-148a-3p/SYNJ1 axis

Jian Xu、Mingqiang Sun、Xiaodong Li
Maternal and Child Health Hospital of Weifang Medical University

Febrile seizures (FSs) are common neurological disorders in both infants and children, although the precise underlying mechanism remains to be explored, especially in the expression pattern and function of microRNAs (miRNAs). In this report, we aimed to screen new potential miRNAs and examine the role of miR-148a-3p in hippocampal neurons in FS rats via Synaptojanin-1 (SYNJ1). Thirty rats were randomly divided into the normal and FS model groups, which were investigated by miRNA array. This process identifed 31 diferentially expressed (20 upregulated and 11 downregulated) miRNAs and potential miRNA target genes. In addition, hippocampal neurons were assigned into fve groups for diferent transfections. Apoptosis was

detected by TUNEL and fow cytometry. SYNJ1 was identifed as a target gene of miR-148-3p. In vitro experiments revealed that inhibition of miR-148a-3p decreased neuronal cell apoptosis. Moreover, overexpression of miR-148a-3p resulted in activation of PI3K/Akt signaling pathway and the apoptosis of hippocampal neurons. MiR-148a-3p inhibitor could reverse the above events. Taken together, our data demonstrated that the hippocampal miRNA expression profles of a rat model of FS provide a large database of candidate miRNAs and neuron_x0002_related target genes. Furthermore, miR-148a-3p acted as a apoptosis enhcaner via the activation of the SYNJ1/PI3K/Akt signaling pathway, highlighting a potential therapeutic target in the treatment of infants with hyperthermia-induced brain injury

PU-4387

FLT3 internal tandem duplication mutation up-regulates protein tyrosine phosphatase C1-TEN in AML blast

Mansheng Luo、Yan Lin
The Affiliated Ganzhou Hospital of Nanchang University

Context Due to the interactions between C1-TEN and other protein tyrosine kinase, this study aims to explore whether this phosphatase correlates with the FLT3-ITD mutation on AML blast.
Materials and Methods Primary blasts were separated from bone marrow of AML patient, after which qRT-PCR was carried out to detect C1-TEN mRNA. Two AML cell lines, namely HL-60 and MV4-11, were subject to treatments by tyrosine kinase inhibitor Sorafenib and or PKC412 for 18 h, respectively. The sensitivity of these cell lines towards these two TKI was analyzed through MTT, while the expression of FLT3 and C1-TEN was examined via qRT-PCR. Moreover, Western blot was used to analyze C1-TEN and FLT3 activation in terms of translation. In another experiment, CCK-8 assay was employed to assess the effect of C1-TEN suppression on FLT3-ITD phosphorylation of MV4-11.
Results Primary blasts were revealed to highly express C1-TEN in FLT3-ITD mutant AML but moderately in FLT3-WT AML. With respect to TKI sensitivity, HL-60 (FLT3-WT) performed tolerance while MV4-11 (FLT3-ITD) showed obviously sensitive to the TKI tested in this experiment. Another outcome demonstrated that FLT3 mRNA decreased on MV4-11 after both TKI treatments while this phenomenon did not occur on HL-60. Western blot revealed C1-TEN inhibitory effects of these TKI on MV4-11 but not HL-60. In addition, this study turned out that C1-TEN blocking could coordinate with TKI to sensitize MV4-11 cell line, but fail to influence FLT3 activation when used alone.
Conclusion In short, evidenced by the results obtained in this study and related reports elsewhere, we reason that on FLT3-ITD AML blast protein tyrosine phosphatase C1-TEN may be regulated by FLT3-ITD mutation, furthermore contribute to TKI's inhibitory effects, which has not be reported elsewhere till now, even though the mechanism undermining remains to be elaborated.

PU-4388

Effect of sample size and the traditional parametric, nonparametric, and robust Methods on the establishment of reference intervals: Evidence from real world data

Chaochao Ma、Ling Qiu
Department of Clinical Laboratory, Peking Union Medical College Hospital, Peking Union Medical College & Chinese Academy of Medical Science

Sample size and statistical Methods are critical for establishing reference intervals (RIs) but they tend to be overlooked. In this study, we used R (3.6.3) to stratify the reference individuals by sex, and then stratified them using the random sampling method. Fourteen sub-data sets with a sample size of 40, 80, 120, 160, 200, 500, 800, 1000, 1500, 2000, 2500, 3000, 3500, and 4000 were extracted, respectively. The sex ratios of all sub-data sets were 1:1. Transformed parametric (using log transformation), nonparametric, and robust approaches as described in the Clinical and Laboratory Standards Institute guidelines were adopted to establish the RIs and the 90% confidence interval of the thyroid-stimulating hormone (TSH) using data from the sub-data sets. The Bland-Altman plot was used to evaluate the consistency of the upper and lower limits of the RIs established using the three Methods The upper and lower limits of TSH RI tended to be stable starting from the data set with a sample size of 1500. The RIs established using the three Methods were more consistent when using a sample size greater than or equal to 2000

PU-4389

A novel compound heterozygous mutation of MTO1 gene associated with complex oxidative phosphorylation deficiency type 10

Qing Luo、Xia Wen、Jiahong Zhou、Zhiyu Lv、Jinbo Liu
Affiliated Hospital of Southwest Medical University

Background The Mitochondrial tRNA Translation Optimization 1 (MTO1) gene, closely related to defective mitochondrial oxidative phosphorylation, is an evolutionarily conserved protein expressed in high energy-demanding tissues, associated with complex oxidative phosphorylation deficiency type 10 (COXPD10) in humans. While related cases and studies are still scarce and have not been reported in the Chinese region. In this study, we reported the first patient from China carrying a compound heterozygous mutation from each of his parents by whole-exome sequencing technology combined with computer analysis. And bioinformatics software as well as protein constructs were used to predict the pathogenicity of the variants.
Material and Methods Detailed clinical assessment was applied to the patient. Based on next-generation sequencing technology, we performed whole-exome sequencing of patient and parents. Sanger sequencing was used for the validation. And bioinformatics software (SIFT, PolyPhen-2, MutationTaster and Mutation Assessor) to predict the pathogenicity of the variants as well as protein construct ed using SwissModel, which were visualized by the PyMOL software package.
Results The patient was diagnosed with a possible association with mitochondrial disease according to the clinical manifestations and physical examination. A novel frameshift mutation c.344delA (p.Asn115Thrfs*11) and a novel point mutation c.1055C>T (p.Thr352Met) in the MTO1 gene were identified. By predicting biochemical tools that may be pathogenic, they were found to be predisposed to pathogenic potential. The allele frequencies of the two variants in the gnomAD database were much smaller than in the normal population. And the variant c.344delA was categorized as “likely pathogenic” and the variant c.1055C>T was categorized as “uncertain”

according to the ACMG guidelines. The p.Asn115Thr was conserved in the remaining eight speciesm, while p.Thr352Met was conserved in the remaining seven species, while in S. cerevisiae the amino acid site was Ile. The c.344delA (p.Asn115Thrfs*11) variant is a base deletion variant resulting in a frameshift mutation that is predicted to introduce a stop codon after an aberrant sequence of 11 amino acids. The mutation causes early termination of translation of the MOT1 protein and the mutant protein changes from the normal 693 amino acids to 126 amino acids and becomes a truncated enzyme. The c.1055C>T (p.Thr352Met) variant is located in the loop region and changes from a polar uncharged threonine (hydrophilic) T to a non-polar methionine (hydrophobic) M. Most of the loops are located on the surface of protein molecules and contain more hydrophilic amino acids, which have a flexible conformation and can be used as binding sites for proteins as well as catalytic sites for enzymes; this variant may lead to a change in the hydrophilicity of this loop region and thus affect the activity of the enzyme. Two structural domains, MnmG_N (38-435), GidA-ASSOC_3 (438-657), were found when the structure was predicted using Interpro software.

Conclusion We presented two novel and possibly pathogenic variants in the MTO1 gene in a Chinese Han family，which is the first report in China. Although MTO1 related mutations is rare, it is still necessary to screen MTO1 gene in patients with mitochondrial disorders, especially using next generation sequencing technology. The functional validation of the two variants reported here is particularly important, which is what we will subsequently work on.

PU-4390

NDM-1-positive K.pneumoniae at a teaching hospital in southwestern China: Clinical Characteristics, Antimicrobial Resistance, Molecular characterization, Biofilm assay and Virulence

Kai Yang[1]、Shumin Liu[1]、Huanqin Li[2]、Na Du[2]、Jing Yao[2]、Qiuyue He[1]、Yan Du[1]
1. The First Affiliated Hospital of Kunming Medical University
2. Department of Clinical Laboratory, The No. 1 Affiliated Hospital of Yunnan University of Chinese Medicine, Kunming, China

Background The emergence of the NDM-1-positive Klebsiella pneumoniae (K. pneumoniae) strains has led to limited therapeutic options for clinical treatment. Understanding the Clinical Characteristics, Antimicrobial Resistance, Biofilm assayand the virulence genes of these isolated strains is of great significance.

Methods Polymerase chain reaction (PCR)was used to screen isolated NDM-1-positive K.pneumoniae. The clinical information of the patients was collected from medical records. The NDM-1-positiveK.pneumoniaeisolates were subjected to antimicrobial susceptibility testing and multi-locus sequence typing. 60 strains of NDM-1-negative K.pneumoniaeisolated during the same period were collected as the control group for the virulence analysis. The virulence phenotype of the strains were preliminarily evaluated by string testand crystal violet semi-quantitative biofilm formation experiment. PCR combined with gene sequencing was used to detect common high toxicity Capsule genes (K1, K2, K5, K20, K54, K57) and common virulence-related genes (entB, ybtS, ureA, ycf, WabG, FimH, uge, iutA, KfuB, aerobactin, rmpA, magA, Alls, IrnN and VatD).

Results In the 30 non-duplicated NDM-1-positive K.pneumoniaeisolates, 43.33% (13/30) of the patients had a history of a stay in the neonatal intensive care unit (NICU). All of the isolates exhibited multidrug resistance. 9 STs were identified, 77% (10/13) trains from NICU were ST11. NDM-1-positive K.pneumoniaestring testwere all negative, and 35% (21/60) NDM-1-negative K.pneumoniaewere positive. The ratios of NDM-1-positive K.pneumoniaeisolates biofilm formation ability according to strong, medium and weak classification were 67%, 23% and 10%, respectively. NDM-1-negative K.pneumoniaeisolates were 60%, 25% and 15%,

respectively.There was no statistical difference between the two groups (t=0.61, P = 0.2723).The virulence-associated genes with more than 80% of detection rates among the 30 NDM-1-positive K.pneumoniaeisolates included entB(100%, 30/30),ybtS (93.33%, 28/30), ureA(90%, 27/30), ycf(83.33%, 25/30), wabG(90%, 27/30). KfuBandiutAwere detected at prevalence of 3.33% and 13.33%. vatD, allS, iroN, aerobactin,and rmpAwere not detected. In the NDM-1-negative K.pneumoniae, all other 14 virulence genes except VatDwere detected. After statistical analysis, FimH, WabG, ycf, iutA, kfuB, aerobactin, rmpA, and Allsvirulence genes, P <0.005, there was a statistical difference.

Conclusion NDM-1-positive K.pneumoniaeexhibited multidrug resistance, MLST typing is mainly ST11, there is small clonal dissemination in NICU in the hospital, and the NDM-1-positive K.pneumoniaevirulence genes carrier rate is lower thanthe NDM-1-negative K.pneumoniaevirulence genes carrier rate.

PU-4391

Mechanism of circ-0007766 acting as a miRNA sponge to regulate HER2 expression

Yi Zhu
Department of Laboratory Medicine, The Sixth Affiliated Hospital of Guangzhou Medical University, Qingyuan People's Hospital

BACKGROUND & OBJECTIVE Circular RNA(circRNA)， an endogenous non-coding RNA(ncRNA), which is widely found in eukaryotic transcriptome and is closely related to gene expression regulation. As a molecular sponge, circRNA is a supplement to the traditional regulation of gene expression. Many studies have found that the occurrence and development of a variety of tumors are related to circRNA, and the mechanism of circRNA in tumor development has become a hot topic.

METHODS By comparing the circRNA sequencing data of MDA-MB-231 and SK-BR-3 cells, the differentially expressed circRNAs in HER2+ breast cancer were screened out, and the ceRNA regulatory network was selected. QPCR and Western blot were used to preliminarily determine the regulatory relationship. The circRNA-binding proteins were pulled down and analyzed by mass spectrometry, and then verified by WB and RIP experiments. The expression of EMT-related proteins in cells was detected by WB.

RESULTS According to the sequencing results, the circRNA hsa_circ_0007766 significantly overexpressed in HER2-positive breast cancer cells was selected. CIRC_0007766 was highly expressed in breast cancer cell lines.Fluorescence in situ hybridization (FISH) experiments showed that circ-0007766 was mainly localized to the cytoplasm. The results of qPCR and WB showed that circ_0007766 could regulate ERBB3 and ERBB4 in the ERBB family. CircRNA pull down assay showed that circ-0007766 could pull down proteins associated with epithelial mesenchymal process (EMT).

CONCLUSIONS The expression of circRNA circ-0007766 in breast cancer cells is significantly higher than that in normal breast cells, especially in HER2+ breast cancer cells, which can regulate the expression of the erbB family and bind to EMT-related proteins to affect the process of EMT.

PU-4392

EDTA plasma is suitable for measurement of B-type natriuretic peptide on the mindray CL-6000i

Wei Zhao、Yongtong Cao
china-japan friendship hospital

Background and aims The differences of B-type natriuretic peptide (BNP) concentration and stability are controversial among different BNP immunoassays. In this study we explored the BNP differences and stability and evaluated BNP accuracy in different collection tubes on the mindray CL-6000i.
Methods A prospective study was performed on 36 patients at Jinzhai District People's Hospital. BNP concentrations in heparin/glass, EDTA/glass and EDTA/PET tube were measured at 0.5h, 1h, 2h and 4h after sample collection. The differences were evaluated by Wilcoxon's paired test and Bland–Altman plot. The stability was estimated by Kruskal-Wallis H test. The BNP accuracies were investigated by recovery test.
Results BNP concentrations in EDTA/glass tube were mean 31.4% higher than those in heparin/glass tube, and similar with those in EDTA/PET tube (3.04% lower). The stability of BNP significantly decreased in heparin/glass tube and residual BNP levels over 1h, 2h and 4h are 95.67%±7.49%, 86.46%±9.27% and 73.38%±8.33% respectively ($p<0.001$). However, residual BNP levels in EDTA/glass and EDTA/PET tube over 4h were 98.16%±3.65% and 100.22%±2.77%. BNP recovery rates in heparin/glass, EDTA/glass and EDTA/PET were 77.46%, 86.04% and 88.23% respectively.
Conclusions Plasma in EDTA/glass and EDTA/PET are suitable for BNP measurement on the mindray CL-6000i.

PU-4393

ITIH4, as an inflammation biomarker, mainly increases in bacterial bloodstream infection

Yating Ma、Chengbin Wang
301 PLA Hospital

Background Bloodstream infection (BSI) is usually accompanied with the changes of varieties of inflammation proteins. In our previous study, we identified that inter-α-trypsin inhibitor heavy chain H4 (ITIH4) was highly expressed in the infection arms than the normal control arm. However, the correlated verification and mechanism remain obscure.
Methods Escherichia coli infected mice model and clinical serum samples were used to validate the concentration of interleukin-6 (IL-6), tumor necrosis factor-α (TNF-α), interleukin-10 (IL-10), as well as ITIH4, in ELISA method. Cytokines (IL-6, TNF-α, IL-10 and lipopolysaccharide (LPS)) were used to stimulate the HepG2 cell model to explore which cytokines influence the expression of ITIH4. JAK/STAT inhibitor was treated before IL-6 and LPS stimulation. Westernblot, as well as real-time PCR were performed to detect the expression of ITIH4 in liver tissue from protein and transcription levels. Immunohistochemistry analysis was used to observe the expression of ITIH4 in mice liver tissue.
Results In mice model, IL-6, TNF-α, as well as IL-10 increased in the infection arms than the normal control arm. ITIH4 in serum and liver tissue of mice model increased from 1 h to 128 h, which were remarkably different from that of the normal control arm. Besides, ITIH4 increased in the bacterial infection arm greatly than the fungemia arm, mycoplasma pneumoniae (MP) arm and febrile arm in clinical serum samples. Furthermore, using the HepG2 cell line, we demonstrated that ITIH4 was up-regulated at both protein and mRNA levels upon dose- and time-response treatments with IL-6, as well as LPS. Moreover, IL-6 or LPS mediated induction of ITIH4

expression could be significantly decreased by treatment with an JAK/STAT inhibitor in protein or mRNA level. No changes were observed after TNF-α or IL-10 stimulation.
Conclusion ITIH4 might be a critical inflammatory biomarker which correlated with the development of BSI, especially with bacterial bloodstream infection. It is expected that this study would provide some insights into potential functional mechanisms underlying BSI.

PU-4394

Cell Count-based Parameters and Algorithms for Thalassaemia Minor Screening in the Southern Chinese Population

Jialong Xu、Yinge Wu
the First Affiliated Hospital of Shantou University Medical College

Introduction Microcytic anemia is frequently caused by iron deficiency or thalassaemia. And thalassaemia syndrome is potentially mistaken for microcytic or hypochromic anaemia，such as the iron-deficiency anaemia (IDA). Differentiation between the thalassemic and non- thalassemic microcytic anemia have an important clinical implication, for each has entirely different cause, pathogenesis, treatment and prognosis. Moreover, some patients with thalassaemia present with normocytic traits and current criteria for thalassaemia screening are based solely on erythrocyte mean corpuscular volume (MCV) <80 fl, which implies that thalassaemia carriers with MCV values >80 fl would be missed. Here, we aimed to establish differential functions (DFs) derived from basic RBC parameters and an algorithm for detecting microcytic or normocytic thalassaemia in epidemiological screening.
Methods The receiver operating characteristics (ROC) curve analysis was used to determine the diagnostic performance of the RBC parameters and proposed formulae in differentiating thalassaemia and non-thalassaemia. DFs combined the two blood count parameters with the highest performance, based on the area under the curve (AUC) value, into mathematical formulas, using logistic regression. Notably, the normocytic population consists of three cohorts: normocytic TT cohort, healthy cohort, and normocytic non-TT anaemia cohort. To improve the thalassaemia differential efficiency, we first excluded the non-TT anaemia participants. ROC curve analysis was conducted among the RBC parameters to discriminate the normocytic non-TT patients from the healthy or normocytic TT participants. And the parameters with the highest AUC value was used as the first preconditional step for separating the non-TT anaemia participants from the healthy or normocytic TT participants, and subsequently normocytic TT participants will be distinguished from the healthy subjects. Moreover, the diagnostic efficacy of DFs was also evaluated and validated in 767 participants, and reliability (including adjusted agreement [AA] and Kappa values) and validity (including sensitivity, specificity, likelihood ratio, and Youden's Index) were calculated.
Results Among microcytic participants, the proposed DFs showed good diagnostic performance (in females: AUC=0.892 [DF1==0.015×RDW-CV/RBC-0.096×RDW-SD/RBC+1.29]); in males: AUC=0.861 [DF2=0.025×RDW-SD/RBC-0.035×MCV/RBC+1.415]). Youden's Index, AA, and Kappa values for microcytic thalassaemia detection were 0.72, 0.86, and 0.72 and 0.63, 0.81, and 0.63 for females and males, respectively. In normocytic population, the parameter RDW-CV/RBC with the cutoff value=3.54 have the high performance (AUC= 0.94) to separating the non-TT anemia participants from the healthy or normocytic TT participants. Subsequently, to discriminate normocytic TT from healthy participants, DF3=0.38×MCH-0.02×MCHC+17.37 achieved AUC=0.857 in females, whereas DF4=0.007×MCV-0.113×MCH+2.829 achieved AUC=0.969 in males. The Youden's Index, AA, and Kappa values for the proposed DFs for thalassaemia detection were 0.69, 0.84, and 0.67 and 0.76, 0.91, and 0.71 in females and males, respectively.
Conclusion The proposed DFs derived from basic RBC parameters, performed well in the detection of thalassaemia minor among participants with microcytic and normocytic trait. Overall,

our mathematical formulae can be used as a laboratory-based criteria for the selection of samples for thalassaemia testing, which is a simple and inexpensive way to decrease the risk of conceiving a foetus with severe thalassaemic syndrome.

PU-4395

Mechanism of circ-0007766 acting as a miR1972 sponge to regulate HER2 expression

Yi Zhu
General Hospital of Southern Theatre Command of PLA

BACKGROUND & OBJECTIVE Circular RNA(circRNA)， an endogenous non-coding RNA(ncRNA), which is widely found in eukaryotic transcriptome and is closely related to gene expression regulation. As a molecular sponge, circRNA is a supplement to the traditional regulation of gene expression. Many studies have found that the occurrence and development of a variety of tumors are related to circRNA, and the mechanism of circRNA in tumor development has become a hot topic.
METHODS By comparing the circRNA sequencing data of MDA-MB-231 and SK-BR-3 cells, the differentially expressed circRNAs in HER2+ breast cancer were screened out, and the ceRNA regulatory network was selected. QPCR and Western blot were used to preliminarily determine the regulatory relationship. The circRNA-binding proteins were pulled down and analyzed by mass spectrometry, and then verified by WB and RIP experiments. The expression of EMT-related proteins in cells was detected by WB.
RESULTS According to the sequencing results, the circRNA hsa_circ_0007766 significantly overexpressed in HER2-positive breast cancer cells was selected. CIRC_0007766 was highly expressed in breast cancer cell lines and localized to the cytoplasm. The results of qPCR and WB showed that circ_0007766 could regulate ERBB3 and ERBB4 in the ERBB family.

PU-4396

Exploring the expression and prognostic value of the TCP1 ring complex in hepatocellular carcinoma and Overexpressing its subunit 5 promotes HCC tumorigenesis

Jiahui Liu、Ling Huang、Quan Zhou、Zhaohui Sun
General Hospital of Southern Theatre Command of PLA

T-complex protein-1 ring complex (TRiC), also known2 as CCT: Chaperonin Containing T-complex protein-1, belongs to chaperonins required for folding nascent proteins. Increasing evidence has indicated TRiC complex played an important role in the development and progression of various tumors but limited studies in hepatocellular carcinoma (HCC). We comprehensively evaluated the expression pattern and biological function of TRiC complex subunits based on public data obtained from The Cancer Genome Atlas and Human Protein Atlas. We found the expressions of TCP1, CCT2/3/4/5/6A/7/8 were significantly upregulated in HCC tissues at both transcript and protein level, which predict shorter overall survival (OS). Moreover, high mutation rate was found in several CCT subunits, and patients with altered CCT genes had poorer clinical outcomes. Functional enrichment analysis showed that the biological processes of co-altered genes significantly concentrated on protein folding and microtubule-based process while co-expressed genes with CCT subunits were mainly involved in ribosome and spliceosome. Then, CCT5, a subunit of TRiC, knockdown and overexpression were performed in HCC cell lines. Functional assays demonstrated that CCT5 was closely related to HCC cell proliferation, cycle

transition, migration and invasion. In conclusion, our study suggested that the subunit of TRiC complex may be a potential biomarker for the diagnosis of HCC and play an important role in the occurrence and development of HCC.

PU-4397

Clinical and pathological differences of left and right colorectal cancer and prognostic survival analysis

Xuan Wu[1]、yuanjiang Shang[1]、weifeng Wang[1]、zili Ma[1]、lixia Wu[1]、ke Li[1]、hailin Zheng[1]、Lei Chen[2]、weixin Xu[3]、weiwei Liu[4]
1. Shanghai Tenth People's Hospital
2. 上海市第三军医大学附属东方肝胆外科医院
3. 上海医药卫生大学附属嘉定区中心医院检验科
4. 上海市第十人民医院检验科

Background Colorectal cancer (CRC) was divided into left colon cancer (LCC) and right colon cancer (RCC) as early as 1990. LCC and RCC are two completely different diseases in many aspects such as epidemiology, pathology, and cytogenetics. Hence, they should be distinguished in terms of treatment and treated correctly.
Aim This study aimed to explore the clinical and pathological differences in LCC and RCC, find protein molecules specifically or differentially expressed, and explore the factors affecting prognosis and survival.
Methods In this study, from 2010 to the end of 2018, 277 patients with CRC were enrolled, including 159 patients with LCC and 118 patients with RCC. The LCC and RCC are compared with each other, and the existing statistical analysis tools are applied to conduct comprehensive analysis.
Results This study included 164 male and 113 female patients. The mortality rate of LCC was significantly lower than that of RCC ($P = 0.000$). Patients with LCC were generally younger ($P = 0.001$), but lymph nodes were more likely to metastasize and the number of metastases was greater ($P = 0.0077$). In addition, Cox risk regression analysis also showed that the patient's gender, number of lymph node metastases, CA199, and MSH2 were the risk factors affecting the prognostic survival time ($P < 0.05$).
Conclusions The survival rate of LCC was higher and the number of lymph node metastases and the degree of infiltration were lower compared with those of RCC. Gender, number of lymph node metastases, CA199, and MSH2 were risk factors affecting the prognostic survival time.

PU-4398

A pseudo-targeted metabolomics study based on serum bile acids profiling for the differential diagnosis of breast cancer

Haoran Wang[1,2]、Lianjie Zhang[1]、Chengyu Xu[1]
1. Suzhou Dushu Lake Hospital
2. 重庆医科大学

Objective Breast cancer (BC) has become the leading cause of cancer death among females [1]. Therefore, it is critical for the differential diagnosis between BC and benign breast diseases (BBD) [2]. The characteristics of serum bile acids (BAs) profiling in patients with BBD and BC were elucidated so that potential biomarkers could be find out for the differential diagnosis of BC.
Methods A pseudo-targeted approach was used to perform BAs metabolomics analysis in serum of 28 patients with BBD and 46 patients with BC by ultra-high performance liquid

chromatography/hybrid quadrupole time-of-flight mass spectrometry (UPLC-QTOF-MS). Partial least squares-discriminant analysis (PLS-DA) was used to establish a differential diagnostic model for BC, and the receiver operating characteristic (ROC) curve and logistic regression analysis were used to screen out bile acids as biomarkers for the differential diagnosis of BC.
Results Compared with the BBD group, the serum BAs profile in BC group was quite different, as shown in Fig. 1. The level of chenodeoxycholic acid (CDCA) of BC group was higher than that of BBD group, while the levels of dihydroxy tauro-conjugated BA (Tdi-1) and sulfated dihydroxy glyco-conjuga ted BA (Gdi-S-1) of BC group were lower than those of BBD group. The sensitivity and specificity of PLS-DA model for classification of patients were 100% and 92.3%, respectively. The combined biomarker, CDCA and Tdi-1, had high efficacy for the differential diagnosis (area under the curve was 0.954, 95% CI: 0.880-1.000) of BC. Besides, the diagnostic performance was superior to traditional biomarkers in the differential diagnosis of BC with or without comorbidities. Results are shown in Tab. 1.
Conclusion The profile of serum BAs in women with BC was quite different from that in patients with BBD. Serum BAs profiling analysis could be used as an effective tool for the differential diagnosis of BC.

PU-4399

数字 PCR 检测血流感染常见病原菌的临床应用研究

刘芳瑞、吕琳婷
上海交通大学医学院附属仁济医院(东院)

背景
血流感染是指细菌、真菌等病原微生物入侵血循环，在血液中繁殖,释放毒素和代谢产物,并诱导细胞因子释放,引起全身感染性疾病。目前血流感染的主流病原菌有大肠埃希菌、肺炎克雷伯菌、鲍曼不动杆菌、铜绿假单胞菌以及各类葡萄球菌。大多入侵为呼吸道感染、泌尿系统感染以及腹腔感染。近些年由于抗生素和介入治疗的使用，血流感染的发病率呈持续增高趋势。目前检测血流感染最重要的检查手段是血培养。但血培养周期时间长、用血量大、且无法定量，早期诊断及准确的抗菌治疗对降低疾病死亡率至关重要。
目的 运用领航数字 PCR 系统检测临床血浆样本中的病原菌，以测评该技术的临床应用价值。
方法 采用领航基因五色荧光数字 PCR 系统检测 169 份临床血浆样本，并与传统血培养方法进行比较，计算数字 PCR 技术检测血流感染的敏感度、特异性和符合率。
结果 本次实验检测的 169 份样本中，血培养阳性 27 例，阴性 142 例，阳性率 16%；数字 PCR 阳性 15 例，阴性 154 例，阳性率 8.9%。与传统血培养鉴定技术相比，领航五色荧光数字 PCR 系统检测血流感染样本的敏感度为 24%，特异性为 97.2%，阳性预测值为 60%，阴性预测值为 88%，总体符合率为 88.8%。数字 PCR 系统鉴定阳性的病原菌包括绿假单胞菌（1 例）、大肠埃希菌（5 例）、肺炎克雷伯菌（4 例）、鲍曼不动杆菌（2 例）、屎肠球菌（3 例）、粪肠球菌、嗜麦芽窄食单胞菌（5 例）、表皮葡萄球菌（3 例）。但由于血培养阴性而数字 PCR 检测阳性的病原菌主要集中在嗜麦芽假单胞菌和表面葡萄球菌，所以不能排除污染的可能性。
结论 数字 PCR 技术是一种新型血流感染的检测技术，检测时间短，具有较好的特异性，但敏感性还有待提高，未来或许可以成为临床早期诊断与优化感染治疗的新方法。

PU-4400

检验过程的生物安全风险管理和实践体会

公衍文
山东大学第二医院

目的 总结实验室检验过程生物安全风险管理的实践体会，以期能够提供可以落地有效的风险管理办法。
方法 风险管理是质量管理的根本落脚点，但在实施过程中，多数实验室未能将静态评估和动态监测结果结合起来，一味地依靠所谓的头脑风暴，导致风险管理流于形式，没能识别出真正可能存在的风险，相应的风险控制措施也就没有效果，无法实现持续改进。我们将静态风险评估（基于工作流程和操作，明确每个岗位和操作在实验室环境、生物安全柜、个人防护措施等方面选择，并在此基础上评估存在的风险，以及风险的严重程度和可识别能力）和动态监测（安全管理组定期检查监测安全措施执行情况、风险管控措施执行情况，以及生物安全实验室良好工作行为遵守情况，统计风险可能发生的频次）相结合，计算 RPN 指数，进行客观的风险评估。
结果 共识别出高风险 5 项，中风险 11 项，低风险 25 项。对高风险立即实施针对性的纠正措施，并作为后续监测的重点，评估措施的有效性；对中风险项目，评估其可能的发展趋势，必要时采取预防措施，并监测措施的有效性；对低风险项目，继续列入日常监测项目，持续关注。
结论 检验过程风险管理必须将静态评估和动态监测结合起来，才能真正有效。

PU-4401

运用 PDCA 循环法在三级医院检验科三年质量管理上的研究

周慧聪
南京大学医学院附属泰康仙林鼓楼医院

目的 运用 PDCA 循环法管理检验科检验前、检验后质量指标，探索检验科质量管理方法，提高检验科的工作质量，更好的服务患者。
方法 1、由科主任确定检验科“年度重点质量管理项目”，制定“质量目标”，包括“体液标本采集时间缺失率<10%”、“血液标本采集时间缺失率<10%”、“不合格标本比例<1%”、“门诊患者实验室内周转时间超时率<5%”。2、将上述数据“快捷统计功能”维护到检验科 LIS 系统里，可以按照“时间”、“标本来源”等检索条件获取每月数据。3、每月 5 号前由专人统计并分析上述质量指标涉及的数据，形成图表，清晰可见，内容包含以上四项质量管理项目在上月的数据。4、召开“检验科月度质量小组会议”，分析导致质量目标不佳的原因，由专人根据会议内容撰写“质量小组活动记录”，内容包括“针对本月的质量分析及改进项目”、“针对下月的改进目标和措施”、“对上月质控活动改进措施的落实和成效评价”。5、从人、机、料、法、环五方面进行根因分析，针对不同问题积极整改并与临床沟通，增强培训及考核力度。6、每月按照上述方法进行质量管理，循环往复，计算三年来质量管理成效。
结果 2020 年全年较 2018 年全年体液标本采集时间缺失率下降 31.24%；血液标本采集时间缺失率下降 82.59%；不合格标本率下降 40%；门诊患者实验室内周转时间超时率下降 54.14%。2019 年及 2020 年全年质量目标均在目的范围内。
结论 PDCA 循环法运用到检验科质量管理中可以起到很好的作用，可以大大提高检验科的质量目标，此方法可以运用到更多的检验科质量管理项目中，使检验质量不断进步。

PU-4402

泛癌分析显示同源重组缺乏评分可作为免疫治疗反应者的预测指标

杨璨[2,3]、唐雪梅[1]、张心菊[2]、吴之源[1,2,3]、关明[1,2,3,4]
1. 复旦大学附属华山北院中心实验室
2. 复旦大学附属华山医院中心实验室
3. 复旦大学附属华山医院检验科
4. 复旦大学附属华山北院检验科

目的 肿瘤微环境(TME)的免疫背景是免疫学干预成功的决定性因素，但对免疫敏感性 TME 和免疫治疗反应者识别的 DNA 水平的生物标志物的探索较少。同源重组缺陷(HRD)疤痕是肿瘤基因组不稳定的一个新兴特征，可以触发免疫反应。本研究旨在全面研究主要癌症类型的 HRD 疤痕（评分），并揭示它们与肿瘤微环境和免疫治疗反应的联系。
方法 使用来自癌症基因组图谱(TCGA)的 9088 个肿瘤的基因组学、转录基因组学和免疫表型数据对 HRD 评分进行了功能分析。与 HRD 相关的癌症类型由 HRD 评分累积频率分类来定义。对 HRD 高或低基因型的肿瘤突变负荷(TMB)和新抗原进行比较。肿瘤微环境(TME)用 CIBERSORT、xCell、MCP-counter、EPIC 和 quanTIseq 这五种算法进行了数字分析。微卫星不稳定性(MSI)、TMB 和 HRD 的敏感性和特异性。
结果 来自 TCGA 的 32 种癌症的 9088 名肿瘤患者的 HRD 评分分析显示，7 种主要癌之间的广泛关联，包括膀胱癌、乳腺癌、头颈鳞癌、肺腺癌、肺鳞细胞癌、卵巢癌和肉瘤。HRD 评分高的肿瘤有白细胞浸润和淋巴细胞分数增加，并表现出免疫敏感的 TME。最后，通过 TIDE 模型，我们证实了 HRD 评分的高基因型是 TCGA 乳腺癌队列中免疫反应的潜在预测因子。
结论 HRD 评分高的肿瘤具有免疫敏感的 TME。HRD-高基因型是乳腺癌患者免疫治疗反应的重要指标。

PU-4403

Genetic testing and clinical relevance of patients with thoracic aortic aneurysm and dissection in northwestern China

Liu Yang、jinjie li、yanjun diao、lei zhou、yijuan xin、rui li、juan wang、jiayun liu
Air force medical uiversity xijing hospital

Thoracic aortic aneurysm and dissection (TAAD) is a life-threatening pathology that remains a challenge worldwide. Up to 40% of TAAD cases are hereditary with complex heterogeneous genetic backgrounds. The purposes of this study were to determine the diagnostic rate of patients with TAAD, investigate the molecular pathological spectrum of TAAD by next-generation sequencing (NGS), and explore the future preclinical prospects of genetic diagnosis in patients at high-risk of study.
METHODS:NGS was used to screen 15 genes associated withgenetic TAAD in 212 patients from northwestern China. Clinical data of patients were gathered by Electrocardiography, transthoracic echocardiography and computed tomography.
RESULTS:Of the 212 patients, 67 (31.60%) tested positive for a (likely) pathogenic variant, 42 (19.81%) had a variant of uncertain significance (VUS), and 103 (48.58%) had no variant (likely benign/benign/negative). A total of 135reportable variants were detected in our test, among which 77(57.04%) are first reported in this paper.

PU-4404

核心抗体定量在乙肝相关慢加急性肝衰竭中的表达水平及与预后的关系

李静[1]、龚启明[2]、谢培琳[1]、林君玉[1]、陈嘉[1]、韦栋[1]、于德敏[1]、韩悦[1]、张欣欣[1]
1. 上海交通大学医学院附属瑞金医院临床病毒室
2. 上海交通大学医学院附属瑞金医院感染科

目的 研究乙肝相关慢加急性肝衰竭（HBV-ACLF）患者血清核心抗体定量（qAnti-HBc）的表达水平及与预后的关系。
方法 选取上海交通大学附属瑞金医院 2014 年 1 月-2019 年 12 月 HBV-ACLF 患者 168 例（88 例为训练集，80 例为验证集），和同期慢性乙型肝炎（CHB）患者 216 例（对照组），比较两组 qAnti-HBc 水平。进一步比较 HBV-ACLF 患者生存组与死亡组 qAnti-HBc 水平，建立预后模型，并在验证集验证。动态观察 16 例 HBV-ACLF 组患者入院后 1 月内，3 月，6 月，9 月，12 月时 qAnti-HBc 的变化。
结果 HBV-ACLF 组血清 qAnti-HBc 水平明显高于 CHB 组。HBV-ACLF 患者中，qAnti-HBc 水平在生存组明显高于死亡组，血清 qAnti-HBc 水平与 MELD 评分呈轻度负相关。HBV-ACLF 组患者中合并其他感染患者相比未合并者血清 qAnti-HBc 水平明显降低；合并肝性脑病患者相比未合并者 qAnti-HBc 水平明显降低；合并肝肾综合征患者相比未合并者 qAnti-HBc 水平明显降低；在有无肝硬化患者中无明显统计学差异。ROC 曲线提示血清 qAnti-HBc 水平对 HBV-ACLF 的预后预测价值与 MELD 评分相当。 进一步建立包含 qAnti-HBc 在内的预测模型，预测价值明显优于 MELD 评分，且在验证组中加以验证。16 例 HBV-ACLF 患者在入院 1 月内 qAnti-HBc 水平无明显变化，3 月时显著下降，6 月时再次下降，后趋于稳定。
结论 HBV-ACLF 患者 qAnti-HBc 水平显著高于 CHB 患者，在 HBV-ACLF 患者中，生存组明显高于死亡组，qAnti-HBc 水平对 HBV-ACLF 患者预后的预测价值与 MELD 相当。随着 HBV-ACLF 患者病情好转，于第 3 月和第 6 个月时明显下降，后趋于稳定。

PU-4405

结肠癌微环境中免疫细胞浸润模式及其预后评估

梁艳玲[1,2]、吴智聪[1,2]、马尊雅[3,4]、陈华[3]、吴妮莎[2]、邓凡[3]、曾方银[2]
1. 南方医科大学南方医院检验科
2. 南方医科大学第五附属医院检验医学科
3. 南方医科大学基础医学院细胞生物学教研室
4. 南方医科大学基础医学院基础医学

目的 结直肠癌（colorectal cancer，CRC）是主要的致死性恶性肿瘤之一。其中，结肠癌是结直肠癌中的最常见类型。目前，免疫疗法已被临床验证为许多肿瘤有效治疗的选择。肿瘤浸润免疫细胞作为肿瘤免疫微环境中的主要成分，其与结肠癌患者预后之间的关联尚未明确。本研究旨在探索结肠癌微环境中免疫细胞的浸润模式及其预后价值，为临床个体化治疗提供新方向。
方法 利用 CIBERSORT 软件包从癌症基因组图谱 TCGA（The Cancer Genome Atlas）数据库、GEO（Gene Expression Omnibus）数据库共筛选 38 例正常结肠组织样本及 316 例结肠癌组织样本，基于标准化后的基因表达谱对 22 种浸润免疫细胞进行提取和量化，分析免疫细胞在正常组织和癌组织中的浸润差异。利用多因素 COX 回归构建 Nomogram 风险预测模型。
结果 本研究发现活化的 CD4+记忆性 T 细胞、M0 巨噬细胞、M1 巨噬细胞在结肠癌组织中浸润显著增多，幼稚 B 细胞、浆细胞、单核细胞及未活化的肥大细胞显著减少。高水平活化的肥大细胞及调节性 T 细胞浸润与肿瘤转移和分期进展密切相关（$p<0.05$），低水平活化的 CD4+记忆性 T 细胞

和滤泡辅助性 T 细胞与肿瘤淋巴结播散及分期进展相关（p<0.05）。利用患者年龄、性别、临床病理分期、TNM 分期、组间分析具有差异的免疫细胞构建 Nomogram 风险预测模型，模型预测 1 年、3 年和 5 年生存率的 ROC 曲线 AUC 分别为 0.828、0.794 和 0.754。将 COAD 患者按照风险评分分为高低风险组并进行 Kaplan-Meier 分析，结果显示高风险组 COAD 患者预后较差（p<0.001），提示模型具有良好预测效能。
结论 结肠癌患者中免疫细胞的浸润差异可能在疾病进展中具有重要作用，其预后模型可能为结肠癌患者的生存评估提供理论和数据支持。

PU-4406
肺腺癌外泌体 miR-1290 靶向抑制 SOCS3 调控巨噬细胞极化

吴逸宁、王雪滢、顾嘉慧、徐建
江苏省人民医院（南京医科大学第一附属医院）

目的 肺腺癌严重威胁人类健康。阐明肺腺癌的发病机制，寻找免疫治疗的新方法，对改善预后十分重要。本研究旨在明确肺腺癌外泌体 miR-1290 对巨噬细胞极化的调控作用及其分子机制，为靶向 miR-1290 的治疗提供理论依据。
方法 利用重组慢病毒构建 miR-1290 稳定敲低的肺腺癌细胞株并分离及鉴定其外泌体。流式细胞术和 Transwell 细胞侵袭实验检测与敲低 miR-1290 的外泌体共培养后巨噬细胞表型和功能的改变。通过裸鼠皮下瘤模型在体内验证肺腺癌外泌体 miR-1290 对巨噬细胞极化的作用。采用双荧光素酶报告基因实验、qRT-PCR 和 Western blot 鉴定 miR-1290 的靶基因 SOCS3。改变 miR-1290、SOCS3 的表达水平或与肺腺癌外泌体共培养后，qRT-PCR 和 Western blot 检测巨噬细胞极化标志物及相关信号通路分子的表达变化。
结果 与敲低 miR-1290 的肺腺癌外泌体共培养抑制巨噬细胞向 M2 型极化并减弱其促肺腺癌细胞侵袭的能力。敲低肺腺癌外泌体 miR-1290 可减少裸鼠皮下移植瘤中浸润的 M2 型巨噬细胞数量并减小肿瘤体积。过表达 miR-1290 可活化巨噬细胞 STAT3 通路，同时促进其向 M2 型极化；阻断 STAT3 通路削弱 miR-1290 促巨噬细胞 M2 型极化的效应。miR-1290 能特异性结合 SOCS3 的 3'UTR，靶向抑制 SOCS3 的表达。敲低 SOCS3 可活化 STAT3 并促进巨噬细胞向 M2 型极化；回补 SOCS3 可抵消 miR-1290 上调对 STAT3 活化及 M2 型极化的促进作用。敲低 miR-1290 的肺腺癌细胞外泌体可上调巨噬细胞中 SOCS3 表达, 进而抑制 STAT3 通路及 M2 型极化。
结论 肺腺癌外泌体 miR-1290 通过调控 SOCS3-STAT3 轴, 促进巨噬细胞向 M2 型极化。

PU-4407
Effects of Different Doses of rAAV5-mCherry on the Transcriptome of Hippocampal Pyramidal Neurons in Male Mice

刘忆思
南方医科大学珠江医院

Recombinant adeno-associated virus (rAAV) vectors have been widely used in neuroscience for gene transduction, and high-dose rAAV induces unexpected side effects. However, little is known about the mechanisms underlying rAAV-induced toxicity in brain cells. Here, we evaluated the effects of three different doses of rAAV5 vectors, which are widely used for functional studies in the brain, on hippocampal pyramidal neurons in male mice. There was a strong correlation between rAAV dose and toxicity. As the dose increased, rAAV5-mCherry upregulated genes related to immune and inflammatory responses and neuronal apoptosis and downregulated

genes associated with synaptic and axonal compartments and mitochondria, suggesting that higher doses of rAAV-5-mCherry may induce pyramidal neuronal fragility and impair synaptic transmission. Thus, the dose should be taken into consideration when rAAV vectors are used for gene transduction studies.

PU-4408

Development and validation of a prediction model for malignant pulmonary nodules

Zhen Ren、Hongmei Ding、Zhenzhen Cai
The First Affiliated Hospital of Nanjing Medical University

Background: To develop and validate a preoperative prediction model for malignancy of pulmonary nodules (PNs).
Methods: Data from 409 patients who underwent PN resection at the First Affiliated Hospital of Nanjing Medical University between June 2018 and December 2020 were retrospectively collected. Then, the patients were nonrandomly split into[Y. Mu1] a training cohort and a validation cohort. Logistic regression analysis was used to identify variables significantly associated with malignant pulmonary nodules (MPNs) that were then included in the nomogram. We evaluated the discrimination and calibration ability of the nomogram by using R software.
Results: MPNs were confirmed in 215 (52.6%) patients by a pathological examination. Multivariate logistic regression analysis identified six risk factors independently associated with MPN: Gender [Female, odds ratio (OR) =2.487; 95% confidence interval (CI): 1.313–4.711; P = 0.005], location of nodule (upper lobe of lung, OR = 2.576; 95%CI: 1.380–4.806; P = 0.003), density of nodule (pure ground glass, OR = 16.899; 95%CI: 7.572-37.716; P < 0.001; part-solid nodules, OR = 24.096; 95%CI: 10.153–57.186; P < 0.001), nodule size (OR = 1.100; 95% CI: 1.058–1.145; P < 0.001), GAGE7 (OR = 1.085; 95%CI: 1.011–1.165; P = 0.023) and GBU4-5 (OR = 1.126; 95%CI: 1.054–1.204; P < 0.001). The concordance index was 0.88 (95%CI: 0.83–0.91) and 0.92 (95%CI: 0.85–0.97) in the training and validation cohorts, respectively. The calibration curves showed good agreement between the predicted risk by the nomogram and real outcomes.
Conclusions: We have developed and validated a preoperative prediction model for MPNs. The model could aid physicians in clinical treatment decision making.

PU-4409

核受体 NR2F6 介导乳腺癌铂类药物耐药的分子机制研究

黄玲
广州医科大学附属第六医院

目的 NR2F6 与多种癌症预后不良有关，再此探讨核受体亚族 2，F 组第 6 号成员（NR2F6）对乳腺癌细胞顺铂耐药的影响及其可能的作用机制。
方法 Western blot 和 real-time PCR 检测乳腺癌正常上皮细胞 MCF-10A，5 种乳腺癌细胞 MCF7,MDA-MB-231,UACC812,SK-BR3,BT474 和乳腺癌顺铂耐药细胞株 MCF-7/DDDP 中 NR2F6 的表达水平。CCK8 法检测上述细胞的半抑制浓度 IC50，探究 NR2F6 的表达水平是否与 IC50 有关，根据 NR2F6 表达水平选择 MDA-MB-231 细胞构建 NR2F6 稳转细胞，MCF7 构建敲低细胞，Western blot 法验证细胞是否构建成功。CCK8 细胞增殖，流式凋亡实验，划痕，transwell 法验证 NR2F6 对乳腺癌细胞增殖、侵袭、迁移的影响，CCK8 法验证顺铂的最适浓度，在顺铂作用下，重复上述实验验证顺铂作用下 NR2F6 对乳腺癌细胞增殖、侵袭、迁移的影响。CCK8 法检

测过表达细胞及其亲本细胞，敲低细胞及其亲本细胞的半抑制浓度 IC50。运用 RNA-seq，蛋白质质谱，CHIP 筛选下游分子行进一步机制研究，并进一步行 rescue 实验，双荧光素酶报告基因实验验证其下游基因。
结果 NR2F6 过表达可增加顺铂对 MDA-MB-231 细胞的杀伤活性，而 NR2F6 敲低可降低顺铂对其杀伤活性，根据 RNA-seq 及蛋白质质谱筛选并验证下游基因 BCL2A1。
结论 NR2F6 可通过下调 BCL2A1 增加乳腺癌细胞对顺铂的敏感性。

PU-4410

泛素连接酶 TRIM7 通过调控 HIF-1α 信号抑制肾透明细胞癌的转移与侵袭

袁超、赵敬杰
山东大学第二医院

目的 肾透明细胞癌是一种具有独特发病机制的恶性肿瘤，发生机制尚未完全阐明。我们前期研究结果表明，泛素连接酶 TRIM7 在肾透明细胞癌中低表达。本课题将探讨泛素连接酶 TRIM7 抑制肾透明细胞癌发生发展的机制研究。
方法 本课题结合细胞模型、动物模型和临床病理标本，明确 TRIM7 在肾透明细胞癌中的作用；利用干扰 shRNA、RNA-seq 等分子生物学手段和基因组学方法研究 TRIM7 对 HIF-1α 信号通路的影响，进而阐明 TRIM7 影响肾透明细胞癌发生的分子机制。
结果 我们收集了 40 例 ccRCC 患者的石蜡切片和 25 例 ccRCC 患者的新鲜癌组织，免疫组化、qRT-PCR 和 Western Blot 的结果显示 TRIM7 在 ccRCC 组织中显著低表达。过表达 TRIM7 基因可以抑制乏氧条件下细胞转移和侵袭，并显著降低 HIF-1α 的蛋白水平。我们将不同量的 TRIM7 野生型过表达质粒和 CA 突变体与恒量的 Src 过表达质粒共转染 HEK293 细胞，野生型 TRIM7 可以显著降低 Src 的蛋白水平，而泛素连接酶活性缺失的 CA 突变体对 Src 蛋白水平没有影响；与 CA 突变体相比，野生型 TRIM7 可以明显缩短 Src 的半衰期；蛋白酶体抑制剂 MG132 可以废除 TRIM7 对 Src 蛋白水平的影响。
结论 本研究明确了 TRIM7 在肾透明细胞癌中的作用，揭示了 TRIM7 调控 HIF-1 信号通路的分子机制，将为肾透明细胞癌的防治提供新的策略。

PU-4411

Dysregulated Glutamate Transporter SLC1A1 Propels Cystine Uptake via Xc_x0001_ for Glutathione Synthesis in Lung Cancer

Wenzheng Guo[1,2]、Kaimi Li[3]、Beibei Sun[4]、Shuhai Lin[5]、Jiong Deng[2]
1. 上海市东方医院 检验科 Department of Laboratory Medicine，Shanghai East Hospital, Tongji University School of Medicine
2. 上海交通大学医学院 Shanghai Jiao Tong University School of Medicine
3. 北京协和医学院 Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College
4. 上海交通大学转化医学中心 Translational Medical Research Center, Shanghai Jiao Tong University
5. 厦门大学生命科学学院 School of Life Sciences, Xiamen University

Cancer cells need to generate large amounts of glutathione (GSH) to buffer oxidative stress during tumor development. A ratelimiting step for GSH biosynthesis is cystine uptake via a cystine/ glutamate antiporter Xc_x0001_. Xc_x0001_ is a sodium-independent antiporter

passively driven by concentration gradients from extracellular cystine and intracellular glutamate across the cell membrane. Increased uptake of cystine via Xc_x0001_ in cancer cells increases the level of extracellular glutamate, which would subsequently restrain cystine uptake via Xc_x0001_. Cancer cells must therefore evolve a mechanism to overcome this negative feedback regulation. In this study, we report that glutamate transporters, in particular SLC1A1, are tightly intertwined with cystine uptake and GSH biosynthesis in lung cancer cells. Dysregulated SLC1A1, a sodium-dependent glutamate carrier, actively recycled extracellular glutamate into cells, which enhanced the efficiency of cystine uptake via Xc_x0001_ and GSH biosynthesis as measured by stable isotope-assisted metabolomics. Conversely, depletion of glutamate transporter SLC1A1 increased extracellular glutamate, which inhibited cystine uptake, blocked GSH synthesis, and induced oxidative stress-mediated cell death or growth inhibition. Moreover, glutamate transporters were frequently upregulated in tissue samples of patients with non–small cell lung cancer. Taken together, active uptake of glutamate via SLC1A1 propels cystine uptake via Xc_x0001_ for GSH biosynthesis in lung tumorigenesis.

PU-4412

An Extraction free Isothermal System for Rapid Detection of Eight Common Pathogens Causing Lower Respiratory Tract Infections

Yuying Si、Lieying Fan
Shanghai East Hospital

Lower respiratory tract infections (LRTIs) are a leading cause of morbidity and mortality worldwide and lack of a rapid diagnostic method. To improve the diagnosis of LRTIs, we established an available loop-mediated isothermal amplification (LAMP) assay for the detection of eight common lower respiratory pathogens, including Klebsiella pneumoniae, Pseudomonas aeruginosa, Acinetobacter baumannii, Staphylococcus aureus, Escherichia coli, Haemophilus influenza, Streptococcus pneumoniae, and Moraxella catarrhalis. Furtherly, we established a rapid, high throughput and extraction free detection planform for LRITs using direct nucleic acid releasing strategy without extra nucleic acid extraction steps and encapsulated assay agents saved multiple labor. The whole progress can be shortened to 45min from sample in to results out. 528 sputum samples collected from patients with suspected LRTIs were detected by LAMP assays (8 tests in each sample, a total of 4224 tests), which compared with standard culture method (SCM), and then samples with inconsistent results were verified by Sanger sequencing and High-throughput sequencing (NGS). The results showed that all the Kappa coefficients between LAMP assay and SCM for detecting eight kinds of bacteria exceeded 0.4 as well as $P < 0.001$, indicated fair to good agreement. Besides, LAMP method (44.51%) detected more multiple infections than SCM (12.69%), and 367 inconsistent tests between the two methods were verified by Sanger sequencing. Results showed that 231 tests (62.94%) were concordant with LAMP, presenting higher sensitivity and detection rate than SCM, especially for multiple infection samples. 50 inconsistent samples were randomly selected for NGS and the diagnostic efficiency of LAMP assay was as follows: specific 94.49%, sensitive 75.00%, positive predictive value 90.44%, negative predictive value 84.47%, positive likelihood ratio 13.62, and negative likelihood ratio 0.26. In summary, an extraction free and high throughput LAMP platform was established to detect eight common pathogens causing LRTIs, which was significant for point of care testing and can be implemented in primary hospitals.

PU-4413

肺炎链球菌疫苗蛋白 ΔA146Ply 的矿化纳米颗粒在鼻咽部感染中的研究

吴静雯
成都市第三人民医院

目的 本文旨在研究肺炎链球菌蛋白疫苗 ΔA146Ply 的矿化纳米颗粒在鼻咽部感染中的免疫保护作用。
方法 利用大肠杆菌原核表达系统，通过分子克隆技术表达肺炎链球菌疫苗蛋白 ΔA146Ply 及含有生物矿化肽的疫苗蛋白 ΔA146Ply-PA44，分别经 Ni2+柱纯化、去除内毒素。将 ΔA146Ply-PA44 置于富含 Ca2+和 PO43-的弱碱性溶液中处理后制备成纳米级的生物矿化颗粒（ΔA146Ply-PA44@CaP）。以 ΔA146Ply、ΔA146Ply-PA44@CaP 及 PBS 分别免疫小鼠后取其末梢血检测特异性抗体效价；于末次免疫后取小鼠脾细胞，再刺激并检测上清液中细胞因子分泌量。末次免疫后经鼻腔攻毒肺炎链球菌 CMCC31693，于 3 天后取肺泡灌洗液计数鼻腔及肺部细菌载量，同时取其肺部行 HE 染色评估炎症情况。
结果 以 ΔA146Ply、ΔA146Ply-PA44@CaP 及 PBS 分别免疫小鼠后，测得 ΔA146Ply-PA44@CaP 免疫组小鼠产生的特异性抗体效价较 ΔA146Ply 及 PBS 组均有显著升高；ΔA146Ply-PA44@CaP 免疫组小鼠脾细胞再刺激后产生的细胞因子 IL-4，IFN-γ 较 ΔA146Ply 及 PBS 免疫组均有显著增高。末次免疫后经鼻腔攻毒肺炎链球菌 CMCC31693，于 3 天后取肺泡灌洗液计数鼻腔及肺部细菌载量，结果显示 ΔA146Ply-PA44@CaP 免疫组小鼠肺泡灌洗液中细菌载量较 ΔA146Ply 及 PBS 免疫组明显减少，同时小鼠肺部 HE 染色提示，ΔA146Ply-PA44@CaP 免疫组的小鼠肺部炎症反应较 ΔA146Ply 及 PBS 免疫组明显较弱。
结论 以上结果提示肺炎链球菌蛋白疫苗 ΔA146Ply 的矿化纳米颗粒能诱导小鼠产生较强免疫保护效应并可有效抵抗肺炎链球菌的鼻咽部定植及感染。

PU-4414

POU4F3 基因两个新突变致常染色体显性遗传非综合征型耳聋家系的鉴定分析及其分子标志物价值研究

白晓卉[1]、张凤国[2]、肖云[2]、卢志明[1]、徐磊[2]
1. 山东第一医科大学附属省立医院
2. 山东大学附属省耳鼻喉医院

目的 分析两个遗传性非综合征型耳聋家系的临床听力学特征，并利用遗传性耳聋基因目标区域捕获测序技术鉴定致聋基因,并评价致病突变作为分子标志物的诊断价值及意义。
方法 通过家系调查，收集到两个感音神经性聋家系的临床资料，整理并分析该家系成员的临床听力学和遗传学特征，对家系成员进行调查并绘制系谱图。我们利用进行耳聋基因目标区域捕获技术和大规模平行测序技术，对先证者的 DNA 标本进行了已知耳聋基因突变筛查。继而对获得的测序结果进行分析，确定候选基因。利用 Sanger 测序技术对所有家系成员进行候选基因突变验证，并对氨基酸保守性进行分析。结合临床患者资料，评价 POU4F3 基因 2 个新突变作为分子标志物的价值。
结果 根据绘制的系谱图，该耳聋家系遗传方式为常染色体显性遗传。该家系耳聋特征为双侧对称性的全频感音神经性耳聋，发病特点为语后发病、进展性听力损失。耳聋基因目标区域捕获测序技术分析结果提示，耳聋基因 POU4F3 存在 2 个新突变 c.704_705del (p.T235fs) 和 c.593G>A(p.R198H)，分别为这两个耳聋家系的致病病因。这 2 个位点在多物种之间保守，Sanger 测序确认 2 个新突变与家系耳聋表型共分离，在 200 个正常人群中未发现。

结论 耳聋基因 POU4F3 存在 2 个新突变 c.704_705del (p.T235fs) 和 c.593G>A(p.R198H)，分别是两个耳聋家系的致病病因，在诊断常染色体显性遗传性耳聋致病病因中具有重要意义和临床价值。

PU-4415

流式细胞术检测多发性骨髓瘤患者 NK 细胞及其表面 PD-1 表达的初步研究

王亚奇[1]、张琳[1]、岳保红[2]
1. 郑州大学第五附属医院
2. 郑州大学第一附属医院

目的 本研究旨在探讨多参数流式细胞术（multiparameter flow cytometry，MFCM）检测多发性骨髓瘤患者 NK（CD3-CD56+）细胞及其细胞表面 PD-1 表达，从而为病人的诊断、治疗和预后提供依据。
方法 回顾性分析 2018 年 07 月至 2020 年 11 月收治的多发性骨髓瘤患者的临床资料，随访至少半年时间，并将研究对象分为对照组、初诊组、复发难治组。
结果 97 例患者均经组织病理活检及免疫组化确诊为多发性骨髓瘤，其中男性 55 例，女性 42 例，发病年龄为 60 岁（40~84 岁）。流式细胞术检测显示，相比于对照组，初诊组、复发难治组 NK 细胞的比例增高，但是初诊组 NK 细胞增高没有统计学意义（$P > 0.05$），复发难治组 NK 细胞比例显著增高，差异具有统计学意义（$P < 0.05$）。复发难治组患者骨髓中 NK 细胞与初诊组相比比例增高，差异具有统计学意义（$P < 0.05$）。进一步对 PD-1 在 NK 细胞表面的表达情况进行分析，流式细胞术检测结果显示相比于对照组，在复发难治组多发性骨髓瘤患者骨髓中 NK 细胞上的 PD-1 表达增高，差异有统计学意义（$P < 0.05$）。并且复发难治组多发性骨髓瘤患者骨髓中 NK 细胞上 PD-1 的表达比初诊组增高，差异有统计学意义（$P < 0.05$）。
结论 流式细胞术检测到 PD-1 在多发性骨髓瘤患者的 NK 细胞上表达，并且 PD-1 在多发性骨髓瘤患者骨髓中的表达与疾病的进展相关，PD-1/PD-L1 通路可能与多发性骨髓瘤的预后有关。

PU-4416

伴有-5/del(5q)和/或-7/del(7q)的骨髓增生异常综合征的（相关）基因表观遗传学研究

虞亚菲
中国人民解放军总医院第一医学中心

目的 骨髓增生异常综合征(MDS)是一种克隆性血液学疾病，以造血细胞发育不良、外周血细胞减少和易发生急性髓系白血病(AML)为特征。5 和 7 号染色体的全部或部分缺失[-5/del(5q)和-7/del(7q)]被认为是最常复发的遗传异常，包括骨髓增生异常综合征(MDS)和急性髓系白血病(AML)在内的 10-20%的髓系恶性肿瘤。有研究认为，5、7 号染色体常见缺失区域(common deleted regions, CDRs)的肿瘤抑制基因的单倍性是 MDS 和 AML 的发病机制之一。而表观遗传变化，包括启动子区高甲基化和翻译后组蛋白修饰，可能使肿瘤抑制基因失活，从而导致肿瘤的发生。本研究拟应用高通量测序（NGS）技术，对[-5/del(5q)和-7/del(7q)]阳性患者的常见缺失区域（CDRs）相关基因启动子区的甲基化水平检测，分析表观遗传变化，进一步评估其在携带 del(5q)和/或-7/del(7q)的 MDS/AML 患者中的临床意义。
方法 通过常规细胞遗传学、荧光原位杂交（FISH）筛选出-5/del(5q)和/或-7/del(7q)阳性骨髓标本，对 5、7 号染色体 CDRs（5q32-q33，7q31、7q34、7q35-q36）的候选基因启动子区进行生物信息学预测及验证，并应用二代测序（NGS）方法进行基因启动子区甲基化验证，并结合血液常规及

血细胞形态、骨髓细胞形态与骨髓活检病理、染色体核型分析等相关临床检查，进行单因素和多因素分析，Kaplan－Meier 法和 COX 回归模型分析其生存情况。

预期结果和结论 通过高通量测序技术提取靶向基因特异的甲基化状态，并结合相关临床检查，不同分组之间的预后进行单因素和多因素分析，分析其生存情况。建立和完善 MDS 发生和发展分子评估模型，为 MDS 患者的潜在遗传机制提供了新的见解。